### Model

A simulation of the evolution of a set of retrotransposons can be run using the simulate() function.

The simulation starts with a set of sequences that are either randomly generated, or read from file. Initially, the entire family of retrotransposons are assumed to be the exact same sequence.

Retrotransposons are deemed to be *active* by default, and active retrotransposons are capable of transposition. If the number of active sequences exceeds a certain threshold, some of them are randomly discarded, to simulate extinction events until the total number of copies is within the specified limit.

sequenceParams <- SequenceParams(num\_initial\_copies = 100,   
 seq\_length = 5000)  
  
simulationParams <- SimulationParams(num\_jumps = 20,  
 timestep = 1,  
 max\_active\_copies = 500)

During the simulation, each retrotransposon sequence undergoes point mutations under one of six nucleotide substitution models.

mutationParams <- MutationParams(model = 'K80')

If due to a point mutation, a retrotransposon if affected in a critical region, it might become inactive with a specified probability. If the number of inactive sequences exceeds a threshold, they are discarded in a similar fashion to how active sequences are discarded.

flagParams <- FlagParams(length\_critical\_region = 100,  
 prob\_inactive\_when\_mutated = 0.001,  
 max\_inactive\_copies = 500)

During a transposition (burst event) a retrotransposon increases in copy number. This happens with a specified probability. This package is capable of simulating the burst events under two assumptions - (a) without recombination, where each bursting sequence is copied directly (b) with recombination, where each bursting sequence recombines with another similar sequence before it inserts itself back into the genome.

burstParams <- BurstParams(burst\_probability = 0.1,  
 burst\_mean = 1,  
 recomb\_mean = 1.5  
 recomb\_similarity = 0.85)

During the simulation, sequences that diverge from the initial sequence by a large amount can be discarded to simulate evolutionary pressure. Similarly, speciation events can be simulated by allowing the set of sequences to split into two species, where retrotransposons from different species are not allowed to recombine with each other during transposition.

speciesParams <- SpeciesParams(selection\_threshold = 0.5,  
 species\_similarity = 0.7,  
 species\_coherence = 0.5)

### I/O examples