Sleuth Analysis of Juvenile HFD Data

Dave Bridges

August 19, 2015

```
library(sleuth)
```

```
## Loading required package: ggplot2
## Loading required package: dplyr
##
## Attaching package: 'dplyr'
##
## The following objects are masked from 'package:stats':
##
##     filter, lag
##
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
base_dir <- "../kallisto/kallisto_output"
sample_id <- dir(file.path(base_dir))
kal_dirs <- paste(base_dir, sample_id, sep="/")
annotation_file <- '../sample-mapping.csv'
sample.table <- read.csv(annotation_file)
#duplicate barcode column as sample
sample.table$sample <- sample.table$Barcode
sample.table$condition <- sample.table$Tissue
#make
sample.table.all <- sample.table %>%
  select(sample, condition)

#created separate annotation tables for quadriceps and ewat
sample.table.quad <- subset(sample.table, Tissue=="Quadriceps")%>%
  select(Barcode, Feeding, Diet, SampleID) %>%
  transmute(sample=Barcode)
sample.table.wat <- subset(sample.table, Tissue=="eWAT")%>%
  select(Barcode, Feeding, Diet, SampleID) %>%
  transmute(sample=Barcode)
```

Effects of Tissue Type

This analysis looks for transcripts that are differentially expressed between the two tissue types.

```
so.tissue <- sleuth_prep(kal_dirs, sample.table.all, ~condition)
```

```
## reading in kallisto results
## .....................................
## normalizing est_counts
```

```
## 18313 targets passed the filter
## normalizing tpm
## normalizing bootstrap samples
```

```
#fit the data
so.tissue <- sleuth_fit(so.tissue)
```

```
## summarizing bootstraps
## fitting measurement error models
## shrinkage estimation
## computing variance of betas
```

```
#calculate statistics
so.tissue <- sleuth_test(so.tissue, which_beta='conditionQuadriceps')
#set up interactive plot
#sleuth_live(so.tissue)
results.tissue <- sleuth_results(so.tissue, 'conditionQuadriceps')
results.tissue.file <- 'tissue_differences.csv'
write.csv(results.tissue, results.tissue.file)
```

Wrote these results out to tissue_differences.csv. By this analysis there were 11791 differentially expressed transcripts, with 5885 upregulated transcripts and 5906 downregulated transcripts.

Session Information

```
## R version 3.2.2 (2015-08-14)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
## Running under: OS X 10.10.4 (Yosemite)
##
## 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] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] sleuth_0.27.1 dplyr_0.4.2   ggplot2_1.0.1
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_0.12.0      knitr_1.11       magrittr_1.5     zlibbioc_1.14.0
##  [5] MASS_7.3-43      munsell_0.4.2    colorspace_1.2-6 R6_2.1.0
##  [9] stringr_1.0.0    plyr_1.8.3       tools_3.2.2      parallel_3.2.2
## [13] grid_3.2.2       rhdf5_2.12.0     data.table_1.9.4 gtable_0.1.2
## [17] DBI_0.3.1        htmltools_0.2.6  lazyeval_0.1.10  yaml_2.1.13
## [21] digest_0.6.8     assertthat_0.1   tidyr_0.2.0      reshape2_1.4.1
## [25] formatR_1.2      evaluate_0.7.2   rmarkdown_0.7    stringi_0.5-5
## [29] scales_0.2.5     chron_2.3-47     proto_0.3-10
```