

# solareclipser

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## Introduction and Installation

solareclipser is an R package to interface with [SOLAR-Eclipse](#). solareclipser requires [solar](#).

Install solareclipser from GitHub using devtools with the following:

```
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.

```
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

### Polygenic

```
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.
```

### FPHI

```
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.
```

## SolarFiles

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

```
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
```

## Additional Examples

Using settings to set tcl and stdout\_and\_stderr to TRUE.

```
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 file7e7049f3c377 {} {
#>   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 -l option to skip this)
#> Warning if number of families is greater than one it may
#> cause an issue when loading phi2 matrix.  Use -l 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
#> =====

```

## Additional References

- [education - solar-eclipse-genetics.org](http://education-solar-eclipse-genetics.org)
- [solareclipse.pdf - solar-eclipse-genetics.org](http://solareclipse.pdf-solar-eclipse-genetics.org)
- [www.nitrc.org - solar documents](http://www.nitrc.org-solar-documents)