Assessing substitution Sequence simulation Estimation of model accuracy: data-specific models comparing to the simulation model and simulation tree Constrained ML analyses of the simulated data sets using the simulation tree, data-specific models, gcpREV, cpREV, and Estimate data-specific WAG Simulate sequence data amino-acid substitution using the simulation tree PCA ordination of the models from each and the gcpREV estimated data-specific simulated data set using the (simulation model) with models, gcpREV, cpREV, simulation tree and five 400, 1500, and 8000 sites, and WAG methods, namely, Codeml, with 100 replicates for FastMG, IQ-TREE, P4-ML, each length Unconstrained ML and P4-BI analyses of the simulated data sets using dataspecific models, gcpREV, cpREV, and WAG