

- The authors state:

We focused on pairs highly connected by gene flow previously identified in Rougemont

Am I misunderstanding this statement? It seems to suggest populations were ascertained by previously estimated levels of gene flow. If so, wouldn't this bias the results of the ABC analysis?

- Line 157-158: Not all of these are standard stats, please briefly describe the non-standard ones.
- Line 159,199: please make all R code available online (github, figshare, etc.)
- Line 181: "scaled"
- Line 282: What is the differentiation referred to here? F_{st} is given on line 277. This is something different?
- Am I correct that the variable importance done using Random Forest was estimated using simulated data?
- The results were confusing at times. I think I would present the model selection, and only discuss errors when relevant to the models selected (i.e. do we care about AM vs SI when neither model was selected?). Error rates for models not selected can be reported in a table but probably aren't important to highlight in the text.
- Discussion: do you need to report N_e ? It seems that inference based on relative values from the ABC may be valid, but if the assumed value of 1,000 for the ancestral population isn't regarded as very accurate, why use it to estimate N_e for other populations?
- Regarding estimation of variable importance in RF: my (limited) understanding is that this is difficult to do well if variables are highly correlated. Is that not a problem here?
- Migration was estimated to be highly asymmetric, but some of that is due to differences in N_e . Factoring out N_e , differences in m would appear to be smaller, and the CI for these estimates is high. Given this, how strong are the claims of asymmetrical migration?
- I always like to be able to investigate differences between the posterior for parameters and their prior. Would it be possible to include these graphs as a supplement?
- Figure 1 should be zoomed-in on the actual populations. It might be helpful to include on this figure F_{st} between populations, as I found it hard to keep track of while reading.
- I was hoping for some explanation of differences among populations. The authors offer details for Oir, but why is Bresle so different from the others?
- Similarly, some discussion of the divergence that the authors think is occurring is worthwhile. By analyzing these separately are you assuming 6 independent divergence events? And if so, should the 6 brook lampreys be considered the same thing? Or is it

that these 6 represent 1 divergence event and then 6 colonizations of different streams?

- A number of the posterior predictive sims suggest poor fits to the summary statistics. Is this not a concern?