CUBAP: An Interactive Web Portal for Analyzing Codon Usage Bias Across Populations

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By: Matthew Hodgman, Justin Miller, Taylor Meurs, John Kauwe

What is Codon Usage Bias?
Codon usage bias is the unequal distribution of synonymous codons in a gene. Codon usage biases affect
- Translation rate and efficiency
- Gene expression
- mRNA structure and stability
- Protein secondary structure
- Genetic diseases and disorders

Gene-specific Codon Analysis
View codon usage biases for 17,635 human genes
- Codon frequencies
- Codon aversion – codons that are completely unused in a gene
- Identical codon pairing – when a codon occurs multiple times in a single ribosome footprint
- Co-tRNA codon pairing – when multiple synonymous (but not identical) codons are present in a single ribosome footprint

CUBAP is an interactive web portal that allows users to query population differences in codon usage biases across 17,635 genes. It is freely available at cubap.byu.edu.

Compare Codon Biases in Populations
Compare codon usage biases across alleles from the 1000 Genomes Project
- 2,504 individuals
- 26 subpopulations
- 5 superpopulations

Example analyses on CUBAP:

Visit CUBAP

A screenshot of CUBAP showing average codon frequencies and standard deviations in the gene CR1.