L-lactate_Wound_Healing_Analysis

Import Packages

```
#install.packages("gdata")
#install.packages("cowplot")
#install.packages("gridExtra")
#install.packages("lemon")
```

Import Libraries

```
library(dplyr)

##
## 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

library(ggplot2)
library(tidyverse)

## — Attaching packages ——————————————————————————— tidyverse 1.
3.1 —

## ✓ tibble  3.1.6      ✓ purrr   0.3.4
## ✓ tidyr   1.2.0      ✓ stringr 1.4.0
## ✓ readr   2.1.2      ✓ forcats 0.5.1

## — Conflicts ——————————————————————————— tidyverse_conflict
s() —
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()

library(gdata)

## gdata: read.xls support for 'XLS' (Excel 97-2004) files ENABLED.

##

## gdata: read.xls support for 'XLSX' (Excel 2007+) files ENABLED.

##
## Attaching package: 'gdata'
```

```
## The following object is masked from 'package:purrr':
##
##     keep

## The following objects are masked from 'package:dplyr':
##
##     combine, first, last

## The following object is masked from 'package:stats':
##
##     nobs

## The following object is masked from 'package:utils':
##
##     object.size

## The following object is masked from 'package:base':
##
##     startsWith

library(cowplot)
library(grid)
library(gridExtra)

##
## Attaching package: 'gridExtra'

## The following object is masked from 'package:gdata':
##
##     combine

## The following object is masked from 'package:dplyr':
##
##     combine

library(lemon)

##
## Attaching package: 'lemon'

## The following object is masked from 'package:purrr':
##
##     %||%

## The following objects are masked from 'package:ggplot2':
##
##     CoordCartesian, element_render
```

Import CSV Files

```
imagej_wound_size_day_0 <- read.csv('Results_Day_0.csv', header=TRUE,sep = ",
")
imagej_wound_size_day_1 <- read.csv('Results_Day_1.csv', header=TRUE,sep = ",
```

```
")
imagej_wound_size_day_2 <- read.csv('Results_Day_2.csv', header=TRUE,sep = ",
")
```

Data Labelling and Calculating Percent Migration

```
#Modifying "Day 0" ImageJ Data

imagej_wound_size_day_0_modified <- imagej_wound_size_day_0 %>%
  mutate(time_day=c("Day 0"),.after=Label) %>%
  mutate(Treatment=c(rep("0",8),rep("0.1",8),rep("1",8),rep("10",8)),.after=t
ime_day) %>%
  mutate(percent_migration = (abs(imagej_wound_size_day_0$Area.mm.2-imagej_wo
und_size_day_0$Area.mm.2)/imagej_wound_size_day_0$Area.mm.2)*100)

imagej_wound_size_day_0_grouped <- group_by(imagej_wound_size_day_0_modified,
Treatment)
imagej_wound_size_day_0_aggregated <- summarise(imagej_wound_size_day_0_group
ed, Average_Percent_Migration=mean(percent_migration), sd=sd(percent_migratio
n))


#Modifying "Day 1" ImageJ Data

imagej_wound_size_day_1_modified <- imagej_wound_size_day_1 %>%
  mutate(time_day=c("Day 1"),.after=Label) %>%
  mutate(Treatment=c(rep("0",8),rep("0.1",8),rep("1",8),rep("10",8)),.after=t
ime_day) %>%
  mutate(percent_migration = (abs(imagej_wound_size_day_1$Area.mm.2-imagej_wo
und_size_day_0$Area.mm.2)/imagej_wound_size_day_0$Area.mm.2)*100)

imagej_wound_size_day_1_grouped <- group_by(imagej_wound_size_day_1_modified,
Treatment)
imagej_wound_size_day_1_aggregated <- summarise(imagej_wound_size_day_1_group
ed, Average_Percent_Migration=mean(percent_migration), sd=sd(percent_migratio
n))

#Modifying "Day 2" ImageJ Data

imagej_wound_size_day_2_modified <- imagej_wound_size_day_2 %>%
  mutate(time_day=c("Day 2"),.after=Label) %>%
  mutate(Treatment=c(rep("0",8),rep("0.1",8),rep("1",8),rep("10",8)),.after=t
ime_day) %>%
  mutate(percent_migration = (abs(imagej_wound_size_day_2$Area.mm.2-imagej_wo
und_size_day_0$Area.mm.2)/imagej_wound_size_day_0$Area.mm.2)*100)

imagej_wound_size_day_2_grouped <- group_by(imagej_wound_size_day_2_modified,
Treatment)
imagej_wound_size_day_2_aggregated <- summarise(imagej_wound_size_day_2_group
```

```
ed, Average_Percent_Migration=mean(percent_migration), sd=sd(percent_migratio
n))
```

## Combining the Data Frames and Preparing for Scatterplot

```
wound_size_scatterplot_data <- rbind(imagej_wound_size_day_0_aggregated,image
j_wound_size_day_1_aggregated,imagej_wound_size_day_2_aggregated)

wound_size_scatterplot_data_days <- wound_size_scatterplot_data %>%
    mutate(time_day=c(rep("Day 0", 4),rep("Day 1", 4), rep("Day 2", 4)) ,.bef
ore=Treatment)
```
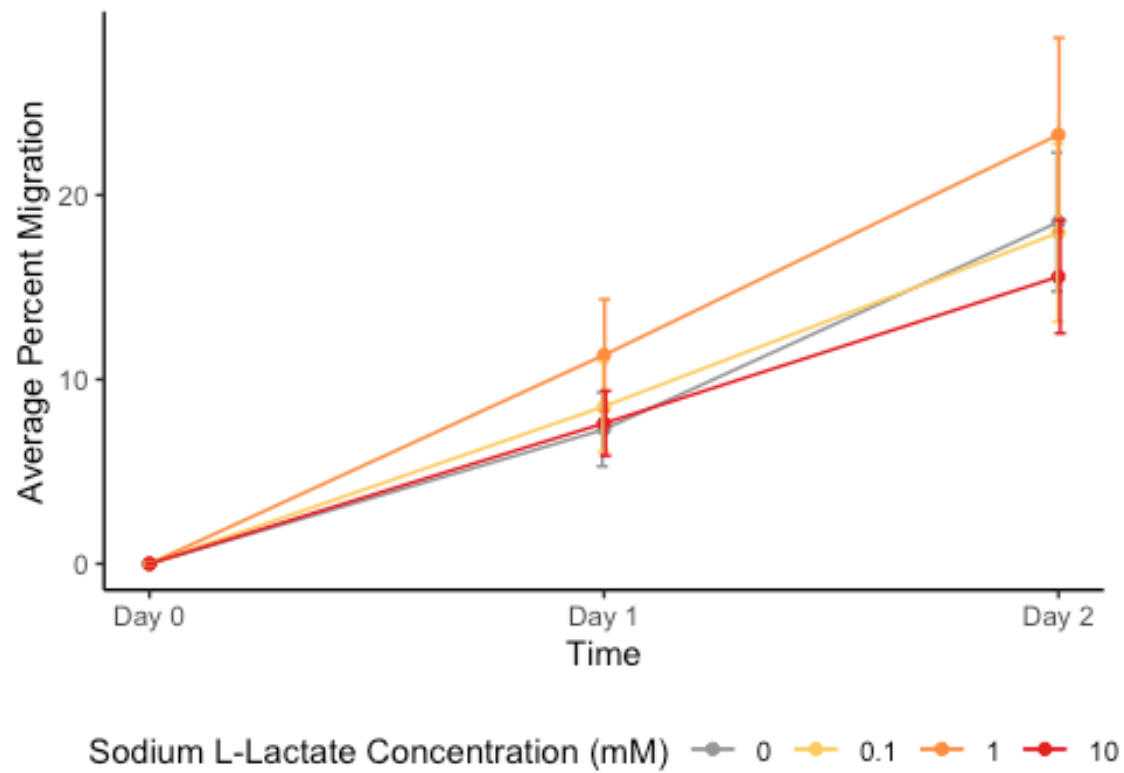
Create Scatterplot

```
lactate_scatterPlot_B <- ggplot(wound_size_scatterplot_data_days, aes(x = tim
e_day, y= Average_Percent_Migration, col = Treatment)) +
    geom_line(aes(group = Treatment)) +
    geom_point() +
    geom_errorbar(aes(ymin=Average_Percent_Migration-sd, ymax=Average_Percent
_Migration+sd), width=.1,
                  position=position_dodge(0.01)) +
    theme_classic() + #classic theme has the white background with black axis
titles +
    scale_color_manual(values=c('#969696','#fecc5c','#fd8d3c','#e31a1c')) +
    ggtitle('') + #plot title
    xlab('Time') + #X-axis title
    ylab('Average Percent Migration') + #Y-axis title
    labs(colour="Sodium L-Lactate Concentration (mM)") + #Legend title
    theme(legend.position="bottom") +
    theme(plot.title = element_text(face="bold", size = rel(2.0))) + #Format
the plot title with bold and increased size
    scale_x_discrete(expand = c(0, .1))

lactate_scatterPlot_B
```
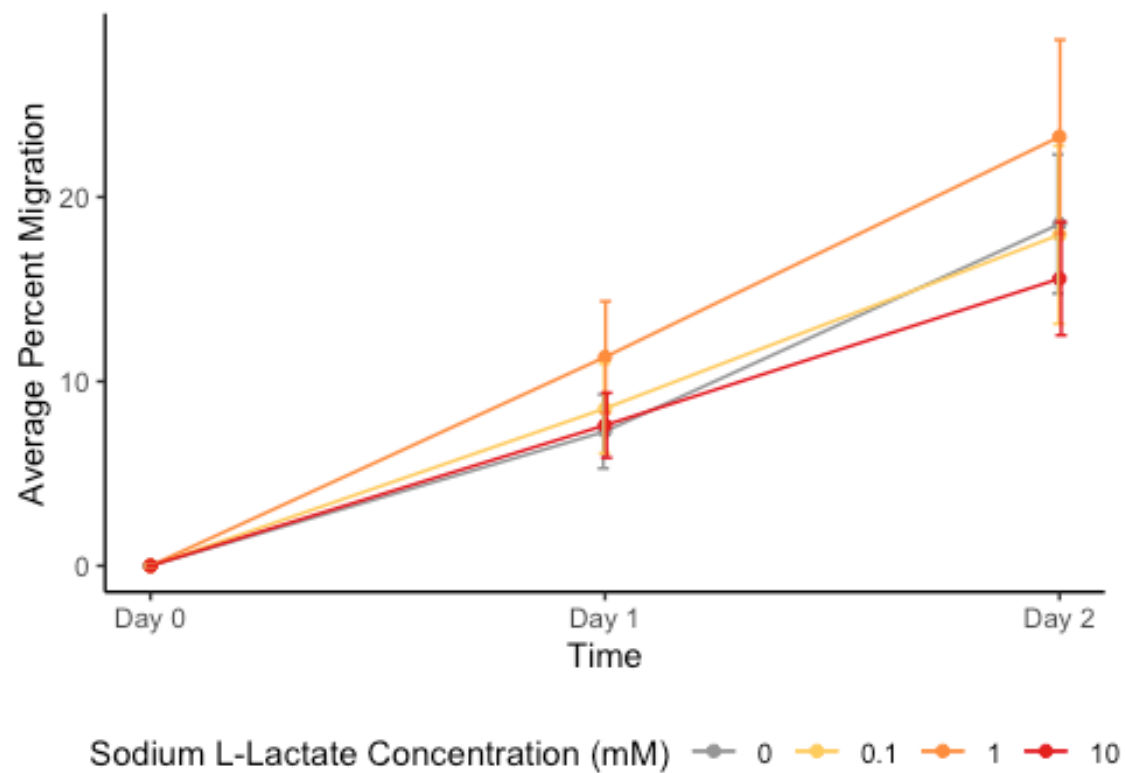
Save Scatterplot

`lactate_scatterPlot_B`

```
ggsave("lactate_scatterPlot_B.png", plot= lactate_scatterPlot_B, width = 30,
height = 20, units = "cm")
```