

# Thesis meeting

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```
#loading libraries
pacman::p_load(rvest, rgbif, tidyverse, rnaturalearth, rnaturalearthdata, rgeos, devRate)
```

## Pulling down data from GBIF

Notes:

- Excluded genres from the final meta analysis dataset that did not have greater than 8 sample size (included *Platyplectum ornatum* (6), *Natrix natrix* (5), *Trachemys scripta* (2), *Leptopilinia bouldarii* (6), *Clematis vitalba* (1))
- Any of the remaining organisms have a sample size of at least 8 when aggregated by genus
- *S. enterica* and *E. coli* had no data on GBIF and was therefore left out.

## Plotting preliminary plot from GBIF data

- The climate reference bands were pulled from Devine et al 2015 with the following groups:

Tropical: 20 N - 20 S Subtropical: 20-40 N, 20-40 S Extratropical: 40-60 N, 40-60 S

Added in my own category of polar: anything above 60 N or below 60 S

```
#generating data for map overlay
regions <- read_csv("gbif_region_data.csv")
```

```
## Parsed with column specification:
## cols(
##   countryCode = col_character(),
##   genus = col_character(),
##   species = col_character(),
##   decimalLongitude = col_double(),
##   decimalLatitude = col_double(),
##   thermal_zone = col_character()
## )
```

```

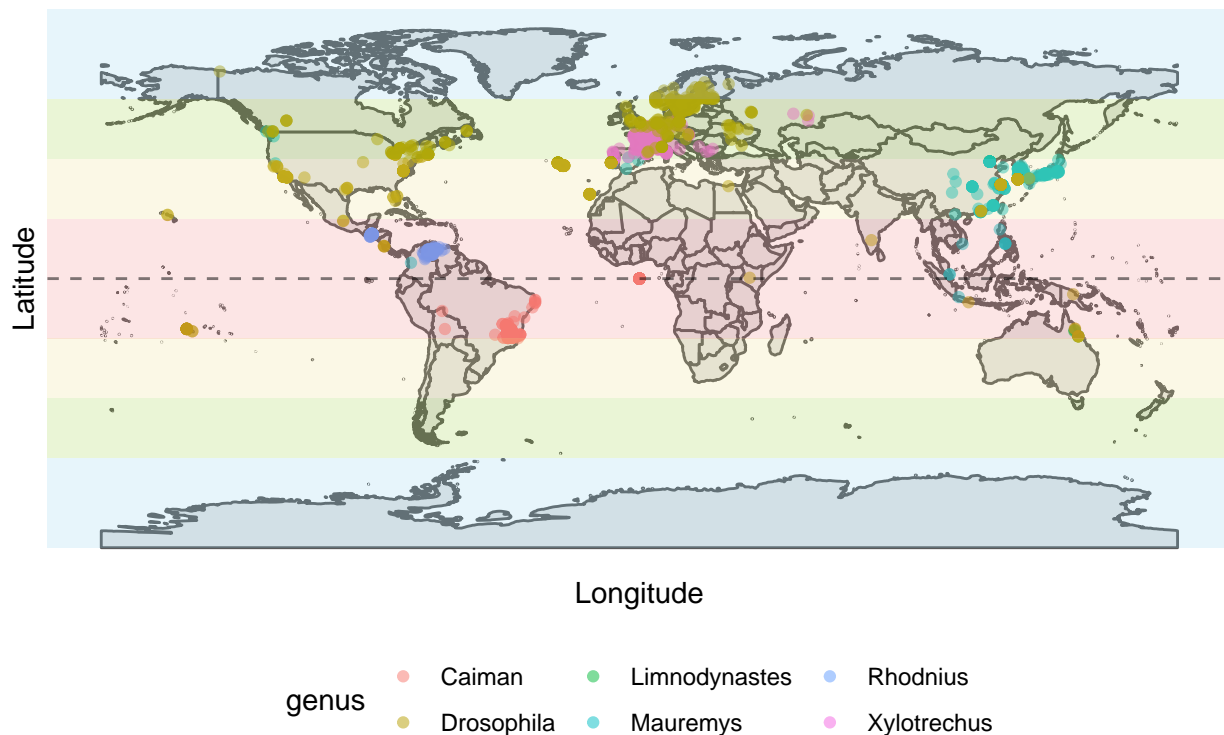
world <- ne_countries(scale = "medium", returnclass = "sf")
#plotting up data
ggplot(data = world)+
  geom_sf()+
  geom_point(data = regions, aes(x=decimalLongitude, y=decimalLatitude, color=genus), alpha = 0.5)+
  annotate("rect",xmin = -Inf, xmax = Inf, ymin = -20, ymax = 20, alpha = 0.2, fill = "lightcoral")+
  annotate("rect",xmin = -Inf, xmax = Inf, ymin = 20, ymax = 40, alpha = 0.2, fill = "lightgoldenrod")+
  annotate("rect",xmin = -Inf, xmax = Inf, ymin = -40, ymax = -20, alpha = 0.2, fill = "lightgoldenrod")+
  annotate("rect",xmin = -Inf, xmax = Inf, ymin = 40, ymax = 60, alpha = 0.2, fill = "yellowgreen")+
  annotate("rect",xmin = -Inf, xmax = Inf, ymin = -60, ymax = -40, alpha = 0.2, fill = "yellowgreen")+
  annotate("rect",xmin = -Inf, xmax = Inf, ymin = 60, ymax = 90, alpha = 0.2, fill = "skyblue")+
  annotate("rect",xmin = -Inf, xmax = Inf, ymin = -90, ymax = -60, alpha = 0.2, fill = "skyblue")+
  geom_hline(yintercept = 0, alpha =0.5, linetype= "dashed")+
  theme_classic()+
  theme(legend.position="bottom")+
  ylab("Latitude")+
  xlab("Longitude")

```

```

## Warning: range backtransformation not implemented in this coord; results may be
## wrong.

```



```

#attempting to pull thermal performance data from devRate
myDf <- exTropicalMoth$raw$egg

```

```
devRateModelAll(dfData = myDf)
devRateFind(species = "Drosophila melanogaster")
devRateFind(species = "Drosophila simulans")
```

## Running Questions:

- How should thermal regimes be designated? By latitude or country code? Losing some occurrence data because country is listed but latitude/longitude are not.
- How can I successfully join this dataset with the meta analysis dataset to run a model that takes into account location? How should I handle some species that span multiple zones (i.e. *Drosophila* )

-Should I be grouping by genus or by species?

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Additional notes/questions from figures last week

- Semenov 2007 and Kern et al 2015 were the two studies with the strangely smooth curves
  - Kern et al 2015–I changed the sample sizes but not sure they are right?
    - \* Looks less curved after sample size change -Not sure about the sample size for Semenov: sample size of 3 for 3 replicates, should I be multiplying that by the original CFU count?
- Removed Piccau et al (the big negative yi)–only study without a comparable constant and fluctuating mean
- How to best determine whether or not the temperatures each species is experiencing are heat stress temperatures? -It looks like in the final processes meta-analysis file there are quite a few species with range of temperatures

-Would it be useful to pull in and extract the thermal performance acclimation studies?