

# Package ‘aroma.affymetrix’

April 16, 2018

**Version** 3.1.1

**Depends** R (>= 3.2.0), R.utils (>= 2.6.0), aroma.core (>= 3.1.1)

**Imports** methods, R.methodsS3 (>= 1.7.1), R.oo (>= 1.21.0), R.cache (>= 0.13.0), R.devices (>= 2.15.1), R.filesets (>= 2.11.0), aroma.apd (>= 0.6.0), MASS, splines, matrixStats (>= 0.52.2), listenv, future

**Suggests** DBI (>= 0.5-1), gsmoothr (>= 0.1.7), RColorBrewer (>= 1.1-2), Biobase (>= 2.28.0), BiocGenerics (>= 0.14.0), affxparser (>= 1.40.0), affy (>= 1.46.0), affyPLM (>= 1.44.0), aroma.light (>= 2.4.0), gcrma (>= 2.40.0), limma (>= 3.24.1), oligo (>= 1.32.0), oligoClasses (>= 1.30.0), pdInfoBuilder (>= 1.32.0), preprocessCore (>= 1.28.0), AffymetrixDataTestFiles, dChipIO (>= 0.1.1)

**SuggestsNote** BioC (>= 3.0), Recommended: preprocessCore, affyPLM, aroma.light, affxparser, DNACopy

**Date** 2018-04-05

**Title** Analysis of Large Affymetrix Microarray Data Sets

**Description** A cross-platform R framework that facilitates processing of any number of Affymetrix microarray samples regardless of computer system. The only parameter that limits the number of chips that can be processed is the amount of available disk space. The Aroma Framework has successfully been used in studies to process tens of thousands of arrays. This package has actively been used since 2006.

**License** LGPL (>= 2.1)

**URL** <http://www.aroma-project.org/>,  
<https://github.com/HenrikBengtsson/aroma.affymetrix>

**BugReports** <https://github.com/HenrikBengtsson/aroma.affymetrix/issues>

**LazyLoad** TRUE

**biocViews** Infrastructure, ProprietaryPlatforms, ExonArray, Microarray, OneChannel, GUI, DataImport, DataRepresentation, Preprocessing, QualityControl, Visualization, ReportWriting, aCGH, CopyNumberVariants, DifferentialExpression, GeneExpression, SNP, Transcription

**RoxygenNote** 6.0.1

**NeedsCompilation** no

**Author** Henrik Bengtsson [aut, cre, cph],  
 James Bullard [ctb],  
 Kasper Hansen [ctb],  
 Pierre Neuvial [ctb],  
 Elizabeth Purdom [ctb],  
 Mark Robinson [ctb],  
 Ken Simpson [ctb]

**Maintainer** Henrik Bengtsson <henrikb@braju.com>

**Repository** CRAN

**Date/Publication** 2018-04-16 18:53:05 UTC

## R topics documented:

aroma.affymetrix-package . . . . .	4
AbstractProbeSequenceNormalization . . . . .	6
AdditiveCovariatesNormalization . . . . .	7
AffineCnPlm . . . . .	10
AffinePlm . . . . .	12
AffineSnpPlm . . . . .	14
AffymetrixCdfFile . . . . .	15
AffymetrixCelFile . . . . .	18
AffymetrixCelSet . . . . .	21
AffymetrixCelSetReporter . . . . .	24
AffymetrixCelSetTuple . . . . .	25
AffymetrixCnChpSet . . . . .	26
AffymetrixFile . . . . .	28
AffymetrixFileSet . . . . .	30
AffymetrixFileSetReporter . . . . .	32
AffymetrixPgfFile . . . . .	33
AlleleSummation . . . . .	36
AllelicCrosstalkCalibration . . . . .	37
AromaChipTypeAnnotationFile . . . . .	39
ArrayExplorer . . . . .	41
AvgCnPlm . . . . .	43
AvgPlm . . . . .	45
AvgSnpPlm . . . . .	47
BackgroundCorrection . . . . .	48
BaseCountNormalization . . . . .	50
BasePositionNormalization . . . . .	52
ChipEffectFile . . . . .	53
ChipEffectSet . . . . .	56
ChipEffectTransform . . . . .	58
CnagCfhFile . . . . .	60
CnagCfhSet . . . . .	63

CnChipEffectFile	64
CnChipEffectSet	67
CnPlm	70
CnProbeAffinityFile	72
CrImmParametersFile	74
CrImmParametersSet	76
DChipCdfBinFile	78
DChipDcpFile	80
DChipDcpSet	83
DChipGenomeInformation	85
DChipQuantileNormalization	87
DChipSnpInformation	88
doCRMAv1	90
doCRMAv2	92
doFIRMA	93
doGCRMA	94
doRMA	95
ExonChipEffectFile	96
ExonChipEffectSet	99
ExonProbeAffinityFile	101
ExonRmaPlm	104
FirmaFile	106
FirmaModel	108
FirmaSet	109
FragmentEquivalentClassNormalization	112
FragmentLengthNormalization	113
GcContentNormalization	115
GcContentNormalization2	117
GcRmaBackgroundCorrection	119
GenericReporter	121
GenomeInformation	122
HetLogAddCnPlm	123
HetLogAddPlm	125
HetLogAddSnpPlm	127
justRMA	129
LimmaBackgroundCorrection	130
LinearModelProbeSequenceNormalization	132
MatNormalization	134
MatSmoothing	136
MbeiCnPlm	137
MbeiPlm	139
MbeiSnpPlm	141
Model	142
MultiArrayUnitModel	144
NormExpBackgroundCorrection	146
OpticalBackgroundCorrection	148
ParameterCelFile	150
ParameterCelSet	153

ProbeAffinityFile . . . . .	155
ProbeLevelModel . . . . .	157
ProbeLevelTransform . . . . .	159
ProbeLevelTransform3 . . . . .	160
QualityAssessmentFile . . . . .	162
QualityAssessmentModel . . . . .	164
QualityAssessmentSet . . . . .	165
QuantileNormalization . . . . .	167
ReseqCrosstalkCalibration . . . . .	169
ResidualFile . . . . .	171
ResidualSet . . . . .	173
RmaBackgroundCorrection . . . . .	176
RmaCnPlm . . . . .	178
RmaPlm . . . . .	180
RmaSnplm . . . . .	182
ScaleNormalization . . . . .	183
ScaleNormalization3 . . . . .	185
SingleArrayUnitModel . . . . .	186
SmoothMultiarrayModel . . . . .	188
SmoothRmaModel . . . . .	189
SnpcpeEffectFile . . . . .	190
SnpcpeEffectSet . . . . .	193
SnpcpeInformation . . . . .	195
SnpcpePlm . . . . .	197
SnpcpeProbeAffinityFile . . . . .	201
SpatialReporter . . . . .	203
TransformReport . . . . .	204
UgpGenomeInformation . . . . .	206
UnitModel . . . . .	208
UnitTypeScaleNormalization . . . . .	209
WeightsFile . . . . .	211
WeightsSet . . . . .	213

<b>Index</b>	<b>216</b>
--------------	------------

---

aroma.affymetrix-package

*Package aroma.affymetrix*

---

## Description

A cross-platform R framework that facilitates processing of any number of Affymetrix microarray samples regardless of computer system. The only parameter that limits the number of chips that can be processed is the amount of available disk space. The Aroma Framework has successfully been used in studies to process tens of thousands of arrays. This package has actively been used since 2006.

## Installation and updates

The preferred way to install this package is:

```
source("http://callr.org/install#aroma.affymetrix")
```

## To get started

To get started, see the online user guides and the vignettes <http://www.aroma-project.org/>.

## How to cite this package

In order to keep improving and providing support for this project, please cite references [1], [2], or any applicable publication listed on <http://aroma-project.org/publications/>, whenever you publish work that have been used any of the Aroma Framework.

## License

The releases of this package is licensed under LGPL version 2.1 or newer.

The development code of the packages is under a private licence (where applicable) and patches sent to the author fall under the latter license, but will be, if incorporated, released under the "release" license above.

## Author(s)

Henrik Bengtsson, James Bullard, Kasper Hansen, Pierre Neuvial, Elizabeth Purdom, Mark Robinson, Ken Simpson

## References

- [1] H. Bengtsson, K. Simpson, J. Bullard, and K. Hansen, *aroma.affymetrix: A generic framework in R for analyzing small to very large Affymetrix data sets in bounded memory*, Tech Report \#745, Department of Statistics, University of California, Berkeley, February 2008.
- [2] H. Bengtsson, R. Irizarry, B. Carvalho, and T. Speed, *Estimation and assessment of raw copy numbers at the single locus level*, Bioinformatics, 2008.
- [3] H. Bengtsson, *The R.oo package - Object-Oriented Programming with References Using Standard R Code*, In Kurt Hornik, Friedrich Leisch and Achim Zeileis, editors, Proceedings of the 3rd International Workshop on Distributed Statistical Computing (DSC 2003), March 20-22, Vienna, Austria. <http://www.ci.tuwien.ac.at/Conferences/DSC-2003/Proceedings/>

For a complete list, see <http://aroma-project.org/publications/>.

---

 AbstractProbeSequenceNormalization

*The AbstractProbeSequenceNormalization class*


---

## Description

Package: aroma.affymetrix

### Class AbstractProbeSequenceNormalization

#### Object

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--ProbeLevelTransform3
~~~~~|
~~~~~+--AbstractProbeSequenceNormalization
  
```

#### Directly known subclasses:

[BaseCountNormalization](#), [BasePositionNormalization](#), [LinearModelProbeSequenceNormalization](#), [MatNormalization](#)

```

public abstract static class AbstractProbeSequenceNormalization
  extends ProbeLevelTransform3
  
```

This abstract class represents a normalization method that corrects for systematic effects in the probe intensities due to differences in probe sequences.

## Usage

```

AbstractProbeSequenceNormalization(..., target=NULL)
  
```

## Arguments

...	Arguments passed to the constructor of <a href="#">ProbeLevelTransform3</a> .
target	A <a href="#">character</a> string specifying type of "target" used. If "zero", all arrays are normalized to have no effects. If <code>NULL</code> , all arrays a normalized to have the same effect as the average array has.

**Fields and Methods****Methods:**

```

getTargetFile -
process -

```

**Methods inherited from ProbeLevelTransform3:**

getAsteriskTags, getCellsTo, getCellsToFit, getCellsToUpdate, getParameters, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Requirements**

This class requires that an [AromaCellSequenceFile](#) is available for the chip type.

**Author(s)**

Henrik Bengtsson

---

AdditiveCovariatesNormalization

*The AdditiveCovariatesNormalization class*

---

**Description**

Package: aroma.affymetrix

**Class AdditiveCovariatesNormalization**

[Object](#)

~~|

```

~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ChipEffectTransform
~~~~~|
~~~~~+--AdditiveCovariatesNormalization

```

#### Directly known subclasses:

[GcContentNormalization2](#)

public abstract static class **AdditiveCovariatesNormalization**  
 extends *ChipEffectTransform*

This class represents a normalization method that corrects for GC-content effects on copy-number chip-effect estimates.

#### Usage

```
AdditiveCovariatesNormalization(dataSet=NULL, ..., target=NULL, subsetToFit="-XY",
  shift=0, onMissing=c("median", "ignore"))
```

#### Arguments

dataSet	A <a href="#">SnpChipEffectSet</a> .
...	Additional arguments passed to the constructor of <a href="#">ChipEffectTransform</a> .
target	(Optional) A <a href="#">character</a> string or a <a href="#">function</a> specifying what to normalize toward.
subsetToFit	The units from which the normalization curve should be estimated. If <code>NULL</code> , all are considered.
onMissing	Specifies how to normalize units for which the GC contents are unknown.
shift	An optional amount the data points should be shifted (translated).

#### Details

For SNPs, the normalization function is estimated based on the total chip effects, i.e. the sum of the allele signals. The normalizing is done by rescale the chip effects on the intensity scale such that the mean of the total chip effects are the same across samples for any given GC content. For allele-specific estimates, both alleles are always rescaled by the same amount. Thus, when normalizing allele-specific chip effects, the total chip effects is change, but not the relative allele signal, e.g. the allele B frequency.



**Fields and Methods**

**Methods:**

```

getCdf -
process -

```

**Methods inherited from ChipEffectTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$. \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

AffineCnPlm

*The AffineCnPlm class*

---

**Description**

Package: aroma.affymetrix

**Class AffineCnPlm**

Object

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--AffinePlm
~~~~~|

```



### Directly known subclasses:

```
public abstract static class AffineCnPlm
extends CnPlm
```

### Usage

```
AffineCnPlm(..., combineAlleles=FALSE)
```

### Arguments

```
...           Arguments passed to AffineSnpPlm.
combineAlleles If FALSE, allele A and allele B are treated seperately, otherwise together.
```

### Fields and Methods

#### Methods:

*No methods defined.*

#### Methods inherited from [CnPlm](#):

[getCellIndices](#), [getChipEffectSet](#), [getCombineAlleles](#), [getParameters](#), [getProbeAffinityFile](#), [setCombineAlleles](#)

#### Methods inherited from [SnpPlm](#):

[getCellIndices](#), [getChipEffectSet](#), [getMergeStrands](#), [getParameters](#), [getProbeAffinityFile](#), [setMergeStrands](#)

#### Methods inherited from [AffineSnpPlm](#):

[getAsteriskTags](#)

#### Methods inherited from [AffinePlm](#):

[getAsteriskTags](#), [getFitUnitGroupFunction](#), [getProbeAffinityFile](#)

#### Methods inherited from [ProbeLevelModel](#):

[calculateResidualSet](#), [calculateWeights](#), [fit](#), [getAsteriskTags](#), [getCalculateResidualsFunction](#), [getChipEffectSet](#), [getProbeAffinityFile](#), [getResidualSet](#), [getRootPath](#), [getWeightsSet](#)

#### Methods inherited from [MultiArrayUnitModel](#):

[getListOfPriors](#), [setListOfPriors](#), [validate](#)

#### Methods inherited from [UnitModel](#):

[findUnitsTodo](#), [getAsteriskTags](#), [getFitSingleCellUnitFunction](#), [getParameters](#)

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

AffinePlm

*The AffinePlm class*

---

**Description**

Package: aroma.affymetrix

**Class AffinePlm**

Object

```

~|
~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--AffinePlm

```

**Directly known subclasses:**

*AffineCnPlm, AffineSnpPlm*

```

public abstract static class AffinePlm
extends ProbeLevelModel

```

This class represents affine model in Bengtsson & Hossjer (2006).

**Usage**

```
AffinePlm(..., background=TRUE)
```

**Arguments**

... Arguments passed to [ProbeLevelModel](#).

background If `TRUE`, background is estimate for each unit group, otherwise not. That is, if `FALSE`, a *linear* (proportional) model without offset is fitted, resulting in very similar results as obtained by the [MbeiPlm](#).

**Fields and Methods****Methods:**

```
getProbeAffinityFile -
```

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Model**

For a single unit group, the affine model is:

$$y_{ik} = a + \theta_i \phi_k + \varepsilon_{ik}$$

where  $a$  is an offset common to all probe signals,  $\theta_i$  are the chip effects for arrays  $i = 1, \dots, I$ , and  $\phi_k$  are the probe affinities for probes  $k = 1, \dots, K$ . The  $\varepsilon_{ik}$  are zero-mean noise with equal variance. The model is constrained such that  $\prod_k \phi_k = 1$ .

Note that with the additional constraint  $a = 0$  (see arguments above), the above model is very similar to [MbeiPlm](#). The differences in parameter estimates is due to difference in assumptions about the error structure, which in turn affects how the model is estimated.

**Author(s)**

Henrik Bengtsson

**References**

Bengtsson \&amp; Hossjer (2006).

AffineSnpPlm

*The AffineSnpPlm class***Description**

Package: aroma.affymetrix

**Class AffineSnpPlm****Object**

```

~|
~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--AffinePlm
~~~~~|
~~~~~+--SnpPlm
~~~~~|
~~~~~+--AffineSnpPlm

```

**Directly known subclasses:**[AffineCnPlm](#)public abstract static class **AffineSnpPlm**extends [SnpPlm](#)**Usage**

AffineSnpPlm(..., mergeStrands=FALSE)

**Arguments**

...	Arguments passed to <a href="#">AffinePlm</a> .
mergeStrands	If <code>TRUE</code> , the sense and the anti-sense strands are fitted together, otherwise separately.

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from SnpPlm:**

getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

**Methods inherited from AffinePlm:**

getAsteriskTags, getFitUnitGroupFunction, getProbeAffinityFile

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**Description**

Package: aroma.affymetrix

**Class AffymetrixCdfFile****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AromaChipTypeAnnotationFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--UnitAnnotationDataFile
~~~~~|
~~~~~+--UnitTypesFile
~~~~~|
~~~~~+--UnitNamesFile
~~~~~|
~~~~~+--AffymetrixCdfFile

```

**Directly known subclasses:**

```

public abstract static class AffymetrixCdfFile
extends UnitNamesFile

```

An AffymetrixCdfFile object represents a generic Affymetrix CDF file.

**Usage**

```
AffymetrixCdfFile(...)
```

**Arguments**

... Arguments passed to [AromaChipTypeAnnotationFile](#).



**Fields and Methods****Methods:**

convert	-
createExonByTranscriptCdf	-
getACSFile	-
getAromaCellSequenceFile	-
getCellIndices	-
getChipType	-
getDimension	-
getFileFormat	-
getGenomeInformation	-
getImage	-
getPlatform	-
getUnitNames	-
getUnitTypes	-
hasUnitTypes	-
isMonocellCdf	-
isPm	-
isUniqueCdf	-
nbrOfCells	-
nbrOfColumns	-
nbrOfQcUnits	-
nbrOfRows	-
nbrOfUnits	-
readDataFrame	-
readUnits	-

**Methods inherited from UnitNamesFile:**

getUnitNames, indexOf, nbrOfUnits

**Methods inherited from UnitTypesFile:**

getUnitTypes, nbrOfUnits

**Methods inherited from UnitAnnotationDataFile:**

byChipType, getAromaUflFile, getAromaUgpFile, getChipType, getDefaultExtension, getPlatform, nbrOfUnits

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaChipTypeAnnotationFile:**

as.character, byChipType, byName, findByChipType, fromFile, getChipType, getDefaultExtension, getHeader, getPlatform

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$. \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson, Ken Simpson

---

AffymetrixCelFile      *The AffymetrixCelFile class*

---

**Description**

Package: aroma.affymetrix

**Class AffymetrixCelFile****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|

```

```

~~~~~+---FileCacheKeyInterface
~~~~~|
~~~~~+---AromaMicroarrayDataFile
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFile
~~~~~|
~~~~~+---AffymetrixCelFile

```

**Directly known subclasses:**

*ChipEffectFile, CnChipEffectFile, CnProbeAffinityFile, ExonChipEffectFile, ExonProbeAffinityFile, FirmaFile, ParameterCelFile, ProbeAffinityFile, QualityAssessmentFile, ResidualFile, SnpChipEffectFile, SnpProbeAffinityFile, WeightsFile*

```

public abstract static class AffymetrixCelFile
extends AffymetrixFile

```

An AffymetrixCelFile object represents a single Affymetrix CEL file.

**Usage**

```
AffymetrixCelFile(..., cdf=NULL)
```

**Arguments**

...	Arguments passed to <a href="#">AromaMicroarrayDataFile</a> .
cdf	An optional <a href="#">AffymetrixCdfFile</a> making it possible to override the default CDF file as specified by the CEL file header. The requirement is that its number of cells must match that of the CEL file. If <code>NULL</code> , the CDF structure is inferred from the the chip type as specified in the CEL file header.

**Fields and Methods****Methods:**

extractMatrix	-
getAm	-
getCdf	-
getFileFormat	-
getImage	-
getUnitNamesFile	-
getUnitTypesFile	-
image270	-
nbrOfCells	-
plotDensity	-
plotImage	-

```

plotMvsA      -
plotMvsX      -
setCdf        -
smoothScatterMvsA -
writeImage    -

```

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUffFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**For developers**

If you subclass this class, please make sure to query the [AffymetrixCdfFile](#) object (see `*getCdf()`) whenever querying CDF information. Do not use the CDF file inferred from the chip type in CEL header, unless you really want it to be hardwired that way, otherwise you will break to possibility to override the CDF structure.

**Author(s)**

Henrik Bengtsson

**See Also**An object of this class is typically part of an [AffymetrixCelSet](#).

---

AffymetrixCelSet      *The AffymetrixCelSet class*


---

**Description**

Package: aroma.affymetrix

**Class AffymetrixCelSet****Object**

```

~~|
~~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFileSet
~~~~~|
~~~~~+---AromaMicroarrayDataSet
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFileSet
~~~~~|
~~~~~+---AffymetrixCelSet

```

**Directly known subclasses:**

[ChipEffectSet](#), [CnChipEffectSet](#), [ExonChipEffectSet](#), [FirmaSet](#), [ParameterCelSet](#), [QualityAssessmentSet](#), [ResidualSet](#), [SnpChipEffectSet](#), [WeightsSet](#)

public static class **AffymetrixCelSet**extends [AffymetrixFileSet](#)An AffymetrixCelSet object represents a set of Affymetrix CEL files with *identical* chip types.**Usage**

AffymetrixCelSet(files=NULL, ...)

**Arguments**

files	A <a href="#">list</a> of <a href="#">AffymetrixCelFile</a> s.
...	Not used.

**Fields and Methods****Methods:**

```

as -
as.AffymetrixCelSet -
byName -
doCRMAv1 -
doCRMAv2 -
doFIRMA -
doGCRMA -
doRMA -
extractAffyBatch -
extractFeatureSet -
extractMatrix -
getAverage -
getAverageAsinh -
getAverageFile -
getAverageLog -
getCdf -
getChipType -
getData -
getIntensities -
getPlatform -
getTimestamps -
getUnitGroupCellMap -
getUnitIntensities -
getUnitNamesFile -
getUnitTypesFile -
justSNPRMA -
plotDensity -
readUnits -
setCdf -
writeSgr -

```

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNames-

TranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApply, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

#### Methods inherited from FullNameInterface:

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

#### Methods inherited from Object:

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

#### Author(s)

Henrik Bengtsson

#### See Also

[AffymetrixCelFile](#).

#### Examples

```
## Not run:
  for (zzz in 0) {

# Find any dataset
path <- NULL
if (is.null(path))
  break

# -----
# Define a dataset object based on all CEL files in a directory
# -----
ds <- AffymetrixCelSet$fromFiles(path)
print(ds)

# Keep at most three arrays for this example
ds <- ds[1:min(3,nbrOfArrays(ds))]
print(ds)
```

```
} # for (zzz in 0)
rm(zzz)
```

```
## End(Not run)
```

---

AffymetrixCelSetReporter

*The AffymetrixCelSetReporter class*

---

## Description

Package: aroma.affymetrix

**Class AffymetrixCelSetReporter**

Object

```
~~|
~~+---GenericReporter
~~~~~|
~~~~~+---AffymetrixFileSetReporter
~~~~~|
~~~~~+---AffymetrixCelSetReporter
```

**Directly known subclasses:**

*SpatialReporter*

public abstract static class **AffymetrixCelSetReporter**

extends *AffymetrixFileSetReporter*

## Usage

```
AffymetrixCelSetReporter(..., .setClass="AffymetrixCelSet")
```

## Arguments

```
...           Arguments passed to AffymetrixFileSetReporter.
.setClass     The name of the class of the input set.
```

## Fields and Methods

**Methods:**

getDataSet -



**Methods inherited from AffymetrixFileSetReporter:**

getFileSet, getInputName, getInputTags

**Methods inherited from GenericReporter:**

as.character, getAlias, getAsteriskTags, getFullName, getInputName, getInputTags, getMainPath, getName, getPath, getReportSet, getRootPath, getTags, process, setAlias, setup

**Methods inherited from Object:**

\$, \$&lt;-, [], [[&lt;-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

 AffymetrixCelSetTuple *The AffymetrixCelSetTuple class*


---

**Description**

Package: aroma.affymetrix

**Class AffymetrixCelSetTuple****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSetList
~~~~~|
~~~~~+--AromaMicroarrayDataSetTuple
~~~~~|
~~~~~+--AffymetrixCelSetTuple

```

**Directly known subclasses:**

ChipEffectSetTuple, CnChipEffectSetTuple

public static class **AffymetrixCelSetTuple**extends *AromaMicroarrayDataSetTuple***Usage**

AffymetrixCelSetTuple(..., .setClass="AffymetrixCelSet")

**Arguments**

... Arguments passed to the constructor of *AromaMicroarrayDataSetTuple*.

.setClass The name of the class of the input set.

**Fields and Methods****Methods:**

byPath -

**Methods inherited from AromaMicroarrayDataSetTuple:**

as, as.AromaMicroarrayDataSetTuple, byPath, getAsteriskTags, getChipTypes, getFullNames, getSets, getTags, indexOf, nbrOfChipTypes

**Methods inherited from GenericDataFileSetList:**

as, as.GenericDataFileSetList, as.character, as.data.frame, as.list, assertDuplicates, clone, extract, getAsteriskTags, getDefaultFullName, getFileList, getFileListClass, getFullNames, getNames, getSet, getSets, getTags, indexOf, length, nbrOfFiles, nbrOfSets, setTags

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$&lt;-, [[, [[&lt;-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

 AffymetrixCnChpSet      *The AffymetrixCnChpSet class*


---

**Description**

Package: aroma.affymetrix

**Class AffymetrixCnChpSet**

Object

~~|

~~+--FullNameInterface

~~~~~|

~~~~~+--GenericDataFileSet

~~~~~|

```

~~~~~+---AromaMicroarrayDataSet
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFileSet
~~~~~|
~~~~~+---AffymetrixCnChpSet

```

### Directly known subclasses:

public abstract static class **AffymetrixCnChpSet**  
 extends *AffymetrixFileSet*

A *AffymetrixCnChpSet* object represents a set of *AffymetrixCnChpFile*:s with *identical* chip types.

### Usage

```
AffymetrixCnChpSet(files=NULL, ...)
```

### Arguments

|       |                                                 |
|-------|-------------------------------------------------|
| files | A <i>list</i> of <i>AffymetrixCnChpFile</i> :s. |
| ...   | Not used.                                       |

### Fields and Methods

#### Methods:

|                       |   |
|-----------------------|---|
| as                    | - |
| as.AffymetrixCnChpSet | - |
| exportTotalCnRatioSet | - |
| extractLogRatios      | - |
| findByName            | - |
| getCdf                | - |
| setCdf                | - |

#### Methods inherited from *AffymetrixFileSet*:

as, as.AffymetrixFileSet, byPath, getDefaultFullName

#### Methods inherited from *AromaPlatformInterface*:

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

#### Methods inherited from *AromaMicroarrayDataSet*:

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAt-

tributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApply, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**See Also**

[AffymetrixCnChpFile](#).

---

AffymetrixFile

*The abstract AffymetrixFile class*

---

**Description**

Package: aroma.affymetrix

**Class AffymetrixFile**

Object

~~|

~~+--FullNameInterface

~~~~~|

~~~~~+--GenericDataFile

```

~~~~~|
~~~~~+---CacheKeyInterface
~~~~~|
~~~~~+---FileCacheKeyInterface
~~~~~|
~~~~~+---AromaMicroarrayDataFile
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFile

```

**Directly known subclasses:**

*AffymetrixCdfFile, AffymetrixCelFile, AffymetrixCnChpFile, AffymetrixPgfFile, AffymetrixTsvFile, AromaChipTypeAnnotationFile, ChipEffectFile, CnChipEffectFile, CnProbeAffinityFile, CnagCfhFile, DChipCdfBinFile, DChipDcpFile, ExonChipEffectFile, ExonProbeAffinityFile, FirmaFile, ParameterCelFile, ProbeAffinityFile, QualityAssessmentFile, ResidualFile, SnpChipEffectFile, SnpProbeAffinityFile, WeightsFile*

```
public abstract static class AffymetrixFile
extends AromaPlatformInterface
```

An AffymetrixFile object represents a single Affymetrix file, e.g. an Affymetrix CEL file or an Affymetrix CDF file. Note that this class is abstract and can not be instantiated, but instead you have to use one of the subclasses or the generic fromFile() method.

**Usage**

```
AffymetrixFile(...)
```

**Arguments**

... Arguments passed to [GenericDataFile](#).

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$. \$<-, [, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**See Also**

An object of this class is typically part of an [AffymetrixFileSet](#).

---

AffymetrixFileSet      *The AffymetrixFileSet class*

---

**Description**

Package: aroma.affymetrix

**Class AffymetrixFileSet****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface

```

```

~~~~~|
~~~~~+--AffymetrixFileSet

```

**Directly known subclasses:**

[AffymetrixCelSet](#), [AffymetrixCnChpSet](#), [ChipEffectSet](#), [CnChipEffectSet](#), [DChipDcpSet](#), [ExonChipEffectSet](#), [FirmaSet](#), [ParameterCelSet](#), [QualityAssessmentSet](#), [ResidualSet](#), [SnpChipEffectSet](#), [WeightsSet](#)

```

public abstract static class AffymetrixFileSet
extends AromaPlatformInterface

```

An [AffymetrixFileSet](#) object represents a set of [AffymetrixFiles](#) with *identical* chip types.

**Usage**

```
AffymetrixFileSet(files=NULL, ...)
```

**Arguments**

|       |                                                              |
|-------|--------------------------------------------------------------|
| files | A <a href="#">list</a> of <a href="#">AffymetrixFile</a> :s. |
| ...   | Arguments passed to <a href="#">GenericDataFileSet</a> .     |

**Fields and Methods****Methods:**

|                      |   |
|----------------------|---|
| as                   | - |
| as.AffymetrixFileSet | - |
| byPath               | - |

**Methods inherited from [AromaPlatformInterface](#):**

[getAromaPlatform](#), [getAromaUflFile](#), [getAromaUgpFile](#), [getChipType](#), [getPlatform](#), [getUnitAnnotationDataFile](#), [getUnitNamesFile](#), [getUnitTypesFile](#), [isCompatibleWith](#)

**Methods inherited from [AromaMicroarrayDataSet](#):**

[as.AromaMicroarrayDataSetList](#), [as.AromaMicroarrayDataSetTuple](#), [getAromaFullNameTranslatorSet](#), [getAverageFile](#), [getChipType](#), [getDefaultFullName](#), [getPlatform](#), [setAttributesBy](#), [setAttributesBySampleAnnotationFile](#), [setAttributesBySampleAnnotationSet](#), [validate](#)

**Methods inherited from [GenericDataFileSet](#):**

[\[](#), [\[\[](#), [anyDuplicated](#), [anyNA](#), [append](#), [appendFiles](#), [appendFullNamesTranslator](#), [appendFullNamesTranslatorByNULL](#), [appendFullNamesTranslatorByTabularTextFile](#), [appendFullNamesTranslatorByTabularTextFileSet](#), [appendFullNamesTranslatorBydata.frame](#), [appendFullNamesTranslatorByfunction](#), [appendFullNamesTranslatorBylist](#), [as.character](#), [as.list](#), [byName](#), [byPath](#), [c](#), [clearCache](#), [clearFullNamesTranslator](#), [clone](#), [copyTo](#), [dsApply](#), [dsApplyInPairs](#), [duplicated](#), [equals](#), [extract](#), [findByName](#), [findDuplicated](#), [getChecksum](#), [getChecksumFileSet](#), [getChecksumObjects](#), [getDefaultFullName](#), [getFile](#), [getFileClass](#), [getFileSize](#), [getFiles](#), [getFullNames](#), [getNames](#), [getOneFile](#),

getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

AffymetrixFileSetReporter

*The AffymetrixFileSetReporter class*

---

**Description**

Package: aroma.affymetrix

**Class AffymetrixFileSetReporter**

**Object**

```

~~|
~~+---GenericReporter
~~~~~|
~~~~~+---AffymetrixFileSetReporter

```

**Directly known subclasses:**

*AffymetrixCelSetReporter, SpatialReporter*

```

public abstract static class AffymetrixFileSetReporter
extends GenericReporter

```

**Usage**

```

AffymetrixFileSetReporter(set=NULL, ..., .setClass="AffymetrixFileSet")

```



**Arguments**

set            An *AffymetrixFileSet* object.  
 ...           Arguments passed to *GenericReporter*.  
 .setClass     The name of the class of the input set.

**Fields and Methods****Methods:**

                  getInputName    -  
                   getInputTags    -

**Methods inherited from *GenericReporter*:**

as.character, getAlias, getAsteriskTags, getFullName, getInputName, getInputTags, getMainPath, getName, getPath, getReportSet, getRootPath, getTags, process, setAlias, setup

**Methods inherited from *Object*:**

\$. \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

AffymetrixPgfFile        *The AffymetrixPgfFile class*

---

**Description**

Package: aroma.affymetrix

**Class *AffymetrixPgfFile*****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaMicroarrayDataFile

```

```

~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AromaChipTypeAnnotationFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--UnitAnnotationDataFile
~~~~~|
~~~~~+--UnitTypesFile
~~~~~|
~~~~~+--UnitNamesFile
~~~~~|
~~~~~+--AffymetrixPgfFile

```

### Directly known subclasses:

```

public abstract static class AffymetrixPgfFile
extends UnitNamesFile

```

An AffymetrixPgfFile object represents a generic Affymetrix Probe Group File (PGF). A PGF file "provides information about what probes are contained within a probeset and information about the nature of the probes necessary for analysis. The current PGF file format (version 1) is only specified for expression style probesets." [1]

### Usage

```
AffymetrixPgfFile(...)
```

### Arguments

... Arguments passed to [AromaChipTypeAnnotationFile](#).

### Fields and Methods

#### Methods:

```

getChipType -
getDimension -
getPlatform -
getUnitNames -
nbrOfCells -
nbrOfColumns -
nbrOfRows -
nbrOfUnits -

```

**Methods inherited from UnitNamesFile:**

getUnitNames, indexOf, nbrOfUnits

**Methods inherited from UnitTypesFile:**

getUnitTypes, nbrOfUnits

**Methods inherited from UnitAnnotationDataFile:**

byChipType, getAromaUflFile, getAromaUgpFile, getChipType, getDefaultExtension, getPlatform, nbrOfUnits

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaChipTypeAnnotationFile:**

as.character, byChipType, byName, findByChipType, fromFile, getChipType, getDefaultExtension, getHeader, getPlatform

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$. \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**References**

[1] ...

---

AlleleSummation      *The AlleleSummation class*


---

**Description**

Package: aroma.affymetrix

**Class AlleleSummation**

Object

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--AlleleSummation

```

**Directly known subclasses:**

```

public abstract static class AlleleSummation
extends UnitModel

```

This class takes allele-specific chip effect estimates of a SnpChipEffectSet and returns a CnChipEffectSet holding the summed allele estimates.

**Usage**

```
AlleleSummation(dataSet=NULL, ignoreNAs=TRUE, ...)
```

**Arguments**

```

dataSet      A SnpChipEffectSet.
ignoreNAs    If TRUE, missing values are excluded when summing the signals from the two
alleles.
...          Arguments passed to UnitModel.

```

**Fields and Methods****Methods:**

```

findUnitsTodo      -
getChipEffectSet   -
process            -

```

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

AllelicCrosstalkCalibration

*The AllelicCrosstalkCalibration class*

---

**Description**

Package: aroma.affymetrix

**Class AllelicCrosstalkCalibration****Object**

```
~~|
```

```
~~+--ParametersInterface
```

```
~~~~~|
```

```
~~~~~+--AromaTransform
```

```
~~~~~|
```

```
~~~~~+--Transform
```

```
~~~~~|
```

```
~~~~~+--ProbeLevelTransform
```

```
~~~~~|
```

```
~~~~~+--AllelicCrosstalkCalibration
```

**Directly known subclasses:**

```
public static class AllelicCrosstalkCalibration
extends ProbeLevelTransform
```

This class represents a calibration function that transforms the probe-level signals such that the signals from the two alleles are orthogonal. The method fits and calibrates PM signals only. MM signals will not affect the model fitting and are unaffected.

### Usage

```
AllelicCrosstalkCalibration(dataSet=NULL, ..., model=c("asis", "auto", "CRMA", "CRMAv2"),
  rescaleBy=c("auto", "groups", "all", "none"), targetAvg=c(2200, 2200),
  subsetToAvg="-XY", mergeShifts=TRUE, B=1, flavor=c("sfit", "expectile"),
  alpha=c(0.1, 0.075, 0.05, 0.03, 0.01), q=2, Q=98, lambda=2,
  pairBy=c("CDF", "sequence"))
```

### Arguments

|                     |                                                                                                                                                                                                      |
|---------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| dataSet             | An <a href="#">AffymetrixCelSet</a> .                                                                                                                                                                |
| ...                 | Arguments passed to the constructor of <a href="#">ProbeLevelTransform</a> .                                                                                                                         |
| model               | A <a href="#">character</a> string for quickly specifying default parameter settings.                                                                                                                |
| rescaleBy           | A <a href="#">character</a> string specifying what sets of cells should be rescaled towards a target average, if any. Default is to rescale all cells together. If "none", no rescaling is done.     |
| targetAvg           | The signal(s) that either the average of the sum (if one target value) or the average of each of the alleles (if two target values) should have after calibration. Only used if rescaleBy != "none". |
| subsetToAvg         | The indices of the cells (taken as the intersect of existing indices) used to calculate average in order to rescale to the target average. If <code>NULL</code> , all probes are considered.         |
| mergeShifts         | If <code>TRUE</code> , the shift of the probe sequence relative to the SNP position is ignored, otherwise not.                                                                                       |
| B                   | An <a href="#">integer</a> specifying by how many nucleotides the allelic groups should be stratified by. If zero, all SNPs are put in one group.                                                    |
| flavor              | A <a href="#">character</a> string specifying what algorithm is used to fit the crosstalk calibration.                                                                                               |
| alpha, q, Q, lambda | Model fitting parameters.                                                                                                                                                                            |
| pairBy              | A <a href="#">character</a> string specifying how allele probe pairs are identified.                                                                                                                 |

### What probe signals are updated?

Calibration for crosstalk between allele signals applies by definition only SNP units. Furthermore, it is only SNP units with two or four unit groups that are calibrated. For instance, in at least on custom SNP CDFs we know of, there is a small number of SNP units that have six groups. *Currently these units are not calibrated (at all)*. It is only PM probes that will be calibrated. Note that, non-calibrated signals will be saved in the output files.

**What probe signals are used to fit model?**

All PM probe pairs are used to fit the crosstalk model. In the second step where signals are rescaled to a target average, it is possible to specify the set of cells that should be included when estimating the target average.

**Important about rescaling towards target average**

Rescaling each allele-pair group (e.g. AC, AG, AT, CG, CT, GC) towards a target average (`rescaleBy="groups"`) *must not* be used for multi-enzyme chip types, e.g. GenomeWideSNP\_6. If still done, due to confounded effects of non-perfect enzyme mixtures etc, there will be a significant bias between raw CNs for SNPs and CN probes. Instead, for such chip types *all probe signals* should be rescaled together towards the target average (`rescaleBy="all"`).

**Fields and Methods****Methods:**

process -

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

AromaChipTypeAnnotationFile

*The AromaChipTypeAnnotationFile class*

---

**Description**

Package: aroma.affymetrix

**Class AromaChipTypeAnnotationFile****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AromaChipTypeAnnotationFile

```

**Directly known subclasses:**

[AffymetrixCdfFile](#), [AffymetrixPgfFile](#)

public abstract static class **AromaChipTypeAnnotationFile**  
 extends [AffymetrixFile](#)

An AromaChipTypeAnnotationFile object represents an annotation file for a specific chip type.

**Usage**

```
AromaChipTypeAnnotationFile(...)
```

**Arguments**

... Arguments passed to [AffymetrixFile](#).

**Fields and Methods****Methods:**

```

byChipType -
getChipType -
getHeader -
getPlatform -

```



**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$. \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

ArrayExplorer

*The ArrayExplorer class*

---

**Description**

Package: aroma.affymetrix

**Class ArrayExplorer**

[Object](#)

~~|

```

~+---Explorer
~~~~~|
~~~~~+---ArrayExplorer

```

### Directly known subclasses:

```

public abstract static class ArrayExplorer
extends Explorer

```

### Usage

```
ArrayExplorer(csTuple=NULL, ...)
```

### Arguments

|         |                                    |
|---------|------------------------------------|
| csTuple | An <i>AffymetrixCelSet</i> object. |
| ...     | Not used.                          |

### Fields and Methods

#### Methods:

|                |   |
|----------------|---|
| addColorMap    | - |
| getColorMaps   | - |
| getDataSet     | - |
| getSetTuple    | - |
| nbrOfChipTypes | - |
| process        | - |
| setArrays      | - |
| setColorMaps   | - |

#### Methods inherited from Explorer:

addIncludes, addIndexFile, as.character, display, getAlias, getArrayOfInput, getAsteriskTags, getFullName, getIncludePath, getMainPath, getName, getNameOfInput, getNames, getPath, getReportPathPattern, getRootPath, getSampleLayerPrefix, getSubname, getTags, getTagsOfInput, getTemplatePath, getVersion, nbrOfArrays, process, setAlias, setArrays, setReportPathPattern, setSubname, setup, splitByReportPathPattern, updateSetupExplorerFile

#### Methods inherited from Object:

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

AvgCnPlm

*The AvgCnPlm class***Description**

Package: aroma.affymetrix

**Class AvgCnPlm****Object**

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--AvgPlm
~~~~~|
~~~~~+--AvgSnpPlm
~~~~~|
~~~~~+--SnpPlm
~~~~~|
~~~~~+--CnPlm
~~~~~|
~~~~~+--AvgCnPlm

```

**Directly known subclasses:**

```

public abstract static class AvgCnPlm
extends CnPlm

```

**Usage**

```

AvgCnPlm(..., combineAlleles=FALSE)

```

**Arguments**

... Arguments passed to [AvgSnpPlm](#).  
 combineAlleles If [FALSE](#), allele A and allele B are treated separately, otherwise together.

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from CnPlm:**

getCellIndices, getChipEffectSet, getCombineAlleles, getParameters, getProbeAffinityFile, setCombineAlleles

**Methods inherited from SnpPlm:**

getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

**Methods inherited from AvgSnpPlm:**

getAsteriskTags

**Methods inherited from AvgPlm:**

getAsteriskTags, getCalculateResidualsFunction, getParameters, validate

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

AvgPlm

*The AvgPlm class***Description**

Package: aroma.affymetrix

**Class AvgPlm****Object**

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--AvgPlm

```

**Directly known subclasses:***AvgCnPlm, AvgSnpPlm*

```

public abstract static class AvgPlm
extends ProbeLevelModel

```

This class represents a PLM where the probe intensities are averaged assuming identical probe affinities. For instance, one may assume that replicated probes with identical sequences have the same probe affinities, cf. the GenomeWideSNP\_6 chip type.

**Usage**

```
AvgPlm(..., flavor=c("median", "mean"))
```

**Arguments**

|        |                                                                                                                                                             |
|--------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ...    | Arguments passed to <a href="#">ProbeLevelModel</a> .                                                                                                       |
| flavor | A <a href="#">character</a> string specifying what model fitting algorithm to be used. This makes it possible to get identical estimates as other packages. |

## Fields and Methods

### Methods:

*No methods defined.*

### Methods inherited from ProbeLevelModel:

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

### Methods inherited from MultiArrayUnitModel:

getListOfPriors, setListOfPriors, validate

### Methods inherited from UnitModel:

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

### Methods inherited from Model:

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

### Methods inherited from ParametersInterface:

getParameterSets, getParameters, getParametersAsString

### Methods inherited from Object:

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

## Model

For a single unit group, the averaging PLM of  $K$  probes is:

$$y_{ik} = \theta_i + \varepsilon_{ik}$$

where  $\theta_i$  are the chip effects for arrays  $i = 1, \dots, I$ . The  $\varepsilon_{ik}$  are zero-mean noise with equal variance.

## Different flavors of model fitting

The above model can be fitted in two ways, either robustly or non-robustly. Use argument `flavor="mean"` to fit the model non-robustly, i.e.

$$\hat{\theta}_i = 1/K \sum_k y_{ik}$$

.

Use argument `flavor="median"` to fit the model robustly, i.e.

$$\hat{\theta}_i = \text{median}_k y_{ik}$$

.

Missing values are always excluded.

## Author(s)

Henrik Bengtsson

AvgSnpPlm

*The AvgSnpPlm class***Description**

Package: aroma.affymetrix

**Class AvgSnpPlm****Object**

```

~|
~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--AvgPlm
~~~~~|
~~~~~+--SnpPlm
~~~~~|
~~~~~+--AvgSnpPlm

```

**Directly known subclasses:**[AvgCnPlm](#)public abstract static class **AvgSnpPlm**extends [SnpPlm](#)**Usage**

AvgSnpPlm(..., mergeStrands=FALSE)

**Arguments**

|              |                                                                                                  |
|--------------|--------------------------------------------------------------------------------------------------|
| ...          | Arguments passed to <a href="#">AvgPlm</a> .                                                     |
| mergeStrands | If <b>TRUE</b> , the sense and the anti-sense strands are fitted together, otherwise separately. |

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from SnpPIm:**

getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

**Methods inherited from AvgPIm:**

getAsteriskTags, getCalculateResidualsFunction, getParameters, validate

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$. \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

BackgroundCorrection *The BackgroundCorrection class*

---

**Description**

Package: aroma.affymetrix

**Class BackgroundCorrection**

Object

~~|

~~+--ParametersInterface

~~~~~|

~~~~~+--AromaTransform

~~~~~|



```

~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--BackgroundCorrection

```

**Directly known subclasses:**

[GcRmaBackgroundCorrection](#), [LimmaBackgroundCorrection](#), [NormExpBackgroundCorrection](#), [OpticalBackgroundCorrection](#), [RmaBackgroundCorrection](#)

```

public abstract static class BackgroundCorrection
  extends ProbeLevelTransform

```

This class represents a background adjustment function.

**Usage**

```

BackgroundCorrection(..., subsetToUpdate=NULL, typesToUpdate=NULL)

```

**Arguments**

... Arguments passed to the constructor of [ProbeLevelTransform](#).  
subsetToUpdate The probes to be updated. If `NULL`, all probes are updated.  
typesToUpdate Types of probes to be updated.

**Fields and Methods****Methods:**

process -

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach,

equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

### Author(s)

Ken Simpson, Henrik Bengtsson

---

BaseCountNormalization

*The BaseCountNormalization class*

---

### Description

Package: aroma.affymetrix

#### Class BaseCountNormalization

#### Object

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--ProbeLevelTransform3
~~~~~|
~~~~~+--AbstractProbeSequenceNormalization
~~~~~|
~~~~~+--BaseCountNormalization

```

#### Directly known subclasses:

```

public static class BaseCountNormalization
extends AbstractProbeSequenceNormalization

```

This class represents a normalization method that corrects for systematic effects in the probe intensities due to differences in the number of A, C, G, and T:s in the probe sequences.

### Usage

```
BaseCountNormalization(..., model=c("robustSmoothSpline", "lm"), bootstrap=FALSE)
```

**Arguments**

|           |                                                                                             |
|-----------|---------------------------------------------------------------------------------------------|
| ...       | Arguments passed to the constructor of <a href="#">AbstractProbeSequenceNormalization</a> . |
| model     | A <a href="#">character</a> string specifying the model used to fit the base-count effects. |
| bootstrap | If <a href="#">TRUE</a> , the model fitting is done by bootstrap in order to save memory.   |

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from AbstractProbeSequenceNormalization:**

fitOne, getAromaCellSequenceFile, getParameters, getTargetFile, indexOfMissingSequences, predictOne, process

**Methods inherited from ProbeLevelTransform3:**

getAsteriskTags, getCellsTo, getCellsToFit, getCellsToUpdate, getParameters, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Requirements**

This class requires that an aroma probe sequence file is available for the chip type.

**Author(s)**

Henrik Bengtsson

---

 BasePositionNormalization

*The BasePositionNormalization class*


---

## Description

Package: aroma.affymetrix

### Class BasePositionNormalization

#### Object

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--ProbeLevelTransform3
~~~~~|
~~~~~+--AbstractProbeSequenceNormalization
~~~~~|
~~~~~+--LinearModelProbeSequenceNormalization
~~~~~|
~~~~~+--BasePositionNormalization
  
```

#### Directly known subclasses:

```

public abstract static class BasePositionNormalization
  extends LinearModelProbeSequenceNormalization
  
```

This class represents a normalization method that corrects for systematic effects in the probe intensities due to differences in positioning of A, C, G, and T:s in the probe sequences.

## Usage

```
BasePositionNormalization(..., model=c("smooth.spline"), df=5)
```

## Arguments

|       |                                                                                                |
|-------|------------------------------------------------------------------------------------------------|
| ...   | Arguments passed to the constructor of <a href="#">LinearModelProbeSequenceNormalization</a> . |
| model | A <a href="#">character</a> string specifying the model used to fit the base-count effects.    |
| df    | The degrees of freedom of the model.                                                           |

**Fields and Methods****Methods:***No methods defined.***Methods inherited from LinearModelProbeSequenceNormalization:**

fitOne, getDesignMatrix, getNormalEquations, getSignalTransform, predictOne

**Methods inherited from AbstractProbeSequenceNormalization:**

fitOne, getAromaCellSequenceFile, getParameters, getTargetFile, indexOfMissingSequences, predictOne, process

**Methods inherited from ProbeLevelTransform3:**

getAsteriskTags, getCellsTo, getCellsToFit, getCellsToUpdate, getParameters, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$&lt;-, [], [[&lt;-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson, Mark Robinson

ChipEffectFile

*The ChipEffectFile class***Description**

Package: aroma.affymetrix

**Class ChipEffectFile**

Object

~~|

~~+--FullNameInterface

~~~~~|

~~~~~+--GenericDataFile

```

~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--ParameterCelFile
~~~~~|
~~~~~+--ChipEffectFile

```

**Directly known subclasses:**

*CnChipEffectFile*, *ExonChipEffectFile*, *SnpChipEffectFile*

```

public abstract static class ChipEffectFile
extends ParameterCelFile

```

This class represents estimates of chip effects in the probe-level models.

**Usage**

```
ChipEffectFile(..., probeModel=c("pm"))
```

**Arguments**

```

...           Arguments passed to ParameterCelFile.
probeModel   The specific type of model, e.g. "pm".

```

**Fields and Methods****Methods:**

```

extractMatrix -
extractTheta  -
findUnitsTodo -
getAM         -
readUnits     -

```

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, readUnits

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelFile:**

allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUfflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$&lt;-, [[, [[&lt;-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**See Also**

An object of this class is typically obtained through the `getChipEffectSet()` method for the [ProbeLevelModel](#) class. An object of this class is typically part of a [ChipEffectSet](#).

---

 ChipEffectSet

*The ChipEffectSet class*


---

**Description**

Package: aroma.affymetrix

**Class ChipEffectSet****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--ParameterCelSet
~~~~~|
~~~~~+--ChipEffectSet
  
```

**Directly known subclasses:**

[CnChipEffectSet](#), [ExonChipEffectSet](#), [SnpChipEffectSet](#)

```
public static class ChipEffectSet
```

```
extends ParameterCelSet
```

This class represents estimates of chip effects in the probe-level models.

**Usage**

```
ChipEffectSet(..., probeModel=c("pm"))
```



**Arguments**

... Arguments passed to [AffymetrixCelSet](#).  
 probeModel The specific type of model, e.g. "pm".

**Fields and Methods****Methods:**

```

boxplotStats -
extractExpressionSet -
extractMatrix -
extractTheta -
findUnitsTodo -
getAM -
getAverageFile -
getCellIndices -
plotBoxplot -
readUnits -

```

**Methods inherited from ParameterCelSet:**

extractDataFrame, extractMatrix

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelSet:**

append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

[, [], anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorBy-

function, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApply, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**See Also**

An object of this class is typically obtained through the `getChipEffectSet()` method for the [ProbeLevelModel](#) class.

---

ChipEffectTransform    *The ChipEffectTransform class*

---

**Description**

Package: aroma.affymetrix  
**Class ChipEffectTransform**

```
Object
~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
```

~~~~~+---ChipEffectTransform

**Directly known subclasses:**

[AdditiveCovariatesNormalization](#), [ChipEffectGroupMerge](#), [FragmentEquivalentClassNormalization](#), [FragmentLengthNormalization](#), [GcContentNormalization](#), [GcContentNormalization2](#), [SnpChipEffectGroupMerge](#)

public abstract static class **ChipEffectTransform**  
extends [Transform](#)

This abstract class represents a transform that transforms chip-effect estimates obtained from probe-level modelling.

**Usage**

ChipEffectTransform(dataSet=NULL, ...)

**Arguments**

dataSet           The input data set as an [ChipEffectSet](#).  
...                Arguments passed to the constructor of [Transform](#).

**Details**

Subclasses must implement the process() method.

**Fields and Methods**

**Methods:**

*No methods defined.*

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

CnagCfhFile

*The CnagCfhFile class***Description**

Package: aroma.affymetrix

**Class CnagCfhFile****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--CnagCfhFile

```

**Directly known subclasses:**

```

public abstract static class CnagCfhFile
extends AffymetrixFile

```

A CnagCfhFile object represents a single CNAG CFH file.

**Usage**

```
CnagCfhFile(..., cdf=NULL)
```

**Arguments**

```

...           Arguments passed to AromaMicroarrayDataFile.
cdf          An optional AffymetrixCdfFile

```

**Fields and Methods**

**Methods:**

```

getCdf -
nbrOfCells -
nbrOfSnps -
setCdf -

```

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**See Also**

An object of this class is typically part of an [CnagCfhSet](#).

---

CnagCfhSet                      *The CnagCfhSet class*

---

## Description

Package: aroma.affymetrix

### Class CnagCfhSet

Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--CnagCfhSet

```

### Directly known subclasses:

```

public static class CnagCfhSet
extends GenericDataFileSet

```

An CnagCfhSet object represents a set of CNAG CFH files with *identical* chip types.

## Usage

```
CnagCfhSet(files=NULL, ...)
```

## Arguments

|       |                                 |
|-------|---------------------------------|
| files | A <i>list</i> of CnagCfhFile:s. |
| ...   | Not used.                       |

## Fields and Methods

### Methods:

|                 |   |
|-----------------|---|
| as              | - |
| as.CnagCfhSet   | - |
| byName          | - |
| getAverage      | - |
| getAverageAsinh | - |
| getAverageFile  | - |
| getAverageLog   | - |
| getCdf          | - |

```

getData          -
getTimestamps    -
readUnits        -
setCdf           -

```

#### Methods inherited from GenericDataSet:

[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApply, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

#### Methods inherited from FullNameInterface:

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

#### Methods inherited from Object:

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

#### Author(s)

Henrik Bengtsson

#### See Also

[CnagCfhFile](#).



**Description**

Package: aroma.affymetrix

**Class CnChipEffectFile**

Object

```

~|
~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--ParameterCelFile
~~~~~|
~~~~~+--ChipEffectFile
~~~~~|
~~~~~+--SnpChipEffectFile
~~~~~|
~~~~~+--CopyNumberDataFile
~~~~~|
~~~~~+--CnChipEffectFile

```

**Directly known subclasses:**public abstract static class **CnChipEffectFile**extends *CopyNumberDataFile*

This class represents estimates of chip effects in a copy-number probe-level models.

**Usage**

CnChipEffectFile(..., combineAlleles=FALSE)

**Arguments**

... Arguments passed to [SnpChipEffectFile](#).  
 combineAlleles A **logical** indicating if the signals from allele A and allele B are combined or not.

**Fields and Methods****Methods:**

```

exportTotalAndFracB -
extractTheta -
extractTotalAndFreqB -
hasAlleleBFractions -
hasStrandiness -
mergeStrands -
readUnits -

```

**Methods inherited from CopyNumberDataFile:**

as, as.CopyNumberDataFile, getNumberOfFilesAveraged, hasAlleleBFractions, hasStrandiness

**Methods inherited from SnpChipEffectFile:**

exportTotalAndFracB, extractCNT, extractTheta, extractTotalAndFracB, getCellIndices, getExpandedCellMap, getParameters, mergeStrands, readUnits, writeCNT

**Methods inherited from ChipEffectFile:**

as.character, extractChromosomalDataFrame, extractMatrix, extractTheta, findUnitsTodo, getAM, getAsFullCelFile, getCellIndices, getCellMapForMainCdf, getExpandedCellMap, getParameters, getUnitGroupCellArrayMap, getUnitGroupCellMatrixMap, getXAM, mergeGroups, readUnits, writeAsFullCelFile

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, readUnits

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelFile:**

allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**See Also**

An object of this class is typically part of a [CnChipEffectSet](#).

---

CnChipEffectSet

*The CnChipEffectSet class*


---

**Description**

Package: aroma.affymetrix

**Class CnChipEffectSet**

Object

~~|

~~+--FullNameInterface

~~~~~|

~~~~~+--GenericDataFileSet

~~~~~|

~~~~~+--AromaMicroarrayDataSet

```

~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--ParameterCelSet
~~~~~|
~~~~~+--ChipEffectSet
~~~~~|
~~~~~+--SnpChipEffectSet
~~~~~|
~~~~~+--CopyNumberDataSet
~~~~~|
~~~~~+--CnChipEffectSet

```

### Directly known subclasses:

```

public static class CnChipEffectSet
extends CopyNumberDataSet

```

This class represents estimates of chip effects in the probe-level models.

### Usage

```
CnChipEffectSet(..., combineAlleles="byFirstFile")
```

### Arguments

```

...           Arguments passed to SnpChipEffectSet.
combineAlleles A logical indicating if the signals from allele A and allele B are combined or
not.

```

### Fields and Methods

#### Methods:

```

as.CopyNumberDataSetTuple -
exportTotalAndFracB       -
extractTheta              -
extractTotalAndFreqB     -
getAverageFile            -
getCombineAlleles        -

```

```

hasAlleleBFractions      -
hasStrandiness           -
setCombineAlleles        -
writeWig                  -

```

**Methods inherited from CopyNumberDataSet:**

as, as.CopyNumberDataSet, doCBS, hasAlleleBFractions, hasStrandiness

**Methods inherited from SnpChipEffectSet:**

byPath, exportTotalAndFracB, extractAlleleSet, extractCNT, extractSnpCnvQSet, extractSnpQSet, extractTheta, extractTotalAndFreqB, getAverageFile, getBaseline, getMergeStrands, setMergeStrands, writeCNT

**Methods inherited from ChipEffectSet:**

as.character, boxplotStats, byPath, calculateBaseline, calculateFieldBoxplotStats, calculateNuseBoxplotStats, calculateRleBoxplotStats, extractAffyBatch, extractChromosomalDataFrame, extractExpressionSet, extractMatrix, extractTheta, findByName, findUnitsTodo, fromDataSet, getAM, getAsFullCelSet, getAverageFile, getBaseline, getCellIndices, getXAM, plotBoxplot, readUnits, updateUnits

**Methods inherited from ParameterCelSet:**

extractDataFrame, extractMatrix

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelSet:**

append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, get Intensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApply, dsApplyInPairs, duplicated, equals, extract,

findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

CnP1m

*The CnP1m class*

---

**Description**

Package: aroma.affymetrix

**Class CnP1m**

**Interface**

```
~~|
~~+--SnpP1m
~~~~~|
~~~~~+--CnP1m
```

**Directly known subclasses:**

*[AffineCnP1m](#), [AvgCnP1m](#), [HetLogAddCnP1m](#), [MbeiCnP1m](#), [RmaCnP1m](#)*

```
public class CnP1m
  extends SnpP1m
```

This support class represents a [SnpP1m](#) specially designed for copy-number analysis.

**Usage**

```
CnPlm(...)
```

**Arguments**

```
...           Arguments passed to SnpPlm.
```

**Details**

Models implementing this copy-number PLM, provides either allele-specific or total copy-number estimates. For allele-specific CNs the underlying [SnpPlm](#) model is fitted as is, i.e. for each allele separately with or without the strands first being merged.

For total CNs the probe signals for the two alleles are combined (=summed; not averaged) on the intensity scale before fitting underlying [SnpPlm](#) model, again with or without the strands first being merged.

**Methods****Methods:**

```
getCellIndices      -
getChipEffectSet    -
getCombineAlleles   -
getProbeAffinityFile -
setCombineAlleles   -
```

**Methods inherited from SnpPlm:**

```
getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands
```

**Methods inherited from Interface:**

```
extend, print, uses
```

**Requirements**

Classes inheriting from this [Interface](#) must provide the following fields, in addition to the ones according to [SnpPlm](#):

- combineAllelesA [logical](#) indicating if total or allele-specific copy numbers should be estimated according to the above averaging.

**Author(s)**

```
Henrik Bengtsson
```

---

CnProbeAffinityFile    *The CnProbeAffinityFile class*

---

## Description

Package: aroma.affymetrix

### Class CnProbeAffinityFile

#### Object

```

~|
~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--ParameterCelFile
~~~~~|
~~~~~+--ProbeAffinityFile
~~~~~|
~~~~~+--SnpProbeAffinityFile
~~~~~|
~~~~~+--CnProbeAffinityFile

```

#### Directly known subclasses:

```

public abstract static class CnProbeAffinityFile
extends SnpProbeAffinityFile

```

This class represents estimates of probe affinities in SNP probe-level models.



**Usage**

```
CnProbeAffinityFile(..., combineAlleles=FALSE)
```

**Arguments**

... Arguments passed to [SnpProbeAffinityFile](#).

combineAlleles If [FALSE](#), allele A and allele B are treated separately, otherwise together.

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from SnpProbeAffinityFile:**

getCellIndices, setMergeStrands

**Methods inherited from ProbeAffinityFile:**

as.character, getCellIndices, getParameters, readUnits

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, readUnits

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelFile:**

allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

CrlmmParametersFile    *The CrlmmParametersFile class*

---

**Description**

Package: aroma.affymetrix

**Class CrlmmParametersFile****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--ColumnNamesInterface
~~~~~|
~~~~~+--GenericTabularFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaTabularBinaryFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AromaUnitSignalBinaryFile
~~~~~|
~~~~~+--CrlmmParametersFile

```

**Directly known subclasses:**

public static class **CrlmmParametersFile**  
 extends [AromaUnitSignalBinaryFile](#)

An CrlmmParametersFile is a [AromaUnitSignalBinaryFile](#).

**Usage**

```
CrlmmParametersFile(...)
```

**Arguments**

... Arguments passed to [AromaUnitSignalBinaryFile](#).

**Fields and Methods****Methods:**

```
allocate          -
findUnitsTodo    -
readParameter    -
updateParameter  -
```

**Methods inherited from AromaUnitSignalBinaryFile:**

allocate, allocateFromUnitAnnotationDataFile, allocateFromUnitNamesFile, as.character, extractMatrix, extractRawGenomicSignals, fromFile, getChipType, getExtensionPattern, getFilenameExtension, getNumberOfFilesAveraged, getPlatform, isAverageFile, nbrOfUnits, readDataFrame, writeDataFrame

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaTabularBinaryFile:**

[, [<-, [[, allocate, as.character, colApply, colMeans, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getDefaultColumnNames, getRootName, importFrom, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericTabularFile:**

[, as.character, dim, extractMatrix, head, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, tail, writeColumnsToFiles

**Methods inherited from ColumnNamesInterface:**

appendColumnNamesTranslator, appendColumnNamesTranslatorByNULL, appendColumnNamesTranslatorBycharacter, appendColumnNamesTranslatorByfunction, appendColumnNamesTranslatorBylist, clearColumnNamesTranslator, clearListOfColumnNamesTranslators, getColumnNames, getColumnNamesTranslator, getDefaultColumnNames, getListOfColumnNamesTranslators, nbrOfColumns, setColumnNames, setColumnNamesTranslator, setListOfColumnNamesTranslators, updateColumnNames

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$. \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

CrlmmParametersSet      *The CrlmmParametersSet class*

---

**Description**

Package: aroma.affymetrix

**Class CrlmmParametersSet**

Object

~~|

~~+--FullNameInterface

~~~~~|

~~~~~+--GenericDataFileSet

~~~~~|

```

~~~~~+---GenericTabularFileSet
~~~~~|
~~~~~+---AromaTabularBinarySet
~~~~~|
~~~~~+---AromaUnitSignalBinarySet
~~~~~|
~~~~~+---CrlmmParametersSet

```

### Directly known subclasses:

```

public static class CrlmmParametersSet
extends AromaUnitSignalBinarySet

```

An CrlmmParametersSet object represents a set of [CrlmmParametersFiles](#) with *identical* chip types.

### Usage

```
CrlmmParametersSet(...)
```

### Arguments

... Arguments passed to [AromaUnitSignalBinarySet](#).

### Fields and Methods

#### Methods:

```

byName      -
byPath      -
findUnitsTodo -

```

#### Methods inherited from [AromaUnitSignalBinarySet](#):

byName, findByName, getAromaFullNameTranslatorSet, getAromaUgpFile, getChipType, getPlatform, validate, writeDataFrame

#### Methods inherited from [AromaTabularBinarySet](#):

getDefaultFullName, getRootName, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, setAttributesByTags

#### Methods inherited from [GenericTabularFileSet](#):

extractMatrix, calculateAverageColumnAcrossFiles

#### Methods inherited from [GenericDataFileSet](#):

[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorBy-

function, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApply, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

DChipCdfBinFile

*The DChipCdfBinFile class*

---

**Description**

Package: aroma.affymetrix

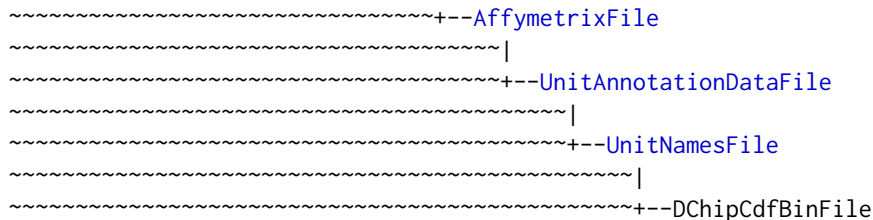
**Class DChipCdfBinFile**

**Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|

```



**Directly known subclasses:**

```

public abstract static class DChipCdfBinFile
extends UnitNamesFile
    
```

A DChipCdfBinFile object represents a DChip CDF.bin file.

**Usage**

```

DChipCdfBinFile(...)
    
```

**Arguments**

... Arguments passed to *AffymetrixFile*.

**Fields and Methods**

**Methods:**

- byChipType -
- getChipType -
- getFileFormat -
- getHeader -
- getPlatform -
- getUnitNames -
- getUnitSizes -
- nbrOfCells -
- nbrOfUnits -
- readDataFrame -

**Methods inherited from UnitNamesFile:**

getUnitNames, indexOf, nbrOfUnits

**Methods inherited from UnitAnnotationDataFile:**

byChipType, getAromaUflFile, getAromaUgpFile, getChipType, getDefaultExtension, getPlatform, nbrOfUnits

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$. \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

DChipDcpFile

*The DChipDcpFile class*

---

**Description**

Package: aroma.affymetrix

**Class DChipDcpFile**

[Object](#)

~~|

~~+--[FullNameInterface](#)



```

~~~~~|
~~~~~+---GenericDataFile
~~~~~|
~~~~~+---CacheKeyInterface
~~~~~|
~~~~~+---FileCacheKeyInterface
~~~~~|
~~~~~+---AromaMicroarrayDataFile
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFile
~~~~~|
~~~~~+---DChipDcpFile

```

### Directly known subclasses:

```

public abstract static class DChipDcpFile
extends AffymetrixFile

```

A DChipDcpFile object represents a DChip DCP file.

### Usage

```
DChipDcpFile(...)
```

### Arguments

... Arguments passed to *AffymetrixFile*.

### Fields and Methods

#### Methods:

```

dim -
extractTheta -
getCalls -
getExcludes -
getFileFormat -
getHeader -
getNormalizedIntensities -
getRawIntensities -
getThetaStds -
getThetas -
getThetasAB -
hasMbeiData -
hasNormalizedData -

```

|            |   |
|------------|---|
| nbrOfCells | - |
| nbrOfUnits | - |

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**See Also**

[DChipDcpSet](#).

DChipDcpSet

*The DChipDcpSet class***Description**

Package: aroma.affymetrix

**Class DChipDcpSet****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--DChipDcpSet

```

**Directly known subclasses:**

```

public abstract static class DChipDcpSet
extends AffymetrixFileSet

```

A DChipDcpSet object represents a set of DChip DCP files for *identical* chip types.

**Usage**

```
DChipDcpSet(files=NULL, ...)
```

**Arguments**

|       |                                                           |
|-------|-----------------------------------------------------------|
| files | A <a href="#">list</a> of <a href="#">DChipDcpFile</a> s. |
| ...   | Not used.                                                 |

**Fields and Methods****Methods:**

|                |   |
|----------------|---|
| as             | - |
| as.DChipDcpSet | - |

```

byName -
exportTotalAndFracB -
extractTheta -
getCdfBin -
getChipType -

```

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApply, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**See Also**

[DChipDcpFile](#).

---

DChipGenomeInformation

*The DChipGenomeInformation class*


---

## Description

Package: aroma.affymetrix

### Class DChipGenomeInformation

#### Object

```

~|
~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--GenomeInformation
~~~~~|
~~~~~+--DChipGenomeInformation

```

#### Directly known subclasses:

public abstract static class **DChipGenomeInformation**  
 extends *GenomeInformation*

This class represents dChip genome information files, which typically contains information about chromosomal locations of the units.

## Usage

```
DChipGenomeInformation(...)
```

## Arguments

... Arguments passed to *GenomeInformation*.

## Details

The dChip genome information files for various chip types can be downloaded from <https://sites.google.com/site/dchipsoft/>. Put each file in a directory named identically as the corresponding chip type under the *annotations/* directory, e.g. *annotations/Mapping50K\_Hind240/50k\_hind\_genome\_info\_AfAm\_june\_05\_hg17.xls*. Note that dChip changes the filename and file format

slightly between chip types, but currently the `*byChipType()` basically searches for files with names consisting of "genome\_info" or "genome\_info". At least for the most common chip types, there is no need to rename the files in order for this class to recognize them.

## Fields and Methods

### Methods:

```
byChipType      -
readDataFrame   -
```

### Methods inherited from GenomeInformation:

as.character, byChipType, fromCdf, fromDataSet, getChipType, getChromosomeStats, getChromosomes, getData, getPositions, getUnitIndices, getUnitsOnChromosome, getUnitsOnChromosomes, isCompatibleWithCdf, nbrOfUnits, plotDensity, readDataFrame, verify

### Methods inherited from FileCacheKeyInterface:

getCacheKey

### Methods inherited from CacheKeyInterface:

getCacheKey

### Methods inherited from GenericDataFile:

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

### Methods inherited from FullNameInterface:

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

### Methods inherited from Object:

\$, \$<-, [, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

## Author(s)

Henrik Bengtsson

---

DChipQuantileNormalization

*The DChipQuantileNormalization class*


---

## Description

Package: aroma.affymetrix

### Class DChipQuantileNormalization

#### Object

```

~|
~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--QuantileNormalization
~~~~~|
~~~~~+--DChipQuantileNormalization

```

#### Directly known subclasses:

```

public static class DChipQuantileNormalization
extends QuantileNormalization

```

This class represents a special [QuantileNormalization](#) using smooth-splines.

## Usage

```
DChipQuantileNormalization(..., robust=FALSE)
```

## Arguments

|        |                                                                                         |
|--------|-----------------------------------------------------------------------------------------|
| ...    | Arguments passed to the constructor of <a href="#">QuantileNormalization</a> .          |
| robust | If <code>TRUE</code> , the normalization function is estimated robustly, otherwise not. |

## Details

This normalization method implements the two-pass algorithm described in Bengtsson et al. (2008).

**Fields and Methods****Methods:**

process -

**Methods inherited from QuantileNormalization:**

findTargetDistributionFile, getParameters, process

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$&lt;-, [], [[&lt;-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**References**

[1] H. Bengtsson, R. Irizarry, B. Carvalho, & T.P. Speed. Estimation and assessment of raw copy numbers at the single locus level, *Bioinformatics*, 2008.

---

DChipSnpInformation    *The DChipSnpInformation class*

---

**Description**

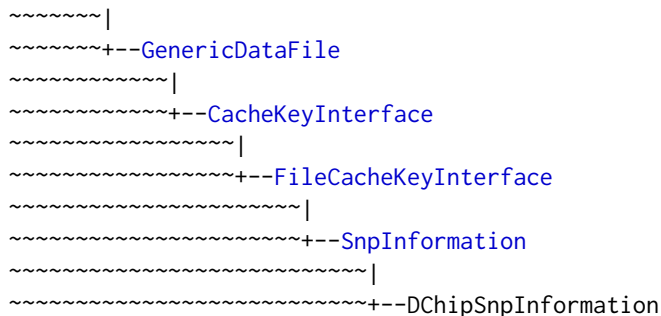
Package: aroma.affymetrix

**Class DChipSnpInformation**[Object](#)

~~|

~~+--[FullNameInterface](#)





**Directly known subclasses:**

public abstract static class **DChipSnpInformation**  
 extends *SnpInformation*

This class represents dChip genome information files, which typically contains information on nucleotide sequences and fragment lengths of the units.

**Usage**

DChipSnpInformation(...)

**Arguments**

... Arguments passed to *SnpInformation*.

**Details**

The dChip SNP information files for various chip types can be downloaded from <https://sites.google.com/site/dchipsoft/>. Put each file in a directory named identically as the corresponding chip type under the *annotations/* directory, e.g. *annotations/Mapping50K\Hind240/50k hind snp info AfAm june 05 hg17.xls*. Note that dChip changes the filename and file format slightly between chip types, but currently the *\*byChipType()* basically searches for files with names consisting of "snp info" or "snp\_info". At least for the most common chip types, there is no need to rename the files in order for this class to recognize them.

**Fields and Methods**

**Methods:**

- byChipType -
- readDataFrame -

**Methods inherited from SnpInformation:**

as.character, byChipType, fromCdf, fromDataSet, getChipType, getData, getFields, getFragmentLengths, getFragmentStarts, getFragmentStops, isCompatibleWithCdf, nbrOfEnzymes, nbrOfUnits, read-DataFrame, verify

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [, [ [<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

doCRMAv1

*Estimation and assessment of raw copy numbers at the single locus level (CRMA v1)*

---

**Description**

Estimation and assessment of raw copy numbers at the single locus level (CRMA v1) based on [1]. The algorithm is processed in bounded memory, meaning virtually any number of arrays can be analyzed on also very limited computer systems.

**Usage**

```
## S3 method for class 'AffymetrixCelSet'
doCRMAv1(csR, shift=+300, combineAlleles=TRUE, lengthRange=NULL, arrays=NULL, drop=TRUE,
  verbose=FALSE, ...)
## Default S3 method:
doCRMAv1(dataSet, ..., verbose=FALSE)
## Default S3 method:
doASCRMAv1(...)
```

**Arguments**

|                |                                                                                                                                     |
|----------------|-------------------------------------------------------------------------------------------------------------------------------------|
| csR, dataSet   | An <a href="#">AffymetrixCelSet</a> (or the name of an <a href="#">AffymetrixCelSet</a> ).                                          |
| shift          | An tuning parameter specifying how much to shift the probe signals before probe summarization.                                      |
| combineAlleles | A <a href="#">logical</a> specifying whether allele probe pairs should be summed before modelling or not.                           |
| lengthRange    | An optional <a href="#">numeric</a> vector of length two passed to <a href="#">FragmentLengthNormalization</a> .                    |
| arrays         | A <a href="#">integer vector</a> specifying the subset of arrays to process. If <a href="#">NULL</a> , all arrays are considered.   |
| drop           | If <a href="#">TRUE</a> , the summaries are returned, otherwise a named <a href="#">list</a> of all intermediate and final results. |
| verbose        | See <a href="#">Verbose</a> .                                                                                                       |
| ...            | Additional arguments used to set up <a href="#">AffymetrixCelSet</a> (when argument dataSet is specified).                          |

**Value**

Returns a named [list](#), iff drop == FALSE, otherwise only [ChipEffectSet](#) object.

**Allele-specific or only total-SNP signals**

If you wish to obtain allele-specific estimates for SNPs, which are needed to call genotypes or infer parent-specific copy numbers, then use argument `combineAlleles=FALSE`. Total copy number signals are still available. If you know for certain that you will not use allele-specific estimates, you will get slightly less noisy signals (very small difference) if you use `combineAlleles=TRUE`.

`doASCRMAv1(...)` is a wrapper for `doCRMAv1(..., combineAlleles=FALSE)`.

**Author(s)**

Henrik Bengtsson

**References**

[1] H. Bengtsson, R. Irizarry, B. Carvalho & T.P. Speed. *Estimation and assessment of raw copy numbers at the single locus level*, Bioinformatics, 2008.

**See Also**

For CRMA v2 (recommended by authors), which is a single-array improvement over CRMA v1, see [doCRMAv2\(\)](#).

---

|          |                                                                                                                                            |
|----------|--------------------------------------------------------------------------------------------------------------------------------------------|
| doCRMAv2 | <i>A single-array preprocessing method for estimating full-resolution raw copy numbers from all Affymetrix genotyping arrays (CRMA v2)</i> |
|----------|--------------------------------------------------------------------------------------------------------------------------------------------|

---

**Description**

A single-array preprocessing method for estimating full-resolution raw copy numbers from all Affymetrix genotyping arrays (CRMA v2) based on [1]. The algorithm is processed in bounded memory, meaning virtually any number of arrays can be analyzed on also very limited computer systems.

We recommend CRMA v2 for estimating allele-specific as well total SNP signals from Affymetrix SNP chips.

**Usage**

```
## S3 method for class 'AffymetrixCelSet'
doCRMAv2(csR, combineAlleles=TRUE, lengthRange=NULL, arrays=NULL,
  plm=c("AvgCnPlm", "RmaCnPlm"), drop=TRUE, verbose=FALSE, ...)
## Default S3 method:
doCRMAv2(dataSet, ..., verbose=FALSE)
## Default S3 method:
doASCRMAv2(...)
```

**Arguments**

|                |                                                                                                                                     |
|----------------|-------------------------------------------------------------------------------------------------------------------------------------|
| csR, dataSet   | An <a href="#">AffymetrixCelSet</a> (or the name of an <a href="#">AffymetrixCelSet</a> ).                                          |
| combineAlleles | A <a href="#">logical</a> specifying whether allele probe pairs should be summed before modelling or not.                           |
| lengthRange    | An optional <a href="#">numeric</a> vector of length two passed to <a href="#">FragmentLengthNormalization</a> .                    |
| arrays         | A <a href="#">integer vector</a> specifying the subset of arrays to process. If <a href="#">NULL</a> , all arrays are considered.   |
| plm            | A <a href="#">character</a> string specifying which type of probe-summarization model to used.                                      |
| drop           | If <a href="#">TRUE</a> , the summaries are returned, otherwise a named <a href="#">list</a> of all intermediate and final results. |
| verbose        | See <a href="#">Verbose</a> .                                                                                                       |
| ...            | Additional arguments used to set up <a href="#">AffymetrixCelSet</a> (when argument dataSet is specified).                          |

**Value**

Returns a named [list](#), iff `drop == FALSE`, otherwise only [ChipEffectSet](#) object.

**Allele-specific or only total-SNP signals**

If you wish to obtain allele-specific estimates for SNPs, which are needed to call genotypes or infer parent-specific copy numbers, then use argument `combineAlleles=FALSE`. Total copy number signals are still available. If you know for certain that you will not use allele-specific estimates, you will get slightly less noisy signals (very small difference) if you use `combineAlleles=TRUE`.

`doASCRMAv2(...)` is a wrapper for `doCRMAv2(..., combineAlleles=FALSE)`.

**Author(s)**

Henrik Bengtsson

**References**

[1] H. Bengtsson, P. Wirapati & T.P. Speed. *A single-array preprocessing method for estimating full-resolution raw copy numbers from all Affymetrix genotyping arrays including GenomeWideSNP 5 & 6*, Bioinformatics, 2009.

**See Also**

For CRMA v1, which is a multi-array methods that precedes CRMA v2, see [doCRMAv1\(\)](#).

---

doFIRMA

*Finding Isoforms using Robust Multichip Analysis (FIRMA)*

---

**Description**

Finding Isoforms using Robust Multichip Analysis (FIRMA) based on [1].

**Usage**

```
## S3 method for class 'AffymetrixCelSet'
doFIRMA(csR, ..., flavor=c("v1b", "v1a"), drop=TRUE, verbose=FALSE)
## Default S3 method:
doFIRMA(dataSet, ..., verbose=FALSE)
```

**Arguments**

`csR`, `dataSet` An [AffymetrixCelSet](#) (or the name of an [AffymetrixCelSet](#)).

`...` Additional arguments passed to [FirmaModel](#), and to set up [AffymetrixCelSet](#) (when argument `dataSet` is specified).

`flavor` A [character](#) string specifying the flavor of FIRMA to use.

|         |                                                                                                                                  |
|---------|----------------------------------------------------------------------------------------------------------------------------------|
| drop    | If <code>TRUE</code> , the FIRMA scores are returned, otherwise a named <code>list</code> of all intermediate and final results. |
| verbose | See <a href="#">Verbose</a> .                                                                                                    |

**Value**

Returns a named `list`, iff `drop == FALSE`, otherwise only `FirmaSet` object (containing the FIRMA scores).

**Using a custom exon-by-transcript CDF**

It is strongly recommended to use a custom CDF, e.g. "core", "extended" or "full" [1]. To use a custom CDF, set it before calling this method, i.e. `setCdf(csR, cdf)`. Do not set the standard "non-supported" Affymetrix CDF (see also Section 'Flavors').

**Flavors**

If `flavor == "v1b"` (default), then the standard "non-supported" Affymetrix CDF is used for background correction and the quantile normalization steps, and the custom CDF is used for the probe summarization and everything that follows. The advantage of this flavor is that those two first preprocessing steps will remain the same if one later changes to a different custom CDF.

If `flavor == "v1a"`, then the custom CDF is used throughout all steps of FIRMA, which means that if one changes the custom CDF all steps will be redone.

**Author(s)**

Henrik Bengtsson

**References**

[1] E. Purdom, K. Simpson, M. Robinson, J. Conboy, A. Lapuk & T.P. Speed, *FIRMA: a method for detection of alternative splicing from exon array data*, Bioinformatics, 2008.

**Description**

Robust Multichip Analysis (GCRMA) based on [1]. The algorithm is processed in bounded memory, meaning virtually any number of arrays can be analyzed on also very limited computer systems. The method replicates the results of `gcrma` (package `gcrma`) with great precision.

**Usage**

```
## S3 method for class 'AffymetrixCelSet'
doGCRMA(csR, arrays=NULL, type=c("fullmodel", "affinities"), uniqueP1m=FALSE, drop=TRUE,
        verbose=FALSE, ...)
## Default S3 method:
doGCRMA(dataSet, ..., verbose=FALSE)
```

**Arguments**

|              |                                                                                                                                                                                                                                |
|--------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| csR, dataSet | An <a href="#">AffymetrixCelSet</a> (or the name of an <a href="#">AffymetrixCelSet</a> ).                                                                                                                                     |
| arrays       | A <a href="#">integer vector</a> specifying the subset of arrays to process. If <a href="#">NULL</a> , all arrays are considered.                                                                                              |
| type         | A <a href="#">character</a> string specifying what type of model to use for the GCRMA background correction. For more details, see <a href="#">GcRmaBackgroundCorrection</a> .                                                 |
| uniqueP1m    | If <a href="#">TRUE</a> , the log-additive probe-summarization model is done on probeset with <i>unique</i> sets of probes. If <a href="#">FALSE</a> , the summarization is done on "as-is" probesets as specified by the CDF. |
| drop         | If <a href="#">TRUE</a> , the summaries are returned, otherwise a named <a href="#">list</a> of all intermediate and final results.                                                                                            |
| verbose      | See <a href="#">Verbose</a> .                                                                                                                                                                                                  |
| ...          | Additional arguments used to set up <a href="#">AffymetrixCelSet</a> (when argument dataSet is specified).                                                                                                                     |

**Value**

Returns a named [list](#), iff drop == FALSE, otherwise only [ChipEffectSet](#) object.

**Author(s)**

Henrik Bengtsson

**References**

[1] Z. Wu, R. Irizarry, R. Gentleman, F.M. Murillo & F. Spencer. *A Model Based Background Adjustment for Oligonucleotide Expression Arrays*, JASA, 2004.

---

doRMA

*Robust Multichip Analysis (RMA)*


---

**Description**

Robust Multichip Analysis (RMA) based on [1]. The algorithm is processed in bounded memory, meaning virtually any number of arrays can be analyzed on also very limited computer systems. The method replicates the results of [fitPLM](#) (package [affyPLM](#)) with great precision.

**Usage**

```
## S3 method for class 'AffymetrixCelSet'
doRMA(csR, arrays=NULL, flavor=c("affyPLM", "oligo"), uniqueP1m=FALSE, drop=TRUE,
      verbose=FALSE, ...)
## Default S3 method:
doRMA(dataSet, ..., verbose=FALSE)
```

**Arguments**

|              |                                                                                                                                                                                                                                |
|--------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| csR, dataSet | An <a href="#">AffymetrixCelSet</a> (or the name of an <a href="#">AffymetrixCelSet</a> ).                                                                                                                                     |
| arrays       | A <a href="#">integer vector</a> specifying the subset of arrays to process. If <a href="#">NULL</a> , all arrays are considered.                                                                                              |
| flavor       | A character string specifying what model fitting algorithm to be used, cf. <a href="#">RmaP1m</a> .                                                                                                                            |
| uniqueP1m    | If <a href="#">TRUE</a> , the log-additive probe-summarization model is done on probeset with <i>unique</i> sets of probes. If <a href="#">FALSE</a> , the summarization is done on "as-is" probesets as specified by the CDF. |
| drop         | If <a href="#">TRUE</a> , the summaries are returned, otherwise a named <a href="#">list</a> of all intermediate and final results.                                                                                            |
| verbose      | See <a href="#">Verbose</a> .                                                                                                                                                                                                  |
| ...          | Additional arguments used to set up <a href="#">AffymetrixCelSet</a> (when argument <code>dataSet</code> is specified).                                                                                                        |

**Value**

Returns a named [list](#), iff `drop == FALSE`, otherwise only [ChipEffectSet](#) object.

**Author(s)**

Henrik Bengtsson

**References**

[1] Irizarry et al. *Summaries of Affymetrix GeneChip probe level data*. NAR, 2003, 31, e15.

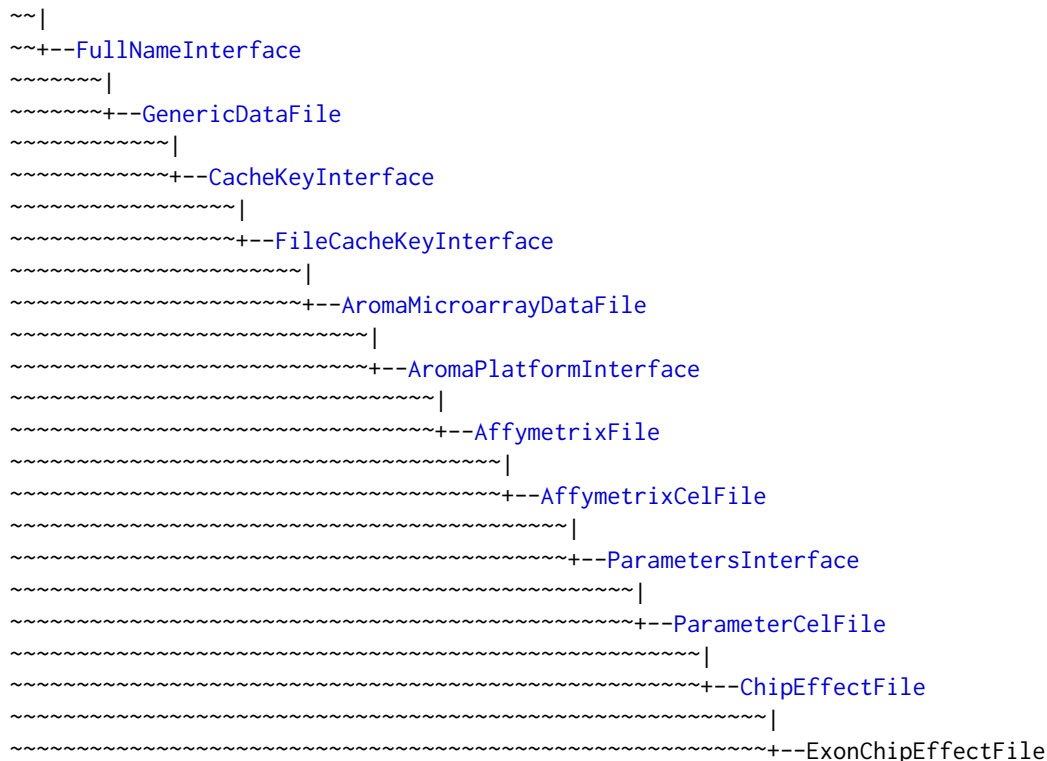


**Description**

Package: aroma.affymetrix

**Class ExonChipEffectFile**

**Object**



**Directly known subclasses:**

```

public abstract static class ExonChipEffectFile
extends ChipEffectFile
    
```

This class represents estimates of chip effects in the probe-level models.

**Usage**

```

ExonChipEffectFile(..., mergeGroups=FALSE)
    
```

**Arguments**

- ... Arguments passed to [ChipEffectFile](#).
- mergeGroups Specifies if the groups are merged or not for these estimates.

**Fields and Methods****Methods:**

readUnits -

**Methods inherited from ChipEffectFile:**

as.character, extractChromosomalDataFrame, extractMatrix, extractTheta, findUnitsTodo, getAM, getAsFullCelFile, getCellIndices, getCellMapForMainCdf, getExpandedCellMap, getParameters, getUnitGroupCellArrayMap, getUnitGroupCellMatrixMap, getXAM, mergeGroups, readUnits, writeAsFullCelFile

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, readUnits

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelFile:**

allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags,

hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [], []<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Ken Simpson, Henrik Bengtsson

**See Also**

An object of this class is typically part of a [ExonChipEffectSet](#).

ExonChipEffectSet      *The ExonChipEffectSet class*

**Description**

Package: aroma.affymetrix

**Class ExonChipEffectSet**

Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--ParameterCelSet
~~~~~|
~~~~~+--ChipEffectSet
~~~~~|
~~~~~+--ExonChipEffectSet

```

**Directly known subclasses:**

public static class **ExonChipEffectSet**  
 extends [ChipEffectSet](#)

This class represents estimates of chip effects in the probe-level models.

**Usage**

```
ExonChipEffectSet(..., mergeGroups=TRUE)
```

**Arguments**

|             |                                                                                                                                                          |
|-------------|----------------------------------------------------------------------------------------------------------------------------------------------------------|
| ...         | Arguments passed to <a href="#">ChipEffectSet</a> .                                                                                                      |
| mergeGroups | Specifies if groups (individual exons in a CDF file) are merged or not for these estimates, i.e. whether transcript-level expression is to be estimated. |

**Fields and Methods****Methods:**

|                |   |
|----------------|---|
| findUnitsTodo  | - |
| getAverageFile | - |
| getMergeGroups | - |
| setMergeGroups | - |

**Methods inherited from [ChipEffectSet](#):**

as.character, boxplotStats, byPath, calculateBaseline, calculateFieldBoxplotStats, calculateNuse-BoxplotStats, calculateRleBoxplotStats, extractAffyBatch, extractChromosomalDataFrame, extractExpressionSet, extractMatrix, extractTheta, findByName, findUnitsTodo, fromDataSet, getAM, getAsFullCelSet, getAverageFile, getBaseline, getCellIndices, getXAM, plotBoxplot, readUnits, updateUnits

**Methods inherited from [ParameterCelSet](#):**

extractDataFrame, extractMatrix

**Methods inherited from [ParametersInterface](#):**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from [AffymetrixCelSet](#):**

append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApply, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Ken Simpson, Henrik Bengtsson

---

ExonProbeAffinityFile *The ExonProbeAffinityFile class*

---

**Description**

Package: aroma.affymetrix

**Class ExonProbeAffinityFile**

```

Object
~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--ParameterCelFile
~~~~~|
~~~~~+--ProbeAffinityFile
~~~~~|
~~~~~+--ExonProbeAffinityFile

```

### Directly known subclasses:

```

public abstract static class ExonProbeAffinityFile
extends ProbeAffinityFile

```

This class represents estimates of probe affinities in exon array probe-level models.

### Usage

```

ExonProbeAffinityFile(..., mergeGroups=FALSE)

```

### Arguments

```

...           Arguments passed to ProbeAffinityFile.
mergeGroups  Specifies if the groups (exons) are merged or not for these estimates.

```

### Fields and Methods

#### Methods:

*No methods defined.*

**Methods inherited from ProbeAffinityFile:**

as.character, getCellIndices, getParameters, readUnits

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, readUnits

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelFile:**

allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$. \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Ken Simpson, Henrik Bengtsson

ExonRmaP1m

*The ExonRmaP1m class***Description**

Package: aroma.affymetrix

**Class ExonRmaP1m****Object**

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--RmaP1m
~~~~~|
~~~~~+--ExonRmaP1m

```

**Directly known subclasses:**

```

public abstract static class ExonRmaP1m
extends RmaP1m

```

This class represents the log-additive model part of the Robust Multichip Analysis (RMA) method described in Irizarry et al (2003), as implemented for exon arrays. The model may be fitted with exons merged into transcripts (all probes fitted together) or on an individual exon basis (probes within an exon treated as a group, but exons fitted separately).

**Usage**

```

ExonRmaP1m(..., mergeGroups=TRUE)

```

**Arguments**

```

...           Arguments passed to RmaP1m.
mergeGroups  A logical flag specifying whether to merge exons into transcripts.

```



**Fields and Methods****Methods:**

```

getCellIndices      -
getChipEffectSet    -
getProbeAffinityFile -
setMergeGroups      -

```

**Methods inherited from RmaPlm:**

getAsteriskTags, getCalculateResidualsFunction, getParameters, getRlmFitFunctions

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$., \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Model**

[RmaPlm](#).

**Author(s)**

Ken Simpson, Henrik Bengtsson, Elizabeth Purdom

**References**

Irizarry et al. *Summaries of Affymetrix GeneChip probe level data*. NAR, 2003, 31, e15.

FirmaFile

*The FirmaFile class***Description**

Package: aroma.affymetrix

**Class FirmaFile****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--ParameterCelFile
~~~~~|
~~~~~+--FirmaFile

```

**Directly known subclasses:**

```

public abstract static class FirmaFile
extends ParameterCelFile

```

This class represents scores calculated by the FIRMA algorithm.

**Usage**

```

FirmaFile(...)

```

**Arguments**

... Arguments passed to [AffymetrixCelFile](#).

**Fields and Methods****Methods:**

```
extractMatrix -
findUnitsTodo -
readUnits -
```

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, readUnits

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelFile:**

allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags,

hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [], []<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Ken Simpson, Henrik Bengtsson

**See Also**

An object of this class is typically part of a [FirmaSet](#).

---

FirmaModel

*The FirmaModel class*

---

**Description**

Package: aroma.affymetrix

**Class FirmaModel**

**Object**

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--FirmaModel

```

**Directly known subclasses:**

```

public abstract static class FirmaModel
extends UnitModel

```

This class represents the FIRMA (Finding Isoforms using RMA) alternative splicing model.

**Usage**

```

FirmaModel(rmaPlm=NULL, summaryMethod=c("median", "upperQuartile", "max"),
operateOn=c("residuals", "weights"), ...)

```

**Arguments**

|               |                                                                                  |
|---------------|----------------------------------------------------------------------------------|
| rmaPlm        | An @RmaPlm object.                                                               |
| summaryMethod | A <a href="#">character</a> specifying what summarization method should be used. |
| operateOn     | A <a href="#">character</a> specifying what statistic to operate on.             |
| ...           | Arguments passed to constructor of <a href="#">UnitModel</a> .                   |

**Fields and Methods****Methods:**

|             |   |
|-------------|---|
| fit         | - |
| getCdf      | - |
| getDataSet  | - |
| getFirmaSet | - |
| getName     | - |
| getPlm      | - |
| getTags     | - |

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Ken Simpson, Henrik Bengtsson

---

FirmaSet

*The FirmaSet class*

---

**Description**

Package: aroma.affymetrix

**Class FirmaSet**

```

Object
~~|
~~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFileSet
~~~~~|
~~~~~+---AromaMicroarrayDataSet
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFileSet
~~~~~|
~~~~~+---AffymetrixCelSet
~~~~~|
~~~~~+---ParametersInterface
~~~~~|
~~~~~+---ParameterCelSet
~~~~~|
~~~~~+---FirmaSet

```

#### Directly known subclasses:

```

public static class FirmaSet
extends ParameterCelSet

```

#### Usage

```
FirmaSet(...)
```

#### Arguments

```
... Arguments passed to constructor of AffymetrixCelSet.
```

#### Fields and Methods

##### Methods:

```

extractMatrix -
findUnitsTodo -
getCellIndices -
readUnits -

```

##### Methods inherited from [ParameterCelSet](#):

```
extractDataFrame, extractMatrix
```

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelSet:**

append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUfflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApply, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Ken Simpson, Henrik Bengtsson

---

 FragmentEquivalentClassNormalization

*The FragmentEquivalentClassNormalization class*


---

## Description

Package: aroma.affymetrix

### Class FragmentEquivalentClassNormalization

#### Object

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ChipEffectTransform
~~~~~|
~~~~~+--FragmentEquivalentClassNormalization
  
```

#### Directly known subclasses:

public static class **FragmentEquivalentClassNormalization**

extends *ChipEffectTransform*

This class represents a normalization method that corrects for systematic effects between loci of different equivalent classes of pairs of sequences that are recognized by the restriction enzymes that cut the DNA studies.

## Usage

```

FragmentEquivalentClassNormalization(dataSet=NULL, ..., targetAvg=NULL,
  subsetToFit="-XY")
  
```

## Arguments

|             |                                                                                                                                  |
|-------------|----------------------------------------------------------------------------------------------------------------------------------|
| dataSet     | A <i>CnChipEffectSet</i> .                                                                                                       |
| ...         | Additional arguments passed to the constructor of <i>ChipEffectTransform</i> .                                                   |
| targetAvg   | An optional list of <i>functions</i> . For each enzyme there is one target averages to which all arrays should be normalized to. |
| subsetToFit | The units from which the normalization curve should be estimated. If <i>NULL</i> , all are considered.                           |



**Fields and Methods****Methods:**

```

getAromaUfcFile -
getCdf          -
process        -

```

**Methods inherited from ChipEffectTransform:**

```
getRootPath
```

**Methods inherited from Transform:**

```
getOutputDataSet, getOutputFiles
```

**Methods inherited from AromaTransform:**

```

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames,
getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles,
getPath, getRootPath, getTags, isDone, process, setTags

```

**Methods inherited from ParametersInterface:**

```
getParameterSets, getParameters, getParametersAsString
```

**Methods inherited from Object:**

```

$, $<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach,
equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstan-
tiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

```

**Requirements**

This class requires an UFC (Unit Fragment Class) annotation file.

**Acknowledgments**

The idea of normalization signals stratified on enzyme recognition sequences is credited to Jim Veitch and Ben Bolstad at Affymetrix Inc. (2008) who have designed a similar method for copy number estimation in the Affymetrix' Genotype Console v2.

**Author(s)**

Henrik Bengtsson

---

FragmentLengthNormalization

*The FragmentLengthNormalization class*

---

**Description**

Package: aroma.affymetrix

**Class FragmentLengthNormalization****Object**

```

~|
~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ChipEffectTransform
~~~~~|
~~~~~+--FragmentLengthNormalization

```

**Directly known subclasses:**

public static class **FragmentLengthNormalization**  
 extends *ChipEffectTransform*

This class represents a normalization method that corrects for PCR fragment length effects on copy-number chip-effect estimates.

**Usage**

```
FragmentLengthNormalization(dataSet=NULL, ..., target=targetFunctions, subsetToFit="-XY",
  lengthRange=NULL, onMissing=c("median", "ignore"), shift=0, targetFunctions=NULL)
```

**Arguments**

|                 |                                                                                                                                                                                                   |
|-----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| dataSet         | A <i>SnpChipEffectSet</i> .                                                                                                                                                                       |
| ...             | Additional arguments passed to the constructor of <i>ChipEffectTransform</i> .                                                                                                                    |
| target          | (Optional) A <i>character</i> string or a list of <i>functions</i> specifying what to normalize toward. For each enzyme there is one target function to which all arrays should be normalized to. |
| subsetToFit     | The units from which the normalization curve should be estimated. If <i>NULL</i> , all are considered.                                                                                            |
| lengthRange     | If given, a <i>numeric vector</i> of length 2 specifying the range of fragment lengths considered. All fragments with lengths outside this range are treated as if they were missing.             |
| onMissing       | Specifies how to normalize units for which the fragment lengths are unknown.                                                                                                                      |
| shift           | An optional amount the data points should be shifted (translated).                                                                                                                                |
| targetFunctions | Deprecated.                                                                                                                                                                                       |

**Details**

For SNPs, the normalization function is estimated based on the total chip effects, i.e. the sum of the allele signals. The normalizing is done by rescale the chip effects on the intensity scale such that the mean of the total chip effects are the same across samples for any given fragment length. For allele-specific estimates, both alleles are always rescaled by the same amount. Thus, when normalizing allele-specific chip effects, the total chip effects is change, but not the relative allele signal, e.g. the allele B frequency.

**Fields and Methods****Methods:**

```
getCdf    -
process   -
```

**Methods inherited from ChipEffectTransform:**

```
getRootPath
```

**Methods inherited from Transform:**

```
getOutputDataSet, getOutputFiles
```

**Methods inherited from AromaTransform:**

```
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames,
getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles,
getPath, getRootPath, getTags, isDone, process, setTags
```

**Methods inherited from ParametersInterface:**

```
getParameterSets, getParameters, getParametersAsString
```

**Methods inherited from Object:**

```
$/, $<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach,
equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstan-
tiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis
```

**Requirements**

This class requires a SNP information annotation file for the chip type to be normalized.

**Author(s)**

Henrik Bengtsson

**Description**

Package: aroma.affymetrix

**Class GcContentNormalization****Object**

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ChipEffectTransform
~~~~~|
~~~~~+--GcContentNormalization

```

**Directly known subclasses:**

```

public static class GcContentNormalization
extends ChipEffectTransform

```

**Usage**

```
GcContentNormalization(dataSet=NULL, ..., targetFunction=NULL, subsetToFit=NULL)
```

**Arguments**

|                |                                                                                                        |
|----------------|--------------------------------------------------------------------------------------------------------|
| dataSet        | A <i>CnChipEffectSet</i> .                                                                             |
| ...            | Additional arguments passed to the constructor of <i>ChipEffectTransform</i> .                         |
| targetFunction | A <i>function</i> . The target function to which all arrays should be normalized to.                   |
| subsetToFit    | The units from which the normalization curve should be estimated. If <i>NULL</i> , all are considered. |

**Fields and Methods****Methods:**

```

getCdf -
process -

```

**Methods inherited from ChipEffectTransform:**

```
getRootPath
```

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$/, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Requirements**

This class requires an Aroma unit GC-content (UGC) file.

**Author(s)**

Henrik Bengtsson

---

GcContentNormalization2

*The GcContentNormalization2 class*

---

**Description**

Package: aroma.affymetrix

**Class GcContentNormalization2****Object**

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ChipEffectTransform
~~~~~|
~~~~~+--AdditiveCovariatesNormalization
~~~~~|
~~~~~+--GcContentNormalization2

```

**Directly known subclasses:**

public static class **GcContentNormalization2**  
 extends [AdditiveCovariatesNormalization](#)

This class represents a normalization method that corrects for annotation-data covariate effects on copy-number chip-effect estimates.

**Usage**

```
GcContentNormalization2(...)
```

**Arguments**

... Arguments passed to the constructor of [AdditiveCovariatesNormalization](#).

**Fields and Methods****Methods:**

plotCovariateEffects -

**Methods inherited from AdditiveCovariatesNormalization:**

getAsteriskTags, getCdf, getCovariates, getOutputDataSet00, getParameters, process

**Methods inherited from ChipEffectTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

GcRmaBackgroundCorrection

*The GcRmaBackgroundCorrection class*


---

## Description

Package: aroma.affymetrix

### Class GcRmaBackgroundCorrection

#### Object

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--BackgroundCorrection
~~~~~|
~~~~~+--GcRmaBackgroundCorrection

```

#### Directly known subclasses:

```

public static class GcRmaBackgroundCorrection
extends BackgroundCorrection

```

This class represents the GCRMA background adjustment function.

## Usage

```

GcRmaBackgroundCorrection(..., indicesNegativeControl=NULL, affinities=NULL,
  type=c("fullmodel", "affinities"), opticalAdjust=TRUE, gsbAdjust=TRUE,
  gsbParameters=NULL, seed=NULL)

```

## Arguments

```

...           Arguments passed to the constructor of ProbeLevelTransform.
indicesNegativeControl
              Locations of any negative control probes (e.g., the anti-genomic controls on the
              human exon array). If NULL and type == "affinities", then all non-PM
              probes are used as the negative controls.

```

|               |                                                                                                                                                                                       |
|---------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| affinities    | A <b>numeric vector</b> of probe affinities, usually as calculated by <code>computeAffinities()</code> of the <code>AffymetrixCdfFile</code> class.                                   |
| type          | Type (flavor) of background correction, which can be either "fullmodel" (uses MMs; requires that the chip type has PM/MM pairs) or "affinities" (uses probe sequence only).           |
| gsbAdjust     | If <b>TRUE</b> , adjustment for specific binding is done, otherwise not.                                                                                                              |
| opticalAdjust | If <b>TRUE</b> , correction for optical effect is done first, utilizing <code>OpticalBackgroundCorrection</code> .                                                                    |
| gsbParameters | Additional argument passed to the internal <code>bgAdjustGcrma()</code> method.                                                                                                       |
| seed          | An (optional) <b>integer</b> specifying a temporary random seed to be used during processing. The random seed is set to its original state when done. If <b>NULL</b> , it is not set. |

## Fields and Methods

### Methods:

process -

### Methods inherited from BackgroundCorrection:

`getParameters`, `process`

### Methods inherited from ProbeLevelTransform:

`getRootPath`

### Methods inherited from Transform:

`getOutputDataSet`, `getOutputFiles`

### Methods inherited from AromaTransform:

`as.character`, `findFilesTodo`, `getAsteriskTags`, `getExpectedOutputFiles`, `getExpectedOutputFullnames`, `getFullName`, `getInputDataSet`, `getName`, `getOutputDataSet`, `getOutputDataSet0`, `getOutputFiles`, `getPath`, `getRootPath`, `getTags`, `isDone`, `process`, `setTags`

### Methods inherited from ParametersInterface:

`getParameterSets`, `getParameters`, `getParametersAsString`

### Methods inherited from Object:

`$`, `$<-`, `[]`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clearLookupCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `getEnvironment`, `getFieldModifier`, `getFieldModifiers`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `names`, `objectSize`, `print`, `save`, `asThis`

## Author(s)

Ken Simpson, Henrik Bengtsson

## References

[1] Z. Wu, R. Irizarry, R. Gentleman, F.M. Murillo & F. Spencer. *A Model Based Background Adjustment for Oligonucleotide Expression Arrays*, JASA, 2004.



---

GenericReporter      *The GenericReporter class*

---

## Description

Package: aroma.affymetrix

### Class GenericReporter

[Object](#)

~~|

~~+--GenericReporter

### Directly known subclasses:

[AffymetrixCelSetReporter](#), [AffymetrixFileSetReporter](#), [SpatialReporter](#)

public abstract static class **GenericReporter**

extends [Object](#)

## Usage

```
GenericReporter(tags="*", ...)
```

## Arguments

|      |                                                                            |
|------|----------------------------------------------------------------------------|
| tags | A <a href="#">character vector</a> of tags to be added to the output path. |
| ...  | Not used.                                                                  |

## Fields and Methods

### Methods:

|             |   |
|-------------|---|
| getFullName | - |
| getName     | - |
| getPath     | - |
| getTags     | - |
| process     | - |
| setup       | - |

### Methods inherited from Object:

\$, \$<-, [, [(<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

 GenomeInformation      *The GenomeInformation class*


---

**Description**

Package: aroma.affymetrix

**Class GenomeInformation****Object**

```

~|
~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--GenomeInformation
  
```

**Directly known subclasses:**

*AffymetrixCsvGenomeInformation, DChipGenomeInformation, UgpGenomeInformation*

```
public abstract static class GenomeInformation
```

```
extends FileCacheKeyInterface
```

**Usage**

```
GenomeInformation(..., .verify=TRUE)
```

**Arguments**

```
...           Arguments passed to GenericDataFile.
.verify      For internal use only.
```

**Fields and Methods****Methods:**

```
byChipType   -
getChipType  -
```

```

getChromosomeStats -
getChromosomes -
getData -
getPositions -
getUnitsOnChromosome -
getUnitsOnChromosomes -
nbrOfUnits -
plotDensity -

```

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**Description**

Package: aroma.affymetrix

**Class HetLogAddCnPlm**

Object

```

~|
~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--RmaPlm
~~~~~|
~~~~~+--HetLogAddPlm
~~~~~|
~~~~~+--HetLogAddSnpPlm
~~~~~|
~~~~~+--SnpPlm
~~~~~|
~~~~~+--CnPlm
~~~~~|
~~~~~+--HetLogAddCnPlm

```

**Directly known subclasses:**

```

public abstract static class HetLogAddCnPlm
extends CnPlm

```

**Usage**

```
HetLogAddCnPlm(..., combineAlleles=FALSE)
```

**Arguments**

... Arguments passed to [HetLogAddCnPlm](#).  
 combineAlleles If **FALSE**, allele A and allele B are treated separately, otherwise together.

**Fields and Methods**

**Methods:**

*No methods defined.*

**Methods inherited from CnPlm:**

getCellIndices, getChipEffectSet, getCombineAlleles, getParameters, getProbeAffinityFile, setCombineAlleles

**Methods inherited from SnpPlm:**

getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

**Methods inherited from HetLogAddSnpPlm:**

getAsteriskTags

**Methods inherited from HetLogAddPlm:**

getAsteriskTags, getFitUnitGroupFunction

**Methods inherited from RmaPlm:**

getAsteriskTags, getCalculateResidualsFunction, getParameters, getRlmFitFunctions

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Model**

TO DO.

**Author(s)**

Henrik Bengtsson

**Description**

Package: aroma.affymetrix

**Class HetLogAddPlm****Object**

```

~|
~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--RmaPlm
~~~~~|
~~~~~+--HetLogAddPlm

```

**Directly known subclasses:**

*HetLogAddCnPlm*, *HetLogAddSnpPlm*

public abstract static class **HetLogAddPlm**  
 extends *RmaPlm*

This class represents a log-additive model similar to the one described in Irizarry et al (2003), except that the errors may have different variances for different probes.

**Usage**

```
HetLogAddPlm(...)
```

**Arguments**

... Arguments passed to *RmaPlm*.

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from RmaPlm:**

getAsteriskTags, getCalculateResidualsFunction, getParameters, getRlmFitFunctions

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**See Also**

[RmaPlm](#).

---

HetLogAddSnpPlm

*The HetLogAddSnpPlm class*

---

**Description**

Package: aroma.affymetrix

**Class HetLogAddSnpPlm**

Object

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--RmaPlm
~~~~~|
~~~~~+--HetLogAddPlm

```

```

~~~~~|
~~~~~+---SnpP1m
~~~~~|
~~~~~+---HetLogAddSnpP1m

```

**Directly known subclasses:**[HetLogAddCnP1m](#)

```

public abstract static class HetLogAddSnpP1m
extends SnpP1m

```

**Usage**

```
HetLogAddSnpP1m(..., mergeStrands=FALSE)
```

**Arguments**

```

...           Arguments passed to HetLogAddP1m.
mergeStrands If TRUE, the sense and the anti-sense strands are fitted together, otherwise separately.

```

**Fields and Methods****Methods:***No methods defined.***Methods inherited from SnpP1m:**

```
getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands
```

**Methods inherited from HetLogAddP1m:**

```
getAsteriskTags, getFitUnitGroupFunction
```

**Methods inherited from RmaP1m:**

```
getAsteriskTags, getCalculateResidualsFunction, getParameters, getRlmFitFunctions
```

**Methods inherited from ProbeLevelModel:**

```
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet
```

**Methods inherited from MultiArrayUnitModel:**

```
getListOfPriors, setListOfPriors, validate
```

**Methods inherited from UnitModel:**

```
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters
```

**Methods inherited from Model:**

```
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags
```

**Methods inherited from ParametersInterface:**

```
getParameterSets, getParameters, getParametersAsString
```



**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

justRMA

*Robust Multichip Analysis (RMA) reproducing the affy package*

---

**Description**

Robust Multichip Analysis (RMA) reproducing the affy package as far as possible. The RMA method is described in [1].

The algorithm is processed in bounded memory, meaning a very large number of arrays can be analyzed on also very limited computer systems. The only limitation is the amount of memory required to load the final chip-effect estimates into memory (as a [ExpressionSet](#)).

**Usage**

```
## S3 method for class 'AffymetrixCelSet'
justRMA(csR, flavor=c("oligo", "affyPLM"), ..., verbose=FALSE)
## Default S3 method:
justRMA(...)
```

**Arguments**

|         |                                                                                                  |
|---------|--------------------------------------------------------------------------------------------------|
| csR     | An <a href="#">AffymetrixCelSet</a> .                                                            |
| flavor  | A <a href="#">character</a> string specifying the estimators used in the RMA summarization step. |
| ...     | Additional arguments passed to <a href="#">doRMA()</a> used internally.                          |
| verbose | See <a href="#">Verbose</a> .                                                                    |

**Value**

Returns an annotated [ExpressionSet](#).

**Reproducibility of affy**

This implementation of the RMA method reproduces [justRMA](#) in [affy](#) package quite well. It does so by still using a constant memory profile, i.e. it is possible to use this implementation to run RMA on a much large data set than what is possible with [affy](#). At least 20-50 *times* more samples should be doable, if not more.

**Author(s)**

Henrik Bengtsson

**References**[1] Irizarry et al. *Summaries of Affymetrix GeneChip probe level data*. NAR, 2003, 31, e15.**See Also**[doRMA\(\)](#).

---

`LimmaBackgroundCorrection`*The LimmaBackgroundCorrection class*

---

**Description**

Package: aroma.affymetrix

**Class LimmaBackgroundCorrection****Object**

```

~|
~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--BackgroundCorrection
~~~~~|
~~~~~+--LimmaBackgroundCorrection

```

**Directly known subclasses:**[NormExpBackgroundCorrection](#)public static class **LimmaBackgroundCorrection**extends *BackgroundCorrection*

This class represents the various "background" correction methods implemented in the **limma** package.

**Usage**

```
LimmaBackgroundCorrection(..., args=NULL, addJitter=FALSE, jitterSd=0.2, seed=6022007)
```

**Arguments**

|           |                                                                                                                                                                                                                            |
|-----------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ...       | Arguments passed to the constructor of <a href="#">BackgroundCorrection</a> .                                                                                                                                              |
| args      | A <a href="#">list</a> of additional arguments passed to the correction algorithm.                                                                                                                                         |
| addJitter | If <a href="#">TRUE</a> , Zero-mean gaussian noise is added to the signals before being background corrected.                                                                                                              |
| jitterSd  | Standard deviation of the jitter noise added.                                                                                                                                                                              |
| seed      | An (optional) <a href="#">integer</a> specifying a temporary random seed to be used for generating the (optional) jitter. The random seed is set to its original state when done. If <a href="#">NULL</a> , it is not set. |

**Details**

By default, only PM signals are background corrected and MMs are left unchanged.

**Fields and Methods****Methods:**

process -

**Methods inherited from BackgroundCorrection:**

getParameters, process

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Jitter noise**

The fitting algorithm of the normal+exponential background correction model may not converge if there too many small and discrete signals. To overcome this problem, a small amount of noise may be added to the signals before fitting the model. This is an ad hoc solution that seems to work. However, adding Gaussian noise may generate non-positive signals.

**Author(s)**

Henrik Bengtsson. Adopted from RmaBackgroundCorrection by Ken Simpson.

**See Also**

Internally, [backgroundCorrect](#) is used.

---

LinearModelProbeSequenceNormalization

*The LinearModelProbeSequenceNormalization class*

---

**Description**

Package: aroma.affymetrix

**Class LinearModelProbeSequenceNormalization****Object**

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--ProbeLevelTransform3
~~~~~|
~~~~~+--AbstractProbeSequenceNormalization
~~~~~|
~~~~~+--LinearModelProbeSequenceNormalization

```

**Directly known subclasses:**

[BasePositionNormalization](#)

```

public abstract static class LinearModelProbeSequenceNormalization
extends AbstractProbeSequenceNormalization

```

This abstract class represents a normalization method that corrects for systematic effects in the probe intensities due to probe-sequence dependent effects that can be modelled using a linear model.

**Usage**

```
LinearModelProbeSequenceNormalization(...)
```

**Arguments**

... Arguments passed to the constructor of [AbstractProbeSequenceNormalization](#).

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from AbstractProbeSequenceNormalization:**

fitOne, getAromaCellSequenceFile, getParameters, getTargetFile, indexOfMissingSequences, predictOne, process

**Methods inherited from ProbeLevelTransform3:**

getAsteriskTags, getCellsTo, getCellsToFit, getCellsToUpdate, getParameters, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Requirements**

This class requires that an aroma probe sequence file is available for the chip type.

**Memory usage**

The model fitting methods of this class are bounded in memory. This is done by first building up the normal equations incrementally in chunks of cells. The generation of normal equations is otherwise the step that consumes the most memory. When the normal equations are available, the [solve\(\)](#) method is used to solve the equations. Note that this algorithm is still exact.

**Author(s)**

Henrik Bengtsson

---

 MatNormalization      *The MatNormalization class*


---

## Description

Package: aroma.affymetrix

### Class MatNormalization

#### Object

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--ProbeLevelTransform3
~~~~~|
~~~~~+--AbstractProbeSequenceNormalization
~~~~~|
~~~~~+--MatNormalization
  
```

#### Directly known subclasses:

```

public static class MatNormalization
  extends AbstractProbeSequenceNormalization
  
```

This class represents a normalization method that corrects for systematic effects in the probe intensities due to differences in the number of A, C, G, and T:s and the match scores according to MAT [1].

## Usage

```
MatNormalization(..., unitsToFit=NULL, model=c("lm"), nbrOfBins=200)
```

## Arguments

|            |                                                                                                              |
|------------|--------------------------------------------------------------------------------------------------------------|
| ...        | Arguments passed to the constructor of <a href="#">AbstractProbeSequenceNormalization</a> .                  |
| unitsToFit | The units from which the normalization curve should be estimated. If <code>NULL</code> , all are considered. |
| model      | A <a href="#">character</a> string specifying the model used to fit the base-count effects.                  |
| nbrOfBins  | The number of bins to use for the variance smoothing step.                                                   |

**Fields and Methods****Methods:**

process -

**Methods inherited from AbstractProbeSequenceNormalization:**

fitOne, getAromaCellSequenceFile, getParameters, getTargetFile, indexOfMissingSequences, predictOne, process

**Methods inherited from ProbeLevelTransform3:**

getAsteriskTags, getCellsTo, getCellsToFit, getCellsToUpdate, getParameters, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$&lt;-, [], [[&lt;-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Requirements**

This class requires that an aroma probe sequence file and aroma match scores file is available for the chip type.

**Author(s)**

Mark Robinson

**References**

[1] Johnson WE, Li W, Meyer CA, Gottardo R, Carroll JS, Brown M, Liu XS. *Model-based analysis of tiling-arrays for ChIP-chip*, PNAS, 2006.

---

 MatSmoothing

*The MatSmoothing class*


---

## Description

Package: aroma.affymetrix

### Class MatSmoothing

#### Object

```

~|
~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--MatSmoothing
  
```

#### Directly known subclasses:

public static class **MatSmoothing**  
 extends *ProbeLevelTransform*

This class represents a function for smoothing data with a trimmed mean.

## Usage

```
MatSmoothing(..., design=NULL, probeWindow=300, nProbes=10, meanTrim=0.1)
```

## Arguments

|             |                                                                                                                |
|-------------|----------------------------------------------------------------------------------------------------------------|
| ...         | Arguments passed to <i>ProbeLevelTransform</i> .                                                               |
| design      | A design <i>matrix</i> .                                                                                       |
| probeWindow | Bandwidth to use. Effectively the width is 2*probeWindow since it looks probeWindow bases in either direction. |
| nProbes     | The minimum number of probes to calculate a MAT score for.                                                     |
| meanTrim    | The amount of trimming of the mean in [0,0.5].                                                                 |

## Fields and Methods

### Methods:



process -

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$&lt;-, [[, [[&lt;-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Mark Robinson, Henrik Bengtsson

MbeiCnPlm

*The MbeiCnPlm class***Description**

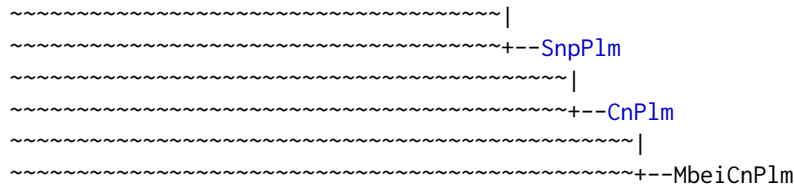
Package: aroma.affymetrix

**Class MbeiCnPlm****Object**

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--MbeiPlm
~~~~~|
~~~~~+--MbeiSnpPlm

```



### Directly known subclasses:

```
public abstract static class MbeiCnPlm
extends CnPlm
```

### Usage

```
MbeiCnPlm(..., combineAlleles=FALSE)
```

### Arguments

```
... Arguments passed to MbeiSnpPlm.
combineAlleles If FALSE, allele A and allele B are treated separately, otherwise together.
```

### Fields and Methods

#### Methods:

*No methods defined.*

#### Methods inherited from CnPlm:

getCellIndices, getChipEffectSet, getCombineAlleles, getParameters, getProbeAffinityFile, setCombineAlleles

#### Methods inherited from SnpPlm:

getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

#### Methods inherited from MbeiSnpPlm:

getAsteriskTags

#### Methods inherited from MbeiPlm:

getAsteriskTags, getFitUnitGroupFunction

#### Methods inherited from ProbeLevelModel:

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

#### Methods inherited from MultiArrayUnitModel:

getListOfPriors, setListOfPriors, validate

#### Methods inherited from UnitModel:

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

MbeiPlm

*The MbeiPlm class*

---

**Description**

Package: aroma.affymetrix

**Class MbeiPlm**

Object

~~|

~~+--ParametersInterface

~~~~~|

~~~~~+--Model

~~~~~|

~~~~~+--UnitModel

~~~~~|

~~~~~+--MultiArrayUnitModel

~~~~~|

~~~~~+--ProbeLevelModel

~~~~~|

~~~~~+--MbeiPlm

**Directly known subclasses:**

*MbeiCnPlm, MbeiSnpPlm*

public abstract static class **MbeiPlm**

extends *ProbeLevelModel*

This class represents the *model-based expression indexes* (MBEI) multiplicative model in Li & Wong (2001).

**Usage**

```
MbeiPlm(...)
```

**Arguments**

... Arguments passed to [ProbeLevelModel](#).

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Model**

For a single unit group, the multiplicative model is:

$$y_{ik} = \theta_i \phi_k + \varepsilon_{ik}$$

where  $\theta_i$  are the chip effects for arrays  $i = 1, \dots, I$ , and  $\phi_k$  are the probe affinities for probes  $k = 1, \dots, K$ . The  $\varepsilon_{ik}$  are zero-mean noise with equal variance. To make parameters identifiable, the constraint  $\prod_k \phi_k = 1$  is added.

**Author(s)**

Henrik Bengtsson

**References**

- Li, C. and Wong, W.H. (2001), *Genome Biology* 2, 1-11.  
 Li, C. and Wong, W.H. (2001), *Proc. Natl. Acad. Sci USA* 98, 31-36.

**See Also**

Internally [fit.li.wong](#) is used.

MbeiSnpPlm

*The MbeiSnpPlm class*

**Description**

Package: aroma.affymetrix

**Class MbeiSnpPlm**

Object

```

~|
~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--MbeiPlm
~~~~~|
~~~~~+--SnpPlm
~~~~~|
~~~~~+--MbeiSnpPlm
    
```

**Directly known subclasses:**

[MbeiCnPlm](#)

public abstract static class **MbeiSnpPlm**  
 extends [SnpPlm](#)

**Usage**

MbeiSnpPlm(..., mergeStrands=FALSE)

**Arguments**

... Arguments passed to [MbeiPlm](#).  
 mergeStrands If **TRUE**, the sense and the anti-sense strands are fitted together, otherwise separately.

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from SnpPIm:**

getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

**Methods inherited from MbeiPIm:**

getAsteriskTags, getFitUnitGroupFunction

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$. \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

Model

*The Model class*

---

**Description**

Package: aroma.affymetrix

**Class Model**

Object

~~|

~~+--ParametersInterface

~~~~~|

~~~~~+--Model

**Directly known subclasses:**

*AffineCnPlm, AffinePlm, AffineSnpPlm, AlleleSummation, AvgCnPlm, AvgPlm, AvgSnpPlm, CrlmModel, ExonRmaPlm, FirmaModel, HetLogAddCnPlm, HetLogAddPlm, HetLogAddSnpPlm, MbeiCnPlm, MbeiPlm, MbeiSnpPlm, MultiArrayUnitModel, ProbeLevelModel, RmaCnPlm, RmaPlm, RmaSnpPlm, SingleArrayUnitModel, UnitModel*

public abstract static class **Model**  
 extends [ParametersInterface](#)

This class is abstract and represents a generic model that applies to a data set.

**Usage**

```
Model(dataSet=NULL, tags="*", ..., .onUnknownArgs=c("error", "warning", "ignore"))
```

**Arguments**

|                |                                                                                                       |
|----------------|-------------------------------------------------------------------------------------------------------|
| dataSet        | The data set to which this model should be fitted.                                                    |
| tags           | A <a href="#">character vector</a> of tags to be appended to the tags of the input data set.          |
| ...            | Not used.                                                                                             |
| .onUnknownArgs | A <a href="#">character</a> string specifying what should occur if there are unknown arguments in ... |

**Fields and Methods****Methods:**

|                 |   |
|-----------------|---|
| fit             | - |
| getAsteriskTags | - |
| getDataSet      | - |
| getFullName     | - |
| getName         | - |
| getPath         | - |
| getTags         | - |
| setTags         | - |

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

MultiArrayUnitModel    *The MultiArrayUnitModel class*


---

**Description**

Package: aroma.affymetrix

**Class MultiArrayUnitModel****Object**

```

~|
~+---ParametersInterface
~~~~~|
~~~~~+---Model
~~~~~|
~~~~~+---UnitModel
~~~~~|
~~~~~+---MultiArrayUnitModel

```

**Directly known subclasses:**

*AffineCnPlm, AffinePlm, AffineSnpPlm, AvgCnPlm, AvgPlm, AvgSnpPlm, ExonRmaPlm, HetLogAddCnPlm, HetLogAddPlm, HetLogAddSnpPlm, MbeiCnPlm, MbeiPlm, MbeiSnpPlm, ProbeLevelModel, RmaCnPlm, RmaPlm, RmaSnpPlm*

```

public abstract static class MultiArrayUnitModel
extends UnitModel

```

This abstract class represents a unit model that fits one model per unit based on signals for all arrays in the data set. The nature of a multi-array unit model is that all arrays must be available at the time of the fit and the estimated parameters will depend on the data from all arrays. Thus, if the signals in one array changes the model has to be refitted.

**Usage**

```
MultiArrayUnitModel(..., listOfPriors=NULL)
```

**Arguments**

```

...           Arguments passed to UnitModel.
listOfPriors  A list of priors to be used when fitting the model.

```



**Fields and Methods**

**Methods:**

```

getListOfPriors -
setListOfPriors -

```

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

NormExpBackgroundCorrection

*The NormExpBackgroundCorrection class*

---

**Description**

Package: aroma.affymetrix

**Class NormExpBackgroundCorrection****Object**

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--BackgroundCorrection
~~~~~|
~~~~~+--LimmaBackgroundCorrection
~~~~~|
~~~~~+--NormExpBackgroundCorrection

```

**Directly known subclasses:**

public static class **NormExpBackgroundCorrection**  
 extends [LimmaBackgroundCorrection](#)

This class represents the normal exponential background correction model. Estimators of the **limma** package is used.

**Usage**

```
NormExpBackgroundCorrection(..., method=c("rma", "saddle", "mle"))
```

**Arguments**

|        |                                                                                                                        |
|--------|------------------------------------------------------------------------------------------------------------------------|
| ...    | Arguments passed to the constructor of <a href="#">LimmaBackgroundCorrection</a> .                                     |
| method | The estimator used, cf. argument normexp.method of <a href="#">backgroundCorrect</a> in <b>limma</b> for more details. |

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from LimmaBackgroundCorrection:**

getAsteriskTags, getParameters, process

**Methods inherited from BackgroundCorrection:**

getParameters, process

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**See Also**

Internally, [backgroundCorrect](#) is used.

---

OpticalBackgroundCorrection

*The OpticalBackgroundCorrection class*

---

**Description**

Package: aroma.affymetrix

**Class OpticalBackgroundCorrection****Object**

```

~|
~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--BackgroundCorrection
~~~~~|
~~~~~+--OpticalBackgroundCorrection

```

**Directly known subclasses:**

```

public static class OpticalBackgroundCorrection
extends BackgroundCorrection

```

This class represents "optical" background adjustment.

**Usage**

```

OpticalBackgroundCorrection(..., minimum=1)

```

**Arguments**

|         |                                                                              |
|---------|------------------------------------------------------------------------------|
| ...     | Arguments passed to the constructor of <a href="#">ProbeLevelTransform</a> . |
| minimum | The minimum signal allowed after adjustment.                                 |

**Fields and Methods**

**Methods:**

process -

**Methods inherited from BackgroundCorrection:**

getParameters, process

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$&lt;-, [], [[&lt;-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Ken Simpson

ParameterCelFile

*The ParameterCelFile class***Description**

Package: aroma.affymetrix

**Class ParameterCelFile****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface

```

```

~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--ParameterCelFile

```

**Directly known subclasses:**

*ChipEffectFile, CnChipEffectFile, CnProbeAffinityFile, ExonChipEffectFile, ExonProbeAffinityFile, FirmaFile, ProbeAffinityFile, ResidualFile, SnpChipEffectFile, SnpProbeAffinityFile, WeightsFile*

```
public abstract static class ParameterCelFile
extends ParametersInterface
```

A ParameterCelFile object represents parameter estimates.

**Usage**

```
ParameterCelFile(..., encodeFunction=NULL, decodeFunction=NULL)
```

**Arguments**

... Arguments passed to [AffymetrixCelFile](#).  
 encodeFunction A [function](#) taking a single [list](#) structure as its argument.  
 decodeFunction A [function](#) taking a single [list](#) structure as its argument.

**Fields and Methods****Methods:**

```
extractDataFrame -
extractMatrix -
readUnits -
```

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelFile:**

allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$. \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

## File format

The idea behind this class is store data fields which by nature have one value per probe (per field) in CEL files. A perfect example is to store probe-affinity estimates and their standard deviations. There is one probe affinity per probe so the structure of a CEL file (and its coupled CDF file) is well suited to read/write such information.

Consider a unit group with L probes. A CEL file stores intensities (L floats), stdvs (L floats), and pixels (L integers). Thus, for each probe  $l=1, \dots, L$ , a (float, float, integer) tuple is stored. We can use this for any information we want. If we want a slightly different structure, we can choose to encode/decode our structure/information to fit the structure of the CEL file. This abstract class provides transparent methods for encoding and decoding such information through methods `encodeUnitGroup()` and `decodeUnitGroup()`. By subclassing you can implement different types of data structures.

## Author(s)

Henrik Bengtsson



---

ParameterCelSet      *The ParameterCelSet class*

---

## Description

Package: aroma.affymetrix

### Class ParameterCelSet

#### Object

```

~|
~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--ParameterCelSet

```

#### Directly known subclasses:

[ChipEffectSet](#), [CnChipEffectSet](#), [ExonChipEffectSet](#), [FirmaSet](#), [SnpChipEffectSet](#)

```
public static class ParameterCelSet
```

```
extends ParametersInterface
```

A ParameterCelSet object represents a set of [ParameterCelFile](#):s.

## Usage

```
ParameterCelSet(...)
```

## Arguments

...                    Arguments passed to [AffymetrixCelSet](#).

## Fields and Methods

### Methods:

```
extractDataFrame -
extractMatrix -
```

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelSet:**

append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUffFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApply, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

 ProbeAffinityFile      *The ProbeAffinityFile class*


---

**Description**

Package: aroma.affymetrix

**Class ProbeAffinityFile****Object**

```

~~|
~~+---FullNameInterface
~~~~~|
~~~~~+---GenericDataFile
~~~~~|
~~~~~+---CacheKeyInterface
~~~~~|
~~~~~+---FileCacheKeyInterface
~~~~~|
~~~~~+---AromaMicroarrayDataFile
~~~~~|
~~~~~+---AromaPlatformInterface
~~~~~|
~~~~~+---AffymetrixFile
~~~~~|
~~~~~+---AffymetrixCelFile
~~~~~|
~~~~~+---ParametersInterface
~~~~~|
~~~~~+---ParameterCelFile
~~~~~|
~~~~~+---ProbeAffinityFile

```

**Directly known subclasses:***CnProbeAffinityFile, ExonProbeAffinityFile, SnpProbeAffinityFile*public abstract static class **ProbeAffinityFile**extends *ParameterCelFile*

This class represents estimates of probe affinities in probe-level models.

**Usage**

```
ProbeAffinityFile(..., probeModel=c("pm", "mm", "pm-mm", "min1(pm-mm)", "pm+mm"))
```

**Arguments**

... Arguments passed to [ParameterCelFile](#).  
 probeModel The specific type of probe model.

**Fields and Methods****Methods:**

readUnits -

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, readUnits

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelFile:**

allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags,

hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**See Also**

An object of this class is typically obtained through the `getProbeAffinityFile()` method for the [ProbeLevelModel](#) class.

---

|                 |                                  |
|-----------------|----------------------------------|
| ProbeLevelModel | <i>The ProbeLevelModel class</i> |
|-----------------|----------------------------------|

---

**Description**

Package: aroma.affymetrix

**Class ProbeLevelModel**

Object

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel

```

**Directly known subclasses:**

*AffineCnPlm, AffinePlm, AffineSnpPlm, AvgCnPlm, AvgPlm, AvgSnpPlm, ExonRmaPlm, HetLogAddCnPlm, HetLogAddPlm, HetLogAddSnpPlm, MbeiCnPlm, MbeiPlm, MbeiSnpPlm, RmaCnPlm, RmaPlm, RmaSnpPlm*

public abstract static class **ProbeLevelModel**

extends *MultiArrayUnitModel*

This abstract class represents a probe-level model (PLM) as defined by the **affyPLM** package: "A [...] PLM is a model that is fit to probe-intensity data. More specifically, it is where we fit a model

with probe level and chip level parameters on a probeset by probeset basis", where the more general case for a probeset is a *unit group* in Affymetrix CDF terms.

### Usage

```
ProbeLevelModel(..., standardize=TRUE)
```

### Arguments

... Arguments passed to `MultiArrayUnitModel`.

standardize If `TRUE`, chip-effect and probe-affinity estimates are rescaled such that the product of the probe affinities is one.

### Details

In order to minimize the risk for mistakes, but also to be able compare results from different PLMs, all PLM subclasses must meet the following criteria:

1. All parameter estimates must be (stored and returned) on the intensity scale, e.g. log-additive models such as `RmaPlm` have to transform the parameters on the log-scale to the intensity scale.
2. The probe-affinity estimates  $\phi_k$  for a unit group must be constrained such that  $\prod_k \phi_k = 1$ , or equivalently if  $\phi_k > 0, \sum_k \log(\phi_k) = 0$ .

Note that the above probe-affinity constraint guarantees that the estimated chip effects across models are on the same scale.

### Fields and Methods

#### Methods:

```
fit -
getChipEffectSet -
getProbeAffinityFile -
getResidualSet -
getWeightsSet -
```

#### Methods inherited from `MultiArrayUnitModel`:

getListOfPriors, setListOfPriors, validate

#### Methods inherited from `UnitModel`:

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

#### Methods inherited from `Model`:

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

#### Methods inherited from `ParametersInterface`:

getParameterSets, getParameters, getParametersAsString

#### Methods inherited from `Object`:

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

### Author(s)

Henrik Bengtsson

### See Also

For more details on probe-level models, please see the **preprocessCore** package.

---

ProbeLevelTransform    *The ProbeLevelTransform class*

---

### Description

Package: aroma.affymetrix

#### Class ProbeLevelTransform

#### Object

```

~~|
~~+---ParametersInterface
~~~~~|
~~~~~+---AromaTransform
~~~~~|
~~~~~+---Transform
~~~~~|
~~~~~+---ProbeLevelTransform

```

#### Directly known subclasses:

*AbstractProbeSequenceNormalization*, *AllelicCrosstalkCalibration*, *BackgroundCorrection*, *BaseCountNormalization*, *BasePositionNormalization*, *DChipQuantileNormalization*, *GcRmaBackgroundCorrection*, *LimmaBackgroundCorrection*, *LinearModelProbeSequenceNormalization*, *MatNormalization*, *MatSmoothing*, *NormExpBackgroundCorrection*, *OpticalBackgroundCorrection*, *ProbeLevelTransform3*, *QuantileNormalization*, *ReseqCrosstalkCalibration*, *RmaBackgroundCorrection*, *ScaleNormalization*, *ScaleNormalization3*, *SpatialRowColumnNormalization*, *UnitTypeScaleNormalization*

```

public abstract static class ProbeLevelTransform
extends Transform

```

This abstract class represents a transformation methods that transforms probe-level signals, typically intensities.

### Usage

```

ProbeLevelTransform(...)

```

**Arguments**

... Arguments passed to the constructor of [Transform](#).

**Details**

Subclasses must implement the `process()` method.

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from Transform:**

`getOutputDataSet`, `getOutputFiles`

**Methods inherited from AromaTransform:**

`as.character`, `findFilesTodo`, `getAsteriskTags`, `getExpectedOutputFiles`, `getExpectedOutputFullnames`, `getFullName`, `getInputDataSet`, `getName`, `getOutputDataSet`, `getOutputDataSet0`, `getOutputFiles`, `getPath`, `getRootPath`, `getTags`, `isDone`, `process`, `setTags`

**Methods inherited from ParametersInterface:**

`getParameterSets`, `getParameters`, `getParametersAsString`

**Methods inherited from Object:**

`$`, `$<-`, `[]`, `[[<-`, `as.character`, `attach`, `attachLocally`, `clearCache`, `clearLookupCache`, `clone`, `detach`, `equals`, `extend`, `finalize`, `getEnvironment`, `getFieldModifier`, `getFieldModifiers`, `getFields`, `getInstantiationTime`, `getStaticInstance`, `hasField`, `hashCode`, `ll`, `load`, `names`, `objectSize`, `print`, `save`, `asThis`

**Author(s)**

Henrik Bengtsson

---

ProbeLevelTransform3 *The ProbeLevelTransform3 class*

---

**Description**

Package: aroma.affymetrix

**Class ProbeLevelTransform3****Object**

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform

```



```

~~~~~|
~~~~~+--ProbeLevelTransform3

```

**Directly known subclasses:**

[AbstractProbeSequenceNormalization](#), [BaseCountNormalization](#), [BasePositionNormalization](#), [LinearModelProbeSequenceNormalization](#), [MatNormalization](#), [ScaleNormalization3](#), [UnitTypeScaleNormalization](#)

```

public abstract static class ProbeLevelTransform3
extends ProbeLevelTransform

```

This abstract class is specialized from [ProbeLevelTransform](#) and provides methods to identify subsets and types of probes that are used for fitting and/or updating the signals.

**Usage**

```

ProbeLevelTransform3(dataSet=NULL, ..., unitsToFit="-XY", typesToFit=typesToUpdate,
unitsToUpdate=NULL, typesToUpdate="pm", shift=0)

```

**Arguments**

|               |                                                                                                              |
|---------------|--------------------------------------------------------------------------------------------------------------|
| dataSet       | A <a href="#">AffymetrixCelSet</a> .                                                                         |
| ...           | Arguments passed to the constructor of <a href="#">ProbeLevelTransform</a> .                                 |
| unitsToFit    | The units from which the normalization curve should be estimated. If <code>NULL</code> , all are considered. |
| typesToFit    | Types of probes to be used when fitting the model.                                                           |
| unitsToUpdate | The units to be updated. If <code>NULL</code> , all are considered.                                          |
| typesToUpdate | Types of probes to be updated.                                                                               |
| shift         | An optional amount to shift data before fitting and updating.                                                |

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

QualityAssessmentFile *The QualityAssessmentFile class*

---

**Description**

Package: aroma.affymetrix

**Class QualityAssessmentFile****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--QualityAssessmentFile

```

**Directly known subclasses:**

```

public abstract static class QualityAssessmentFile
extends AffymetrixCelFile

```

This class represents probe-level QC information (residuals, weights, etc.)

**Usage**

```
QualityAssessmentFile(...)
```

**Arguments**

```
... Arguments passed to AffymetrixCelFile.
```

**Fields and Methods****Methods:**

```
findUnitsTodo -
```

**Methods inherited from AffymetrixCelFile:**

allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Ken Simpson

**See Also**

An object of this class is typically part of a [QualityAssessmentSet](#).

---

QualityAssessmentModel

*The QualityAssessmentModel class*

---

**Description**

Package: aroma.affymetrix

**Class QualityAssessmentModel****Object**

~~|

~~+--QualityAssessmentModel

**Directly known subclasses:**

```
public static class QualityAssessmentModel
  extends Object
```

**Usage**

```
QualityAssessmentModel(plm=NULL, tags="*", ...)
```

**Arguments**

|      |                                             |
|------|---------------------------------------------|
| plm  | A <a href="#">ProbeLevelModel</a> .         |
| tags | A <a href="#">character vector</a> of tags. |
| ...  | Not used.                                   |

**Fields and Methods****Methods:**

```

getChipEffectSet -
getDataSet      -
getFullName     -
getName         -
getPath         -
getPlm         -
getResiduals   -
getTags        -
getWeights     -
nbrOfArrays    -
plotNuse       -
plotRle        -
    
```

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Ken Simpson, Henrik Bengtsson

---

QualityAssessmentSet    *The QualityAssessmentSet class*

---

**Description**

Package: aroma.affymetrix  
**Class QualityAssessmentSet**

```

Object
~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet
~~~~~|
    
```

~~~~~+--QualityAssessmentSet

### Directly known subclasses:

public static class **QualityAssessmentSet**  
 extends [AffymetrixCelSet](#)

### Usage

QualityAssessmentSet(...)

### Arguments

... Arguments passed to constructor of [AffymetrixCelSet](#).

### Fields and Methods

#### Methods:

*No methods defined.*

#### Methods inherited from [AffymetrixCelSet](#):

append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

#### Methods inherited from [AffymetrixFileSet](#):

as, as.AffymetrixFileSet, byPath, getDefaultFullName

#### Methods inherited from [AromaPlatformInterface](#):

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

#### Methods inherited from [AromaMicroarrayDataSet](#):

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

#### Methods inherited from [GenericDataFileSet](#):

[, [, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApply, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep,

resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Ken Simpson

---

QuantileNormalization *The QuantileNormalization class*

---

**Description**

Package: aroma.affymetrix

**Class QuantileNormalization**

**Object**

```

~|
~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--QuantileNormalization

```

**Directly known subclasses:**

[DChipQuantileNormalization](#)

```
public static class QuantileNormalization
```

```
extends ProbeLevelTransform
```

This class represents a normalization function that transforms the probe-level signals towards the same empirical distribution.

**Usage**

```
QuantileNormalization(..., subsetToUpdate=NULL, typesToUpdate=NULL,
  targetDistribution=NULL, subsetToAvg=subsetToUpdate, typesToAvg=typesToUpdate)
```

**Arguments**

... Arguments passed to the constructor of `ProbeLevelTransform`.

subsetToUpdate The probes to be updated. If `NULL`, all probes are updated.

typesToUpdate Types of probes to be updated.

targetDistribution A `numeric vector`. The empirical distribution to which all arrays should be normalized to.

subsetToAvg The probes to calculate average empirical distribution over. If a single `numeric` in (0,1), then this fraction of all probes will be used. If `NULL`, all probes are considered.

typesToAvg Types of probes to be used when calculating the average empirical distribution. If "pm" and "mm" only perfect-match and mismatch probes are used, respectively. If "pmm" both types are used.

**Fields and Methods****Methods:**

process -

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson



**Examples**

```
## Not run:
  for (zzz in 0) {

# Setup verbose output
verbose <- Arguments$getVerbose(-2)
timestampOn(verbose)

# -----
# Define an example dataset
# -----
# Find any dataset
path <- NULL
if (is.null(path))
  break

ds <- AffymetrixCelSet$fromFiles(path)
print(ds)

# -----
# Normalization
# -----
norm <- QuantileNormalization(ds, subsetToAvg=1/3)
dsQN <- process(norm, verbose=verbose)
print(dsQN)

} # for (zzz in 0)
rm(zzz)

## End(Not run)
```

---

ReseqCrosstalkCalibration  
*The ReseqCrosstalkCalibration class*

---

**Description**

Package: aroma.affymetrix  
**Class ReseqCrosstalkCalibration**

Object  
 ~|  
 ~+--ParametersInterface  
 ~~~~~|  
 ~~~~~+--AromaTransform  
 ~~~~~~|  
 ~~~~~~+--Transform

```

~~~~~|
~~~~~+---ProbeLevelTransform
~~~~~|
~~~~~+---ReseqCrosstalkCalibration

```

### Directly known subclasses:

```

public static class ReseqCrosstalkCalibration
extends ProbeLevelTransform

```

This class represents a calibration function that transforms the probe-level signals such that the signals from the four nucleotides (A, C, G, T) are orthogonal.

### Usage

```

ReseqCrosstalkCalibration(dataSet=NULL, ..., targetAvg=2200, subsetToAvg=NULL,
mergeGroups=FALSE, flavor=c("sfit", "expectile"), alpha=c(0.1, 0.075, 0.05, 0.03,
0.01), q=2, Q=98)

```

### Arguments

|             |  |
|-------------|--|
| dataSet     | An <i>AffymetrixCelSet</i> .   |
| ...         | Arguments passed to the constructor of <i>ProbeLevelTransform</i> .  |
| targetAvg   | The signal(s) that the average of the sum of the probe quartets should have after calibration.   |
| subsetToAvg | The indices of the cells (taken as the intersect of existing indices) used to calculate average in order to rescale to the target average. If <i>NULL</i> , all probes are considered. |
| mergeGroups | A <i>logical</i> ...   |
| flavor      | A <i>character</i> string specifying what algorithm is used to fit the crosstalk calibration.  |
| alpha, q, Q | Additional arguments passed to <i>fitMultiDimensionalCone()</i> .  |

### Fields and Methods

#### Methods:

process -

#### Methods inherited from *ProbeLevelTransform*:

getRootPath

#### Methods inherited from *Transform*:

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

 ResidualFile

*The ResidualFile class*


---

**Description**

Package: aroma.affymetrix

**Class ResidualFile****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--ParameterCelFile
~~~~~|

```

~~~~~+---ResidualFile

### Directly known subclasses:

public abstract static class **ResidualFile**  
 extends *ParameterCelFile*

This class represents estimates of residuals in the probe-level models.

### Usage

```
ResidualFile(..., probeModel=c("pm"))
```

### Arguments

... Arguments passed to *ParameterCelFile*.  
 probeModel The specific type of model, e.g. "pm".

### Fields and Methods

#### Methods:

```
findUnitsTodo -  
getImage      -  
readUnits    -  
writeImage   -
```

#### Methods inherited from *ParameterCelFile*:

extractDataFrame, extractMatrix, readUnits

#### Methods inherited from *ParametersInterface*:

getParameterSets, getParameters, getParametersAsString

#### Methods inherited from *AffymetrixCelFile*:

allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

#### Methods inherited from *AromaPlatformInterface*:

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

#### Methods inherited from *AromaMicroarrayDataFile*:

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

#### Methods inherited from *FileCacheKeyInterface*:

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Ken Simpson, Henrik Bengtsson

**See Also**

An object of this class is typically obtained through the `getResidualSet()` method for the [ProbeLevelModel](#) class. An object of this class is typically part of a [ResidualSet](#).

ResidualSet

*The ResidualSet class***Description**

Package: aroma.affymetrix

**Class ResidualSet**

Object

~~|

~~+--FullNameInterface

~~~~~|

~~~~~+--GenericDataFileSet

~~~~~|

```

~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--ResidualSet

```

### Directly known subclasses:

```

public static class ResidualSet
extends ParametersInterface

```

This class represents probe-level residuals from probe-level models.

### Usage

```
ResidualSet(..., probeModel=c("pm"))
```

### Arguments

```

...           Arguments passed to AffymetrixCelSet.
probeModel    The specific type of model, e.g. "pm".

```

### Fields and Methods

#### Methods:

```

findUnitsTodo -
getAverageFile -
getCellIndices -
readUnits -

```

#### Methods inherited from ParametersInterface:

```
getParameterSets, getParameters, getParametersAsString
```

#### Methods inherited from AffymetrixCelSet:

```

append, as, as.AffymetrixCelSet, as.character, averageQuantile,
byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2,
doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet,
extractMatrix, extractSnpFeatureSet, findByName, getAverage,
getAverageAsinh, getAverageFile, getAverageLog, getCdf,
getChipType, getData, getIntensities, getPlatform, getTimestamps,

```

getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUffFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApply, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Ken Simpson, Henrik Bengtsson

**See Also**

An object of this class is typically obtained through the `getResidualSet()` method for the [ProbeLevelModel](#) class.

---

RmaBackgroundCorrection

*The RmaBackgroundCorrection class*


---

## Description

Package: aroma.affymetrix

### Class RmaBackgroundCorrection

#### Object

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--BackgroundCorrection
~~~~~|
~~~~~+--RmaBackgroundCorrection

```

#### Directly known subclasses:

public static class **RmaBackgroundCorrection**

extends *BackgroundCorrection*

This class represents the RMA background adjustment function.

## Usage

```
RmaBackgroundCorrection(..., addJitter=FALSE, jitterSd=0.2, seed=6022007)
```

## Arguments

|           |  |
|-----------|--|
| ...       | Arguments passed to the constructor of <i>BackgroundCorrection</i> .   |
| addJitter | If <b>TRUE</b> , Zero-mean gaussian noise is added to the signals before being background corrected.   |
| jitterSd  | Standard deviation of the jitter noise added.  |
| seed      | An (optional) <b>integer</b> specifying a temporary random seed to be used for generating the (optional) jitter. The random seed is set to its original state when done. If <b>NULL</b> , it is not set. |



**Details**

Internally `bg.adjust` is used to background correct the probe signals. The default is to background correct PM signals only.

**Fields and Methods****Methods:**

process -

**Methods inherited from BackgroundCorrection:**

getParameters, process

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Jitter noise**

The fitting algorithm of the RMA background correction model may not converge if there too many small and discrete signals. To overcome this problem, a small amount of noise may be added to the signals before fitting the model. This is an ad hoc solution that seems to work. However, add Gaussian noise may generate non-positive signals.

**Author(s)**

Ken Simpson, Henrik Bengtsson

RmaCnPlm

*The RmaCnPlm class***Description**

Package: aroma.affymetrix

**Class RmaCnPlm****Object**

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--RmaPlm
~~~~~|
~~~~~+--RmaSnpPlm
~~~~~|
~~~~~+--SnpPlm
~~~~~|
~~~~~+--CnPlm
~~~~~|
~~~~~+--RmaCnPlm

```

**Directly known subclasses:**

```

public abstract static class RmaCnPlm
extends CnPlm

```

**Usage**

```
RmaCnPlm(..., combineAlleles=FALSE)
```

**Arguments**

```

...           Arguments passed to RmaSnpPlm.
combineAlleles If FALSE, allele A and allele B are treated seperately, otherwise together.

```

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from CnPlm:**

getCellIndices, getChipEffectSet, getCombineAlleles, getParameters, getProbeAffinityFile, setCombineAlleles

**Methods inherited from SnpPlm:**

getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

**Methods inherited from RmaSnpPlm:**

getAsteriskTags

**Methods inherited from RmaPlm:**

getAsteriskTags, getCalculateResidualsFunction, getParameters, getRlmFitFunctions

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Model**

TO DO.

**Author(s)**

Henrik Bengtsson

RmaPlm

*The RmaPlm class***Description**

Package: aroma.affymetrix

**Class RmaPlm****Object**

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--RmaPlm

```

**Directly known subclasses:**

*ExonRmaPlm, HetLogAddCnPlm, HetLogAddPlm, HetLogAddSnpPlm, RmaCnPlm, RmaSnpPlm*

```

public abstract static class RmaPlm
extends ProbeLevelModel

```

This class represents the log-additive model part of the Robust Multichip Analysis (RMA) method described in Irizarry et al (2003).

**Usage**

```
RmaPlm(..., flavor=c("affyPLM", "oligo"))
```

**Arguments**

|        |   |
|--------|---|
| ...    | Arguments passed to <a href="#">ProbeLevelModel</a> .   |
| flavor | A <a href="#">character</a> string specifying what model fitting algorithm to be used. This makes it possible to get identical estimates as other packages. |

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Model**

For a single unit group, the log-additive model of RMA is:

$$\log_2(y_{ik}) = \beta_i + \alpha_k + \varepsilon_{ik}$$

where  $\beta_i$  are the chip effects for arrays  $i = 1, \dots, I$ , and  $\alpha_k$  are the probe affinities for probes  $k = 1, \dots, K$ . The  $\varepsilon_{ik}$  are zero-mean noise with equal variance. The model is constrained such that  $\sum_k \alpha_k = 0$ .

Note that all PLM classes must return parameters on the intensity scale. For this class that means that  $\theta_i = 2^{\beta_i}$  and  $\phi_k = 2^{\alpha_k}$  are returned.

**Different flavors of model fitting**

There are a few differ algorithms available for fitting the same probe-level model. The default and recommended method (`flavor="affyPLM"`) uses the implementation in the **preprocessCore** package which fits the model parameters robustly using an M-estimator (the method used to be in **affyPLM**).

Alternatively, other model-fitting algorithms are available. The algorithm (`flavor="oligo"`) used by the **oligo** package, which originates from the **affy** packages, fits the model using median polish, which is a non-robust estimator. Note that this algorithm does not constraint the probe-effect parameters to multiply to one on the intensity scale. Since the internal function does not return these estimates, we can neither rescale them.

**Author(s)**

Henrik Bengtsson, Ken Simpson

## References

Irizarry et al. *Summaries of Affymetrix GeneChip probe level data*. NAR, 2003, 31, e15.

---

RmaSnpP1m

*The RmaSnpP1m class*

---

## Description

Package: aroma.affymetrix

### Class RmaSnpP1m

#### Object

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--Model
~~~~~|
~~~~~+--UnitModel
~~~~~|
~~~~~+--MultiArrayUnitModel
~~~~~|
~~~~~+--ProbeLevelModel
~~~~~|
~~~~~+--RmaP1m
~~~~~|
~~~~~+--SnpP1m
~~~~~|
~~~~~+--RmaSnpP1m

```

#### Directly known subclasses:

[RmaCnP1m](#)

public abstract static class **RmaSnpP1m**

extends [SnpP1m](#)

## Usage

```
RmaSnpP1m(..., mergeStrands=FALSE)
```

## Arguments

... Arguments passed to [RmaP1m](#).

mergeStrands If **TRUE**, the sense and the anti-sense strands are fitted together, otherwise separately.

**Fields and Methods****Methods:***No methods defined.***Methods inherited from SnpPIm:**

getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

**Methods inherited from RmaPIm:**

getAsteriskTags, getCalculateResidualsFunction, getParameters, getRlmFitFunctions

**Methods inherited from ProbeLevelModel:**

calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

**Methods inherited from MultiArrayUnitModel:**

getListOfPriors, setListOfPriors, validate

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$&lt;-, [], [[&lt;-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

ScaleNormalization      *The ScaleNormalization class*


---

**Description**

Package: aroma.affymetrix

**Class ScaleNormalization****Object**

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform

```

```

~~~~~|
~~~~~+---ProbeLevelTransform
~~~~~|
~~~~~+---ScaleNormalization

```

### Directly known subclasses:

```

public static class ScaleNormalization
extends ProbeLevelTransform

```

This class represents a normalization function that transforms the probe-level signals towards the same scale.

### Usage

```

ScaleNormalization(dataSet=NULL, ..., targetAvg=4400, subsetToUpdate=NULL,
  typesToUpdate=NULL, subsetToAvg="-XY", typesToAvg=typesToUpdate, shift=0)

```

### Arguments

|                |   |
|----------------|---|
| dataSet        | <a href="#">AffymetrixCelSet</a> to be normalized.  |
| ...            | Arguments passed to the constructor of <a href="#">ProbeLevelTransform</a> .  |
| targetAvg      | A <a href="#">numeric</a> value.  |
| subsetToUpdate | The probes to be updated. If <code>NULL</code> , all probes are updated.  |
| typesToUpdate  | Types of probes to be updated.  |
| subsetToAvg    | The probes to calculate average signal over. If a single <a href="#">numeric</a> in (0,1), then this fraction of all probes will be used. If <code>NULL</code> , all probes are considered. |
| typesToAvg     | Types of probes to be used when calculating the average signal. If "pm" and "mm" only perfect-match and mismatch probes are used, respectively. If "pmmm" both types are used.              |
| shift          | Optional amount of shift if data before fitting/normalizing.  |

### Fields and Methods

#### Methods:

process -

#### Methods inherited from [ProbeLevelTransform](#):

getRootPath

#### Methods inherited from [Transform](#):

getOutputDataSet, getOutputFiles



**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

ScaleNormalization3    *The ScaleNormalization3 class*

---

**Description**

Package: aroma.affymetrix

**Class ScaleNormalization3****Object**

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|
~~~~~+--ProbeLevelTransform3
~~~~~|
~~~~~+--ScaleNormalization3

```

**Directly known subclasses:**

```

public static class ScaleNormalization3
extends ProbeLevelTransform3

```

This class represents a normalization function that transforms the probe-level signals towards the same scale.

**Usage**

```
ScaleNormalization3(..., targetAvg=4400)
```

**Arguments**

... Arguments passed to the constructor of `ProbeLevelTransform3`.  
 targetAvg A numeric value.

**Fields and Methods****Methods:**

```
process -
```

**Methods inherited from ProbeLevelTransform3:**

getAsteriskTags, getCellsTo, getCellsToFit, getCellsToUpdate, getParameters, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

**Methods inherited from ProbeLevelTransform:**

getRootPath

**Methods inherited from Transform:**

getOutputDataSet, getOutputFiles

**Methods inherited from AromaTransform:**

as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**Description**

Package: aroma.affymetrix

**Class SingleArrayUnitModel**

Object

~~|

~~+--ParametersInterface

~~~~~|

~~~~~+--Model

~~~~~|

~~~~~+--UnitModel

~~~~~|

~~~~~+--SingleArrayUnitModel

**Directly known subclasses:**

public abstract static class **SingleArrayUnitModel**  
extends *UnitModel*

This abstract class represents a unit model that fits one model per unit based on signals from a single arrays. The nature of a single-array unit model is that each array can be fitted independently of the others.

**Usage**

SingleArrayUnitModel(...)

**Arguments**

... Arguments passed to *UnitModel*.

**Fields and Methods****Methods:**

fit -

**Methods inherited from UnitModel:**

findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

**Methods inherited from Model:**

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRoot-Path, getTags, setAlias, setTags

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from Object:**

\$, \$<-, [], [<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

SmoothMultiarrayModel *The SmoothMultiarrayModel class*

---

**Description**

Package: aroma.affymetrix

**Class SmoothMultiarrayModel****Object**

```

~~|
~~+--ChromosomalModel
~~~~~|
~~~~~+--SmoothMultiarrayModel

```

**Directly known subclasses:**

*SmoothRmaModel*, *SmoothSaModel*

public abstract static class **SmoothMultiarrayModel**  
 extends *ChromosomalModel*

This abstract class represents a chromosomal smoothing method done chromosome by chromosome.

**Usage**

```
SmoothMultiarrayModel(..., typeOfWeights=c("none", "1/s2"), bandwidth=10000, tags="*")
```

**Arguments**

|               |   |
|---------------|---|
| ...           | Arguments passed to the constructor of <i>ChromosomalModel</i> .                    |
| typeOfWeights | A <b>character</b> string.  |
| bandwidth     | A single <b>numeric</b> specifying the smoothing bandwidth in units of nucleotides. |
| tags          | A <b>character vector</b> of tags to be added.                                      |

**Fields and Methods****Methods:**

```

getBandwidth -
getOutputTuple -
setBandwidth -

```

**Methods inherited from ChromosomalModel:**

as.character, fit, getAlias, getAromaGenomeTextFile, getAsteriskTags, getChipType, getChipTypes, getChromosomes, getFullName, getFullNames, getGenome, getGenomeData, getGenomeFile, getListOfAromaUgpFiles, getName, getNames, getParentPath, getPath, getReportPath, getRootPath, getSetTuple, getSets, getTags, indexOf, nbrOfArrays, nbrOfChipTypes, setChromosomes, setGenome, getListOfGenomeInformations, getPcuTheta, getPositionChipTypeUnit

**Methods inherited from Object:**

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

**See Also**

[CopyNumberSegmentationModel](#).

---

SmoothRmaModel

*The SmoothRmaModel class*

---

**Description**

Package: aroma.affymetrix

**Class SmoothRmaModel****Object**

```

~~|
~~+--ChromosomalModel
~~~~~|
~~~~~+--SmoothMultiarrayModel
~~~~~|
~~~~~+--SmoothRmaModel

```

**Directly known subclasses:**

```

public abstract static class SmoothRmaModel
extends SmoothMultiarrayModel

```

This class represents the Chromosomal Smoothing Robust Multichip Analysis method.

**Usage**

```
SmoothRmaModel(...)
```

**Arguments**

... Arguments passed to the constructor of [SmoothMultiarrayModel](#).

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from SmoothMultiarrayModel:**

as.character, createOutputTuple, fitOneChromosome, getAsteriskTags, getBandwidth, getFitUnitGroupFunction, getOutputTuple, getRootPath, setBandwidth

**Methods inherited from ChromosomalModel:**

as.character, fit, getAlias, getAromaGenomeTextFile, getAsteriskTags, getChipType, getChipTypes, getChromosomes, getFullName, getFullNames, getGenome, getGenomeData, getGenomeFile, getListOfAromaUgpFiles, getName, getNames, getParentPath, getPath, getReportPath, getRootPath, getSetTuple, getSets, getTags, indexOf, nbrOfArrays, nbrOfChipTypes, setChromosomes, setGenome, getListOfGenomeInformations, getPcuTheta, getPositionChipTypeUnit

**Methods inherited from Object:**

\$. \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

SnpChipEffectFile      *The SnpChipEffectFile class*

---

**Description**

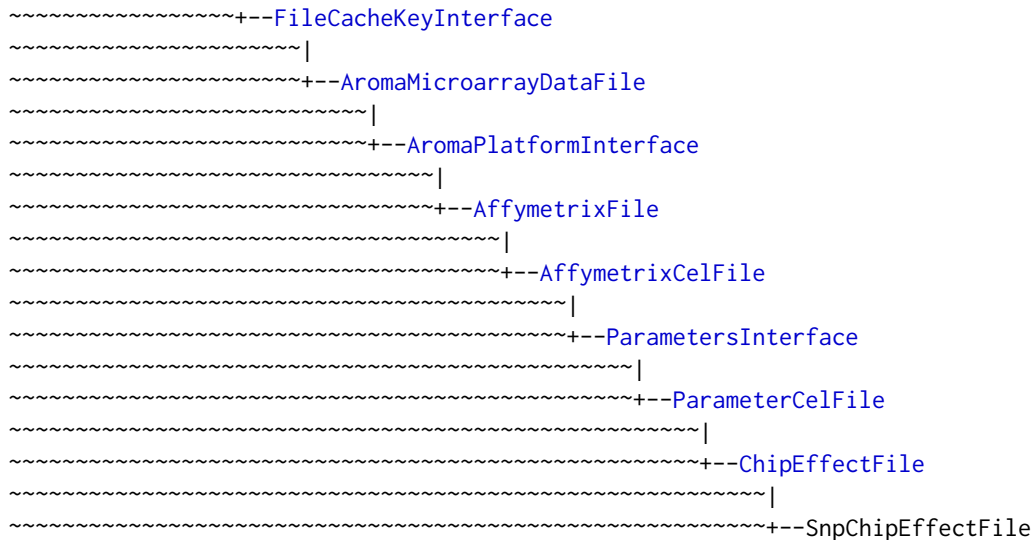
Package: aroma.affymetrix

**Class SnpChipEffectFile****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|

```



**Directly known subclasses:**

*CnChipEffectFile*

public abstract static class **SnpChipEffectFile**  
 extends *ChipEffectFile*

This class represents estimates of chip effects in the probe-level models.

**Usage**

SnpChipEffectFile(..., mergeStrands=FALSE)

**Arguments**

- ... Arguments passed to *ChipEffectFile*.
- mergeStrands Specifies if the strands are merged or not for these estimates.

**Fields and Methods**

**Methods:**

- extractTheta -
- extractTotalAndFracB -
- readUnits -

**Methods inherited from ChipEffectFile:**

as.character, extractChromosomalDataFrame, extractMatrix, extractTheta, findUnitsTodo, getAM, getAsFullCelFile, getCellIndices, getCellMapForMainCdf, getExpandedCellMap, getParameters,

getUnitGroupCellArrayMap, getUnitGroupCellMatrixMap, getXAM, mergeGroups, readUnits, writeAsFullCelFile

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, readUnits

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelFile:**

allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson



**See Also**

An object of this class is typically part of a [SnpChipEffectSet](#).

SnpChipEffectSet      *The SnpChipEffectSet class*

**Description**

Package: aroma.affymetrix

**Class SnpChipEffectSet**

**Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--ParameterCelSet
~~~~~|
~~~~~+--ChipEffectSet
~~~~~|
~~~~~+--SnpChipEffectSet
    
```

**Directly known subclasses:**

[CnChipEffectSet](#)

public static class **SnpChipEffectSet**

extends [ChipEffectSet](#)

This class represents estimates of chip effects in the probe-level models.

**Usage**

SnpChipEffectSet(..., mergeStrands="byFirstFile")

**Arguments**

- ... Arguments passed to [ChipEffectSet](#).
- mergeStrands Specifies if the strands are merged or not for these estimates.

**Fields and Methods****Methods:**

```

extractAlleleSet -
extractSnpCnvQSet -
extractSnpQSet -
extractTheta -
extractTotalAndFreqB -
getAverageFile -
getMergeStrands -
setMergeStrands -

```

**Methods inherited from ChipEffectSet:**

as.character, boxplotStats, byPath, calculateBaseline, calculateFieldBoxplotStats, calculateNuseBoxplotStats, calculateRleBoxplotStats, extractAffyBatch, extractChromosomalDataFrame, extractExpressionSet, extractMatrix, extractTheta, findByName, findUnitsTodo, fromDataSet, getAM, getAsFullCelSet, getAverageFile, getBaseline, getCellIndices, getXAM, plotBoxplot, readUnits, updateUnits

**Methods inherited from ParameterCelSet:**

extractDataFrame, extractMatrix

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelSet:**

append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApply, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

SnpInformation

*The SnpInformation class*

---

**Description**

Package: aroma.affymetrix

**Class SnpInformation****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|

```

~~~~~+--SnpInformation

**Directly known subclasses:**

*DChipSnpInformation, UflSnpInformation*

public abstract static class **SnpInformation**  
 extends [FileCacheKeyInterface](#)

**Usage**

SnpInformation(...)

**Arguments**

... Arguments passed to [GenericDataFile](#).

**Fields and Methods**

**Methods:**

|                    |   |
|--------------------|---|
| byChipType         | - |
| getChipType        | - |
| getData            | - |
| getFragmentLengths | - |
| getFragmentStarts  | - |
| getFragmentStops   | - |
| nrOfEnzymes        | - |
| nrOfUnits          | - |
| readDataFrame      | - |

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTab-

ularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

SnpPlm

*The SnpPlm interface class*

---

**Description**

Package: aroma.affymetrix

**Class SnpPlm**

**Interface**

```
~~|
~~+--SnpPlm
```

**Directly known subclasses:**

*AffineCnPlm, AffineSnpPlm, AvgCnPlm, AvgSnpPlm, CnPlm, HetLogAddCnPlm, HetLogAddSnpPlm, MbeiCnPlm, MbeiSnpPlm, RmaCnPlm, RmaSnpPlm*

```
public class SnpPlm
```

```
extends Interface
```

An [Interface](#) implementing methods special for [ProbeLevelModels](#) specific to SNP arrays.

**Usage**

```
SnpPlm(...)
```

**Arguments**

```
...          Not used.
```

**Methods**

**Methods:**

```

getCellIndices      -
getChipEffectSet    -
getMergeStrands     -
getProbeAffinityFile -
setMergeStrands     -

```

### Methods inherited from Interface:

extend, print, uses

### Requirements

Classes inheriting from this [Interface](#) must provide the following fields:

- mergeStrandsA [logical](#) value indicating if strands should be merged or not.

### Author(s)

Henrik Bengtsson

### Examples

```

for (zzz in 0) {

# Setup verbose output
verbose <- Arguments$getVerbose(-2)
timestampOn(verbose)

# -----
# Define an example dataset using this path
# -----
# Find any SNP dataset
path <- NULL
if (is.null(path))
  break

if (!exists("ds")) {
  ds <- AffymetrixCelSet$fromFiles(path)
}
print(ds)

# -----
# Create a set of various PLMs for this dataset
# -----
if (!exists("models", mode="list")) {
  mergeStrands <- TRUE
  models <- list(
    rma = RmaSnpPlm(ds, mergeStrands=mergeStrands),
    mbei = MbeiSnpPlm(ds, mergeStrands=mergeStrands)
  # affine = AffineSnpPlm(ds, background=FALSE, mergeStrands=mergeStrands)
  )
}
}

```

```

}
print(models)

# -----
# For each model, fit a few units
#
# Note, by fitting the same set of units across models, the internal
# caching mechanisms of aroma.affymetrix makes sure that the data is
# only read into memory once. See log for reading speed.
# -----
units <- 55+1:100

for (model in models) {
  ruler(verbose)
  fit(model, units=units, force=TRUE, verbose=verbose)
}

# -----
# For each unit, plot the estimated (thetaB,thetaA) for all models
# -----
# Should we plot the on the log scale?
log <- TRUE

# Do only user to press ENTER if more than one unit is plotted
opar <- par(ask=(length(units) > 1))

Alab <- expression(theta[A])
Blab <- expression(theta[B])
if (log) {
  lim <- c(6, 16)
} else {
  lim <- c(0, 2^15)
}

# For each unit...
for (unit in units) {
  # For all models...
  for (kk in seq_along(models)) {
    ces <- getChipEffects(models[[kk]])
    ceUnit <- ces[unit]
    snpName <- names(ceUnit)[1]
    theta <- ceUnit[[1]]
    thetaA <- theta[[1]]$theta
    thetaB <- theta[[2]]$theta
    if (log) {
      thetaA <- log(thetaA, base=2)
      thetaB <- log(thetaB, base=2)
    }

    # Create the plot?
    if (kk == 1) {
      plot(NA, xlim=lim, ylim=lim, xlab=Blab, ylab=Alab, main=snpName)
    }
  }
}

```



```

    abline(a=0, b=1, lty=2)
  }

  # Plot the estimated parameters
  points(thetaB, thetaA, col=kk, pch=19)
}
} # for (unit ...)

# Reset graphical parameter settings
par(opar)

} # for (zzz in 0)
rm(zzz)

```

SnpProbeAffinityFile *The SnpProbeAffinityFile class*

**Description**

Package: aroma.affymetrix  
**Class SnpProbeAffinityFile**

**Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--ParameterCelFile
~~~~~|
~~~~~+--ProbeAffinityFile
~~~~~|
~~~~~+--SnpProbeAffinityFile

```

**Directly known subclasses:***CnProbeAffinityFile*

public abstract static class **SnpProbeAffinityFile**  
 extends *ProbeAffinityFile*

This class represents estimates of probe affinities in SNP probe-level models.

**Usage**

```
SnpProbeAffinityFile(..., mergeStrands=FALSE)
```

**Arguments**

... Arguments passed to *ProbeAffinityFile*.  
 mergeStrands Specifies if the strands are merged or not for these estimates.

**Fields and Methods****Methods:**

*No methods defined.*

**Methods inherited from ProbeAffinityFile:**

as.character, getCellIndices, getParameters, readUnits

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, readUnits

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelFile:**

allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern,

getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

SpatialReporter

*The SpatialReporter class*

---

**Description**

Package: aroma.affymetrix

**Class SpatialReporter**

**Object**

```

~~|
~~+--GenericReporter
~~~~~|
~~~~~+--AffymetrixFileSetReporter
~~~~~|
~~~~~+--AffymetrixCelSetReporter
~~~~~|
~~~~~+--SpatialReporter

```

**Directly known subclasses:**

public abstract static class **SpatialReporter**  
 extends *AffymetrixCelSetReporter*

A SpatialReporter generates image files of spatial representations of cell signals for each of the arrays in the input set.

### Usage

```
SpatialReporter(..., reference=NULL)
```

### Arguments

... Arguments passed to [AffymetrixCelSetReporter](#).  
reference An optional reference [AffymetrixCelFile](#).

### Fields and Methods

#### Methods:

```
addColorMap -
getColorMaps -
plotMargins -
process -
setColorMaps -
```

#### Methods inherited from AffymetrixCelSetReporter:

as.character, getChipType, getDataSet, getPath, nbrOfArrays

#### Methods inherited from AffymetrixFileSetReporter:

getFileSet, getInputName, getInputTags

#### Methods inherited from GenericReporter:

as.character, getAlias, getAsteriskTags, getFullName, getInputName, getInputTags, getMainPath, getName, getPath, getReportSet, getRootPath, getTags, process, setAlias, setup

#### Methods inherited from Object:

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

### Author(s)

Henrik Bengtsson

**Description**

Package: aroma.affymetrix

**Class TransformReport****Object**

~~|

~~+--TransformReport

**Directly known subclasses:**

public static class **TransformReport**

extends [Object](#)

**Usage**

TransformReport(inSet=NULL, outSet=NULL, ...)

**Arguments**

|        |                                                              |
|--------|--------------------------------------------------------------|
| inSet  | The input data set as an <a href="#">AffymetrixCelSet</a> .  |
| outSet | The output data set as an <a href="#">AffymetrixCelSet</a> . |
| ...    | Not used.                                                    |

**Fields and Methods****Methods:**

|                    |   |
|--------------------|---|
| getCdf             | - |
| getFullName        | - |
| getInputDataSet    | - |
| getName            | - |
| getOutputDataSet   | - |
| getPath            | - |
| getTags            | - |
| getUnitNamesFile   | - |
| getUnitTypesFile   | - |
| getYY              | - |
| nbrOfArrays        | - |
| plotXYCurve        | - |
| plotXYCurveLog2    | - |
| seq                | - |
| writeImageCombined | - |
| writeImages        | - |

**Methods inherited from Object:**

\$, \$<-, [], [<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson

---

UgpGenomeInformation    *The UgpGenomeInformation class*

---

**Description**

Package: aroma.affymetrix

**Class UgpGenomeInformation**

Object

```

~|
~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--GenomeInformation
~~~~~|
~~~~~+--UgpGenomeInformation

```

**Directly known subclasses:**

```

public abstract static class UgpGenomeInformation
extends GenomeInformation

```

This class represents Aroma UGP genome information files.

**Usage**

```

UgpGenomeInformation(..., .ugp=NULL, .verify=TRUE)

```

**Arguments**

|         |                                                         |
|---------|---------------------------------------------------------|
| ...     | Arguments passed to <a href="#">GenomeInformation</a> . |
| .ugp    | For internal use only.                                  |
| .verify | For internal use only.                                  |

**Fields and Methods****Methods:**

|                      |   |
|----------------------|---|
| byChipType           | - |
| getChipType          | - |
| getChromosomes       | - |
| getData              | - |
| getUnitsOnChromosome | - |
| isCompatibleWithCdf  | - |
| nrOfUnits            | - |
| readDataFrame        | - |

**Methods inherited from GenomeInformation:**

as.character, byChipType, fromCdf, fromDataSet, getChipType, getChromosomeStats, getChromosomes, getData, getPositions, getUnitIndices, getUnitsOnChromosome, getUnitsOnChromosomes, isCompatibleWithCdf, nrOfUnits, plotDensity, readDataFrame, verify

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach,

equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

### Author(s)

Henrik Bengtsson

---

UnitModel

*The UnitModel class*

---

### Description

Package: aroma.affymetrix

#### Class UnitModel

Object

```

~|
~+---ParametersInterface
~~~~~|
~~~~~+---Model
~~~~~|
~~~~~+---UnitModel

```

#### Directly known subclasses:

*AffineCnPlm, AffinePlm, AffineSnpPlm, AlleleSummation, AvgCnPlm, AvgPlm, AvgSnpPlm, ExonRmaPlm, FirmaModel, HetLogAddCnPlm, HetLogAddPlm, HetLogAddSnpPlm, MbeiCnPlm, MbeiPlm, MbeiSnpPlm, MultiArrayUnitModel, ProbeLevelModel, RmaCnPlm, RmaPlm, RmaSnpPlm, SingleArrayUnitModel*

```

public abstract static class UnitModel
extends Model

```

This class is abstract and represents a generic unit model, i.e. a model that is applied to each unit separately.

### Usage

```

UnitModel(dataSet=NULL, probeModel=c("pm", "mm", "pm-mm", "min1(pm-mm)", "pm+mm"),
  shift=0, ...)

```

### Arguments

dataSet            An *AffymetrixCelSet* to which this model should be fitted.

probeModel        A *character* string specifying how PM and MM values should be modelled. By default only PM signals are used.



shift            An optional amount the signals should be shifted (translated) before fitting the model.

...              Arguments passed to the constructor of [Model](#).

## Fields and Methods

### Methods:

findUnitsTodo -

### Methods inherited from Model:

as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

### Methods inherited from ParametersInterface:

getParameterSets, getParameters, getParametersAsString

### Methods inherited from Object:

\$, \$<-, [], [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

## Author(s)

Henrik Bengtsson

---

UnitTypeScaleNormalization

*The UnitTypeScaleNormalization class*

---

## Description

Package: aroma.affymetrix

### Class UnitTypeScaleNormalization

#### Object

```

~~|
~~+--ParametersInterface
~~~~~|
~~~~~+--AromaTransform
~~~~~|
~~~~~+--Transform
~~~~~|
~~~~~+--ProbeLevelTransform
~~~~~|

```

```

~~~~~+---ProbeLevelTransform3
~~~~~|
~~~~~+---UnitTypeScaleNormalization

```

### Directly known subclasses:

```

public static class UnitTypeScaleNormalization
extends ProbeLevelTransform3

```

This class represents a normalization function that transforms the probe signals such that each unit type gets the same average.

### Usage

```
UnitTypeScaleNormalization(..., targetAvg=4400)
```

### Arguments

```

...           Arguments passed to the constructor of ProbeLevelTransform3.
targetAvg     A numeric value.

```

### Fields and Methods

#### Methods:

```
process -
```

#### Methods inherited from *ProbeLevelTransform3*:

```
getAsteriskTags, getCellsTo, getCellsToFit, getCellsToUpdate, getParameters, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals
```

#### Methods inherited from *ProbeLevelTransform*:

```
getRootPath
```

#### Methods inherited from *Transform*:

```
getOutputDataSet, getOutputFiles
```

#### Methods inherited from *AromaTransform*:

```
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags
```

#### Methods inherited from *ParametersInterface*:

```
getParameterSets, getParameters, getParametersAsString
```

#### Methods inherited from *Object*:

```
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis
```

**Author(s)**

Henrik Bengtsson

WeightsFile

*The WeightsFile class***Description**

Package: aroma.affymetrix

**Class WeightsFile****Object**

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFile
~~~~~|
~~~~~+--CacheKeyInterface
~~~~~|
~~~~~+--FileCacheKeyInterface
~~~~~|
~~~~~+--AromaMicroarrayDataFile
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFile
~~~~~|
~~~~~+--AffymetrixCelFile
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--ParameterCelFile
~~~~~|
~~~~~+--WeightsFile

```

**Directly known subclasses:**

```

public abstract static class WeightsFile
extends ParameterCelFile

```

This class represents weights calculated from residuals of probe-level models.

**Usage**

```

WeightsFile(..., probeModel=c("pm"))

```

**Arguments**

... Arguments passed to [ParameterCelFile](#).  
 probeModel The specific type of model, e.g. "pm".

**Fields and Methods****Methods:**

```

findUnitsTodo -
getImage      -
readUnits     -
writeImage    -

```

**Methods inherited from ParameterCelFile:**

extractDataFrame, extractMatrix, readUnits

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelFile:**

allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataFile:**

getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

**Methods inherited from FileCacheKeyInterface:**

getCacheKey

**Methods inherited from CacheKeyInterface:**

getCacheKey

**Methods inherited from GenericDataFile:**

as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBychar-

acter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

#### Methods inherited from Object:

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

#### Author(s)

Henrik Bengtsson, Ken Simpson

#### See Also

An object of this class is typically obtained through the `getWeightsSet()` method for the [ProbeLevelModel](#) class. An object of this class is typically part of a [WeightsSet](#).

---

WeightsSet

*The WeightsSet class*

---

#### Description

Package: aroma.affymetrix

#### Class WeightsSet

##### Object

```

~~|
~~+--FullNameInterface
~~~~~|
~~~~~+--GenericDataFileSet
~~~~~|
~~~~~+--AromaMicroarrayDataSet
~~~~~|
~~~~~+--AromaPlatformInterface
~~~~~|
~~~~~+--AffymetrixFileSet
~~~~~|
~~~~~+--AffymetrixCelSet
~~~~~|
~~~~~+--ParametersInterface
~~~~~|
~~~~~+--WeightsSet

```

**Directly known subclasses:**

public static class **WeightsSet**  
 extends [ParametersInterface](#)

This class represents probe-level weights.

**Usage**

```
WeightsSet(..., probeModel=c("pm"))
```

**Arguments**

... Arguments passed to [AffymetrixCelSet](#).  
 probeModel The specific type of model, e.g. "pm".

**Fields and Methods****Methods:**

```
findUnitsTodo -
getAverageFile -
getCellIndices -
readUnits -
```

**Methods inherited from ParametersInterface:**

getParameterSets, getParameters, getParametersAsString

**Methods inherited from AffymetrixCelSet:**

append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

**Methods inherited from AffymetrixFileSet:**

as, as.AffymetrixFileSet, byPath, getDefaultFullName

**Methods inherited from AromaPlatformInterface:**

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

**Methods inherited from AromaMicroarrayDataSet:**

as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

**Methods inherited from GenericDataFileSet:**

[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApply, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

**Methods inherited from FullNameInterface:**

appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

**Methods inherited from Object:**

\$, \$<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

**Author(s)**

Henrik Bengtsson, Ken Simpson

**See Also**

An object of this class is typically obtained through the `getWeightsSet()` method for the [ProbeLevelModel](#) class.

# Index

## \*Topic **IO**

ParameterCelFile, [150](#)  
ParameterCelSet, [153](#)

## \*Topic **classes**

AbstractProbeSequenceNormalization, [6](#)  
AdditiveCovariatesNormalization, [7](#)  
AffineCnPlm, [10](#)  
AffinePlm, [12](#)  
AffineSnpPlm, [14](#)  
AffymetrixCdfFile, [15](#)  
AffymetrixCelFile, [18](#)  
AffymetrixCelSet, [21](#)  
AffymetrixCelSetReporter, [24](#)  
AffymetrixCelSetTuple, [25](#)  
AffymetrixCnChpSet, [26](#)  
AffymetrixFile, [28](#)  
AffymetrixFileSet, [30](#)  
AffymetrixFileSetReporter, [32](#)  
AffymetrixPgffFile, [33](#)  
AlleleSummation, [36](#)  
AllelicCrosstalkCalibration, [37](#)  
AromaChipTypeAnnotationFile, [39](#)  
ArrayExplorer, [41](#)  
AvgCnPlm, [43](#)  
AvgPlm, [45](#)  
AvgSnpPlm, [47](#)  
BackgroundCorrection, [48](#)  
BaseCountNormalization, [50](#)  
BasePositionNormalization, [52](#)  
ChipEffectFile, [53](#)  
ChipEffectSet, [56](#)  
ChipEffectTransform, [58](#)  
CnagCfhFile, [60](#)  
CnagCfhSet, [63](#)  
CnChipEffectFile, [64](#)  
CnChipEffectSet, [67](#)  
CnPlm, [70](#)  
CnProbeAffinityFile, [72](#)

CrlmmParametersFile, [74](#)  
CrlmmParametersSet, [76](#)  
DChipCdfBinFile, [78](#)  
DChipDcpFile, [80](#)  
DChipDcpSet, [83](#)  
DChipGenomeInformation, [85](#)  
DChipQuantileNormalization, [87](#)  
DChipSnpInformation, [88](#)  
ExonChipEffectFile, [96](#)  
ExonChipEffectSet, [99](#)  
ExonProbeAffinityFile, [101](#)  
ExonRmaPlm, [104](#)  
FirmaFile, [106](#)  
FirmaModel, [108](#)  
FirmaSet, [109](#)  
FragmentEquivalentClassNormalization, [112](#)  
FragmentLengthNormalization, [113](#)  
GcContentNormalization, [115](#)  
GcContentNormalization2, [117](#)  
GcRmaBackgroundCorrection, [119](#)  
GenericReporter, [121](#)  
GenomeInformation, [122](#)  
HetLogAddCnPlm, [123](#)  
HetLogAddPlm, [125](#)  
HetLogAddSnpPlm, [127](#)  
LimmaBackgroundCorrection, [130](#)  
LinearModelProbeSequenceNormalization, [132](#)  
MatNormalization, [134](#)  
MatSmoothing, [136](#)  
MbeiCnPlm, [137](#)  
MbeiPlm, [139](#)  
MbeiSnpPlm, [141](#)  
Model, [142](#)  
MultiArrayUnitModel, [144](#)  
NormExpBackgroundCorrection, [146](#)  
OpticalBackgroundCorrection, [148](#)  
ParameterCelFile, [150](#)



- ParameterCelSet, 153
- ProbeAffinityFile, 155
- ProbeLevelModel, 157
- ProbeLevelTransform, 159
- ProbeLevelTransform3, 160
- QualityAssessmentFile, 162
- QualityAssessmentModel, 164
- QualityAssessmentSet, 165
- QuantileNormalization, 167
- ReseqCrosstalkCalibration, 169
- ResidualFile, 171
- ResidualSet, 173
- RmaBackgroundCorrection, 176
- RmaCnPlm, 178
- RmaPlm, 180
- RmaSnPPlm, 182
- ScaleNormalization, 183
- ScaleNormalization3, 185
- SingleArrayUnitModel, 186
- SmoothMultiarrayModel, 188
- SmoothRmaModel, 189
- SnPChipEffectFile, 190
- SnPChipEffectSet, 193
- SnPInformation, 195
- SnPPlm, 197
- SnPProbeAffinityFile, 201
- SpatialReporter, 203
- TransformReport, 204
- UgpGenomeInformation, 206
- UnitModel, 208
- UnitTypeScaleNormalization, 209
- WeightsFile, 211
- WeightsSet, 213
- \*Topic **methods**
  - justRMA, 129
- \*Topic **package**
  - aroma.affymetrix-package, 4
- \*byChipType, 86, 89
- \*getCdf, 20
- AbstractProbeSequenceNormalization, 6, 50–52, 132–134, 159, 161
- AdditiveCovariatesNormalization, 7, 59, 117, 118
- AffineCnPlm, 10, 12, 14, 70, 143, 144, 157, 197, 208
- AffinePlm, 10, 12, 14, 15, 143, 144, 157, 208
- AffineSnPPlm, 11, 12, 14, 143, 144, 157, 197, 208
- AffymetrixCdfFile, 15, 19, 20, 29, 40, 60, 120
- AffymetrixCelFile, 18, 21, 23, 29, 54, 65, 72, 97, 102, 106, 107, 151, 155, 162, 163, 171, 191, 201, 204, 211
- AffymetrixCelSet, 21, 21, 31, 38, 42, 56, 57, 68, 91–93, 95, 96, 99, 110, 129, 153, 161, 165, 166, 170, 174, 184, 193, 205, 208, 213, 214
- AffymetrixCelSetReporter, 24, 32, 121, 203, 204
- AffymetrixCelSetTuple, 25
- AffymetrixCnChpFile, 27–29
- AffymetrixCnChpSet, 26, 31
- AffymetrixCsvGenomeInformation, 122
- AffymetrixFile, 16, 19, 28, 31, 34, 40, 54, 60, 65, 72, 79, 81, 97, 102, 106, 151, 155, 162, 171, 191, 201, 211
- AffymetrixFileSet, 21, 27, 30, 30, 33, 56, 68, 83, 99, 110, 153, 165, 174, 193, 213
- AffymetrixFileSetReporter, 24, 32, 121, 203
- AffymetrixPgffFile, 29, 33, 40
- AffymetrixTsvFile, 29
- AlleleSummation, 36, 143, 208
- AllelicCrosstalkCalibration, 37, 159
- aroma.affymetrix
  - (aroma.affymetrix-package), 4
- aroma.affymetrix-package, 4
- AromaCellSequenceFile, 7
- AromaChipTypeAnnotationFile, 16, 29, 34, 39
- AromaMicroarrayDataFile, 16, 19, 29, 33, 40, 54, 60, 65, 72, 78, 81, 97, 102, 106, 150, 155, 162, 171, 191, 201, 211
- AromaMicroarrayDataSet, 21, 27, 30, 56, 67, 83, 99, 110, 153, 165, 174, 193, 213
- AromaMicroarrayDataSetTuple, 25
- AromaPlatformInterface, 16, 19, 21, 27, 29–31, 34, 40, 54, 56, 60, 65, 68, 72, 74, 78, 81, 83, 97, 99, 102, 106, 110, 150, 153, 155, 162, 165, 171, 174, 191, 193, 201, 211, 213
- AromaTabularBinaryFile, 74
- AromaTabularBinarySet, 77
- AromaTransform, 6, 8, 37, 48, 50, 52, 58, 87,

- 112, 114, 116, 117, 119, 130, 132, 134, 136, 146, 148, 159, 160, 167, 169, 176, 183, 185, 209*  
 AromaUnitSignalBinaryFile, *74, 75*  
 AromaUnitSignalBinarySet, *77*  
 ArrayExplorer, *41*  
 AvgCnPlm, *43, 45, 47, 70, 143, 144, 157, 197, 208*  
 AvgPlm, *43, 45, 47, 143, 144, 157, 208*  
 AvgSnpPlm, *43–45, 47, 143, 144, 157, 197, 208*  
  
 backgroundCorrect, *132, 147, 148*  
 BackgroundCorrection, *48, 119, 130, 131, 146, 148, 159, 176*  
 BaseCountNormalization, *6, 50, 159, 161*  
 BasePositionNormalization, *6, 52, 132, 159, 161*  
 bg.adjust, *177*  
  
 CacheKeyInterface, *16, 18, 29, 33, 40, 54, 60, 65, 72, 74, 78, 81, 85, 89, 97, 102, 106, 122, 150, 155, 162, 171, 190, 195, 201, 206, 211*  
 character, *6, 8, 38, 45, 51, 52, 92, 93, 95, 109, 114, 121, 129, 134, 143, 164, 170, 180, 188, 208*  
 ChipEffectFile, *19, 29, 53, 65, 97, 151, 191*  
 ChipEffectGroupMerge, *59*  
 ChipEffectSet, *21, 31, 56, 56, 59, 68, 91, 93, 95, 96, 99, 100, 153, 193, 194*  
 ChipEffectSetTuple, *25*  
 ChipEffectTransform, *8, 58, 112, 114, 116, 117*  
 ChromosomalModel, *188, 189*  
 CnagCfhFile, *29, 60, 63, 64*  
 CnagCfhSet, *62, 63*  
 CnChipEffectFile, *19, 29, 54, 64, 151, 191*  
 CnChipEffectSet, *21, 31, 56, 67, 67, 112, 116, 153, 193*  
 CnChipEffectSetTuple, *25*  
 CnPlm, *11, 43, 70, 124, 138, 178, 197*  
 CnProbeAffinityFile, *19, 29, 72, 151, 155, 202*  
 ColumnNamesInterface, *74*  
 CopyNumberDataFile, *65*  
 CopyNumberDataSet, *68*  
 CopyNumberSegmentationModel, *189*  
 CrImmModel, *143*  
 CrImmParametersFile, *74, 77*  
  
 CrImmParametersSet, *76*  
  
 DChipCdfBinFile, *29, 78*  
 DChipDcpFile, *29, 80, 83, 84*  
 DChipDcpSet, *31, 82, 83*  
 DChipGenomeInformation, *85, 122*  
 DChipQuantileNormalization, *87, 159, 167*  
 DChipSnpInformation, *88, 196*  
 doASCRMAv1 (doCRMAv1), *90*  
 doASCRMAv2 (doCRMAv2), *92*  
 doCRMAv1, *90, 93*  
 doCRMAv2, *92, 92*  
 doFIRMA, *93*  
 doGCRMA, *94*  
 doRMA, *95, 129, 130*  
  
 ExonChipEffectFile, *19, 29, 54, 96, 151*  
 ExonChipEffectSet, *21, 31, 56, 99, 99, 153*  
 ExonProbeAffinityFile, *19, 29, 101, 151, 155*  
 ExonRmaPlm, *104, 143, 144, 157, 180, 208*  
 Explorer, *42*  
 ExpressionSet, *129*  
  
 FALSE, *11, 13, 44, 73, 95, 96, 124, 138, 178*  
 FileCacheKeyInterface, *16, 19, 29, 33, 40, 54, 60, 65, 72, 74, 78, 81, 85, 89, 97, 102, 106, 122, 150, 155, 162, 171, 191, 195, 196, 201, 206, 211*  
 FirmaFile, *19, 29, 106, 151*  
 FirmaModel, *93, 108, 143, 208*  
 FirmaSet, *21, 31, 94, 108, 109, 153*  
 fit.li.wong, *141*  
 fitPLM, *95*  
 FragmentEquivalentClassNormalization, *59, 112*  
 FragmentLengthNormalization, *59, 91, 92, 113*  
 FullNameInterface, *16, 18, 21, 25, 26, 28, 30, 33, 40, 53, 56, 60, 63, 65, 67, 72, 74, 76, 78, 80, 83, 85, 88, 97, 99, 102, 106, 110, 122, 150, 153, 155, 162, 165, 171, 173, 190, 193, 195, 201, 206, 211, 213*  
 function, *8, 112, 114, 116, 151*  
  
 GcContentNormalization, *59, 115*  
 GcContentNormalization2, *8, 59, 117*  
 gcrma, *94*

- GcRmaBackgroundCorrection, 49, 95, 119, 159
- GenericDataFile, 16, 18, 28, 29, 33, 40, 53, 60, 65, 72, 74, 78, 81, 85, 89, 97, 102, 106, 122, 150, 155, 162, 171, 190, 195, 196, 201, 206, 211
- GenericDataFileSet, 21, 26, 30, 31, 56, 63, 67, 76, 83, 99, 110, 153, 165, 173, 193, 213
- GenericDataFileSetList, 25
- GenericReporter, 24, 32, 33, 121, 203
- GenericTabularFile, 74
- GenericTabularFileSet, 77
- GenomeInformation, 85, 122, 206, 207
- HetLogAddCnPlm, 70, 123, 124, 126, 128, 143, 144, 157, 180, 197, 208
- HetLogAddPlm, 124, 125, 127, 128, 143, 144, 157, 180, 208
- HetLogAddSnplm, 124, 126, 127, 143, 144, 157, 180, 197, 208
- integer, 38, 91, 92, 95, 96, 120, 131, 176
- Interface, 70, 71, 197, 199
- justRMA, 129, 129
- LimmaBackgroundCorrection, 49, 130, 146, 147, 159
- LinearModelProbeSequenceNormalization, 6, 52, 132, 159, 161
- list, 21, 27, 31, 63, 83, 91–96, 131, 144, 151
- logical, 66, 68, 71, 91, 92, 104, 170, 199
- MatNormalization, 6, 134, 159, 161
- matrix, 136
- MatSmoothing, 136, 159
- MbeiCnPlm, 70, 137, 139, 141, 143, 144, 157, 197, 208
- MbeiPlm, 13, 137, 139, 141, 143, 144, 157, 208
- MbeiSnplm, 137–139, 141, 143, 144, 157, 197, 208
- Model, 10, 12, 14, 36, 43, 45, 47, 104, 108, 124, 126, 127, 137, 139, 141, 142, 144, 157, 178, 180, 182, 187, 208, 209
- MultiArrayUnitModel, 10, 12, 14, 43, 45, 47, 104, 124, 126, 127, 137, 139, 141, 143, 144, 157, 158, 178, 180, 182, 208
- NormExpBackgroundCorrection, 49, 130, 146, 159
- NULL, 6, 8, 19, 38, 49, 91, 92, 95, 96, 112, 114, 116, 119, 120, 131, 134, 161, 168, 170, 176, 184
- numeric, 91, 92, 114, 120, 168, 184, 186, 188, 210
- Object, 6, 7, 10, 12, 14, 16, 18, 21, 24–26, 28, 30, 32, 33, 36, 37, 40, 41, 43, 45, 47, 48, 50, 52, 53, 56, 58, 60, 63, 65, 67, 72, 74, 76, 78, 80, 83, 85, 87, 88, 97, 99, 102, 104, 106, 108, 110, 112, 114, 116, 117, 119, 121, 122, 124, 126, 127, 130, 132, 134, 136, 137, 139, 141, 142, 144, 146, 148, 150, 153, 155, 157, 159, 160, 162, 164, 165, 167, 169, 171, 173, 176, 178, 180, 182, 183, 185, 187–190, 193, 195, 201, 203, 205, 206, 208, 209, 211, 213
- OpticalBackgroundCorrection, 49, 120, 148, 159
- ParameterCelFile, 19, 29, 54, 65, 72, 97, 102, 106, 150, 153, 155, 156, 171, 172, 191, 201, 211, 212
- ParameterCelSet, 21, 31, 56, 68, 99, 110, 153, 193
- ParametersInterface, 6, 8, 10, 12, 14, 36, 37, 43, 45, 47, 48, 50, 52, 54, 56, 58, 65, 68, 72, 87, 97, 99, 102, 104, 106, 108, 110, 112, 114, 116, 117, 119, 124, 126, 127, 130, 132, 134, 136, 137, 139, 141–144, 146, 148, 151, 153, 155, 157, 159, 160, 167, 169, 171, 174, 176, 178, 180, 182, 183, 185, 187, 191, 193, 201, 208, 209, 211, 213, 214
- ProbeAffinityFile, 19, 29, 72, 102, 151, 155, 201, 202
- ProbeLevelModel, 10, 12–14, 43, 45, 47, 56, 58, 104, 124, 126, 127, 137, 139–141, 143, 144, 157, 157, 164, 173, 175, 178, 180, 182, 197, 208, 213, 215
- ProbeLevelTransform, 6, 37, 38, 49, 50, 52, 87, 119, 130, 132, 134, 136, 146,

- 148, 159, 160, 161, 167, 168, 170,  
 176, 184, 185, 209  
 ProbeLevelTransform3, 6, 50, 52, 132, 134,  
 159, 160, 185, 186, 210  
 QualityAssessmentFile, 19, 29, 162  
 QualityAssessmentModel, 164  
 QualityAssessmentSet, 21, 31, 164, 165  
 QuantileNormalization, 87, 159, 167  
 ReseqCrosstalkCalibration, 159, 169  
 ResidualFile, 19, 29, 151, 171  
 ResidualSet, 21, 31, 173, 173  
 RmaBackgroundCorrection, 49, 159, 176  
 RmaCnPlm, 70, 143, 144, 157, 178, 180, 182,  
 197, 208  
 RmaPlm, 96, 104, 105, 124, 126, 127, 143, 144,  
 157, 158, 178, 180, 182, 208  
 RmaSnpPlm, 143, 144, 157, 178, 180, 182, 197,  
 208  
 ScaleNormalization, 159, 183  
 ScaleNormalization3, 159, 161, 185  
 SingleArrayUnitModel, 143, 186, 208  
 SmoothMultiarrayModel, 188, 189, 190  
 SmoothRmaModel, 188, 189  
 SmoothSaModel, 188  
 SnpChipEffectFile, 19, 29, 54, 65, 66, 151,  
 190  
 SnpChipEffectGroupMerge, 59  
 SnpChipEffectSet, 8, 21, 31, 36, 56, 68, 114,  
 153, 193, 193  
 SnpInformation, 89, 195  
 SnpPlm, 11, 14, 43, 47, 70, 71, 124, 128, 138,  
 141, 178, 182, 197  
 SnpProbeAffinityFile, 19, 29, 72, 73, 151,  
 155, 201  
 solve, 133  
 SpatialReporter, 24, 32, 121, 203  
 SpatialRowColumnNormalization, 159  
 Transform, 6, 8, 37, 49, 50, 52, 58, 59, 87,  
 112, 114, 116, 117, 119, 130, 132,  
 134, 136, 146, 148, 159, 160, 167,  
 169, 176, 183, 185, 209  
 TransformReport, 204  
 TRUE, 13, 15, 36, 38, 47, 51, 87, 91, 92, 94–96,  
 120, 128, 131, 141, 158, 176, 182  
 UflSnpInformation, 196  
 UgpGenomeInformation, 122, 206  
 UnitAnnotationDataFile, 16, 34, 79  
 UnitModel, 10, 12, 14, 36, 43, 45, 47, 104,  
 108, 109, 124, 126, 127, 137, 139,  
 141, 143, 144, 157, 178, 180, 182,  
 187, 208  
 UnitNamesFile, 16, 34, 79  
 UnitTypeScaleNormalization, 159, 161,  
 209  
 UnitTypesFile, 16, 34  
 vector, 91, 92, 95, 96, 114, 120, 121, 143,  
 164, 168, 188  
 Verbose, 91, 92, 94–96, 129  
 WeightsFile, 19, 29, 151, 211  
 WeightsSet, 21, 31, 213, 213