Matters Arising: Re-examining the correlations between codon usage and dihedral bond angles using a population genetics model

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Codon usage bias (CUB), or the non-uniform usage of synonymous codons, has been observed across all domains of life (1). CUB is driven by a combination of both non-adaptive (e.g. mutation biases) and adaptive (e.g. natural selection for translation efficiency/accuracy) evolutionary forces (2; 3; 4; 5; 6). Empirical work has shown that changes to synonymous codon usage can affect co-translational protein folding and various computational studies have sought to determine if there is a general connection between codon usage and protein structure (see (7) for a review). In a recent manuscript, (8) explored the relationship between synonymous codon usage and the dihedral bond angles that form a protein's backbone. Using a method they developed to compare dihedral bond angle distributions across synonymous codons, they detected statistically significant differences between the dihedral bond angle distributions of synonymous codons within the *E. coli* proteome. Although they rightly note that correlation does not imply causation, they hypothesize that differences in dihedral bond angle distributions between synonymous codons could be due to differences in elongation speed (see Figure 5 in (8)). Here, we present results using simulated data suggesting the findings of (8) may be a statistical artifact due to failure to control for a significant factor shaping a gene's synonymous CUB: gene expression.

It is well known that gene expression is the strongest correlate with CUB, with highly expressed genes biased towards codons that are translated more efficiently or accurately and lowly expressed genes biased towards codons favored by mutational biases (5; 6). Analyses attempting to correlate codon usage with other genomic, transcriptomic, or proteomic factors must account for the variation in codon usage due to variation in gene expression. Previous work showed that failure to control for gene expression and other biases known to impact codon usage (e.g. amino acid biases) led to spurious differences in the codon usage biases of signal peptides and protein secondary structure (9; 10). (8) did not control for gene expression in their permutation test for comparing dihedral bond angle distributions (i.e. codons were allowed to be permuted across genes), potentially leading to spurious significant differences between the dihedral bond angles of synonymous codons. We examined if the correlations observed by (8) could be a statistical artifact.

To answer this question, we used a population genetics model of coding sequence evolution, called the Ribosome Overhead Costs version of the Stochastic Evolutionary Model of Protein Production Rate (ROC-SEMPPR) (11). ROC-SEMPPR assumes codon usage is at selection-mutation-drift equilibrium and is able to estimate parameters reflecting natural selection on codon usage and mutation biases by accounting for variation in gene expression across protein-coding sequences. Notably, ROC-SEMPPR does not consider position specific effects on codon usage, making it blind to dihedral bond angle distributions and any other aspect of protein structure.

The *E. coli* K12 MG1655 was downloaded from NCBI-RefSeq (GCF_000005845.2). (8) did not restrict their analysis to a single strain of *E. coli*. Non-K12 MG1655 protein-coding sequences used by (8) were downloaded from the European Nucleotide Archive and appended to the *E. coli* K12 MG1655 protein-coding sequence FASTA file. We note that one protein-coding sequence (ENA AAL21040.1) used by (8) was annotated in the ENA as a *S. enterica* gene, but this was included for completeness. Excluding positions with missing codons in the real data, the simulated data contained 99% of the amino acid sites included in the real data. ROC-SEMPPR was fit to these protein-coding sequences using the AnaCoDa R package (12) to estimate parameters reflecting natural selection on codon usage, mutation bias, and an evolutionary average estimate gene expression. We note that ROC-SEMPPR estimates of gene expression were well-correlated with estimates taken from Ribo-seq data (Figure 1A, Spearman $R = 0.48$), suggesting an overall good model fit. Parameters from ROC-SEMPPR were then used to simulate codon usage in *E. coli* protein sequences (i.e. the amino acid sequences were the same between the real and simulated data, but the codon usage could differ). Overall, the real and simulated protein-coding sequences had similar codon counts per gene, as expected (Figure 1B, Spearman $R = 0.83$).

The computational pipeline and the publicly-available data used to recreate their analysis were downloaded from the sources specified in (8). The pipeline was applied using the default settings to the real data

reflecting the true codon usage patterns and the simulated data. Although codon usage within the simulated protein-coding sequences is similar to the real sequences, the positions of these synonymous codons within the sequences are effectively randomized compared to the real sequences (Figure 1C). For example, for the 4-codon amino acid Valine (V), the percentage of times the same codon occurred at the same position within a protein-coding sequence between the two datasets is approximately 25%. For most amino acids, there does tend to be a small upward bias relative to the uniform expectation (Figure 1C, dashed lines). This is likely due to the fact that some protein-coding sequences will be strongly biased towards certain synonymous codons. Given the overall lack of agreement between the real and simulated data on a position-specific basis, analysis of our simulated data should show little agreement with the analysis of the real data if there is truly a general relationship between synonymous codon usage and dihedral bond angle distributions.

Overall, we found striking agreement between the analysis of the real and simulated data. 90.5% of the cases determined to be statistically significant in the real data were also found to be significant in the simulated data, despite the overall randomization of codon usage by position. In agreement with this, the p-values between the two analyses are highly correlated (Figure 1D, Spearman $R = 0.83$). Additionally, the distribution distance (DDist, to use the column name from pipeline output) statistics between the two analyses are also highly correlated (Figure 1E, Spearman $R = 0.98$). In cases where a synonymous codon pair was only significant in one of the datasets, the same synonymous pair tended to have a lower, but not significant, p-value in the other dataset (Figure 1F). Given that the simulated data accurately reflects gene-specific codon usage patterns, but not position-specific codon usage patterns, it is likely the significant results obtained by (8) reflect a statistical artifact due to gene-specific biases. In the context of our results, the correlation between their distance metric and differences in codon-specific elongation speed (Figure 5 in (8)) suggests they are detecting signals related to selection for translation efficiency, as their analysis did not account for gene expression.

Much like (8), we cannot definitively say if synonymous codon usage shapes dihedral bond angles or vice versa. However, our results strongly suggests that the correlations between codon usage and dihedral bond angles are a statistical artifact caused by the correlation between codon usage and gene expression. Importantly, highly expressed genes are also known to be subject to various other biases that might impact dihedral bond angles, including amino acid biases (13). Our findings further emphasize the importance of controlling for gene expression when testing the relationship of biological factors with codon usage.

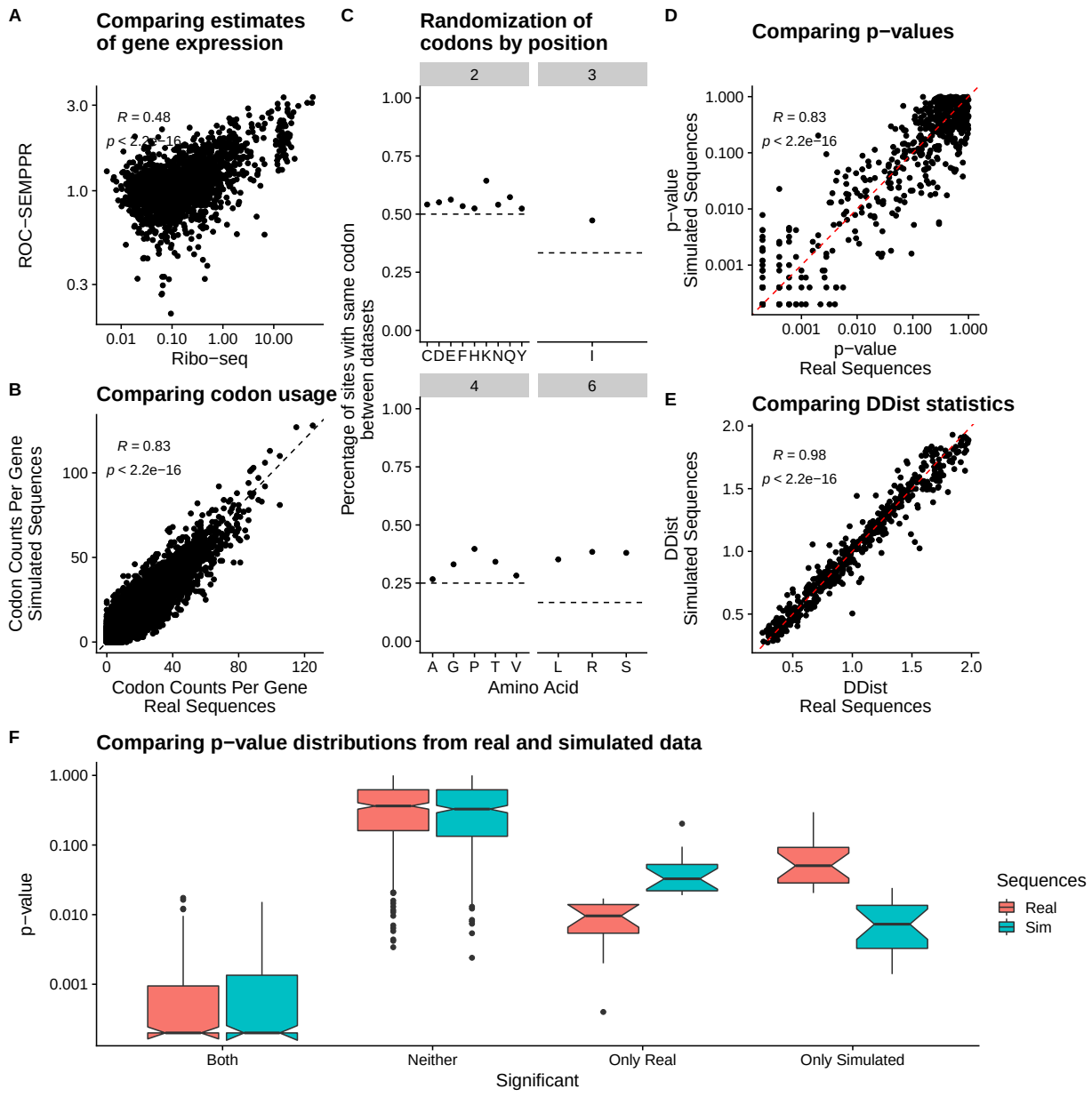

Figure 1: (A) Comparing estimates of ROC-SEMPPR predicted gene expression to Ribo-seq estimates taken from (14). (B) Comparing codon counts across all protein-coding sequences in the real and simulated data. Each dot represents the number of occurrences of codon within a given gene (C) Percentage of amino acid sites that have the same codon at the same position in the same protein-coding sequence between the real and simulated data. The dashed line indicates the expectation under a completely random distribution. (D) Comparison of p-values estimated from the Rosenberg *et al.* pipeline applied to the real and simulated data. (E) Comparison of distribution distance statistics estimated from the Rosenberg *et al.* pipeline applied to the real and simulated data. (F) Comparing p-value distributions for synonymous codon pairs that were significant in both, neither, or only one of the real and simulated data analyses.

Data availability

Relevant data and scripts can be found at https://github.com/acope3/Codon_usage_prot_structure_angles.

Competing interests

The author's declare no competing interest.

Contributions

O.J.A. contributed to the analysis, and the writing and editing of the manuscript. A.L.C. conceptualized the project, contributed to the analysis, and helped write and edit the manuscript.

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