

## **Towards improving dynamic vegetation structure and distribution in DGVMs**

H. Lischke (1), M. Scherstjanoi (1), B. Poulter (1), and J. Kaplan (2)

(1) Swiss Federal Institute for Forest, Snow and Landscape Research, Ecological Process Modelling, Birmensdorf, Switzerland (lischke@wsl.ch), (2) ARVE research group, Ecole Polytechnique Federale de Lausanne, Switzerland

Besides current vegetation distribution, on time scales relevant for climate change also vegetation dynamics influences global biogeochemistry. In traditional DGVMs, vegetation dynamics is simulated by rules for competition between PFTs or simulating the dynamics of populations of average PFTs with temporally changing properties.

Yet, vegetation horizontal and vertical structure influences the light regime within the canopy, due to non-linear relationships the ecophysiology, via birth, growth and mortality the population dynamics of PFTs and consequently the biogeochemistry. By using average individuals, the current large-scale DGVMs neglect this horizontal and vertical structure. Other approaches (e.g. LPJ-GUESS, SEIB-DGVM) explicitly simulate structure by stochastic individuals or cohorts of PFTs. This however requires long computing times, restricting the models to small areas or coarse resolutions.

We present how to include structural dynamics in DGVMs by dynamically changing height and spatial distributions of plants. Simulations with this approach are considerably faster than simulations of the individual (or cohort) based model, however producing similar results.

On longer time scales, migration by seed dispersal can affect vegetation distribution and thus biogeochemistry and the feedbacks to the Earth System. With the above mentioned efficient distribution based approach, simulation of dispersal and migration becomes feasible for the regional to continental scale at sufficiently fine resolution (ca. 1km<sup>2</sup>). Simulations on a sample transect through Siberia with the forest landscape model TreeMig indicate that migration can slow down the climate change induced northward shift of the taiga into the tundra for centuries as compared to simulations where seeds are already present.

Global simulations with such fine resolutions are still hampered by immense computing times and memory requirements, despite parallelization and large computing clusters. Simulating migration with coarser grid cells, however, introduces large discretization errors. These can be limited by appropriate upscaling methods, which take into account the within cell migration speed depending on seed dispersal distance, the within-cell-pattern of habitat suitability and generation times. We present concepts and first results of upscaling migration by such metamodeling and multiscale methods.