## Assignment

My name

```
library(knitr)
library(tidyverse)
```

## Download data

```
download.file("http://www.esapubs.org/archive/ecol/E096/269/Data_Files/Amniote_Database_Aug_2015.csv",
# Read data
Amniote<-read.csv("./data/Amniote_Database_Aug_2015.csv")</pre>
```

## Explore data

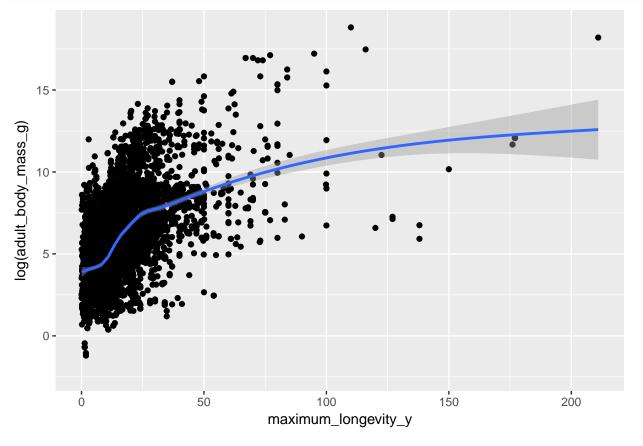
```
names(Amniote)
```

```
##
   [1] "class"
  [2] "order"
## [3] "family"
## [4] "genus"
## [5] "species"
## [6] "subspecies"
## [7] "common_name"
## [8] "female_maturity_d"
  [9] "litter_or_clutch_size_n"
## [10] "litters_or_clutches_per_y"
## [11] "adult_body_mass_g"
## [12] "maximum_longevity_y"
## [13] "gestation_d"
## [14] "weaning_d"
## [15] "birth_or_hatching_weight_g"
## [16] "weaning_weight_g"
## [17] "egg_mass_g"
## [18] "incubation_d"
## [19] "fledging_age_d"
## [20] "longevity_y"
## [21] "male_maturity_d"
## [22] "inter_litter_or_interbirth_interval_y"
## [23] "female_body_mass_g"
## [24] "male_body_mass_g"
## [25] "no_sex_body_mass_g"
## [26] "egg_width_mm"
## [27] "egg_length_mm"
## [28] "fledging_mass_g"
## [29] "adult_svl_cm"
## [30] "male_svl_cm"
## [31] "female_svl_cm"
## [32] "birth_or_hatching_svl_cm"
```

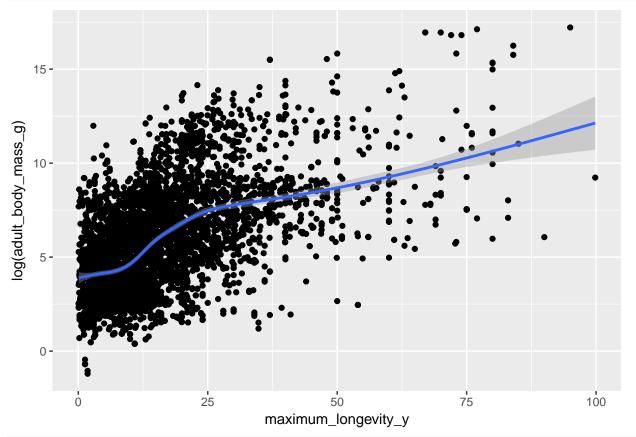
class	N_order	N_families	N_species
Aves	40	230	5525
Mammalia	29	152	3473
Reptilia	3	83	4692

```
# Replace -999 for NAs
Amniote[Amniote==-999] <-NA

ggplot(Amniote, aes(x=maximum_longevity_y, y=log(adult_body_mass_g))) +
    geom_point()+
    stat_smooth()</pre>
```



```
Amniote %>%
  filter(maximum_longevity_y<100) %>%
  ggplot(aes(x=maximum_longevity_y, y=log(adult_body_mass_g))) +
  geom_point()+
  stat_smooth()
```



```
Amniote %>%
  filter(class=="Mammalia" & maximum_longevity_y < 100) %>%
  ggplot(aes(x=maximum_longevity_y, y=log(adult_body_mass_g))) +
  geom_point()+
  stat_smooth(model="lm")
```

