

Worksheet - Lesson 3: Concision and Simplicity

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

Answer: The most frequently used CTSSs in the PMA time course are typically around 450 bp from an H3K9 AC island.

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

Answer: Gata1 forms a complex with Ldb1 and Tal1 proteins in hematopoietic transcription.

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.

Answer: The relationship between gene expression patterns and morphology shapes evolution through development constraints and channels.

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.

Answer: Natural selection scrutinizes exons more than intron sequences due to their explicit encoding of molecular function.

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

Answer: A phylogenetic tree based on gene expression differences mirrors the known phylogeny of species.

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*.

Answer: Changes in the trichome pattern in insects, whether induced in the laboratory or occurring through evolutionary diversification, are solely linked to variations in the expression of *svb*.

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

Answer: Later discussions hinge on the fact that each block can only contain 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.

Answer: These sequences, typically less constrained in the genome, serve as a credible neutral standard, reflecting regional variation in mutation and recombination rates.

9. The reasons for S_n 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.

Answer: Differences in S_n among datasets are of significant interest. Recent studies indicate that genes related to developmental and transcriptional regulation have tightly constrained CRMs, while the HBB gene complex has been extensively studied.