

## Worksheet - Lesson 1: Subjects and Actions

### Principles:

1. Put actions in verbs
2. Put characters in subjects
3. Keep subjects near verbs

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

1. Tyrosine phosphorylation by activated JAKs of cytokine-receptor cytoplasmic domains then provides binding sites for the Src-homology-2 domain of the STAT proteins.

**The activation of JAKs of cytokine-receptor cytoplasmic domains in tyrosine phosphorylation provides binding sites for the Src-homology-2 domain of the STAT proteins.**

2. We subjected yeast to 20 min of amino acid deprivation and made ribosome-footprint and mRNA-abundance measurements.

**We subjected yeast to 20 min of amino acid deprivation and measured ribosome-footprint and mRNA-abundance.**

3. The assumptions that all sites evolve at one of two evolutionary rates (conserved and nonconserved), that these rates are uniform across the genome, that sites evolve independently conditional on whether they are in conserved or nonconserved regions, and that the phylogenetic models for conserved and nonconserved regions have the same branch-length proportions, base compositions, and substitution patterns, all represent oversimplifications of the complex process of sequence evolution in eukaryotic genomes.

**The complex process of sequence evolution in eukaryotic genomes is oversimplified as a result of several assumptions: that all sites evolve at one of two evolutionary rates (conserved and nonconserved), that these rates are uniform across the genome, that sites evolve independently conditional on whether they are in conserved or nonconserved regions, and that the phylogenetic models for conserved and nonconserved regions have the same branch-length proportions, base compositions, and substitution patterns.**

4. The number of different mechanisms that may exist for cells to interpret morphogens, and the importance of design features such as feedback or local cell-cell communication, is unclear.

**It is unclear how many different cellular morphogen interpretation mechanisms may exist and how important design features such as feedback or local cell-cell communication are.**

**We do not fully understand either the variety of cellular morphogen interpretation mechanisms or the importance of design features such as feedback or local cell-cell communication.**

5. Furthermore, the application of new technologies to further understand the biology of the adipocyte, including location analysis, global DNase hypersensitivity, high-throughput RNA-interference screens and computational strategies, promises to enhance our knowledge of this once-neglected cell.

**Furthermore, new technologies promise to improve our understanding of previously neglected adipocyte biology, including location analysis, global DNase hypersensitivity, high-throughput RNA-interference screens and computational strategies.**

6. Indeed, in the mouse, the sequences of large noncoding RNAs, which probably have no 3' polyA tail, were reconstructed from the fragments of truncated cDNAs.

**In the mouse, truncated cDNA fragments helped (us) reconstruct sequences of large noncoding RNAs which probably have no 3' polyA tail.**

**Indeed, in the mouse, the fragments of truncated cDNAs were reconstructed and resulted in sequences of large noncoding RNAs, which probably have no 3' polyA tail.**

7. Localized fluctuations in substitution rate are widely employed to draw inference concerning the phenotypic significance of genomic sequence.

**Localized fluctuations in substitution rate are widely employed to infer the phenotypic significance of genomic sequence.**

8. A number of promoters exhibited significant positive correlations between the footprinting estimated distribution of K and nucleosome score estimated from T-Cells.

9. In this study, we subjected seven different primate species to comparative analysis of the radial distribution pattern of human chromosome 18- and 19-homologous chromatin by three-dimensional fluorescence in situ hybridization.

**In this study, we used three-dimensional fluorescence in situ hybridization to analyze the radial distribution pattern of human chromosome 18- and 19-homologous chromatin in seven different primate species.**