ONLINE APPENDIX: Supplementary figures

Scenario	M	S_0.005	F_0.00125	F_0.005	F_0.02	F_0.08
No migration						
4	0	1.0	0.96	0.96	0.96	0.92
Isolation-migration (A-B)						
4	0.001	0.99	1.0	1.0	1.0	0.92
4	0.01	0.99	0.96	1.0	1.0	0.96
4	0.1	0.99	1.0	0.96	0.96	0.96
4	1.0	1.0	1.0	1.0	1.0	0.92
Paraphyly (B-C)						
4	0.001	0.99	1.0	1.0	1.0	0.92
4	0.01	1.0	0.96	0.96	1.0	0.96
4	0.1	0.47	0.32	0.36	0.68	0.88
4	1.0	0.10	0.16	0.16	0.20	0.80
Ancestral (AB-C)						
4	0.001	0.99	1.0	0.96	0.96	0.92
4	0.01	1.0	1.0	1.0	1.0	1.0
4	0.1	0.99	0.96	0.96	0.96	0.96
4	1.0	0.99	1.0	1.0	1.0	0.92
No migration						
4	0	1.0	0.96	0.96	0.96	0.92
Single migrant (B-A)						
4	Sister species (B-A)	1.0	1.0	1.0	1.0	0.92
4	Non-sister species (B-C)	0.98	0.84	0.96	0.96	0.92
Single locus introgression						
4	Sister species (B-A)	1.0	1.0	1.0	1.0	0.92
4	Non-sister species (B-C)	0.98	0.96	0.96	1.0	0.92

Table S1: Coverage for 4-species scenarios, and different settings in DENIM. S_0.005 stands for the simple model with prior mean 0.005 on the migration rate, F_0.00125 for the flexible one with prior mean 0.00125, and so on.

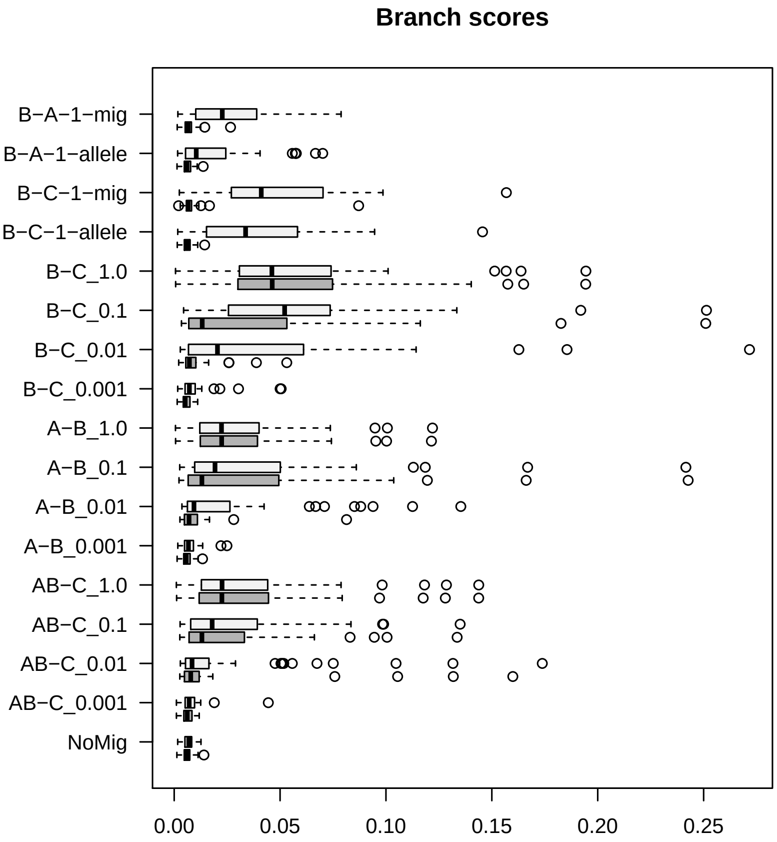


Figure S1: Branch scores for the 4-species scenarios, based on 50 replicates. For each scenario, the results for DENIM are in mid-gray and below those for *BEAST which are in pale gray. See the text for a decscription of the scenarios. The simple model was used with prior mean of 0.005.

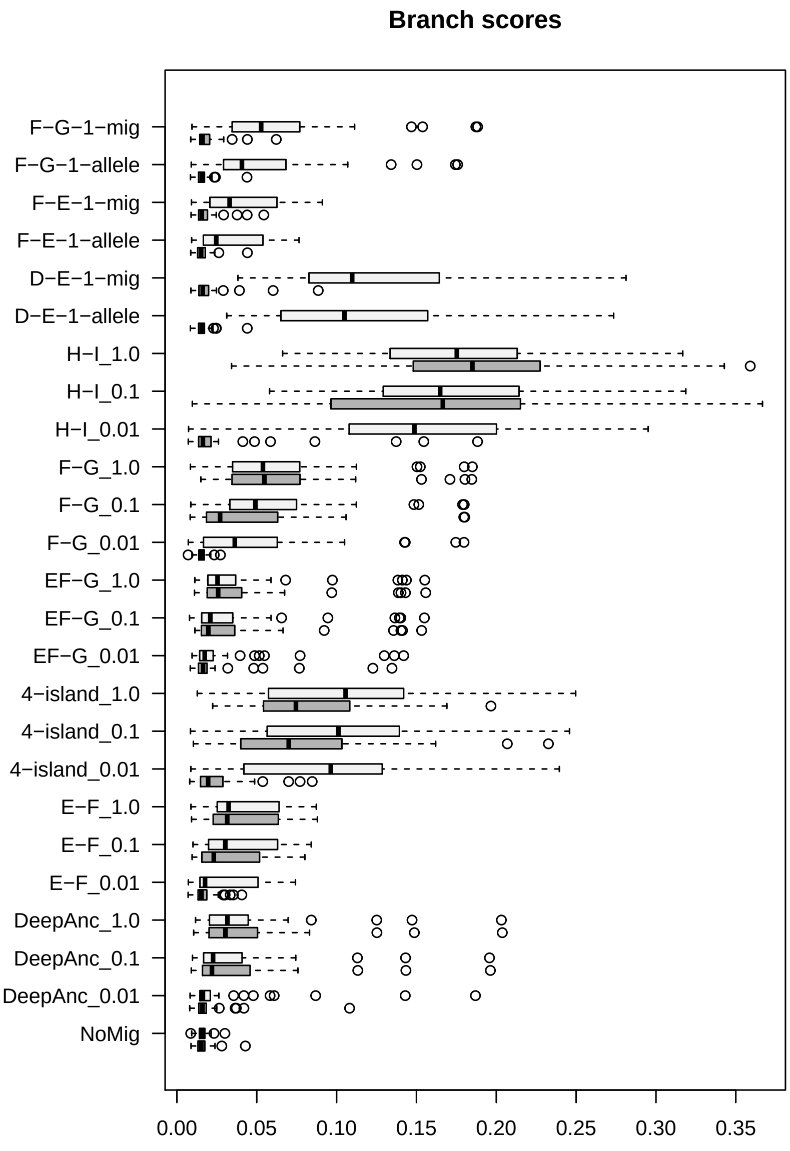


Figure S2: Branch scores for the 10-species scenarios. Other details as Fig. S1.

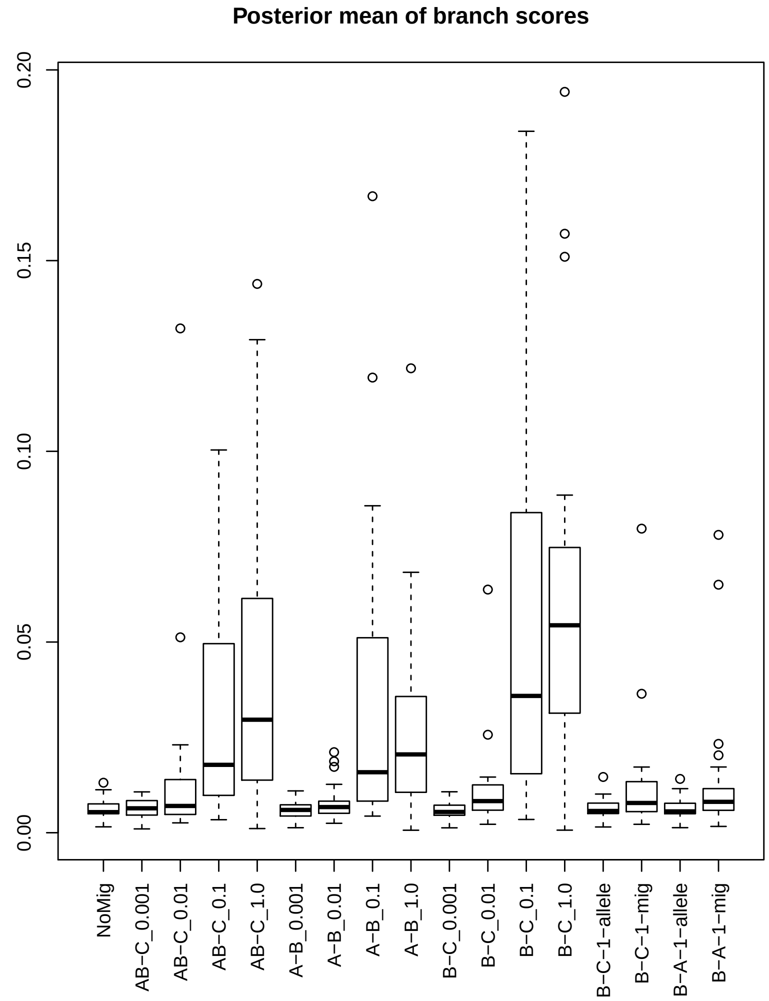


Figure S3: Branch scores for the 4-species scenarios, based on 100 replicates. "NoMig" is the scenario with no migration. The other names describe the pairs of species tree branches which have migration, followed by the migration rate, or "allele" meaning a single locus introgression, or "mig", meaning a single migrant. The flexible model was used with a prior mean of 0.00125.

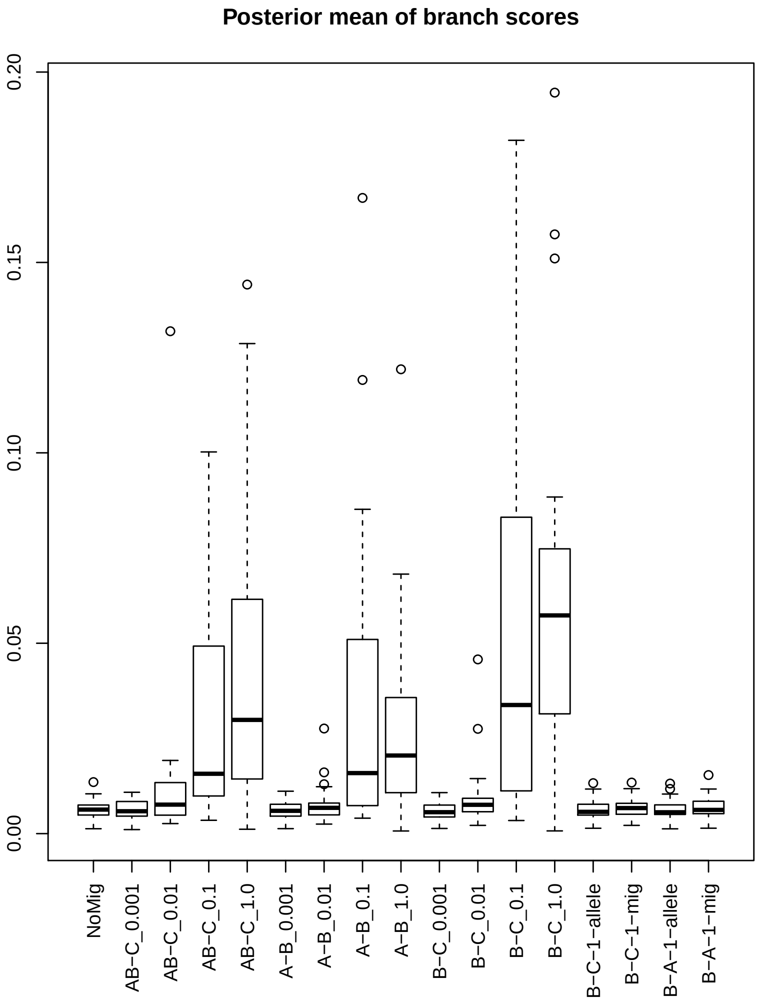


Figure S4: As Figure S3 except that the prior mean was 0.005.

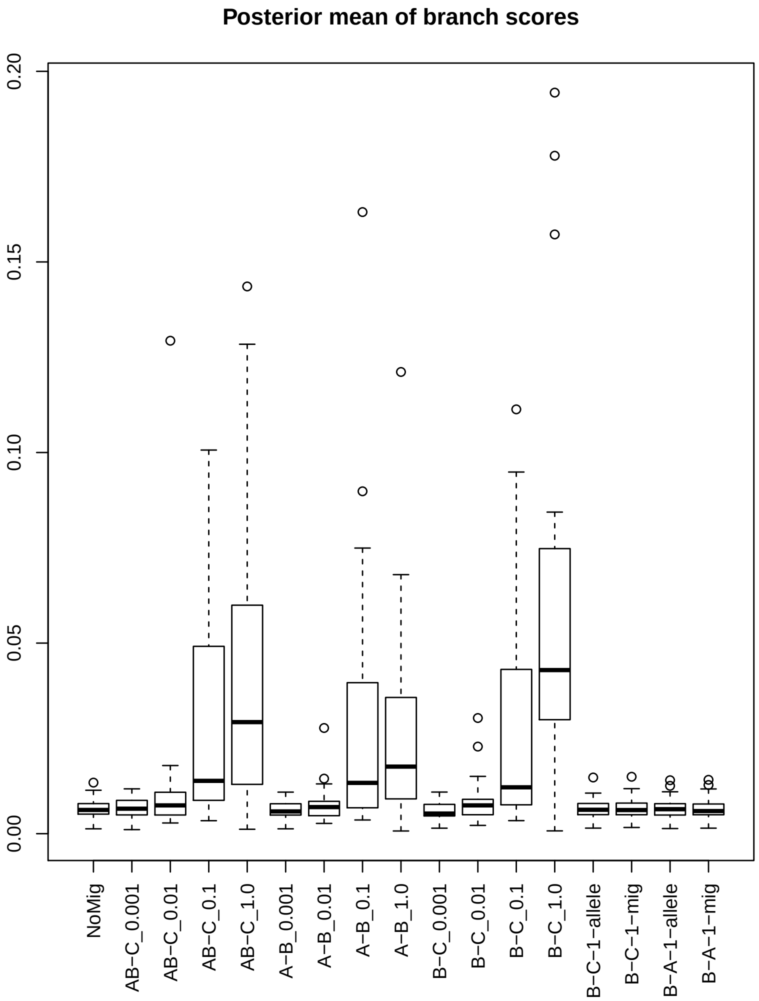


Figure S5: As Figure S3 except that the prior mean was 0.02.

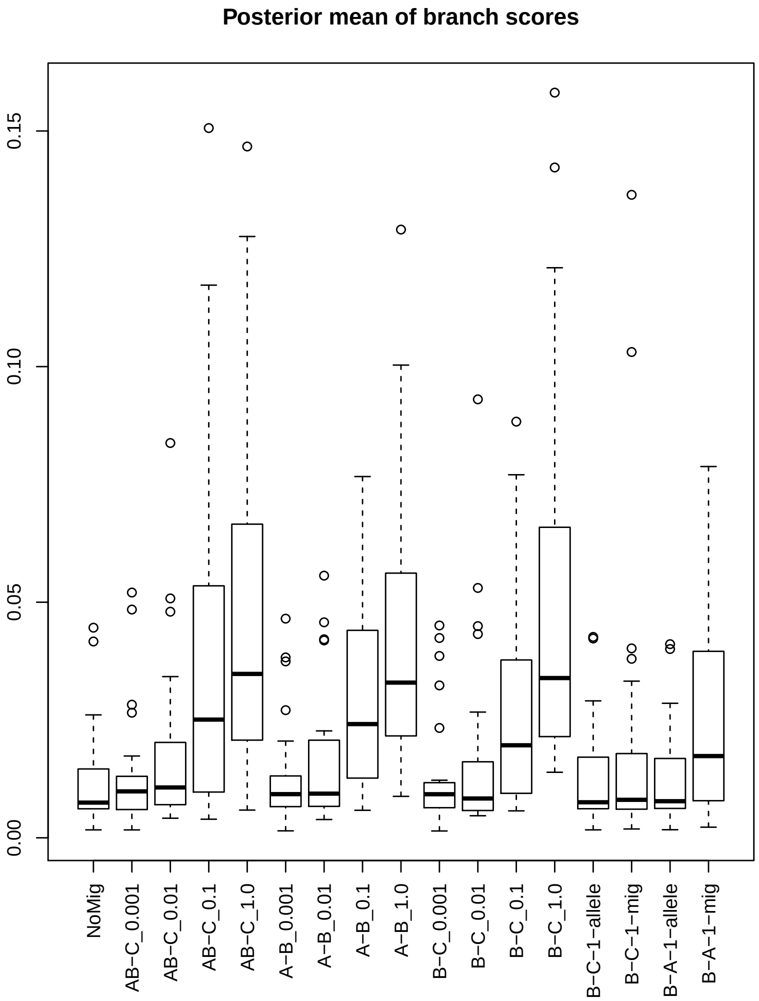
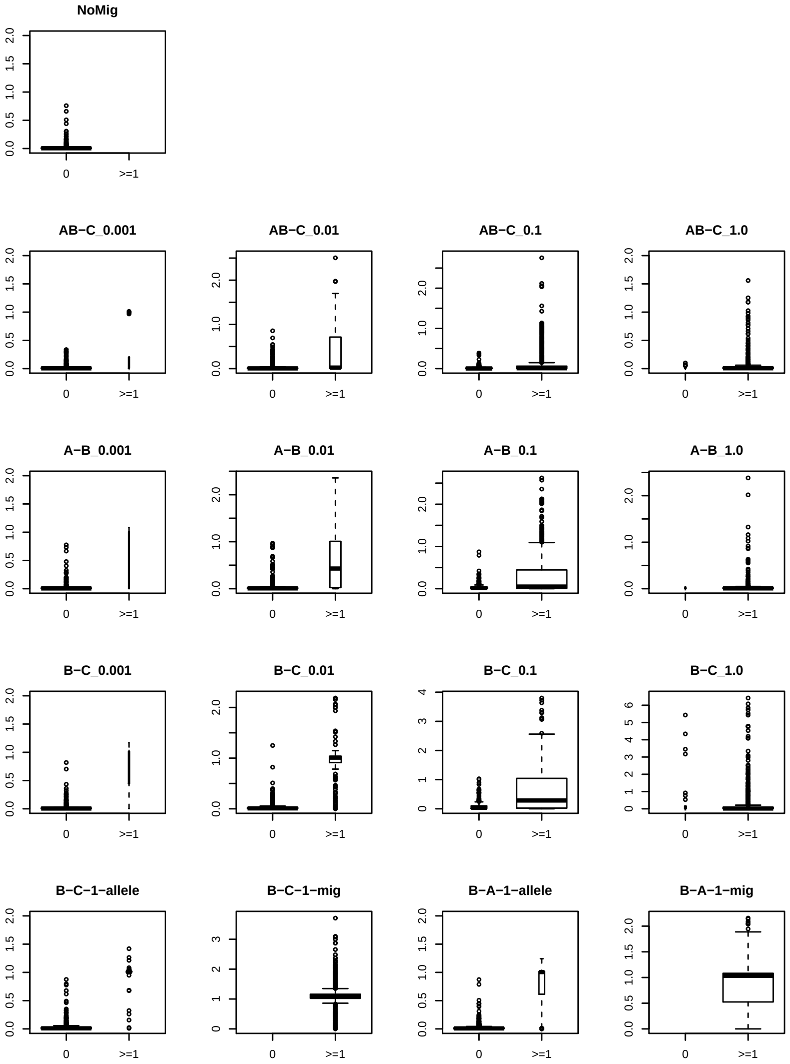


Figure S6: As Figure S3 except that the prior mean was 0.08.



NoMig

AB−C_0.001

AB−C_0.01

AB−C_0.1

AB−C_1.0

A−B_0.001

A−B_0.01

A−B_0.1

A−B_1.0

B−C_0.001

B−C_0.01

B−C_0.1

B−C_1.0

B−C−1−allele

B−C−1−mig

B−A−1−allele

B−A−1−mig

Figure S7: Mean migration counts for the 4-species scenarios. Each boxplot show the posterior mean count of migrations for the two cases that migration is present or absent in a locus in the simulated data. The width of the boxes is proportional to the number of cases.

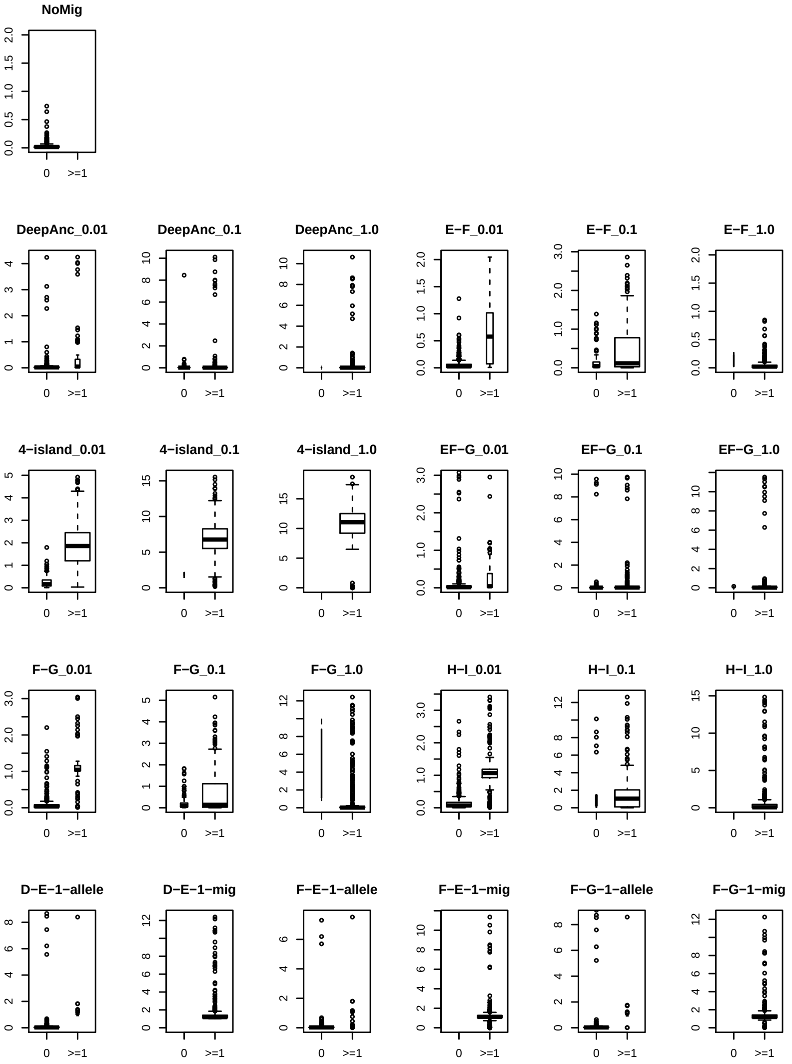


Figure S8: Mean migration counts for the 10-species scenarios. Other details are as Figure S7.