

Getting started with the biogas package

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1 Introduction

Anaerobic digestion is a popular technology for production of renewable energy and stabilisation of organic wastes, and research on the topic is carried out in laboratories in many countries. Transformation of raw data collected in laboratory experiments into quantities and rates of methane (CH_4) production requires a sequence of simple calculations. Although conceptually simple, these steps are time-consuming, and seldom described in detail in publications, so results may not be reproducible among laboratories or experiments. We developed the biogas package to address these issues. This document provides a brief introduction to the biogas package for new users. We have assumed that readers are familiar with biogas data collection and R.

2 Overview of functions

The package includes seven “low-level” functions (Table 1) and three “high-level” functions (Table 2). To go from data collected in the laboratory to biogas and methane (CH_4) production or biochemical methane potential (BMP), two high-level functions are needed: `cumBg()` and `summBg()`. Comparing results to theory is facilitated by the remaining high-level function: `predBg()`. The low-level functions support the calculations carried out by the high-level functions, and may also be useful for some simple operations (e.g., converting reported biogas volumes to different standard conditions). This document describes the use of the high-level functions.

Table 1: Operations done with the low-level functions in the biogas package. All functions are vectorized. See help files for more details.

Operation	Function
Standardise gas volume	<code>stdVol()</code>
Interpolate composition etc.	<code>interp()</code>
Calculate oxygen demand of a compound	<code>calcCOD()</code>
Calculate molar mass of a compound	<code>molMass()</code>
Calculate biogas volume from mass loss	<code>mass2vol()</code>
Calculate mass loss from biogas volume	<code>vol2mass()</code>
Convert gas volume to moles	<code>vol2mol()</code>

Table 2: Operations done with the high-level functions in the biogas package. The `cumBg()` and `summBg()` functions can handle data from any number of reactors. `predBg()` is vectorized.

Operation	Function
Calculate cumulative CH ₄ production and rates from volume (mass), composition	<code>cumBg()</code>
Calculate biochemical methane potential, summarise cumulative production or rates	<code>summBg()</code>
Predict biogas production based on substrate composition	<code>predBg()</code>

3 An example: calculation and prediction of biochemical methane potential

Calculation of biochemical methane potential (BMP) typically requires three data frames: initial mass, biogas quantity (volume, pressure, or bottle mass loss), and biogas composition. Input data may be structured in one of three ways: “long”, “wide”, or “combined”. In a “long” format (`data.struct = 'long'`, the default), the measured variable (e.g., biogas volume) is in a single column (Fig. 1). In this case columns with unique reactor IDs and time allow the `biogas` functions to link observations in the two data frames¹. Any order of observations can be used in input data frames.

Reactor ID	Time	Response variable (volume or mass)
R1	1	$y_{1,1}$
R2	1	$y_{2,1}$
...
R_n	1	$y_{i,1}$
R1	2	$y_{1,2}$
R2	2	$y_{2,2}$
R_n	2	$y_{i,2}$
...
R_n	t_k	$y_{n,k}$

Reactor ID	Time	Response variable (Composition)
R1	2	$y_{1,2}$
R2	2	$y_{2,2}$
...
R_n	2	$y_{n,2}$
...
R_n	t_k	$y_{n,k}$

Figure 1: General structure of time-dependent data frames for the `dat` (left) and `comp` (right) arguments to the `cumBg()` function.

The third data frame on initial conditions is used by the `summBg()` function. It should contain at least a reactor ID column and a description of the reactor contents. If the contribution of an inoculum is to be subtracted (as in the BMP test), the mass of inoculum added should be included here. Any measurements to be used to normalise biogas or CH₄ production are included here, using a “wide” format (Fig. 2). Note that there is no time column in this data frame—these values are independent of time.

With the “wide” data structure (`data.struct = 'wide'`) the biogas quantity data frame contains a separate column for each bottle. And in the “combined” option (`data.struct = 'longcombo'`) a single data frame contains both biogas quantity and composition in a “long” structure.

¹ But observations need not be for the same times. Interpolation by `interp` takes care of this. Note that the time columns can be date/time objects as well as numeric or integer.

Reactor ID	Description	Substrate VS mass	Inoculum total mass	...
R1	Substrate A	10.2	302	...
R2	Substrate A	9.85	301	...
R3	Substrate A	10.3	298	...
R4	Substrate B	8.5	300	...
...
R6	Inoculum only		502	...
...
R _n

Figure 2: General structure of initial conditions data frame for the `setup` argument to the `summBg()` function.

In this example, we will use the example data sets included with the package: `vol` for biogas volumes, `comp` for composition, and `setup` for grouping and substrate and inoculum masses. These data are from a BMP test that was carried out on two different substrates A and B, and cellulose (included as a “control”). The experiment included 12 batch reactors:

- 3 reactors with substrate A and inoculum
- 3 reactors with substrate B and inoculum
- 3 reactors with cellulose and inoculum
- 3 reactors with inoculum only

Reactors consisted of 500 mL or 1.0 L glass bottles, and were sealed with a butyl rubber septum and a screw cap. Initial substrate and inoculum masses were determined. A typical volumetric method was used to measure biogas production: accumulated biogas was measured and removed intermittently using syringes, and composition was measured for some of these samples.

```
library(biogas)

data("vol")

dim(vol)

## [1] 288  4

head(vol)

##      id      date.time days vol
## 1 2_1 2014-06-07 13:00:00 1.98 393
## 2 2_1 2014-06-08 13:00:00 2.98 260
## 3 2_1 2014-06-09 13:00:00 3.98 245
## 4 2_1 2014-06-10 13:00:00 4.98 225
## 5 2_1 2014-06-11 13:00:00 5.98 200
## 6 2_1 2014-06-12 14:00:00 7.02 175

summary(vol)
```

```
##          id          date.time          days
## 2_1      : 24    Min.      :2014-06-07 13:00:00    Min.      : 1.98
## 2_2      : 24    1st Qu.:2014-06-14 02:00:00    1st Qu.: 8.52
## 2_3      : 24    Median  :2014-06-28 12:00:00    Median : 22.94
## 2_4      : 24    Mean     :2014-07-16 21:29:22    Mean     : 41.33
## 2_5      : 24    3rd Qu.:2014-07-26 04:45:00    3rd Qu.: 50.63
## 2_6      : 24    Max.      :2014-12-19 10:30:00    Max.      :196.92
## (Other):144
##          vol
## Min.      : 98.0
## 1st Qu.:171.5
## Median :225.0
## Mean      :271.7
## 3rd Qu.:300.0
## Max.      :840.0
##
```

```
data("comp")
```

```
dim(comp)
```

```
## [1] 132 4
```

```
head(comp)
```

```
##          id          date.time  days      xCH4
## 516 2_1 2014-06-12 14:00:00  7.02 0.7104731
## 519 2_1 2014-06-19 14:00:00 14.02 0.7024937
## 522 2_1 2014-06-26 11:00:00 20.90 0.6659919
## 524 2_1 2014-07-03 10:00:00 27.85 0.6789466
## 525 2_1 2014-07-10 09:00:00 34.81 0.6951429
## 528 2_1 2014-07-24 10:00:00 48.85 0.6693053
```

```
summary(comp)
```

```
##          id          date.time          days
## 2_1      :11    Min.      :2014-06-12 14:00:00    Min.      : 7.02
## 2_2      :11    1st Qu.:2014-06-26 11:00:00    1st Qu.: 20.90
## 2_3      :11    Median  :2014-07-24 10:00:00    Median : 48.85
## 2_4      :11    Mean     :2014-07-31 13:47:43    Mean     : 56.01
## 2_5      :11    3rd Qu.:2014-08-28 10:00:00    3rd Qu.: 83.85
## 2_6      :11    Max.      :2014-10-13 13:00:00    Max.      :129.98
## (Other):66
##          xCH4
## Min.      :0.5647
## 1st Qu.:0.6393
## Median :0.6598
## Mean      :0.6587
## 3rd Qu.:0.6786
## Max.      :0.7115
##
```

```
data("setup")
```

```
setup
```

```
##      id descrip  msub  minoc    mvs.sub mvs.inoc  mcod.sub mcod.inoc
## 1  2_1      A 178.96 328.82  3.839567 12.92268  5.527522 19.09109
## 5  2_2      A 178.58 350.90  3.831414 13.79043  5.515785 20.37305
## 6  2_3      A 178.58 326.61  3.831414 12.83583  5.515785 18.96278
## 7  2_4      B  40.21 465.32  5.333816 18.28716  8.325115 27.01620
## 8  2_5      B  40.04 461.90  5.311266 18.15275  8.289918 26.81764
## 9  2_6      B  40.13 475.61  5.323204 18.69156  8.308551 27.61363
## 10 2_7  cellu   5.75 500.94  5.507470 19.68703  7.762500 29.08428
## 11 2_8  cellu   5.76 498.10  5.517048 19.57542  7.776000 28.91939
## 12 2_9  cellu   5.71 504.65  5.469157 19.83283  7.708500 29.29968
## 2  2_10  inoc 501.50 501.50 19.709037 19.70904 29.116792 29.11679
## 3  2_11  inoc 502.27 502.27 19.739298 19.73930 29.161498 29.16150
## 4  2_12  inoc 502.12 502.12 19.733403 19.73340 29.152789 29.15279
##      m.tot  mvs.tot mcod.tot
## 1  657.78 16.76225 24.61862
## 5  679.79 17.62184 25.88883
## 6  654.68 16.66724 24.47857
## 7  655.22 23.62097 35.34132
## 8  652.56 23.46402 35.10756
## 9  665.76 24.01476 35.92219
## 10 656.68 25.19450 36.84678
## 11 653.02 25.09246 36.69539
## 12 659.28 25.30199 37.00818
## 2  652.07 19.70904 29.11679
## 3  752.37 19.73930 29.16150
## 4  650.66 19.73340 29.15279
```

3.1 Cumulative production

The first step in processing these data is to calculate cumulative production of biogas and CH₄ and production rates. We can do this with the `cumBg()` function, using `vol` and `comp` data frames as input. The arguments for the function are:

```
args(cumBg)
```

```
## function (dat, dat.type = "vol", comp = NULL, temp = NULL, pres = NULL,
##      interval = TRUE, data.struct = "long", id.name = "id", time.name = "time",
##      dat.name = dat.type, comp.name = "xCH4", pres.resid = NULL,
##      temp.init = NULL, pres.init = NULL, rh.resid.init = 1, headspace = NULL,
##      vol.hs.name = "vol.hs", headcomp = "N2", absolute = TRUE,
##      pres.amb = NULL, mol.f.name = NULL, vol.syr = NULL, cmethod = "removed",
##      imethod = "linear", extrap = FALSE, addt0 = TRUE, showt0 = TRUE,
##      dry = FALSE, std.message = TRUE, check = TRUE, temp.std = getOption("temp.std",
##      0), pres.std = getOption("pres.std", 1), unit.temp = getOption("unit.temp",
##      "C"), unit.pres = getOption("unit.pres", "atm"))
## NULL
```

Most of the arguments have default values, but to calculate CH₄ production we must provide values for at least **dat** (we will use **vol**), **comp** (we will use **comp**), **temp** (biogas temperature), and **pres** (biogas pressure)², along with the names of a few columns in our input data frames. We need to specify the name of the time column in **vol** and **comp** using the **time.name** argument. This name must be the same in both data frames. Similarly, there is an **id.name** argument for the reactor ID column (used to match up volume and composition data), but we can use the default value ("id") here because it matches the column name in **vol** and **comp**. And, the **comp.name** argument is used to indicate which column within the **comp** data frame contains the CH₄ content (as mole fraction in dry biogas, normalised so the sum of mole fractions of CH₄ and CO₂ sum to unity). We can use the default ("xCH4") because it matches the name in **comp**. Lastly, the name of the column that contains the response variable in the **dat** data frame (**vol** here) can be specified with the **dat.name** argument. Here too we can use the default ("vol" for volumetric measurements or "mass" for gravimetric). By default (**cmethod** = "removed") the function calculates volumes following [2] as the product of standardised volume of biogas removed and normalised CH₄ content.

```
cum.prod <- cumBg(vol, comp = comp, time.name = "days", temp = 35, pres = 1,
                  extrap = TRUE)

## Biogas composition is interpolated.
## Working with volume data, applying volumetric method.
## Using a standard pressure of 1 atm and standard temperature of 0 C for standardizing
## volume.
```

Note the message about standard temperature and pressure—it is important to make sure these values are correct, therefore users are reminded by a message³. The output looks like this:

```
head(cum.prod)

##      id      date.time days vol      xCH4 temperature pressure      vBg
## 1 2_1      <NA> 0.00  NA      NA          NA          NA      0.0000
## 2 2_1 2014-06-07 13:00:00 1.98 393 0.7104731      35          1 328.9470
## 3 2_1 2014-06-08 13:00:00 2.98 260 0.7104731      35          1 217.6240
## 4 2_1 2014-06-09 13:00:00 3.98 245 0.7104731      35          1 205.0687
## 5 2_1 2014-06-10 13:00:00 4.98 225 0.7104731      35          1 188.3284
## 6 2_1 2014-06-11 13:00:00 5.98 200 0.7104731      35          1 167.4031
##      vCH4      cvBg      cvCH4      rvBg      rvCH4
## 1  0.0000  0.0000  0.0000      NA      NA
## 2 234.0036 328.9470 234.0036 166.1348 118.1837
## 3 154.8116 546.5710 388.8152 217.6240 154.8116
## 4 145.8801 751.6397 534.6954 205.0687 145.8801
## 5 133.9716 939.9681 668.6669 188.3284 133.9716
## 6 119.0858 1107.3712 787.7527 167.4031 119.0858

dim(cum.prod)

## [1] 300 13
```

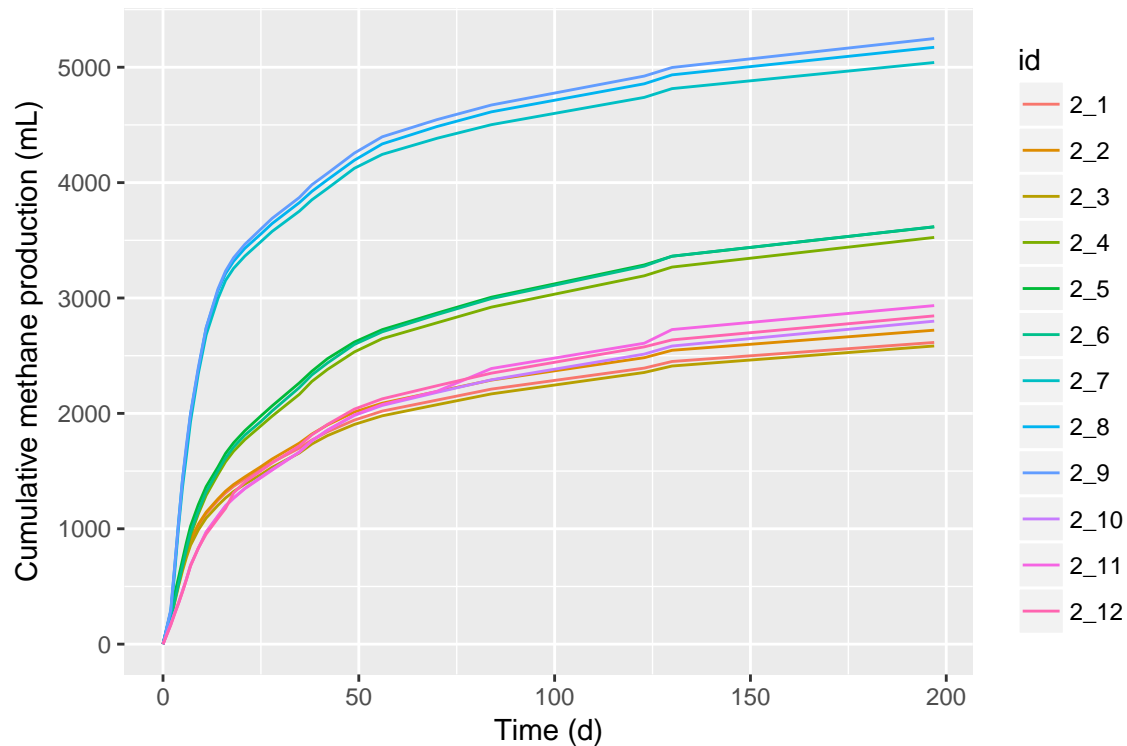
² By default, temperature is in °C and pressure in atm, but these can be changed in the function call with the **temp.unit** and **pres.unit** arguments, or globally with **options**.

³ Remember that standard conditions can be set in the function call with **temp.std** and **pres.std**, or globally with **options()**.

The data frame that is returned has all the original columns in `vol`, plus others. In these columns, `v` stands for (standardised) volume, `cv` (standardised) cumulative volume, `rv` stands for (standardised) volume production rate, and `Bg` and `CH4` for biogas and methane. So `cvCH4` contains standardised cumulative CH₄ production. It is probably easier to understand the data in the output graphically. Here we'll use the `qplot` function from the `ggplot2` package to plot it.

```
library(ggplot2)

qplot(x = days, y = cvCH4, data = cum.prod, xlab = "Time (d)",
      ylab = "Cumulative methane production (mL)", color = id,
      geom = "line")
```



3.2 Other data structures

As of bigoas version 1.5.0, the "long" data structures described above are not the other options. In addition, "wide" and combined "long" structures are possible. We can compare the three possible approaches using the same dataset.

Let's load data on biogas production from three bottles with wastewater sludge.

```
data("s3voll")
data("s3compl")
data("s3volw")
data("s3compw")
data("s3lcombo")
```

The "long" structure described above looks like this:

```
s3voll

##      id  time.d  vol.ml  cvol.ml
##  1    D   0.9438    103    103
##  2    E   0.9451    106    106
##  3    F   0.9472    107    107
##  4    D   2.9060    192    295
##  5    E   2.9090    181    287
##  6    F   2.9100    203    310
##  7    D   5.8860    141    436
##  8    E   5.8880    133    420
##  9    F   5.8900    140    450
## 10    D  10.0000    112    548
## 11    E  10.0000    111    531
## 12    F  10.0100    110    560
## 13    D  23.1000    200    748
## 14    E  23.1000    190    721
## 15    F  23.1000    200    760
## 16    D  34.0100    109    857
## 17    E  34.0100    110    831
## 18    F  34.0100    112    872
## 19    D  57.8400    146   1003
## 20    E  57.8400    136    967
## 21    F  57.8400    138   1010
```

```
s3compl

##      id  time.d   xCH4
##  1    D   2.906 0.6983
##  2    E   2.909 0.6817
##  3    F   2.910 0.6869
##  4    D  10.000 0.6646
##  5    E  10.000 0.6644
##  6    F  10.010 0.6632
##  7    D  23.100 0.6946
##  8    E  23.100 0.6871
##  9    F  23.100 0.6829
## 10    D  34.010 0.6626
## 11    E  34.010 0.6556
## 12    F  34.010 0.6527
## 13    D  57.840 0.6651
## 14    E  57.840 0.6600
```

The "wide" format contains (mostly) the same data, but there are separate columns for each reactor.

```
s3volw

##      time.d    D    E    F
##  1   0.9438  103  106  107
```



```
## 2  2.9060 192 181 203
## 3 34.0100 109 110 112
## 4  5.8860 141 133 140
## 5 10.0000 112 111 110
## 6 23.1000 200 190 200
## 7 57.8400 146 136 138
```

s3compw

```
##   time.d      D      E      F
## 1  2.906 0.6983 0.6817 0.6869
## 2 34.010 0.6626 0.6556 0.6527
## 3 10.000 0.6646 0.6644 0.6632
## 4 23.100 0.6946 0.6871 0.6829
## 5 57.840 0.6651 0.6600      NA
```

Note the missing composition value in **s3compw**. With the "long" structure, a row was simply omitted. Both approaches will result in the same output though. With the "wide" approach all bottles must be measured at the same times.

Finally, in the combined approach both volume and composition are in the same "long" data frame.

s3lcombo

```
##   id  time.d vol.ml  xCH4
## 1  D  0.9438   103     NA
## 2  E  0.9451   106     NA
## 3  F  0.9472   107     NA
## 4  D  2.9060   192 0.6983
## 5  E  2.9090   181 0.6817
## 6  F  2.9100   203 0.6869
## 7  D  5.8860   141 0.6800
## 8  E  5.8880   133 0.6800
## 9  F  5.8900   140 0.6800
## 10 D 10.0000   112 0.6646
## 11 E 10.0000   111 0.6644
## 12 F 10.0100   110 0.6632
## 13 D 23.1000   200 0.6946
## 14 E 23.1000   190 0.6871
## 15 F 23.1000   200 0.6829
## 16 D 34.0100   109 0.6626
## 17 E 34.0100   110 0.6556
## 18 F 34.0100   112 0.6527
## 19 D 57.8400   146 0.6651
## 20 E 57.8400   136 0.6600
## 21 F 57.8400   138     NA
```

Each of these structures can be used by **cumBg** by changing the **comp** argument.

```

cpl <- cumBg(s3lcombo, comp = s3compl, temp = 25, pres = 1,
             id.name = 'id', time.name = 'time.d',
             dat.name = 'vol.ml', comp.name = 'xCH4',
             extrap = TRUE)

## Biogas composition is interpolated.
## Working with volume data, applying volumetric method.
## Using a standard pressure of 1 atm and standard temperature of 0 C for standardizing
volume.

cpw <- cumBg(s3volw, comp = s3compw, temp = 25, pres = 1,
             time.name = 'time.d',
             data.struct = 'wide',
             dat.name = 'D', comp.name = 'D',
             extrap = TRUE)

## Biogas composition is interpolated.
## Working with volume data, applying volumetric method.
## Using a standard pressure of 1 atm and standard temperature of 0 C for standardizing
volume.

cpc <- cumBg(s3lcombo, temp = 25, pres = 1,
             id.name = 'id', time.name = 'time.d',
             data.struct = 'longcombo',
             dat.name = 'vol.ml', comp.name = 'xCH4',
             extrap = TRUE)

## Biogas composition is interpolated.
## Working with volume data, applying volumetric method.
## Using a standard pressure of 1 atm and standard temperature of 0 C for standardizing
volume.

```

Output is nearly identical here. The small differences result from the use of unique times for each bottle in the long formats.

```

head(cpl)

##   id  time.d vol.ml      xCH4 temperature pressure      vBg      vCH4
## 1  D  0.0000    NA      NA      NA      NA    0.00000  0.00000
## 2  D  0.9438   103 0.6983000    25      1  91.40334  63.91110
## 3  D  2.9060   192 0.6983000    25      1 170.38293 119.13525
## 4  D  5.8860   141 0.6841435    25      1 125.12497  85.72159
## 5  D 10.0000   112 0.6646000    25      1  99.39004  66.15145
## 6  D 23.1000   200 0.6946000    25      1 177.48222 123.44367
##      cvBg    cvCH4    rvBg    rvCH4
## 1  0.00000  0.0000    NA      NA
## 2  91.40334  63.9111  96.84609 67.716783
## 3 261.78628 183.0464  86.83260 60.715143

```

```
## 4 386.91124 268.7679 41.98824 28.765635
## 5 486.30129 334.9194 24.15898 16.079593
## 6 663.78351 458.3631 13.54826 9.423181
```

```
head(cpw)
```

```
##   id  time.d vol      xCH4 temperature pressure      vBg      vCH4
## 1  D  0.0000  NA          NA          NA      NA  0.00000  0.00000
## 2  D  0.9438 103 0.6983000      25      1  91.40334  63.91110
## 3  D  2.9060 192 0.6983000      25      1 170.38293 119.13525
## 4  D  5.8860 141 0.6841435      25      1 125.12497  85.72159
## 5  D 10.0000 112 0.6646000      25      1  99.39004  66.15145
## 6  D 23.1000 200 0.6946000      25      1 177.48222 123.44367
##      cvBg      cvCH4      rvBg      rvCH4
## 1  0.00000  0.0000      NA      NA
## 2  91.40334  63.9111 96.84609 67.716783
## 3 261.78628 183.0464 86.83260 60.715143
## 4 386.91124 268.7679 41.98824 28.765635
## 5 486.30129 334.9194 24.15898 16.079593
## 6 663.78351 458.3631 13.54826 9.423181
```

```
head(cpc)
```

```
##   id  time.d vol.ml      xCH4 temperature pressure      vBg      vCH4
## 1  D  0.0000      NA      NA          NA      NA  0.00000  0.00000
## 2  D  0.9438  103 0.6983      25      1  91.40334  63.91110
## 3  D  2.9060  192 0.6983      25      1 170.38293 119.13525
## 4  D  5.8860  141 0.6800      25      1 125.12497  85.20396
## 5  D 10.0000  112 0.6646      25      1  99.39004  66.15145
## 6  D 23.1000  200 0.6946      25      1 177.48222 123.44367
##      cvBg      cvCH4      rvBg      rvCH4
## 1  0.00000  0.0000      NA      NA
## 2  91.40334  63.9111 96.84609 67.716783
## 3 261.78628 183.0464 86.83260 60.715143
## 4 386.91124 268.2503 41.98824 28.591933
## 5 486.30129 334.4018 24.15898 16.079593
## 6 663.78351 457.8454 13.54826 9.423181
```

3.3 Calculating BMP from cumulative production

To calculate BMP we need to subtract the contribution of the inoculum to CH_4 production for each reactor, normalise by substrate volatile solids (VS), and calculate means and standard deviations. This is done by the `summBg()` function using the results from `cumBg()`, along with the `setup` data frame. The arguments for `summBg()` are:

```
args(summBg)
```

```
## function (vol, setup, id.name = "id", time.name = "time", descrip.name = "descrip",
##      inoc.name = NULL, inoc.m.name = NULL, norm.name = NULL, norm.sd.name = NULL,
```

```
##      vol.name = "cvCH4", imethod = "linear", extrap = FALSE, when = 30,
##      show.obs = FALSE, sort = TRUE)
## NULL
```

This is a flexible function, and is useful for more than just calculating BMP. For example, to simply determine the mean cumulative CH₄ production for each substrate at 30 d, we could use:

```
summBg(cum.prod, setup = setup, time.name = "days", descrip.name = "descrip",
        when = 30)

## Response variable (volume) is cum.prod$cvCH4.
## Inoculum contribution not subtracted.
## No normalization by substrate mass.

##      descrip days      mean      sd n
## 1          A    30 1610.518 38.23170 3
## 2          B    30 2081.235 46.00754 3
## 3      cellu    30 3692.615 57.80451 3
## 4        inoc    30 1577.433 33.30427 3
```

Here, the response variable was `cvCH4` (cumulative CH₄ production, the default—but `vol.name` could be used to specify any column). The argument `descrip.name` is the name of the column in `setup` that gives a description of the reactor. Here it is used for grouping reactors. We could have used the default value in this call.

To calculate BMP, we need to provide information on where inoculum and substrate VS masses can be found. To subtract the inoculum contribution, we need to provide a value for the `inoc.name` argument, which should be the value in the `setup$descrip.name` column that indicates that the reactor contained inoculum only. In our `setup` data frame, the value is `"inoc"`. Inoculum mass is given in the `minoc` column, and we need to provide this information using the `inoc.m.name` argument (although here also, we could use the default value). The last step is normalisation of cumulative CH₄ production, based on substrate VS mass. This mass must be stored in the `setup` data frame and the name of column is given using the `norm.name` argument. Here, it is `"mvs.sub"`. We will evaluate CH₄ production at 60 days (`when` argument).

```
BMP <- summBg(cum.prod, setup = setup, time.name = "days", inoc.name = "inoc",
              inoc.m.name = "minoc", norm.name = "mvs.sub", when = 60)

## Response variable (volume) is cum.prod$cvCH4.
## Inoculum contribution subtracted based on setup$minoc.
## Response normalized by setup$mvs.sub.

BMP

##      descrip days      mean      sd n
## 1          A    60 166.4386  6.627077 3
## 2          B    60 142.1766 10.988131 3
## 3      cellu    60 408.8386 15.359236 3
```

Note the messages—because any response variable could be used and subtraction of an inoculum contribution and normalisation are optional, it is important to check these messages and be sure that `summBg()` did what you think it did. Additionally, it is good practice to view and save results from individual reactors, and check the apparent contribution of the inoculum to each reactor’s biogas production. This additional information can be returned by setting `show.obs = TRUE`.

3.4 Predicting methane production

The function `predBg()` provides a flexible approach for predicting methane potential, and in our example can be used to quickly check our experimental values. Predictions can be based on an empirical chemical formula, chemical oxygen demand (COD), or macromolecule composition.

Our BMP test included cellulose as a control. Using its chemical formula ($C_6H_{10}O_5$), we can calculate theoretical methane potential to compare to our measurements⁴.

```
predBg("C6H10O5")

## [1] 413.7274
```

So we see that theoretical methane potential of cellulose is 414 mL g^{-1} . Comparing expected cellulose BMP to measurements is an important way to check BMP experiments. How does this compare to our measurements?

```
BMP

##   descrip days      mean      sd n
## 1      A    60 166.4386  6.627077 3
## 2      B    60 142.1766 10.988131 3
## 3   cellu    60 408.8386 15.359236 3
```

The measured value is a bit lower, which is reasonable. It is common to assume that 5 – 10% of substrate is used to produce microbial biomass, and so not converted to biogas. We can incorporate this assumption into our prediction using the `fs` argument, which is the fraction of substrate electrons used for cell synthesis.

```
predBg("C6H10O5", fs = 0.1)

## [1] 372.3547
```

Measured and predicted values are close after making this correction.

We don’t have empirical formulas for substrates A and B, but we can predict theoretical potential by using the COD. Initial COD masses are in the `setup` data frame, and from these we can calculate COD:VS ratios for substrates A and B of 1.439 and 1.561 $g\ g^{-1}$. Cellulose has a calculated oxygen demand (COD’)⁵ of 1.184 $g\ g^{-1}$. Predicted CH_4 production per g VS is therefore:

⁴ In this case, the calculation is based on Eq. (13.5) in Rittmann and McCarty [3]. When the input is COD, it is based on the COD of CH_4 , as described in [3].

⁵ Oxygen demand can be calculated with the `calcCOD` function.

```
predBg(COD = c(A = 1.439, B = 1.561, cellu = 1.184))

## [1] 502.7638 545.3887 413.6709
```

Measured BMP was substantially lower for substrates A and B, indicating very low degradability. In fact, we could use `predBg()` to estimate effective degradability (ignoring synthesis of microbial biomass).

```
BMP$mean/predBg(COD = c(A = 1.439, B = 1.561, cellu = 1.184))

## [1] 0.3310472 0.2606886 0.9883184
```

We see that substrates A and B had low degradability, while degradability of cellulose was high. Both substrates A and B were digestate from digesters, i.e., they had already been anaerobically digested once before these measurements, and so we should expect low degradability. We can conclude that our measured results are reasonable.

4 Continuing with the biogas package

The three functions demonstrated in this document can be used in other ways not described here. For example, `cumBg()` can be used with measurements of reactor mass over time to determine biogas production[1], `summBg()` can return results for multiple times, and `predBg()` function can predict microbial nitrogen requirements and biogas composition. More details can be found in the help files for these functions, or, for `predBg`, in the `predBg` vignette. The low-level functions are straight-forward to use, and details can also be found in the help files.

To receive updates on the biogas package, you can subscribe to a mailing list by sending an e-mail to either of us. And please send us a message if you find a bug or have a suggestion for improving an existing function or adding a new one.

References

- [1] S.D. Hafner, C. Rennuit, J.M. Triolo, and B.K. Richards. Validation of a simple gravimetric method for measuring biogas production in laboratory experiments. *Biomass and Bioenergy*, 83:297–301, 2015.
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