Questions and To Do’s

ASE Paper

10-26-2015

* What is the concordance of cis and trans in mated and virgin?
  + Trans in mated and virgin, Pearson=0.723
  + Cis in mated and virgin, Pearson=0.838
* What are the genes that differ between mated and virgin in AI?
  + There are some genes involved with reproduction response and determination of adult lifespan that may be of interest in Mated only vs Virgin only
  + Count genes in categories: mated only, virgin only, both
  + Summarize exons across lines and then across fusions
* Is AI common among lines tested in a given fusion?
  + Most fusions have between 0-25% of lines with AI
* How pervasive is cis and trans in a gene?
  + Calculate proportion of cis and trans, assume normality, then compare across genes
* What types of genes have cis? Are these genes constrained or not?
  + Check interaction database for 1st and 2nd degree neighbors of genes with cis
* Genes with 2+ fusion with AI, do estimates of AI agree or are they different?
* What does cis really mean in terms of expression? Is it tied to expression?
  + Sum of both/line/tester counts (log)
  + Simple expression model- log=line; random=plate;
  + Compare: fusion, sig/not\_sig, AI/not\_AI
* Pathway associations: in a pathway, is AI upstream predictive of AI downstream?
  + Use sex det as an example pathway since it’s so transcriptionally responsive
  + Ex: are AI estimates in sxl correlated with fru?
  + Proc corr on AI estimates in sex det
  + There may be a program that looks at distribution of correlation
* Do some lines have more AI than others?
  + Count AI by line
* If no cis and no gene is expressed, what does it mean?
  + Is the regulation more pervasive and you just don’t see it when expression is low?
* Cis vs trans by fusion: filter to a minimum of 5 lines, run regression; find slope and count diff than 0
  + Is this regression slope associated with direction of AI? Cis or trans direction?
* Cis vs trans by line: how different is the line to the tester?
  + Sort the graphs made by genetic distance to the tester (relatedness)
  + How do the patterns sort out?
* Is there a difference in AI across chromosomes?
  + X vs autosomes difference? In some lines, yes
* Test associations of gene lists with AI to Rita’s and John Pool’s gene lists
  + Chi-squared enrichment
* Tajima’s D- calculate on the CEGs 49 lines used
  + Or use Langley data or USC browser?
  + Is Tajima’s D associated with the level of cis in the region?
* SNP counts
  + How are the levels of SNP counts related to level of cis and trans?
  + Are there known TSS’s or TF’s near cis and trans?
  + How are levels of cis and trans related to areas of non-synonymous alleles?