

## ***Interactive comment on “Dispersal distances and migration rates at the arctic treeline in Siberia – a genetic and simulation based study” by Stefan Kruse et al.***

### **Anonymous Referee #2**

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This paper uses the LAVESI model to explore the rate of northward *Larix* migration on the southern portion of the Taimyr Peninsula in Siberia. The study uses recent field data collected in the area to drive the simulation work. The focus of the model parameterization/calibration was to improve the *Larix* dispersal functionality using genetic parentage, and then apply the model to understand how the *Larix* dispersal characteristics will play out in given some climate scenarios. The site of this modelling work is of particular interest, as it is near the northernmost forest stands where paleoecological records have indicated past presence of trees north of where they are currently found. Given the unique nature of *Larix* forests (deciduous conifers linked to continuous permafrost distribution) and the fact that across their broad spatial domain (central and

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eastern Siberia) this class of trees coincides with marked changes in climate, and the potential for changes in tree distribution to alter the dynamics of high latitude systems (through changes to albedo and permafrost), this study is of great interest. I think the paper is for the most part clear and well-structured. Perhaps there can be some modification of the Discussion based on my main critique.

Main critiques: 1. At the scale of this study, are south-north assumptions of tree migration robust? At fine scales, the migrations may occur according to the patterns of favorable microsites, and primarily be confined to corridors with favorable active layer dynamics, and direct insolation. Such landforms seem important for explaining the current pattern of trees. A study with such an individual model that doesn't account for the conditions that are associated with the germination, survival, and growth of those individuals that are being dispersed should probably discuss in some detail this issue of the micro-site constraints that may contribute to broad error bars associated with migration rates. In other words, would the velocity of migration change between different microsites? If so, what is the relative prevalence of such favorable sites across the landscape, and how are they connected to the seed sources? These may be questions for follow-up work, and may be beyond the scope of this study, but I think a section in the Discussion could serve as a link between this study and some potentially viable next steps (one that incorporates landforms and micro-sites details).

2. This area is the northernmost forest ecotone. Some discussion for why this may be the case (paleoecological history) could be interesting and help contextualize predictions of future treeline velocities.

3. In Figure 1, a simple schematic of the sampling design could be useful.

Other comments: In the abstract, might it be possible to replace some of the technical wording associated with the genetic analysis with other more recognizable terminology that would be more likely to be understood by most of the readers of this journal?

Figure 4. Nice figure that shows how a few individuals dominate the reproduction. I

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think it needs to be graphically enhanced. Suggestion: Put an alpha (i.e., transparency) on the green lines, and put the dots on top.

Section 4.3 Line 336 - "However, further processes . . . and should therefore [NOT?] be neglected in simulation studies:..."

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