

# Assessing Uncorrected Insertions and Deletions - Flye Assemblies

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*6/14/2019*

Load the packages

Read files into R

```
polished <- "/Users/Taruna/Dropbox/Wilbanks-lab/MinION/annie-row/genome-assemblies/blast/flye-largestCor  
unpolished <- "/Users/Taruna/Dropbox/Wilbanks-lab/MinION/annie-row/genome-assemblies/blast/flye-largestCor  
polishedTable <- read.table(file.path(polished), sep = "\t", header = FALSE, check.names = FALSE)  
unpolishedTable <- read.table(file.path(unpolished), sep = "\t", header = FALSE, check.names = FALSE)  
head(unpolishedTable)
```

```
##           V1  V2           V3  V4  
## 1 IOPLDOMB_00001 276 sp|Q88EM0|DADA1_PSEPK 432  
## 2 IOPLDOMB_00002 449 sp|A4WPF7|SYDND_RHOS5 591  
## 3 IOPLDOMB_00003  33 sp|A1B431|SYDND_PARDP 591  
## 4 IOPLDOMB_00004 158 sp|Q8YS92|NICK_NOSS1 351  
## 5 IOPLDOMB_00005  97 sp|C1F3C4|DXS_ACIC5 627  
## 6 IOPLDOMB_00006 152 sp|PODM78|PHOP_SALTY 224
```

Assign colnames to each table

```
colnames(polishedTable) <- c("queryID", "qLen", "subjectID", "sLen" )  
colnames(unpolishedTable) <- c("queryID", "qLen", "subjectID", "sLen" )
```

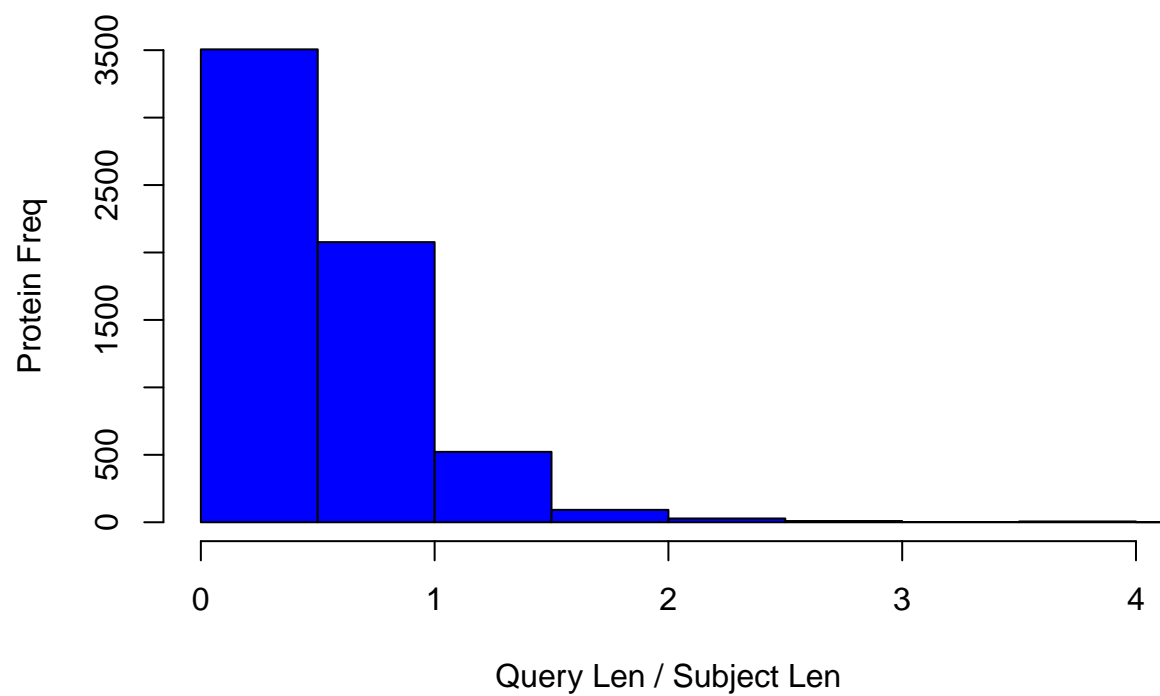
Divide the qLen with sLen and create a new column

```
newPolish <- transform(polishedTable, ratio = qLen/sLen)  
newUnpolish <- transform(unpolishedTable, ratio = qLen/sLen)
```

Create histogram for the Polished Assembly

```
unp_hist <- hist(newUnpolish$ratio, col = "blue",  
                 xlab = "Query Len / Subject Len",  
                 ylab = "Protein Freq",  
                 main = "Histogram for Unpolished Flye Assembly",  
                 xlim = c(0.0,4))
```

## Histogram for Unpolished Flye Assembly



Create histogram for the Unpolished Assembly

```
p_hist <- hist(newPolish$ratio, col = "gold",  
               xlab = "Query Len / Subject Len",  
               ylab = "Protein Freq",  
               main = "Histogram for Polished Flye Assembly",  
               xlim = c(0.0,4))
```

**Histogram for Polished Flye Assembly**

