

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...
#> Error in system2("solar", args = tcl_proc_name, stdout = TRUE, stderr = TRUE): error in running command
```

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...
#> Error in system2("solar", args = tcl_proc_name, stdout = TRUE, stderr = TRUE): error in running command
```

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()
#> Error in str_replace_all(polygenic_files$trait_d, " ", "."): could not find function "str_replace_all"
trait_d_files <- sfc$get_polygenic_trait_d_files()

mod_files <- sfc$get_mod_files()
#> Error in str_detect(str, ".mod$"): could not find function "str_detect"
out_files <- sfc$get_out_files()
#> Error in str_detect(str, ".out$"): could not find function "str_detect"
stat_files <- sfc$get_stats_files()
#> Error in str_detect(str, ".stats$"): could not find function "str_detect"

summary <- readLines(out_files[str_detect(out_files, "polygenic.out")])
#> Error in readLines(out_files[str_detect(out_files, "polygenic.out")]): object 'out_files' not found
cat(str_trim(summary), sep = "\n")
#> Error in str_trim(summary): could not find function "str_trim"
```

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 file4a55548eca14 {} {
#>   load pedigree HCP_imputed_filtered_ped.csv -t 0
#>   load phenotypes HCP_WM_ave_norm.csv
#>   trait CC
#>   polygenic
#> }
#> =====
#> Error in system2("solar", args = tcl_proc_name, stdout = TRUE, stderr = TRUE): error in running command
```

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)