Workflow

① Assign SNPs to tree branches → ② Call informative SNPs in aDNA samples, filtering for deamination (C/T, G/A) and error. → ③ For each ancient sample, add derived/ancestral state information at each branch of the tree. → ④ Traverse tree and find optimal path for each sample, based on branch state information and allowing for missing data.

①
loci

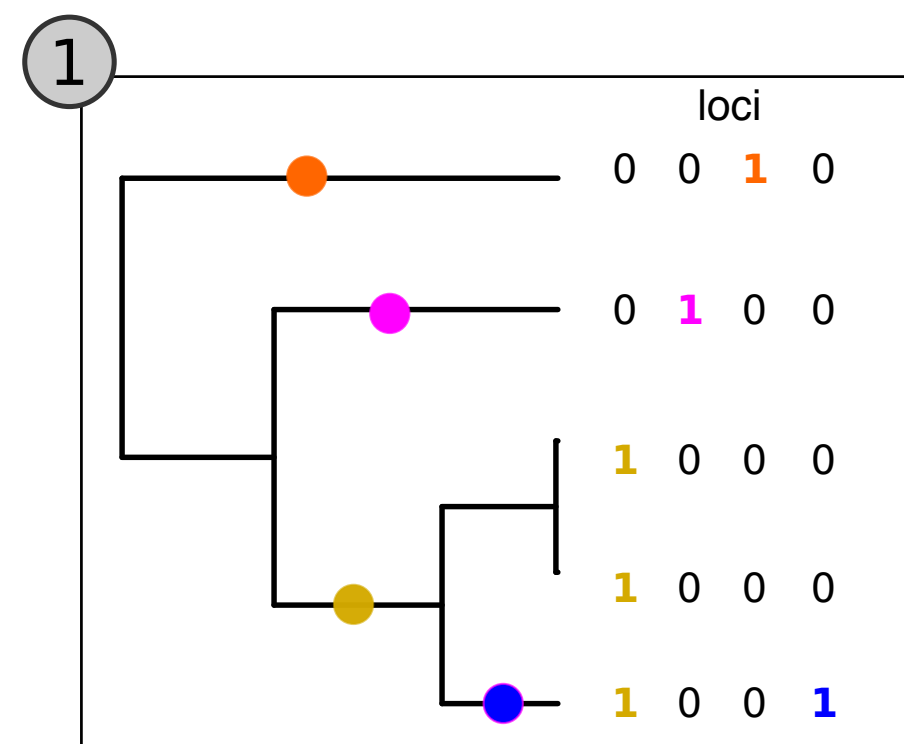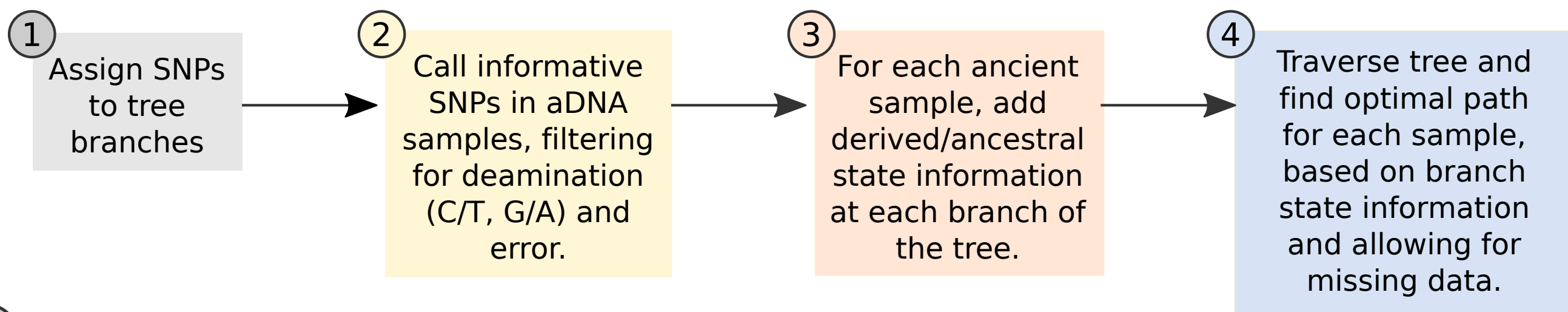0 0 **1** 0

0 **1** 0 0

1 0 0 0

1 0 0 0

1 0 0 **1**

Starting with a phylogeny estimated with high-coverage individuals and a VCF file, we assign SNPs to each branch if all the individuals belonging to that branch carry one allele and individuals outside that branch carry the other.

③

④

best path

best node

R2

R1a

R1b

R1b-L21

#s number of markers **supporting** assignment to branch

#ns number of markers **not supporting** assignment to branch