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# Tracking the Genetic Legacy of Past Human Populations through the Grid

*Wednesday, 26 August 2009 09:45 (45 minutes)*

Knowing the past demography of human populations over the last 100'000 years is a fascinating, but difficult endeavor. Inferring this past demography has been classically approached through data from the archaeological record, but more recently by the use of genetic data from contemporary samples. Building realistic demographic models at the continental scale is also a necessary step toward the improvement of current genomic methods aiming at finding genes under selection, which may be linked to genetic adaptations or disorders. In light of recent advances in Bayesian statistical inference, we discuss here the importance of considering spatially-explicit approaches for modeling population expansion and dispersal. Due to the large parameter space to explore and the computationally intensive spatial simulations, grid computing is an important tool to be able to compare several realistic scenarios for human evolution.

Our main simulation tool, SPLATCHE (SPatiaL And Temporal Coalescences in Heterogeneous Environment), will be presented. SPLATCHE has been ported to the EGEE infrastructure. We will discuss the porting process and give several examples of how the tool has been used to shed light on important demographic and genetic processes that have occur during the evolution of our species.

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