

## Supplement Figures

### Tree migration in the dynamic, global vegetation model LPJ-GM 1.1: Efficient uncertainty assessment and improved dispersal kernels of European trees

Deborah Zani<sup>1,2</sup>, Veiko Lehsten<sup>1,2</sup>, Heike Lischke<sup>1</sup>

<sup>1</sup>Dynamic Macroecology/Land Change Science, Swiss Federal Institute for Forest, Snow and Landscape Research WSL, Birmensdorf, Switzerland

<sup>2</sup>Department of Physical Geography and Ecosystem Science, Lund University, Lund, Sweden

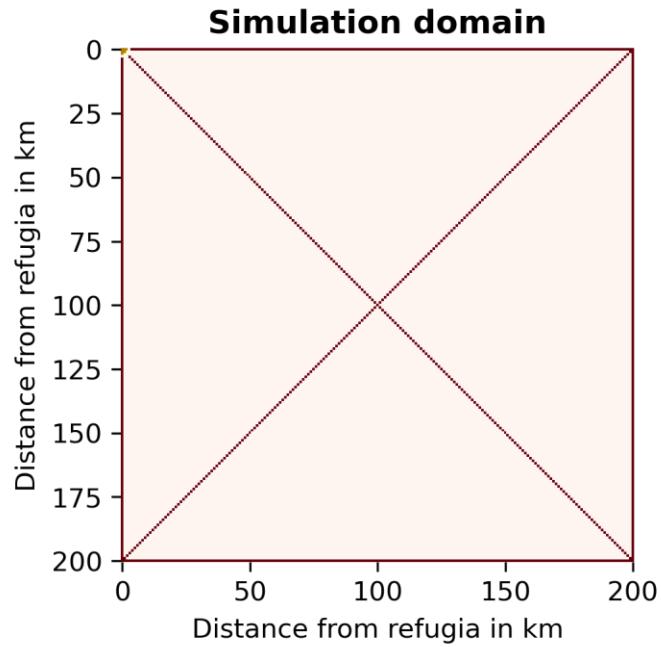
*Correspondence to:* Deborah Zani ([deborah.zani01@gmail.com](mailto:deborah.zani01@gmail.com))

**Figure S1:** Spatial domain of the LPJ-GM simulations.

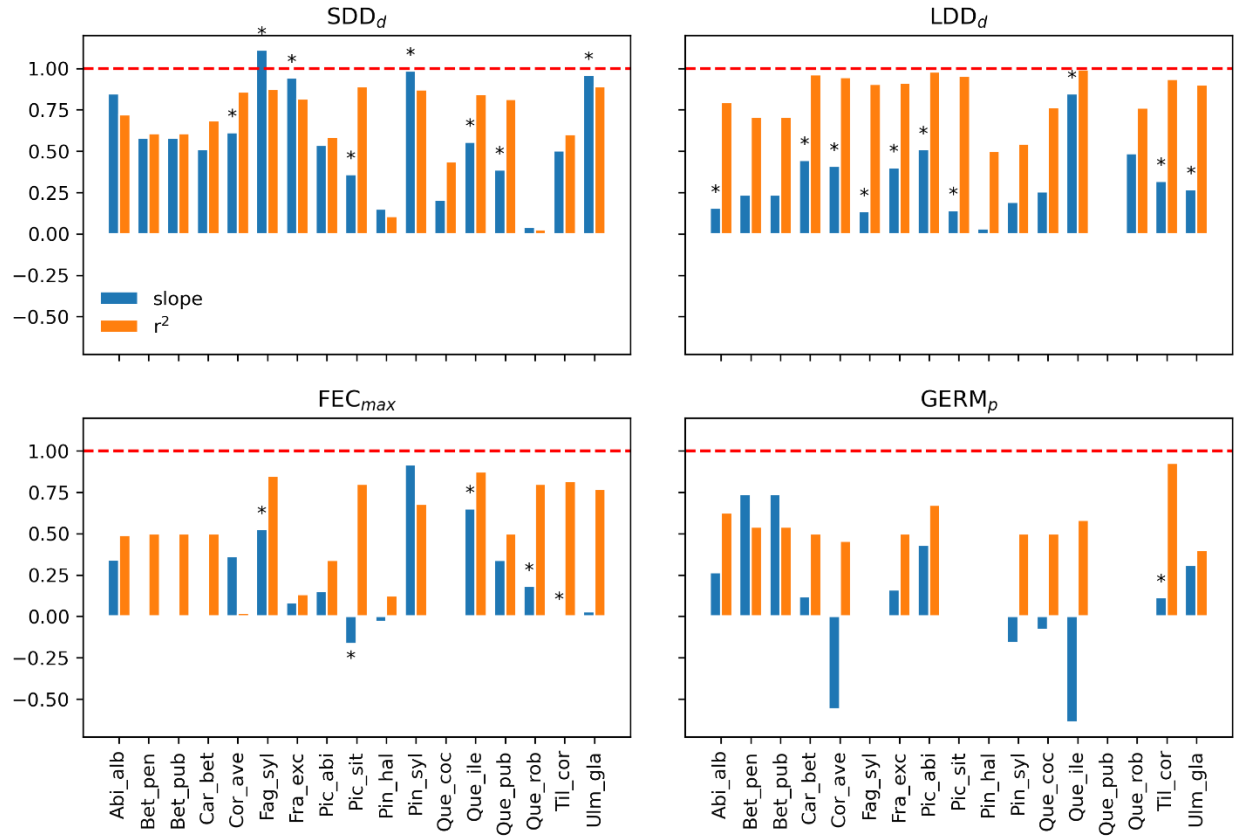
**Figure S2:** Species-specific slope coefficients and coefficients of determination ( $r^2$ ).

**Figure S3:** Shape of sensitivity functions of simulated migration rates vs. mean-normalized migration parameters.

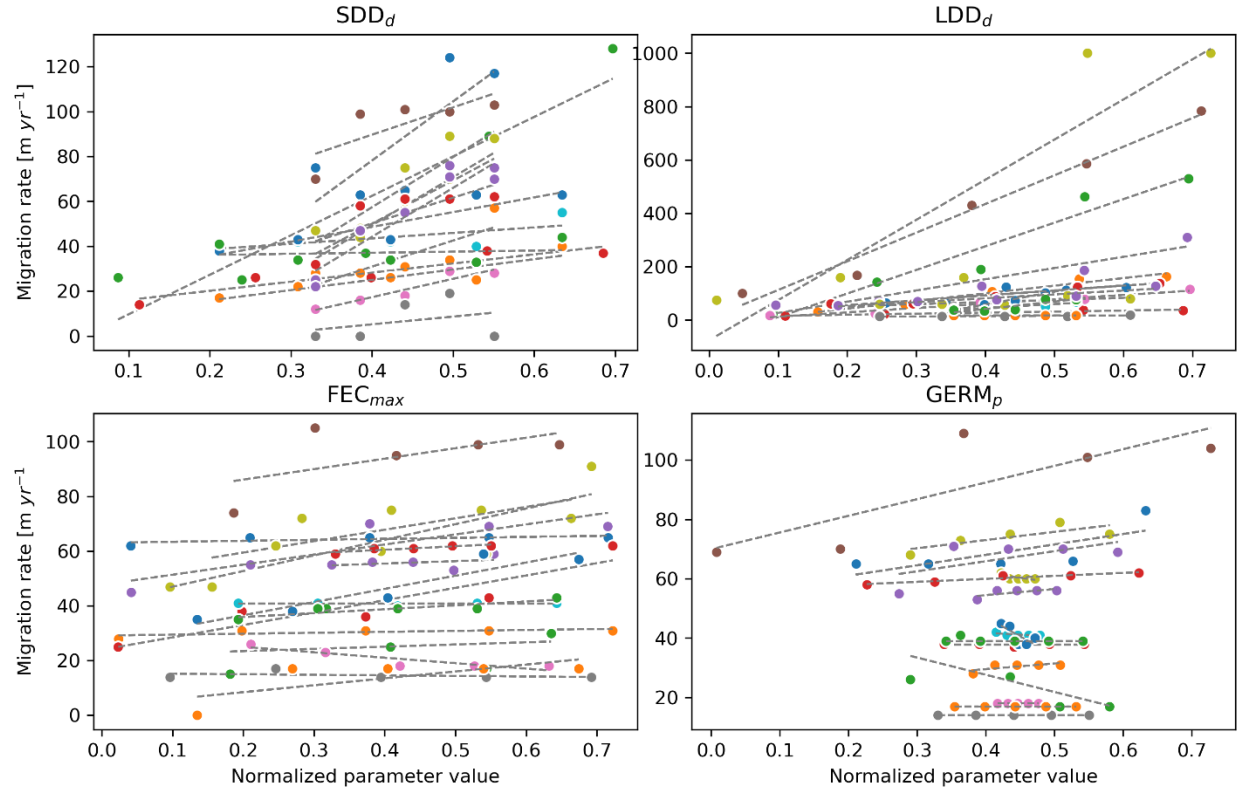
**Figure S4:** Relationship between dispersal syndromes, migration parameters and speed.



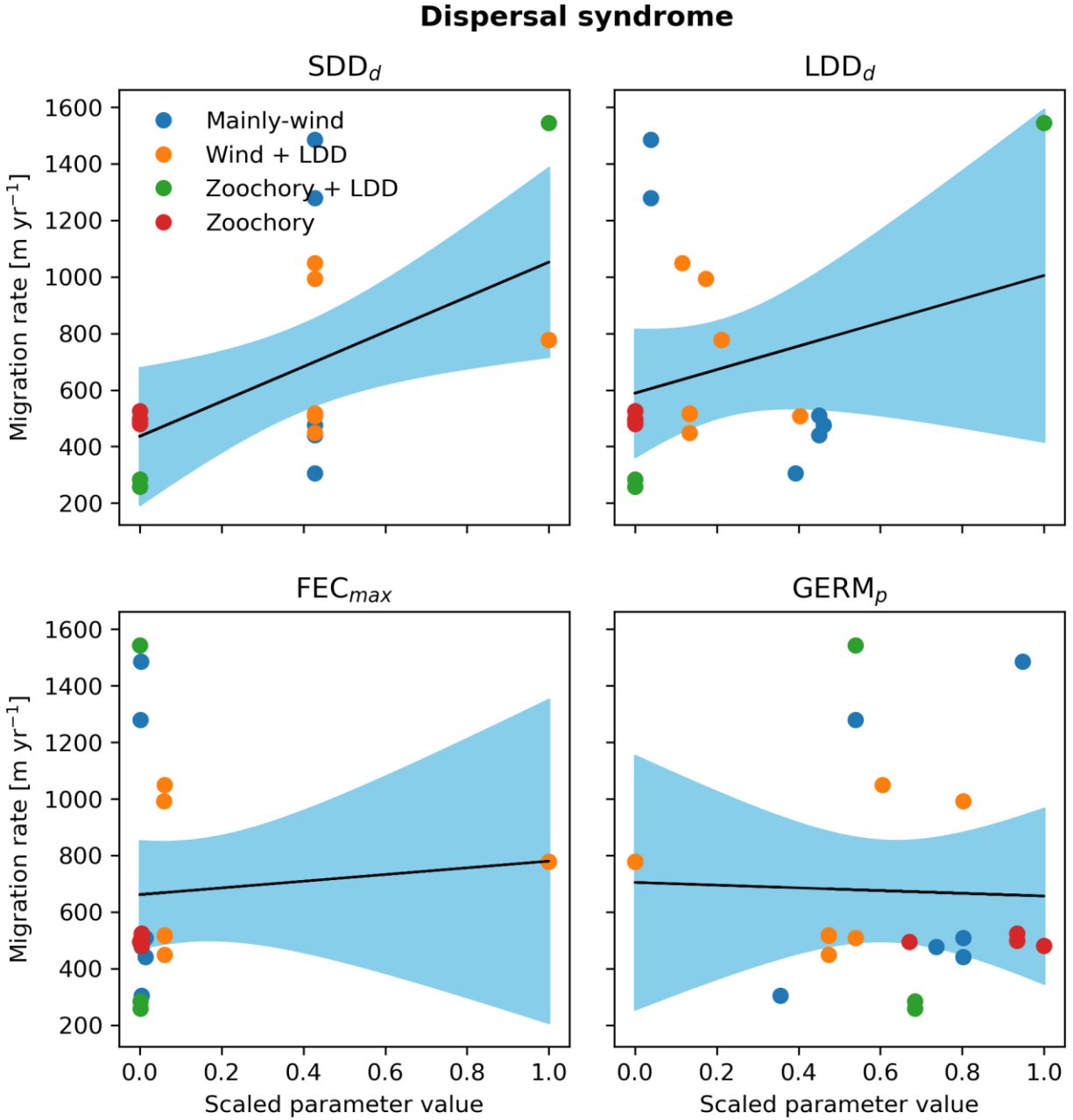
**Figure S1: Spatial domain of the LPJ-GM simulations.** The simulation domain covers an area of 201 x 201 cells (1 km<sup>2</sup> each, for a total of 40,401 cells). Dark red indicates corridors, where local dynamics and seed production are simulated (for a total of 1,197 cells with dispersal simulation); seed production is then interpolated onto all grid cells of the spatial domain. The starting point of migration (refugium) is located in the upper left corner (single cell highlighted by the yellow circle).



**Figure S2: Species-specific slope coefficients and coefficients of determination ( $r^2$ ).** Coefficients were obtained from linear regression analyses of the type  $y \sim x_i$ , where  $y$  = simulated migration rates, and  $x_i$  = parameter  $i$ : average short dispersal distance ( $SDD_d$ , meters), 1 % average long dispersal distance ( $LDD_d$ , meters), maximum fecundity per tree ( $FEC_{max}$ , no. seeds in 100 per year), and seed germination rate ( $GERM_p$ , %). Coefficient values ( $r^2$ ) close to 1 indicate a linear shape of the migration rate-parameter relationship (cf. species-specific LI in Table S1). Asterisks ‘\*’ indicate a significant linear regression (p-value < 0.05). See Fig. S3 for an explicit visualization of species-specific linear regressions.



**Figure S3: Shape of sensitivity functions of simulated migration rates vs. mean-normalized migration parameters:** average short dispersal distance ( $SDD_d$ , meters), 1 % average long dispersal distance ( $LDD_d$ , meters), maximum fecundity per tree ( $FEC_{max}$ , no. seeds in 100 per year), and seed germination rate ( $GERM_p$ , %). Different colors correspond to the 17 tree species implemented in LPJ-GM (see Table 1). Dashed lines represent species-specific linear regressions of the type  $y \sim x_i$ , where  $y$  = simulated migration rates, and  $x_i$  = parameter  $i$ .



**Figure S4: Relationship between dispersal syndromes, migration parameters and speed.** Simulated migration rates are plotted against best-fitted parameter values for the 17 tree species implemented in LPJ-GM. Color indicates dispersal syndrome categories defined as follows: primarily dispersed by wind with no additional LDD mechanisms (Mainly-wind), primarily dispersed by wind with additional LDD mechanisms such as water current and/or large/migratory animals (Wind + LDD), primarily dispersed by animals with additional LDD mechanisms (Zoochory + LDD), and only dispersed by animals (Zoochory). For species-specific dispersal syndromes, see Table 1 and Table B1.