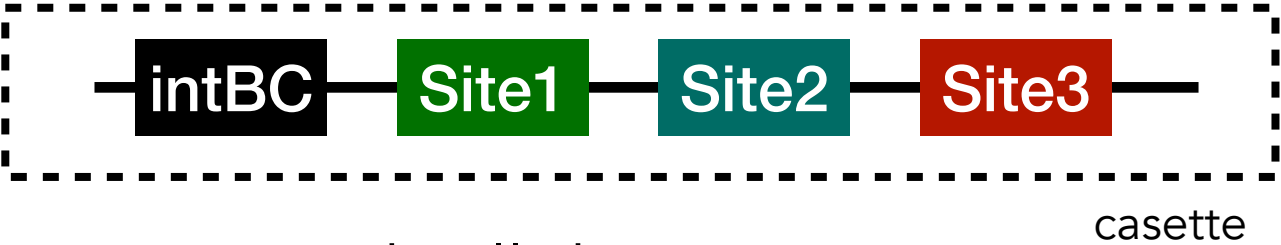
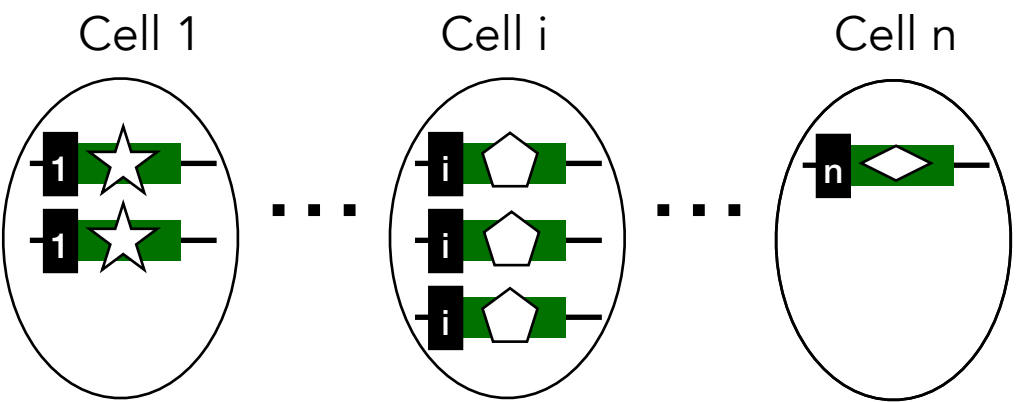


Input

(1) Lineage tracing system

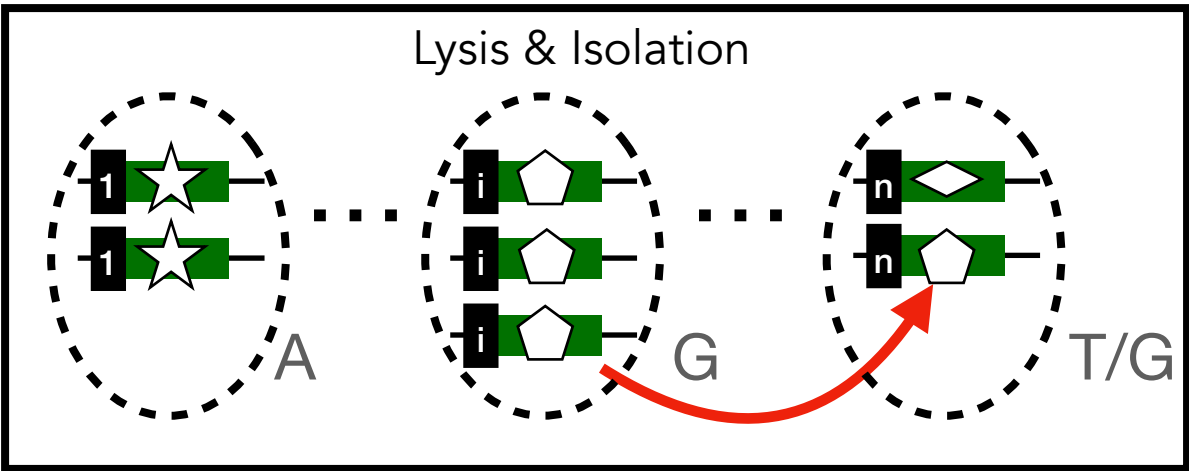


(2) Integration and cell division

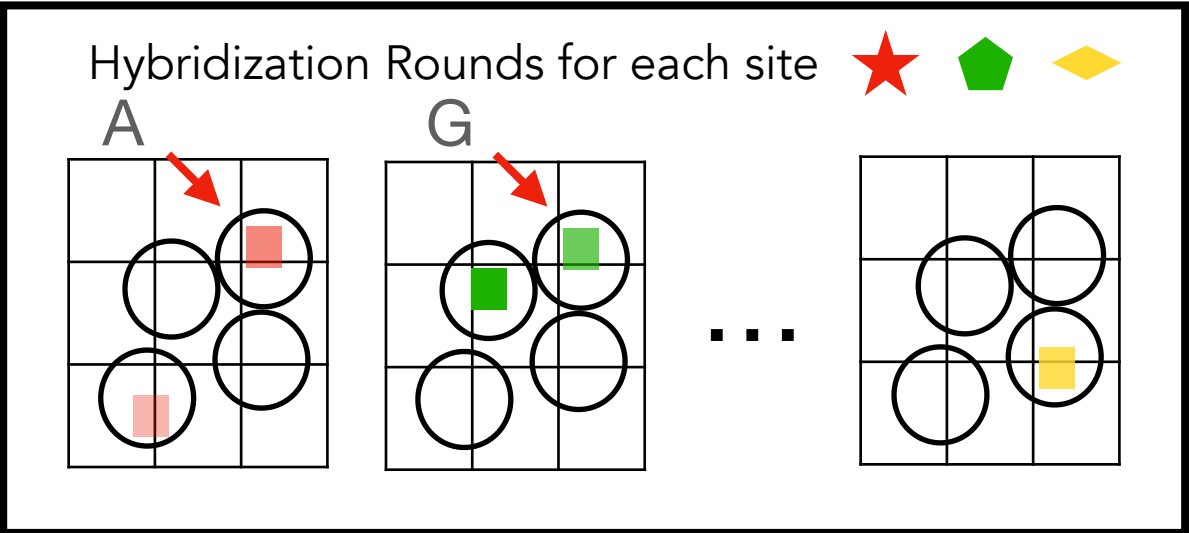


(3) Observation Process

Sequencing-based



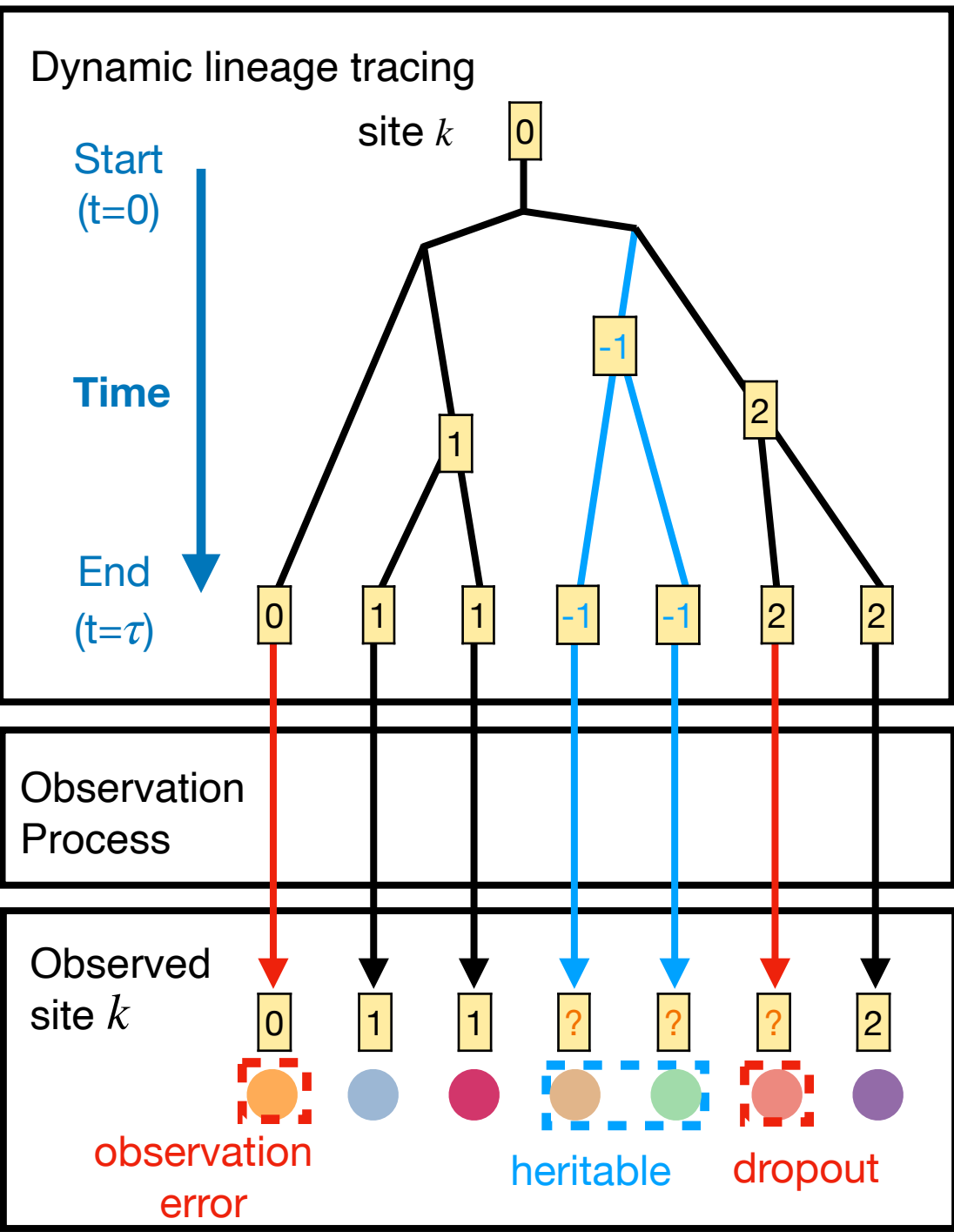
Imaging-based



LAML-Pro

maximum likelihood tree inference
 $\max_{T, \Theta} \log L(T, \Theta; \mathbf{D})$

calculate $L(T, \Theta; \mathbf{D})$ under the IUCM

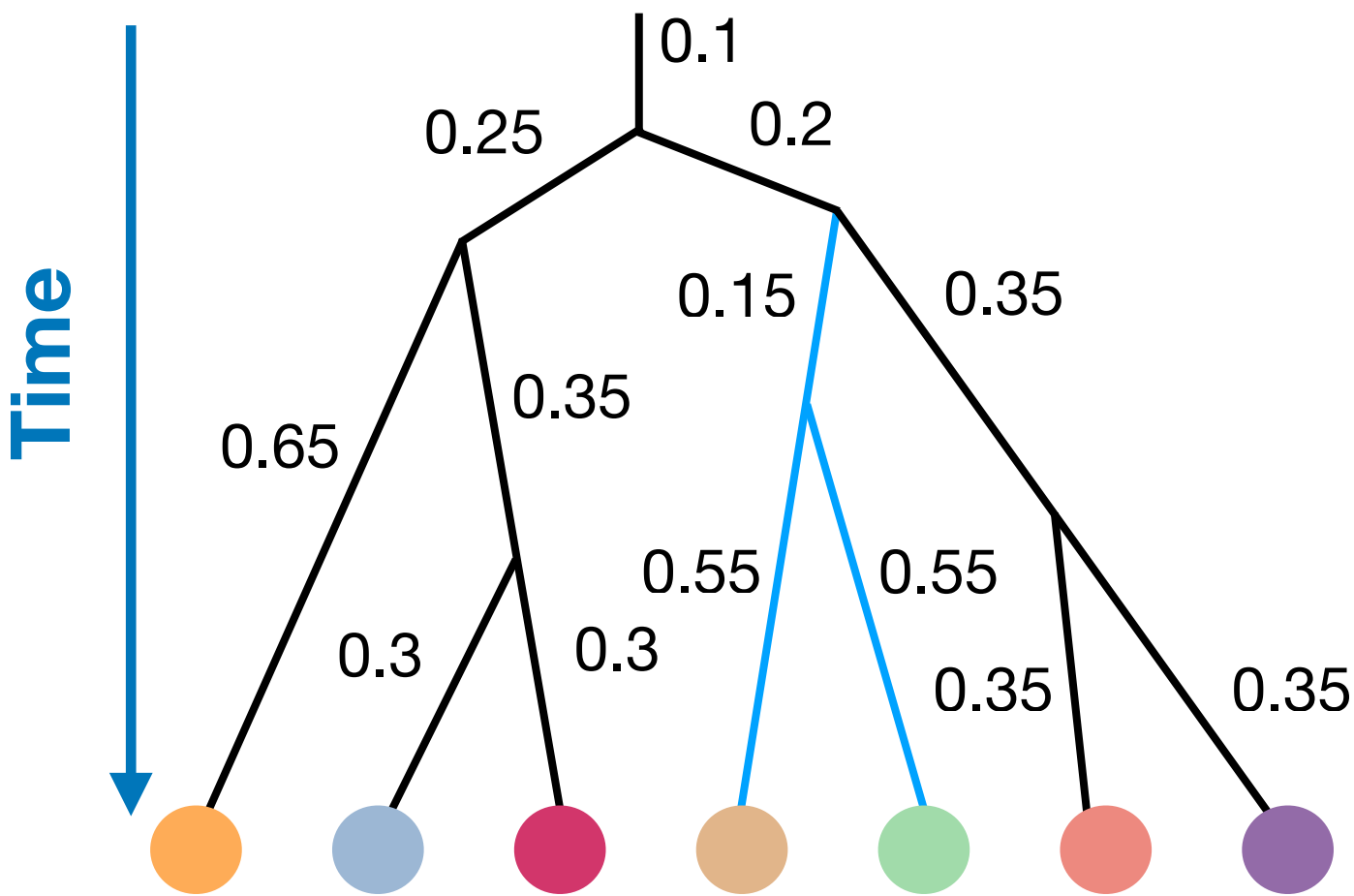


Output

(1) Imputed genotype matrix

target sites	1	3	3	0	0	2	2
	0	1	1	0	0	2	2
	4	3	3	1	1	2	2

(2) Time-resolved lineage tree



(3) Editing rate $\hat{\lambda}$, heritable missing rate $\hat{\nu}$, dropout probability $\hat{\phi}$, and readout accuracy $\hat{\rho}$