Alexander Skupin
Luxembourg Centre for Systems Biomedicine, University of Luxembourg, Luxembourg
e-mail: alexander.skupin@uni.lu
Moritz Schütte
MPI of Molecular Plant Physiology, Potsdam-Golm, Germany
e-mail: schuette@mpimp-golm.mpg.de
Oliver Ebenhöh
Institute of Complex Systems and Mathematical Biology, University of Aberdeen, U.K.
e-mail: ebenhoeh@abdn.ac.uk

Modeling the dynamics of enzyme-pathway coevolution

Metabolic pathways must have coevolved with the corresponding enzyme gene sequences. However, the evolutionary dynamics ensuing from the interplay between metabolic networks and genomes is still poorly understood. Here, we present a computational model that generates putative evolutionary walks on the metabolic network using a parallel evolution of metabolic reactions with their catalyzing enzymes. Starting from an initial set of compounds and enzymes, we expand the metabolic network iteratively by adding new enzymes with a probability that depends on their sequence-based similarity to already present enzymes. Thus, we obtain simulated time courses of chemical evolution in which we can monitor the appearance of new metabolites, enzyme sequences, or even entire organisms. We observe that new enzymes do not appear gradually but rather in clusters which correspond to enzyme classes. A comparison with Brownian motion dynamics indicates that our system displays biased random walks similar to diffusion on the metabolic network with long range correlations. This suggests that a quantitative molecular principle may underlie the concept of punctuated equilibrium as enzymes occur in bursts rather than by phyletic gradualism. Moreover, the simulated time courses lead to a putative time-order of enzyme and organism appearance. Among the patterns we detect in these evolutionary trends is a significant correlation between the time of appearance and their enzyme repertoire size. Hence, our approach to metabolic evolution may help understand the rise in complexity at the biochemical and genomic levels.