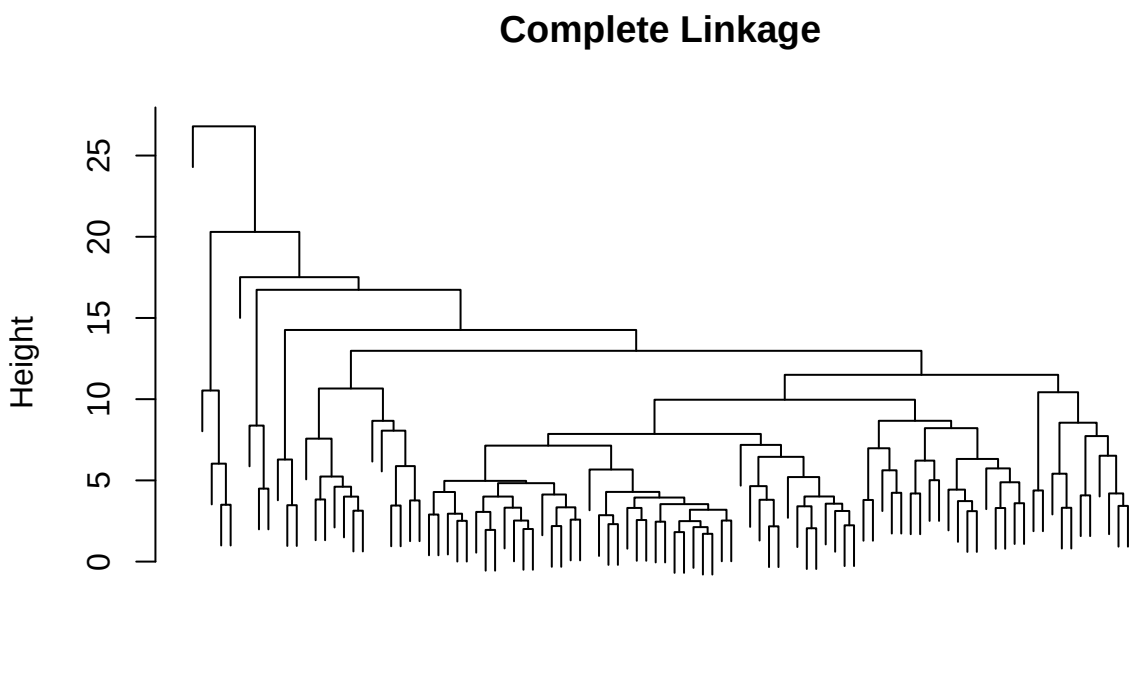
Project

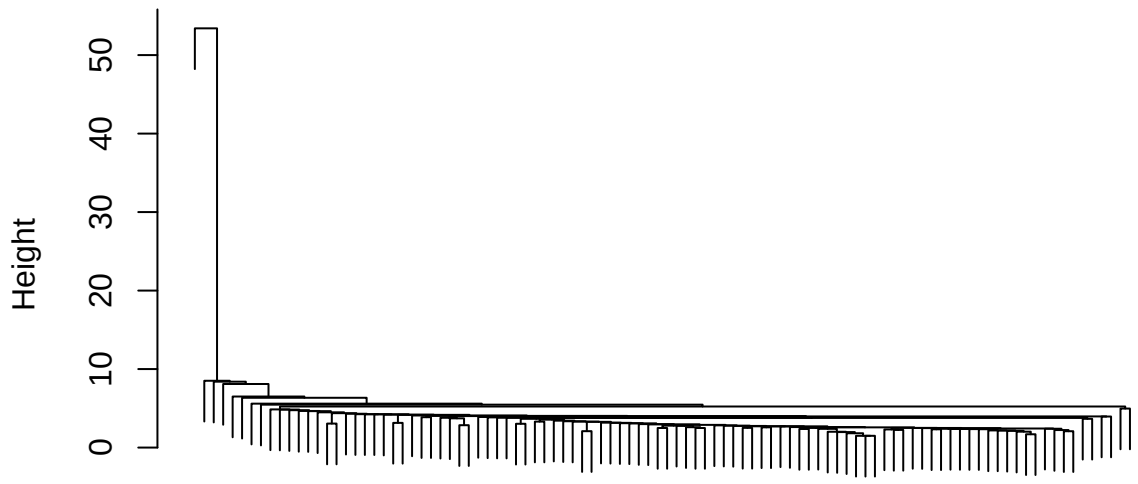
Travis Benedict

October 30, 2018

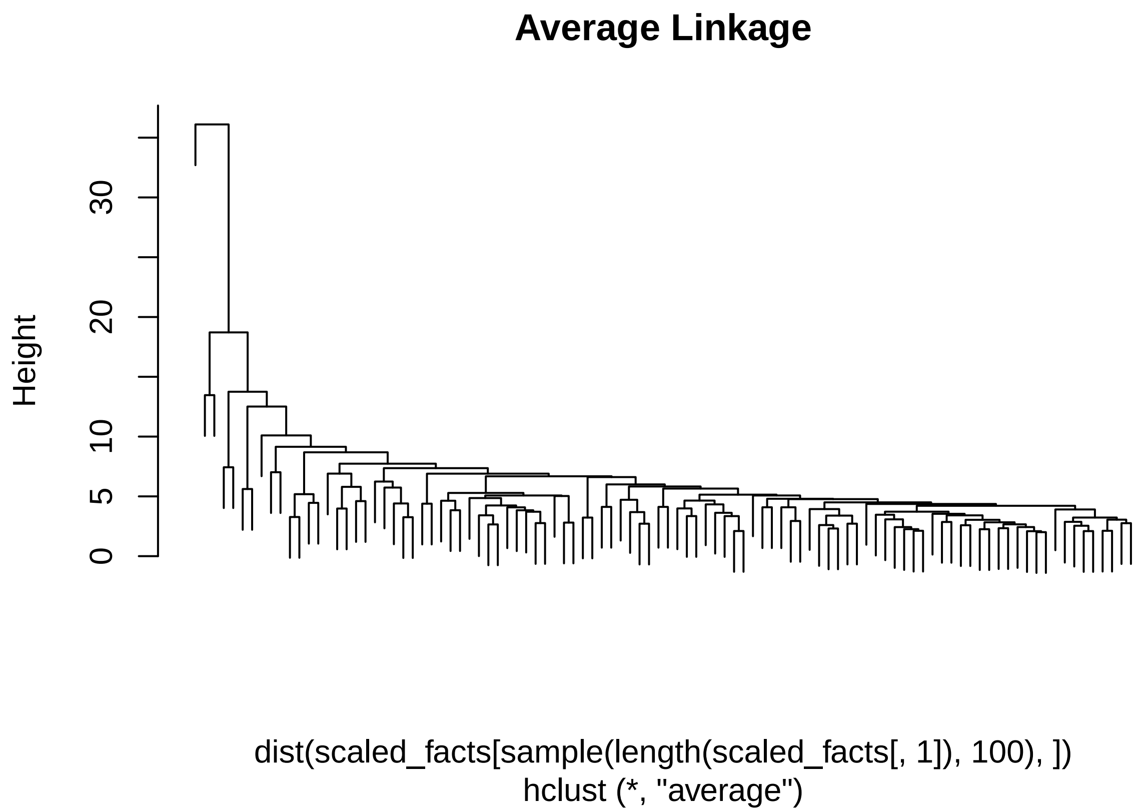
```
set.seed(1)

# Predictors are separated from vote results join on FIPS
results = read.csv('CountyLevelResults.csv')
facts = read.csv('county_facts.csv')

# Remove statewide information and identifiers from facts leave only data
cleaned_facts = data.frame(facts[c(-1, -2, -3)])
cleaned_facts = cleaned_facts[facts[3] != "",]

##### BE CAREFUL JOINING THE INFORMATION BACK WITH THE IDENTIFIERS

# View(cleaned_facts)
# View(results)


scaled_facts = scale(cleaned_facts)



plot(hclust(dist(scaled_facts[sample(length(scaled_facts[,1]), 100),]), method="complete"), main="Compl
```




```
plot(hclust(dist(scaled_facts[sample(length(scaled_facts[,1]), 100),]), method="single"), main="Single
```




```
plot(hclust(dist(scaled_facts[sample(length(scaled_facts[,1]), 100),]), method="average"), main="Averag
```




```r
#Col
dim(scaled_facts)
```

```
## [1] 3143   51
```

```r
# plot(as.dendrogram(hclust(dist(scaled_facts[sample(length(scaled_facts[,1]), 100),]))), ylim=c(0, 50)
# plot(as.dendrogram(hclust(dist(scaled_facts[sample(length(scaled_facts[,1]), 100),]))), ylim=c(0, 50)
# plot(as.dendrogram(hclust(dist(scaled_facts[sample(length(scaled_facts[,1]), 100),]))), ylim=c(0, 50)
# plot(as.dendrogram(hclust(dist(scaled_facts[sample(length(scaled_facts[,1]), 100),]))), ylim=c(0, 50)
# plot(as.dendrogram(hclust(dist(scaled_facts[sample(length(scaled_facts[,1]), 100),]))), ylim=c(0, 50)
# plot(as.dendrogram(hclust(dist(scaled_facts[sample(length(scaled_facts[,1]), 100),]))), ylim=c(0, 50)
# plot(as.dendrogram(hclust(dist(scaled_facts[sample(length(scaled_facts[,1]), 100),]))), ylim=c(0, 50)
# plot(as.dendrogram(hclust(dist(scaled_facts[sample(length(scaled_facts[,1]), 100),]))), ylim=c(0, 50)
```