

# BDMS example

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The possible “states” that a line can be in. Showing the different genotypic states in this simulation

The beginning state of the tree. Chosen from the list of provided states, inputted above.

A valid stochastic matrix. All of the rows must sum up to a total of one. Each entry must be non-negative.

This shows the mutator, how often and when it mutates.

```
time_to_sampling = 2.0
states = (0, 1, 2)
tree = bdms.Tree(state=0)

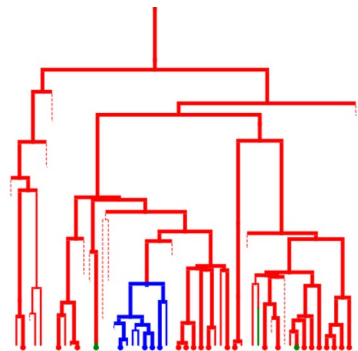
tree.evolve(
    time_to_sampling,
    birth_process=bdms.poisson.DiscreteProcess([2.0, 6.0, 2.0]),
    death_process=bdms.poisson.ConstantProcess(0.8),
    mutation_process=bdms.poisson.ConstantProcess(0.8),
    mutator=bdms.mutators.DiscreteMutator(states, np.array(
        [
            [0.5, 0.25, 0.25],
            [0, 1, 0],
            [0, 0, 1]
        ]
    )),
    seed=np.random.default_rng(seed=0),
)
```

The birth rates for each different state, in order.

The rate at which all processes die off.

The rate at which processes mutate

The seed. For reproducible results.



To the right is our end result! This tree shows the process of evolution within our modeling system.

This allows researchers to produce Tree simulations for Birth-Death-mutation-sampling processes