Worksheet - Lesson 1: Actors and Actions
(Subjects and Actions)

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*.

   Answer: Activated JAKs catalyze the tyrosine phosphorylation of cytokine-receptor cytoplasmic domains, facilitating the creation of 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*.

   Answer: We exposed yeast to 20 minutes of amino acid deprivation and conducted measurements of ribosome footprints 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 overs implications* of the complex process of sequence evolution in eukaryotic genomes.

   Answer : The assumptions regarding the uniformity of evolutionary rates across the genome, the independent evolution of sites based on their conservation status, and the equivalence of phylogenetic models for conserved and nonconserved regions oversimplify the complex process of sequence evolution in eukaryotic genomes.

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*.

   Answer: The clarity regarding both the variety of mechanisms that cells may employ to interpret morphogens and the significance of design features such as feedback or local cell-cell communication remains uncertain.

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.

   Answer: Furthermore, applying new technologies to further understand the biology of the adipocyte, such as location analysis, global DNase hypersensitivity, high-throughput

RNA-interference screens, and computational strategies, holds promise for enhancing our knowledge of this once-neglected cell.

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*.

   Answer: In the mouse, the sequences of large noncoding RNAs, likely lacking a 3' polyA tail, were reconstructed from truncated cDNA fragments.

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

   Answer: Localized fluctuations in substitution rate are commonly utilized to infer the phenotypic significance of genomic sequences.

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

   Answer: Several promoters showed significant positive correlations between the estimated distribution of K from footprinting and the 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*.

   Answer: In this study, we conducted a comparative analysis of the radial distribution pattern of human chromosome 18- and 19-homologous chromatin across seven different primate species using three-dimensional fluorescence in situ hybridization.