

1 Introduction

1.1 Synopsis

Package `cgmisc` contains miscellaneous functions, hopefully useful for extending genome-wide association study (GWAS) analyses.

1.2 Getting help

Like every other R function, the functions provided in this package are documented in the standard R-help (Rd) format and can be easily accessed by issuing `help()` or its shorter version, `?` function. For instance, if you want to get more information on how to use the `clump.markers()` function, type either `help(clumpmarkers)` or `?clump.markers` and press return/enter. To see this document from within R you type `vignette('cgmisc')`.

1.3 Purpose of this document

This document aims at presenting how to use functions provided in this package in a typical GWAS data analyses workflow. It is, however, not pretending to be a GWAS tutorial as such.

1.4 Conventions

- All R commands are written in terminal type: `myfun(foo=T, bar=54)`
- In the above example: `myfun` is a *function* and both `foo` and `bar` are its *arguments*

2 Working with cgmisc

2.1 Installation

In order to install `cgmisc`, you either use one of the R GUIs (native R GUI, RStudio etc.) or type the following command:

```
install.packages("cgmisc", repos = "")
```

Functions in the `cgmisc` package often complement or use `GenABEL` ?? package functions and data structures. `GenABEL` is an excellent and widely-used R package for performing genome-wide association studies and much more... Therefore `GenABEL` will be loaded automatically. If for some mysterious reason this does not happen, you can install and load `GenABEL` by typing:

```
install.packages("GenABEL")
require("GenABEL")
```

You load `cgmisc` package in exactly the same way (both `require` and `library` will do):

```
require("cgmisc")  
library("cgmisc") # Alternative to require
```