

## Worksheet - Lesson 2: Cohesion, Coherence, and Emphasis

1. These data were then subjected to hierarchical clustering using the Pearson correlation as the distance metric.

**Answer:** The data underwent hierarchical clustering, employing the Pearson correlation as the distance metric.

2. We designated the putative GRB target genes as the human TFs that were under a HCNE density peak and whose orthologs were in conserved synteny with an array of HCNEs in human:zebrafish alignments. Density peaks and syntenic regions were downloaded from the Ancora Genome Browser.

**Answer:** 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. By analyzing all of the available mouse cDNA sequences, it was found that the mouse genome encodes at least 44 000 distinct transcriptional units; a transcriptional unit comprises all the RNAs that share a common exonic sequence transcribed from the same genomic strand.

**Answer:** 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. Improvements are expected in the predictive power of all the scores being computed on multispecies alignments.

**Answer:** Calculating multispecies alignment in anticipation of improvements in predictive power.

5. With the development of molecular embryology and the coming of the post-genomic era, the molecular mechanisms of morphological evolution have recently begun to be elucidated.

**Answer:** 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 assess the degree of enrichment of enhancer activities in predicted tissues, we compared the relative frequency of enhancers for each of the three tissues examined here with a background set of 528 previously tested sequences predicted to be developmental enhancers on the basis of extreme sequence constraint that were not associated with a prior tissue specificity prediction.

**Answer:** 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.