Comparing

Loading data and computing coverages

```
source("helper_func.R")
suppressPackageStartupMessages(library(SummarizedExperiment))
load("environment/seList.RData")
load("../../real_data/out_1/sim_counts_matrix.rda")

se100 <- seList[["100"]]
se100 <- computeSizeFactors(se100, counts_matrix[,1])
```

```
## [1] 1
## [1] 2
## [1] 3
```

```
se100 <- computeConfInt(se100, sf = T)
covInds <- computeCoverage(counts_matrix[,1], se100, list(seq(nrow(counts_matrix))), prop = F)[[1]]
```

Number of transcripts that are covered by all the 3 methods

```
commInds <- Reduce(intersect, covInds)
print(length(commInds))
```
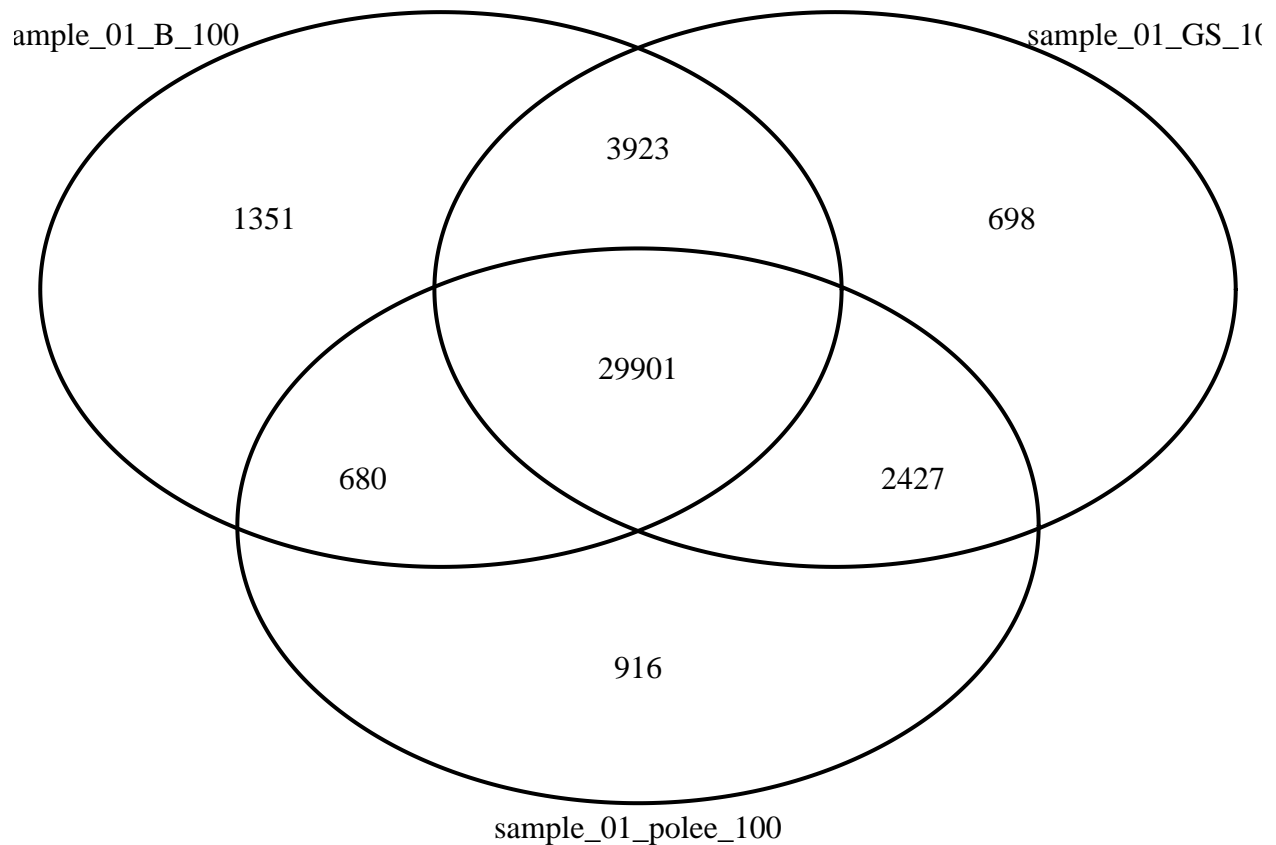
```
## [1] 29901
```

Transcripts that are covered by only 1 method

```
library(VennDiagram)
```

```
## Loading required package: grid
```

```
## Loading required package: futile.logger
```

```
bootOnly <- setdiff(setdiff(covInds[[1]],covInds[[2]]), covInds[[3]])
gibbsOnly <- setdiff(setdiff(covInds[[2]],covInds[[1]]), covInds[[3]])
poleeOnly <- setdiff(setdiff(covInds[[3]],covInds[[1]]), covInds[[2]])

g <- venn.diagram(covInds, category.names=names(covInds), filename=NULL, output=T)
grid.draw(g)
```

sample_01_B_100

sample_01_GS_10

3923

1351

698

29901

680

2427

916

sample_01_polee_100

Number of transcripts for which the width is lower across the common covered transcripts

```
minInds <- apply(assays(se100)[["Width"]][commInds, ], 1, which.min)
tb <- table(minInds)
names(tb) <- c("Boot", "Gibbs", "Polee")
print(tb)

##  Boot Gibbs Polee
##  9747  8930 11224
```

Number of transcripts for which the width is lower across the common covered transcripts only b/w boots and GS removing other common transcripts

```
bGSInds <- setdiff(intersect(covInds[[1]], covInds[[2]]), commInds)
minInds <- apply(assays(se100)[["Width"]][bGSInds, 1:2], 1, which.min)
tb <- table(minInds)
names(tb) <- c("Boot", "Gibbs")
print(tb)

##  Boot Gibbs
##  1613  2310
```

Number of transcripts for which the width is lower across the common covered transcripts only b/w boots and Polee removing other common transcripts

```
bPolInds <- setdiff(intersect(covInds[[1]], covInds[[3]]), commInds)
minInds <- apply(assays(se100)[["Width"]][bPolInds, c(1,3)], 1, which.min)
tb <- table(minInds)
names(tb) <- c("Boot", "Polee")
print(tb)
```

```
##  Boot Polee
##   269   411
```

Number of transcripts for which the width is lower across the common covered transcripts only b/w Gibbs and Polee removing other common transcripts

```
gPolInds <- setdiff(intersect(covInds[[2]], covInds[[3]]), commInds)
minInds <- apply(assays(se100)[["Width"]][gPolInds, c(2,3)], 1, which.min)
tb <- table(minInds)
names(tb) <- c("Gibbs", "Polee")
print(tb)
```

```
## Gibbs Polee
##  1156  1271
```