IUCN_dat_intro

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Read Data

```
data = read_csv('iucn_dat.csv')

# make data set smaller to just columns interested in
imp_data = data %>% select(scientificName, redlistCategory, populationTrend, BodyMass)

imp_data2 = data %>% select(redlistCategory, populationTrend, BodyMass, cat_change, cat_change_bi, syste
```

Data Set Basics

- there are 35451 total species in the data set
- there are 13400 species with body mass data

How many species are in each distinct category?

```
imp_data %>% group_by(redlistCategory) %>% summarize(Sum = n()) %>% arrange(-Sum)
```

```
## # A tibble: 10 x 2
##    redlistCategory                     Sum
##    <chr>                             <int>
##  1 Least Concern                     20473
##  2 Data Deficient                     5152
##  3 Vulnerable                         2928
##  4 Endangered                         2740
##  5 Near Threatened                    2333
##  6 Critically Endangered              1521
##  7 Extinct                             285
##  8 Extinct in the Wild                  15
##  9 Lower Risk/least concern              3
## 10 Lower Risk/conservation dependent     1
```

```
imp_data %>% group_by(populationTrend) %>% summarize(Sum = n()) %>% arrange(-Sum)
```

```
## # A tibble: 5 x 2
##   populationTrend   Sum
##   <chr>           <int>
## 1 Unknown         12754
## 2 Decreasing      11508
```

```
## 3 Stable           9848
## 4 Increasing        900
## 5 <NA>              441
```

```
imp_data2 %>% group_by(cat_change) %>% summarize(Sum = n()) %>% arrange(-Sum)
```

```
## # A tibble: 10 x 2
##    cat_change   Sum
##         <dbl> <int>
##  1         NA 32749
##  2          1  1011
##  3         -1   881
##  4          2   352
##  5         -2   311
##  6          3    69
##  7         -3    35
##  8          0    27
##  9          4    10
## 10         -4     6
```

```
imp_data2 %>% group_by(cat_change_bi) %>% summarize(Sum = n()) %>% arrange(-Sum)
```

```
## # A tibble: 3 x 2
##   cat_change_bi   Sum
##   <chr>         <int>
## 1 <NA>          32776
## 2 decline        1442
## 3 improve        1233
```

```
imp_data2 %>% group_by(systems) %>% summarize(Sum = n()) %>% arrange(-Sum)
```

```
## # A tibble: 10 x 2
##    systems                                          Sum
##    <chr>                                          <int>
##  1 Terrestrial                                    19595
##  2 Terrestrial|Freshwater (=Inland waters)         6712
##  3 Marine                                          5202
##  4 Freshwater (=Inland waters)                     2851
##  5 Terrestrial|Freshwater (=Inland waters)|Marine   494
##  6 Terrestrial|Marine                               408
##  7 Freshwater (=Inland waters)|Marine               171
##  8 <NA>                                              10
##  9 Marine|Marine                                      7
## 10 Freshwater (=Inland waters)|Marine|Marine          1
```

```
imp_data2 %>% group_by(realm) %>% summarize(Sum = n()) %>% arrange(-Sum)
```

```
## # A tibble: 128 x 2
##    realm                      Sum
##    <chr>                    <int>
##  1 Neotropical              10608
```

```
##   2 Afrotropical            5200
##   3 Indomalayan             4719
##   4 <NA>                    2789
##   5 Australasian            2288
##   6 Oceanian                1842
##   7 Nearctic                1684
##   8 Palearctic              1680
##   9 Indomalayan|Palearctic  1446
##  10 Nearctic|Neotropical    1003
## # ... with 118 more rows
```

```
imp_data2 %>% group_by(kingdomName) %>% summarize(Sum = n()) %>% arrange(-Sum)
```

```
## # A tibble: 2 x 2
##   kingdomName   Sum
##   <chr>       <int>
## 1 animalia    32286
## 2 plantae      3165
```

```
imp_data2 %>% group_by(phylumName) %>% summarize(Sum = n()) %>% arrange(-Sum)
```

```
## # A tibble: 4 x 2
##   phylumName     Sum
##   <chr>        <int>
## 1 chordata     27968
## 2 tracheophyta  3165
## 3 arthropoda    2935
## 4 mollusca      1383
```

```
imp_data2 %>% group_by(orderName) %>% summarize(Sum = n()) %>% arrange(-Sum)
```

```
## # A tibble: 106 x 2
##    orderName        Sum
##    <chr>          <int>
##  1 passeriformes   6659
##  2 anura           6098
##  3 decapoda        2864
##  4 rodentia        2364
##  5 perciformes     1684
##  6 caryophyllales  1477
##  7 chiroptera      1304
##  8 neogastropoda    633
##  9 caudata          611
## 10 pinales          610
## # ... with 96 more rows
```

```
imp_data2 %>% group_by(className) %>% summarize(Sum = n()) %>% arrange(-Sum)
```

```
## # A tibble: 13 x 2
##    className        Sum
##    <chr>          <int>
```

```
##  1 aves           11147
##  2 amphibia        6892
##  3 mammalia        5899
##  4 malacostraca    2935
##  5 actinopterygii  2595
##  6 magnoliopsida   2248
##  7 chondrichthyes  1134
##  8 cephalopoda      750
##  9 gastropoda       633
## 10 pinopsida        610
## 11 cycadopsida      307
## 12 reptilia         225
## 13 myxini            76
```

Number of species in each category of population trend for each category of red list

```
list_pop = imp_data %>% group_by(populationTrend, redlistCategory) %>% summarize(Sum = n())
df = as.data.frame(list_pop)

df %>% pivot_wider(names_from=populationTrend, values_from=Sum)
```

```
## # A tibble: 10 x 6
##    redlistCategory                    Decreasing Increasing Stable Unknown  `NA`
##    <chr>                                   <int>      <int>  <int>   <int> <int>
##  1 Critically Endangered                    1108         19     42     343     9
##  2 Data Deficient                            228         NA     72    4834    18
##  3 Endangered                               2197         28     81     427     7
##  4 Extinct                                     1         NA      1       4   279
##  5 Extinct in the Wild                         1         NA     NA      NA    14
##  6 Least Concern                            4469        775   9013    6170    46
##  7 Near Threatened                          1558         36    314     424     1
##  8 Vulnerable                               1946         42    325     552    63
##  9 Lower Risk/conservation dependent          NA         NA     NA      NA     1
## 10 Lower Risk/least concern                   NA         NA     NA      NA     3
```

Species in each category for each category of red list and class

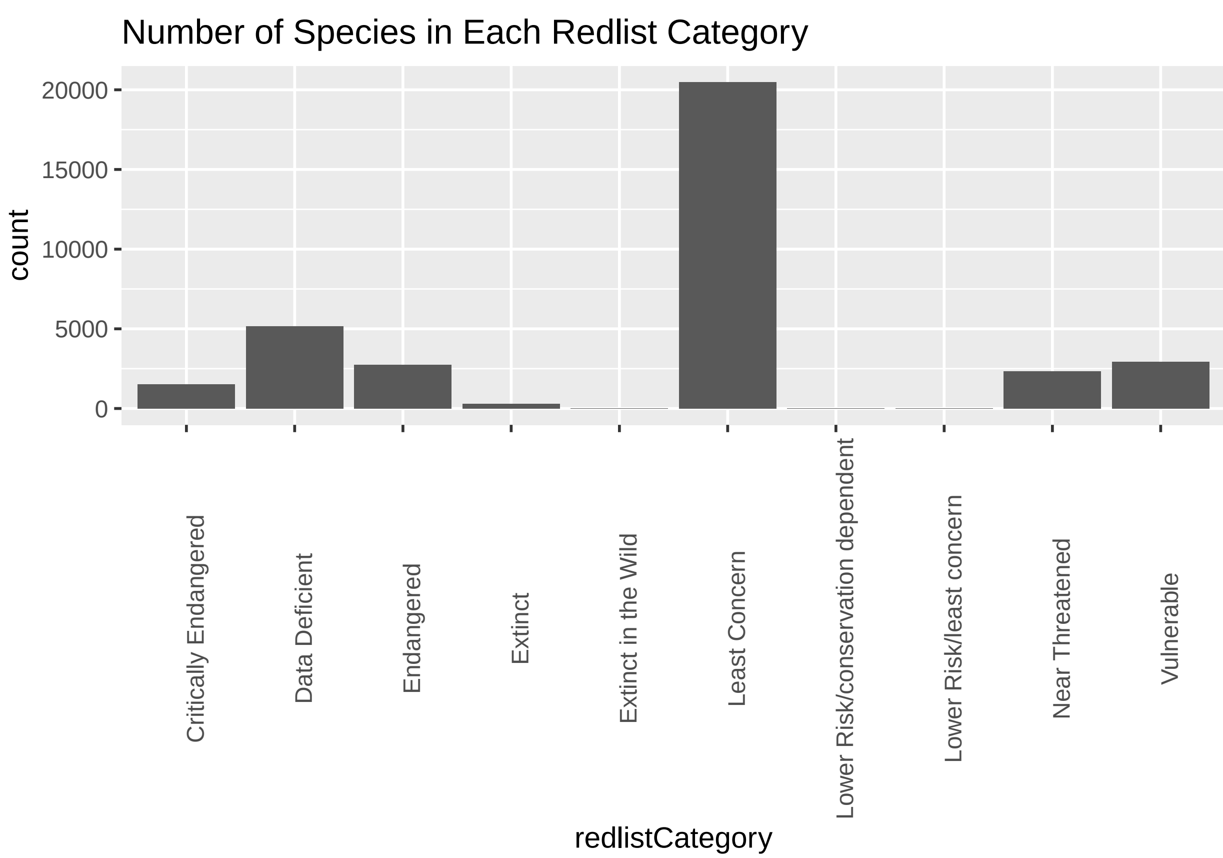
```
list_order = imp_data2 %>% group_by(redlistCategory, className) %>% summarize(Sum = n())
df2 = as.data.frame(list_order)

df3 = df2 %>% pivot_wider(names_from=redlistCategory, values_from=Sum)

knitr::kable(df3)
```

className	Critically Endangered	Data Deficient	Endangered	Extinct	Extinct in the Wild	Least Concern	Lower Risk/conservation dependent	Lower Risk/least concern	Near Threatened	Vulnerab
actinopterygii	10	444	34	NA	NA	1953	NA	NA	49	105
amphibia	610	1336	993	35	2	2856	NA	NA	387	673
aves	225	53	461	159	5	8427	NA	NA	1017	800
cephalopoda	1	419	2	NA	NA	324	NA	NA	2	2
chondrichthyes	43	420	62	NA	NA	382	NA	NA	115	112

className	Critically Endangered	Data Deficient	Endangered	Extinct	Extinct in the Wild	Least Concern	Lower Risk/conservation dependent	Lower Risk/least concern	Near Threatened	Vulnerab
cycadopsida	53	3	65	NA	4	45	NA	NA	63	74
gastropoda	3	88	11	NA	NA	478	NA	NA	26	27
magnoliopsida	185	348	297	NA	2	1107	NA	NA	110	199
malacostraca	122	1124	143	7	NA	1189	NA	NA	71	279
mammalia	222	869	532	84	2	3292	NA	NA	353	545
myxini	1	30	2	NA	NA	35	NA	NA	2	6
pinopsida	29	8	96	NA	NA	298	NA	NA	99	80
reptilia	17	10	42	NA	NA	87	1	3	39	26

Redlist Categories

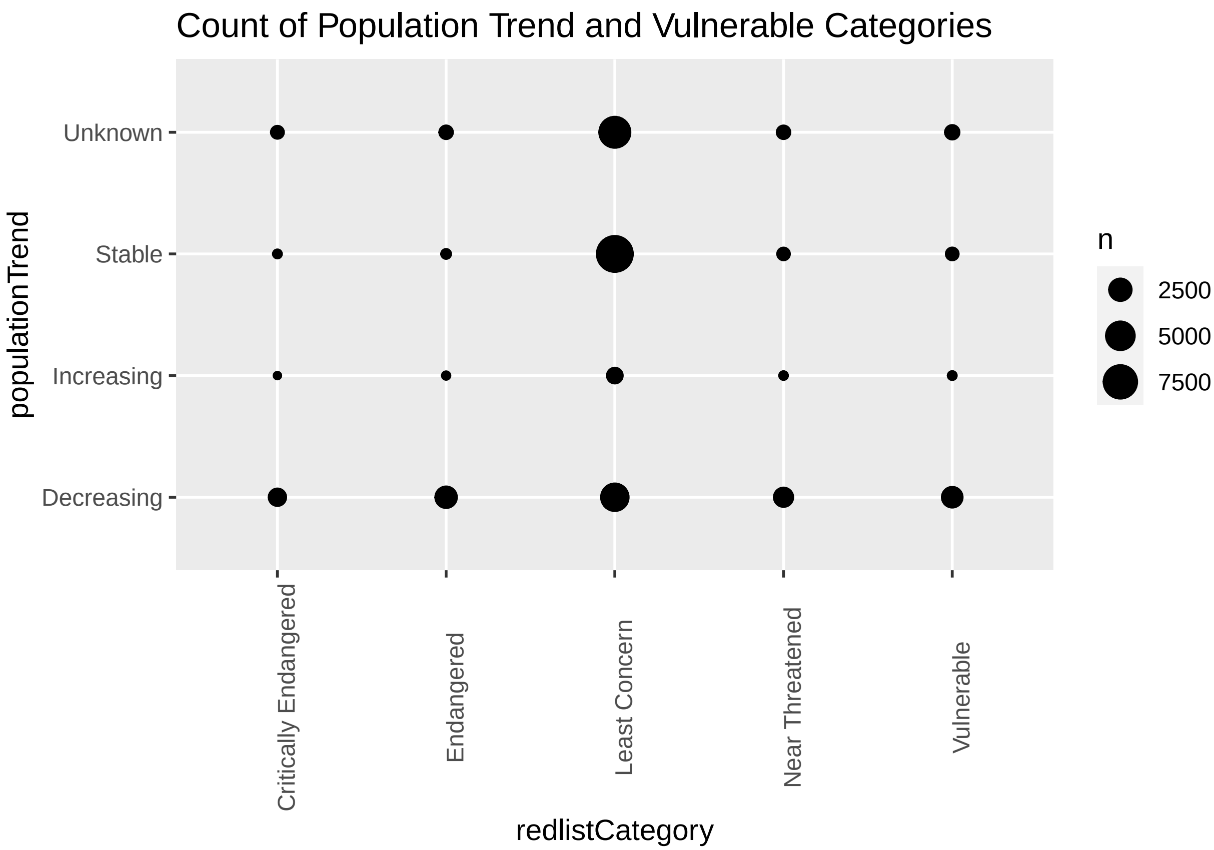
```
# redlist distribution
ggplot(imp_data, aes(x=redlistCategory)) + geom_bar() + theme(axis.text.x = element_text(angle = 90)) +
```



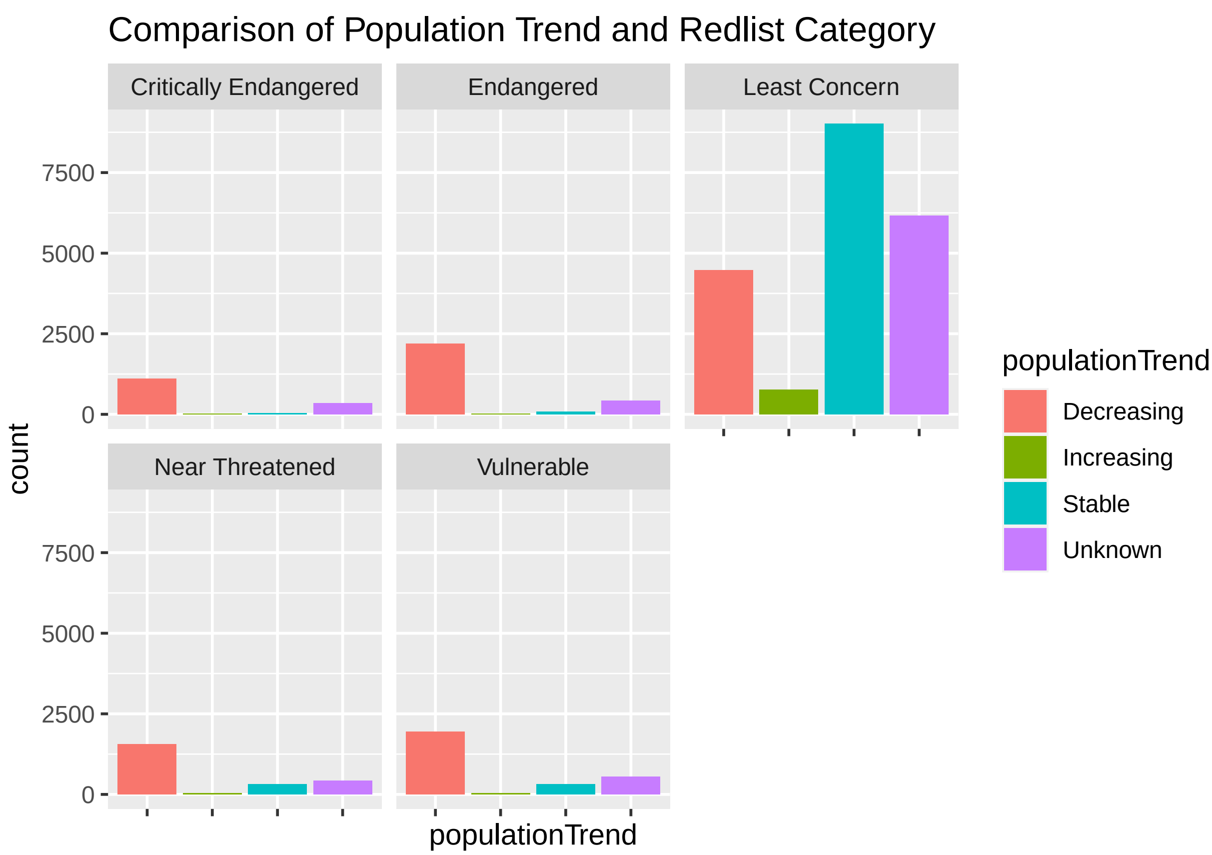

```
# filter data for high risk species
vul_data = imp_data %>% filter(redlistCategory == 'Vulnerable' | redlistCategory == 'Near Threatened' |
```

Compare populationTrend and redlistCategory

```
pop = imp_data %>% filter(populationTrend != 'NA') %>% filter(redlistCategory != 'Data Deficient') %>% 

ggplot(pop, aes(redlistCategory, populationTrend)) + geom_count() + theme(axis.text.x = element_text(an
```




```
ggplot(pop, aes(x=populationTrend, fill=populationTrend)) + geom_bar() + facet_wrap(~redlistCategory) +
```

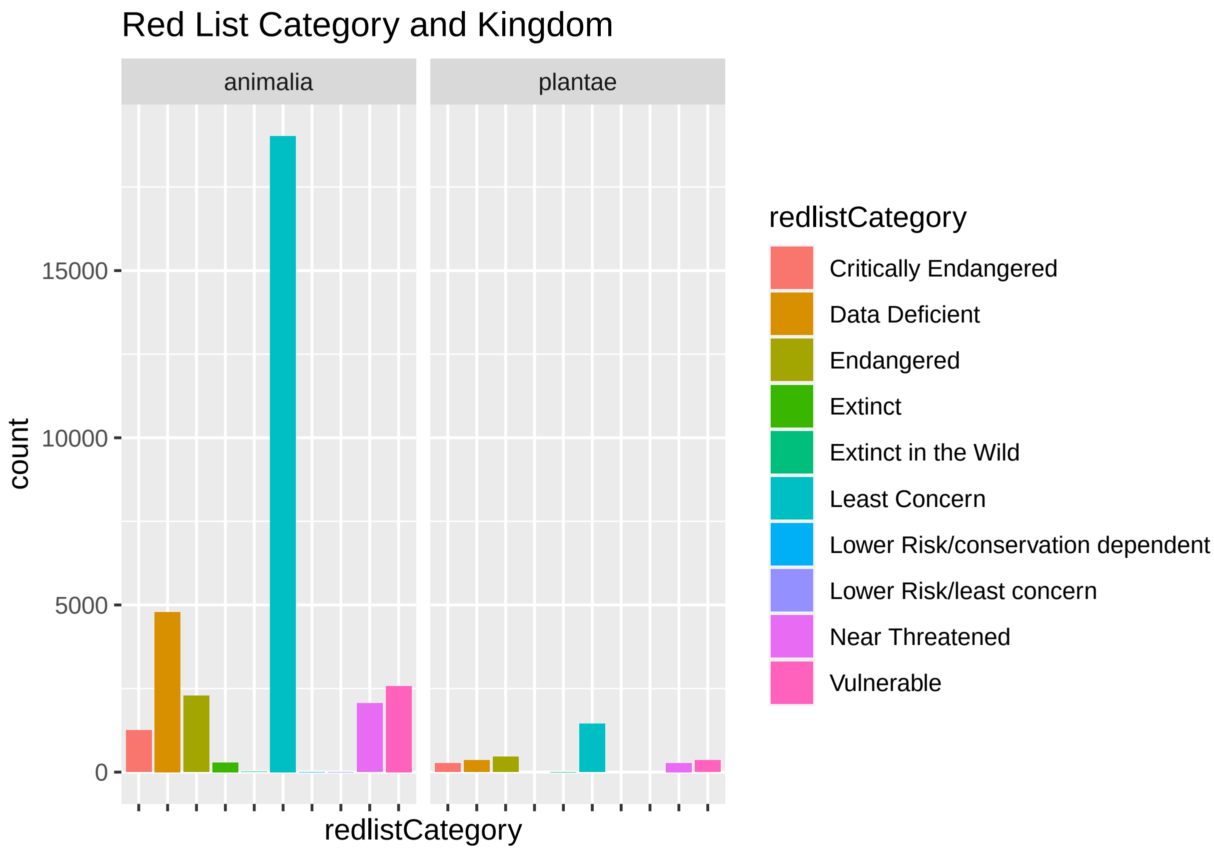


The largest redlistCategory is Least Concern, of which the population trends are more stable or decreasing (unknown excluded). Of the other redlist categories, greater numbers have decreasing population trends than stable/increasing.

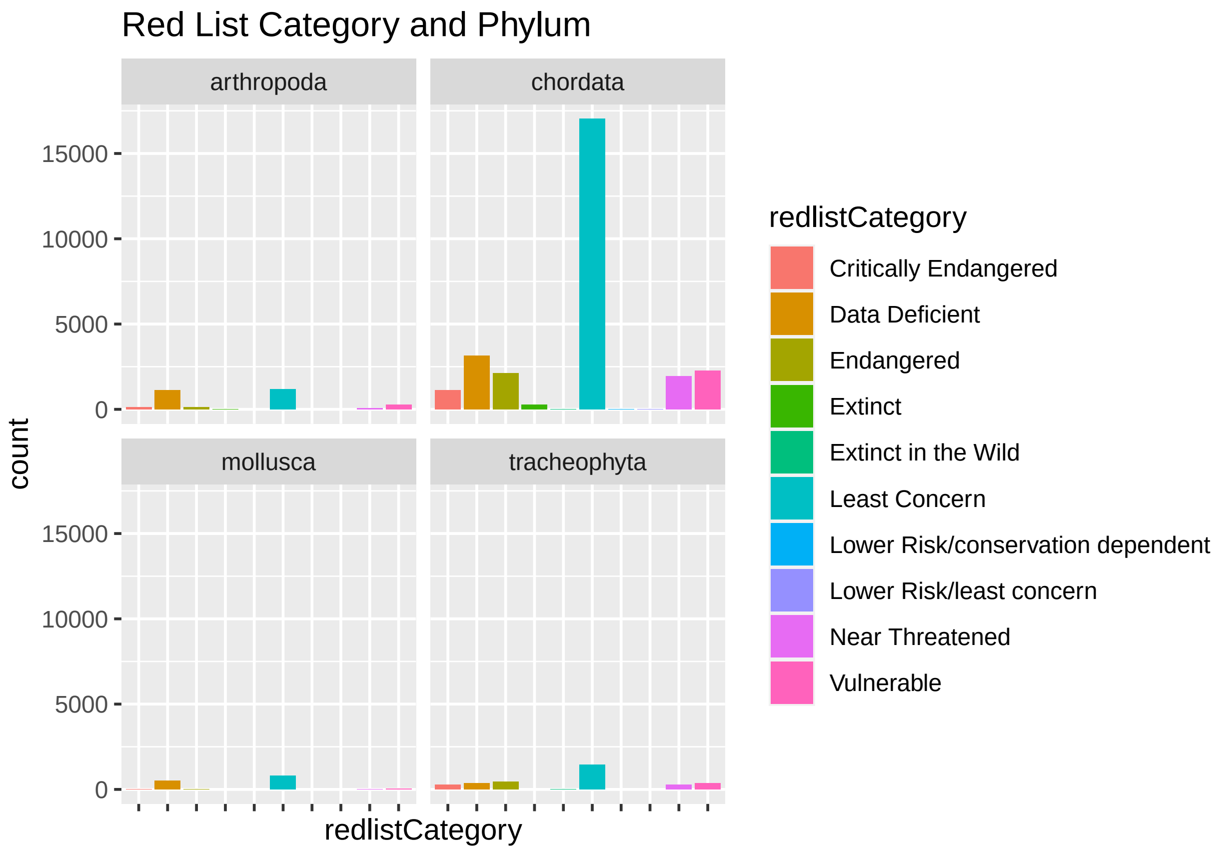
Of the populations decreasing, the categories affected in order are least concern, endangered, vulnerable, near threatened, and critically endangered. The majority of populations that are stable or increasing are in the least concern category.

Comparison of redlistCategory and taxonomy

```
# comparison with kingdom
ggplot(imp_data2, aes(x=redlistCategory, fill=redlistCategory)) + geom_bar() + facet_wrap(~kingdomName)
```




```r
# comparison with phylum
ggplot(imp_data2, aes(x=redlistCategory, fill=redlistCategory)) + geom_bar() + facet_wrap(~phylumName) +
```

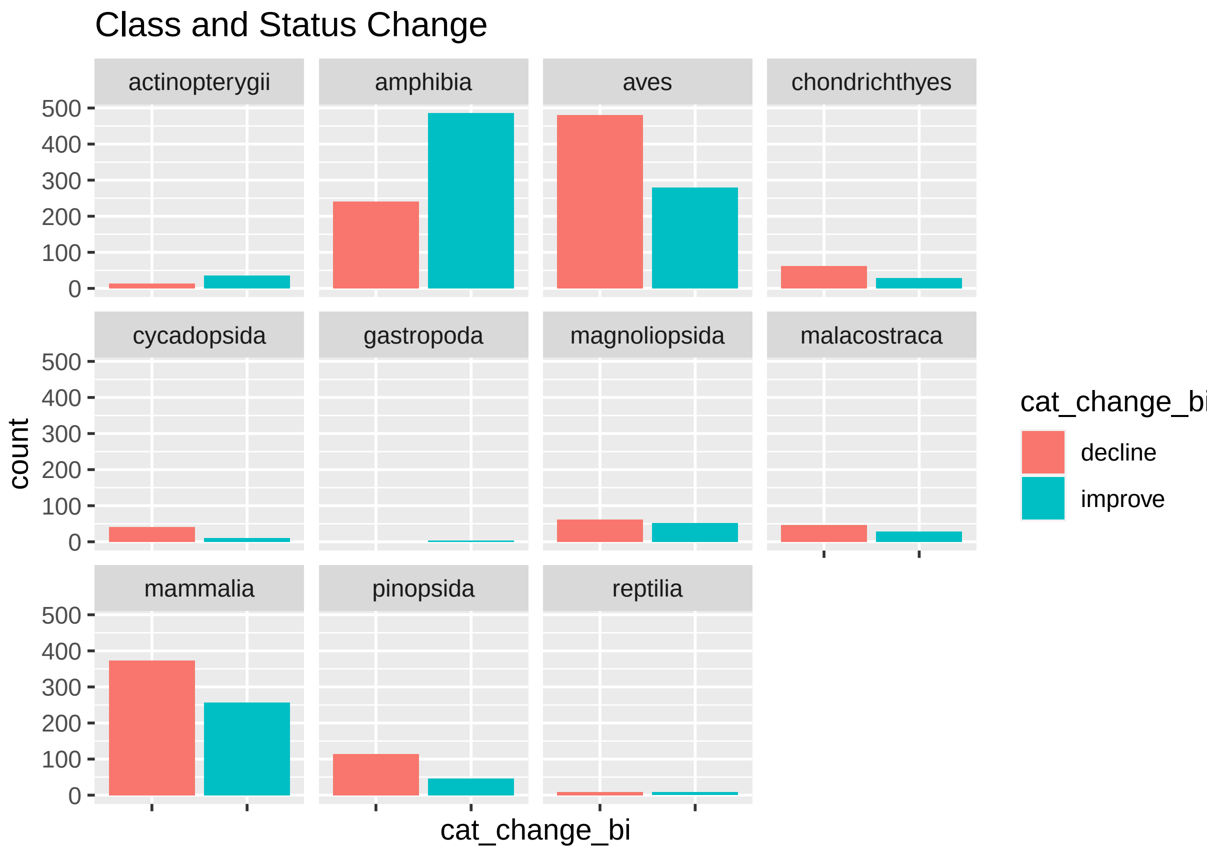



```
# comparison with classes that have over 1000 species in the dataset
class_data = imp_data2 %>% filter(className != 'cephalopoda') %>% filter(className != 'gastropoda') %>%

ggplot(class_data, aes(x=redlistCategory, fill=redlistCategory)) + geom_bar() + facet_wrap(~className) +
```

Amphibians (and mammals second) have the highest proportions with critically endangered, endangered, and vulnerable populations. Birds have high proportions of near threatened and vulnerable populations, but they also hav the highest count of species in the least concern category.

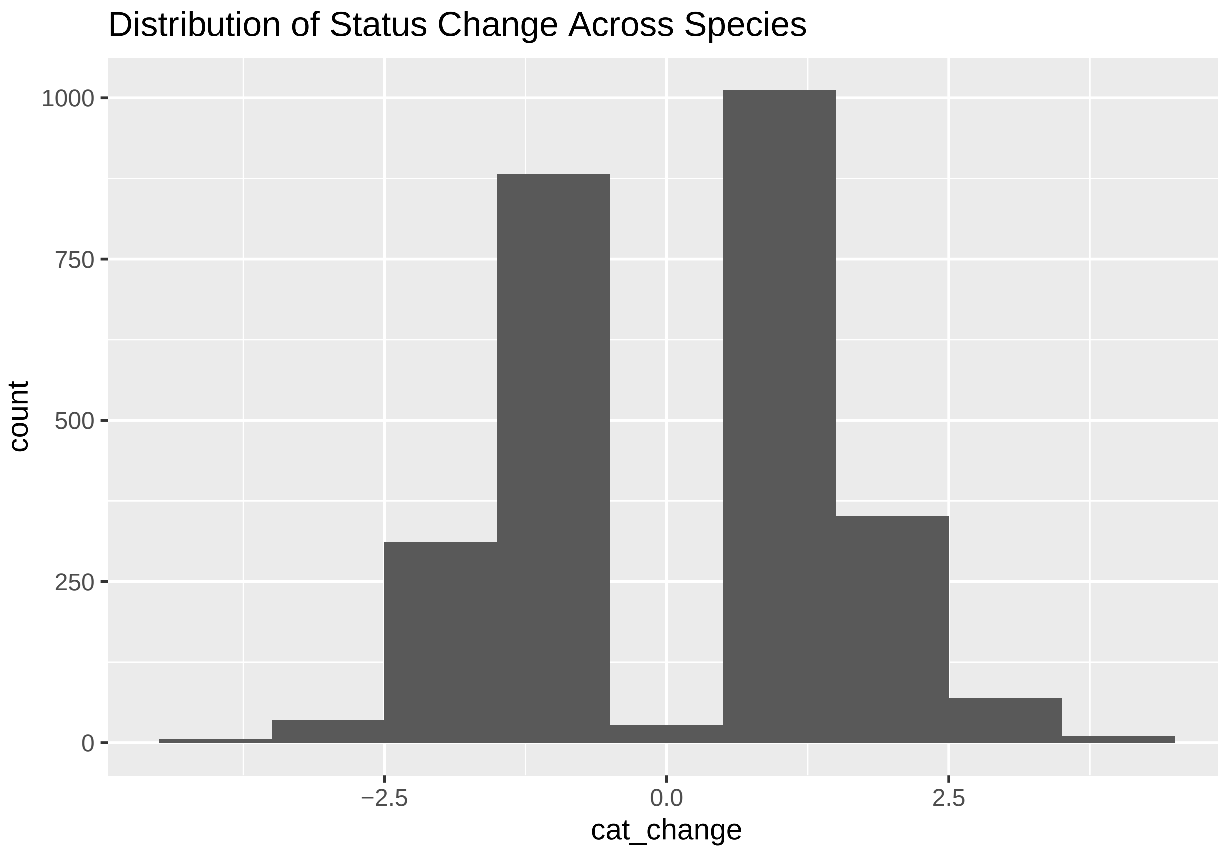
Status Change variables

```
# binary change (NA removed)
change_bi = imp_data2 %>% filter(cat_change_bi != 'NA')

ggplot(change_bi, aes(x=cat_change_bi, fill=cat_change_bi)) + geom_bar() + facet_wrap(~className) + the
```

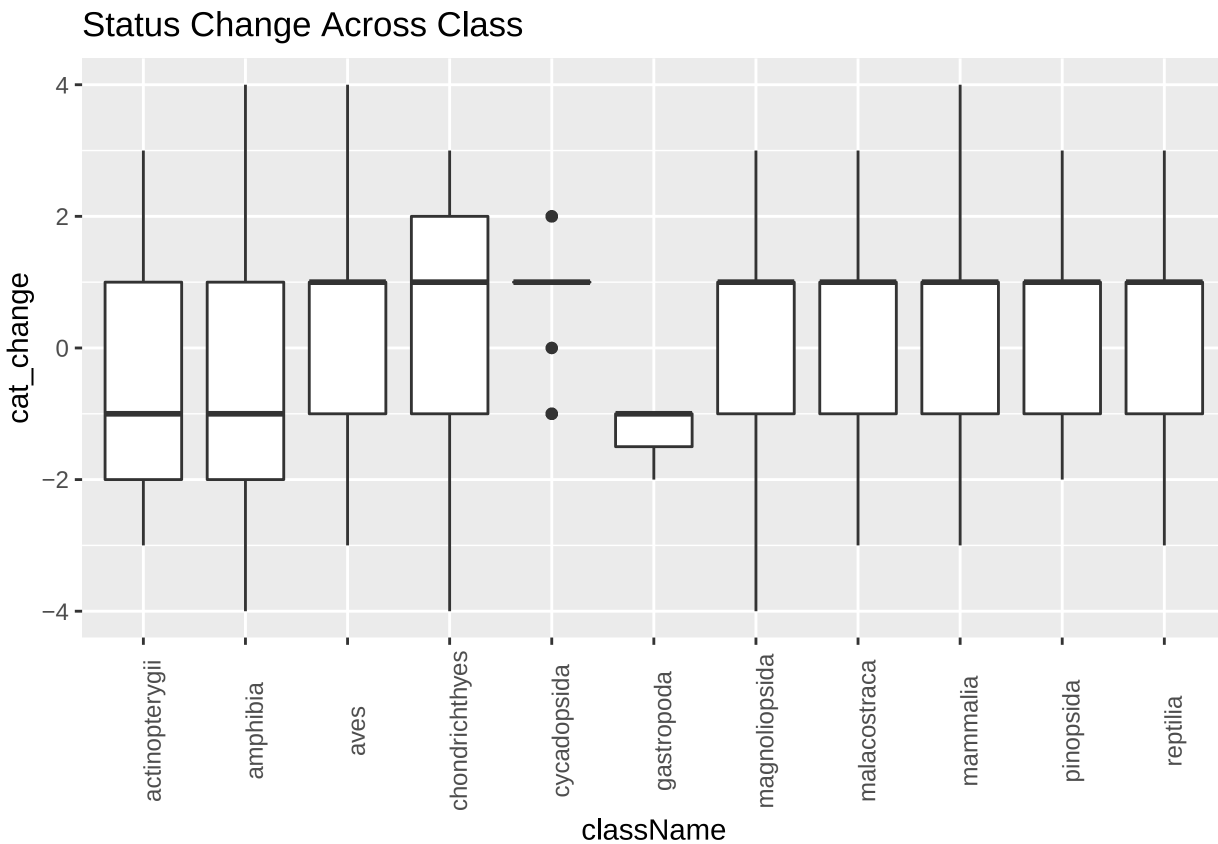


For binary changes, more amphibian and ray-finned fish (actinopterygii) species improved than declined. More bird, mammal, conifer, cycad, and cartilaginous fish species declined than improved (in decreasing order).

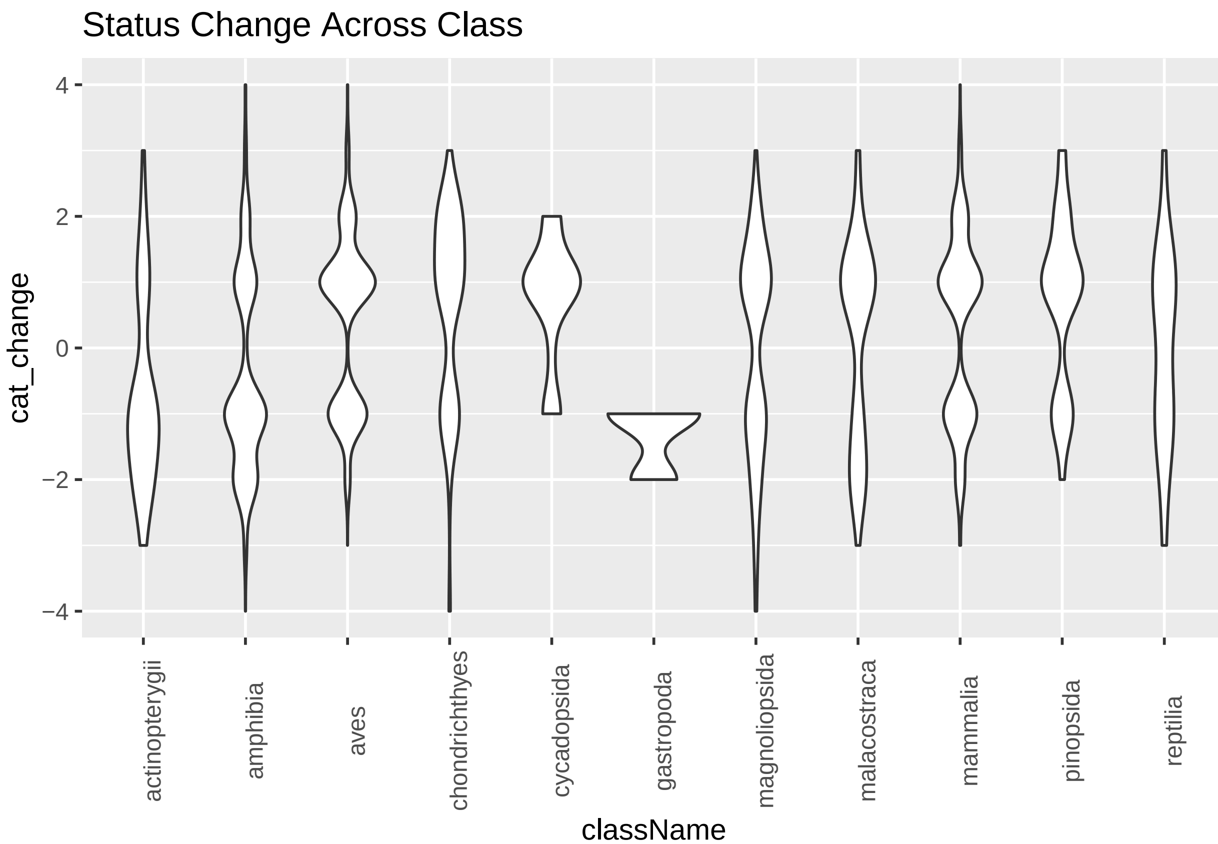
```
# non-binary change
change = imp_data2 %>% filter(cat_change != 'NA')

ggplot(change, aes(x=cat_change)) + geom_histogram(binwidth=1) + ggtitle("Distribution of Status Change
```




```
ggplot(change, aes(x=className, y=cat_change)) + geom_boxplot() + theme(axis.text.x = element_text(angl
```




```
ggplot(change, aes(x=className, y=cat_change)) + geom_violin() + theme(axis.text.x = element_text(angle
```



For nonbinary changes, the classes with the median cat_change below 0 are ray-finned fish, amphibians, and gastropoda. The remaining species have a median change above 0. However, it is notable that all species have an interquartile range that encompasses 0 except for cycadopsida and gastropoda. Birds, mammals, reptiles, and most plants have the median at the upper end of the IQR and above 0.

Body Mass Calculations

```
# average body mass of each red list category and overall
mass = imp_data2 %>% filter(BodyMass != 'NA')
mean(mass$BodyMass)
```

```
## [1] 55947.81
```

```
mass_list = mass %>% group_by(redlistCategory) %>% summarize(AvgMass = mean(BodyMass), MedMass = median
mass_list
```

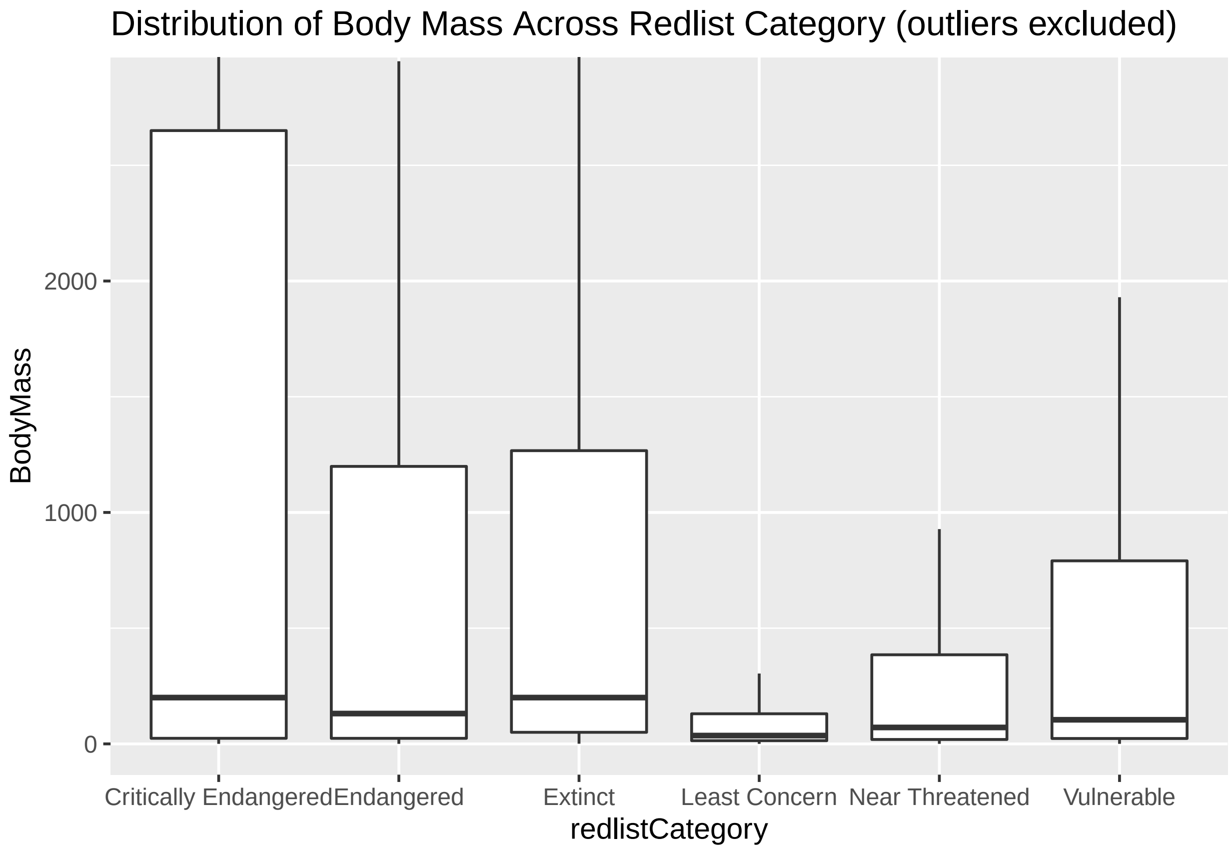
```
## # A tibble: 8 x 3
##   redlistCategory       AvgMass MedMass
##   <chr>                   <dbl>   <dbl>
## 1 Endangered            299307.   131
## 2 Data Deficient        116923.    33.4
## 3 Extinct in the Wild    87280. 74531.
## 4 Critically Endangered  86282.   200.
## 5 Vulnerable             80451.   104.
```

```
## 6 Near Threatened         41419.    71
## 7 Least Concern           29065.    36.0
## 8 Extinct                  8582.   200
```

```
# same but with population trend
mass_pop = mass %>% group_by(populationTrend) %>% summarize(AvgMass = mean(BodyMass), MedMass = median(
mass_pop
```

```
## # A tibble: 5 x 3
##   populationTrend AvgMass MedMass
##   <chr>             <dbl>   <dbl>
## 1 Increasing      667111.    78.5
## 2 Unknown          91307.    37.3
## 3 <NA>             13426.   200
## 4 Decreasing        9422.    69
## 5 Stable            8280.    30.0
```

```
# body mass boxplot without outliers
body_out = imp_data %>% filter(BodyMass != 'NA') %>% filter(redlistCategory != 'Data Deficient') %>% fi

ggplot(body_out, aes(x=redlistCategory, y=BodyMass)) + geom_boxplot(outlier.shape = NA) + coord_cartesi
```



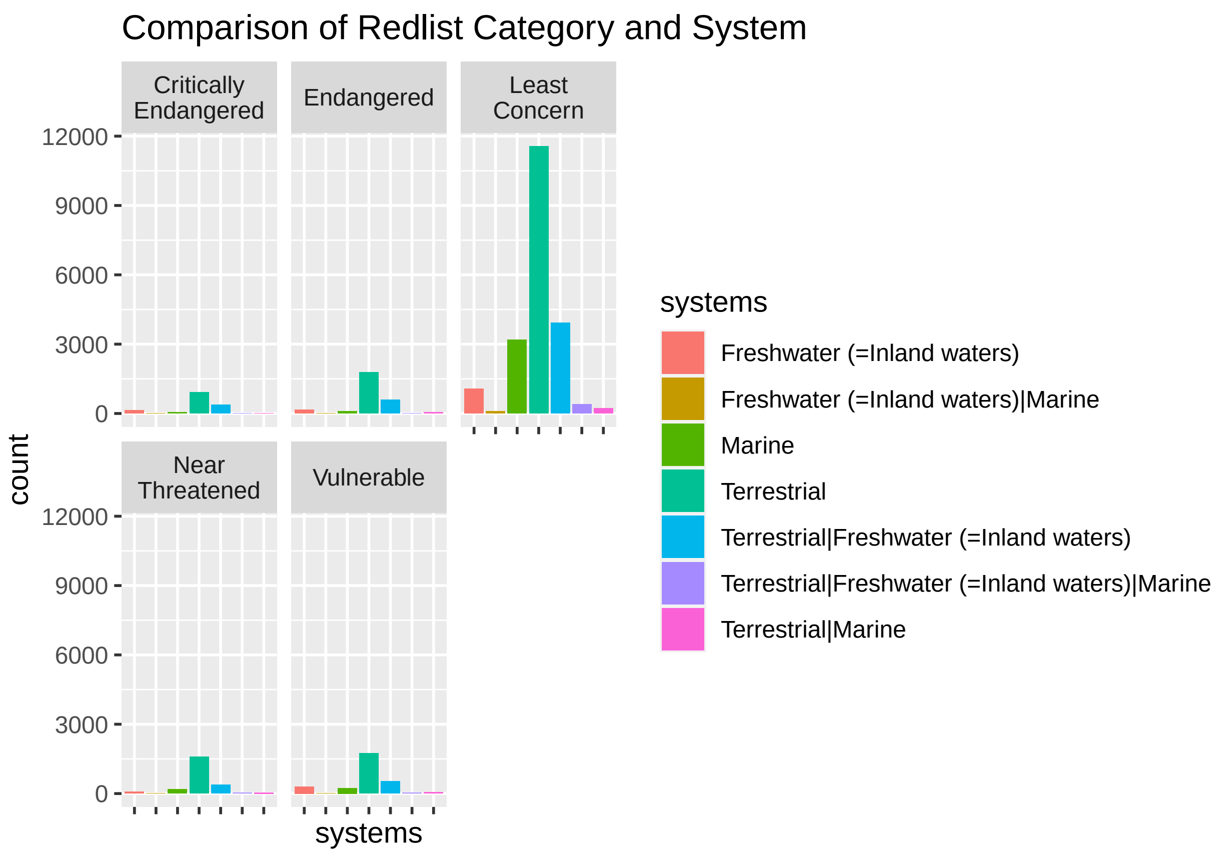
The average body mass is generally higher for uplisted species on the red list. The average body mass is generally higher for species who have increasing population trends as compared to those with decreasing or stable trends (this may be in part due to differences in sample size).

The median body mass is lower for species of least concern and near threatened as compared to the median body mass of other categories. (when outliers are ignored)

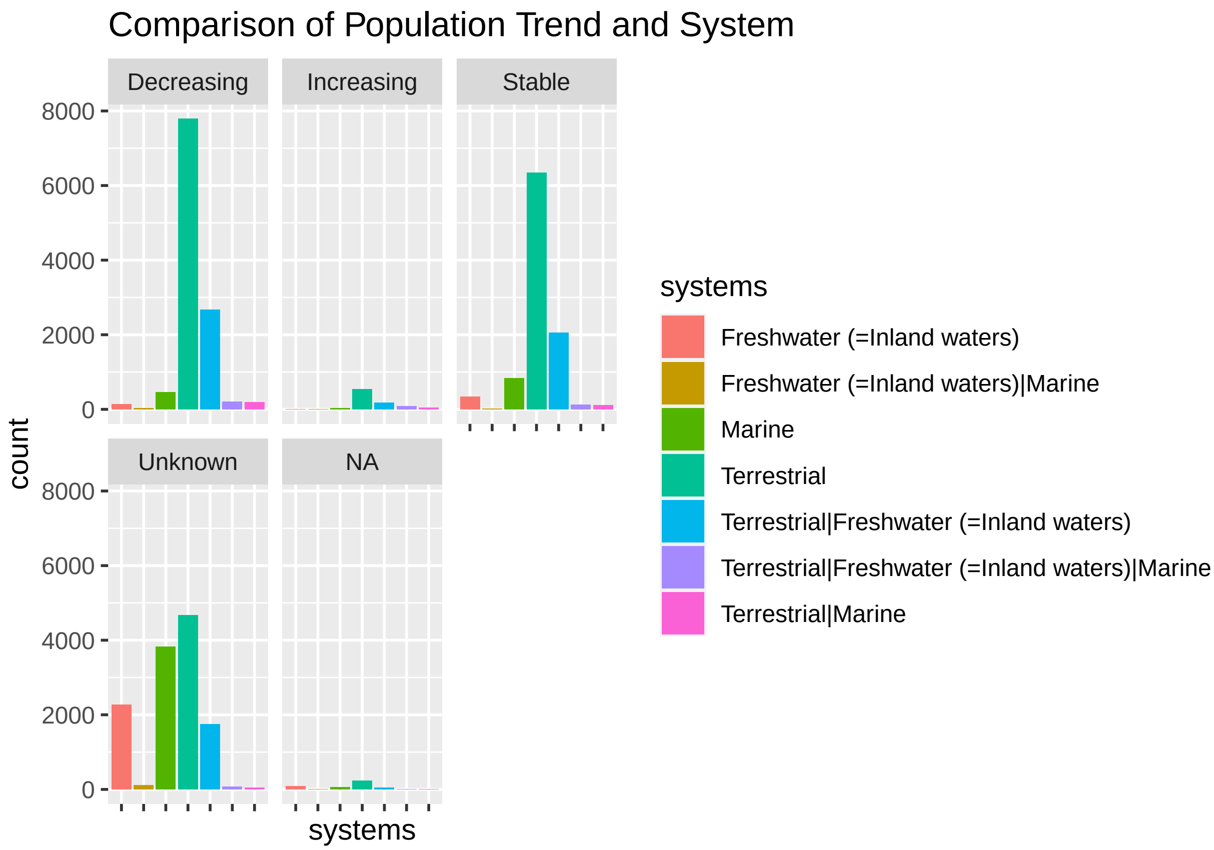
Systems

I thought this might be interesting, even though you didn't mention looking at it.

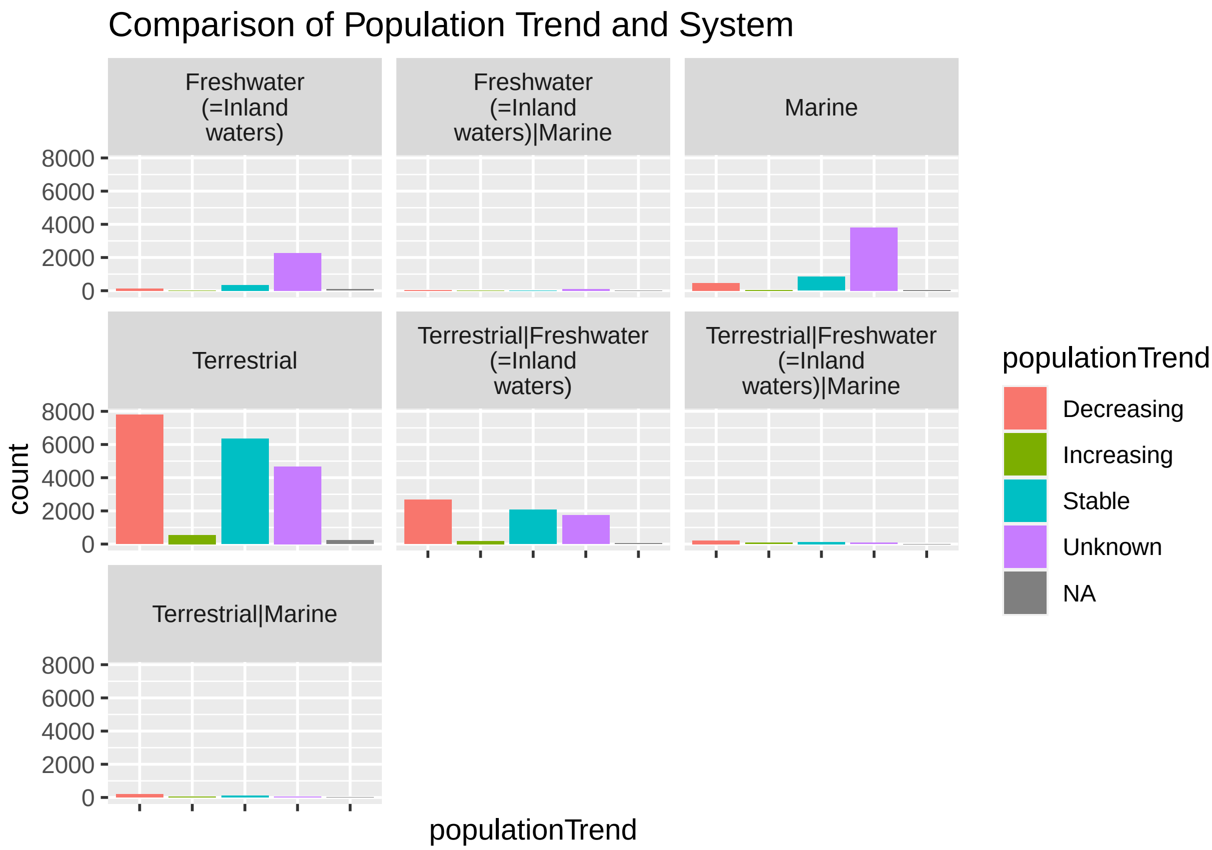
```
# filter out small, NA systems
system = imp_data2 %>% filter(systems != '<NA>') %>% filter(systems != 'Marine|Marine') %>% filter(syste

# filter irrelevant categories
system2 = system %>% filter(redlistCategory == 'Critically Endangered' | redlistCategory == 'Endangered

# compare system and redlistCategory
ggplot(system2, aes(x=systems, fill=systems)) + geom_bar() + facet_wrap(~redlistCategory, labeller = lab
```



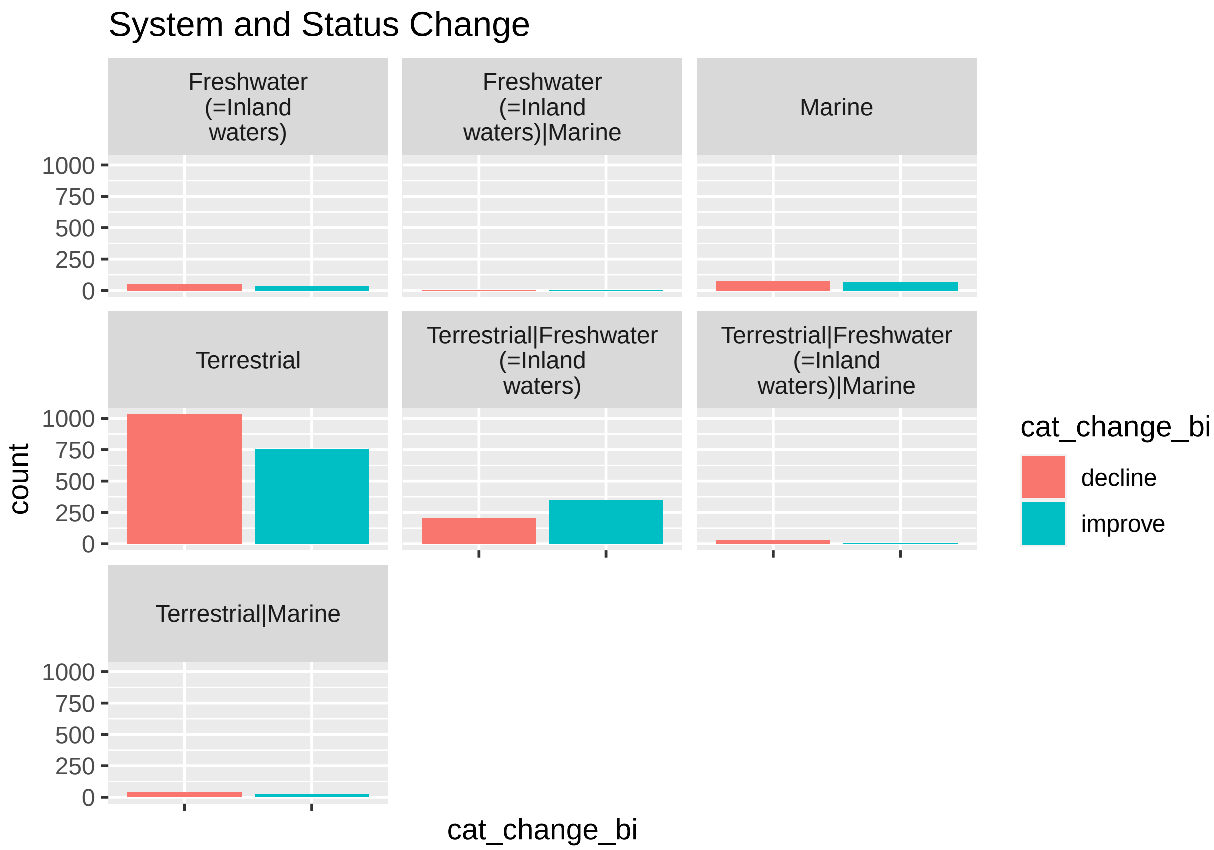

```
# compare system and populationTrend
ggplot(system, aes(x=systems, fill=systems)) + geom_bar() + facet_wrap(~populationTrend) + theme(axis.te
```



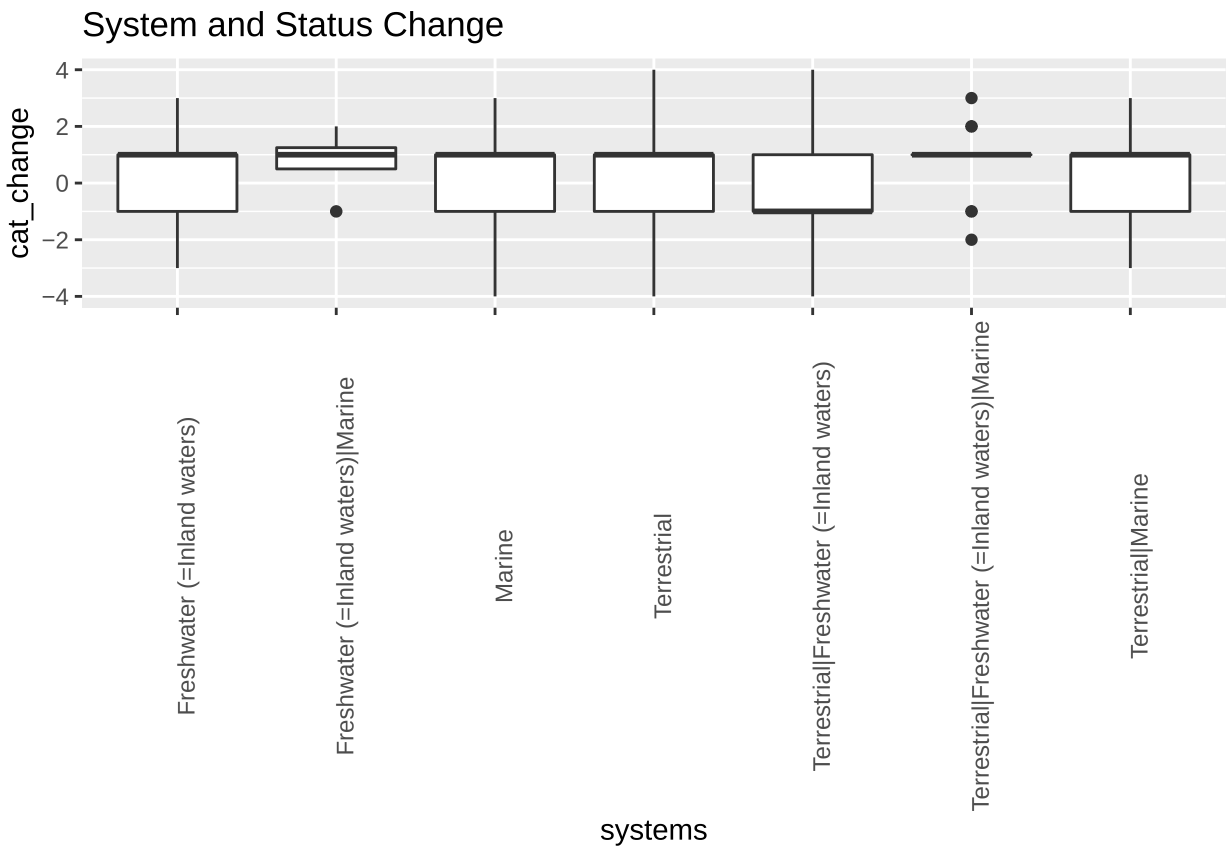

```
ggplot(system, aes(x=populationTrend, fill=populationTrend)) + geom_bar() + facet_wrap(~systems, labell
```




```
# compare system and cat_change_bi
system_bi = system %>% filter(cat_change_bi != 'NA')

ggplot(system_bi, aes(x=cat_change_bi, fill=cat_change_bi)) + geom_bar() + facet_wrap(~systems, labelle
```




```r
# system and cat_change
system_change = system %>% filter(cat_change != 'NA')

ggplot(system_change, aes(x=systems, y=cat_change)) + geom_boxplot() + theme(axis.text.x = element_text
```



The majority of systems are in the least concern category. However, of the categories that are not least concern, the systems with the most species are terrestrial and freshwater inland waters. A small portion of Near Threatened and Vulnerable are marine.

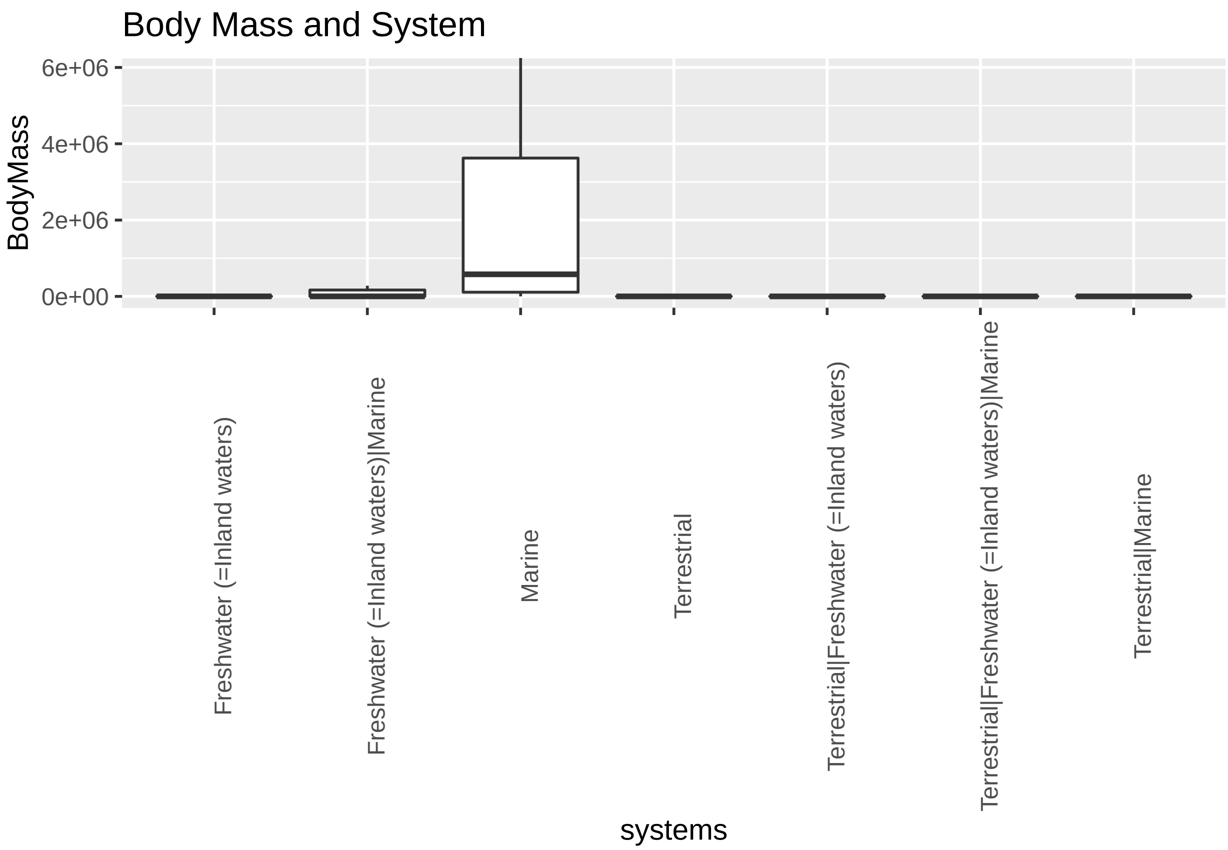
Similarly, terrestrial and freshwater inland water systems have the highest number of species with decreasing population trends. The systems with stable species are in decreasing order: terrestrial, terrestrial freshwater inland, marine, freshwater. Only terrestrial has a noticeable number of species that have increasing trends.

Within the binary change categories, terrestrial had the most change, with more species in decline than improving. Terrestrial freshwater inland had more improved than decline. Marine systems were relatively equal.

Within nonbinary change, the species with median negative -1 change were terrestrial inland freshwater. The remaining systems had a median positive +1 change. ALL IQRs were from -1 to 1 except for freshwater/marine and terrestrial/freshwater/marine, which both had IQRs above 0 cat_change.

For fun

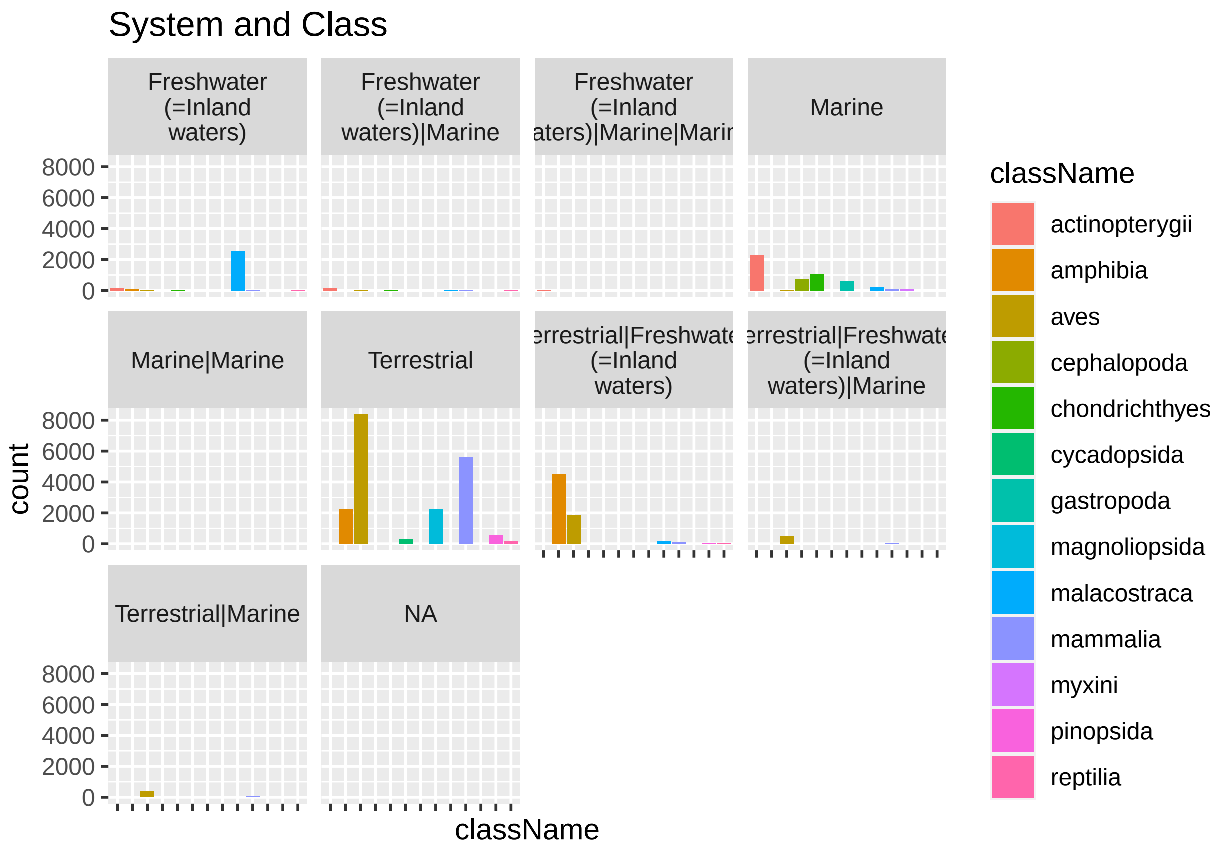
```
# compare system and class, bodymass
ggplot(system, aes(x=systems, y=BodyMass)) + geom_boxplot(outlier.shape = NA) + coord_cartesian(ylim = c
```



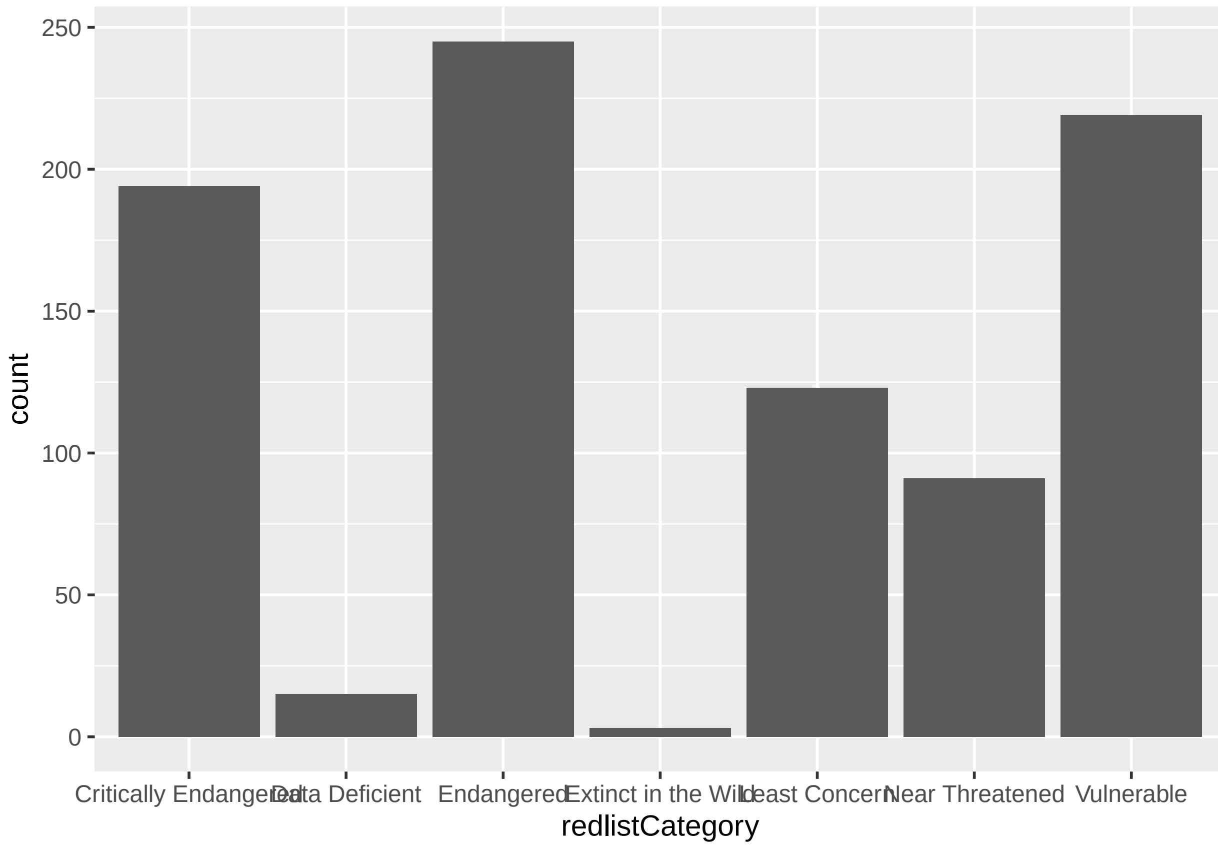

```r
# average body mass of each system
mass_system = mass %>% group_by(systems) %>% summarize(AvgMass = mean(BodyMass), MedMass = median(BodyMa
mass_system
```

```
## # A tibble: 7 x 3
##   systems                                          AvgMass  MedMass
##   <chr>                                              <dbl>    <dbl>
## 1 Marine                                          8676310. 578750
## 2 Freshwater (=Inland waters)|Marine               104567.   1156.
## 3 Freshwater (=Inland waters)                       27856.    681.
## 4 Terrestrial|Marine                                25999.    490.
## 5 Terrestrial|Freshwater (=Inland waters)|Marine     5061.    323.
## 6 Terrestrial                                        3650.     39.9
## 7 Terrestrial|Freshwater (=Inland waters)            2300.     34.9
```

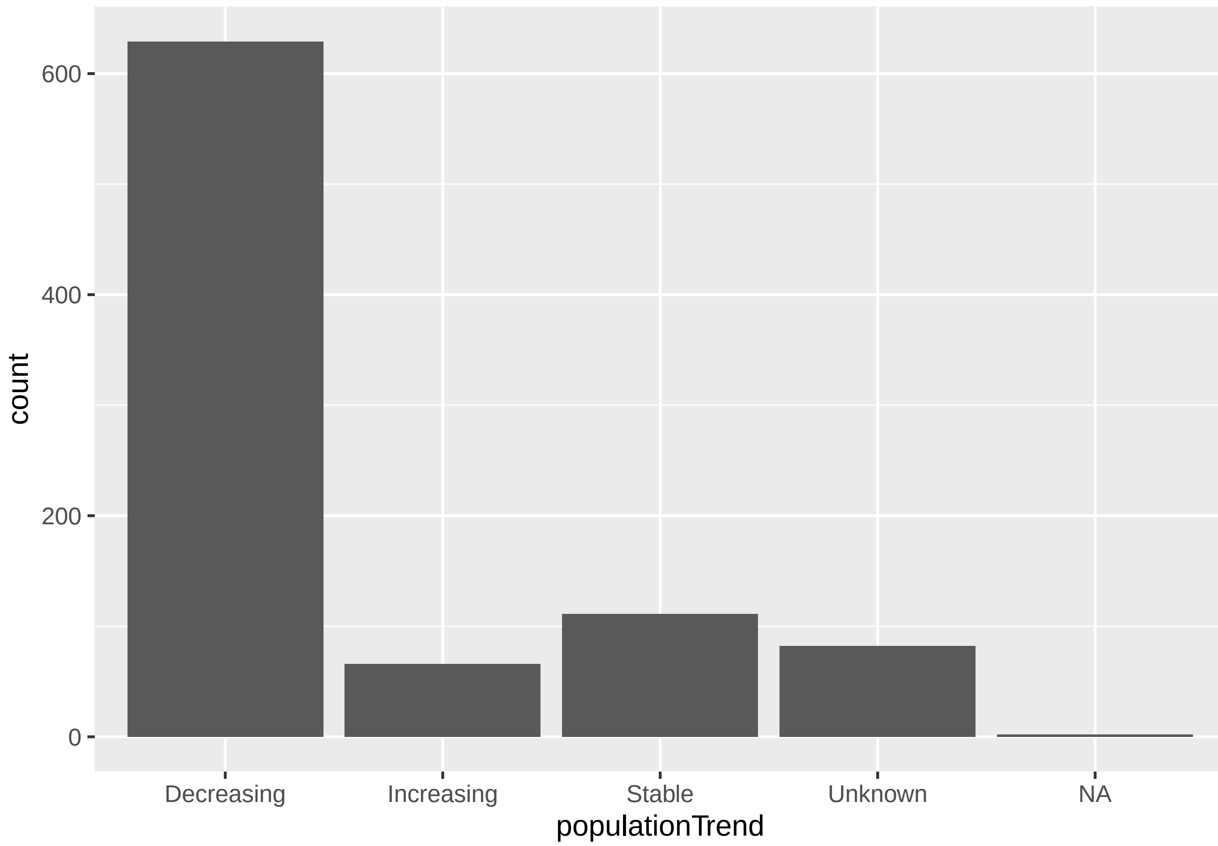
```r
# turns out marine is like wayyyyy bigger !!

# class
ggplot(imp_data2, aes(x=className, fill=className)) + geom_bar() + facet_wrap(~systems, labeller = label
```




```
# education
# it seems education is focused on more threatened species
edu = data %>% filter(education == TRUE)
ggplot(edu, aes(x=redlistCategory)) + geom_bar()
```




```
ggplot(edu, aes(x=populationTrend)) + geom_bar()
```


600
400
200
0
count
Decreasing
Increasing
Stable
Unknown
NA
populationTrend