Untitled

Loading and setting up data

```r
library(tximeta)
dir <- "../../real_data/out"
load("../../real_data/out_1/sim_counts_matrix.rda")
source("helper_func.R")

files <- file.path(dir, c("sample_01_B_100", "sample_01_GS_100"), "quant.sf")
coldata <- data.frame(files, names = c("sample_01_B_100", "sample_01_GS_100"), infType = c("Boot", "GS")
se <- tximeta(coldata)

### Extracting common transcripts
mInds <- match(rownames(counts_matrix), rownames(se))
seNonZero <- se[mInds,]

### Loading the transcripts from the experiment
eqTrans <- read.table("../../real_data/networkx/thought_exp.txt", sep = "\t", header = T)
```

Normalization by scaling factor

```r
library(DESeq2)
reqMat <- cbind(assays(seNonZero)[["counts"]][,1], counts_matrix[,1])
colnames(reqMat) <- c("Estimated", "True")
sizeFac <- estimateSizeFactorsForMatrix(reqMat)

print(sizeFac)
```

```
## Estimated      True
## 0.8902351 1.1232988
```

```r
asNames <- assayNames(seNonZero)
asNames <- asNames[grepl("inf*",asNames) | grepl("counts",asNames)]

for(assay in asNames)
    assays(seNonZero)[[assay]] <- assays(seNonZero)[[assay]]/sizeFac[1]

seNonZero <- computeConfInt(seNonZero)
se <- computeConfInt(se)
trueCounts <- counts_matrix[,1]/sizeFac[2]
```

Actual Coverage

```r
coverage <- computeCoverage(trueCounts, seNonZero, list(seq(nrow(counts_matrix))))
print(coverage)
```

```
##   sample_01_B_100 sample_01_GS_100
## 1       0.7598177        0.7823249
```

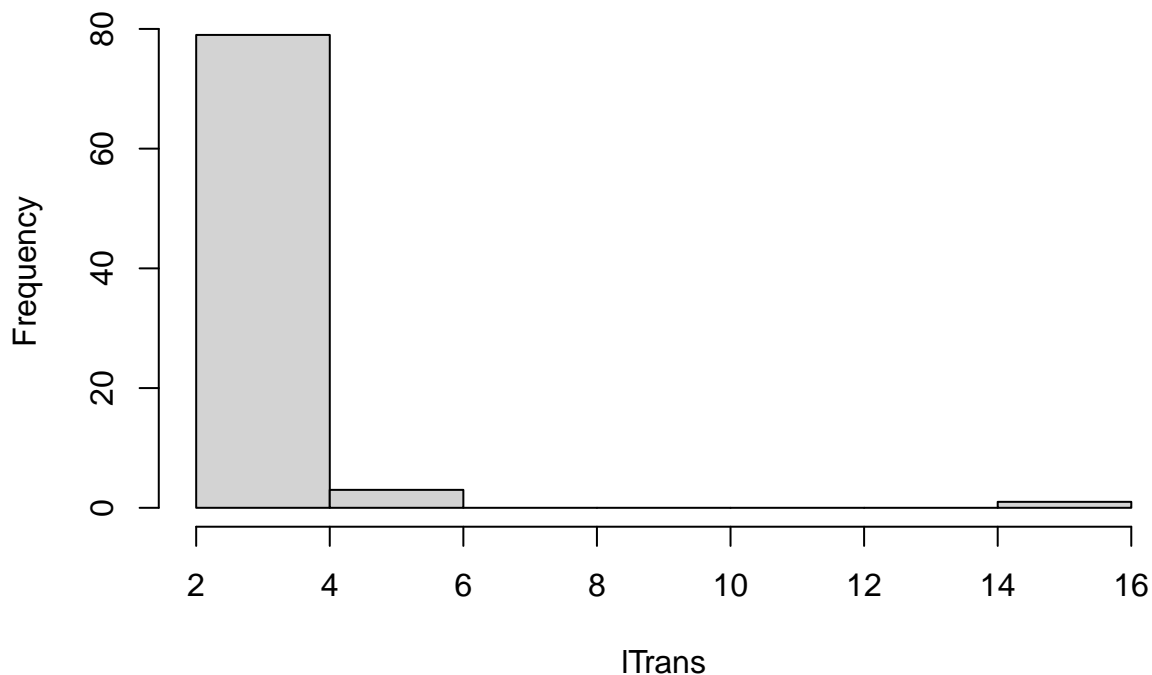**Looking at the transcripts in the experiment**

A total of 83 equivalence classes Most classes contain only 2 transcripts

```
print(nrow(eqTrans))
```

```
## [1] 83
```

```
trans <- strsplit(eqTrans[,1], split = ",", fixed = T)
lTrans <- sapply(trans, length)
hist(lTrans)
```

Histogram of lTrans

However only 88 of the 215 transcripts are in the precomputed simulated counts

```
transAll <- unlist(trans)
print(sum(transAll %in% rownames(seNonZero)))
```

```
## [1] 88
```

```
sumStat <- c("infRV", "means", "LowC", "HighC")
infType <- c("Boot", "GS")

for(s in sumStat)
{
    for(i in seq_along(infType))
    {
        cName <- paste(s, infType[i], sep = "_")
        eqTrans[,cName] <- sapply(trans, function(x) paste(round(assays(se)[[s]][x,i],4), collapse = ",
    }
}
write.table(eqTrans, "../../real_data/networkx/thought_exp.txt", sep = "\t", row.names = F)
```