regspec

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Functions:

- Help functions: simulates mutations based on branch length
- Simulates DNA sequence based on a fixed population size
- Simulates DNA sequence based on a variable (continuous) population size
- Simulates DNA sequence based on a variable (bottleneck) population size
- Various functions that provides different properties of the simulated data. For example: site frequency spectrum (SFS), visualization of ancestral tree, total number of mutations (S_total)

Classes

- Population with fixed size
- Population with variable (continuous) size
- Population with variable (bottleneck) size