

---

# Combining species distribution models with dispersal kernels to predict range shifts in wind-dispersed organisms under changing climate conditions

Florian Zanatta<sup>1</sup>, Robin Engler<sup>2</sup>, Flavien Collart<sup>1</sup>, Olivier Broenimann<sup>3</sup>, Jesús Muñoz<sup>4</sup>, Rubén Mateo<sup>5</sup>, Antoine Guisan<sup>3</sup>, and Alain Vanderpoorten<sup>\*1</sup>

<sup>1</sup>University of Liège – B22 Sart Tilman 4000 Liège, Belgium

<sup>2</sup>Swiss Institute of Bioinformatics – Quartier Sorge, Bâtiment Amphipole, 1015 Lausanne, Switzerland

<sup>3</sup>Spatial Ecology Group, Department of Ecology and Evolution, University of Lausanne – Biophore  
1015 Lausanne, Switzerland

<sup>4</sup>Real Jardín Botánico de Madrid – Plaza de Murillo, 2, 28014 Madrid, Spain

<sup>5</sup>Centro de Investigación en Biodiversidad y Cambio Global (CIBC-UAM), Universidad Autónoma de Madrid – 28049 Madrid, Spain

## Abstract

Species distribution models have been the most widely used tool to assess the impact of climate change on biodiversity patterns. One of the main assumptions of these models is that species are at equilibrium with their environment, as if they had no dispersal limitations. We test this hypothesis in spore-producing plants, wherein experimental evidence suggests that efficient short-distance dispersal coupled with random long-distance dispersal leads to an inverse isolation effect. Under the latter, a higher genetic diversity of colonizing propagules is expected with increasing isolation, counteracting differentiation beyond the range of short-distance dispersal. We employ spatial genetic structure analyses to show that the inverse isolation effect is not a rule in spore dispersal and that geographic distance remains a significant proxy of spore colonization rates, even in organisms with efficient dispersal capacities. We therefore present an integrative model to make predictions of range shifts in wind-dispersed organisms under changing environmental conditions, taking the spatial variation of species dispersal capacities into account. We combined species intrinsic biomechanical features (i.e., the settling velocity of diaspores and their release height) and environmental variables (i.e., canopy height, wind intensity and turbulence) into a mechanistic analytical long-distance dispersal model. We then implemented this dispersal model using a new version of MigClim's cellular automaton that allows migration simulations of species across the landscape under competing environmental change scenarios. The new version of MigClim was adapted for wind dispersal by implementing spatially-explicit dispersal kernels taking variation in wind conditions and canopy structure across the landscape into account. We show an example of application of this method to predict how climate changes will impact future distribution ranges in bryophytes, which are particularly sensitive to climatic variations due to their poikilohydric condition.

**Keywords:** dispersal ecology, dispersal kernel, climate change, spores

---

\*Speaker