

**Using sensitive methods for positive selection detection to detect *(and filter out)* coding sequence alignment errors**

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## Hypothesis Testing using Phylogenies

An open-source software package

for comparative sequence analysis  
using stochastic evolutionary models

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- Evolutionary analyses of multiple sequence alignments
- Specific focus on coding sequence evolution

# Datamonkey

A Collection of State of the Art Statistical Models and Bioinformatics Tools

What evolutionary process would you like to detect?

Selection

Recombination