

Abstract Submitted  
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**Studying Codon Usage: From sequence to function**<sup>1</sup> TERRY HWA, STEFAN KLUMPP, Center for Theoretical Biological Physics, UCSD, JIAJIA DONG, Dept. of Physics, Virginia Tech — Protein coding sequences exhibit strong variances in the use of codons. Highly expressed genes such as those encoding ribosomal proteins use codons corresponding to the highly abundant tRNAs (“optimized codons”). High expression of heterologous genes also requires codon optimization, but even the codon usage of very weakly expressed genes tends to be far from random. To understand this biased choice of codon usage, we develop a theory based on the concept of “ribosomal load.” Ribosome is the key limiting commodity for rapidly growing organisms so that the use of “non-optimal” codons in any gene prolongs the translational elongation time, thus reducing the effective ribosome concentration. This presents a fitness cost, the magnitude of which depends on the amount of that protein being translated. We formulated and solved an evolution equation based on the above ingredients. This provides a quantitative relation between codon usage and protein abundance, which is found to be in good agreement with the available data for E.coli. This result suggests a convenient way to quantitatively predict protein abundances based on genome sequence data.

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