

```
#L:W Regession Graphs  
#create relevant graphics for L:W regression poster  
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```

```
#import packages  
library(ggplot2)  
library(tidyverse)
```

```
## -- Attaching packages -----
```

```
## v tibble  2.1.3      v dplyr   0.8.3  
## v tidyr   1.0.0      v stringr 1.4.0  
## v readr   1.3.1      v forcats 0.4.0  
## v purrr   0.3.3
```

```
## -- Conflicts -----  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag()     masks stats::lag()
```

```
library(maps)
```

```
## Warning: package 'maps' was built under R version 3.6.3
```

```
##  
## Attaching package: 'maps'
```

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

```
library(mapproj)
```

```
## Warning: package 'mapproj' was built under R version 3.6.3
```

```
library(egg)
```

```
## Warning: package 'egg' was built under R version 3.6.3
```

```
## Loading required package: gridExtra
```

```
##  
## Attaching package: 'gridExtra'
```

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

```
library(grid)
# library(sf)
# library(rnaturalearth)
```

```
#import data
rawDat <- read_csv('C:/R/FishRegressions/BiomassRegression_RawEdited.csv')
```

```
## Parsed with column specification:
## cols(
##   .default = col_double(),
##   SpeciesCode = col_character(),
##   CommonName = col_character(),
##   SciName = col_character(),
##   Gender = col_character(),
##   LengthType = col_character(),
##   Country = col_character(),
##   Locality = col_character(),
##   Ref = col_character(),
##   Source = col_character()
## )

## See spec(...) for full column specifications.
```

```
compDat <- read_csv('C:/R/FishRegressions/BiomassRegression_CompiledEdited.csv')
```

```
## Parsed with column specification:
## cols(
##   SpeciesCode = col_character(),
##   `Species Name` = col_character(),
##   SciName = col_character(),
##   a_cm_g = col_double(),
##   b = col_double(),
##   SD_log10_a = col_double(),
##   SD_b = col_double(),
##   SD_log10_W = col_double(),
##   n_Studies = col_double(),
##   n_Fish = col_double(),
##   `Length Measurement` = col_character(),
##   Gender = col_character(),
##   Country = col_character(),
##   Source = col_character()
## )
```

```
countryCoords <- read_csv('C:/R/FishRegressions/countryCoords.csv')
```

```
## Parsed with column specification:
## cols(
##   Country = col_character(),
##   lat = col_double(),
##   lon = col_double()
## )
```

```
#output filepath
```

```
fpOutput <- 'C:/R/FishRegressions/plots/'
```

```
countryDat <- data.frame(table(rawDat$Country))
```

```
countryDat <- countryDat %>% rename(Country = Var1)
```

```
countryCoords <- merge(countryDat, countryCoords, by = 'Country')
```

```
world <- map_data('world')
```

```
ggplot(fill = 'blue') +
```

```
#plot world
```

```
geom_polygon(  
  data = world,  
  aes(x = long, y = lat, group = group),  
  fill = '#ede4cc'  
) +
```

```
borders('world') +
```

```
ylim(-61.7,90) +
```

```
#coord_map() +
```

```
#theme_void() +
```

```
theme(  
  panel.background = element_rect(fill = 'white',#'#e6f5fc'),  
  plot.background = element_rect(fill = 'white',#'#e6f5fc'),  
  panel.border = element_blank(),  
  panel.grid.major = element_blank(),  
  panel.grid.minor = element_blank(),  
  axis.title.x=element_blank(),  
  axis.text.x=element_blank(),  
  axis.ticks.x=element_blank(),  
  axis.title.y=element_blank(),  
  axis.text.y=element_blank(),  
  axis.ticks.y = element_blank()  
) +
```

```
#plot data
```

```
geom_point(  
  data = countryCoords,  
  aes(x = lon, y = lat, size = Freq, pch = 21, fill = '#edf7f7', color = 'black')  
) +
```

```
#aesthetics
```

```
scale_shape_identity() +
```

```
scale_color_identity() +
```

```
scale_fill_identity() +
```

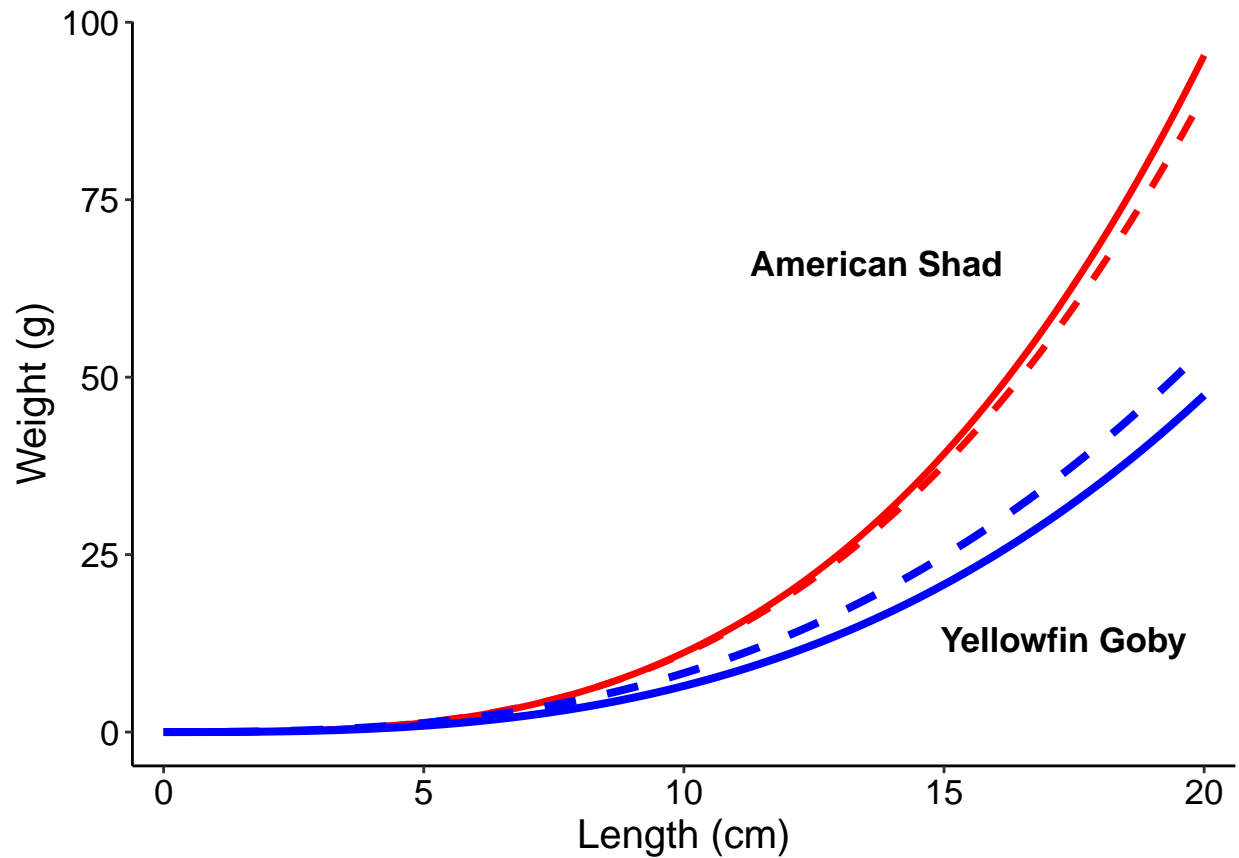
```
theme(legend.position = 'none') +
```

```
scale_size(name = 'Frequency', range = c(5,15)) +
```

```
geom_text(data = countryCoords, aes(x = lon, y = lat, label = Freq))
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```

```
## Warning: Removed 1 rows containing missing values (geom_text).
```

compDat

```
## # A tibble: 84 x 14
##   SpeciesCode `Species Name` SciName  a_cm_g    b SD_log10_a  SD_b
##   <chr>        <chr>         <chr>    <dbl> <dbl>    <dbl>    <dbl>
## 1 AMS        American Shad  Alosa ~ 0.0091  3.09    NA      0.06
## 2 BGS        Bluegill    Lepomi~ 0.0117  3.25    0.17    0.135
## 3 BGS        Bluegill    Lepomi~ 0.0309  3.1     0.169   0.158
## 4 BGS        Bluegill    Lepomi~ 0.0117  3.18    0.249   0.228
## 5 BKB        Black Bullhead Ameiur~ 0.0417  2.87    0.105   0.0548
## 6 BKB        Black Bullhead Ameiur~ 0.01     3.11    0.212   0.177
## 7 BKS        Black Crappie  Pomoxi~ 0.0112  3.08    0.105   0.0781
## 8 BPF        Bay Pipefish  Syngna~ 0.0002  3.12    NA      NA
## 9 BRB        Brown Bullhead Ameiur~ 0.00909  3.13    NA      NA
## 10 BRB       Brown Bullhead Ameiur~ 0.0135  2.98    0.206   0.141
## # ... with 74 more rows, and 7 more variables: SD_log10_W <dbl>,
## #   n_Studies <dbl>, n_Fish <dbl>, `Length Measurement` <chr>, Gender <chr>,
## #   Country <chr>, Source <chr>
```

```
# Heatmap
pltStudies <- ggplot(compDat, aes(`Length Measurement`, `Species Name`, fill= n_Studies)) +
  geom_tile(color = 'black', size = 1.01) +
  scale_fill_distiller(
    name = '# of Studies',
    trans = 'log',
```

```

palette = 'YlOrBr',
direction = 'horizontal',
breaks = c(1,5,20,90),
labels = c(1,5,20,90),
guide = guide_colorbar(frame.colour = 'black', ticks.colour = 'black', frame.linewidth = 2, ticks.l
scale_x_discrete(position = 'top') +
scale_y_discrete(limits = unique(rev(compDat$`Species Name`))) +
theme_bw() +
theme(
  panel.border = element_rect(color = 'black', size = 2),
  axis.text.x = element_text(size = 14, color = 'black'),#, face = 'bold',
  axis.text.y = element_text(size = 14, color = 'black'),#, face = 'bold',
  axis.title.y = element_blank(),#element_text(size = 18, color = 'black', face = 'bold'),
  axis.title.x = element_text(size = 18, color = 'white', face = 'bold'),
  legend.position = 'bottom',
  legend.title = element_text(size = 18),
  legend.title.align = 0.5,
  legend.key.size = unit(0.4, 'in'),
  legend.text = element_text(size = 14, colour = 'black'),
  panel.grid.major = element_blank(),
  plot.margin = unit(c(1,-0.002,1,1), 'in')
)

pltStudies <- set_panel_size(pltStudies,
  width = unit(4, 'in'),
  height = unit(13.5, 'in'))

pltFish <- ggplot(compDat, aes(`Length Measurement`, `Species Name`, fill= n_Fish)) +
  geom_tile(color = 'black', size = 1.01) +
  scale_fill_distiller(
    name = '# of Fish',
    trans = 'log',
    palette = 'YlGnBu',
    direction = 'horizontal',
    breaks = c(1,10,1000,100000),
    labels = c(1,10,1000,100000),
    guide = guide_colorbar(frame.colour = 'black', ticks.colour = 'black', frame.linewidth = 2, ticks.l
scale_x_discrete(position = 'top') +
scale_y_discrete(limits = unique(rev(compDat$`Species Name`))) +
theme_bw() +
theme(
  axis.ticks.y = element_blank(),
  panel.border = element_rect(color = 'black', size = 2),
  axis.text.x = element_text(size = 14, color = 'black'),
  axis.text.y = element_blank(),
  axis.title.y = element_blank(),
  axis.title.x = element_text(size = 18, color = 'white', face = 'bold'),
  legend.position = 'bottom',
  legend.title = element_text(size = 18),
  legend.title.align = 0.5,
  legend.key.size = unit(0.4, 'in'),
  legend.key = element_rect(fill = 'white', color = 'black'),
  legend.text = element_text(size = 14, colour = 'black'),

```

```

    panel.grid.major = element_blank(),
    plot.margin = unit(c(1,1,1,-0.002), 'in')
  )

pltFish <- set_panel_size(pltFish,
  width  = unit(4, 'in'),
  height = unit(13.5, 'in'))

pltComb <- arrangeGrob(
  pltStudies,
  pltFish,
  ncol = 2,
  top = textGrob('Length Measurement', gp = gpar(fontsize = 18, fontface = 'bold'), hjust = 0.32, vjust = 0)
)

ggsave(filename = paste(fpOutput, 'heatmap.png', sep = ''), plot = pltComb, width = 13.5, height = 15.2)

```