

Highlighted text are parts of this code that may need to be optimized to match your dataset

```
# Use this code to reformat your raw data from total instances into an excel  
# spreadsheet listing each observation as a separate row.
```

```
library(readxl) #read excel spreadsheets into R  
library(writexl) #write R data frames to excel  
library(tidyr) # Load the tidyr package
```

Change this to match the name of your raw dataset in the input folder

```
df <- read_excel("input/Male_Supplement_Aged_Control_AD2_5.xlsx")
```

```
reshape_data <- function(df) {  
  # Create a list to store individual worm observations  
  data <- list()
```

```
  # Loop through each observation in the dataset  
  for (i in 1:nrow(df)) {  
    row <- df[i, ]
```

Change these variables to match the column headers in your dataset

```
  # Extract original data except the title of the column, in this case "Exopher" and  
  "No_Exopher"  
  original_data <- row[!(names(row) %in% c("Exopher", "No_Exopher"))]
```

```
  # Add rows for instances where the data is positive for "Exopher" with original data  
  if (row$Exopher > 0) {  
    for (j in 1:row$Exopher) {  
      data[[length(data) + 1]] <- c(original_data, Exopher = 1, No_Exopher = 0)  
    }  
  }
```

```
  # Add rows for "No_Exophers" events with original data  
  if (row$No_Exopher > 0) {  
    for (j in 1:row$No_Exopher) {  
      data[[length(data) + 1]] <- c(original_data, Exopher = 0, No_Exopher = 1)  
    }  
  }
```

```
  # Combine worm observations into a data frame  
  do.call(rbind, data)  
}
```

```
# Reshape the data frame- this will require tidyr later to format it as a table  
df_expanded <- reshape_data(df)  
# Print the expanded data frame  
print(df_expanded)
```

```
data_expanded <- as.data.frame(df_expanded)  
str(data_expanded) #checks the structure of the data- if the result is a "list" then you  
need to use tidyr to clean it up
```

```
#use tidyr to make the lists individual columns, this is formatting the data back into a  
table
```

```
data_trial_unnested <- unnest(data_expanded, Trial)  
data_treatment_unnested <- unnest(data_trial_unnested, Treatment)  
data_exopher_unnested <- unnest(data_treatment_unnested, Exopher)  
data_final <- unnest(data_exopher_unnested, No_Exopher)
```

These variables reference the column titles in your dataset

```
print(data_final) #check your work  
write_xlsx(data_final, "input/aged_exopher_final.xlsx") #write to an excel file
```

Indicate where you want to save the reformatted data and what you want to name the final spreadsheet