Positive selection analysis

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Abstract

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Protocol

Protein sequences were aligned by PROBCONS (version 1.12) using the default parameters,except for the option of iterative refinement, for which we used 1,000 iterations.

Step 1.

   SOFTWARE PACKAGE (Linux -)

   PROBCONS, 1.12 ↗

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we obtain the conserved blocks from the sequence alignment using Gblocks (version 0.91b).

Step 2.

   SOFTWARE PACKAGE (Linux -)

   Gblocks, 0.91b ↗

   http://molevol.cmima.csic.es/castresana/Gblocks_server.html

We use jModelTest (version 2.1.6) to find the best model according to the Bayesian Information Criterion

Step 3.

   SOFTWARE PACKAGE (Linux -)

   jModelTest, 2.1.6 ↗

   http://evomics.org/learning/phylogenetics/jmodeltest/

We use PhyML (release 20141106) to reconstruct the phylogenetic tree under the best model, with bootstrapping of 1,000 replicates.

Step 4.

   SOFTWARE PACKAGE (Linux -)

   PhyML, 3.0 ↗

   http://www.atgc-montpellier.fr/phyml/

Finally, certain branches selected from the phylogenetic tree were examined in a positive selection analysis using PAML (version 4.8) and a branch-site model

Step 5.

   SOFTWARE PACKAGE (Linux -)

   PAML, 4.5 ↗