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Dear Editors,

It is our pleasure to submit for your consideration our latest work, "*Modeling the process of speciation using a multiscale framework including a posteriori error estimates*". We confirm that this work is original and has not been published elsewhere, nor is it currently under consideration for publication elsewhere, and nor will it be submitted to other journals during the reviewing process.

The work treats the conceptually challenging problem of speciation within biology: While modeling the ecology (and evolution) of species is by now well understood, the concept of a species itself by definition breaks down when speciation occurs. As a consequence, more fundamental, i.e. population-level models need to be employed.

Our contribution is therefore to resolve this problem through a heterogeneous multiscale method, in the following sense: Away from speciation events, we use a formally derived *species-level model*, in the form of family of ODEs. On the other hand, locally in time and "space" (the spatial coordinate represents biological traits), we use a *population-level model*, in the form of a PDE for the population density. The choice of models is adaptive, by application of a posteriori error bounds.

Our mathematical contribution is to establish well-posedness and a posteriori error bounds for the time-discrete population-level model, under certain assumptions on the parameters. By guiding the multiscale algorithm by the error bounds, we thereby establish a multiscale simulation framework. Our numerical results indicate very satisfactory performance when our assumptions are satisfied, and acceptable performance also outside the assumptions of the proof.

Overall we hope you will agree with our view, that our results provide both new mathematical results and methods, for a problem of great interest in biology.

Best regards on behalf of the authors,

Mats K. Brun