

Worksheet - Lesson 2: Cohesion, Coherence, and Emphasis

Principles:

1. Put new information last
2. Use passive voice judiciously
3. Make sure the first and last sentences of a paragraph match

Exercises (revise these sentences for clarity using the principles of this lesson):

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

We subjected the data to hierarchical clustering using 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.

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.

We analyzed all available mouse cDNA sequences and found that the mouse genome encodes at least 44,000 distinct transcriptional units. A transcriptional unit comprises all RNAs that share a common exonic sequence transcribed from the same genomic strand.

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

We expect the predictive power of all scores computed on multispecies alignments to improve.

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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.

The development of molecular embryology and the coming of the post-genomic era have recently begun to elucidate the molecular mechanisms of morphological evolution.

Thanks to the development of molecular embryology and the coming of the post-genomic era, we are beginning to understand the molecular mechanisms of morphological evolution.

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.

We conducted an analysis to assess the degree of enrichment of enhancer activities in predicted tissues. We used a background set of 528 previously tested sequences predicted to be developmental enhancers on the basis of extreme sequence constraint. We used this background set to compare the relative frequency of enhancers for each of the three tissues examined here. None of the three tissues were associated with a prior tissue specificity prediction.