Bayesian inference for correlated diffusions in shape spaces with applications to phylogenetics

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We consider Bayesian phylogenetics using models of correlated evolution for positions in DNA or protein sequences and corresponding 3D positions in protein structures. Addition of correlation signficantly enhances the realism of the model, but raises significant computational challenges; in particular convolution with standard birth-death process models for insertion and deletion leads to intractable likelihoods that must be approximated by MCMC or sequential MC methods. We demonstrate the effect of adding correlation on inferred evolutionary divergence times for proteins studied previously under independent models. We compare with results of exact calculations on models where correlation is limited by block structures.