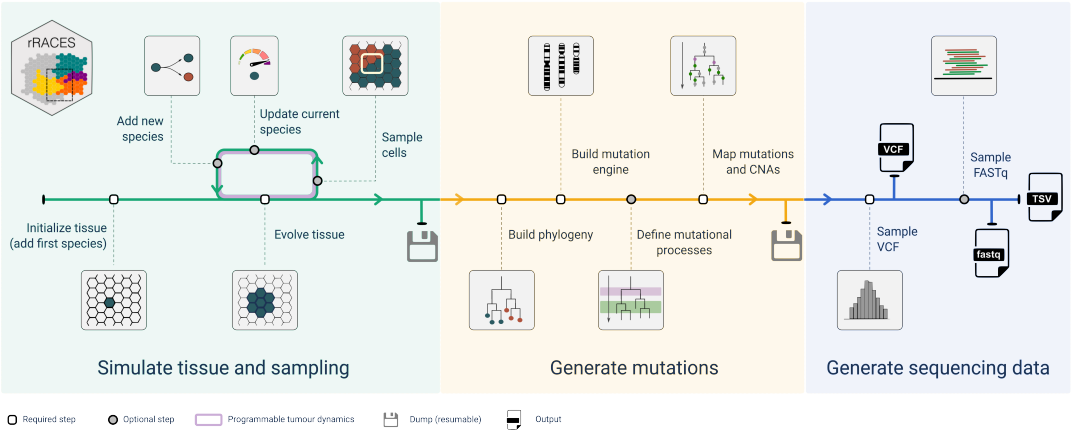
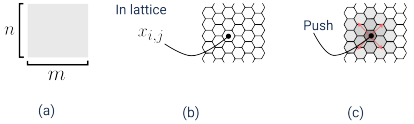


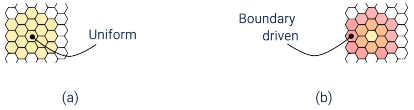
In lattice tissue simulation

A tissue is a squared lattice (a), with cells positioned in a discrete coordinate system (b), and pushing each other during simulation.



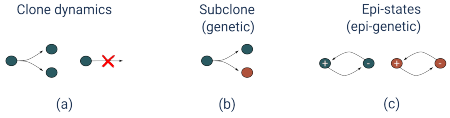
Modes of cell divison on the tissue

Tissue evolution is stochastic and depends on cell parameters. Divisions happen uniformly on the lattice (a) or on boundaries (b).



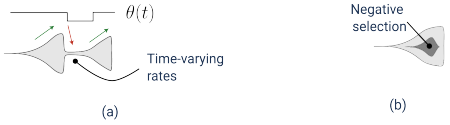
Advanced birth-death process

A stochastic birth-death process (a) with subclones that have custom parameters (b), and reversible epi-genetic events (c).



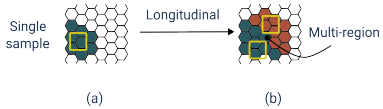
Time-varying evolutionary parameters

The parameters of the birth-death process can vary in time to simulate therapy (a) effect and model negative selection (b).



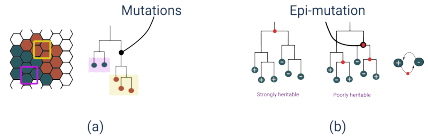
Advanced tissue-sampling strategies

The tissue can be sampled at single (a) or multiple time-points, and in multiple spatially-separated positions (b).



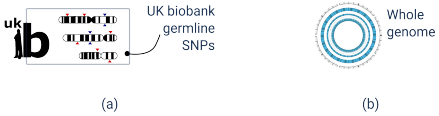
Single-cell phylogenies

Single-cell phylogenies are generaeted from tissue samples (a), capturing epi-mutations with different heritability patterns (b).



Realistic reference genomes

Germline reference from the UK biobank samples (a), with possibility of simulating whole-genome sequencing datasets (b).



Realistic mutational processes

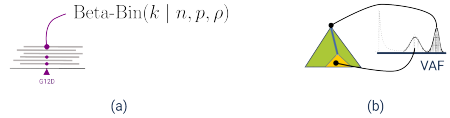
Custom rates of passenger mutations and copy numbers (a), as well as time-varying mutational processes (e.g., therapy) (b).

Custom driver mutations

Custom driver events per clone (a), as well as passenger events mapped on branches of the simulated phylogeny (b).

VCF outputs

Read-counts data in VCF format, with Beta-Binomial sequencing noise (a), bulk purity, to create variant allele frequency data (b).



FASTq outputs

SAM/FASTq outputs with a NovaSeq error model (a), which can be streamlined with standard bioinformatics pipelines (b).