

Reproduce SVA problem

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Setup

What happens to the number of Surrogate Variables as we increase the number of studies in recount3?

To illustrate this, we examined 4 studies that involved case/control prostate tumor and normal samples, with a minimal of 25 samples per study. For each study, we examined the number of SVs (using method = “be”), and we also aggregated them one by one and examined the number of SVs iteratively. When using method = “leek”, we always get 0 estimated SVs, which is strange.

1. SRP118614: “Overall design: Matched high-grade (GS=7(4+3)) prostate tumor and adjacent normal specimens from 16 patients (8 AAM and 8 EAM) were subjected to two replicate runs of RNA-sequencing.”
2. SRP212704: “Overall design: Strand specific total RNA seq was performed using frozen patient matched prostate cancer tissue in biological duplicates. Purpose: The goal of present study is to compare transcript level changes between normal and tumor of same individuals”
3. SRP002628: “Overall design: We sequenced the transcriptome (polyA+) of 20 prostate cancer tumors and 10 matched normal tissues using Illumina GAII platform. Then we used bioinformatic approaches to identify prostate cancer specific aberrations which include gene fusion, alternative splicing, somatic mutation.”
4. SRP027258: “We utilized RNA sequencing to test the hypothesis that SFN modifies the expression of genes that are critical in prostate cancer progression. Normal prostate epithelial cells, and androgen-dependent and androgen-independent prostate cancer cells were treated with 15 μ M SFN and the transcriptome was determined at 6 and 24 hour time points.”

```
#1.  
#Overall design: Matched high-grade (GS=7(4+3)) prostate tumor and adjacent  
#normal specimens from 16 patients (8 AAM and 8 EAM) were subjected to two  
#replicate runs of RNA-sequencing.  
  
proj_info <- subset(  
  human_projects,  
  project == "SRP118614"  
)  
  
rse_gene_SRP118614 <- create_rse(proj_info)  
phenotype = data.frame(colData(rse_gene_SRP118614))  
genotype = data.frame(rowData(rse_gene_SRP118614))  
  
phenotype$phenotype_tumor = grepl("prostate tumor", phenotype$sra.sample_attributes)
```

```

mod_SRP118614 = model.matrix(~phenotype_tumor, data = phenotype)

geneCounts_SRP118614 = assays(rse_gene_SRP118614)$raw_counts
geneCounts_SRP118614 = geneCounts_SRP118614 / colSums(geneCounts_SRP118614) #normalize by bases sequenc

n_sv[1] = num.sv(geneCounts_SRP118614, mod_SRP118614, method = "be", vfilter = 10000)
n_sv_agg[1] = NA

#2.
#Overall design: Strand specific total RNA seq was performed using frozen
#patient matched prostate cancer tissue in biological duplicates.
#Purpose: The goal of present study is to compare transcript level changes
#between normal and tumor of same individuals

proj_info <- subset(
  human_projects,
  project == "SRP212704"
)

rse_gene_SRP212704 <- create_rse(proj_info)
phenotype = data.frame(colData(rse_gene_SRP212704))
genotype = data.frame(rowData(rse_gene_SRP212704))

phenotype$phenotype_tumor = grepl("Tumor", phenotype$sra.sample_attributes)
mod_SRP212704 = model.matrix(~phenotype_tumor, data = phenotype)

geneCounts_SRP212704 = assays(rse_gene_SRP212704)$raw_counts
geneCounts_SRP212704 = geneCounts_SRP212704 / colSums(geneCounts_SRP212704)

geneCounts_2 = cbind(geneCounts_SRP118614, geneCounts_SRP212704)
mod_2 = rbind(mod_SRP118614, mod_SRP212704)

n_sv[2] = num.sv(geneCounts_SRP212704, mod_SRP212704, method = "be", vfilter = 10000)
n_sv_agg[2] = num.sv(geneCounts_2, mod_2, method = "be", vfilter = 10000)

#3
#Overall design: We sequenced the transcriptome (polyA+) of 20 prostate cancer
#tumors and 10 matched normal tissues using Illumina GAII platform.
#Then we used bioinformatic approaches to identify prostate cancer specific
#aberrations which include gene fusion, alternative splicing, somatic mutation
proj_info <- subset(
  human_projects,
  project == "SRP002628"
)

rse_gene_SRP002628 <- create_rse(proj_info)
phenotype = data.frame(colData(rse_gene_SRP002628))
genotype = data.frame(rowData(rse_gene_SRP002628))

phenotype$phenotype_tumor = grepl("Prostate cancer tissue", phenotype$sra.sample_attributes)
mod_SRP002628 = model.matrix(~phenotype_tumor, data = phenotype)

geneCounts_SRP002628 = assays(rse_gene_SRP002628)$raw_counts

```

```

geneCounts_SRP002628 = geneCounts_SRP002628 / colSums(geneCounts_SRP002628)

geneCounts_3 = cbind(geneCounts_SRP118614, geneCounts_SRP212704, geneCounts_SRP002628)
mod_3 = rbind(mod_SRP118614, mod_SRP212704, mod_SRP002628)

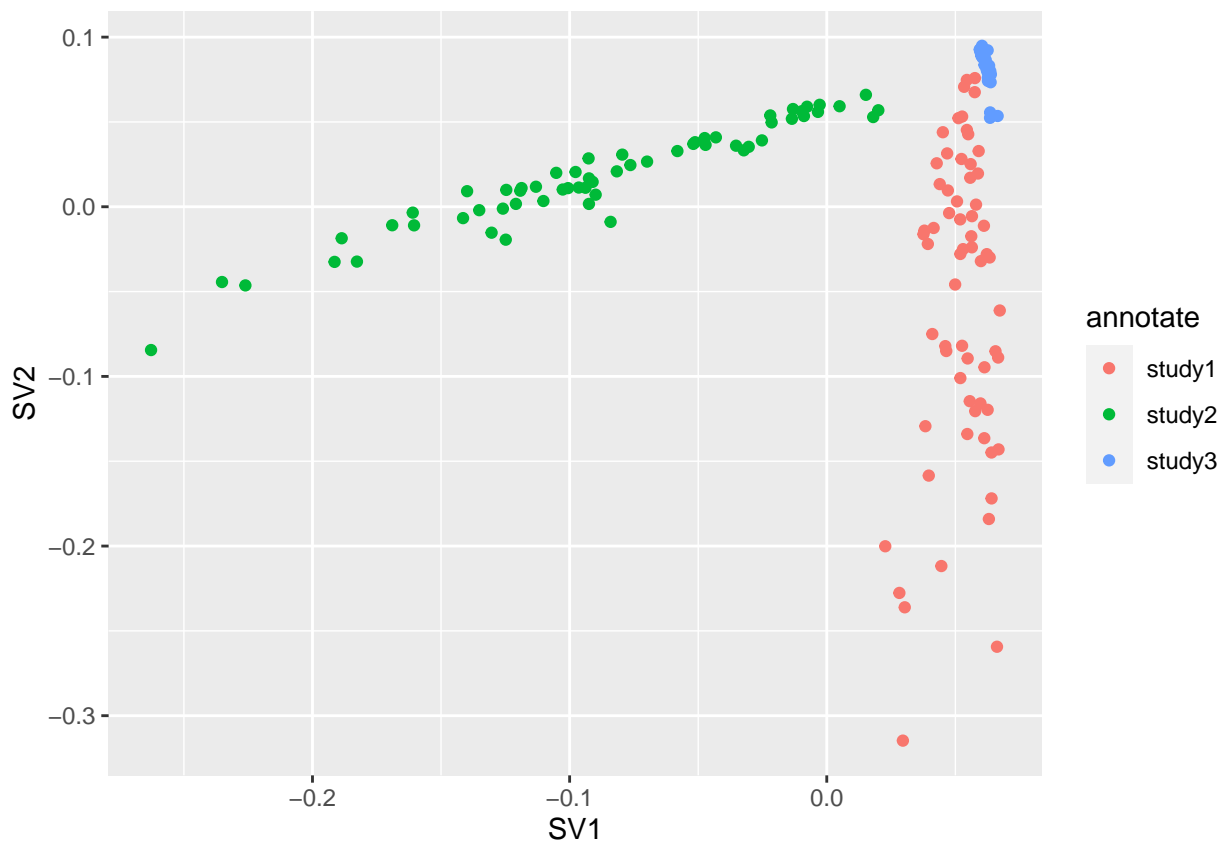
n_sv[3] = num.sv(geneCounts_SRP002628, mod_SRP002628, method = "be", vfilter = 10000)
n_sv_agg[3] = num.sv(geneCounts_3, mod_3, method = "be", vfilter = 10000)

#try plotting the SV variables
svobj = sva(geneCounts_3, mod_3, mod_3[, 1], n_sv = n_sv_agg[3], vfilter = 10000)

## Number of significant surrogate variables is: 2
## Iteration (out of 5):1 2 3 4 5

annotate = c(rep("study1", ncol(geneCounts_SRP118614)),
              rep("study2", ncol(geneCounts_SRP212704)),
              rep("study3", ncol(geneCounts_SRP002628)))
qplot(svobj$sv[,1], svobj$sv[,2], color = annotate, xlab = "SV1", ylab = "SV2")

```



```

#4
#We utilized RNA sequencing to test the hypothesis that SFN modifies the
#expression of genes that are critical in prostate cancer progression.
#Normal prostate epithelial cells, and androgen-dependent and androgen-independent
#prostate cancer cells were treated with 15  $\mu$ M SFN and the transcriptome was
#determined at 6 and 24 hour time points.

```

```

proj_info <- subset(
  human_projects,
  project == "SRP027258"
)
rse_gene_SRP027258 <- create_rse(proj_info)
phenotype = data.frame(colData(rse_gene_SRP027258))
genotype = data.frame(rowData(rse_gene_SRP027258))

phenotype$phenotype_tumor = grepl("prostate cancer", phenotype$sra.sample_attributes)
mod_SRP027258 = model.matrix(~phenotype_tumor, data = phenotype)

geneCounts_SRP027258 = assays(rse_gene_SRP027258)$raw_counts
geneCounts_SRP027258 = geneCounts_SRP027258 / colSums(geneCounts_SRP027258)

geneCounts_4 = cbind(geneCounts_SRP118614, geneCounts_SRP212704, geneCounts_SRP002628, geneCounts_SRP027258)
mod_4 = rbind(mod_SRP118614, mod_SRP212704, mod_SRP002628, mod_SRP027258)

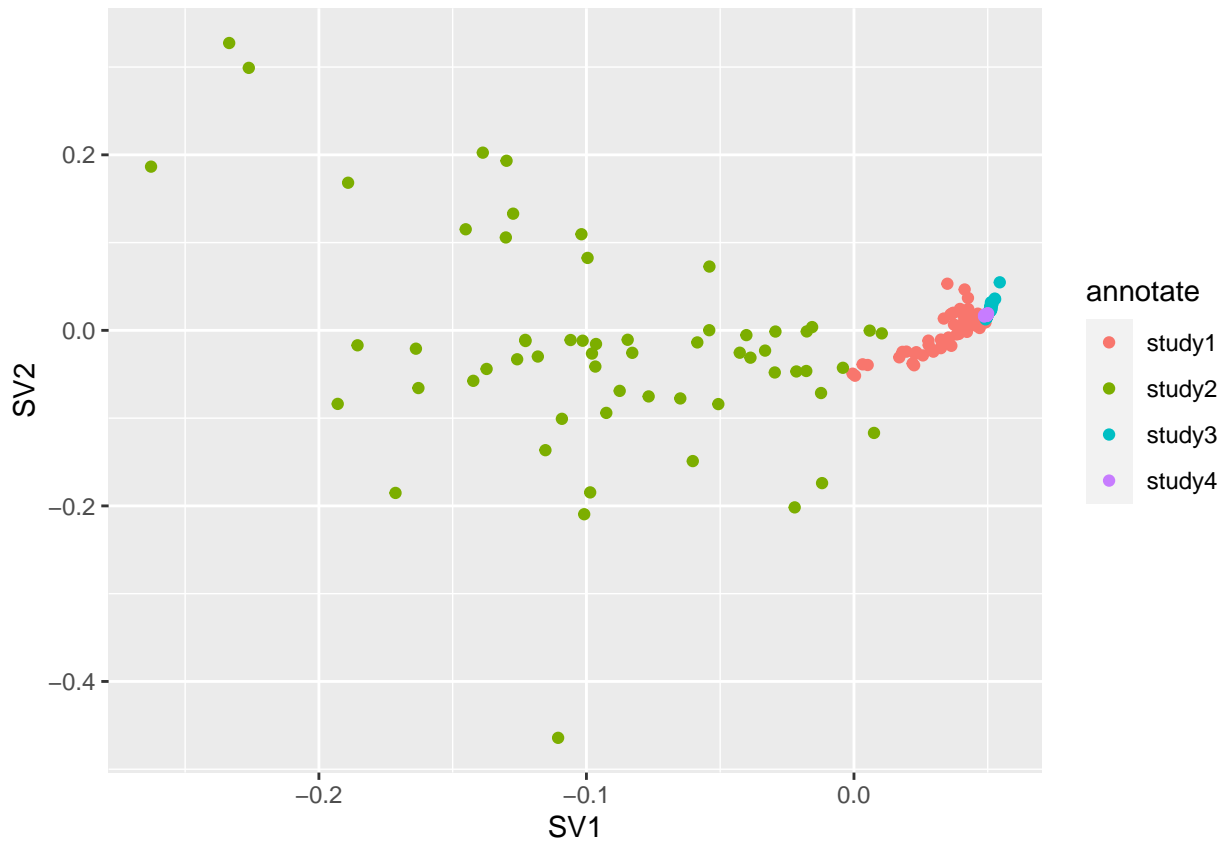
n_sv[4] = num.sv(geneCounts_SRP027258, mod_SRP027258, method = "be", vfilter = 10000)
n_sv_agg[4] = num.sv(geneCounts_4, mod_4, method = "be", vfilter = 10000)

#try plotting the SV variables
svobj = sva(geneCounts_4, mod_4, mod_4[, 1], n.sv = n_sv_agg[4], vfilter = 10000)

## Number of significant surrogate variables is: 2
## Iteration (out of 5):1 2 3 4 5

annotate = c(rep("study1", ncol(geneCounts_SRP118614)),
  rep("study2", ncol(geneCounts_SRP212704)),
  rep("study3", ncol(geneCounts_SRP002628)),
  rep("study4", ncol(geneCounts_SRP027258)))
qplot(svobj$sv[,1], svobj$sv[,2], color = annotate, xlab = "SV1", ylab = "SV2")

```



Results

The number of SVs for each study: 4, 1, 6, 2.

The number of SVs for each aggregation (study 1+2, 1+2+3, 1+2+3+4): NA, 1, 2, 2.

Follow-up

We then consider the following: Is there a difference between study 1 and study 2 just using control samples with SVs? When we run DE, we would expect the adj. p-values look uniform.

```
#We then consider the following:
#Is there a difference between study 1 and study 2 just using control samples with SVs?
#Run DE: Do adj. p-values look uniform?
mod_2controls = c(rep(0, ncol(geneCounts_SRP118614)),
                  rep(1, ncol(geneCounts_SRP212704)))
controls = which(mod_2[, 2] == 0)
geneCounts_2controls = geneCounts_2[, controls]
mod_2controls = mod_2controls[controls]
mod_2controls = model.matrix(~ mod_2controls)

n.sv = num.sv(geneCounts_2controls, mod_2controls, method = "be", vfilter = 10000)
svobj = sva(geneCounts_2controls, mod_2controls, mod_2controls[, 1], n.sv = n.sv, vfilter = 10000)

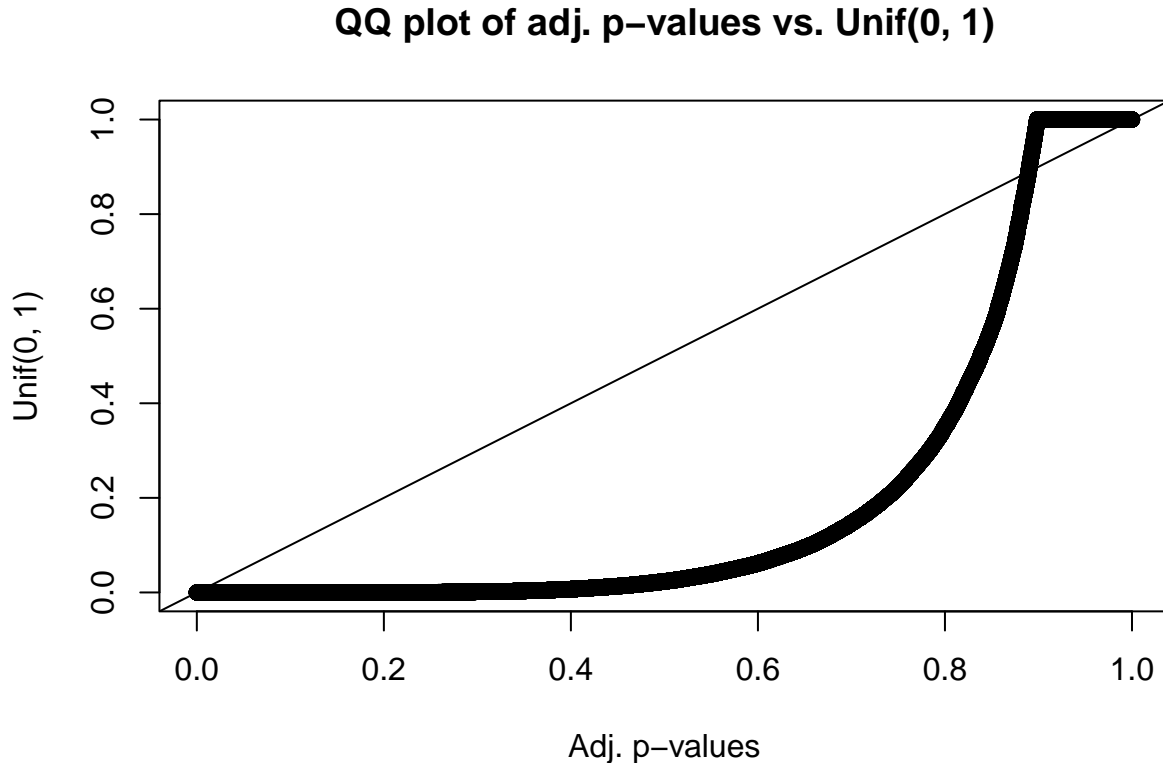
## Number of significant surrogate variables is: 2
## Iteration (out of 5 ):1 2 3 4 5
```

```

mod_2controls_sv = cbind(mod_2controls, svobj$sv)
#run limma for DE
fit = lmFit(geneCounts_2controls, mod_2controls_sv)
eb = eBayes(fit)
result = topTable(eb, adjust = "BH", number = nrow(geneCounts_2controls))

plot(1:nrow(result)/(nrow(result)+1), sort(result$adj.P.Val), xlab="Adj. p-values", ylab="Unif(0, 1)")
abline(a = 0, b = 1)
title(main="QQ plot of adj. p-values vs. Unif(0, 1)")

```



That looks weird. A even more simple case is to take control samples from study 1, split it into two random groups (sample sizes of 12 and 12), run SVA, and perform DE.

```

geneCounts_SRP118614_controls = geneCounts_SRP118614[, phenotype$phenotype_tumor == F]
case_control = rep(0, ncol(geneCounts_SRP118614_controls))
case_control[sample(1:ncol(geneCounts_SRP118614_controls), size = ncol(geneCounts_SRP118614_controls)/2)] = 1
mod = model.matrix(~ case_control)

n.sv = num.sv(geneCounts_SRP118614_controls, mod, method = "be", vfilter = 10000)
svobj = sva(geneCounts_SRP118614_controls, mod, mod[, 1], n.sv = n.sv, vfilter = 10000)

## Number of significant surrogate variables is: 2
## Iteration (out of 5): 1 2 3 4 5

mod_sv = cbind(mod, svobj$sv)

#run limma for DE

```

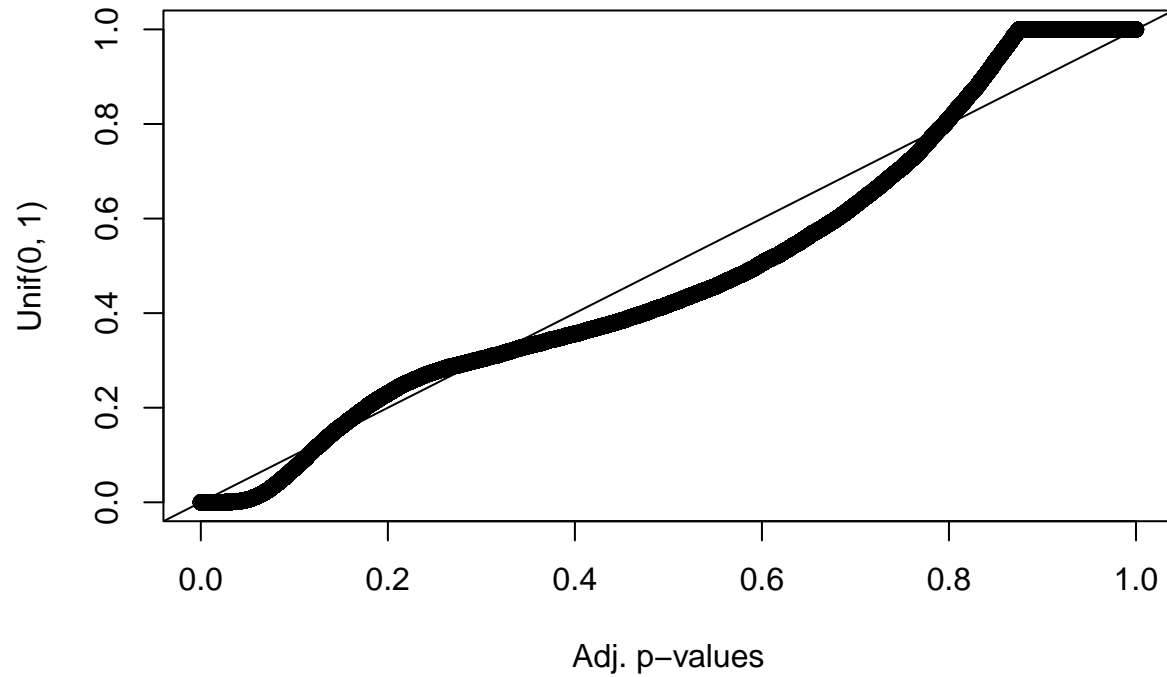
```

fit = lmFit(geneCounts_SRP118614_controls, mod_sv)
eb = eBayes(fit)
result = topTable(eb, adjust = "BH", number = nrow(geneCounts_SRP118614_controls))

plot(1:nrow(result)/(nrow(result)+1), sort(result$adj.P.Val), xlab="Adj. p-values", ylab="Unif(0, 1)")
abline(a = 0, b = 1)
title(main="QQ plot of adj. p-values vs. Unif(0, 1)")

```

QQ plot of adj. p-values vs. Unif(0, 1)



Looks... better?