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Probabilistic Methods for Pathogen and Copy Number Evolution

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ABSTRACT

Biology is becoming increasingly quantitative, with large genomic datasets being curated at a rapid rate. Sound mathematical modeling as well as data science approaches are both needed to take advantage of these newly available datasets. I will describe two projects that span these approaches. The first is a Markov chain model of natural selection acting at two scales, motivated by the virulence-transmission tradeoff from pathogen evolution. This stochastic model, under a natural scaling, converges to a nonlinear deterministic system for which we can analytically derive steady-state behavior. The second project is a bioinformatics pipeline that quantifies gene copy number variants, currently a difficult problem in modern genomics. This quantification of copy number variation in turn generates new mathematical questions that require the type of probabilistic modeling used in the first project.