

A Estimating probability of elongation at a codon during one tRNA insertion attempt

The kinetic model of tRNA selection as adapted from Gromadski and Rodnina (2004)

Using Eqn. (5) from Fluitt, et.al. (2007), we estimated the probability of elongation as

$$p = \frac{P_{23}P_{34}P_{67}}{P_{23}P_{34} + P_{21}} \tag{1}$$

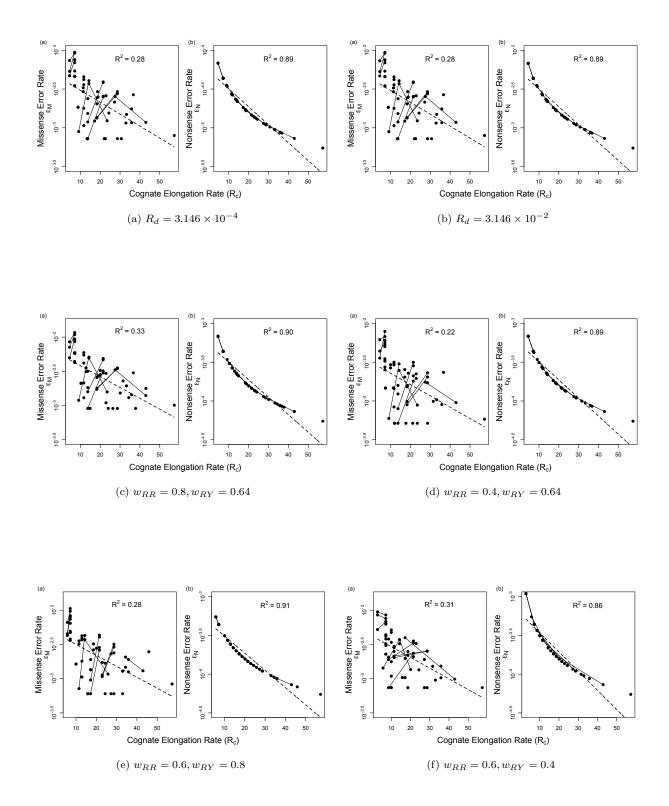
$$P_{23} = \frac{k_2}{k_2 + k_{-1}} \qquad P_{34} = \frac{k_3}{k_3 + k_{-2}} \qquad P_{67} = \frac{k_5}{k_5 + k_7} \qquad P_{21} = \frac{k_{-1}}{k_{-1} + k_2}$$
(2)

Plugging in the values for cognate and near-cognate tRNAs, we find $p_c = 6.52 \times 10^{-1}$ and $p_n = 6.2 \times 10^{-4}$.

B Parameter Sensitivity

Since our model was parametrized using empirical data for *E. coli*, we checked for the sensitivity of our analyses to changes in underlying parameters. Specifically, we changed the wobble parameters (w_{RR} and w_{RY}) and the rate of premature termination (R_d). We checked for the sensitivity to parameters by visually comparing the correlation of error rates (ε_M and ε_N) versus cognate elongation rate (R_c) as well as by comparing the distribution of these correlations across amino acids both intra- and inter-specifically.

Cognate elongation rate versus error rates We find no qualitative difference in the relationship between cognate elongation and error rates when the rate of premature termination (R_d) was both increased and decreased by an order of magnitude. However, we did see a corresponding change in the overall nonsense error rate of codons, as expected.



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