PSODA: Open Source Phylogenetic Search and DNA Analysis

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PSODA
Open Source Phylogenetic Search and DNA Analysis

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http://dna.cs.byu.edu/psoda --- svn co http://dna.cs.byu.edu/opensvn/psoda

Abstract

PSODA (s0-d0) is an open source (GPL v2) sequence analysis package that implements sequence alignment using biochemical properties, phylogeny search with parsimony or maximum likelihood criteria and selection detection using biochemical properties (TreeSAAP). PSODA is compatible with PAUP® and the search algorithms are competitive with those in PAUP®. PSODA also adds a basic scripting language to the PAUP block, making it possible to easily create advanced meta-searches. Because PSODA is open-source, we have also been able to easily add in advanced search techniques and characterize the benefits of various optimizations. PSODA is available for Macintosh OS X, Windows, and Linux.

Advantages of PSODA
• High Performance
• Open Source (:- FREE :-)• Modular Design (easy algorithm development)
• Advanced Scripting Language
  • makes advanced meta-searches simple
• Reads and Executes PAUP nexus files
• PSODA is competitive with PAUP®

PSODA Features
• Parsimony and Likelihood (RAxML) search
• Bayesian methods (Mr. Bayes)
• Consensus (strict and majority rules)
• Selection Detection (TreeSAAP)
• Graphical User Interface
• Binaries for Mac OS X, Windows and Linux
• Object-oriented C++
  • easy to contribute to new algorithm development
• Available via subversion
  • svn checkout http://dna.cs.byu.edu/opensvn/psoda

Advanced Scripting Language
• Added functionality for PAUP blocks.
• Decision Statements & Loops
• Advanced Functions & User-defined Functions
• Easily Extensible
• Easy scripting of advanced meta-searches such as:
  • Ratchet (Parsimony and Likelihood)
  • DCM and more.

PAUP® Ratchet

```
BEGIN PAUP;
set criterion=parsimony;
set maxtrees=1;
BEGIN Ratchet
begin randomReweight
numChars = getWeightsLength();
numWeights = numChars / percent;
j = 0;
while (j < numWeights)
   weight = random(max = range);
   col = random(max = numChars) + 1;
   weight:col;
j++;
end;
END Ratchet;
```

PSODA Likelihood Ratchet

```
BEGIN PAUP;
set criterion=likelihood;
set maxtrees=1 reps = 5;
BEGIN Ratchet
begin randomReweight
   numChars = getWeightsLength();
   numWeights = numChars / percent;
   while (true)
      randomReweight(percent = 10);
      set criterion=parsimony;
      hsearch start = current swap = tbr;
set criterion=likelihood;
      hsearch start = current swap = tbr;
end;
```

Repeated text must continue. However, it is unclear when to stop.