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Brenae L. Bailey* (bbailey@math.arizona.edu), Program in Applied Mathematics, University of Arizona, PO Box 210089, Tucson, AZ 85721-0089. Stochastic Modeling of Ribosomal Frameshifting.

Many viruses can produce different proteins from the same RNA sequence by encoding them in overlapping genes. One mechanism that causes the ribosomes of infected cells to decode both genes is called programmed ribosomal frameshifting (PRF). Although PRF has been recognized for 25 years, the mechanism is not well understood. We have developed a model that treats RNA translation as a stochastic process in which the transition probabilities are based on the free energies of local molecular interactions. The model reproduces observed translation rates and frameshift efficiencies, and can be used to predict the effects of mutations in the viral RNA sequence on the frameshift efficiency. (Received September 15, 2011)