week-8-hw

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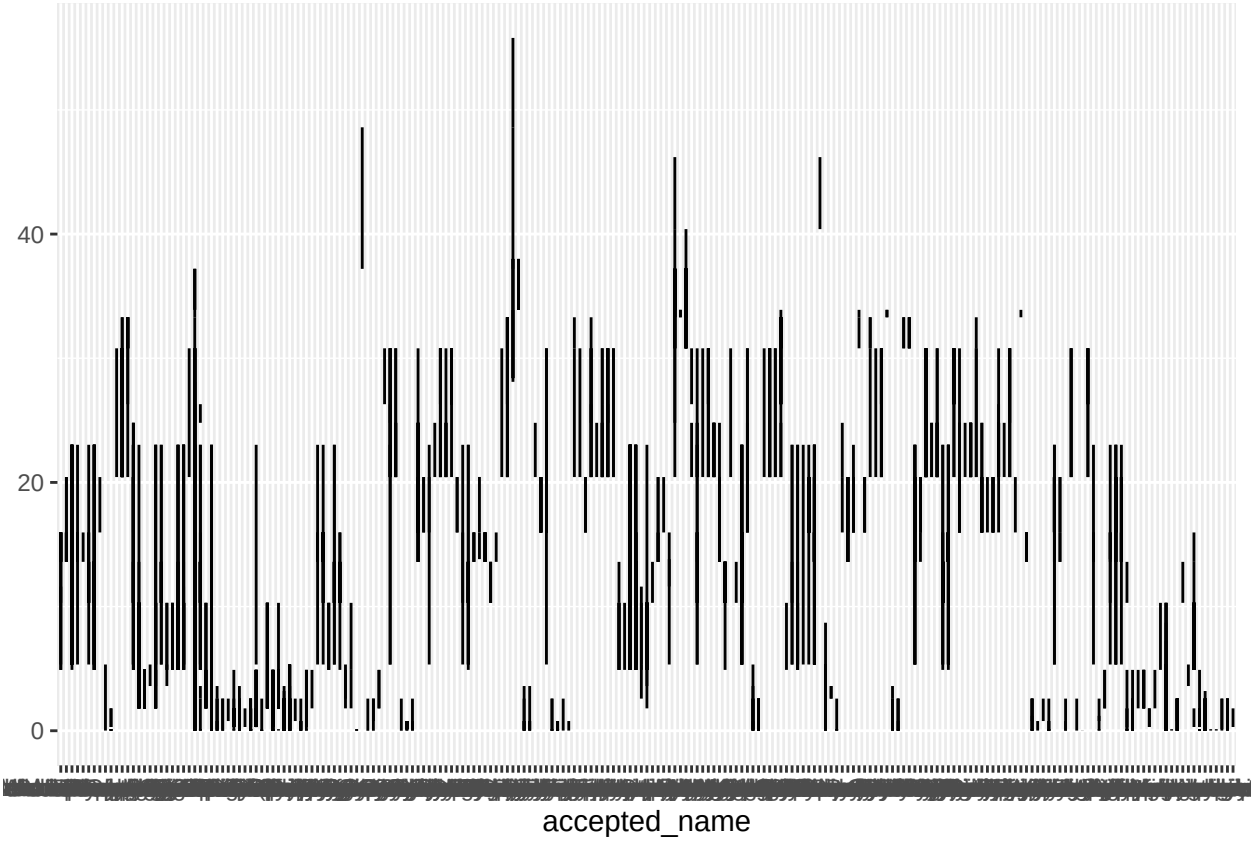
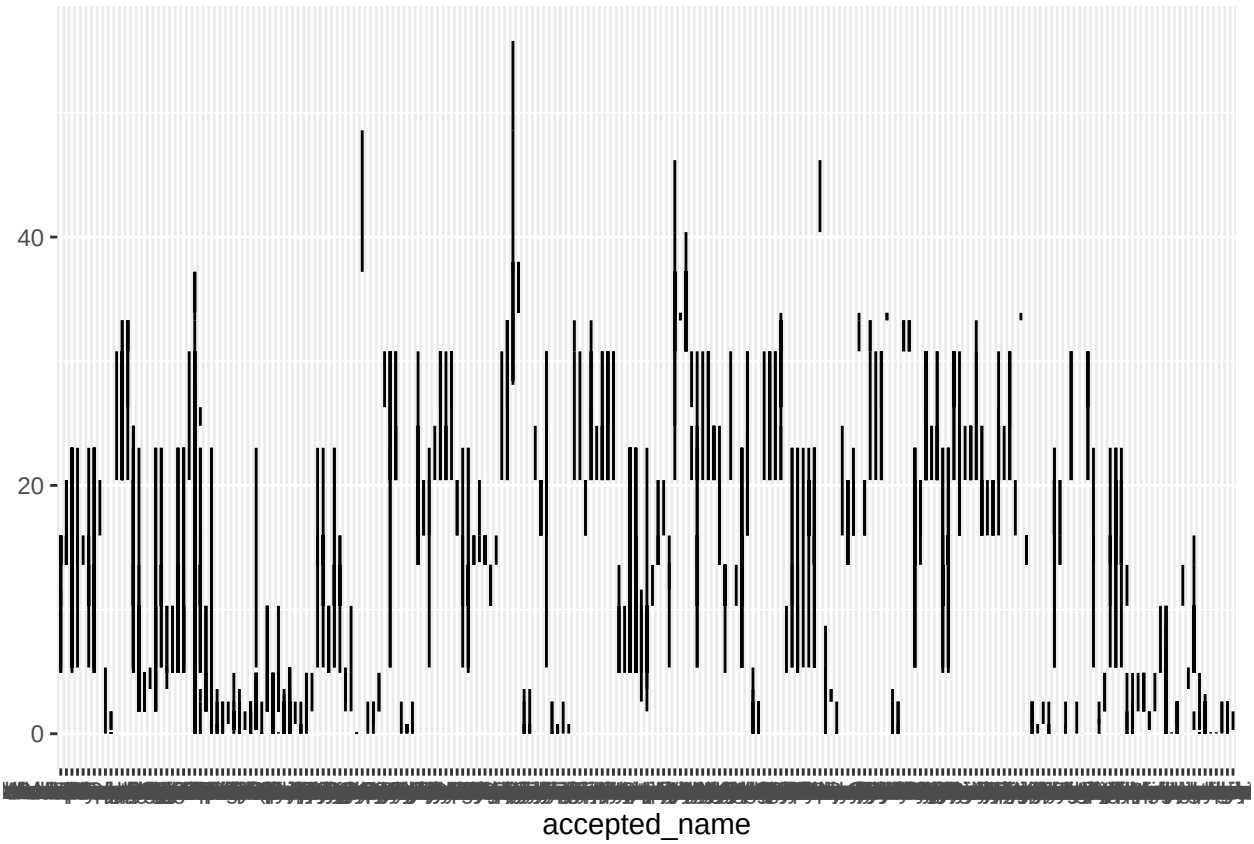
```
library(ggplot2)
setwd("/home/eeb177-student/Desktop/eeb-177/homework-folder/week-8-hw/")
canid <- read.csv("/home/eeb177-student/Desktop/eeb-177/homework-folder/week-8-hw/canids_3.csv", header
names(canid) <- c("occurrence_no", "record_type", "reid_no", "flags", "collection_no", "accepted_name",
head(canid)
```

```
##   occurrence_no record_type reid_no flags collection_no
## 1        117266         occ      NA    NA          9070
## 2        150070         occ      NA    NA         13293
## 3        176227         occ    3083    NA         16626
## 4        176384         occ      NA    NA         16647
## 5        177551         occ      NA    NA         16840
## 6        177611         occ    3336    NA         16845
##           accepted_name accepted_rank accepted_no     early_interval
## 1  Cynodictis lacustris       species      349281        Late Eocene
## 2                 Cuon         genus       41204 Middle Pleistocene
## 3           Hesperocyon         genus       41217        Late Uintan
## 4 Neovulpavus washakius       species       49147             Uintan
## 5           Hesperocyon         genus       41217         Duchesnean
## 6 Hesperocyon gregarius       species       44845         Duchesnean
##      late_interval max_ma  min_ma    NA
## 1                  37.200 33.9000 11154
## 2 Late Pleistocene  0.781  0.0117  4412
## 3                  46.200 40.4000  1139
## 4                  46.200 40.4000  2495
## 5       Chadronian 40.400 33.9000  3359
## 6                  40.400 37.2000  6226
```

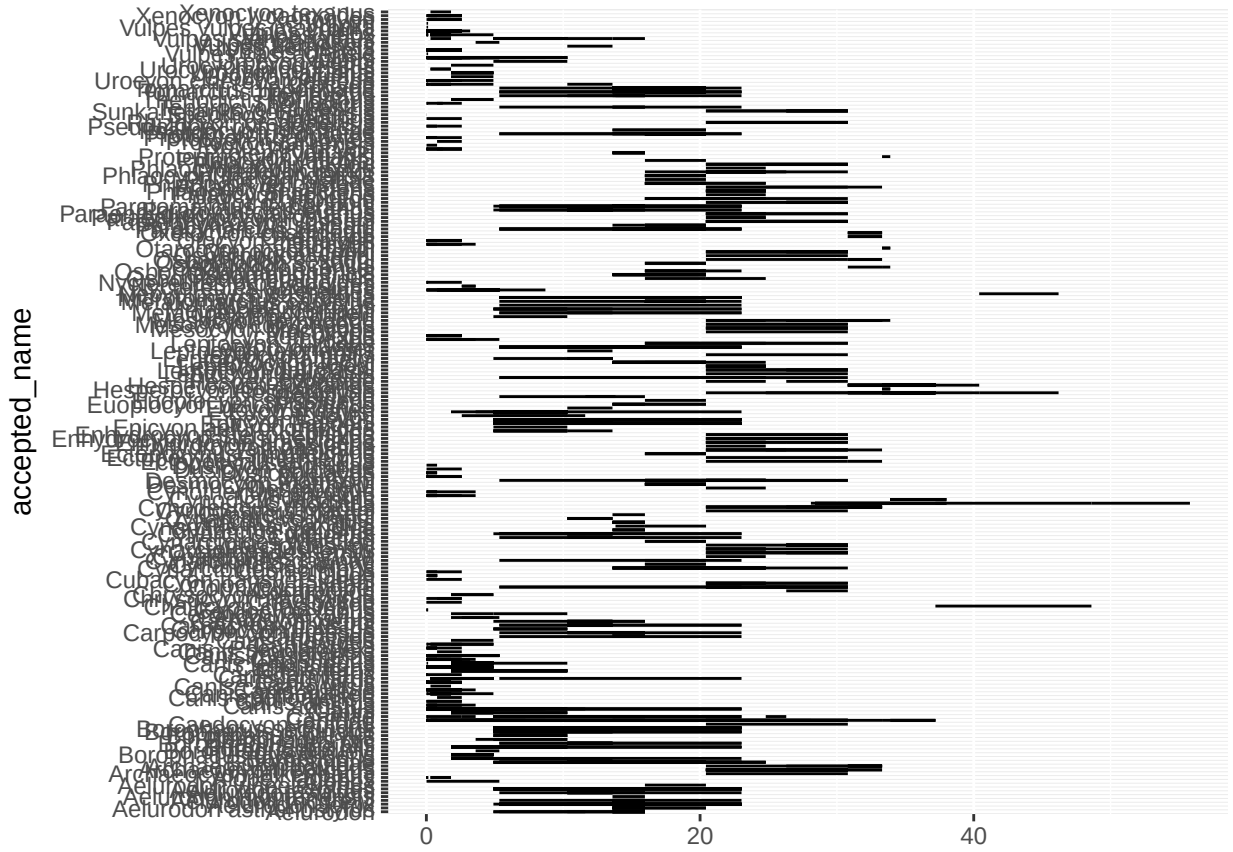
```
canid_occ <- ggplot(canid, aes(accepted_name, ymax =max_ma, ymin=min_ma), color = accepted_rank)
canid_occ <- canid_occ + geom_linerange()
canid_occ
```



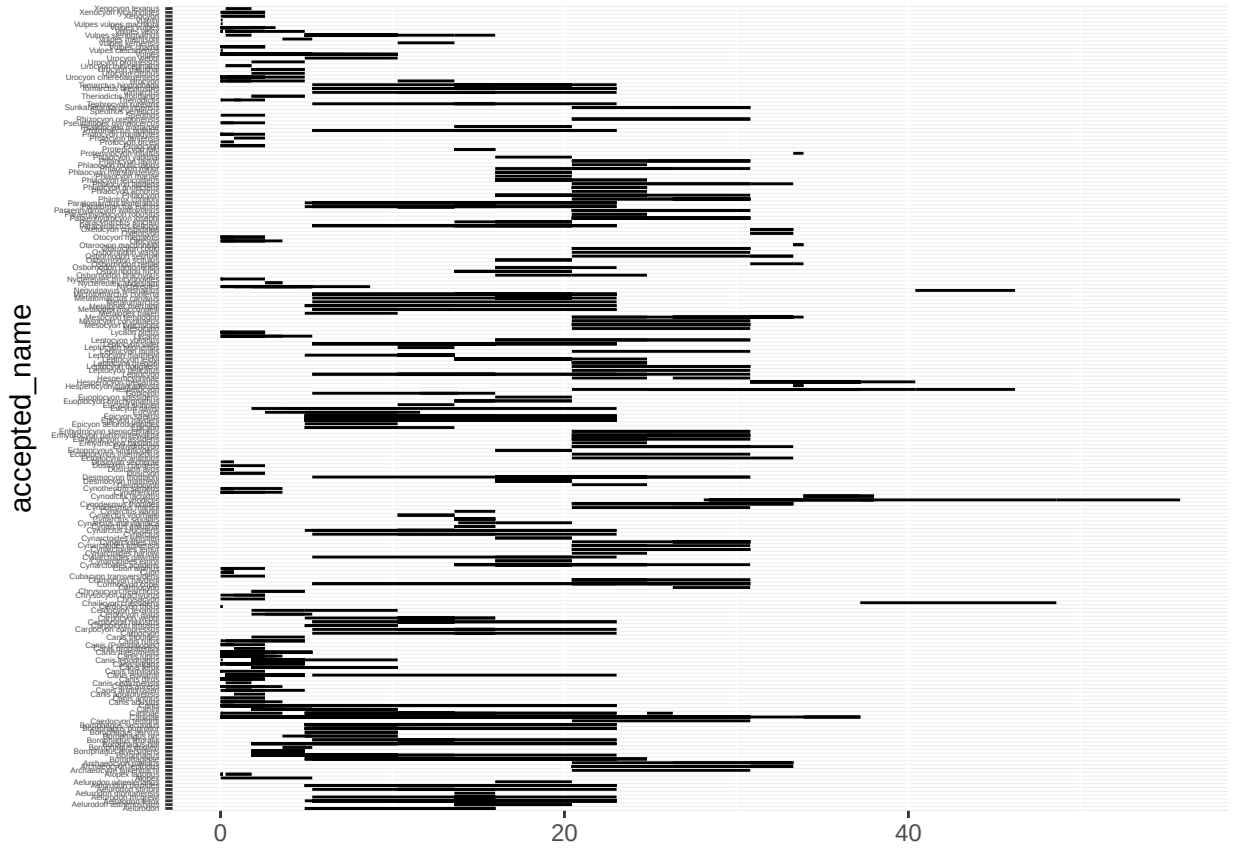

```
canid_occ <- canid_occ + theme(legend.position="none")
canid_occ
```



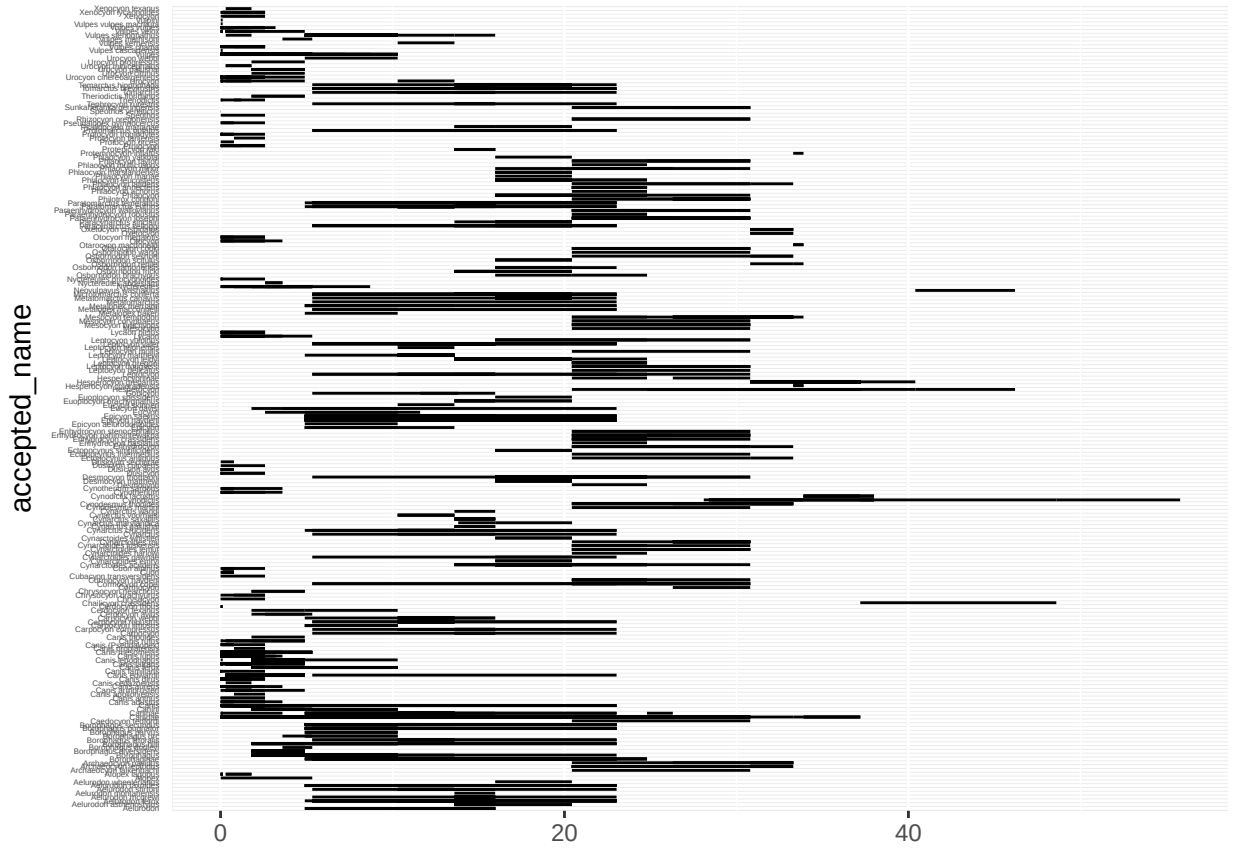

```
canid_occ <- canid_occ + coord_flip()
canid_occ
```




```
canid_occ <- canid_occ +  theme(axis.text.y = element_text(size=3))
canid_occ
```

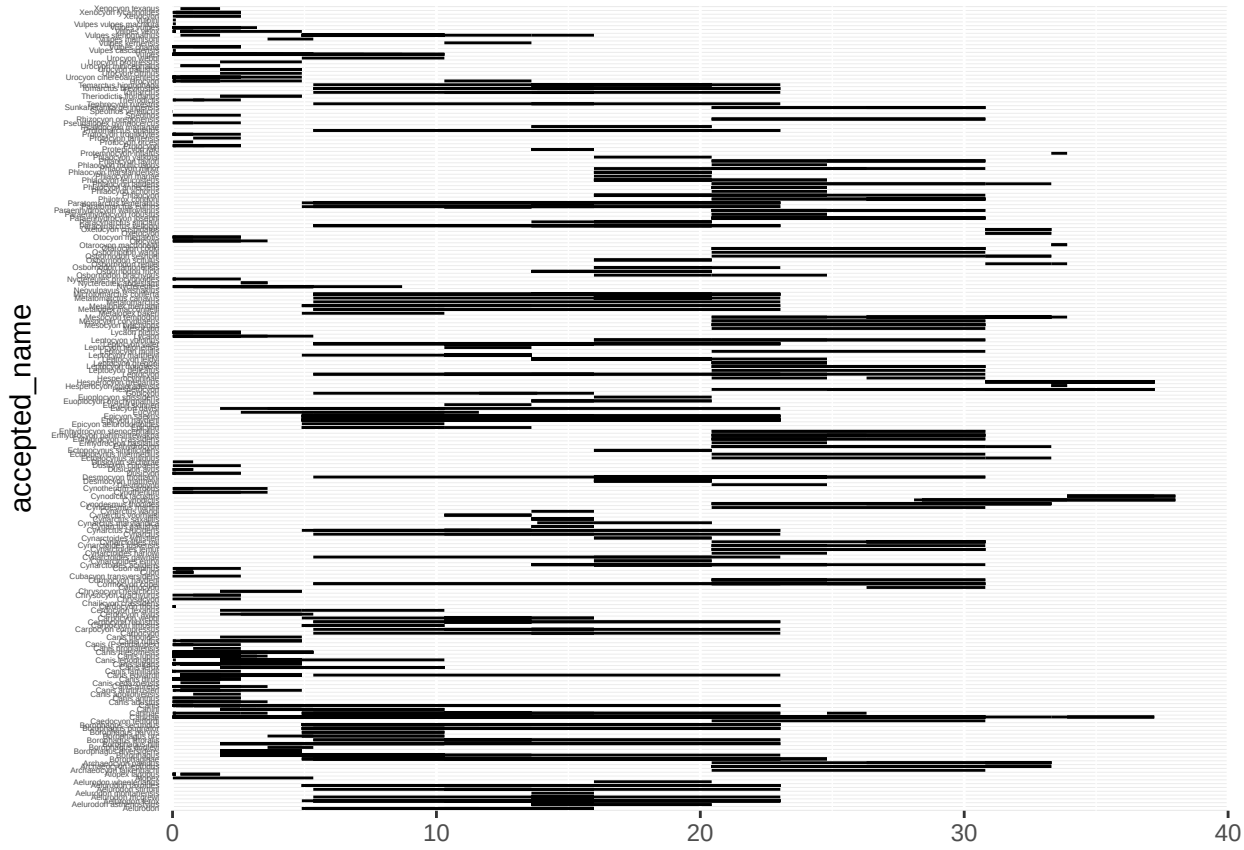



```
canid_occ <- canid_occ + theme(axis.ticks.y=element_blank())
canid_occ
```



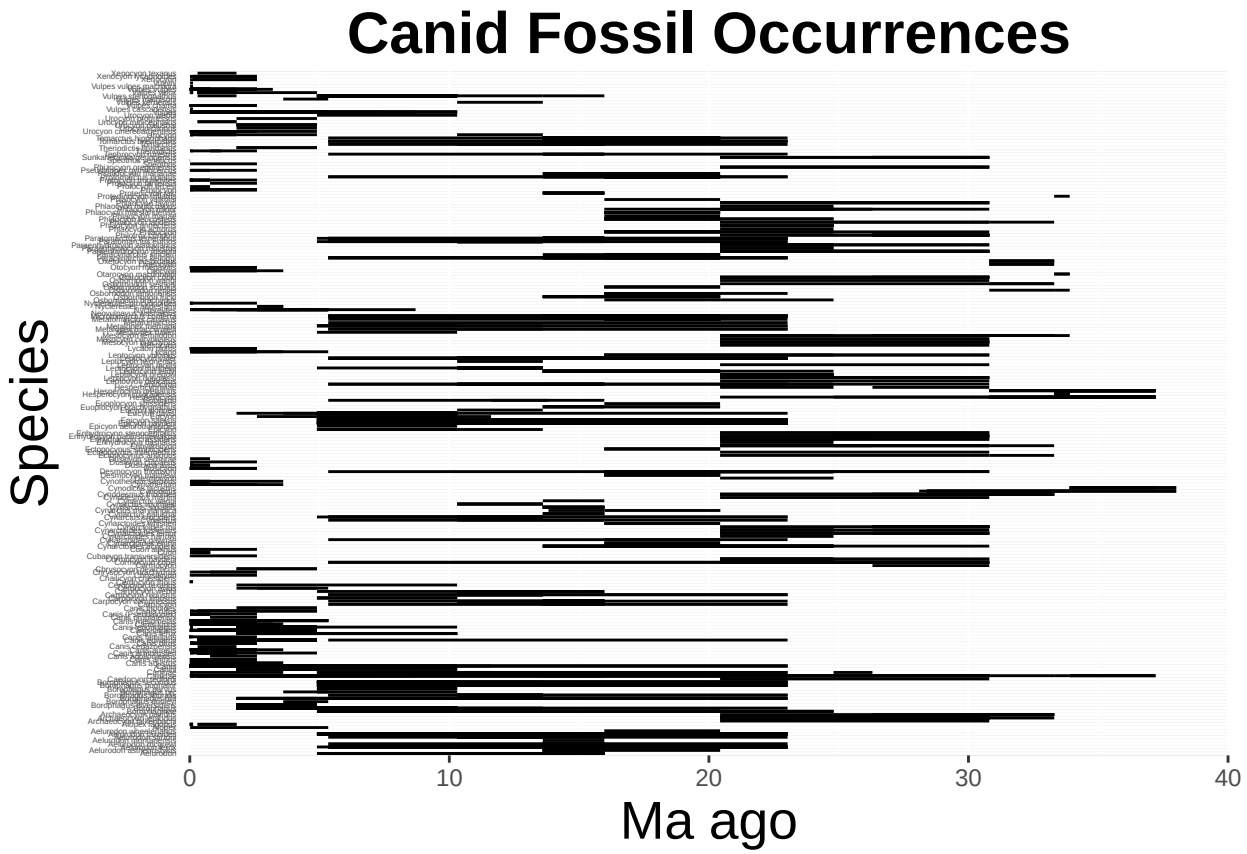

```
canid_occ <- canid_occ + scale_y_continuous(limits=c(0, 40), expand = c(0, 0), breaks=c(0, 10, 20, 30, 4
canid_occ
```

```
## Warning: Removed 7 rows containing missing values (geom_linerange).
```




```
canid_occ <- canid_occ + labs(title = "Canid Fossil Occurrences", x = "Species", y = "Ma ago") + theme(
canid_occ
```

```
## Warning: Removed 7 rows containing missing values (geom_linerange).
```



canids

uniq species = 211

uniq genera = 614?

4. what species has the longest... what?