Summary of Python Modules in Forward-Equivalent Simulation

1 Overview

The Python files define the implementation of the Forward-Equivalent (FE) simulation framework, including:

- Precomputing FE-adjusted birth, death, and mutation rates to avoid simulating unobserved lineages.
- Modeling evolutionary state transitions using Poisson processes.
- Applying mutations based on FE parameters in a phylogenetic tree.
- Providing utility functions for interpolation, numerical computations, and tree statistics.

2 File Summaries

2.1 modulators.py - Core Computation of FE Parameters

This file defines the FEModulator class, which precomputes and stores all forward-equivalent model parameters for efficient simulation.

Key Features:

- Computes survival probabilities $s_a(\tau)$.
- Computes integral survival values $S_a(\tau)$ used for birth, death, and mutation rate adjustments.
- Computes **FE-adjusted mutation rates** $m_a(\tau)$.

Important Methods:

- $_s(t, phenotype)$: Returns survival probability at time t.
- _S(t, phenotype): Computes integral of survival probability.
- _m(t, phenotype): Returns FE-adjusted mutation rate.

Why is this file important?

- FEModulator precomputes all essential FE parameters, making simulations significantly more efficient.
- Without it, the simulation would need to recompute rates dynamically, making it much slower.

2.2 my_bdms.py - Evolutionary Processes and Mutations

This file defines how birth, death, and mutation events occur within the FE simulation framework. It includes:

Key Classes:

- DiscreteProcess: A Poisson process for constant-rate (birth, death, or mutation) transitions.
- CustomProcess: A more flexible Poisson process allowing time- and statedependent transition rates.
- CustomMutator: Handles FE-based mutations and applies them to a phylogenetic tree.

Key Functionalities:

- DiscreteProcess simulates fixed-rate evolutionary events.
- CustomProcess allows time-dependent birth, death, and mutation rate modifications.
- CustomMutator uses FEModulator to apply FE-adjusted mutations to tree nodes.

Why is this file important?

- It allows the FE model to dynamically adjust transition rates instead of assuming static values.
- CustomMutator ensures that mutations follow FE-adjusted probabilities, maintaining statistical equivalence to FullSim.

2.3 utils.py - Helper Functions for Computation and Analysis

This file provides utility functions for:

- Interpolating precomputed values (for fast retrieval of FE parameters).
- Computing tree statistics (e.g., comparing FullSim vs. FE).
- Ensuring numerical stability in simulations.

Key Functions:

- grid_interp(t, array, t_min, dt): Interpolates values from a precomputed time grid.
- compute_tree_stats(tree): Computes tree statistics for validation and comparison.
- clamp(value, min_val, max_val): Ensures values remain within valid ranges.

Why is this file important?

- Supports efficient lookup of FE-adjusted parameters.
- Provides statistical analysis tools to validate FE simulation accuracy.

3 How These Files Work Together

- 1. modulators.py precomputes FE-adjusted rates.
- 2. my_bdms.py uses these rates to simulate birth, death, and mutation processes.
- 3. utils.py provides numerical tools for computation and analysis.

4 Comparison to FullSim

- FullSim computes and prunes all lineages, while FE **skips unobserved lineages**.
- This reduces computational complexity from O(M) (FullSim) to O(N) (FE), where $N \ll M$.
- FE is 2-6× faster than FullSim while preserving statistical accuracy.

5 Potential Questions from the Professor

- 1. What is the most important file? Answer: modulators.py because it computes all FE-adjusted rates, making the simulation efficient.
- 2. How do these files interact? Answer: modulators.py computes rates, my_bdms.py applies them, and utils.py supports numerical operations.
- 3. Why is FE faster than FullSim? Answer: FE avoids computing unobserved lineages, making it $2\text{-}6\times$ faster than FullSim.