Ribo-Seq project report template: Some Descriptive Title

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Contents

1 Introduction

Note: this workflow is currently under construction!

1.1 Background and objectives

This workflow contains most of the relevant data analysis steps used by the study from Juntawong et al. (2014). It includes functionalities for both Ribo-Seq and ribosome footprinting (RF-Seq) experiments. To improve re-usability and adapt to the mose recent versions of software (*e.g.* R, Bioconductor and short read aligners), the code has been optimized accordingly. Thus, the results obtained here are expected to be similar but not necessarily identical with the published ones described in the original paper.

1.2 Experimental design

Typically, users want to specify here all information relevant for the analysis of their NGS study. This includes detailed descriptions of FASTQ files, experimental design, reference genome, gene annotations, etc.

2 Load workflow environment

2.1 Load packages and sample data

The *systemPipeR* package needs to be loaded to perform the analysis steps shown in this report (Girke, 2014).

```
library(systemPipeR)
```

Load workflow environment with sample data into your current working directory. The sample data are described here.

```
library(systemPipeRdata)
genWorkenvir(workflow="chipseq")
setwd("chipseq")
```

In the workflow environments generated by `genWorkenvir` all data inputs are stored in a `data/` directory and all analysis results will be written to a separate `results/` directory, while the `systemPipeRIBOseq.Rnw` script and the `targets` file are expected to be located in the parent directory. The R session is expected to run from this parent directory. Additional parameter files are stored under `param/`.

To work with real data, users want to organize their own data similarly and substitute all test data for their own data. To rerun an established workflow on new data, the initial `targets` file along with the corresponding FASTQ files are usually the only inputs the user needs to provide.

If applicable users can load custom functions not provided by *systemPipeR*. Skip this step if this is not the case.

```
source("systemPipeRIBOseq_Fct.R")
```

2.2 Experiment definition provided by `targets` file

The `targets` file defines all FASTQ files and sample comparisons of the analysis workflow.

```
targetspath <- system.file("extdata", "targets.txt", package="systemPipeR")
targets <- read.delim(targetspath, comment.char = "#")[,1:4]
targets
```

```
                   FileName SampleName Factor SampleLong
1   ./data/SRR446027_1.fastq        M1A     M1  Mock.1h.A
2   ./data/SRR446028_1.fastq        M1B     M1  Mock.1h.B
3   ./data/SRR446029_1.fastq        A1A     A1   Avr.1h.A
4   ./data/SRR446030_1.fastq        A1B     A1   Avr.1h.B
5   ./data/SRR446031_1.fastq        V1A     V1   Vir.1h.A
6   ./data/SRR446032_1.fastq        V1B     V1   Vir.1h.B
7   ./data/SRR446033_1.fastq        M6A     M6  Mock.6h.A
8   ./data/SRR446034_1.fastq        M6B     M6  Mock.6h.B
9   ./data/SRR446035_1.fastq        A6A     A6   Avr.6h.A
10 ./data/SRR446036_1.fastq        A6B     A6   Avr.6h.B
11 ./data/SRR446037_1.fastq        V6A     V6   Vir.6h.A
12 ./data/SRR446038_1.fastq        V6B     V6   Vir.6h.B
13 ./data/SRR446039_1.fastq       M12A    M12 Mock.12h.A
14 ./data/SRR446040_1.fastq       M12B    M12 Mock.12h.B
15 ./data/SRR446041_1.fastq       A12A    A12  Avr.12h.A
16 ./data/SRR446042_1.fastq       A12B    A12  Avr.12h.B
17 ./data/SRR446043_1.fastq       V12A    V12  Vir.12h.A
18 ./data/SRR446044_1.fastq       V12B    V12  Vir.12h.B
```

3 Read preprocessing

3.1 Demultiplexing

...

3.2 Quality filtering and adaptor trimming

The following example shows how one can design a custom read preprocessing function using utilities provided by the *ShortRead* package, and then apply it with `preprocessReads` in batch mode to all FASTQ samples referenced in the corresponding `SYSargs` instance (`args` object below). More detailed information on read preprocessing is provided in *systemPipeR*'s main vignette.

```
args <- systemArgs(sysma="param/trim.param", mytargets="targets_chip.txt")
filterFct <- function(fq, cutoff=20, Nexceptions=0) {
    qcount <- rowSums(as(quality(fq), "matrix") <= cutoff)
    fq[qcount <= Nexceptions] # Retains reads where Phred scores are >= cutoff with N exceptions
}
preprocessReads(args=args, Fct="filterFct(fq, cutoff=20, Nexceptions=0)", batchsize=100000)
writeTargetsout(x=args, file="targets_chip_trim.txt", overwrite=TRUE)
```

3.3 FASTQ quality report

The following `seeFastq` and `seeFastqPlot` functions generate and plot a series of useful quality statistics for a set of FASTQ files including per cycle quality box plots, base proportions, base-level quality trends, relative k-mer diversity, length and occurrence distribution of reads, number of reads above quality cutoffs and mean quality distribution. The results are written to a PDF file named `fastqReport.pdf`.

```
args <- systemArgs(sysma="tophat.param", mytargets="targets.txt")
fqlist <- seeFastq(fastq=infile1(args), batchsize=100000, klength=8)
```

```
pdf("./results/fastqReport.pdf", height=18, width=4*length(fqlist))
seeFastqPlot(fqlist)
dev.off()
```

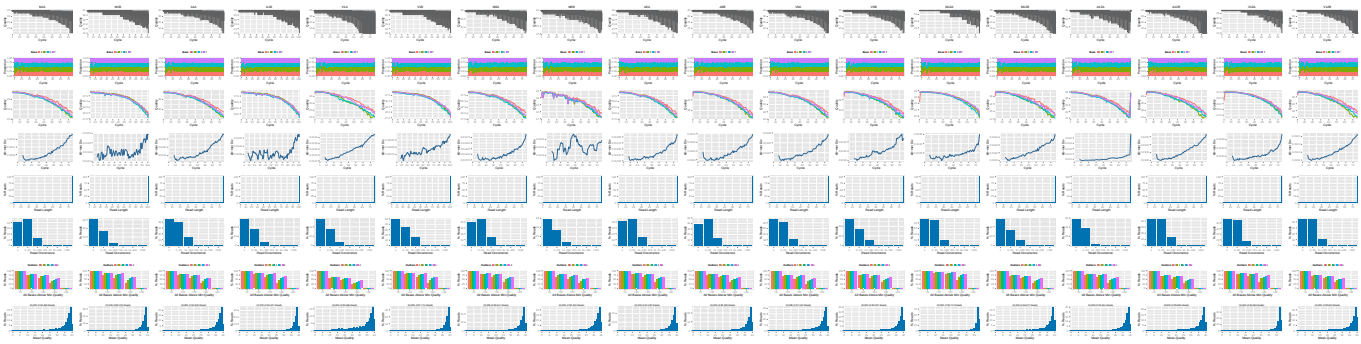

Figure 1: QC report for 18 FASTQ files.

4 Alignments

4.1 Read mapping with Bowtie2/Tophat2

The NGS reads of this project will be aligned against the reference genome sequence using Bowtie2/TopHat2 (Kim et al., 2013; Langmead and Salzberg, 2012). The parameter settings of the aligner are defined in the tophat.param file.

```
args <- systemArgs(sysma="tophat.param", mytargets="targets.txt")
sysargs(args)[1] # Command-line parameters for first FASTQ file
```

Submission of alignment jobs to compute cluster, here using 72 CPU cores (18 qsub processes each with 4 CPU cores).

```
moduleload(modules(args))
system("bowtie2-build ./data/tair10.fasta ./data/tair10.fasta")
resources <- list(walltime="20:00:00", nodes=paste0("1:ppn=", cores(args)), memory="10gb")
reg <- clusterRun(args, conffile=".BatchJobs.R", template="torque.tmpl", Njobs=18, runid="01",
                  resourceList=resources)
waitForJobs(reg)
```

Check whether all BAM files have been created

```
file.exists(outpaths(args))
```

4.2 Read and alignment stats

The following provides an overview of the number of reads in each sample and how many of them aligned to the reference.

```
read_statsDF <- alignStats(args=args)
write.table(read_statsDF, "results/alignStats.xls", row.names=FALSE, quote=FALSE, sep="\t")
```

```
read.table(system.file("extdata", "alignStats.xls", package="systemPipeR"), header=TRUE)[1:4,]
```

```
  FileName Nreads2x Nalign Perc_Aligned Nalign_Primary Perc_Aligned_Primary
1      M1A   192918 177961     92.24697         177961             92.24697
2      M1B   197484 159378     80.70426         159378             80.70426
3      A1A   189870 176055     92.72397         176055             92.72397
4      A1B   188854 147768     78.24457         147768             78.24457
```

4.3 Create symbolic links for viewing BAM files in IGV

The `symLink2bam` function creates symbolic links to view the BAM alignment files in a genome browser such as IGV. The corresponding URLs are written to a file with a path specified under `urlfile`, here IGVurl.txt.

```
symLink2bam(sysargs=args, htmldir=c("~/.html/", "somedir/"),
            urlbase="http://biocluster.ucr.edu/~tgirke/",
            urlfile="./results/IGVurl.txt")
```

5 Read distribution across genomic features

The following provides utilities useful for evaluating read distributions across genomic feature types.

The first step is the generation of the feature type ranges based on annotations provided by a GFF file that can be transformed into a `TxDb` object. This includes ranges for mRNAs, exons, introns, UTRs, CDSs, miRNAs, rRNAs, tRNAs, promoter and intergenic regions. In addition, any number of custom annotations can be included in this routine.

```
library(GenomicFeatures)
file <- system.file("extdata/annotation", "tair10.gff", package="systemPipeRdata")
txdb <- makeTxDbFromGFF(file=file, format="gff3", organism="Arabidopsis")
feat <- genFeatures(txdb, featuretype="all", reduce_ranges=TRUE, upstream=1000, downstream=0, verbose=TRUE
```

Generate and plot feature counts for any read length

```
fc <- featuretypeCounts(bfl=BamFileList(outpaths(args), yieldSize=50000), grl=feat, singleEnd=TRUE, readle
p <- plotfeaturetypeCounts(x=featureCounts2, graphicsfile="featureCounts.pdf", graphicsformat="pdf", scale
```

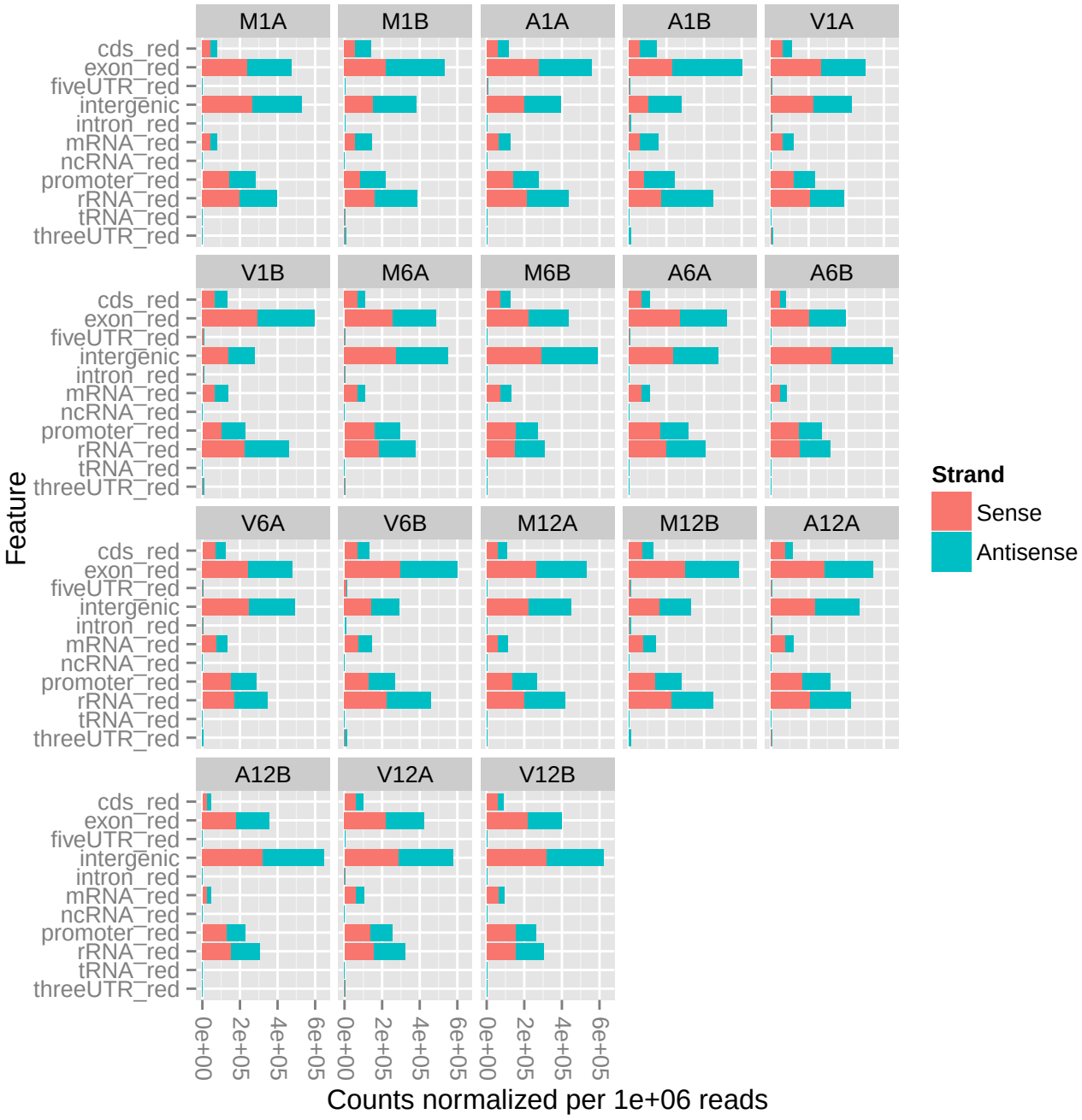

Figure 2: Read distribution plot across annotation features for any read length.

Generate and plot feature counts for specific read lengths

```
fc2 <- featuretypeCounts(bfl=BamFileList(outpaths(args), yieldSize=50000), grl=feat, singleEnd=TRUE, readl
p2 <- plotfeaturetypeCounts(x=fc2, graphicsfile="featureCounts2.pdf", graphicsformat="pdf", scales="fixed"
```

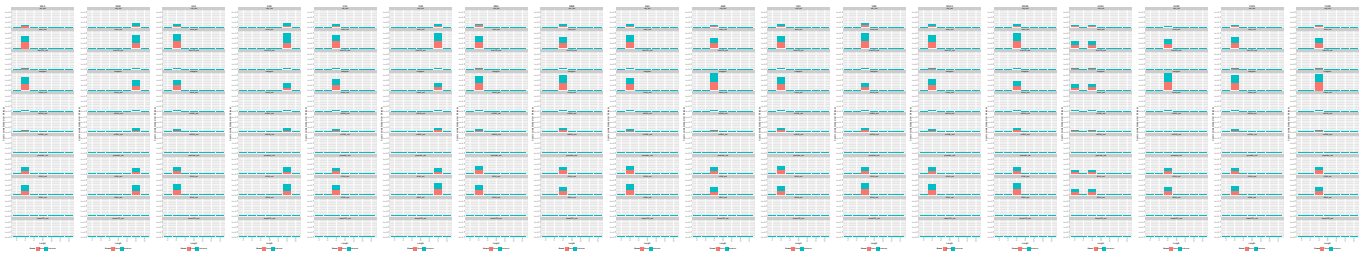

Figure 3: Read distribution plot across annotation features for specific read lengths.

6 Read quantification per annotation range

6.1 Read counting with `summarizeOverlaps` in parallel mode using multiple cores

Reads overlapping with annotation ranges of interest are counted for each sample using the `summarizeOverlaps` function (Lawrence et al., 2013). The read counting is preformed for exonic gene regions in a non-strand-specific manner while ignoring overlaps among different genes. Subsequently, the expression count values are normalized by *reads per kp per million mapped reads* (RPKM). The raw read count table (countDFeByg.xls) and the correspoding RPKM table (rpkmDFeByg.xls) are written to separate files in the `results` directory of this project. Parallelization is achieved with the *BiocParallel* package, here using 8 CPU cores.

```
library("GenomicFeatures"); library(BiocParallel)
txdb <- loadDb("./data/tair10.sqlite")
eByg <- exonsBy(txdb, by=c("gene"))
bfl <- BamFileList(outpaths(args), yieldSize=50000, index=character())
multicoreParam <- MulticoreParam(workers=8); register(multicoreParam); registered()
counteByg <- bplapply(bfl, function(x) summarizeOverlaps(eByg, x, mode="Union",
                                                         ignore.strand=TRUE,
                                                         inter.feature=FALSE,
                                                         singleEnd=TRUE))
countDFeByg <- sapply(seq(along=counteByg), function(x) assays(counteByg[[x]])$counts)
rownames(countDFeByg) <- names(rowRanges(counteByg[[1]])); colnames(countDFeByg) <- names(bfl)
rpkmDFeByg <- apply(countDFeByg, 2, function(x) returnRPKM(counts=x, ranges=eByg))
write.table(countDFeByg, "results/countDFeByg.xls", col.names=NA, quote=FALSE, sep="\t")
write.table(rpkmDFeByg, "results/rpkmDFeByg.xls", col.names=NA, quote=FALSE, sep="\t")
```

Sample of data slice of count table

```
read.delim("results/countDFeByg.xls", row.names=1, check.names=FALSE)[1:4,1:5]
```

Sample of data slice of RPKM table

```
read.delim("results/rpkmDFeByg.xls", row.names=1, check.names=FALSE)[1:4,1:4]
```

Note, for most statistical differential expression or abundance analysis methods, such as *edgeR* or *DESeq2*, the raw count values should be used as input. The usage of RPKM values should be restricted to specialty applications required by some users, *e.g.* manually comparing the expression levels among different genes or features.

6.2 Sample-wise correlation analysis

The following computes the sample-wise Spearman correlation coefficients from the `rlog` normalized expression values generated with the *DESeq2* package. After transformation to a distance matrix, hierarchical clustering is performed with the `hclust` function and the result is plotted as a dendrogram (sample_tree.pdf).

```
library(DESeq2, quietly=TRUE); library(ape,  warn.conflicts=FALSE)
countDF <- as.matrix(read.table("./results/countDFeByg.xls"))
colData <- data.frame(row.names=targetsin(args)$SampleName, condition=targetsin(args)$Factor)
dds <- DESeqDataSetFromMatrix(countData = countDF, colData = colData, design = ~ condition)
d <- cor(assay(rlog(dds)), method="spearman")
hc <- hclust(dist(1-d))
pdf("results/sample_tree.pdf")
plot.phylo(as.phylo(hc), type="p", edge.col="blue", edge.width=2, show.node.label=TRUE, no.margin=TRUE)
dev.off()
```

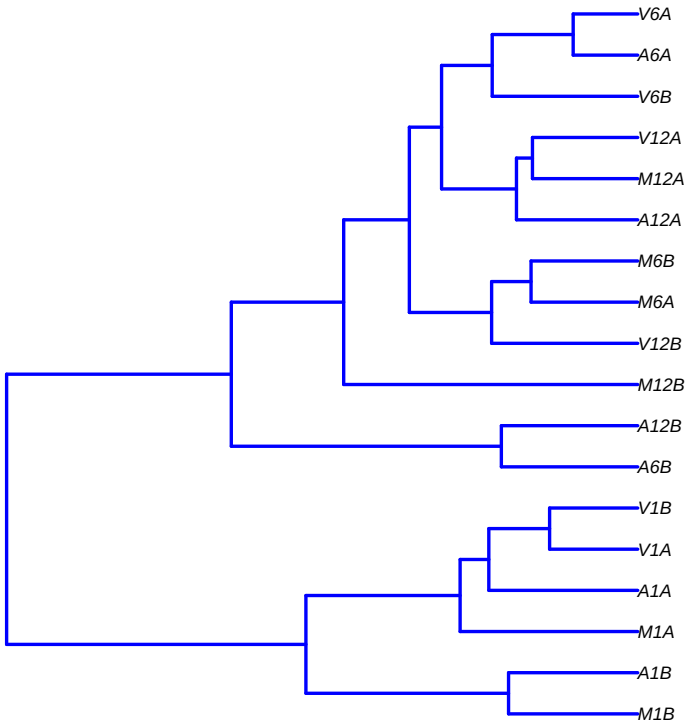

Figure 4: Correlation dendrogram of samples.

7 Analysis of differentially expressed genes with edgeR

The analysis of differentially expressed genes (DEGs) is performed with the glm method from the *edgeR* package (Robinson et al., 2010). The sample comparisons used by this analysis are defined in the header lines of the `targets` file starting with `<CMP>`.

```
library(edgeR)
countDF <- read.delim("countDFeByg.xls", row.names=1, check.names=FALSE)
targets <- read.delim("targets.txt", comment="#")
cmp <- readComp(file="targets.txt", format="matrix", delim="-")
```

```
edgeDF <- run_edgeR(countDF=countDF, targets=targets, cmp=cmp[[1]], independent=FALSE, mdsplot="")
```

Add functional descriptions

```
desc <- read.delim("data/desc.xls")
desc <- desc[!duplicated(desc[,1]),]
descv <- as.character(desc[,2]); names(descv) <- as.character(desc[,1])
edgeDF <- data.frame(edgeDF, Desc=descv[rownames(edgeDF)], check.names=FALSE)
write.table(edgeDF, "./results/edgeRglm_allcomp.xls", quote=FALSE, sep="\t", col.names = NA)
```

Filter and plot DEG results for up and down regulated genes. The definition of '*up*' and '*down*' is given in the corresponding help file. To open it, type `?filterDEGs` in the R console.

```
edgeDF <- read.delim("results/edgeRglm_allcomp.xls", row.names=1, check.names=FALSE)
pdf("results/DEGcounts.pdf")
DEG_list <- filterDEGs(degDF=edgeDF, filter=c(Fold=2, FDR=1))
dev.off()
write.table(DEG_list$Summary, "./results/DEGcounts.xls", quote=FALSE, sep="\t", row.names=FALSE)
```

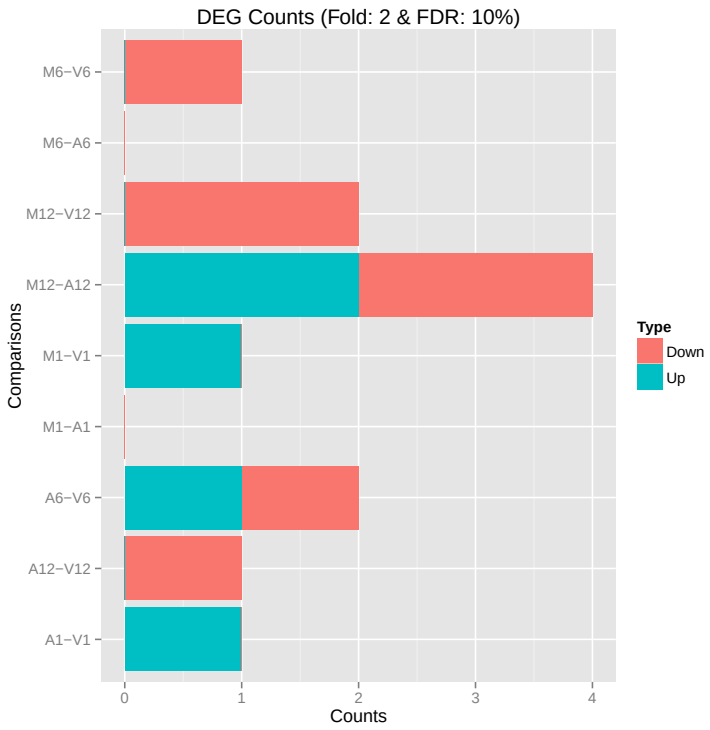

Figure 5: Up and down regulated DEGs with FDR of 1%.

The function `overLapper` can compute Venn intersects for large numbers of sample sets (up to 20 or more) and `vennPlot` can plot 2-5 way Venn diagrams. A useful feature is the possiblity to combine the counts from several Venn comparisons with the same number of sample sets in a single Venn diagram (here for 4 up and down DEG sets).

```
vennsetup <- overLapper(DEG_list$Up[6:9], type="vennsets")
vennsetdown <- overLapper(DEG_list$Down[6:9], type="vennsets")
pdf("results/vennplot.pdf")
vennPlot(list(vennsetup, vennsetdown), mymain="", mysub="", colmode=2, ccol=c("blue", "red"))
dev.off()
```

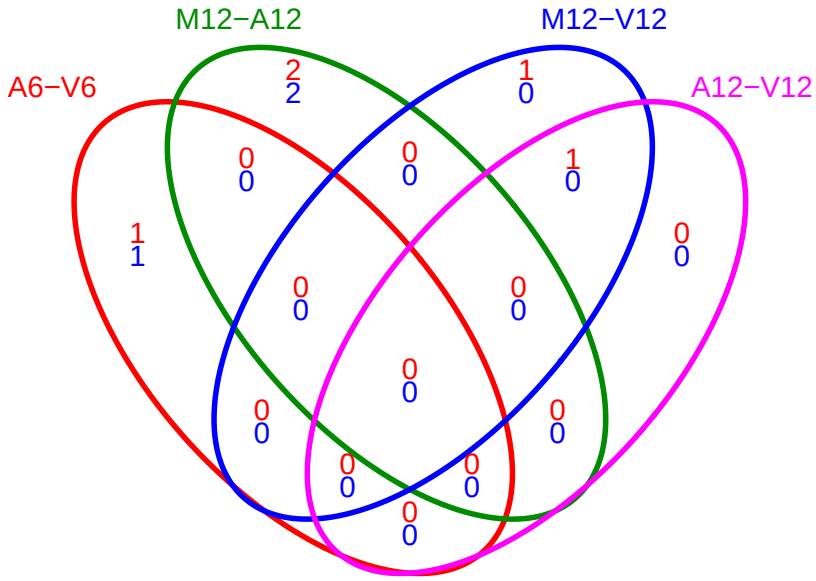

Figure 6: Venn Diagram for 4 Up and Down DEG Sets.

7.1 GO term enrichment analysis of DEGs

7.1.1 Obtain gene-to-GO mappings

The following shows how to obtain gene-to-GO mappings from *biomaRt* (here for *A. thaliana*) and how to organize them for the downstream GO term enrichment analysis. Alternatively, the gene-to-GO mappings can be obtained for many organisms from Bioconductor's `*.db` genome annotation packages or GO annotation files provided by various genome databases. For each annotation this relatively slow preprocessing step needs to be performed only once. Subsequently, the preprocessed data can be loaded with the `load` function as shown in the next subsection.

```
library("biomaRt")
listMarts() # To choose BioMart database
m <- useMart("ENSEMBL_MART_PLANT"); listDatasets(m)
m <- useMart("ENSEMBL_MART_PLANT", dataset="athaliana_eg_gene")
listAttributes(m) # Choose data types you want to download
go <- getBM(attributes=c("go_accession", "tair_locus", "go_namespace_1003"), mart=m)
go <- go[go[,3]!="",]; go[,3] <- as.character(go[,3])
```

```
go[go[,3]=="molecular_function", 3] <- "F"; go[go[,3]=="biological_process", 3] <- "P"; go[go[,3]=="cellul
go[1:4,]
dir.create("./data/GO")
write.table(go, "data/GO/GOannotationsBiomart_mod.txt", quote=FALSE, row.names=FALSE, col.names=FALSE, sep
catdb <- makeCATdb(myfile="data/GO/GOannotationsBiomart_mod.txt", lib=NULL, org="", colno=c(1,2,3), idconv
save(catdb, file="data/GO/catdb.RData")
```

7.1.2 Batch GO term enrichment analysis

Apply the enrichment analysis to the DEG sets obtained the above differential expression analysis. Note, in the following example the FDR filter is set here to an unreasonably high value, simply because of the small size of the toy data set used in this vignette. Batch enrichment analysis of many gene sets is performed with the `GOCluster_Report` function. When `method="all"`, it returns all GO terms passing the p-value cutoff specified under the `cutoff` arguments. When `method="slim"`, it returns only the GO terms specified under the `myslimv` argument. The given example shows how a GO slim vector for a specific organism can be obtained from BioMart.

```
load("data/GO/catdb.RData")
DEG_list <- filterDEGs(degDF=edgeDF, filter=c(Fold=2, FDR=50), plot=FALSE)
up_down <- DEG_list$UporDown; names(up_down) <- paste(names(up_down), "_up_down", sep="")
up <- DEG_list$Up; names(up) <- paste(names(up), "_up", sep="")
down <- DEG_list$Down; names(down) <- paste(names(down), "_down", sep="")
DEGlist <- c(up_down, up, down)
DEGlist <- DEGlist[sapply(DEGlist, length) > 0]
BatchResult <- GOCluster_Report(catdb=catdb, setlist=DEGlist, method="all", id_type="gene", CLSZ=2, cutoff
library("biomaRt"); m <- useMart("ENSEMBL_MART_PLANT", dataset="athaliana_eg_gene")
goslimvec <- as.character(getBM(attributes=c("goslim_goa_accession"), mart=m)[,1])
BatchResultslim <- GOCluster_Report(catdb=catdb, setlist=DEGlist, method="slim", id_type="gene", myslimv=g
```

7.1.3 Plot batch GO term results

The `data.frame` generated by `GOCluster_Report` can be plotted with the `goBarplot` function. Because of the variable size of the sample sets, it may not always be desirable to show the results from different DEG sets in the same bar plot. Plotting single sample sets is achieved by subsetting the input data frame as shown in the first line of the following example.

```
gos <- BatchResultslim[grep("M6-V6_up_down", BatchResultslim$CLID), ]
gos <- BatchResultslim
pdf("GOslimbarplotMF.pdf", height=8, width=10); goBarplot(gos, gocat="MF"); dev.off()
goBarplot(gos, gocat="BP")
goBarplot(gos, gocat="CC")
```

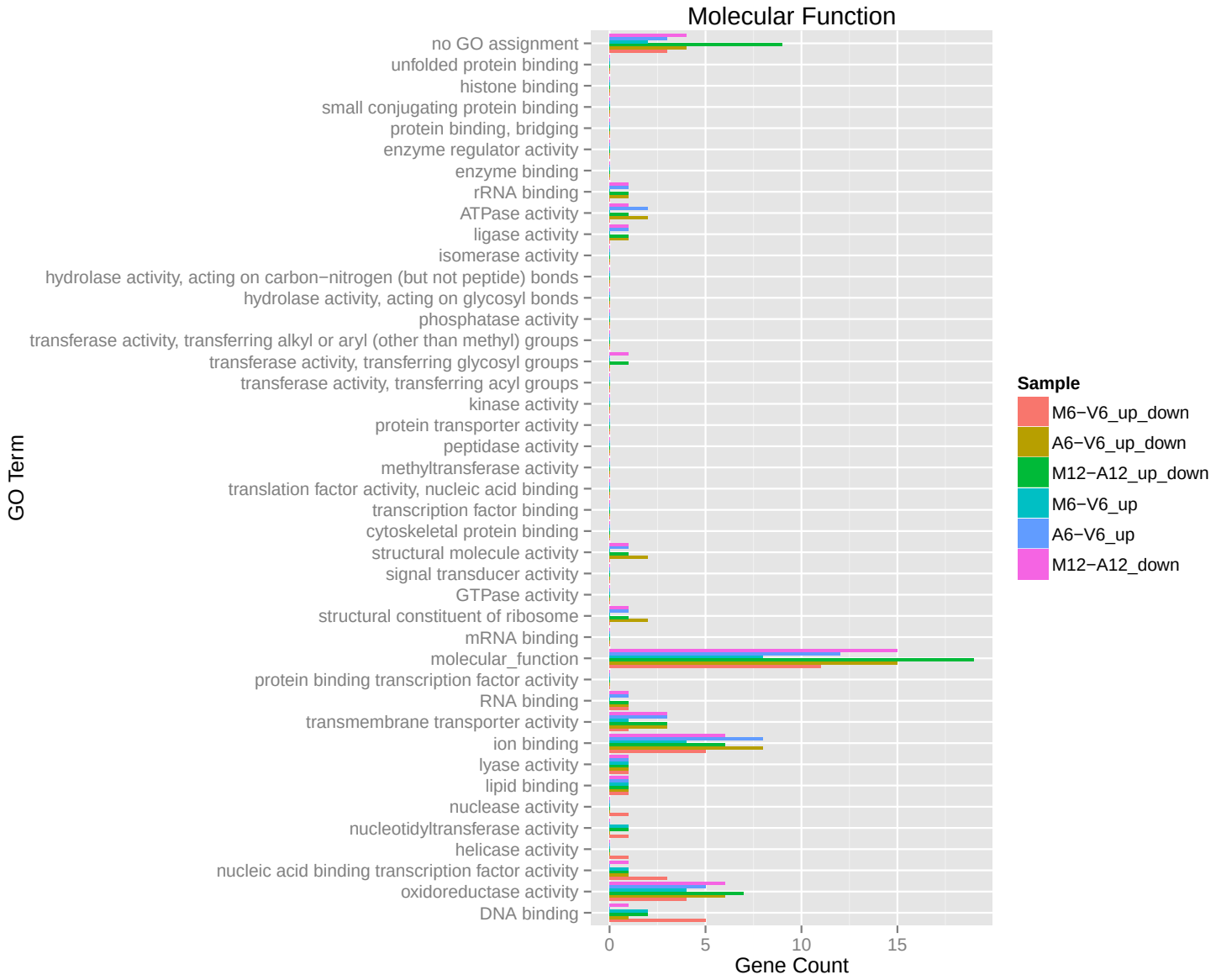

Figure 7: GO Slim Barplot for MF Ontology.

8 Clustering and heat maps

The following example performs hierarchical clustering on the RPKM normalized expression matrix subsetted by the DEGs identified in the above differential expression analysis. It uses a Pearson correlation-based distance measure and complete linkage for cluster joining.

```
library(pheatmap)
geneids <- unique(as.character(unlist(DEG_list[[1]])))
y <- rpkmDFeByg[geneids, ]
pdf("heatmap1.pdf")
pheatmap(y, scale="row", clustering_distance_rows="correlation", clustering_distance_cols="correlation")
```

```
dev.off()
```

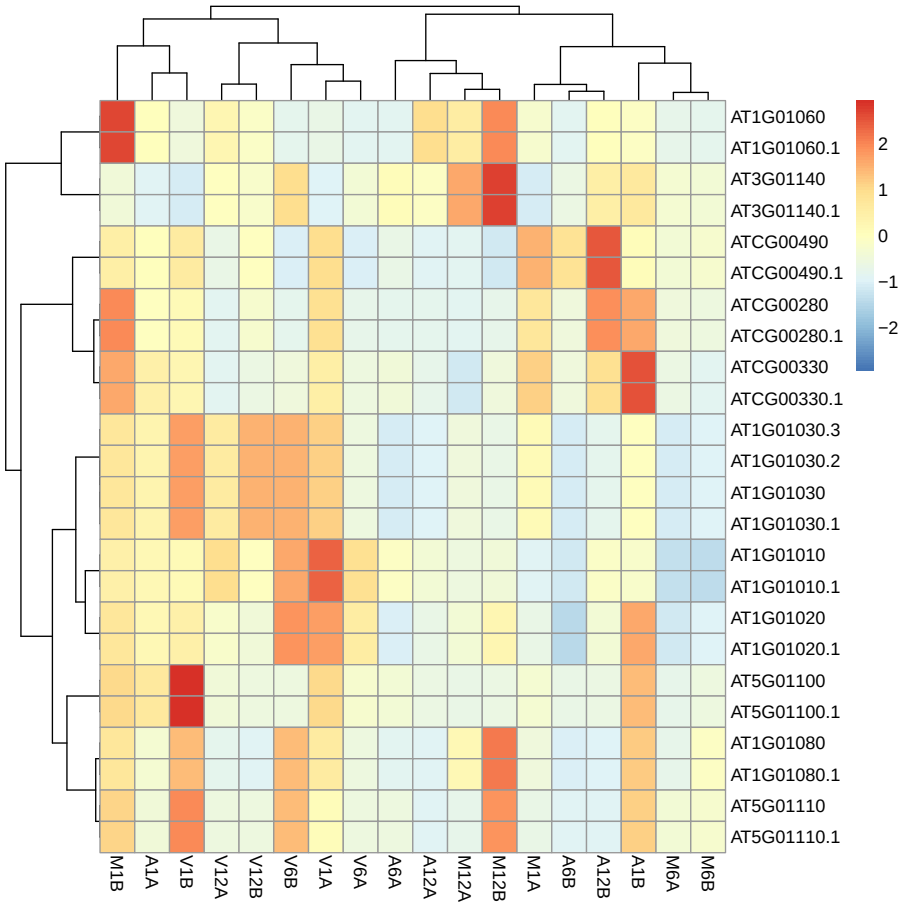

Figure 8: Heat map with hierarchical clustering dendrograms of DEGs.

9 Version Information

```
toLatex(sessionInfo())
```

- R version 3.2.2 (2015-08-14), x86_64-pc-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8, LC_COLLATE=en_US.UTF-8, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=en_US.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.UTF-8, LC_IDENTIFICATION=C
- Base packages: base, datasets, graphics, grDevices, methods, parallel, stats, stats4, utils
- Other packages: Biobase 2.29.1, BiocGenerics 0.15.6, BiocParallel 1.3.51, Biostrings 2.37.8, DBI 0.3.1, GenomeInfoDb 1.5.13, GenomicAlignments 1.5.12, GenomicRanges 1.21.19, IRanges 2.3.18, knitr 1.11, Rsamtools 1.21.15, RSQLite 1.0.0, S4Vectors 0.7.13, ShortRead 1.27.5, SummarizedExperiment 0.3.3, systemPipeR 1.3.31, XVector 0.9.3
- Loaded via a namespace (and not attached): annotate 1.47.4, AnnotationDbi 1.31.17, AnnotationForge 1.11.18, base64enc 0.1-3, BatchJobs 1.6, BBmisc 1.9, BiocStyle 1.7.6, biomaRt 2.25.1, bitops 1.0-6, brew 1.0-6, Category 2.35.1, checkmate 1.6.2, colorspace 1.2-6, digest 0.6.8, edgeR 3.11.2, evaluate 0.7.2, fail 1.2, formatR 1.2, futile.logger 1.4.1, futile.options 1.0.0, genefilter 1.51.0, GenomicFeatures 1.21.18, ggplot2 1.0.1, GO.db 3.2.1, GOstats 2.35.1, graph 1.47.2, grid 3.2.2, GSEABase 1.31.3, gtable 0.1.2, highr 0.5, hwriter 1.3.2, lambda.r 1.1.7, lattice 0.20-33, latticeExtra 0.6-26, limma 3.25.15, magrittr 1.5, MASS 7.3-43, Matrix 1.2-2,

munsell 0.4.2, pheatmap 1.0.7, plyr 1.8.3, proto 0.3-10, RBGL 1.45.1, RColorBrewer 1.1-2, Rcpp 0.12.0, RCurl 1.95-4.7, reshape2 1.4.1, rjson 0.2.15, rtracklayer 1.29.20, scales 0.3.0, sendmailR 1.2-1, splines 3.2.2, stringi 0.5-5, stringr 1.0.0, survival 2.38-3, tools 3.2.2, XML 3.98-1.3, xtable 1.7-4, zlibbioc 1.15.0

10 Funding

This project was supported by funds from the National Institutes of Health (NIH).

11 References

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