solareclipser

Contents

Introduction

`solareclipser` is an R package to interface with SOLAR-Eclipse.

Installation

Prerequisites

`solareclipser` requires `solar`.

solareclipser

```r
install.packages("devtools")
devtools::install_github("txbrain-org/solareclipser")
```

Usage

`solareclipser` defaults to using a tmp directory for the output files. However, this can be overridden by passing settings to the `Solar` class.

Solar S6 class

Set the settings for `Solar` class.

```r
library(solareclipser)

settings <- list(
  output = list(
    dir = "tests/output/solar",
    tcl = FALSE,
    stdout_and_stderr = FALSE
  )
)
```

Note: setting `dir` to a directory from a previous run will allow not needing to load the pedigree and phenotypes again.

Models

```
solar <- Solar$new(settings = settings)
solar$cmd$load(obj = "pedigree",
               fpath = "tests/input/solar/HCP_imputed_filtered_ped.csv",
               cond = "-t 0")
solar$cmd$load(obj = "phenotypes",
               fpath = "tests/input/solar/HCP_WM_ave_norm.csv")
solar$cmd$trait("CC")$polygenic()
solar$run()
#> Executing solar command... Done.
```

Polygenic

```
library(solareclipser)

solar <- Solar$new(settings = settings)
solar$cmd$load(obj = "pedigree",
               fpath = "tests/input/solar/HCP_imputed_filtered_ped.csv",
               cond = "-t 0")
solar$cmd$load(obj = "phenotypes",
               fpath = "tests/input/solar/HCP_WM_ave_norm.csv")
solar$cmd$trait("CC")
solar$cmd$create_evd_data(output_fbasename = "evd_data")
solar$cmd$fphi(evd_data = "evd_data")
solar$run()
#> Executing solar command... Done.
```

FPHI

Output

Using SolarFiles SolarFiles class can be used to get all/individual output files.

```
# trait_d => trait directory
sf <- SolarFiles$new(settings = settings)
sf$set_polygenic_trait_d(trait_d = "CC")
sfc <- SolarFilesController$new(sf = sf)
sfc$set_polygenic_trait_d_files()
trait_d_files <- sfc$get_polygenic_trait_d_files()

mod_files <- sfc$get_mod_files()
out_files <- sfc$get_out_files()
stat_files <- sfc$get_stats_files()

summary <- readLines(out_files[str_detect(out_files, "polygenic.out")])
cat(str_trim(summary), sep = "\n")
#> Pedigree:    HCP_imputed_filtered_ped.csv empirical
#> Phenotypes:  HCP_WM_ave_norm.csv
#> Trait:       CC                         Individuals:  999
#>
#> H2r is 0.9344430  p = 8.148806e-70   (Significant)
#> H2r Std. Error:  0.0104121
#>
#> Warning.  Unexpectedly high heritabilities might result from
#> numerical problems, especially if mztwins are present.
```

```
#>
#>
#> Loglikelihoods and chi's are in CC/polygenic.logs.out
#> Best model is named poly and null0
#> Final models are named poly, spor
#>
#> Residual Kurtosis is -0.0900, within normal range
```

```r
library(solareclipser)

settings <- list(
  output = list(
    dir = "tests/output/solar",
    tcl = TRUE,
    stdout_and_stderr = TRUE
  )
)

solar <- Solar$new(settings = settings)
solar$cmd$load(obj = "pedigree",
               fpath = "tests/input/solar/HCP_imputed_filtered_ped.csv",
               cond = "-t 0")
solar$cmd$load(obj = "phenotypes",
               fpath = "tests/input/solar/HCP_WM_ave_norm.csv")
solar$cmd$trait("CC")$polygenic()
solar$run()
#> =============================> tcl <===============================
#>
#> proc file178af4abaa39 {} {
#>    load pedigree HCP_imputed_filtered_ped.csv -t 0
#>    load phenotypes HCP_WM_ave_norm.csv
#>    trait CC
#>    polygenic
#> }
#> ==================================================================
#> ======================> stdout_and_stderr <======================
#> Unloading current pedigree data ...
#> Loading Empirical Pedigree...
#> There are 2284 people.  If not correct, be sure ID's are unique.
#> Determining families (use -1 option to skip this)
#> Warning if number of families is greater than one it may
#> cause an issue when loading phi2 matrix.  Use -1 option to
#> avoid any potential issues.
#> *****************************************************************
#> *  Maximize sporadic model                                      *
#> *****************************************************************
#>
#>     *** Loglikelihood of sporadic model is -487.520945
#>
#> *****************************************************************
#> *  Maximize polygenic model                                     *
#> *****************************************************************
```

```
#>
#>     *** Loglikelihood of polygenic model is -332.229219
#>     *** H2r in polygenic model is 0.9344430
#>
#>     *** Determining significance of H2r
#>     *** Comparing polygenic and sporadic models
#>     *** chi = 310.5835, deg = 1, p = 8.148806e-70
#>
#> *****************************************************************************
#> *                        Summary of Results                                *
#> *****************************************************************************
#>
#>  Pedigree:    HCP_imputed_filtered_ped.csv empirical
#>  Phenotypes:  HCP_WM_ave_norm.csv
#>  Trait:       CC                          Individuals:   999
#>
#>          H2r is 0.9344430   p = 8.148806e-70   (Significant)
#>        H2r Std. Error:   0.0104121
#>
#>  Warning.   Unexpectedly high heritabilities might result from
#>  numerical problems, especially if mztwins are present.
#>
#>
#>  Output files and models are in directory CC/
#>  Summary results are in CC/polygenic.out
#>  Loglikelihoods and chi's are in CC/polygenic.logs.out
#>  Best model is named poly and null0 (currently loaded)
#>  Final models are named poly, spor
#>
#>  Residual Kurtosis is -0.0900, within normal range
#> ===================================================================
```

Using **settings**

Additional References

- education - solar-eclipse-genetics.org
- solareclipse.pdf - solar-eclipse-genetics.org
- www.nitrc.org - solar documents