

Recreation, Ogran et al. 2019, figure 3

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Step 1: finding the data

-Data were fairly easily accessible through a link in the paper (<https://doi.10.5061/dryad.b2rbnzs93>). Clicking the link directly would not load the page for me, so I went to <https://doi.org> and typed in 10.5061/dryad.b2rbnzs93 to the search bar, which loaded this DRYAD page: <https://datadryad.org/stash/dataset/doi:10.5061/dryad.b2rbnzs93>. From that page I was able to download the complete .xlsx dataset for the paper.

-I then converted the .xlsx dataset to a .csv file.

-I was not able to find any code.

Step 2: loading data into R

-Data loaded into R fine, but due to formatting every other row was blank and showed as NA. To eliminate the empty rows I used a function from dplyr (see `#remove blank rows`).

Step 3: manipulating the data

-Stuck on getting the dataset sorted to individual trait:treatment sets so I can plot them. I tried to group by population and treatment and then summarize for mean glucosinolates first, which didn't work, but I thought it might be because of its units symbol.

-Tried `str()` on the full dataset to see if any spaces were throwing off the table (hopefully this is the right function that would remove stray spaces?)

-So then I tried `summary` next for dry weight (DW) and got the same result - the `group_by` works but the rest of the table says NA.

-SOLUTION: had to use fancy " symbols for the names of columns to get the commands to work!

```
library("tidyverse")
library("dplyr")
library("ggplot2")
library("magrittr")

full_dataset<-read_csv("./data/Full_dataset_Ogran_et_al.csv")
#remove blank rows
full_dataset <- full_dataset %>% filter_all(any_vars(!is.na(.)))

#grouping subset of treatments and groups plotted
subset_trt <- full_dataset %>% group_by(Population, Treatment) %>% summarize(Glucosinolates = mean(`Tot
```

Step 4: creating the reaction norm figures

-Using ggplot 2, I assembled a very basic graph starting with glucosinolates first.

-Used `geom_point` at first and tried `geom_line` to get lines to connect between points, but it connected points within treatments instead.

-SOLUTION: used aes(group) to group by population, which made lines between population points!

-Now doing stylistic edits to get the graph to really look like the figures from the paper.

-STUCK: formatting the y axis to show the scaling it does in the paper.

-STUCK: Need to figure out what I need to do to make error bars on each point.

```
gluc <- ggplot(data=subset_trt)+  
  aes(x=Treatment)+  
  aes(y=Glucosinolates)+  
  aes(group=Population)+  
  aes(color=Treatment)+  
  aes(fill=Treatment)+  
  aes(shape=Population)+  
  geom_point()+  
  geom_line()+  
  scale_shape_manual(values=c(17,15))+  
  scale_color_manual(values=c("black","black"))+  
  scale_fill_manual(values=c("black","black"))+  
  ylab("Glucosinolates")+  
  scale_y_continuous(limits=c(9, 22))+  
  theme_bw()+  
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())  
plot(gluc)
```

