

# Supporting information: Dynamics of adaptation in spatially heterogeneous metapopulations

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## Appendix S4: definition of measures on simulated evolution

At each time step the metapopulation composition was summarised by the means and standard deviation of a two-component Gaussian mixture that was fitted by the EM algorithm (Meng and Rubin, 1993) using the function *normalmixEM* of the R package *mixtools* (Young et al., 2010, Version 0.4.4.). The time to reach the singular strategy ( $T_{\text{branch}}$ ) was defined as the first time step when two distinct populations were identified. The estimated singular strategy ( $\hat{x}^*$ ) was then defined as the mean metapopulation phenotype at  $t = T_{\text{branch}} - 1$ . Trait values of specialists (ESS) were estimated by the means of the two Gaussian mixture components at the end of evolution. The time to reach the specialists ( $T_{\text{ESS}}$ ) was defined as the first time step when the means of the two Gaussian mixture components were contained in the  $\pm 5\%$  interval around the trait values of the specialist strategies. Figure S1 of this appendix illustrates these measures on an example.

Finally, in patch  $j$ , the mean phenotype was calculated as a weighted average of the existing

phenotypes, the weights being the proportions of each phenotype in the local population:

$$\bar{x}_j(t) = \sum_{i=1}^I \frac{n_{ij}(t)}{K_j} x_i.$$

Then we defined the level of local adaptation in patch  $j$  as the mismatch between the mean phenotype ( $\bar{x}_j(t)$ ) and the optimal phenotype ( $\beta_{h(j)}$ ):  $|\bar{x}_j(t) - \beta_{h(j)}|$ .

## References

- X.L. Meng and D.B. Rubin. Maximum likelihood estimation via the ECM algorithm: a general framework. *Biometrika*, 80:267–278, 1993.
- D. Young, T. Benaglia, D. Chauveau, R. Elmore, T. Hettmansperger, D. Hunter, H. Thomas, and F. Xuan. Tools for analyzing finite mixture models. Technical report, R CRAN, 2010, Version 0.4.4.