

distribution-summary

```
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.0 --

## v ggplot2 3.3.3     v purrr   0.3.4
## v tibble  3.1.0     v dplyr    1.0.5
## v tidyr   1.1.2     v stringr  1.4.0
## v readr   1.4.0     v forcats 0.5.1

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

library(rnaturalearth)
library(rnaturalearthdata)
library(raster)

## Loading required package: sp

##
## Attaching package: 'raster'

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

## The following object is masked from 'package:tidyrr':
##       extract

library(rgeos)

## rgeos version: 0.5-5, (SVN revision 640)
## GEOS runtime version: 3.8.1-CAPI-1.13.3
## Linking to sp version: 1.4-5
## Polygon checking: TRUE

library(sf)

## Linking to GEOS 3.8.1, GDAL 3.0.4, PROJ 6.3.2
```

```

mosquito_points <- st_read("data/interim/mosquito_points.dbf")

## Reading layer 'mosquito_points' from data source '/home/daniel/Projects/mosquito-jsdm/data/interim/mosquito_points.dbf'
## Simple feature collection with 8072 features and 1 field
## geometry type:  POINT
## dimension:      XY
## bbox:           xmin: -15.91 ymin: 23.79 xmax: 60.1 ymax: 66.4
## geographic CRS: WGS 84

```

Species Summary

```

data <- mosquito_points %>% as.data.frame()

data %>% count(species) %>% knitr::kable()

```

species	n
Aedes aegypti	494
Aedes albopictus	1104
Aedes cantans	123
Aedes caspius	162
Aedes cinereus	136
Aedes japonicus	317
Aedes koreicus	408
Aedes vexans	176
Anopheles atroparvus	147
Anopheles claviger	230
Anopheles labranchiae	150
Anopheles maculipennis	343
Anopheles plumbeus	321
Anopheles sacharovi	176
Coquillettidia richiardii	197
Culex modestus	400
Culex perexiguus	198
Culex pipiens	1495
Culex theileri	143
Culex torrentium	363
Culex tritaeniorhynchus	358
Culiseta annulata	631

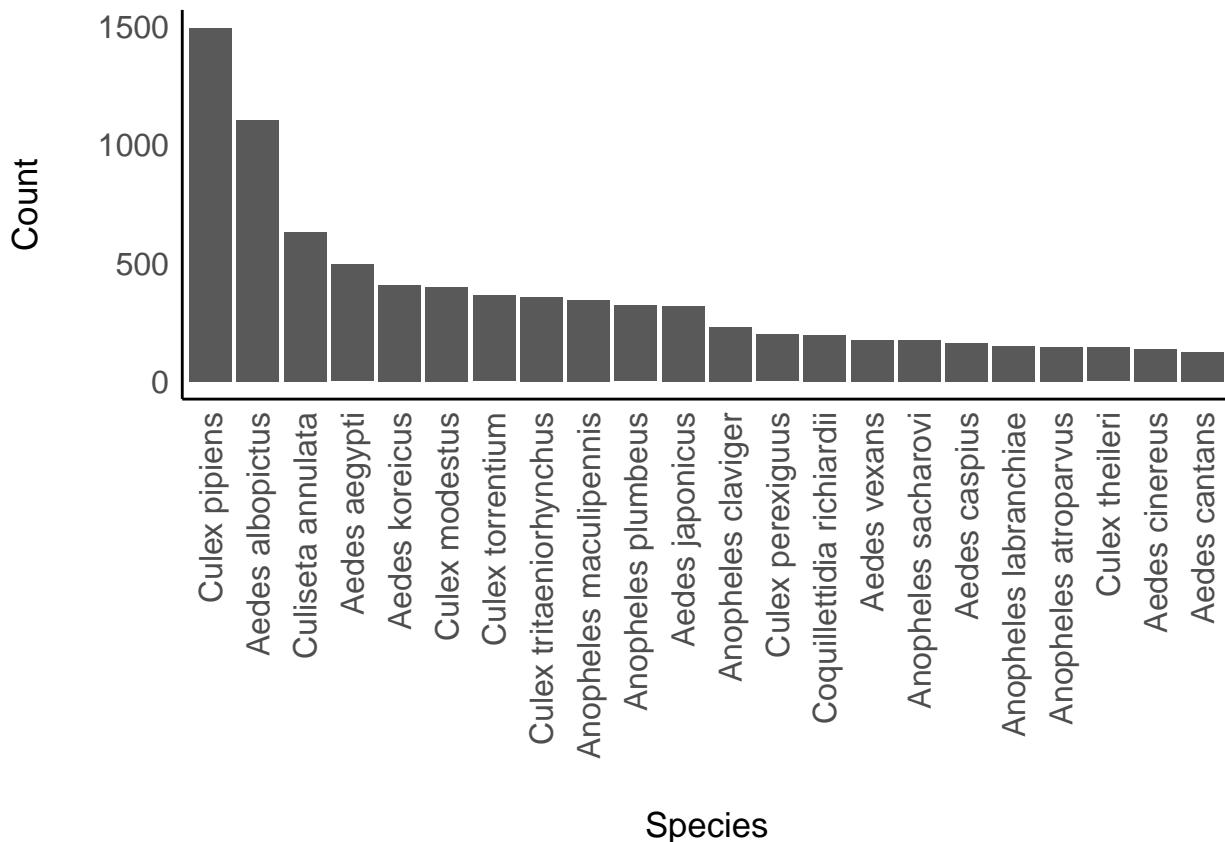
Graphed

```

data %>%
  count(species) %>%
  ggplot(aes(x = reorder(species, -n), y = n)) +
  geom_col() +
  ylab("Count") +
  xlab("Species") +

```

```
see::theme_modern() +
theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1))
```



```
world <- ne_countries(scale = "medium", returnclass = "sf")

world_mod <- st_transform(world, 3035)
mosquito_mod <- st_transform(mosquito_points, 3035)

ggplot(data = world_mod) +
  geom_sf() +
  geom_sf(data = mosquito_mod, size = 1) +
  coord_sf(
    xlim = c(1651007 + 100000, 7567579 + 100000),
    ylim = c(525513.3 + 100000, 4878584 + 100000),
    expand = FALSE
  ) +
  facet_wrap(~species)
```

