# Exploring The Essen and Densmore

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## Import Data

First thing needed is to import all of the data.

```
library(data.table)

## Warning: package 'data.table' was built under R version 3.4.2

library(ggplot2)

densmore <- fread("../data/feature_data/densmoreFeatures.csv") # Native American Songs
essen <- fread("../data/feature_data/essenFeatures.csv") # Essen Collection</pre>
```

## **Explore Data**

Check out all the variables listed.

```
names(essen)
```

```
[1] "folksong"
                                                      "mean.productivity"
                               "mean.entropy"
   [4] "mean.Simpsons.D"
                               "mean.Yules.K"
                                                      "mean.Sichels.S"
## [7] "mean.Honores.H"
                               "p.range"
                                                      "p.entropy"
## [10] "p.std"
                               "i.abs.range"
                                                      "i.abs.mean"
## [13] "i.abs.std"
                               "i.mode"
                                                      "i.entropy"
                                                      "d.mode"
## [16] "d.range"
                               "d.median"
## [19] "d.entropy"
                               "d.eq.trans"
                                                      "d.half.trans"
## [22] "d.dotted.trans"
                               "len"
                                                      "glob.duration"
## [25] "note.dens"
                               "tonalness"
                                                      "tonal.clarity"
## [28] "tonal.spike"
                               "int.cont.grad.mean"
                                                      "int.cont.grad.std"
## [31] "int.cont.dir.change"
                               "step.cont.glob.var"
                                                      "step.cont.glob.dir"
## [34] "step.cont.loc.var"
                               "mode"
                                                      "h.contour"
## [37] "int.cont.glob.dir"
                               "int.contour.class"
                                                      "Country"
## [40] "Country.ID"
                               "Region"
```

Special subset of this data has region of Germany associated with it.

```
unique(essen$Region)
```

```
## [1] NA    "fink"    "erk1"    "erk2"    "boehme"    "ballad"
## [7] "allerkbd" "altdeu1"    "dva"    "zuccal"    "variant"
unique(densmore$Country)
```

```
## [1] "ojibwa" "pawnee" "sioux" "siouxa" "siouxb" "siouxc"
```

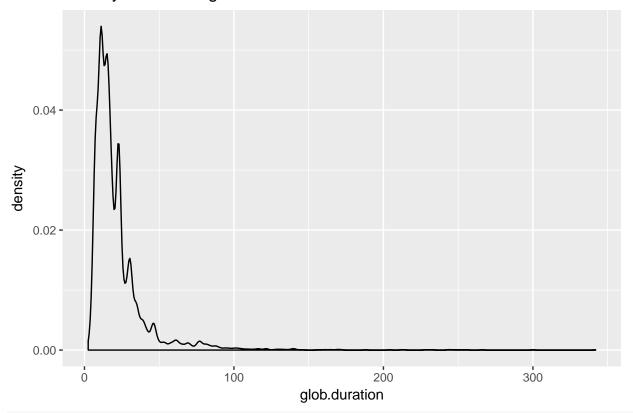
# Link to what key of each one is can be found here http://kern.humdrum.org/cgi-bin/browse?l=essen/euro

#### **Explore Large Level Features of Corpus**

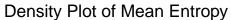
Swap in other variables below!

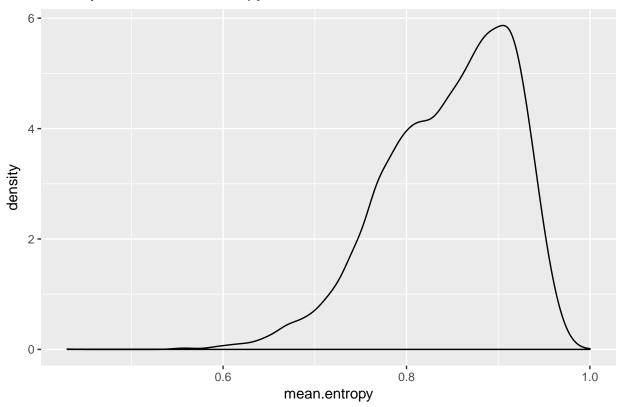
ggplot(essen, aes(glob.duration)) + geom\_density() + labs(title = "Density Plot of Length")

# **Density Plot of Length**



ggplot(essen, aes(mean.entropy)) + geom\_density() + labs(title = "Density Plot of Mean Entropy")

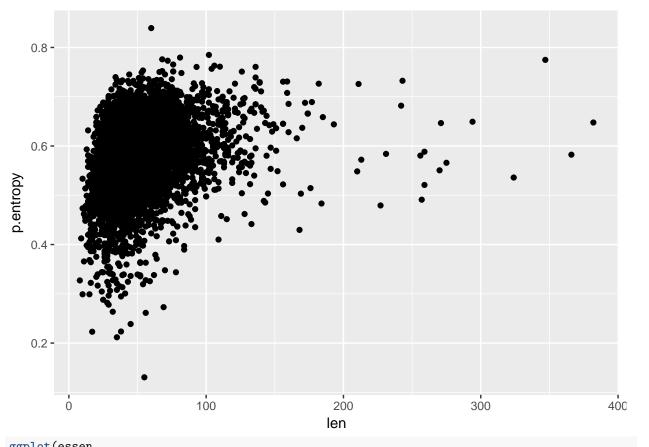




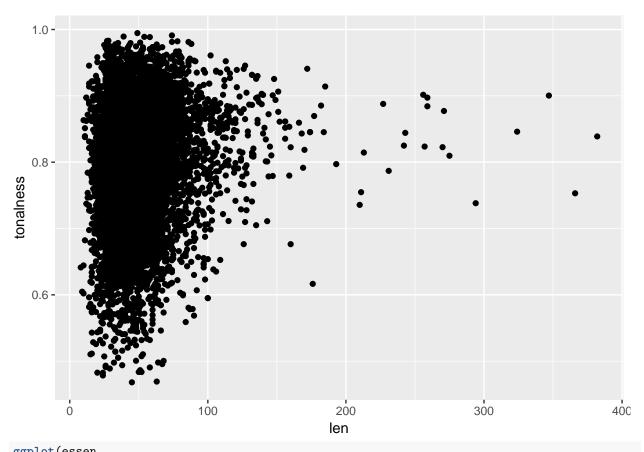
# Relationship Between Variables

You can use ggplot2 to explore the relationship between different variables. Try to swap out the x and y variables with others on a continuous scale. You can also group by categorical variables.

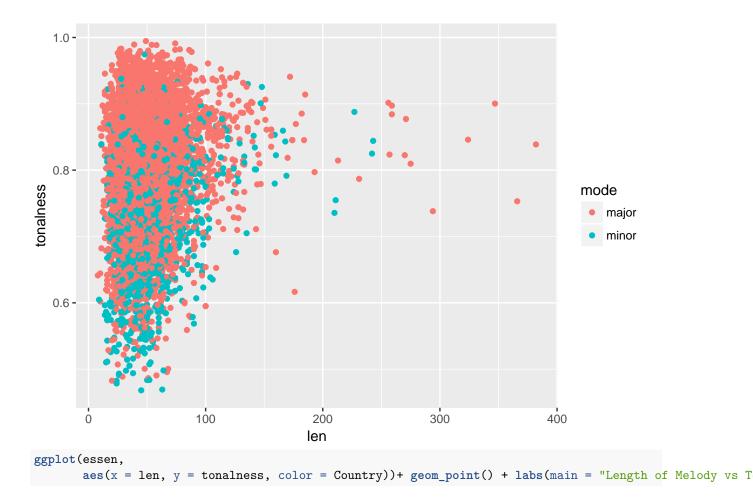
```
ggplot(essen,
    aes(x = len, y = p.entropy))+ geom_point() + labs(main = "Length of Melody vs Pitch Entropy")
```

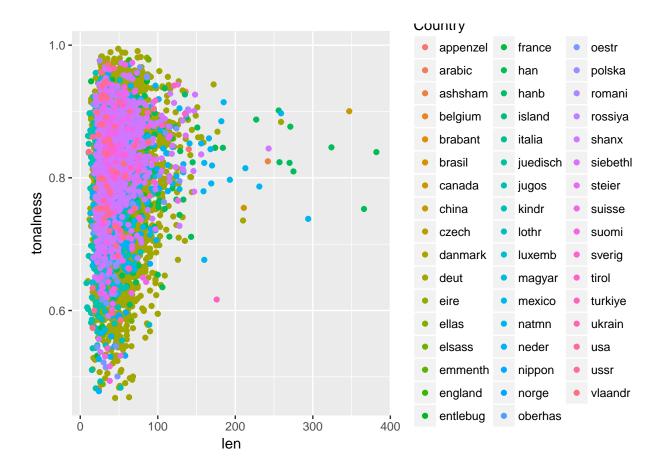


ggplot(essen,
 aes(x = len, y = tonalness))+ geom\_point() + labs(main = "Length of Melody vs Tonalness")



ggplot(essen,
 aes(x = len, y = tonalness, color = mode))+ geom\_point() + labs(main = "Length of Melody vs Tonalness)

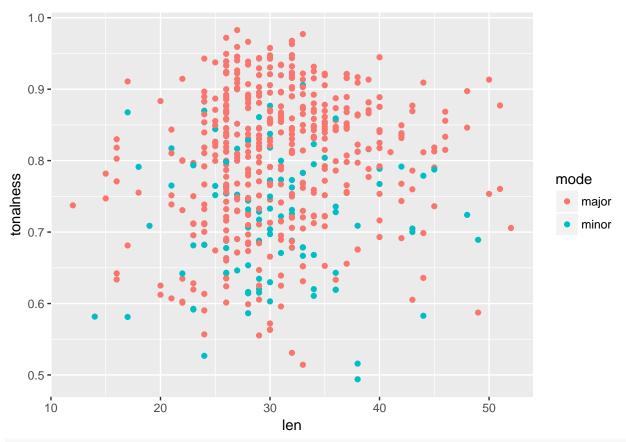


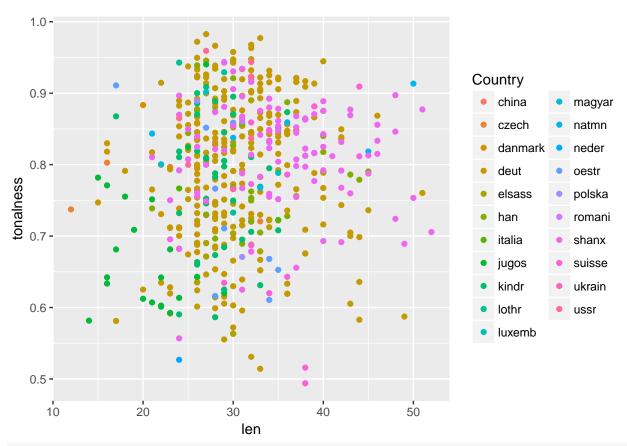


#### Subsetting

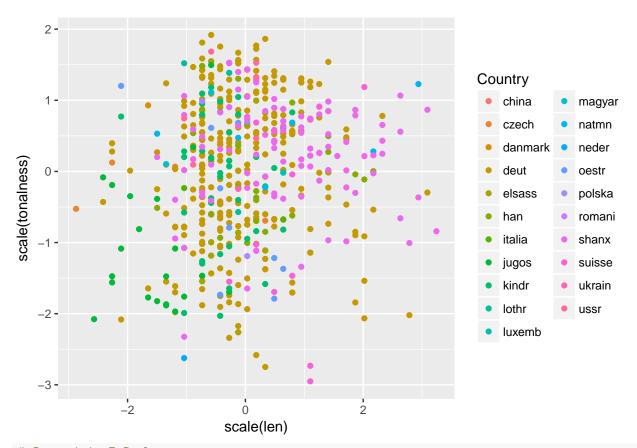
You can "zoom" in on some variables using R's indexing functions.

```
# Index within the plot
ggplot(essen[glob.duration > 7 & glob.duration < 9],
    aes(x = len, y = tonalness, color = mode))+ geom_point() + labs(main = "Length of Melody vs Tona")</pre>
```

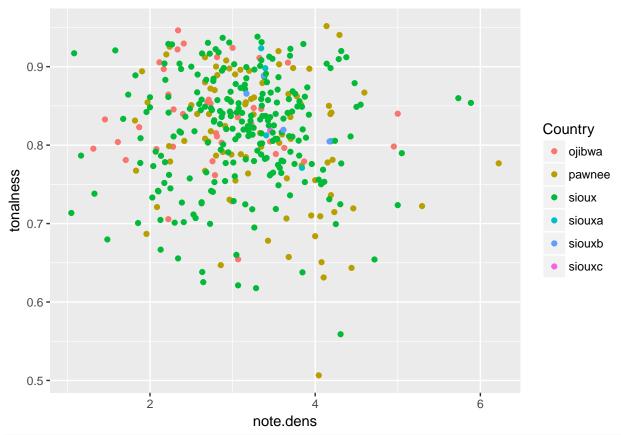




```
# Convert to Z Scale
ggplot(essen[glob.duration > 7 & glob.duration < 9],
    aes(x = scale(len), y = scale(tonalness), color = Country))+ geom_point() + labs(main = "Length")</pre>
```

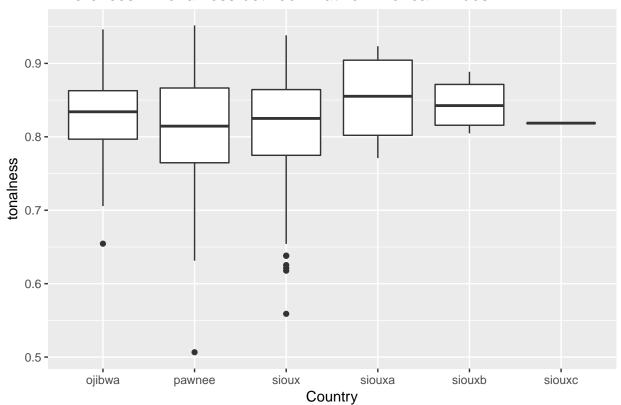


```
# Convert to Z Scale
ggplot(densmore,
    aes(x = note.dens, y = tonalness, color = Country))+ geom_point() + labs(main = "Densmore Density")
```



```
# Look at Group Differences
ggplot(densmore,
       aes(y = tonalness, x = Country)) + geom_boxplot() + labs(title = "Differences in Tonalness between the country))
```

# Differences in Tonalness between Native American Tribes



ggplot(essen,
 aes(y = tonalness, x = mode)) + geom\_boxplot() + labs("Differences in Tonalness in Essen Collect

