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## **Using mathematical models of ribosome movement and allele fixation to extract information on protein translation from genomic datasets**

Due to the inherent redundancy in the genetic code, there are a multitude of ways of coding for any given protein. Often organisms are biased in which codons they use for a particular amino acid. This codon usage bias (CUB) is most evident in, but not restricted to, highly expressed genes. The nature of this bias is generally thought to be caused by natural selection for greater efficiency in producing functional proteins. However, how different codons lead to different translational efficiencies is hotly debated. In this study we present two models that related codon usage to translational efficiency and demonstrate how these models can be used to predict gene expression levels for individual genes based on their codon bias and/or estimate the relative efficiencies of different synonymous codons. This work differs from most studies of CUB in the analysis is based on mathematical descriptions of cellular and evolutionary processes.