

# DAM\_Runs\_Integrator User Guide

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## Overview

**DAM\_Runs\_Integrator.R** is an R program designed to combine data from different behavioral experiments conducted using the Drosophila Activity Monitoring (DAM) system. The main purposes of this program are:

1. **Combine Monitor Files:** Merge different monitor files generated by the DAM system across various experiments (runs).
2. **Rename Monitor Files:** Avoid conflicts by renaming monitor files if they share the same name in different runs.
3. **Combine Genotype Specification Files:** Prepare a combined genotype specification file for analysis using SleepMat, a behavioral analysis software program for the DAM system.

These processes enable multiple run analyses using SleepMat.

## Prerequisites

Before running the DAM\_Runs\_Integrator program, ensure you have the following installed on your computer:

- **R**
- **RStudio**

Additionally, download the R program `DAM_Runs_Integrator.R` from the GitHub repository.

## Instructions

### Step 1: Create the Location Info File

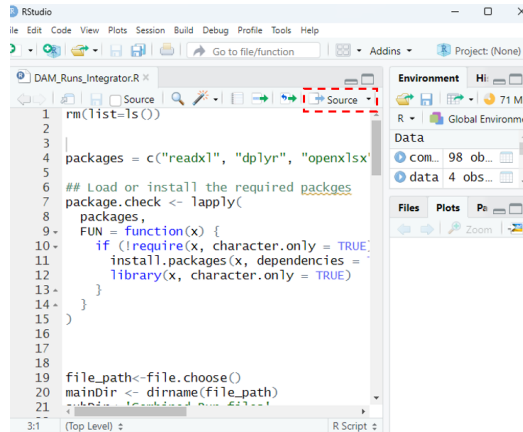
	A	B	C
1	Run_number	Location	
2		600 C:\Users\shijusis\OneDrive - Michigan Medicine\Desktop\Re_Sleep architecture_rebound for paper\GWMM6	
3		900 C:\Users\shijusis\OneDrive - Michigan Medicine\Desktop\Re_Sleep architecture_rebound for paper\GWMM9	
4		1400 C:\Users\shijusis\OneDrive - Michigan Medicine\Desktop\Re_Sleep architecture_rebound for paper\GWMM14	
5		2200 C:\Users\shijusis\OneDrive - Michigan Medicine\Desktop\Re_Sleep architecture_rebound for paper\GWMM22	
6			

1. Open a new Excel file and name it as you like (e.g., `location_info.xlsx`).

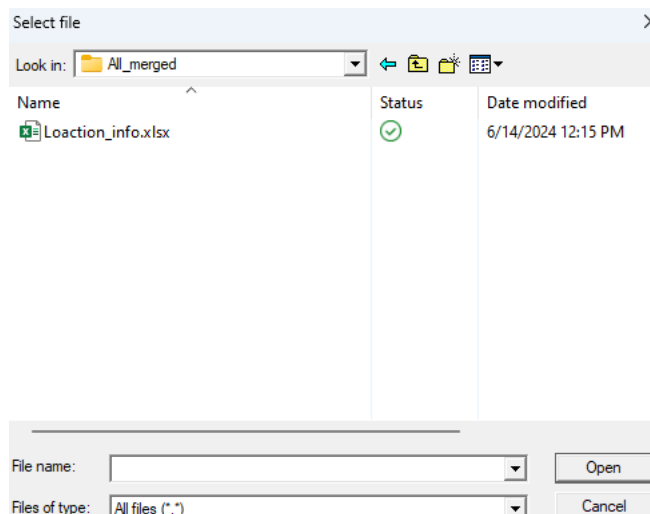
2. In the first row, create headers for your columns:
  - **First Column (Run Number):** You can use any header name. Enter the run numbers below this header. The run number should be a unique numeric value. For example, if your original genotype specification file has a run number M612, you can write it as 612 or any other unique number.
  - **Second Column (Location):** You can use any header name. Enter the file locations of the monitor files corresponding to each run. You can copy and paste the file locations here.
3. Enter all the run numbers and their corresponding monitor file locations.
4. Save the Excel file.

## Step 2: Run the DAM\_Runs\_Integrator Program

1. Open RStudio.
2. Open the DAM\_Runs\_Integrator.R program in RStudio.
3. Click the 'Source' tab at the top left of the program window.



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



5. Click the 'Open' button.

### **Step 3: Complete the Integration**

1. Once the integration is completed, the following message will appear in the console:

"Files integration has been successfully completed."

1. Check the folder where you saved the `location_info.xlsx` file. A new folder named `Combined_Run_files` will be created. This folder contains the combined genotype specification file and renamed monitor files for SleepMat analysis.

## **Conclusion**

You have successfully combined and prepared your monitor files and genotype specification files for analysis using SleepMat. Enjoy your data analysis!