Biogeographic history of individuals

$J_m(time)$
common ancestor
t_∞
Jm_6
t_4
vicariance
Jm_5
t_3
Jm_2
t_2
migration
Jm_1
t_1
Jm_0
t_0
time (in generations before present)
sampled individuals (n_1 and n_2)
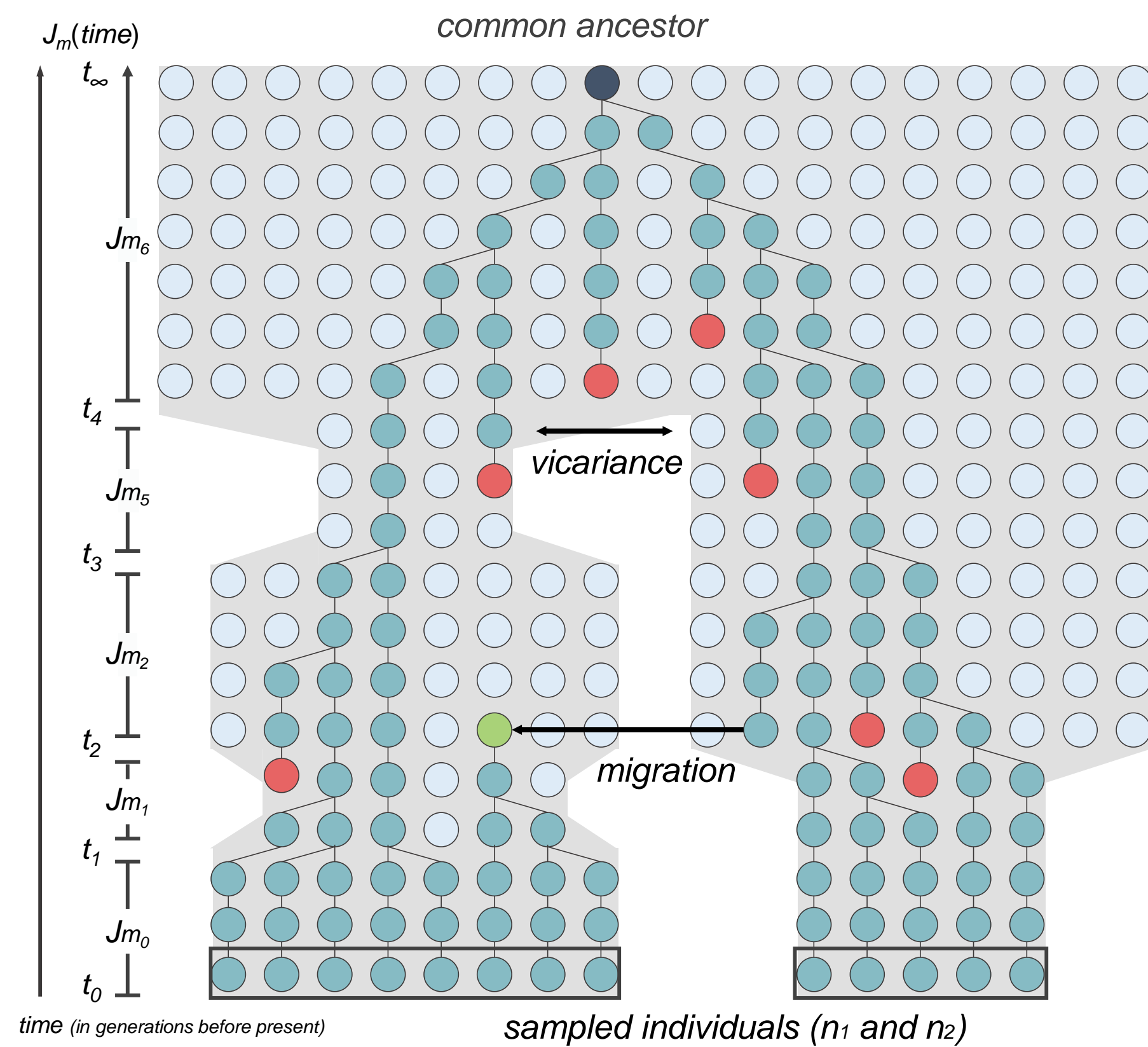
Model parameters

→ The size of the differents assemblages in the past (*deme_sizes*) along with the corresponding dates (*changetimes*)

→ The migration history linking demes (*migr* and *migr_times*)

→ The vicariance history linking demes (*splits*)

→ The point mutation rate (*mu*)

→ The speciation model (*spmodel*, *tau*)

Evolutionary relationships of species

$J_m(time)$
common ancestor
t_∞
Jm_6
t_4
Jm_5
t_3
Jm_2
t_2
Jm_1
t_1
Jm_0
t_0
time (in generations before present)
sampled individuals (n_1 and n_2)

$J_m(time)$
t_∞
Jm_6
t_4
Jm_5
t_3
Jm_2
t_2
Jm_1
t_1
Jm_0
t_0
time (in generations before present)
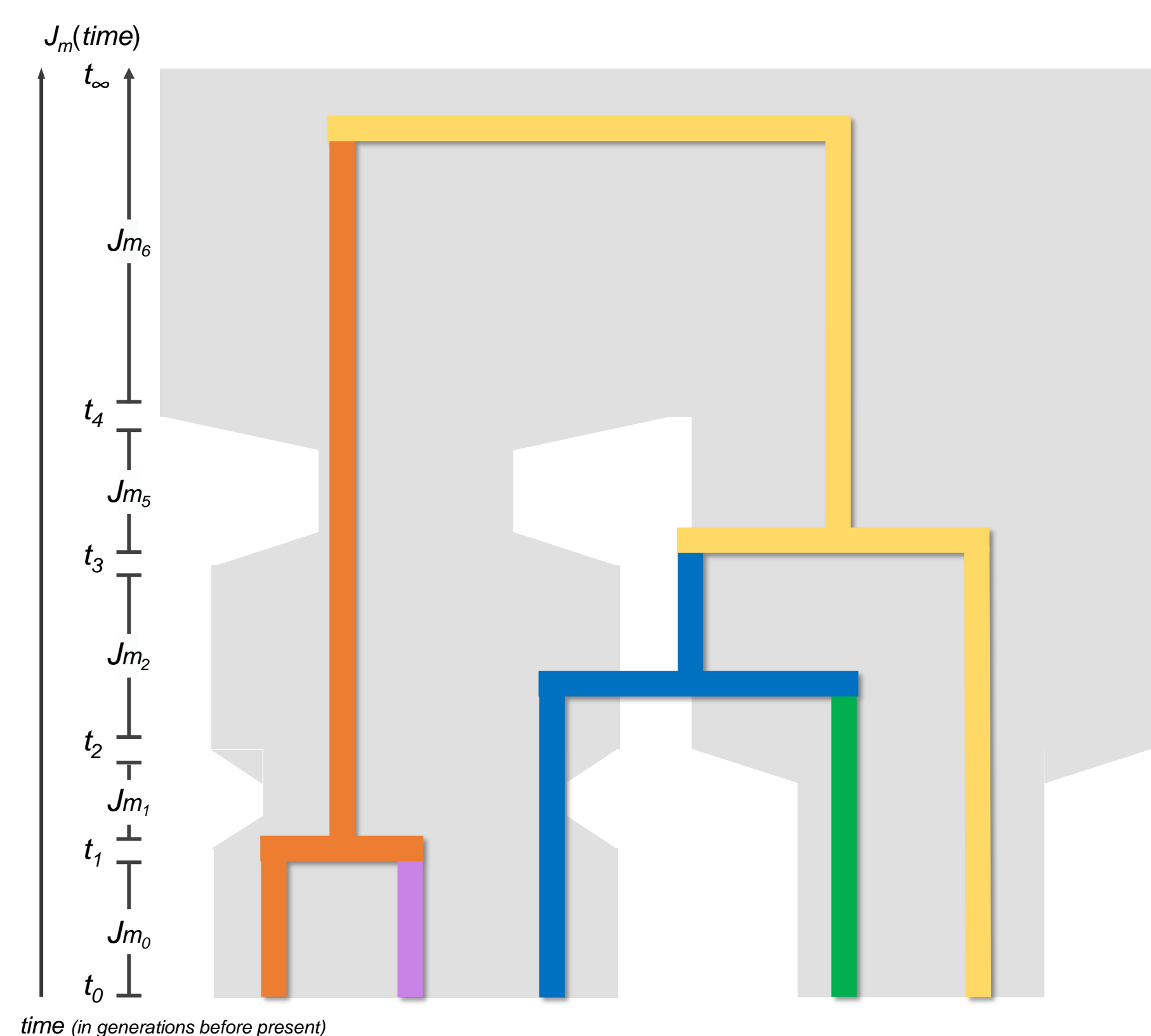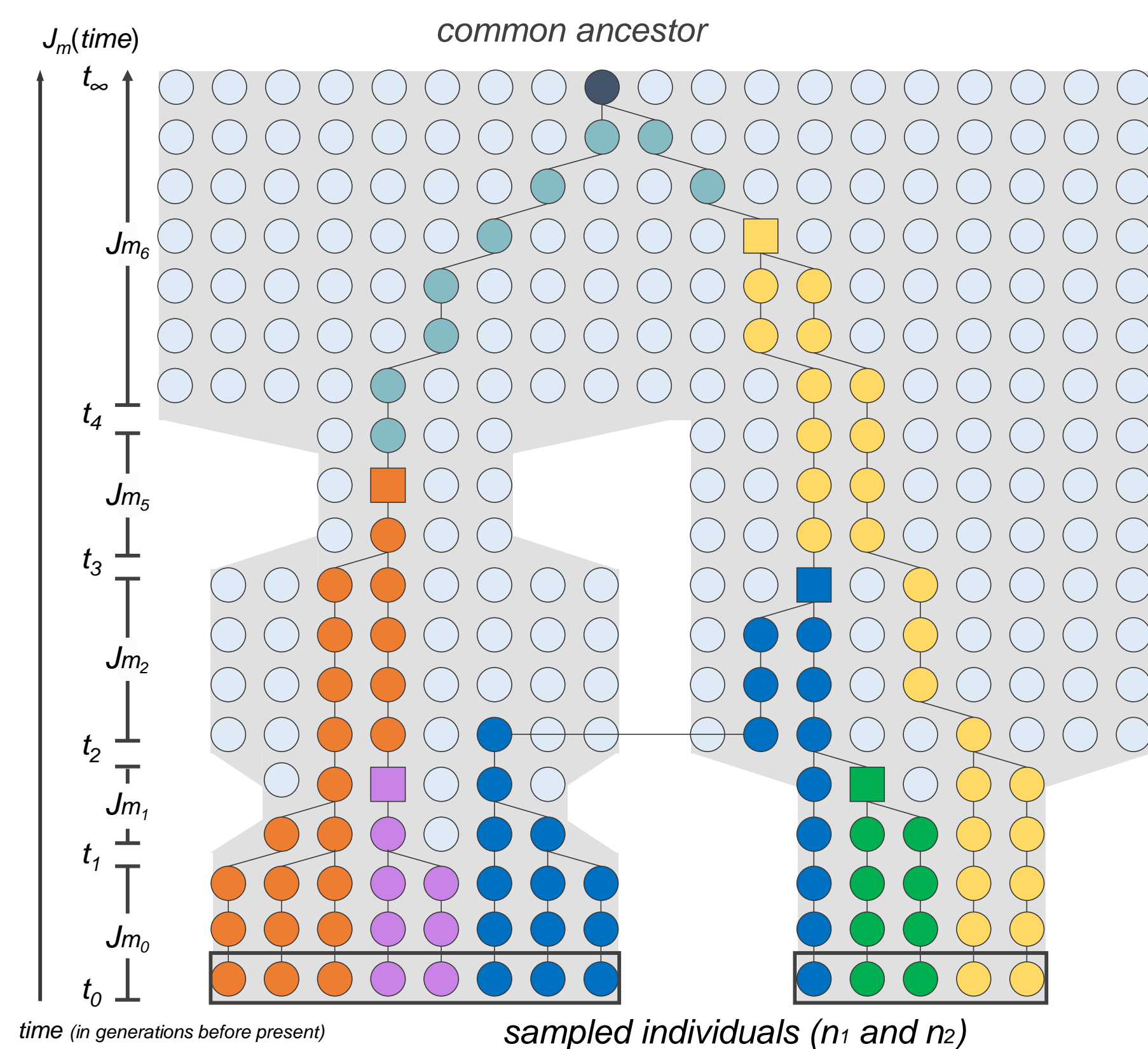
From these users can derive a wide range of summary statistics of interest (species richness, Shannon's or Simpson's diversity indexes, phylogenetic diversity metric etc.)

3 2 4 2 2

species relative abundances

Observations