

# Conservancy Analysis

*BEACN*

*March 23, 2018*

## Setup

Downloading the data

```
library(tidyverse)
```

```
## -- Attaching packages -----  
## v ggplot2 2.2.1.9000      v purrr  0.2.4  
## v tibble  1.4.2          v dplyr  0.7.4  
## v tidyr   0.7.2          v stringr 1.2.0  
## v readr   1.1.1          v forcats 0.2.0
```

```
## -- Conflicts -----  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag()     masks stats::lag()  
## x dplyr::vars()    masks ggplot2::vars()
```

```
library(ggplot2)  
library(stringr)  
library(gridExtra)
```

```
## Warning: package 'gridExtra' was built under R version 3.4.4
```

```
##
```

```
## Attaching package: 'gridExtra'
```

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

```
##
```

```
##      combine
```

```
library(grid)
```

```
conservancy_names <- function(name) {  
  return(paste0("conservancy_", name, ".csv"))  
}
```

```
ucnrs_names <- function(name) {  
  return(paste0("ucnrs_", name, ".csv"))  
}
```

```
conservancyNames <- c("birds", "herpetofauna", "invertebrates", "mammals", "plants")
```

```
ucnrsNames <- c("animal_list", "plant_list")
```

```
fullConservancyNames <- conservancy_names(conservancyNames)
```

```
fullUCNRSNames <- ucnrs_names(ucnrsNames)
```

```
allFiles <- c(fullConservancyNames, fullUCNRSNames)
```

```
path <- paste0("./ucnrs_data/", allFiles)
```

```

data <- lapply(path, read_csv)

## Parsed with column specification:
## cols(
##   species = col_character()
## )

## Parsed with column specification:
## cols(
##   species = col_character()
## )

## Parsed with column specification:
## cols(
##   Species = col_character()
## )

## Parsed with column specification:
## cols(
##   species = col_character()
## )

## Parsed with column specification:
## cols(
##   species = col_character()
## )

## Parsed with column specification:
## cols(
##   Reserve = col_character(),
##   Taxon = col_character(),
##   Family = col_character(),
##   `Scientific Name` = col_character(),
##   `Accepted Name` = col_character(),
##   `Common Name` = col_character()
## )

## Warning: Missing column names filled in: 'X17' [17], 'X18' [18],
## 'X19' [19], 'X20' [20], 'X21' [21], 'X22' [22]

## Parsed with column specification:
## cols(
##   .default = col_character(),
##   `Reserve count (values)` = col_integer(),
##   `Reserve count (formula)` = col_integer()
## )

## See spec(...) for full column specifications.
head(data)

```

## Combining UCNRS and Conservancy into four datasets

```

# Separating out columns of data for conservancy data and removing irrelevant values

conservancyAnimalData <- bind_rows(data[[1]], data[[2]], data[[3]], data[[4]]) %>%
  distinct(species) %>%

```

```

separate(species, into = c("genus", "species", "sublabel1", "sublabel2"), sep = " ", extra = "merge")
filter(!(genus %in% c("Tejon", "Undefined")))

## Warning: Too few values at 351 locations: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10,
## 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, ...

conservancyPlantData <- data[[5]] %>% distinct(species) %>%
  separate(species, into = c("genus", "species", "separator_label", "sublabel"), sep = " ", extra = "merge")
  filter(!(genus %in% c("Tejon", "Undefined")))

## Warning: Too few values at 652 locations: 2, 4, 5, 6, 11, 12, 13, 14, 15,
## 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, ...

# Loading Plant and Animal data from UCNRS

ucnrsPlantData <- data[[7]]
ucnrsAnimalData <- data[[6]]

# Relabeling data

names(ucnrsPlantData)[7:8] <- c("separator_label", "sublabel")
names(ucnrsAnimalData)[4] <- "scientific_name"

# Cleaning UCNRS Animal data

ucnrsAnimalDataSubsetTemp <- ucnrsAnimalData %>%
  select(Reserve, scientific_name) %>%
  separate(scientific_name, into = c("genus", "species", "sublabel1", "sublabel2"), sep = " ", extra = "merge")
  distinct()

## Warning: Too few values at 8696 locations: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10,
## 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, ...

ucnrsAnimalDataSubset <- mutate(ucnrsAnimalDataSubsetTemp,
                                sublabel1 = gsub("\\(", "", sublabel1), sublabel2 = gsub("\\(", "", sublabel2),
                                sublabel1 = gsub("\\)", "", sublabel1), sublabel2 = gsub("\\)", "", sublabel2),
                                sublabel1 = gsub("\\.", "", sublabel1), sublabel2 = gsub("\\.", "", sublabel2),
                                species = tolower(species))

# Cleaning UCNRS Plant Data

ucnrsPlantDataSubset <- ucnrsPlantData %>%
  select(Reserve, Genus, Species, separator_label, sublabel) %>%
  distinct()

# Relabeling column headers

names(ucnrsPlantDataSubset)[1:3] <- c("reserve", "genus", "species")
names(ucnrsAnimalDataSubset)[1] <- c("reserve")

# Print results

head(ucnrsAnimalDataSubset)

## # A tibble: 6 x 5
##   reserve      genus      species      sublabel1 sublabel2

```

```
##   <chr>                <chr>          <chr>      <chr>      <chr>
## 1 Angelo Coast Range Reserve Ambystoma   gracile    <NA>      <NA>
## 2 Angelo Coast Range Reserve Aneides     ferreus    <NA>      <NA>
## 3 Angelo Coast Range Reserve Aneides     flavipunct~ <NA>      <NA>
## 4 Angelo Coast Range Reserve Aneides     vagrans    <NA>      <NA>
## 5 Angelo Coast Range Reserve Ascaphus     truei      <NA>      <NA>
## 6 Angelo Coast Range Reserve Batrachoseps attenuatus <NA>      <NA>
```

```
head(ucnrsPlantDataSubset)
```

```
## # A tibble: 6 x 5
##   reserve                genus  species  separator_label sublabel
##   <chr>                <chr>  <chr>    <chr>          <chr>
## 1 Landells-Hill Big Creek Abies  bracteata <NA>          <NA>
## 2 James San Jacinto Mountains Abies  concolor <NA>          <NA>
## 3 Valentine              Abies  concolor <NA>          <NA>
## 4 Valentine              Abies  magnifica var.      magnifica
## 5 Bodega                  Abronia latifolia <NA>          <NA>
## 6 Younger Lagoon          Abronia latifolia <NA>          <NA>
```

```
head(conservancyAnimalData)
```

```
## # A tibble: 6 x 4
##   genus species  sublabel1 sublabel2
##   <chr> <chr>    <chr>    <chr>
## 1 Aix   sponsa    <NA>     <NA>
## 2 Anas  acuta     <NA>     <NA>
## 3 Anas  americana <NA>     <NA>
## 4 Anas  clypeata <NA>     <NA>
## 5 Anas  crecca    <NA>     <NA>
## 6 Anas  cyanoptera <NA>     <NA>
```

```
head(conservancyPlantData)
```

```
## # A tibble: 6 x 4
##   genus      species  separator_label sublabel
##   <chr>      <chr>    <chr>          <chr>
## 1 Sambucus   nigra      subsp.         caerulea
## 2 Apocynum   cannabinum <NA>           <NA>
## 3 Chlorogalum pomeridianum var.      pomeridianum
## 4 Hesperoyucca whipplei    <NA>           <NA>
## 5 Yucca       brevifolia <NA>           <NA>
## 6 Allium      burlewii   <NA>           <NA>
```

## Match Ratio of Plants per Reserve

```
# Find shared genies and species of plants
matchingPlants <- semi_join(ucnrsPlantDataSubset, conservancyPlantData, by = c("genus", "species", "subl
  select(reserve, genus, species, sublabel)

# Calculate how similar plant species composition is by reserve
matchingPlantsCount <- matchingPlants %>%
  group_by(reserve) %>%
  summarize(count = n())
```

```

totalPlantsCount <- ucnrsPlantDataSubset %>%
  group_by(reserve) %>%
  summarize(count = n())

plantsComparisonTable <- left_join(matchingPlantsCount, totalPlantsCount,
                                   by = "reserve", suffix = c("_matching", "_total")) %>%
  mutate(match_ratio = count_matching / count_total) %>%
  arrange(desc(match_ratio))

plantsComparisonTable

## # A tibble: 30 x 4
##   reserve                                count_matching count_total match_ratio
##   <chr>                                <int>          <int>      <dbl>
## 1 Sedgewick                           193           417      0.463
## 2 Motte Rimrock                        85           192      0.443
## 3 Blue Oak Ranch                      193           462      0.418
## 4 Stebbins Cold Canyon                148           372      0.398
## 5 Stunt Ranch Santa Monica Mounta~    113           297      0.380
## 6 Quail Ridge                         107           287      0.373
## 7 Burns Pinon Ridge                   100           272      0.368
## 8 San Joaquin Freshwater Marsh         94           258      0.364
## 9 Hastings                           229           646      0.354
## 10 Dawson Los Monos Canyon            104           294      0.354
## # ... with 20 more rows

```

## Where each plant is found

```

# Find places where each matched species shows up in other reserves

matchingPlantsArranged <- matchingPlants %>%
  arrange(genus, species, sublabel, reserve)

matchingPlantsReserves <- matchingPlantsArranged %>%
  group_by(genus, species, sublabel) %>%
  summarize(count = n())

# Add names of reserves each species is represented in at end:

matchingPlantsArranged$reserve_list <- ""

matchingPlantsArranged$reserve_list[1] <- paste0(matchingPlantsArranged$reserve[1])
idx = 2
idx_max = nrow(matchingPlantsArranged)

while(idx < idx_max) {
  n = 1
  while((setequal(matchingPlantsArranged[idx, 2:4], matchingPlantsArranged[(idx - 1), 2:4])) & (idx < i
    n = n + 1
    idx = idx + 1
  }
  matchingPlantsArranged$reserve_list[(idx - n):(idx - 1)] <-

```

```

    paste(matchingPlantsArranged$reserve[(idx - n):(idx - 1)], collapse = ", ")
    idx = idx + 1
  }

matchingPlantsArranged$reserve_list[idx_max] <-
  paste(matchingPlantsArranged$reserve[idx_max])

# Combine the data

matchingPlantsReservesCombined <- matchingPlantsArranged %>%
  distinct(genus, species, sublabel, reserve_list) %>%
  right_join(matchingPlantsReserves, by = c("genus", "species", "sublabel"))

matchingPlantsReservesCombined

## # A tibble: 603 x 5
##   genus      species      sublabel reserve_list      count
##   <chr>      <chr>      <chr>      <chr>      <int>
## 1 Abies      concolor      <NA>      James San Jacinto Mounta~    2
## 2 Acamptopappus sphaerocephalus hirtellus Sweeney Granite Mountains    1
## 3 Acer       macrophyllum  <NA>      Angelo Coast Range, Blue~    9
## 4 Achillea   millefolium   <NA>      Angelo Coast Range, Blue~   17
## 5 Achyrachaena mollis      <NA>      Blue Oak Ranch, Hastings~    8
## 6 Acourtia    microcephala  <NA>      Dawson Los Monos Canyon,~    5
## 7 Aesculus    californica   <NA>      Angelo Coast Range, Blue~    8
## 8 Agoseris    grandiflora   <NA>      Angelo Coast Range, Bode~   11
## 9 Agoseris    retrorsa      <NA>      Boyd Deep Canyon, Chicke~    4
## 10 Ailanthus  altissima     <NA>      McLaughlin, Quail Ridge,~    3
## # ... with 593 more rows

```

## Match Ratio of Animals

per Reserve

```

# Find shared genies and species of plants
matchingAnimals <- semi_join(ucnrsAnimalDataSubset, conservancyAnimalData, by = c("genus", "species", "sublabel1", "sublabel2"))

# Calculate how similar plant species composition is by reserve
matchingAnimalsCount <- matchingAnimals %>%
  group_by(reserve) %>%
  summarize(count = n())

totalAnimalsCount <- ucnrsAnimalDataSubset %>%
  group_by(reserve) %>%
  summarize(count = n())

animalsComparisonTable <- left_join(matchingAnimalsCount, totalAnimalsCount,
  by = "reserve", suffix = c("_matching", "_total")) %>%
  mutate(match_ratio = count_matching / count_total) %>%
  arrange(desc(match_ratio))

animalsComparisonTable

```

```
## # A tibble: 31 x 4
##   reserve                                count_matching count_total match_ratio
##   <chr>                                <int>         <int>      <dbl>
## 1 <NA>                                1             1        1.00
## 2 Dawson Los Monos Canyon Reserve      96            126        0.762
## 3 Kendall-Frost Missions Bay Mars~    104            151        0.689
## 4 Elliot Chaparral Reserve             107            158        0.677
## 5 Boyd Deep Canyon Desert Researc~    207            325        0.637
## 6 Carpinteria Salt Marsh Reserve       130            205        0.634
## 7 Scripps Coastal Reserve             118            187        0.631
## 8 Box Springs Reserve                  13             21        0.619
## 9 Stunt Ranch Reserve                   84            139        0.604
## 10 Motte Rimrock Reserve               144            249        0.578
## # ... with 21 more rows
```

## Where each plant is found

```
# Find places where each matched species shows up in other reserves

matchingAnimalsArranged <- matchingAnimals %>%
  arrange(genus, species, sublabel1, reserve)

matchingAnimalsReserves <- matchingAnimalsArranged %>%
  group_by(genus, species, sublabel1) %>%
  summarize(count = n())

# Add names of reserves each species is represented in at end:

matchingAnimalsArranged$reserve_list <- ""

matchingAnimalsArranged$reserve_list[1] <- paste0(matchingAnimalsArranged$reserve[1])
idx = 2
idx_max = nrow(matchingAnimalsArranged)

while(idx < idx_max) {
  n = 1
  while((setequal(matchingAnimalsArranged[idx, 2:4], matchingAnimalsArranged[(idx - 1), 2:4])) & (idx <
    n = n + 1
    idx = idx + 1
  }
  matchingAnimalsArranged$reserve_list[(idx - n):(idx - 1)] <-
    paste(matchingAnimalsArranged$reserve[(idx - n):(idx - 1)], collapse = ", ")
  idx = idx + 1
}

matchingAnimalsArranged$reserve_list[idx_max] <-
  paste(matchingAnimalsArranged$reserve[idx_max])

# Combine the data

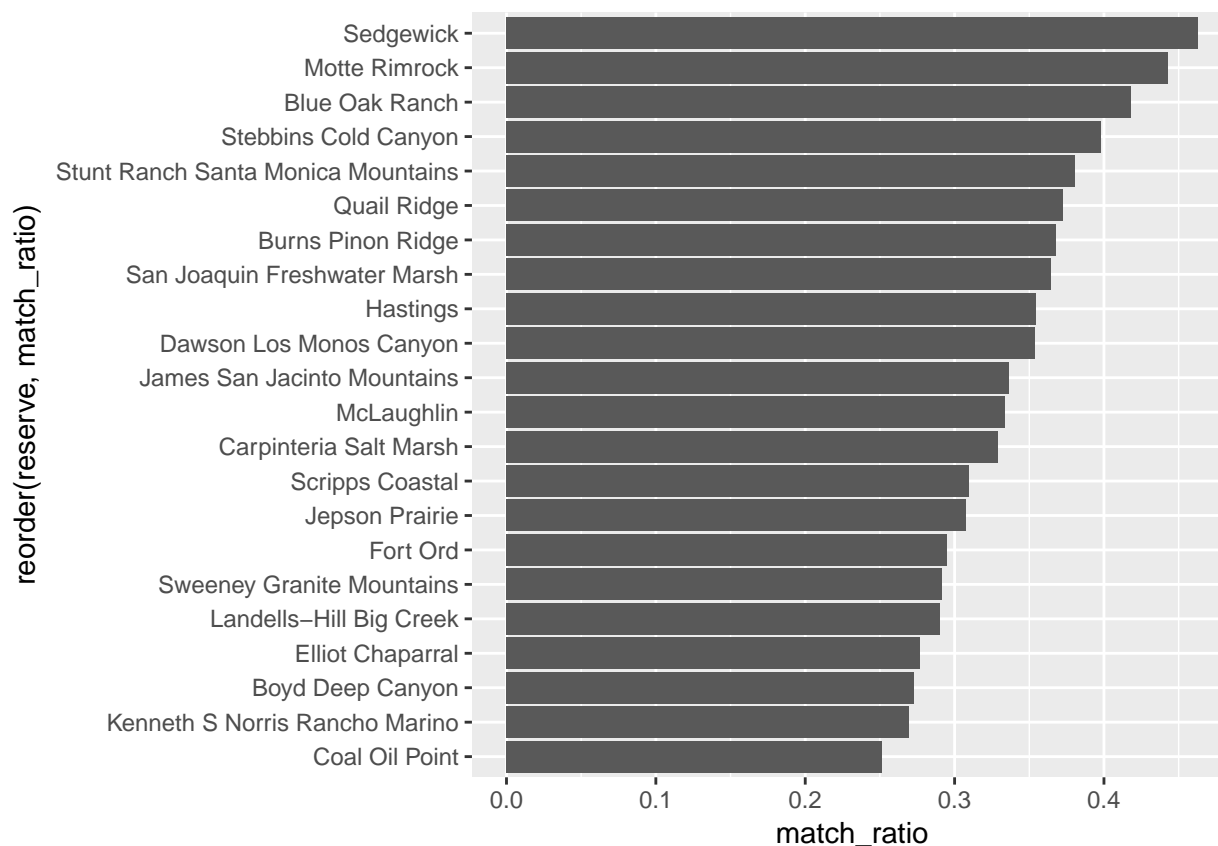
matchingAnimalsReservesCombined <- matchingAnimalsArranged %>%
  distinct(genus, species, sublabel1, reserve_list) %>%
  right_join(matchingAnimalsReserves, by = c("genus", "species", "sublabel1"))
```

```
matchingAnimalsReservesCombined
```

```
## # A tibble: 320 x 5
##   genus      species      sublabel1 reserve_list      count
##   <chr>      <chr>      <chr>      <chr>      <int>
## 1 Accipiter cooperii <NA>      "Angelo Coast Range Reserve,~ 20
## 2 Accipiter gentilis <NA>      "Angelo Coast Range Reserve,~ 6
## 3 Accipiter striatus <NA>      "Angelo Coast Range Reserve,~ 19
## 4 Actinemys marmorata <NA>      Angelo Coast Range Reserve, ~ 3
## 5 Actitis macularia <NA>      "Angelo Coast Range Reserve,~ 10
## 6 Aechmophorus clarkii <NA>      Bodega Marine Reserve, Carpi~ 7
## 7 Aechmophorus occidentalis <NA>      Angelo Coast Range Reserve, ~ 9
## 8 Aegolius acadicus <NA>      Angelo Coast Range Reserve, ~ 11
## 9 Aeronautes saxatalis <NA>      "Blue Oak Ranch Reserve, Box~ 19
## 10 Agelaius phoeniceus <NA>      "Angelo Coast Range Reserve,~ 17
## # ... with 310 more rows
```

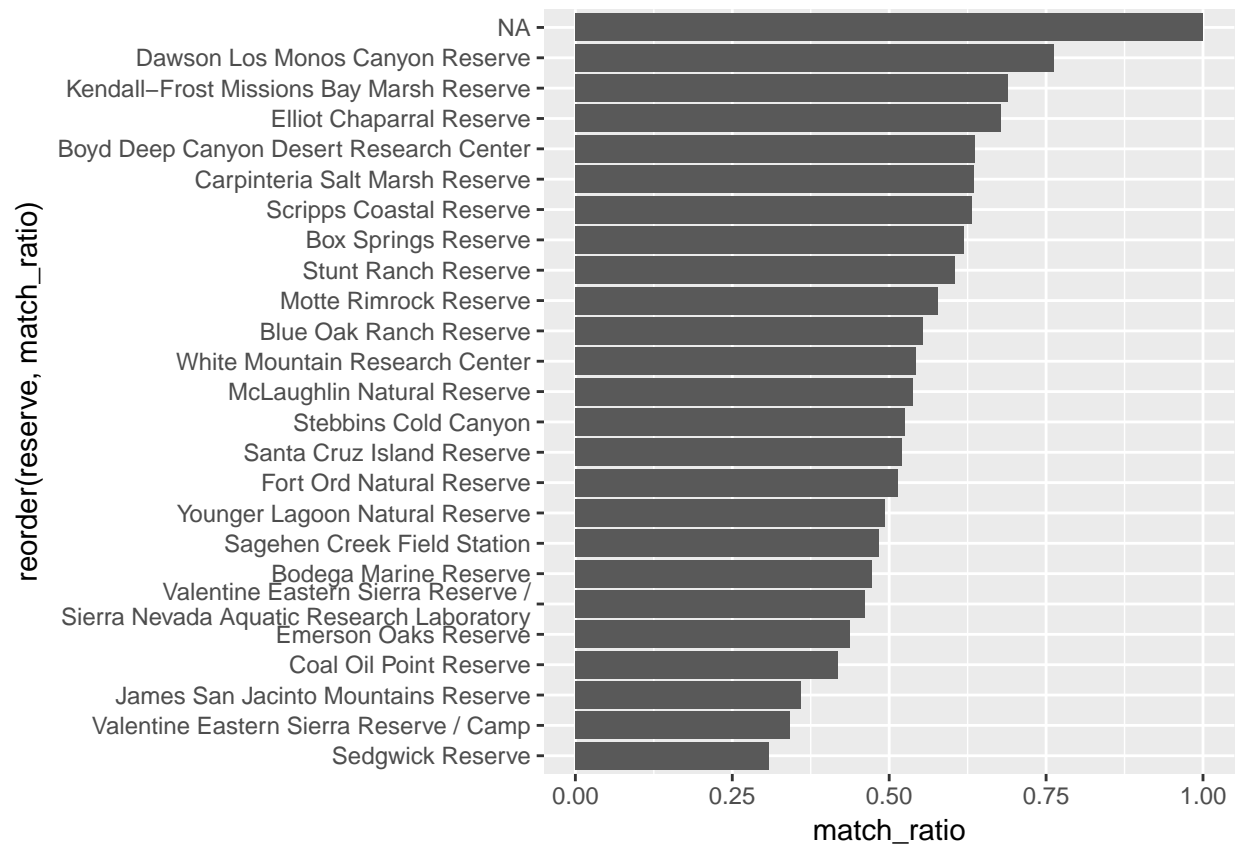
## Visuals & Summary Statistics

```
plantsComparisonTable %>%
  filter(match_ratio > 0.25) %>%
  ggplot(aes(x = reorder(reserve, match_ratio), y = match_ratio)) +
  geom_bar(stat = "identity") +
  coord_flip()
```





```
animalsComparisonTable %>%
  filter(match_ratio > 0.25) %>%
  ggplot(aes(x = reorder(reserve, match_ratio), y = match_ratio)) +
  geom_bar(stat = "identity") +
  coord_flip()
```



## Unique Plants and Animals

```
uniquePlants <- conservancyPlantData %>% anti_join(ucnrsPlantDataSubset, by = c("genus", "species", "subspecies"))
uniqueAnimals <- conservancyAnimalData %>% anti_join(ucnrsAnimalDataSubset, by = c("genus", "species", "subspecies"))

totalPlantsNum <- nrow(conservancyPlantData)
uniquePlantsNum <- nrow(uniquePlants)

totalAnimalsNum <- nrow(conservancyAnimalData)
uniqueAnimalsNum <- nrow(uniqueAnimals)

ratioUniquePlants <- uniquePlantsNum / totalPlantsNum
ratioUniqueAnimals <- uniqueAnimalsNum / totalAnimalsNum

rarePlants <- matchingPlantsReservesCombined %>% filter(count < 4)
rarePlantsNum <- nrow(rarePlants)
rareOrUniquePlantsNum <- uniquePlantsNum + rarePlantsNum
```

```
rareAnimals <- matchingAnimalsReservesCombined %>% filter(count < 4)
rareAnimalsNum <- nrow(rareAnimals)
rareOrUniqueAnimalsNum <- uniqueAnimalsNum + rareAnimalsNum
```

```
ratioRareOrUniquePlants <- rareOrUniquePlantsNum / totalPlantsNum
ratioRareOrUniqueAnimals <- rareOrUniqueAnimalsNum / totalAnimalsNum
```

```
ratioUniquePlants
```

```
## [1] 0.3744813
```

```
ratioRareOrUniquePlants
```

```
## [1] 0.689834
```

```
ratioUniqueAnimals
```

```
## [1] 0.09631728
```

```
ratioRareOrUniqueAnimals
```

```
## [1] 0.2436261
```

```
uniquePlants
```

```
## # A tibble: 361 x 4
```

	genus	species	separator_label	sublabel
	<chr>	<chr>	<chr>	<chr>
## 1	Allium	howellii	var.	howellii
## 2	Allium	lacunosum	var.	davisiae
## 3	Allium	peninsulare	var.	peninsulare
## 4	Rhus	aromatica	<NA>	<NA>
## 5	Cicuta	douglasii	<NA>	<NA>
## 6	Perideridia	pringlei	<NA>	<NA>
## 7	Chaenactis	glabriuscula	var.	megacephala
## 8	Chaenactis	santolinoides	<NA>	<NA>
## 9	Chaenactis	xantiana	<NA>	<NA>
## 10	Crepis	acuminata	<NA>	<NA>

```
## # ... with 351 more rows
```

```
uniqueAnimals
```

```
## # A tibble: 34 x 4
```

	genus	species	sublabel1	sublabel2
	<chr>	<chr>	<chr>	<chr>
## 1	Colinus	virginianus	<NA>	<NA>
## 2	Falco	peregrinus	anatum	<NA>
## 3	Porzana	Carolina	<NA>	<NA>
## 4	Recurvirostra	american	<NA>	<NA>
## 5	Hydroprogne	caspia	<NA>	<NA>
## 6	Strix	occidentalis	occidentalis	<NA>
## 7	Aeronautes	vauxi	<NA>	<NA>
## 8	Hylocichla	mustelina	<NA>	<NA>
## 9	Myadestes	townsendii	<NA>	<NA>
## 10	Setophaga	coronata	coronata	group

```
## # ... with 24 more rows
```

# rarePlants

```
## # A tibble: 304 x 5
##   genus      species      sublabel  reserve_list      count
##   <chr>      <chr>      <chr>      <chr>      <int>
## 1 Abies      concolor    <NA>      James San Jacinto Mou~    2
## 2 Acamptopappus sphaerocephalus hirtellus Sweeney Granite Mount~    1
## 3 Ailanthus    altissima    <NA>      McLaughlin, Quail Rid~    3
## 4 Allium      burlewii     <NA>      Boyd Deep Canyon, Jam~    2
## 5 Allium      fimbriatum   fimbriatum Boyd Deep Canyon, Bur~    3
## 6 Ambrosia    acanthicarpa <NA>      Boyd Deep Canyon, Bur~    3
## 7 Amsinckia   intermedia   <NA>      Landells-Hill Big Cre~    1
## 8 Amsinckia   tessellata   tessellata Boyd Deep Canyon, Swe~    2
## 9 Ancistrocarphus filagineus    <NA>      McLaughlin, Motte Rim~    3
## 10 Anisocoma   acaulis      <NA>      Boyd Deep Canyon, Bur~    3
## # ... with 294 more rows
```

# rareAnimals

```
## # A tibble: 52 x 5
##   genus      species      sublabel1 reserve_list      count
##   <chr>      <chr>      <chr>      <chr>      <int>
## 1 Actinemys    marmorata    <NA>      Angelo Coast Range Reser~    3
## 2 Alectoris    chukar       <NA>      Motte Rimrock Reserve, S~    2
## 3 Ammospermophilus leucurus    <NA>      Boyd Deep Canyon Desert ~    1
## 4 Amphispiza   bilineata    <NA>      Boyd Deep Canyon Desert ~    3
## 5 Anas         penelope     <NA>      Bodega Marine Reserve, C~    3
## 6 Aythya       marila       <NA>      Bodega Marine Reserve    1
## 7 Batrachoseps nigriventris <NA>      Elliot Chaparral Reserve~    2
## 8 Botaurus     lentiginosus <NA>      Boyd Deep Canyon Desert ~    3
## 9 Bubulcus     ibis         <NA>      Boyd Deep Canyon Desert ~    3
## 10 Callisaurus  draconoides   <NA>      Boyd Deep Canyon Desert ~    2
## # ... with 42 more rows
```