MareyMap

Overview

MareyMap is an R package to estimate local recombination rates along the genome.

MareyMap relies on comparing the genetic and the physical maps of a given chromosome to estimate local recombination rates (given by the slope of the curve describing the relationship between both variables), a graphical method called the Marey map method introduced by A. Chakravarti in 1991. MareyMap accepts Marey map data as input (genetic and physical positions of markers for a set of chromosomes of a species) and will return local recombination rate estimates.

MareyMap has many features and possible options (detailed in the present user guideline document) including:

> taking Marey map data from any species, including some Marey map data for a few species provided with the package,

> estimating local recombination rates using different interpolation methods, and

> providing in an automatic way local recombination rates for any given gene (or set of genes) in the genome.

All functionalities of MareyMap are introduced on the vignette of the package.

A web application (a Shiny app) is available to use the functionalities of the MareyMap package in an interactive way: MareyMap Online offers a simpler version of the R package MareyMap. The MareyMap Shiny app can be found at: http://lbbe-shiny.univ-lyon1.fr/MareyMapOnline/ 🗗

References

> Rezvoy C, Charif D, Guéguen L, Marais GAB. (2007). MareyMap: an R-based tool with graphical interface for estimating recombination rates. Bioinformatics. 23(16): 2188-9.

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> A. Siberchicot, A. Bessy, L. Guéguen, G. Marais (2017). MareyMap Online: A User-Friendly Web Application and Database Service for Estimating Recombination Rates Using Physical and Genetic Maps. Genome Biology and Evolution. 9(10): 2506-2509.

https://doi.org/10.1093/gbe/evx178 🗗

Download

You can download MareyMap and its user guide on CRAN, here 🗗
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Contact

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