

deKort 2020 Recreation, Figure 2

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Step 1: locating data

- Finding the data was extremely easy - all I needed to do was click on the URL to the DRYAD repository that the authors put in the Data Availability section near the end of the paper. In the repository was a single .xlsx file that contained the full dataset.
- Code was not available.
- The paper did mention specific R packages used to analyze results - in this case, the package “Plasticity” - but offered no more than a mention.

Step 2: Github and loading data

- I created a Github repository for this recreation project (<https://github.com/jillsyro/DST-deKort>).
- I converted the .xlsx file with data to a .csv file and added it to my project folder to bring in the data.

Step 3: Loading data and packages

```
#install.packages("Plasticity")  
#library("Plasticity")  
library("tidyverse")  
library("dplyr")  
library("ggplot2")  
library("magrittr")  
library("knitr")  
  
full_dataset<-read_csv("./data/Dryad_JEcol-2019-0718.csv")
```

- I ran into a problem while trying to install the Plasticity package (code commented out). It gave me the error “Warning in install.packages : package ‘Plasticity’ is not available (for R version 4.0.2)”.
- I googled “r package plasticity” and the first result was this Github page (<https://github.com/ameztegui/Plasticity>) for the package. In the readme file was different instruction for loading the package:

```
library("devtools")  
devtools::install_github("ameztegui/Plasticity")  
library("Plasticity")  
  
#Dependencies I did not have installed  
library("agricolae")  
library("psych")
```

- After installing the devtools package, the line of code provided in the readme file to install the Plasticity package worked! It is commented out to allow for knitting to PDF, but the # should be removed in line 38 to run the code.
- The readme file also had a section for dependencies to run the Plasticity package, so above I installed the packages I did not already have installed.

-The repository for Plasticity is well-organized and sparsely annotated with brief examples of how to run code producing figures and results.

Step 4: Data analysis

```
library("sciplot")
#growth_plasticity2 <- rdpi(full_dataset, Pop, EarlyGrowth, Treatment)
#growth_plasticity <- rdpi_matrix(full_dataset, EarlyGrowth, North_to_South)
```

-An error when trying to run `rdpi` alerted me that I also needed the package `sciplot`.

-No matter what I put in the code, I can't get the `rdpi` command to run, only `rdpi_matrix`.

-Running "`growth_plasticity <- rdpi_matrix(full_dataset, EarlyGrowth, North_to_South)`" just made a 708,337 element long vector... so that's obviously not the right line of code. A good sign is that all results are from 0-1, which they should be. Maybe the authors split the data into subsets and then ran that through the `rdpi_matrix` command?

-Weirdly, I found in the supplemental Excel file provided at the DOI access page to the paper (<https://besjournals.onlinelibrary.wiley.com/doi/abs/10.1111/1365-2745.13365> under the "Supporting Information" tab) and NOT in the DRYAD repository, more data provided than just the full dataset. That excel file also has their results from all RDPI calculations. But still nowhere do they explain HOW they got all those results...

-At this point with their RDPI data, I think it would be pretty easy to recreate their figures. But I still want to see if I can get the Plasticity package to work for me to reproduce their results.

-I decided to research the foundation of RDPI in Valladares et al. (2006) to see if I could understand the math behind the `rdpi` command. They provide this equation:

$$RDPI = \Sigma(d_{ij} \rightarrow i'j' / (x_{i'j'} + x_{ij})) / n$$

where

d_{ij} = pairwise distance among trait values

i (and i') = different environments

j (and j') = individuals sampled

x = a given trait

n = the total number of distances

-This equation seems like it would be hard for me to write my own function for at my current coding skill level. I think at this point I've reached an impasse for data analysis.

-I will go ahead and use their provided RDPI data to see if the figures I make end up being the same as the figures in the paper.

```
RDPIdataset <- read_csv("./data/jec13365-sup-0002-tables1-s5.csv")
```

```
## Warning: Missing column names filled in: 'X13' [13]
```

```
## Warning: Duplicated column names deduplicated: 'Genotype' => 'Genotype_1' [14],
```

```
## 'Pop' => 'Pop_1' [15], 'Gradient' => 'Gradient_1' [16], 'Elevation' =>
```

```
## 'Elevation_1' [17], 'Nheight' => 'Nheight_1' [18], 'Slope' => 'Slope_1' [20],
```

```
## 'EarlyGrowth' => 'EarlyGrowth_1' [21]
```

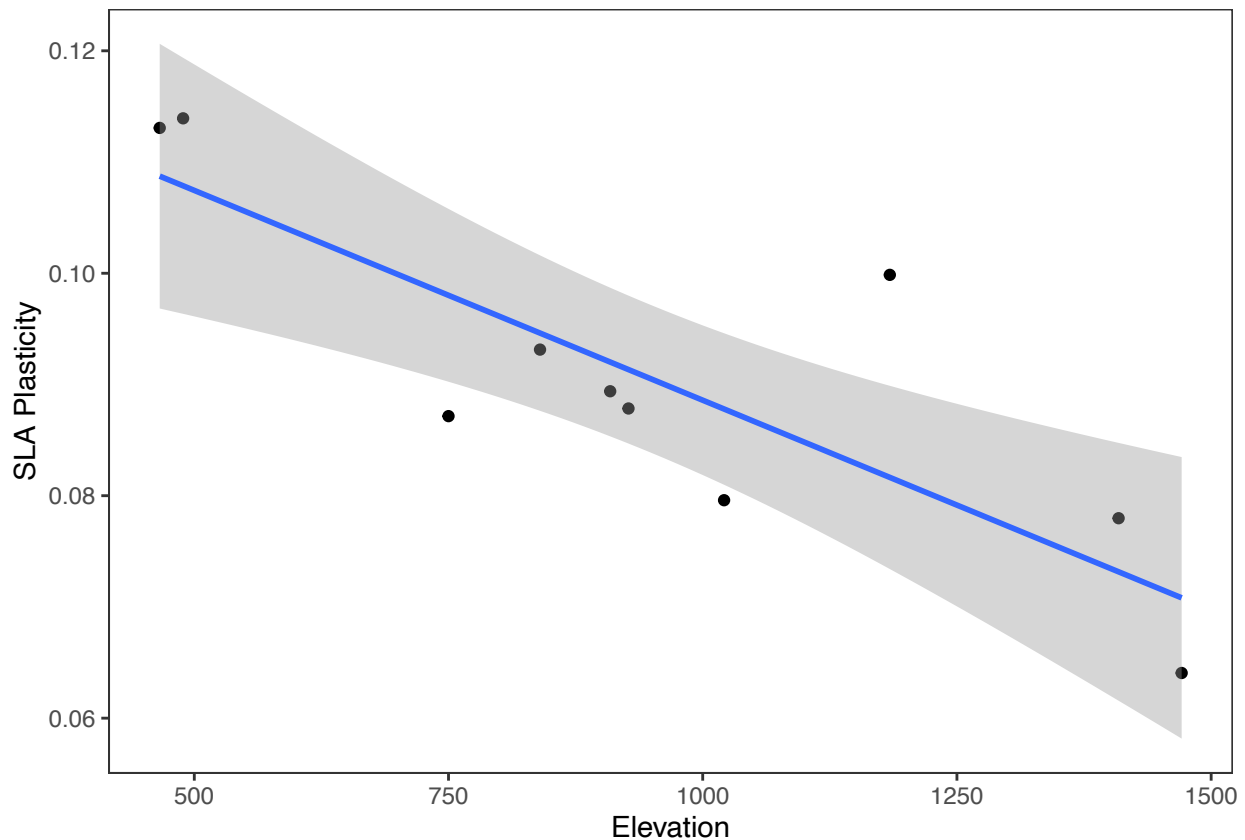
```
RDPI_SUM <- RDPIdataset %>% group_by(Elevation) %>% dplyr::summarize(
  SLA = mean(`SLA`, na.rm = TRUE),
  Running = mean(`Running`, na.rm = TRUE),
  Flowering = mean(`Flowering`, na.rm = TRUE),
  Stomata = mean(`Stomata`, na.rm = TRUE),
  SLA_se = sd(`SLA`, na.rm = TRUE) / sqrt(length(na.omit(`SLA`))),
  Running_se = sd(`Running`, na.rm = TRUE) / sqrt(length(na.omit(`Running`))),
  Flowering_se = sd(`Flowering`, na.rm = TRUE) / sqrt(length(na.omit(`Flowering`))),
  Stomata_se = sd(`Stomata`, na.rm = TRUE) / sqrt(length(na.omit(`Stomata`)))
```

```

)
RDPI_NS <- RDPIdataset %>% group_by(North_to_South) %>% dplyr::summarize(
  SLA = mean(`SLA`, na.rm = TRUE),
  Runnering = mean(`Runnering`, na.rm = TRUE),
  Flowering = mean(`Flowering`, na.rm = TRUE),
  Stomata = mean(`Stomata`, na.rm = TRUE),
  SLA_se = sd(`SLA`, na.rm = TRUE)/sqrt(length(na.omit(`SLA`))),
  Runnering_se = sd(`Runnering`, na.rm=TRUE)/sqrt(length(na.omit(`Runnering`))),
  Flowering_se = sd(`Flowering`, na.rm=TRUE)/sqrt(length(na.omit(`Flowering`))),
  Stomata_se = sd(`Stomata`, na.rm = TRUE)/sqrt(length(na.omit(`Stomata`)))
)
#Standard error calculations aren't working here... not sure why.

#Just going to plot mean data without error bars for right now.
sla_graph <- ggplot(data=RDPI_SUM)+
  aes(x=Elevation)+
  aes(y=SLA)+
  geom_point()+
  geom_smooth(method = "lm")+
  xlab("Elevation")+
  ylab("SLA Plasticity")+
  theme_bw()+
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())
plot(sla_graph)

```



```

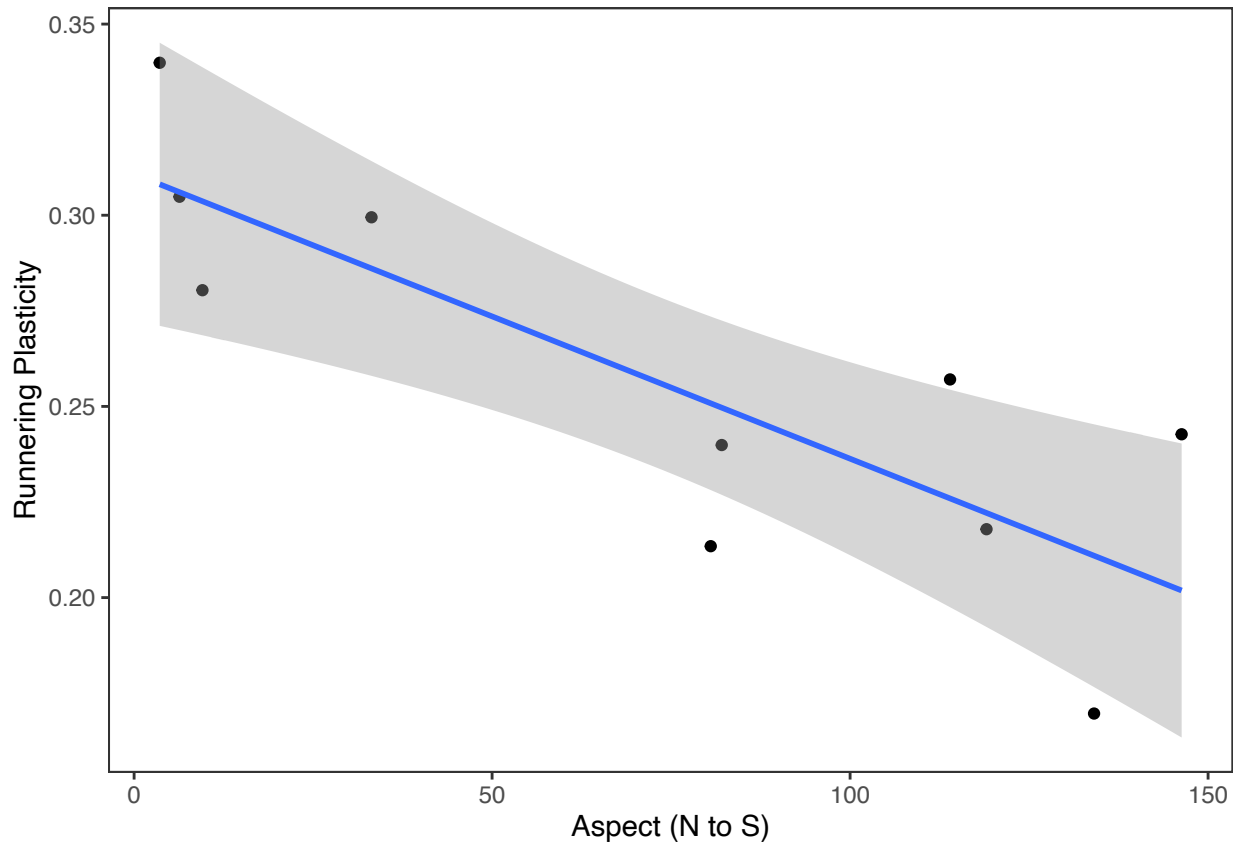
runnering_graph <- ggplot(data=RDPI_NS)+
  aes(x=North_to_South)+

```

```

aes(y=Runnering)+
geom_point()+
geom_smooth(method = "lm")+
xlab("Aspect (N to S)")+
ylab("Runnering Plasticity")+
theme_bw()+
theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())
plot(runnering_graph)

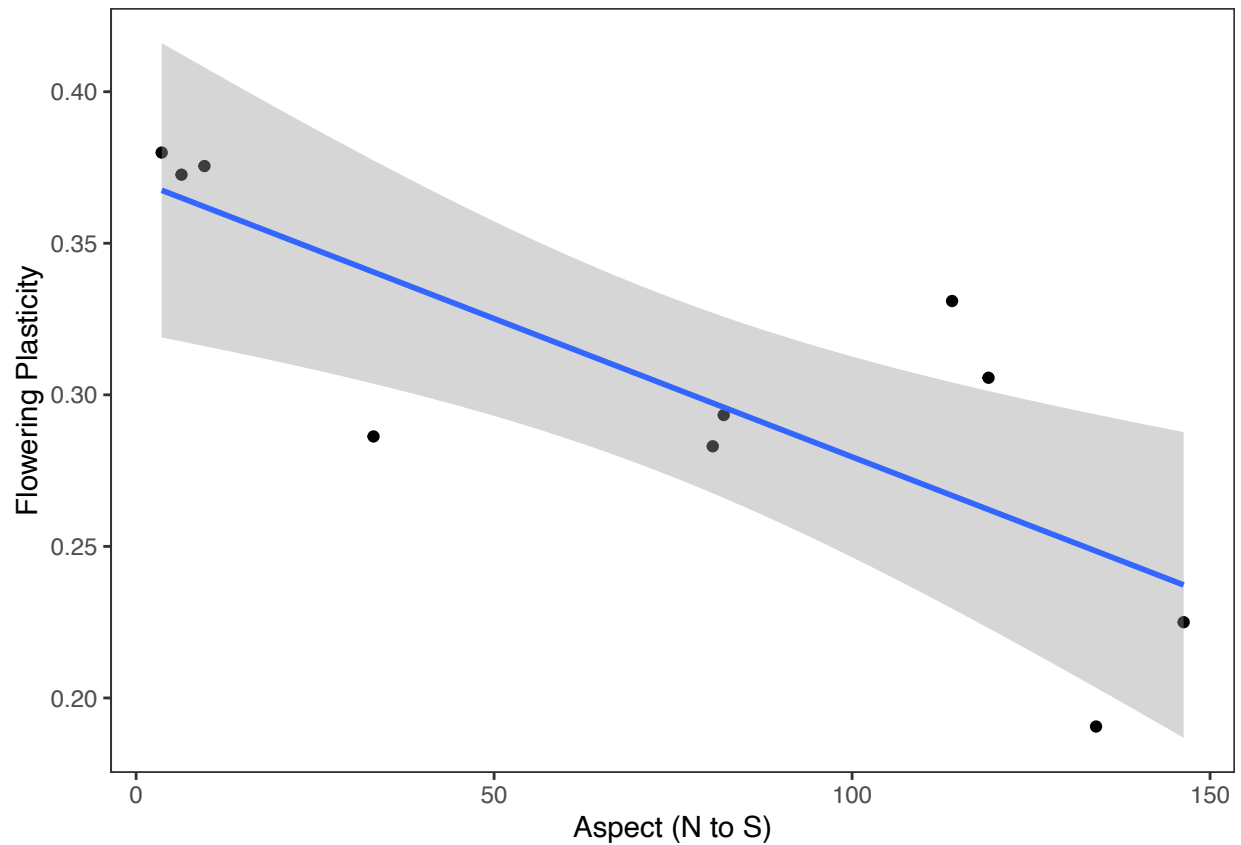
```



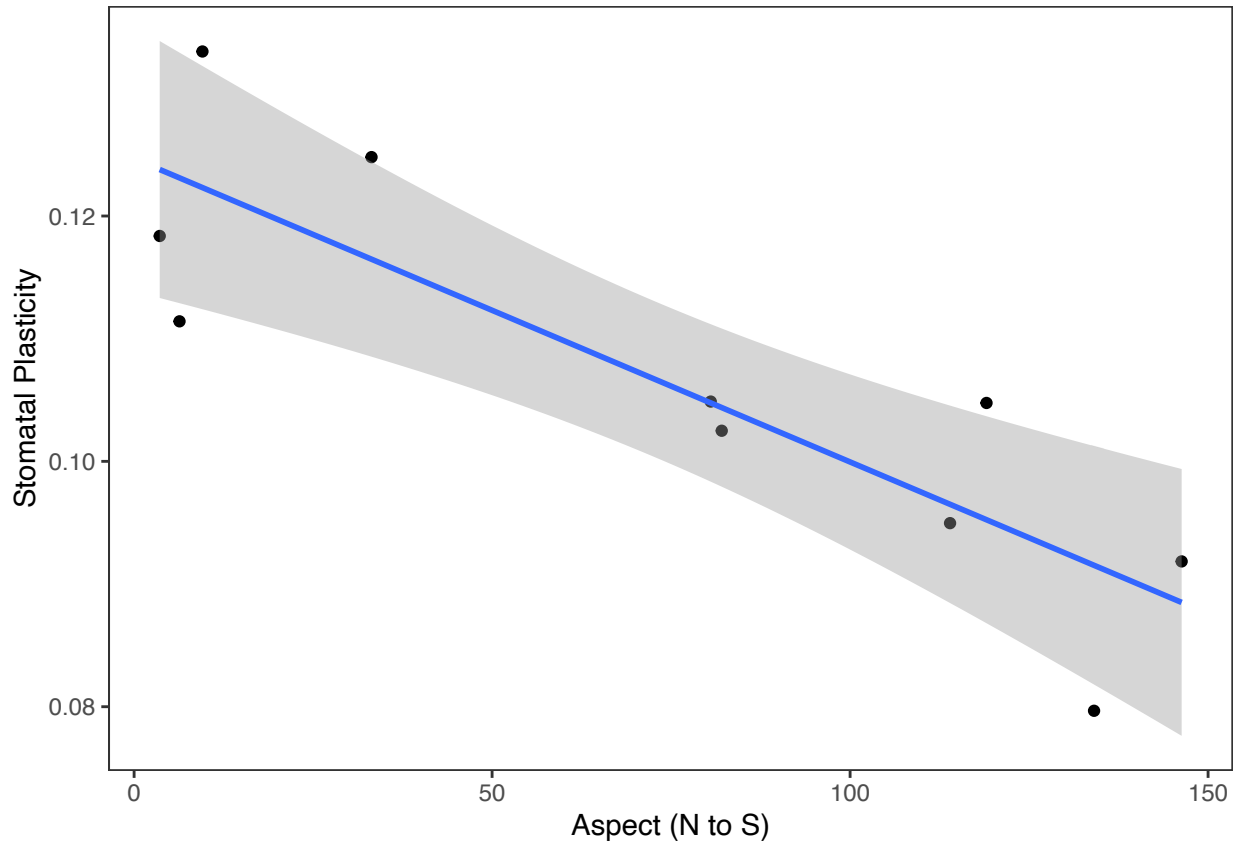
```

flowering_graph <- ggplot(data=RDPI_NS)+
aes(x=North_to_South)+
aes(y=Flowering)+
geom_point()+
geom_smooth(method = "lm")+
xlab("Aspect (N to S)")+
ylab("Flowering Plasticity")+
theme_bw()+
theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())
plot(flowering_graph)

```



```
stomata_graph <- ggplot(data=RDPI_NS)+
  aes(x=North_to_South)+
  aes(y=Stomata)+
  geom_point()+
  geom_smooth(method = "lm")+
  xlab("Aspect (N to S)")+
  ylab("Stomatal Plasticity")+
  theme_bw()+
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank())
plot(stomata_graph)
```



Summary

- I was not able to reproduce their data analysis techniques for RDPI, which is a great detriment to the reproducibility of the paper as a whole.
- I was able to (generally) reproduce each of the four graphs using the authors' supplemented RDPI data, minus issues with my error bar code.
- I would not give this paper a high score for reproducibility due to the issues I encountered when attempting to use the R package Plasticity.

References

- (Ameztegui 2017)
- (De Kort et al. 2020)
- (Valladares, Sanchez-Gomez, and Zavala 2006)
- Ameztegui, A. 2017. "Plasticity." *GitHub Repository*. <https://github.com/ameztegui/Plasticity>; GitHub.
- De Kort, Hanne, Bart Panis, Kenny Helsen, Rolland Douzet, Steven B Janssens, and Olivier Honnay. 2020. "Pre-adaptation to Climate Change Through Topography-driven Phenotypic Plasticity." Edited by Stephen Bonser. *J. Ecol.* 108 (4): 1465–74.
- Valladares, Fernando, David Sanchez-Gomez, and Miguel A Zavala. 2006. "Quantitative Estimation of Phenotypic Plasticity: Bridging the Gap Between the Evolutionary Concept and Its Ecological Applications." *J. Ecol.* 94 (6): 1103–16.