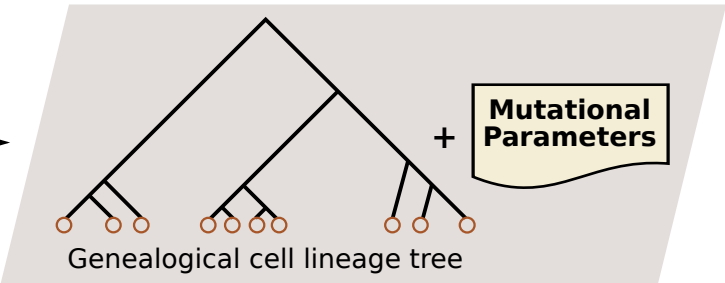
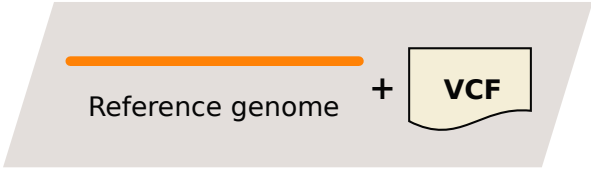


Population genetic modeling of tumor cells

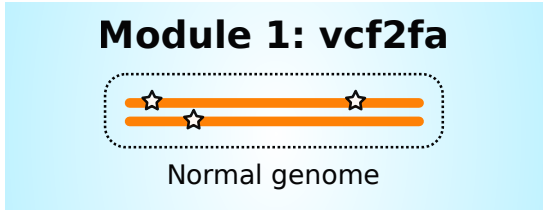


Genealogical cell lineage tree



Reference genome

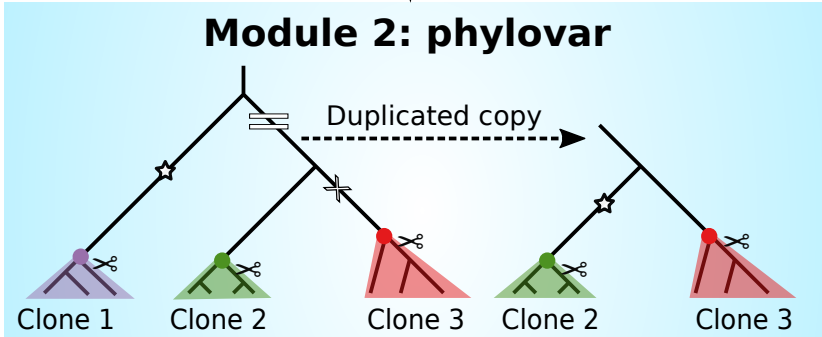
+ VCF



Module 1: vcf2fa

Normal genome

FASTA



Module 2: phylovar

Clone 1

Clone 2

Clone 3

Clone 2

Clone 3

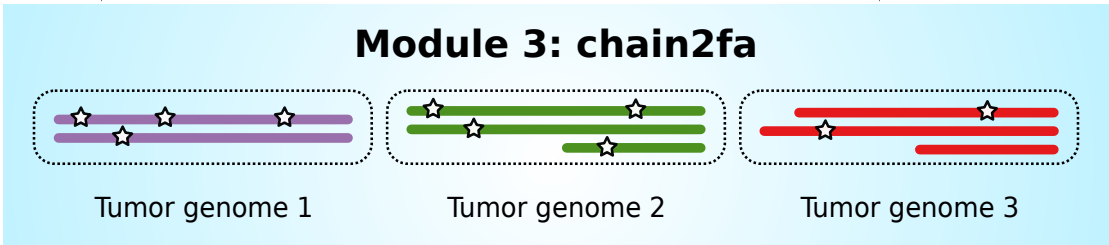
☆ SNV
≡ Amplification
✕ Deletion



CHAIN FILE

CHAIN FILE

CHAIN FILE



Module 3: chain2fa

Tumor genome 1

Tumor genome 2

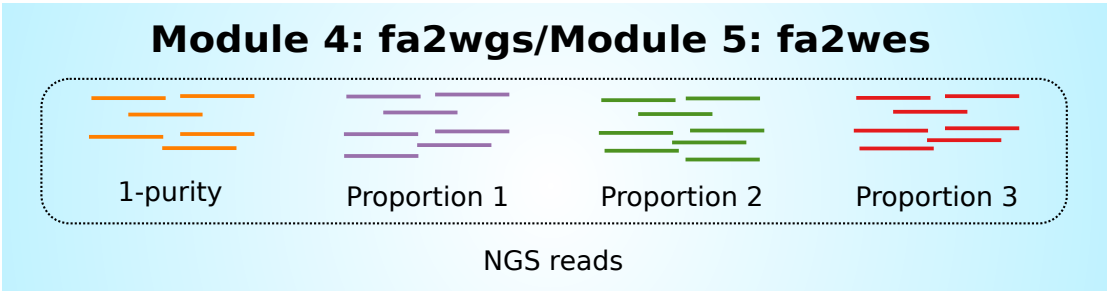
Tumor genome 3



FASTA

FASTA

FASTA



Module 4: fa2wgs/Module 5: fa2wes

1-purity

Proportion 1

Proportion 2

Proportion 3

NGS reads



FASTQ