# **Screening Module User Guide**

Shiju Sisobhan

Allada Lab, University of Michigan

#### **Overview**

Screening\_module.R is an R program designed to collect control genotypes from previous runs and the current run, accumulate them into a single reference group, and re-evaluate parameters against this cumulative control to compute updated P-values

# **Prerequisites**

Before running the Screening\_module.R program, ensure you have the following installed on your computer:

- Matlab
- SleepMat 2025.1 (Alpha)
- R
- RStudio

Additionally, download the R program Screening module.R from the GitHub repository.

Link to download latest version of sleepmat and Screening\_module.R

https://github.com/shijusisobhan/SleepMat\_2025.1-Alpha

# **Instructions**

#### Step 1

SleepMat Analysis: Run your individual analysis using newer version of SleepMat.

## **Step 2: Create the Location Info File**

	Α	В
1	Control	folder
2	attP2 Neg Control	C:\Users\shijusis\OneDrive - Michigan Medicine\Desktop\Screening_module\JM\CSW-TS-2_001\project-attp2\Screening_results
3	attP40 Neg Control	C:\Users\shijusis\OneDrive - Michigan Medicine\Desktop\Screening_module\JM\CSW-TS-2_001\project-attp40\Screening_results
4	58061 Pos Control	C:\Users\shijusis\OneDrive - Michigan Medicine\Desktop\Screening_module\JM\CSW-TS-2_001\project-pos\Screening_results
5		

- 1. Open a new Excel file and name it as you like (e.g., location info.xlsx).
- 2. In the first row, create headers for your columns:

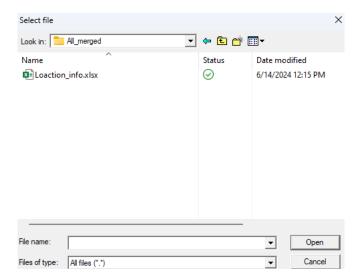
- **First Column (Control):** List of negative control genotypes to accumulate. Unique names only, also there is no order specification.
- o **Second Column (Location):** You can use any header name. Enter the screening results file locations generated by *SleepMat* corresponding to each run. You can copy and paste the file locations here. The last row in the second column should be the run for which cumulative controls are to be applied.
- 3. Save the Excel file.

#### **Step 2: Run the Screening\_module Program**

- 1. Open RStudio.
- 2. Open the Screening module.R program in RStudio.
- 3. Click the 'Source' tab at the top left of the program window.

```
File Edit Code View Plots Session Build Debug Profile Tools Help
🔾 🕶 😭 🚰 🕝 🔒 📗 📥 🖍 Go to file/function
 Screening_module.R ×
 rm(list=ls())
    6 packages = c("readxl", "dplyr", "openxlsx", "stringr")
    8 ## Load or install the required packges
    9 package.check <- lapply(</pre>
       packages,
   10
        FUN = function(x) {
   11 -
   12 -
         if (!require(x, character.only = TRUE)) {
             install.packages(x, dependencies = TRUE)
   13
             library(x, character.only = TRUE)
   14
   15 -
   16 -
   17 )
   18
   19
   20
   21 # Browse and select the Excel file interactively
   22 file_path <- file.choose()</pre>
   23 mainDir <- dirname(file nath)
  4:1
      (Top Level) $
 Console Terminal × Background Jobs ×
```

4. A file browser window will pop up. Browse and select the Excel file (location\_info.xlsx) you created.



- 5. Click the 'Open' button.
- 6. The following line appears on the R console
- Tenter a file name to save the results:
- 8. Enter the file name where you want to save the results (Eg: M127\_M128)
- 9. Once you enter the file name, the P value calculation for combined controls will begin, and the results will be saved in the same folder as your input files with file name M127\_M128\_PValues.xls.