The manuscript « a young age of sub-specific divergence in the desert locust *Schistocerca gregaria* » by Chapuis et al. is a well performed RF-ABC analysis aiming at inferring the most likely divergence history of the species and estimating the associated demographic parameters.

The paper is well written and the author were careful in their analysis, providing justification for the choice of most of their demographic scenario, carefully assessing the robustness of model choice and parameter estimation, which the RF based analysis made easy. The used of the vegetation map at different time periods helps a lot the reader who is unfamiliar with the system to draw expectation regarding the possible scenario of divergence. Generally, more study of these king are needed in non-model species prior to make adaptive hypotheses.

For now I only have few remarks related to the choice of scenario that may perhaps be improved:

i) The author did not allow for bidirectional secondary contact, but only an asymmetric secondary contact (which is modeled like a single discrete admixture pulse in the present study). Although the author provided some verbal argument in the discussion and methods, I think that a formal test of models with bidirectional secondary contact *vs* unidirectional asymmetric contact might be relevant. Once the best models among the two will be chosen, the author could then compare it to models without contact. I think it would make a more rigorous example of how to test for this process without relying too much on priors. Moreover, the conclusions drawn here should not be affected given the nearly absent lack of support for admixture.

ii) Related to this, I find the use of the term secondary contact a little confusing: it seems to me that the author simulated a single discrete admixture pulse at a particular point in time and not really a secondary contact that would last for several generation of ongoing gene-flow (see. e.g. Roux et al. 2013 and 2016 for appropriate definitions). It would have been nice to test for a model with true secondary contacts rather than single discrete admixture pulse and I would be curious to see if the results remains the same or not. (I would expect the model choice not to be affected, but it would be more rigorous to test explicitly for it).

iii) When looking at the evolution of suitable areas on the maps, I was left with the impression that the species range has been continuous (on longer time scale) and may have then been progressively split into two units over a very recent time period (linked to climate variation, as explained by the authors). Under this scenario, there would not be a split without gene-flow, rather I think this could be approximated by a model of split with initial ongoing gene-flow (bi-directional and with the possibility for asymmetry; also referred to as ancient migration models). Although it would even be better if the authors could test for a model of progressive decrease in gene flow following split time, until the model converged to a model of strict isolation. I think this could be more realistic than the "single long-distance migration event of a small fraction of the ancestral population" which is modeled through a bottleneck. Excluding model of initial gene-flow would enriched the discussion line 365 – 382.

Aside from these general remarks, most of my comments are suggestions to improve the manuscripts.

Other comments:
During the reading, I've been wondering several times how many individuals were used, what were the levels of within subspecies genetic diversity, and what were levels of genetic differentiation. I also wondered if their was significant genetic structure within subspecies. This information is only indirectly provided in the methods section through reference to previously published articles. A short paragraph on these topics would be relevant at the beginning of the results.

Also, the discussion was interesting, maybe the author could provide us with some more discussion regarding the advantage and limits of using RF-ABC (this is mostly in the Supp Mat S1). While microsatelitte are less and less used in evolutionary biology, being progressively replaced by SNPs,

maybe the authors should also highlight the fact that such approach is relevant also for SNP/genome-based inference of evolutionary history?

Line 144-145 and 148-155 : One of the first empirical study using RF-ABC was Rougemont et al. (2016). Applying the RF algorithm to the problem of model choice, they find several advantages to the RF algorithm, but with similar difficulties in discriminating complex scenario compared to the neural-network based ABC procedure.

Minor comments:

Line 156 – 165 on model grouping: I am not sure this is entirely new. For instance, Roux et al. (2016) performed grouping of model with gene flow (IM,SC) against models without gene flow (SI, AM). Similarly Leroy et al. (2017) compared groups of IM, SC, AM, and SI models and then statistically compared the best alternative version of the previous "best" model. I guess this procedure is already widely used in the ABC literature.

Fig 2 : Maybe provide separate figures, to ease the understanding for people unfamiliar with these sort of analysis? (or in Supp Mat?).

Line 218- 221 : maybe in the text provide the number of the scenario that are compared against each other, it would also eased the understanding of which scenarios are compared without the need to go reading the table 1 directly.
i) was 1+ 3 +5 +7 vs 2 + 4 +6 +8
ii) was 1+2+5+6 vs 3,4,7,8, and
iii) was 1+2+3+4 vs 5+6+7+8.
It becomes clear only after reading the methods.
Although I would present them in the same order of the colomns of the table in Fig2, (this would also follow the order of events in time (contraction, then bottleneck, then gene-flow)).

Line 280 : Reference for « average of three generations per years »? (it is only provided in the Methods).

Fig 1B is not mentioned (should be with Fig1A or remove?)

Methods :
Prior choice :
It is still not clear to me how Tca was chosen. I think diyABC only allows single admixture event, however, how likely is this? It may be more relevant to allow for a broader time period.
Also, the lower bound of the prior on admixture parameter seem to be very narrow. Why not letting it varying to lower value (i.e. closer to 0). As in models with gene flow?
Line 548 – 553 : it would be nice to have an overview of the dataset, perhaps with a few summary statistics related to the pooled samples (e.g. genetic diversity within pool of subspecies, Fst between subspecies,etc).

References:

Rougemont, Q., Roux, C., Neuenschwander, S., Goudet, J., Launey, S., & Evanno, G. (2016). Reconstructing the demographic history of divergence between European river and brook lampreys using approximate Bayesian computations. *PeerJ*, *4*, e1910. doi: 10.7717/peerj.1910

Roux, C., Fraïsse, C., Romiguier, J., Anciaux, Y., Galtier, N., & Bierne, N. (2016). Shedding Light on the Grey Zone of Speciation along a Continuum of Genomic Divergence. *PLOS Biology*, *14*(12), e2000234. doi: 10.1371/journal.pbio.2000234

Roux, C., Tsagkogeorga, G., Bierne, N., & Galtier, N. (2013). Crossing the species barrier: genomic hotspots of introgression between two highly divergent Ciona intestinalis species. *Molecular Biology and Evolution*, *30*(7), 1574–1587. doi: 10.1093/molbev/mst066