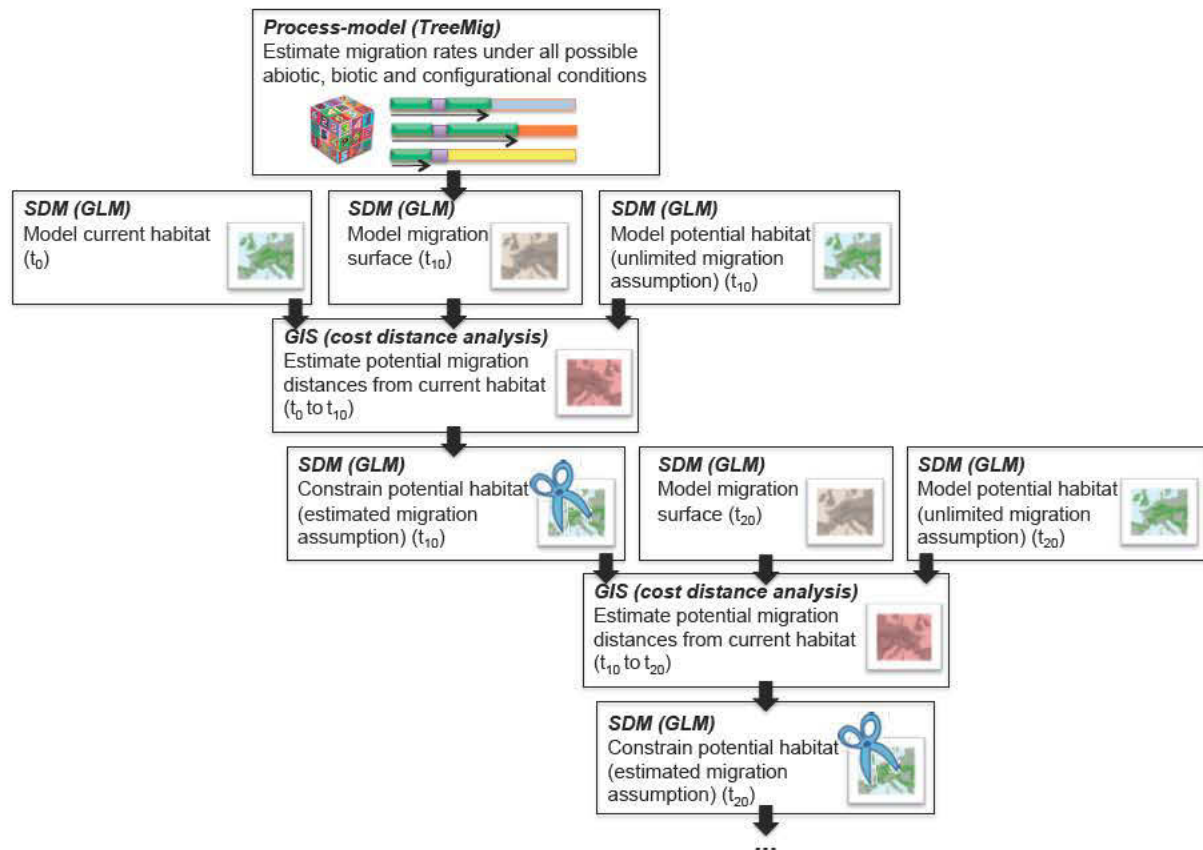


## Appendix S1. Model setup

We estimated with the process-model 'TreeMig' (Lischke *et al.*, 2006) migration rates under all possible combinations of abiotic (i.e. climate, topography and soil), biotic (i.e. inter-specific competition) and contextual (i.e. gap distance between forest patches) conditions. These dependencies were used to model a migration-rate surface over Europe for time  $t_0$  to  $t_{10}$ . This migration-rate surface was then combined with colonisable habitats at  $t_0$  with a cost distance analysis (ESRI, 2006) to constrain potential species distributions at  $t_{10}$  (i.e. 'unlimited migration') to colonizable habitats at  $t_{10}$  (i.e. 'realistic migration'). These steps were repeated for each decade until 2100 for A1fi/GRAS and B1/SEDG climate and land-use scenarios.



## References

- ESRI. (2006) ArcGIS 9.2. Environmental Systems Research Institute, Redlands, CA.
- Lischke, H., Zimmermann, N. E., Bolliger, J., Rickebusch, S. & Löffler, T. J. (2006) TreeMig: A forest-landscape model for simulating spatio-temporal patterns from stand to landscape scale. *Ecological Modelling*, **199**, 409-420.

## Appendix S2. Selection of tree species

We selected 14 species from the ICP Forest Level 1 dataset as focal species for our analyses, which were both abundant enough for fitting statistical models (occurring in >100 forest plots) and were calibrated in the dynamic model TreeMig: four coniferous trees (*Abies alba* Mill., *Larix decidua* Mill., *Picea abies* (L.) H. Karst., *Pinus sylvestris* L.) and ten deciduous trees (*Acer pseudoplatanus* L., *Alnus glutinosa* (L.) Gaertn., *Betula pendula* Roth, *Carpinus betulus* L., *Fagus sylvatica* L., *Fraxinus excelsior* L., *Populus tremula* L., *Quercus petraea* (Mattuschka) Liebl., *Quercus pubescens* Willd., *Quercus robur* L.).

To create the forest matrix in the TreeMig simulations, we used in addition to the selected 14 focal species, 16 fairly common species parameterized in TreeMig: *Pinus cembra* L., *Pinus mugo* Turra, *Taxus baccata* L., *Acer campestre* L., *Acer platanoides* L., *Alnus incana* (L.) Moench, *Alnus viridis* (Chaix) DC., *Castanea sativa* Mill., *Corylus avellana* L., *Populus nigra* L., *Salix alba* L., *Sorbus aria* (L.) Crantz, *Sorbus aucuparia* L., *Tilia cordata* P. Mill., *Tilia platyphyllos* Scop. and *Ulmus glabra* Huds..

### Appendix S3. Design of the migration experiments using TreeMig

Below, we describe the structure of the migration experiments, which we set up in order to estimate realistic and continent-wide migration rate surfaces depending on the climate, competition and habitat-connectivity for the 14 European tree species.

#### *Classifying environmental conditions*

We first analyzed the environmental space between 1950 and 2100 (current climate and A1Fi climate scenario); i.e. we analyzed the absolute minimum and maximum of decadal means and standard deviations of DDEG, MiWiT, DrStr and P0DrStr, which represent the environmental drivers of the TreeMig model (Lischke *et al.*, 2006). We then classified each of the mean variables (i.e. identified with 'av.')

 into 9 equally sized bins, the standard deviation variables (i.e. identified with 'sd.') into 5 equally sized bins, and P0DrStr into 3 equally sized bins. All combinations of bins that occurred under current or future climates were then used for the migration simulations ( $n = 6756$ ), allowing us to evaluate migration rates for all possible current and future climates. See the Data and Methods chapter in the text for a description of these climate variables.

#### *Setting up and running TreeMig*

We used the dynamic, lattice-based, spatio-temporal, height-structured tree species model TreeMig (Lischke *et al.*, 2006) to estimate the migration rates under these various climate conditions. TreeMig is one of very few models that have density-dependent population processes and seed dispersal implemented in a spatially explicit form (Thuiller *et al.*, 2008). The model calculates local tree species population dynamics in each 1 km<sup>2</sup> grid cell, including seed bank dynamics, intra-specific density regulation of the seeds, germination, growth, competition for light, mortality and seed production. The process functions depend on climate variables (DDEG, MiWiT, and DrSt) and on light. The vertical structure leads to hierarchical competition. Within-cell heterogeneity is depicted by frequency distributions of tree density and consequently light intensity. Parameters describing the local dynamics stem from the gap-model ForClim (Bugmann, 1994). Medium scale heterogeneity, e.g. a migration front within a cell, is not taken into account explicitly. Interactions between the cells occur by seed dispersal, described by a dispersal kernel consisting of two negative exponentials, accounting for frequent short- and rare long-distance dispersal events (Lischke & Löffler, 2006). The species-specific mean dispersal distances for wind-dispersed seeds were estimated from sinking velocities and wind speed distributions, and dispersal distances for ballistic and animal dispersal were derived from literature (Lischke & Löffler, 2006). Species parameters reflect trade-offs, e.g. between shade-tolerance and seed production, dispersal distance and maximum growth. Small-scale disturbances are depicted by randomly increased mortality of 80% at return intervals of 1000 years.

For our experiments, we set up transects with the dimension 1\*100 cells and a cell size of 1 km<sup>2</sup>. In order to avoid edge effects, we used cylindrical boundary conditions, assuming periodic boundaries on the narrow sides of the transect.

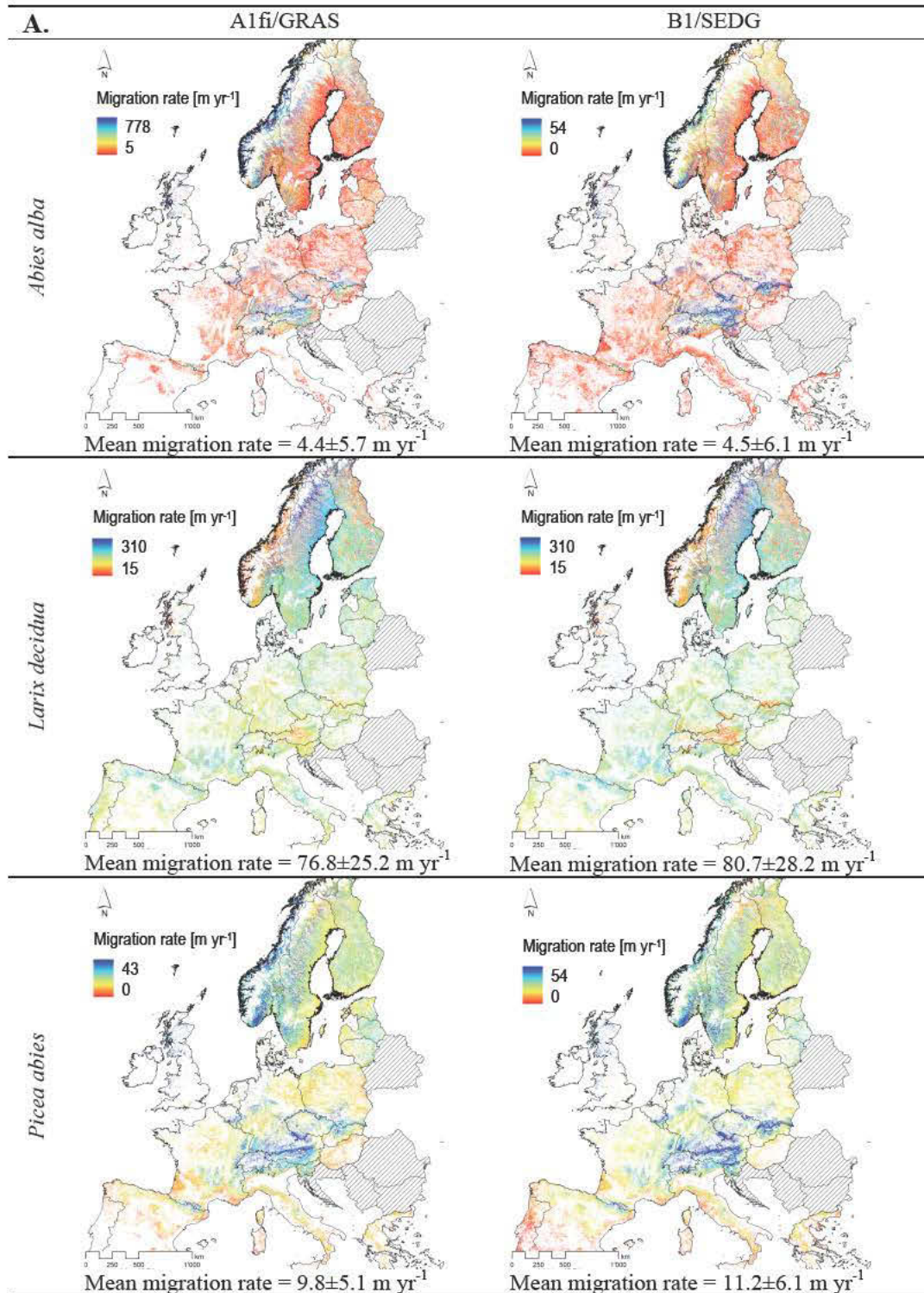
To test the effect of *climate*, we let each focal species migrate under each of the various climate conditions, which were held constant per run. A spin-up of 400 years was run to set up the initial forest conditions on the first cell under each climate condition. To test the effect of *competition*, we ran two tests where, in the first, we excluded the focal species during the spin-up run on all but the first cell, and in the second we kept all but the first cell empty. To test the effect of *habitat connectivity*, we introduced a gap of increasing size with each run along the transect, ranging from 1 km to 90 km in 1 km steps. This means that we repeated the two competition simulations for each gap distance. From these runs, we calculated the time-lags resulting from overcoming increasing gap distances compared to no gap conditions, and we measured the maximum gap distance the focal species was able to overcome. Under all combinations of conditions, we then let all species migrate for 1000 years after spin-up. We estimated the migration rate between the 10<sup>th</sup> (in order to reduce effects of the initialization period) and the 100<sup>th</sup> cell (or the last cell reached after 1000 years). When introducing gaps, we estimated the time lag at the first cell after the gap compared to no gap. Presence of a species was recorded if the species reached a biomass of 10 t/km<sup>2</sup> in a cell. In summary, we run simulations for 6756 climatic conditions, and for each set we ran one simulation without a gap, and an additional 90 simulations with increasing gap size each, both with and without forest as matrix to

migrate through, and for a total of 14 species each. This resulted in  $6756 \times 91 \times 2 \times 14 = 17'214'288$  simulations (or 1'229'592 simulations per focal species).

## References

- Bugmann, H. (1994) *On the ecology of mountainous forests in a changing climate: a simulation study*. Swiss Federal Institute of Technology ETH, Zürich, Switzerland.
- ESRI (2006) *ArcGIS 9.2*. Environmental Systems Research Institute.
- Lischke, H. & Löffler, T. (2006) Intra-specific density dependence is required to maintain diversity in spatio-temporal forest simulations with reproduction. *Ecological Modelling*, **198**, 341-361.
- Lischke, H., Zimmermann, N.E., Bolliger, J., Rickebusch, S. & Löffler, T.J. (2006) TreeMig: A forest-landscape model for simulating spatio-temporal patterns from stand to landscape scale. *Ecological Modelling*, **199**, 409-420.
- Thuiller, W., Albert, C., Araujo, M.B., Berry, P.M., Cabeza, M., Guisan, A., Hickler, T., Midgely, G.F., Paterson, J., Schurr, F.M., Sykes, M.T. & Zimmermann, N.E. (2008) Predicting global change impacts on plant species' distributions: Future challenges. *Perspectives in Plant Ecology Evolution and Systematics*, **9**, 137-152.

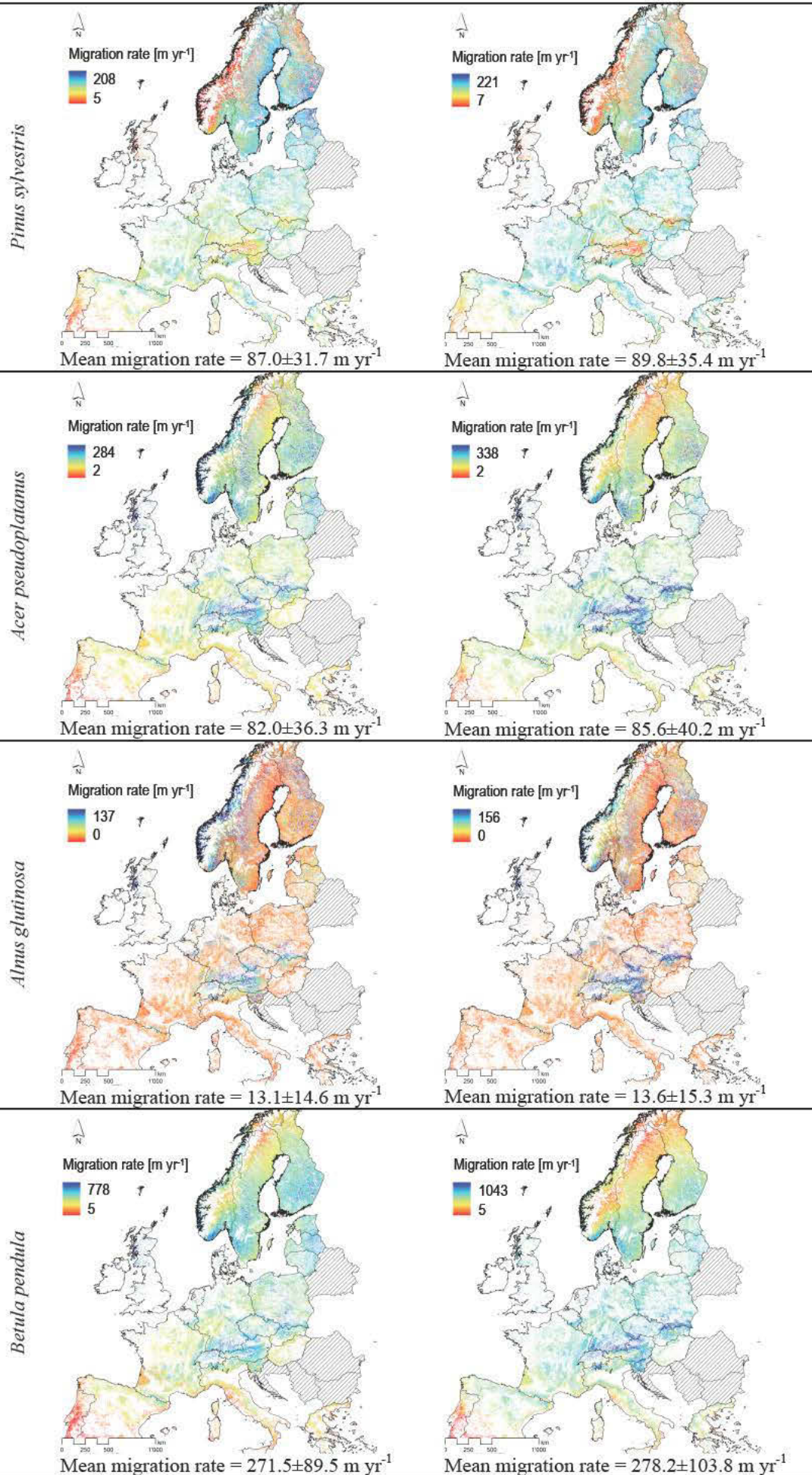
**Appendix S4.** Predicted mean migration rates for the 14 focal tree species (plates A-D) across potentially suitable habitats in the 21st century for the A1fi/GRAS and B1/SEDG climate and land-use scenarios. Minima and maxima of mean migration rates since 2000 are given in the legend; averages and standard deviation of mean migration rates within Europe are indicated below each figure. Countries white highlighted represent areas of model predictions; countries with stripes represent additional areas for model calibration.



**B.**

A1fi/GRAS

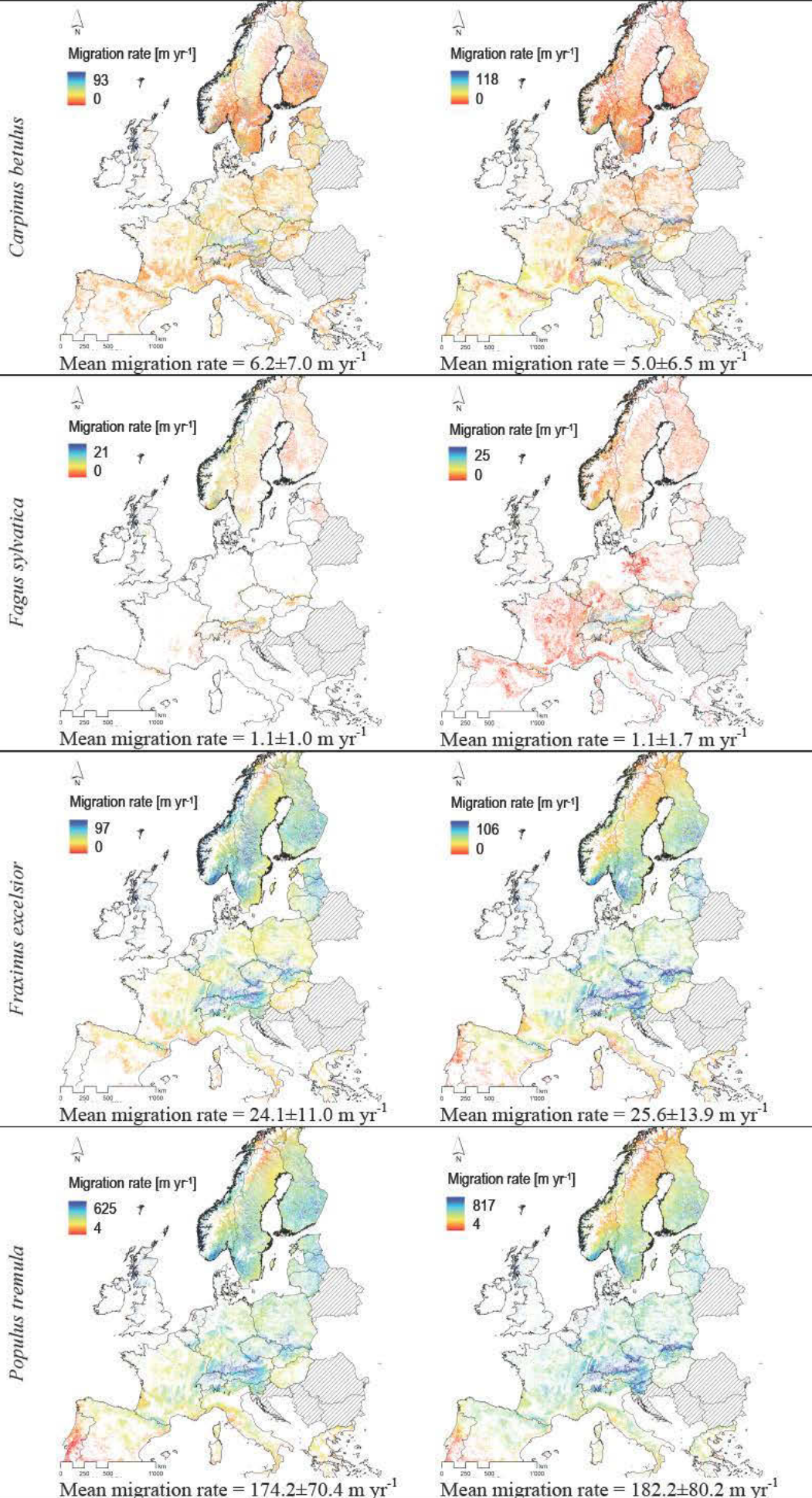
B1/SEDG



C.

A1fi/GRAS

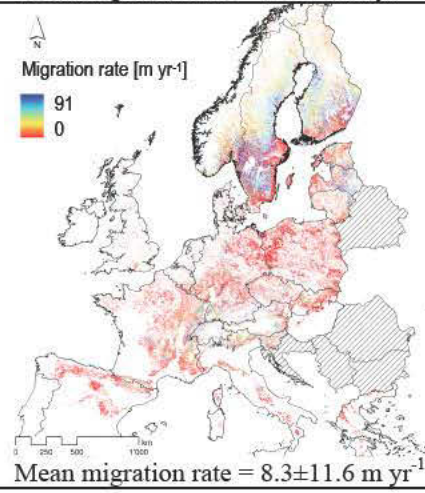
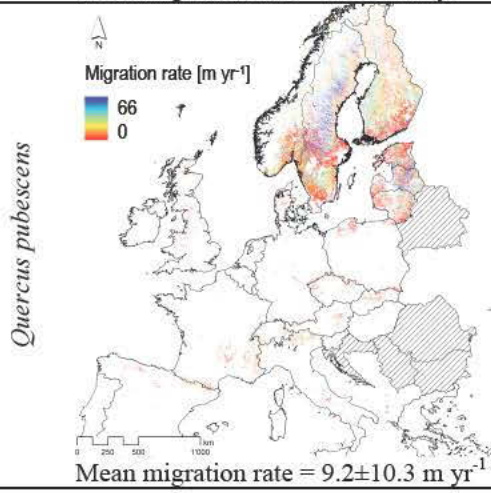
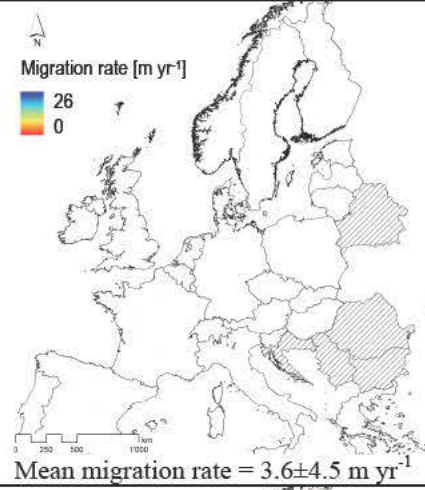
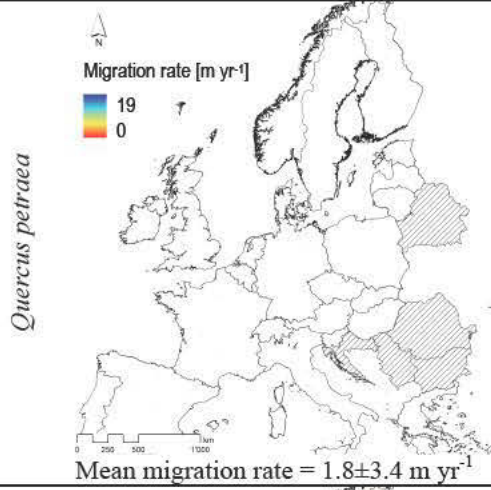
B1/SEDG



D.

A1fi/GRAS

B1/SEDG



**Appendix S5.** Predicted species distributions of the 14 focal tree species (plates A-D) until 2100 (A1fi/GRAS and B1/SEDG climate and land-use scenarios) for no, realistic and unlimited migration scenarios. Predicted species distributions assuming no migration are coloured blue (top layer), distributions assuming realistic migration red (medium layer) and distributions assuming unlimited migration scenarios yellow (bottom layer). Black points in the current distribution represent actual species occurrences in ICP Forest Level 1 data. Countries grey highlighted represent areas of model predictions; countries with stripes represent additional areas for model calibration.

