

Worksheet - 2

1. The data underwent hierarchical clustering, employing the Pearson correlation as the distance metric.
2. We designated putative GRB target genes below an HCNE concentration peak as human TFs whose orthologs were in conserved synteny with the array of HCNEs in the human:zebrafish alignment. Density peaks and syntenic regions were downloaded from the Ancora Genome Browser.
3. Analysis of the mouse cDNA sequence revealed that it encodes at least 44,000 distinct transcriptional units. All RNAs in a transcriptional unit share a common external sequence transcribed from the same genomic strand.
4. Calculating multispecies alignment in anticipation of improvements in predictive power.
5. The molecular mechanisms of morphological evolution have begun to be elucidated with the development of molecular embryology and the advent of the post-genomic era.
6. To gauge the level of enhancer activity enrichment in predicted tissues, we contrasted the occurrence rates of enhancers within the three tissues under investigation against a reference set of 528 previously analyzed sequences. These sequences were identified as developmental enhancers based on stringent sequence constraints but lacked prior predictions of tissue specificity.