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Rinaldo B Schinazi* (rschinaz@uccs.edu), Department of Mathematics, 1530 Austin Bluffs Parkway, Colorado Springs, CO 80933, and **Thomas M Liggett**. *A stochastic model for phylogenetic trees.*

We propose the following simple stochastic model for phylogenetic trees. New types are born and die according to a birth and death chain. At each birth we associate a fitness to the new type sampled from a fixed distribution. At each death the type with the smallest fitness is killed. We show that if the birth (i.e. mutation) rate is sub-critical we get a phylogenetic tree consistent with an influenza tree (few types at any given time and one dominating type lasting a long time). When the birth rate is super-critical we get a phylogenetic tree consistent with an HIV tree (many types at any given time, none dominating very long). (Received August 08, 2010)