

Using multistate mark-recapture mixture models to estimate latent subpopulation structure in survival and state transition probabilities: North Atlantic right whales

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Appendix S1: Detailed results from multistate mixture models simulation studies

¹ In this appendix, we provide details on bias, precision (standard error), and 95% confidence coverage for multistate mixture
² simulations.

³ *Simulation scenario 1: partial migration*

Table 1. Mean estimates, precision (SE), and 95% confidence interval coverage for the partial migration simulation scenario; results are from 817 simulation replicates. A total of 1000 simulations were run but 183 resulted in poor optimizer performance (e.g. estimates on a boundary, non-invertible Hessian matrices).

Parameter	True value	Mean estimate	SE	Coverage
θ_1	0.95	0.948	0.011	0.945
θ_2	0.90	0.896	0.032	0.950
p_1	0.4	0.403	0.015	0.955
p_2	0.4	0.408	0.054	0.953
π	0.333	0.334	0.034	0.988

⁴ *Simulation scenario 2: divergent migration*

Table 2. Mean estimates, precision (SE), and 95% confidence interval coverage for the divergent migration simulation scenario; results are from 1000 simulation replicates.

Parameter	True value	Mean estimate	SE	Coverage
θ_1	0.95	0.951	0.012	0.965
θ_2	0.90	0.900	0.001	0.957
p_A	0.4	0.399	0.015	0.953
p_B	0.2	0.200	0.012	0.943
p_C	0.2	0.200	0.014	0.958
π	0.5	0.500	0.044	0.982

⁵ *Simulation scenario 3: overlapping population*

Table 3. Mean estimates, precision (SE), and 95% confidence interval coverage for the overlapping population simulation scenario; results are from 926 simulation replicates. A total of 1000 simulations were run but 74 resulted in poor optimizer performance (e.g. estimates on a boundary, non-invertible Hessian matrices).

Parameter	True value	Mean estimate	SE	Coverage
θ_1	0.95	0.952	0.013	0.950
θ_2	0.90	0.899	0.015	0.949
p_A	0.7	0.706	0.062	0.943
p_B	0.5	0.505	0.050	0.946
p_C	0.4	0.417	0.169	0.935
π_A	0.5	0.504	0.090	0.927
π_B	0.5	0.502	0.094	0.909
π_C	0.5	0.503	0.121	0.910
ψ_1^{AB}	0.1	0.099	0.026	0.941
ψ_2^{AB}	0.5	0.510	0.203	0.931
ψ_1^{AC}	0.2	0.202	0.051	0.938
ψ_2^{AC}	0.2	0.201	0.187	0.947
ψ_1^{BA}	0.5	0.502	0.113	0.944
ψ_2^{BA}	0.2	0.199	0.046	0.941
ψ_1^{BC}	0.2	0.197	0.160	0.947
ψ_2^{BC}	0.2	0.203	0.057	0.935
ψ_1^{CA}	0.6	0.601	0.117	0.931
ψ_2^{CA}	0.2	0.202	0.114	0.946
ψ_1^{CB}	0.1	0.103	0.116	0.953
ψ_2^{CB}	0.4	0.404	0.111	0.941