Worksheet - Lesson 3: Concision and Simplicity

Principles:

- 1. Omit needless words
- 2. Prefer simple words
- 3. Use simple subjects
- 4. Use adjectives frugally

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

1. Most used CTSSs in the PMA time-course are observed to be, on average, approximately 450 bp away from an H3K9 AC island.

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2. One of the complexes formed by the hematopoietic transcription factor Gata1 is a complex with the Ldb1 and Tal1 proteins

Hematopoietic transcription factor Gata1 forms a complex with the Ldb1 and Tal1 proteins.

3. The mechanistic connections among levels of phenotypic variation, for example, between spatial or temporal patterns of gene expression and morphology, determine how development constrains or channels evolution.

Connections between spatial or temporal patterns of gene expression and morphology are an example of the mechanistic connections between phenotypic variation levels. These connections determine how development constrains or channels evolution.

4. The scrutiny by natural selection is held to be greater for exons than their flanking intron sequences due to the explicit encoding of molecular function by exons.

Natural selection scrutinizes exons more than their flanking intron sequences because exons are explicitly responsible for encoding molecular function.

5. A phylogenetic tree based on the number of differentially expressed genes between species recapitulates their known phylogeny.

A phylogenetic tree represents species phylogeny according to the number of differentially expressed genes.

6. Modifications of the trichome pattern that have been examined in insects (resulting from laboratory-induced mutations or evolutionary diversification) are so far all attributable to changes in expression of svb.

Trichome pattern modifications in insects caused by laboratory-induced mutations or evolutionary diversification may be attributed to changes in svb expression.

7. It is important to note for some of our later discussion that we permit a block to have only one row.

In this case we permit a block to have only one row.

8. These sequences are generally among the least constrained in the genome, so they constitute a plausible neutral standard accounting for regional variation in mutation and recombination rates.

Because these genome sequences are among the least constrained, they are a plausible neutral standard for regional variation in mutation and recombination rates.

9. The reasons for Sn differing among data sets are of considerable interest. Recent studies show that genes encoding proteins involved in developmental and transcriptional regulation tend to have highly constrained CRMs. In contrast, the extensive studies in the HBB gene complex...

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