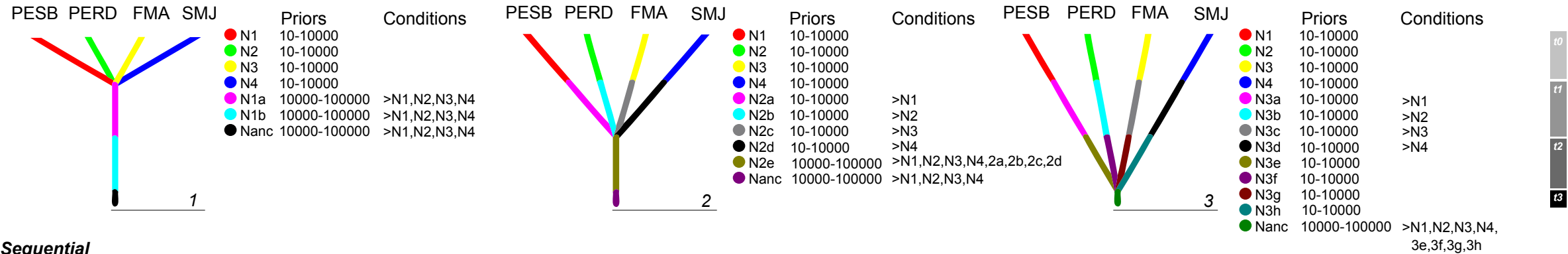
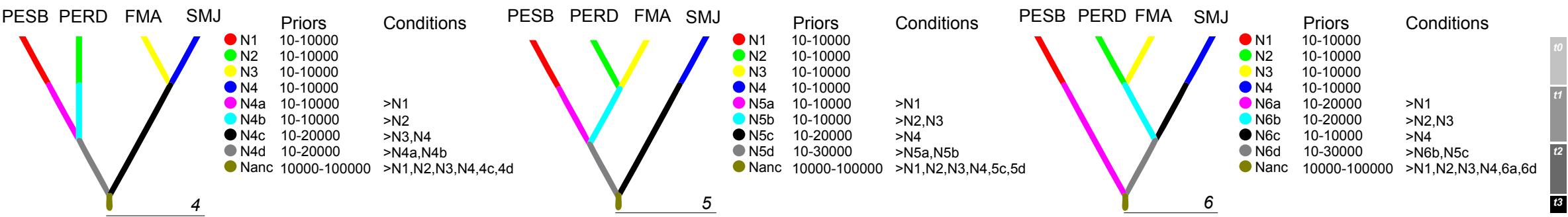


Figure S1: Prior/Scenario settings used in the Approximate Bayesian Computation analysis.

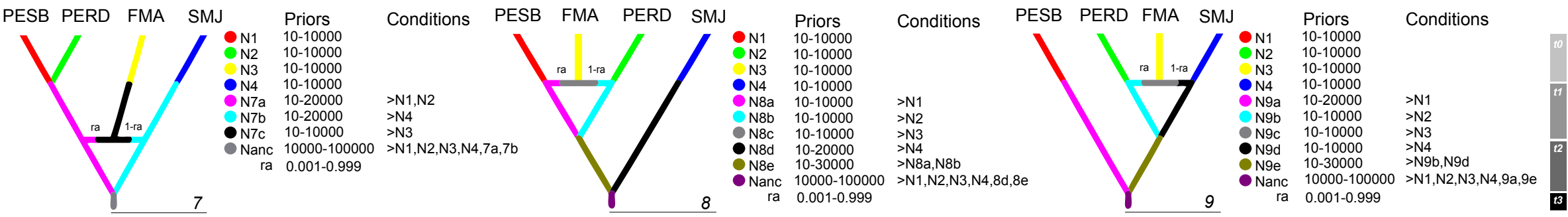
Rapid



Sequential



Sequential with admixture



	Priors present	Conditions	Summary statistics	Mutation model priors
t0			One sample # haplotypes # segregating sites mean pairwise differences Tajima's D	Min. - Max. Mean μ (1/s/generation) 1.0E-7 - 1.0E-6
t1	1-1000		Two sample # haplotypes # segregating sites mean pairwise differences Fst	Mean kappa 25 - 45
t2	1-2000*	>t1	Admixture Samples FMA/PESB/PERD Samples FMA/PERD/SMJ	Model HKY + I
t3	1-30000	>t2		% Inv. sites 90

* All Priors were Uniform, except for t2, which had a Normal distribution with mean 1500 and standard deviation 250. Time is in generations (~10 years/generation).

We followed the DIYABC manual to find appropriate prior model combinations for our data set. We used the same samples from the 106 samples data set to perform the ABC analysis though we included only the four populations shown on the diagrams above (N=90).