I519: Homework 1

Will Shoemaker

04 September, 2015

Overview

Set working directory

```
rm(list=ls())
getwd()
```

```
## [1] "/Users/WRShoemaker/github/PopGen/I519/HW1"
```

```
setwd("~/github/PopGen/I519/HW1/")
```

Import packages

```
library("quantmod")
```

```
## Loading required package: xts
## Loading required package: zoo
##
## Attaching package: 'zoo'
##
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
##
## Loading required package: TTR
## Version 0.4-0 included new data defaults. See ?getSymbols.
```

```
library("ggplot2")
library("reshape2")
library("wesanderson")
library(data.table)
```

```
##
## Attaching package: 'data.table'
##
## The following object is masked from 'package:xts':
##
##     last
```

Import the data and add headers

```
draft <- read.table("./genesize-draft.txt",header=F)
complete <- read.table("./genesize-complete.txt",header=T)

colnames(draft) <- c("Strain", "Genes")
colnames(complete) <- c("Strain", "Genes")
```

Mean gene number

```
mean(draft[,2])
```

```
## [1] 2678.527
```

```
mean(complete[,2])
```

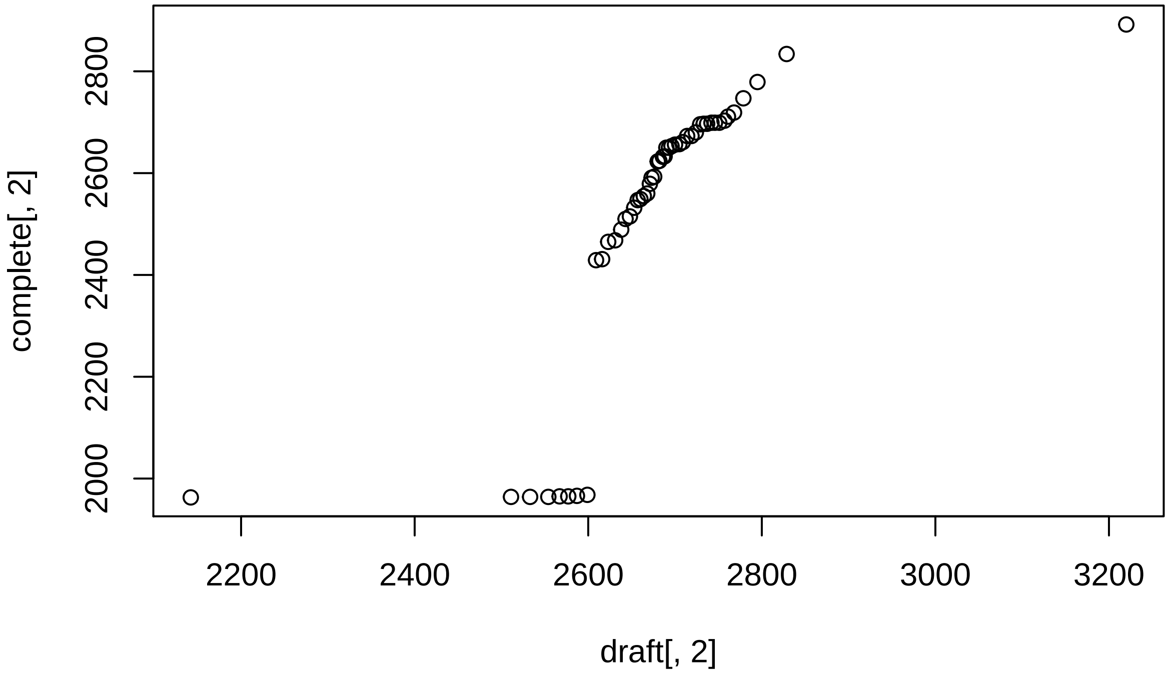
```
## [1] 2521.816
```

So the draft genomes have a mean gene number of ~2,679 and the complete genomes have a mean gene number of ~2522. Let's look if there's a significant difference.

Examine the quantile-quantile plots for the samples

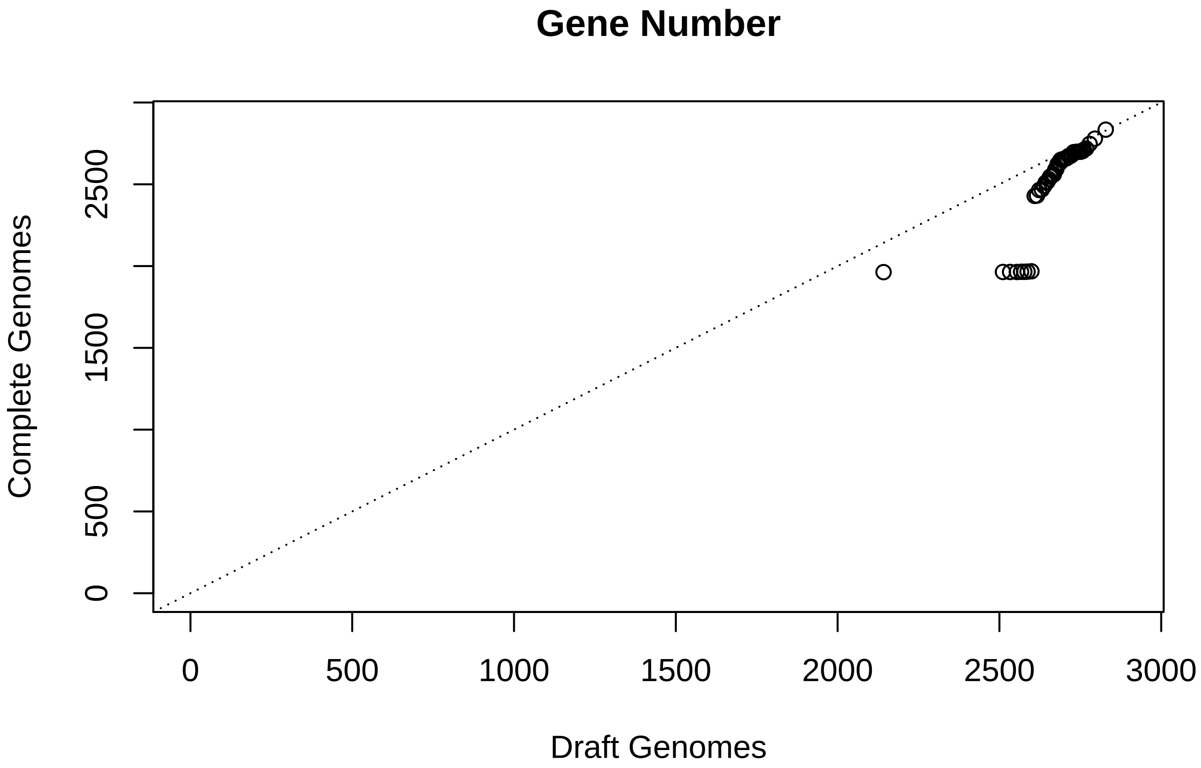
First we make a Q-Q plot that examines both samples.

```
qqplot(draft[,2], complete[,2])
```



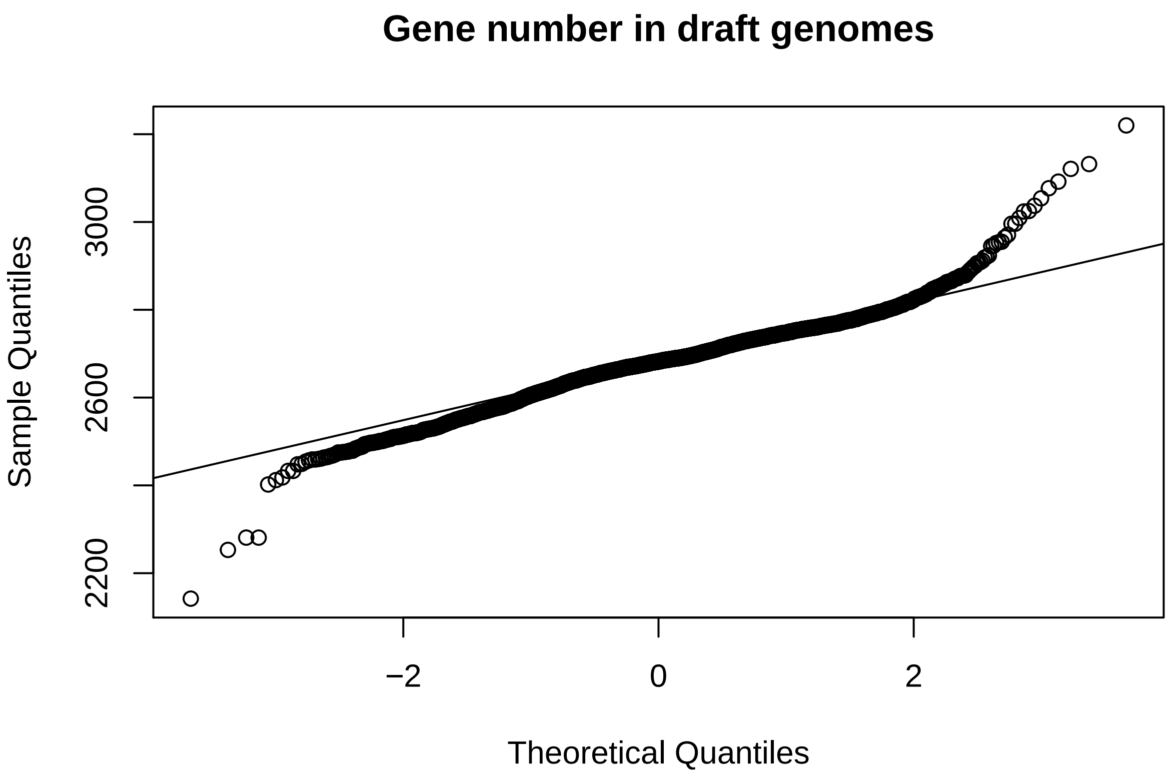
```
xlim = range(1800, draft)
ylim = range(1800, complete)

qqplot(draft[,2], complete[,2],
xlim = ylim, ylim = ylim,
xlab = "Draft Genomes",
ylab = "Complete Genomes",
main = "Gene Number")
abline(a=0, b=1, lty="dotted")
```

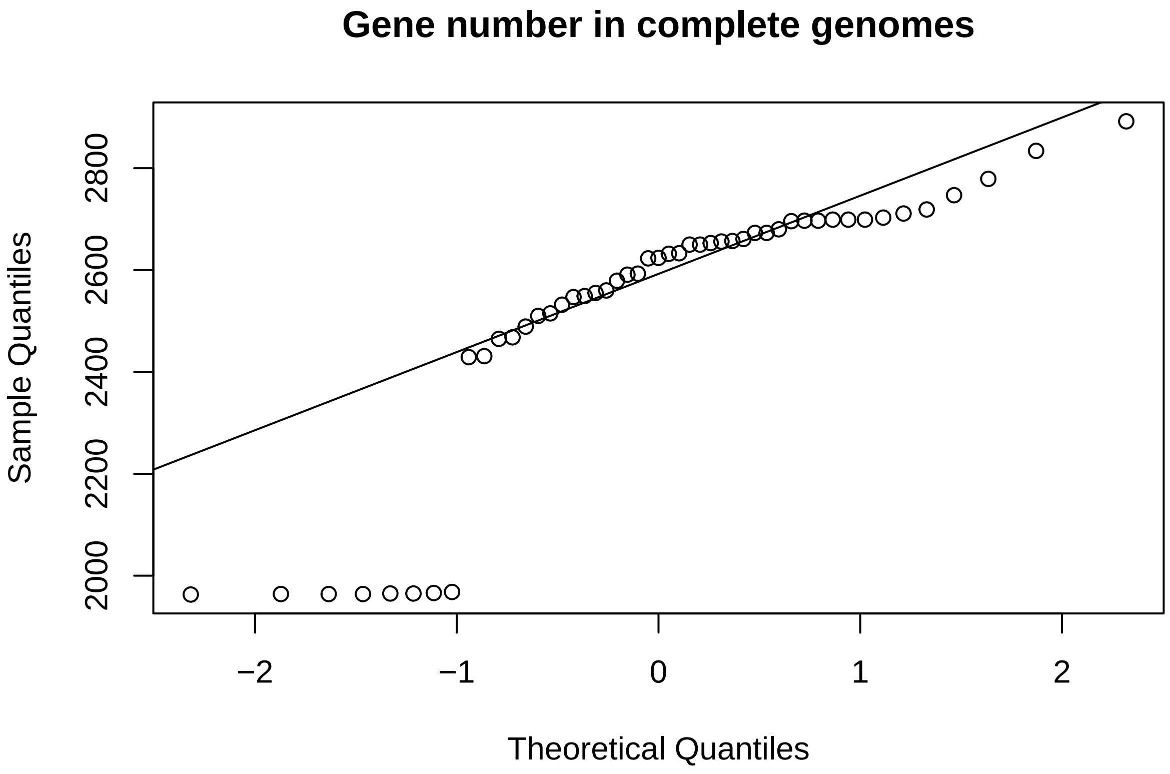


Then we make a Q-Q plot for each sample that compares the theoretical quantiles with sample quantiles.

```
qqnorm(draft[,2],
main = "Gene number in draft genomes")
qqline(draft[,2])
```



```
qqnorm(complete[,2],
main = "Gene number in complete genomes")
qqline(complete[,2])
```



We see from above that there is a clear deviation from the theoretical expectation for each sample, suggesting that it would not be a good idea to assume normality. We can then proceed with a Wilcoxon rank-sum test.

```
wilcox.test(draft[,2], complete[,2], alternative = c("two.sided"), paired = FALSE, conf.level = 0.95)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  draft[, 2] and complete[, 2]
## W = 140410, p-value = 6.078e-07
## alternative hypothesis: true location shift is not equal to 0
```

There is a significant difference in the number of genes between draft and complete genomes.

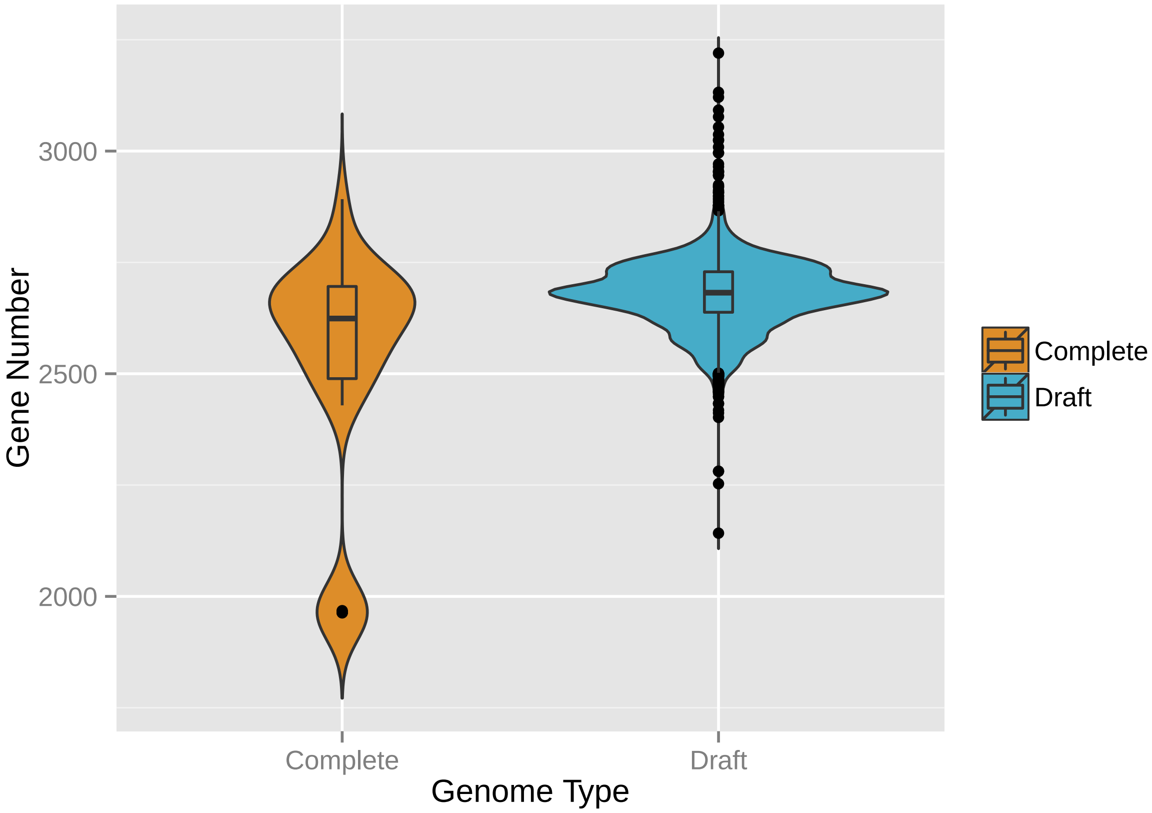
```
draft$Type <- rep("Draft",nrow(draft))
complete$Type <- rep("Complete",nrow(complete))
mergeData <- rbind(draft, complete)
mergeData$logGenes <- log(mergeData[,2])
class(mergeData)
```

```
## [1] "data.frame"
```

```
head(mergeData)
```

```
##                                      Strain Genes  Type logGenes
## 1 Staphylococcus_aureus_06BA18369_uid170654  2804 Draft 7.938802
## 2  Staphylococcus_aureus_07_03450_uid226303  2476 Draft 7.814400
## 3  Staphylococcus_aureus_07_03451_uid226304  2484 Draft 7.817625
## 4  Staphylococcus_aureus_08_01059_uid226297  2566 Draft 7.850104
## 5  Staphylococcus_aureus_08_01062_uid226298  2566 Draft 7.850104
## 6  Staphylococcus_aureus_08_01084_uid226305  2574 Draft 7.853216
```

```
palette <- wes_palette(5, name = "FantasticFox", type = "discrete")
ggplot(mergeData, aes(x=Type, y=Genes, fill = Type)) +
  geom_violin(trim=FALSE) +
  geom_boxplot(width=0.1) +
  scale_fill_manual(values=palette[-2]) +
  xlab("Genome Type") +
  scale_size_area("Genome Type") +
  ylab("Gene Number") +
  guides(fill=guide_legend(title=NULL))
```


3000
2500
2000
Gene Number
Complete
Draft
Genome Type
Complete
Draft