Assignment 6
Hammer Data: RNA-Seq in a Rat Chronic Pain Modle

BST 226

Statistical Methods for Bioinformatics

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Hammer Data

- They performed mRNA-seq on the L4 dorsal root ganglion (DRG) of Sprague Dawley rats with chronic neuropathic pain induced by spinal nerve ligation (SNL) of the neighboring (L5) spinal nerve as well as on control rats.

- This was done at 2 weeks (acute) and at 2 months (chronic).

- There were 2 rats in each condition, for a total of 8 biological replicates.

Initial Processing

- The file `hammer_eset.Rdata` contains the data as a ExpresssionSet object.

- To make a CountDataSet object to use with DESeq, you need to extract the data and reformulate as a CountDataSet

```
> hammer <- newCountDataSet(exprs(hammer.eset),pData(hammer.eset))
```

Exercises

- Find genes significant for the treatment `protocol = control/L5 SNL`

- Find genes significant for the time `Time = 2 weeks/2 months` (edit the variable to change `2months` to `2 months` using `as.factor(as.character())`)

- You can do the first two in an additive model. Now test for the interaction effect of `protocol` and `Time`.

Sources

- http://bowtie-bio.sourceforge.net/recount/

- Paul Hammer, Michaela S. Banck, Ronny Amberg, Cheng Wang, Gabriele Petznick, Shujun Luo, Irina Khrebtukova, Gary P. Schroth, Peter Beyerlein, and Andreas S. Beutler, "mRNA-seq with agnostic splice site discovery for nervous system transcriptomics tested in chronic pain," *Genome Research*, June 2010; **20(6)**: 847–860.