

## Corrigendum

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A recent study investigating the history of gene flow between species of cave-dwelling salamanders (Niemiller *et al.* 2008) used the programme IM (Hey & Nielsen 2004) to: (i) establish that gene flow has occurred, and (ii) qualitatively evaluate the timing of migration to infer whether gene flow was concentrated in the recent past, as might be predicted if recent secondary contact occurred after a period of isolation. In an attempt to achieve the second goal, the ‘-p3’ option (Won & Hey 2005) was used to record the mean times of migration and the posterior distribution of this parameter was used to qualitatively evaluate whether gene flow seemed concentrated or broadly distributed over time. From the evident lack of concentration of mean migration times near the present, Niemiller *et al.* (2008) concluded that gene flow had been continuous or recurrent over a broad timescale. This approach also has been implemented in other studies attempting to infer the timing of migration (Kotlik *et al.* 2008; Berner *et al.* 2009; Nadachowska & Babik 2009).

We now realize that there are at least two problems with making inferences about the timing of migration using this option of IM. First, the IM model does not include variation in rates of gene flow over time, so the true dispersion of migration events is confounded with uncertainty in the parameters describing the timescale of divergence and rates of gene flow. Second and more important, the ‘-p3’ option generates an estimate of the posterior distribution of the *mean* time of migration and not the distribution of migration *events* through time. That is, for each sampled genealogy with migration IM reports only the average time, and not the individual times. The distribution thus reflects the sampling variance of the mean, which is a function of both sample size (number of migration events per simulated genealogy) and the dispersion of migration events over time. Larger sample size will cause the distribution to be narrower and it would be wrong to interpret this as a concentration of migration events near the mean.

While other analyses presented by Niemiller *et al.* (2008) and illustrated by Nosil (2008) support our inference that the signature of gene flow between cave and surface-dwelling *Gyrinophilus* salamanders was not caused by recent secondary contact, our inferences from the posterior distribution of mean migration time represent an over-interpretation of the MCMC results and we do not recommend this procedure for inferring the timing of migration. New methods are required for evaluating heterogeneity of migration over time.

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**1514 CORRIGENDUM**

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