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MFBD Glossary

Sub(super)scripts

- i, j: types in multi type, e.g., a genotype
    - u, v: types in multi type model for discrete space of fitness classes
- a, n, m: lineages in phylogenetic tree
- k, l: genomic sites
- $\hat{}$: estimator (MLE) given approximation

Tree process parameters θ

- λ_i: birth rate for type i
- d_i: death rate ...
- s_i: sampling rate at death ...
- ρ_i: sampling rate at $t = 0$ ...

Mutation process parameters μ

- $\gamma_{i,j}$: (symmetric) transition rate from type i to j

Likelihood terms

- $D_n(t)$: density subtree descending for lineage n evolved between $[t, 0]$ as observed
    - $D_{n,i}(t)$: density subtree ... evolved as observed conditional on type i
- $E_i(t)$: density some lineage of type i not sampled and left no sampled descendants

Fitness terms

- f_n: relative fitness of lineage n
    - $f_{n,k,i}$: relative fitness of lineage n at site k w/ type i
    - $\mathcal{F}$: entire set of $\{\hat{f}_{n,k,i}\}$
- $\omega_{n,g}$: genotype g probability for lineage n
    - $\omega_{n,k,i}$: marginal site density of lineages n at site k w/ type i
- $\sigma_{k,i}$: fitness effect (selection cost) of type i at site k
- g_k: allele at site k for multi site genotype g