## **Gcamp Analysis**

Calvin Cho

2025-03-18

```
library(ggplot2)
Warning: package 'ggplot2' was built under R version 4.3.1
library(tidyr)
Warning: package 'tidyr' was built under R version 4.3.1
library(dplyr)
Warning: package 'dplyr' was built under R version 4.3.1
Attaching package: 'dplyr'
The following objects are masked from 'package:stats':
    filter, lag
The following objects are masked from 'package:base':
    intersect, setdiff, setequal, union
```

```
data_files <- list.files("video", full.names = TRUE)</pre>
data_list <- lapply(data_files, read.csv)</pre>
names(data_list) <- gsub(".csv", "", basename(data_files))</pre>
process_dataset <- function(data, dataset_name) {</pre>
  library(dplyr)
  filtered_data <- data[, seq(1, ncol(data), by = 2)]</pre>
  if (!"x" %in% names(filtered data)) {
    names(filtered_data)[1] <- "x"</pre>
  neuron_columns <- grep("^RawIntDen", names(filtered_data), value = TRUE)</pre>
  new_names <- paste0("Neuron ", seq_along(neuron_columns))</pre>
  names(filtered_data) [names(filtered_data) %in% neuron_columns] <- new_names</pre>
  if (10 %in% filtered_data$x) {
    reference_values <- filtered_data %>%
      filter(x == 10) %>%
      select(all_of(new_names)) %>%
      unlist(use.names = FALSE)
    if (length(reference_values) == length(new_names)) {
      names(reference values) <- new names</pre>
      filtered_data <- filtered_data %>%
        mutate(across(all_of(new_names), ~
        (. - reference values[cur column()]) / reference values[cur column()]))
      warning("Reference values for x == 10 are inconsistent with neuron columns.
               Skipping normalization.")
    }
  }
  total_average_value <- filtered_data %>%
    mutate(average = rowMeans(select(., all_of(new_names)), na.rm = TRUE)) %>%
    select(x, average)
  selected_columns <- filtered_data %>%
```

```
filter(x > 10) \% \%
    select(all_of(new_names)) %>%
    select(where(~ any(. > 0.1, na.rm = TRUE)))
  conditional_average_value <- filtered_data %>%
    mutate(conditional_average =
        rowMeans(select(., all of(names(selected columns))), na.rm = TRUE)) %>%
    select(x, conditional_average)
  names(total_average_value)[2] <- paste0(dataset_name, "_average")</pre>
  names(conditional_average_value)[2] <- paste0(dataset_name, "_caverage")</pre>
  result <- left_join(total_average_value, conditional_average_value, by = "x")</pre>
  return(result)
}
processed_data_list <- lapply(names(data_list), function(name) {</pre>
  process_dataset(data_list[[name]], name)
})
merged_data <-
  Reduce(function(x, y)
    { merge(x, y, by = "x", all = TRUE) }, processed_data_list)
x_column <- merged_data[, 1, drop = FALSE]</pre>
totalaverage_columns <-
totalaverage_columns <- merged_data[, seq(2, ncol(merged_data), by = 2)]
conditionalaverage_columns <- merged_data[, seq(3, ncol(merged_data), by = 2)]</pre>
totalaveragedata <- cbind(x_column, totalaverage_columns)</pre>
conditionalaveragedata <- cbind(x_column, conditionalaverage_columns)</pre>
write.csv(totalaveragedata, "data_total.csv",
          row.names = FALSE)
write.csv(conditionalaveragedata, "data_conditional.csv",
          row.names = FALSE)
```