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BIFX 504

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The following questions are from “Comparative Genomics”

* 1. Different major questions can be asked when comparing sequences at different evolutionary distances. (See figure 1)
     1. What can you learn by comparing sequences across a billion years of evolutionary distance?

The core set of proteins in multicellular organisms.

* + 1. What can you learn by comparing sequences across moderate distances of 70-100 million years?

Which sequences show a signature of purifying selection.

* + 1. What can you learn by the sequences of closely-related genomes across differences of 5 million years or less?

Which sequences account for unique features of an organism.

* 1. What does the fact that there are more signaling pathways in flies and worms than in yeast signify about these species?

They are more complex organisms than yeast.

* 1. What is purifying or negative selection?

The removal of deleterious mutations from a population.

* 1. What is positive selection?

The retention of beneficial mutations from a population.

* 1. What does it mean for a region to have “conserved synteny”

Genes that are on the same chromosome in one species are also on the same chromosome in the comparison species.

* 1. How much of the human genome is under natural selection?

One estimate indicates that only about 5% of the human genome is under purifying selection and thus is functional.

* 1. Are only protein coding sequences under natural selection? How do you know?

The estimated value for the whole genome is about three times larger than that for protein coding regions, which would indicate that more than just the protein coding regions are considered functional by natural selection.

* 1. What percentage of the nucleotides in the human genome match the mouse genome?

About 40% of the human genome aligns with the with mouse genome at the nucleotide level.

* 1. What makes up the parts of the human genome that don’t match the mouse genome?

Lineage-specific mutations, repetitive elements unique to humans, and other things that have established humans as clearly different from mice.

* 1. While comparative genomics is fundamentally the study of the differences between the genomes of species, it can also give clues about functional genomics (the study of the biological functions that rely on genomic sequences i.e. related sequences that encode the various proteins within a family). How? Give an example.

There are large chunks of DNA that are conserved between species. This allows us to study it in one organism, then infer its function on another with the same molecular mechanisms. For example, through human-mouse genome comparisons, some researchers were able to infer the which part of the neural DNA was under selection in humans by looking to mice.