

Evaluation of the variation of RMAE values expected by chance between different replicates of 500 pseudo-observed data sets. Relative median absolute errors (RMAE) were computed for 10 replicates of 500 pseudo-observed data sets simulated under scenario 1. The data sets include 20 (independent) microsatellite loci and were generated under the scenario 1 presented in Figure 1. Parameter values were drawn from the same distributions than the prior distributions given in the legend of Figure 1. The demographic parameters N , $t1$, $t2$, $t3$, $t4$, $t5$, $r1$ and $r2$ are detailed in Figure 1. Standard deviation of RMAE values were equal to 0.009, 0.019, 0.004, 0.017, 0.012, 0.013 and 0.014 for N , $t1$, $t2$, $t3$, $t4$, $t5$, $r1$ and $r2$, respectively. Similar levels of RMAE variation among replicates of 500 pseudo-observed data sets were obtained for other categories of genetic markers (mtDNA and nuclear sequences) and combinations of categories of markers (results not shown).

