

Post-selection inference

Koen Van den Berge

Last compiled on 01 December, 2021

Contents

```
runEdgeR <- function(counts, design){
  d <- DGEList(counts)
  d <- calcNormFactors(d)
  d <- estimateDisp(d, design)
  fit <- glmFit(d, design)
  lrt <- glmLRT(fit, coef=2)
  return(lrt)
}

# simulate data according to a negative binomial distribution
set.seed(99)
n <- 1e4 #number of genes
m <- 100 #number of cells
fprCluster <- c()
fprMock <- c()
par(mfrow=c(1,3))
for(ii in 1:5){
  dss <- DESeq2::makeExampleDESeqDataSet(n=n, m=m)
  counts <- assays(dss)$counts

  # t-SNE on top PCs
  tsneDR <- Rtsne(log1p(t(counts)))

  # cluster in t-SNE space
  km <- kmeans(tsneDR$Y, centers=2)
  group <- as.factor(km$cluster)
  plot(tsneDR$Y, col=group, pch=16, cex=1/2, main="t-SNE on top PCs", xlab="t-SNE1", ylab="t-SNE2")

  # DE based on clustering
  design <- model.matrix(~group)
  lrt <- runEdgeR(counts, design)
  hist(lrt$table$PValue, main=paste("iteration",ii,"cluster comparison"), ylim=c(0,600), xlab="p-value")
  fprCluster[ii] <- sum(lrt$table$PValue <= 0.05)

  # mock DE
  mock <- as.factor(rep(1:2,each=m/2))
  designMock <- model.matrix(~mock)
  lrtMock <- runEdgeR(counts, designMock)
  hist(lrtMock$table$PValue, main=paste("iteration",ii,"mock comparison"), ylim=c(0,600), xlab="p-value")
}
```

```

Sys.sleep(1)
fprMock[ii] <- sum(lrtMock$table$PValue <= 0.05)
}

```

t-SNE on top PCs



iteration 1 cluster comparison



iteration 1 mock comparison



t-SNE on top PCs



iteration 2 cluster comparisor



iteration 2 mock comparison



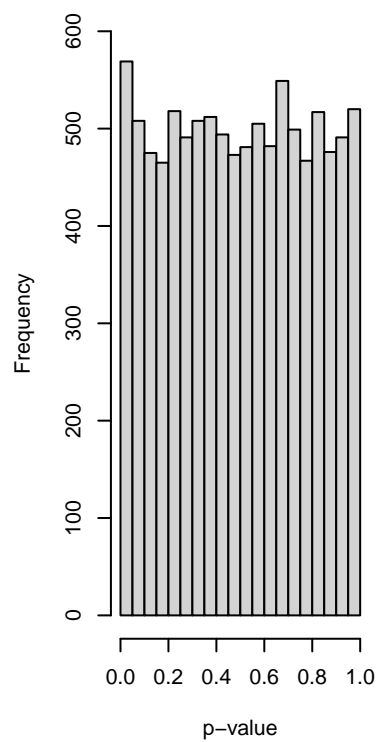
t-SNE on top PCs



iteration 3 cluster comparisor



iteration 3 mock comparison



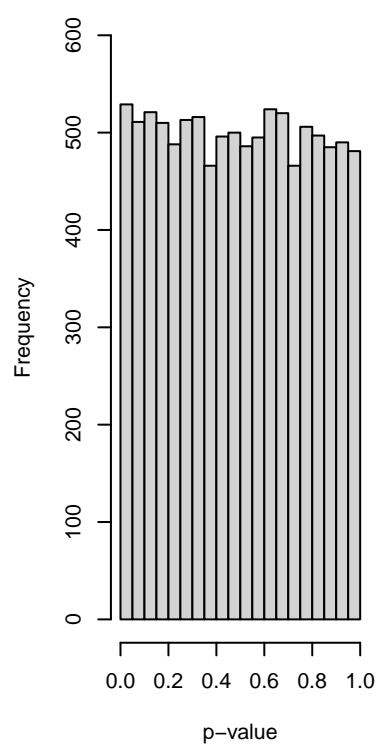
t-SNE on top PCs



iteration 4 cluster comparisor



iteration 4 mock comparison





```
par(mfrow=c(1,1))
boxplot(cbind(fprCluster, fprMock)/n, names=c("cluster-based", "random"), ylab="False positive rate")
```



```
sessionInfo()
```

```
## R version 4.1.2 (2021-11-01)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Catalina 10.15.7
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats4      stats      graphics  grDevices datasets  utils      methods
## [8] base
##
## other attached packages:
## [1] edgeR_3.36.0           limma_3.50.0
## [3] Rtsne_0.15            DESeq2_1.34.0
## [5] SummarizedExperiment_1.24.0 Biobase_2.54.0
## [7] MatrixGenerics_1.6.0    matrixStats_0.61.0
## [9] GenomicRanges_1.46.1    GenomeInfoDb_1.30.0
## [11] IRanges_2.28.0          S4Vectors_0.32.3
## [13] BiocGenerics_0.40.0     rmarkdown_2.10
## [15] knitr_1.33
```

```
##
## loaded via a namespace (and not attached):
## [1] httr_1.4.2          sass_0.4.0          bit64_4.0.5
## [4] jsonlite_1.7.2      splines_4.1.2       bslib_0.3.1
## [7] assertthat_0.2.1    highr_0.9           BiocManager_1.30.16
## [10] blob_1.2.2          renv_0.14.0         GenomeInfoDbData_1.2.7
## [13] yaml_2.2.1          pillar_1.6.2        RSQLite_2.2.8
## [16] lattice_0.20-44     glue_1.4.2          digest_0.6.27
## [19] RColorBrewer_1.1-2  XVector_0.34.0      colorspace_2.0-2
## [22] htmltools_0.5.2     Matrix_1.3-4        pkgconfig_2.0.3
## [25] XML_3.99-0.8        genefilter_1.76.0   zlibbioc_1.40.0
## [28] purrr_0.3.4         xtable_1.8-4        scales_1.1.1
## [31] BiocParallel_1.28.2 tibble_3.1.4        annotate_1.72.0
## [34] KEGGREST_1.34.0     generics_0.1.1      ggplot2_3.3.5
## [37] ellipsis_0.3.2      cachem_1.0.6        survival_3.2-13
## [40] magrittr_2.0.1      crayon_1.4.1        memoise_2.0.1
## [43] evaluate_0.14       fansi_0.5.0         tools_4.1.2
## [46] lifecycle_1.0.0     stringr_1.4.0       locfit_1.5-9.4
## [49] munsell_0.5.0       DelayedArray_0.20.0 AnnotationDbi_1.56.2
## [52] Biostrings_2.62.0   compiler_4.1.2      jquerylib_0.1.4
## [55] rlang_0.4.11        grid_4.1.2          RCurl_1.98-1.5
## [58] bitops_1.0-7        gtable_0.3.0        DBI_1.1.1
## [61] R6_2.5.1            dplyr_1.0.7         utf8_1.2.2
## [64] fastmap_1.1.0       bit_4.0.4           stringi_1.7.4
## [67] parallel_4.1.2      Rcpp_1.0.7          vctrs_0.3.8
## [70] geneplotter_1.72.0  png_0.1-7           tidyselect_1.1.1
## [73] xfun_0.25
```