Geophysical Research Abstracts
Vol. 12, EGU2010-3915, 2010
EGU General Assembly 2010

Using the VERHIB model to reconstruct palaeo-vegetation from preserved biomarker patterns

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One of the most detailed methods available to date to reconstruct past vegetation dynamics is the analysis of fossil pollen. Unfortunately, fossil pollen analysis does not distinguish beyond family or generic level in most cases, while its spatial resolution is limited amongst others by windblown dispersal of pollen, affecting the accuracy of pollen-based reconstructions of UFL positions. To overcome these limitations, we developed a new method based on the analysis of plant-specific groups of biomarkers preserved in suitable archives, such as peat deposits, that are unraveled into the plant species of origin by the newly developed VERHIB model. It consists of a linear forward model to describe the way in which a certain vegetation development over time at a certain location results in accumulation of biomarkers in a suitable archive such as marine or lacustrine sediment, peat deposit or soil. An inversion of the forward model is used to reconstruct paleovegetation on the basis of the observed accumulated biomarker signal. Tikhonov regularization is used to cope with non-uniqueness resulting from the combination of fine-scale output resolution and limited sample numbers. The Bayesian quality control technique by Ingleby & Lorenc is used to deal with heterogeneity in observational errors. Hard as well as soft constraints, derived from biological principles and dynamical models are included to ensure model results are always within physically and biologically realistic limits. Sequential Quadratic Programming is used as the solution technique for the combined non-linear constrained and regularized problem in VERHIB. Here we describe the model and present its first application to reconstruct palaeo-vegetation based on patterns of plant-specific n-alcohols and n-alkanes with chain lengths of C_{20}-C_{36} preserved in a peat sequence from a biodiversity hotspot of montane rainforest in the Ecuadorian Andes. We show how a combination of the new biomarker application using VERHIB with conventional pollen analysis from the same peat sequence yields a reconstruction of past vegetation compositions with previously unattainable detail.