Estimating recombination rates across genomes using MareyMap

Clément Rezvoy
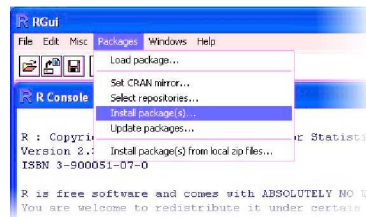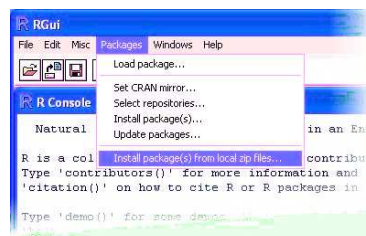
June 29, 2006

1 installing MareyMap

1.1 Install procedure on Windows

First of all you need to install a recent version of R if you don't have one yet (2.2 at least). you can get the latest version from the CRAN[1]. Once R is installed. you need to install tkrplot and MareyMap:

1. In R, go to `packages -> install package(s)...`:

2. In the dialog popping-up select a location near you and click *OK*.

3. A new dialog appears, scroll down until you reach *tkrplot*, select it and click *OK*.

4. Once tkrplot is installed, Download MareyMap from <TODO: url >. In R go to `Packages -> Install package(s) from local zip files...`:

---

[1]Comprehensive R Archive Network: urlhttp://cran.univ-lyon1.fr/bin/windows/base/

5. A file selector dialog appears, select the MareyMap zip file you have previously downloaded and click *Open*.

6. MareyMap is now installed, you can continue to section 2: Using MareyMap.

1.2   Install procedure on MacOS X

First of all you need to install a recent version of R if you don't have one yet (2.2 at least). you can get the latest version from the CRAN[2]. once R is installed. you can get the binary version of tkrplot package from the CRAN as follows:

<screenshots here>

You can now install MareyMap. first of all grab the latest version from <TODO: insert the address here> and install it as follows.

<screenshots here>

1.3   Install procedure on Linux

First of all you need to install a recent version of R if you don't have one yet (2.2 at least). Depending on your distribution, you may find a suitable precompiled version of R in the CRAN[3]. you may as well be able to install R using your distribtion's packaging system (for instance R is available under debian by typing 'su; apt-get install r-base' in a terminal window). Once R is installed. you need to install tkrplot and MareyMap:

1. Start R with administrative rights by typing 'su; R' (or sudo R).

2. From the R prompt, type: 'install.packages()'

3. In the popup window appearing, select a location near you. and click *OK*

4. A second window appears. Scroll down untill you reach tkrplot. select it and click *OK*.

5. Download MareyMap by typing wget <TODO: add url here>

6. Get administrative rights by typing su (sudo su, depending on your distribution)

7. Install the package by typing R CMD INSTALL MareyMap_{version number}.tar.gz[4]

8. Once MareyMap is installed, you may remove the downloaded file: rm MareyMap_{version number}.tar.gz

9. MareyMap is now installed, you can continue to section 2: Using MareyMap.
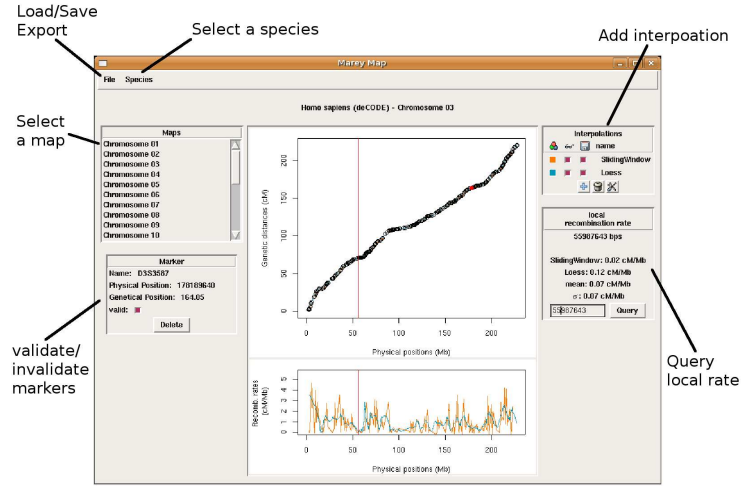
---

[2]Comprehensive R Archive Network: http://cran.univ-lyon1.fr/bin/macosx/
[3]Comprehensive R Archive Network: http://cran.univ-lyon1.fr/bin/linux/
[4]example: MareyMap_1.0.tar.gz

2 Using MareyMap

from the R prompt, you can start the graphical interface of MareyMap as follows:

```
> library(MareyMapGUI)
> startMareyMapGUI()
```


The graphical interface starts by default with the default map collecition. It is however possible to load a different collection via the *file* menu. After selecting a species from the menu, the list of maps for this species is displayed ① and once a map selected, it is displayed in the center part of the interface ②. it is then possible to select markers on the map to get and invalidate them if they seem misplaced ④. Once the map clean, you may apply interpolation method to the map ⑤ in order to calculate local recombination rates ③. The recombination rate at a specific location on the map can then be queried ⑥, you may query several locations at once by seperating them with ':'.

3