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# PSODA: Open Source Phylogenetic Search and DNA Analysis

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**Authors**

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# PSODA

## Open Source Phylogenetic Search and DNA Analysis

Quinn Snell, Mark Clement, Kenneth Sundberg

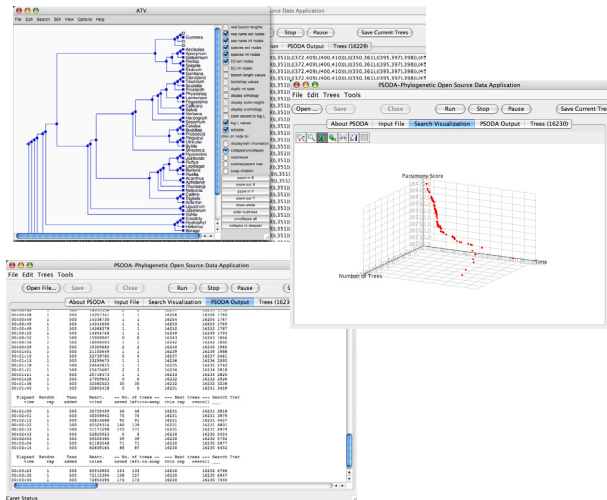
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<http://dna.cs.byu.edu/psoda> --- svn co <http://dna.cs.byu.edu/opensvn/psoda>

### Abstract

PSODA (sō-də) 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.

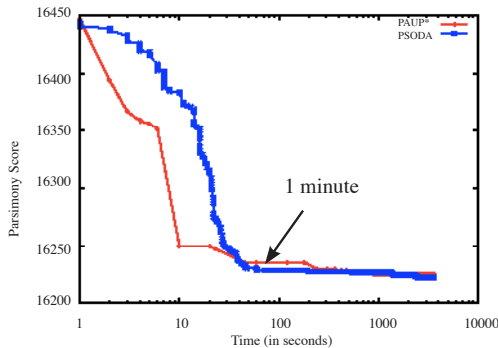


### Advantages of PSODA

- 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\*

### 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

```

%%%% Ratchet
%% criterion=comparimony ;
%% nreps=100 ;
%% nsearches = 10 ;
search start=current swap=PSO ;
weights 2 : 1 16 20 27 31 34 40 50 52 54 57 62 63 64 65 70 77 84 91 92 100 103 107 110 117 121 ;
125 128 137 139 143 146 150 154 158 162 166 170 174 178 183 187 191 195 199 204 208 212 216 220 225 231 241 ;
225 228 230 237 238 240 241 244 246 250 254 255 258 269 276 278 284 288 291 294 295 297 309 310 315 ;
319 323 325 328 332 336 340 344 348 352 354 355 359 362 366 370 373 376 380 384 388 390 394 401 408 412 ;
416 422 426 428 432 436 440 444 448 452 456 460 464 468 472 476 480 484 488 492 496 500 ;
search start=current swap=PSO ;
%%
%%%% RatchetL
weights likeli ;
search start=current swap=PSO ;
%%
weights 2 : 1 17 20 26 31 34 39 44 46 48 51 53 56 57 61 62 63 64 65 71 78 80 85 87 91 94 100 103 107 110 117 121 ;
125 128 130 133 136 140 144 148 152 156 160 164 168 172 176 180 184 188 192 196 200 204 208 212 216 220 224 ;
228 232 236 240 244 248 252 256 260 264 268 272 276 280 284 288 292 296 300 304 308 312 316 320 324 328 ;
332 336 340 344 348 352 356 360 364 368 372 376 380 384 388 392 396 400 404 408 412 416 420 424 428 ;
432 436 440 444 448 452 456 460 464 468 472 476 480 484 488 492 496 500 ;
search start=current swap=PSO ;
%%
weights 2 : 2 3 9 20 22 24 26 28 30 32 34 36 38 40 42 44 46 48 50 52 54 56 58 60 62 64 66 68 70 72 74 76 78 80 82 84 86 88 90 92 94 96 98 100 102 104 ;
106 108 110 112 114 116 118 120 122 124 126 128 130 132 134 136 138 140 142 144 146 148 150 152 154 156 158 160 162 164 166 168 170 172 174 176 178 180 182 184 186 188 190 192 194 ;
196 198 200 202 204 206 208 210 212 214 216 218 220 222 224 226 228 230 232 234 236 238 240 242 244 246 248 250 252 254 256 258 260 262 264 266 268 270 272 274 276 278 280 282 284 286 288 290 292 294 ;
296 298 300 302 304 306 308 310 312 314 316 318 320 322 324 326 328 330 332 334 336 338 340 342 344 346 348 350 352 354 356 358 360 362 364 366 368 370 372 374 376 378 380 382 384 386 388 390 392 394 ;
396 398 400 402 404 406 408 410 412 414 416 418 420 422 424 426 428 430 432 434 436 438 440 442 444 446 448 450 452 454 456 458 460 462 464 466 468 470 472 474 476 478 480 482 484 ;
486 488 490 492 494 496 500 ;
search start=current swap=PSO ;
%%
weights 2 : 1 5 17 22 26 31 34 39 44 46 48 51 53 56 57 61 62 63 64 65 71 78 80 85 87 91 94 100 103 107 110 117 121 125 128 ;
130 133 136 140 144 148 152 156 160 164 168 172 176 180 184 188 192 196 200 204 208 212 216 220 224 228 232 236 240 244 248 252 256 260 264 268 272 276 280 284 288 292 296 300 304 308 312 316 ;
320 324 328 332 336 340 344 348 352 356 360 364 368 372 376 380 384 388 392 396 400 404 408 412 416 420 424 428 432 436 440 444 448 452 456 460 464 468 472 476 480 484 488 492 496 500 ;
search start=current swap=PSO ;
%%
weights 2 : 2 3 9 20 22 24 26 28 30 32 34 36 38 40 42 44 46 48 50 52 54 56 58 60 62 64 66 68 70 72 74 76 78 80 82 84 86 88 90 92 94 96 98 100 102 104 ;
106 108 110 112 114 116 118 120 122 124 126 128 130 132 134 136 138 140 142 144 146 148 150 152 154 156 158 160 162 164 166 168 170 172 174 176 178 180 182 184 186 188 190 192 194 ;
196 198 200 202 204 206 208 210 212 214 216 218 220 222 224 226 228 230 232 234 236 238 240 242 244 246 248 250 252 254 256 258 260 262 264 266 268 270 272 274 276 278 280 282 284 286 288 290 292 294 ;
296 298 300 302 304 306 308 310 312 314 316 318 320 322 324 326 328 330 332 334 336 338 340 342 344 346 348 350 352 354 356 358 360 362 364 366 368 370 372 374 376 378 380 382 384 386 388 390 392 394 ;
396 398 400 402 404 406 408 410 412 414 416 418 420 422 424 426 428 430 432 434 436 438 440 442 444 446 448 450 452 454 456 458 460 462 464 466 468 470 472 474 476 478 480 482 484 ;
486 488 490 492 494 496 500 ;
search start=current swap=PSO ;
%%
weights 2 : 5 6 19 24 27 31 34 37 40 43 46 49 52 55 58 61 64 67 70 73 76 79 82 85 88 91 94 97 100 103 106 109 112 115 118 121 124 127 130 133 136 139 142 145 148 151 154 157 160 163 166 169 172 175 178 181 184 187 190 193 196 199 202 205 208 211 214 217 220 223 226 229 232 235 238 241 244 247 250 253 256 259 262 265 268 271 274 277 280 283 286 289 292 295 298 301 304 307 310 313 316 319 322 325 328 331 334 337 340 343 346 349 352 355 358 361 364 367 370 373 376 379 382 385 388 391 394 397 400 403 406 409 412 415 418 421 424 427 430 433 436 439 442 445 448 451 454 457 460 463 466 469 472 475 478 481 484 487 490 493 496 499 502 505 ;
search start=current swap=PSO ;
%%
weights likeli ;
search start=current swap=PSO ;
end ;

```

### PSODA Likelihood Ratchet

```

BEGIN PAUP;
begin randomReweight
numChars = getWeightsLength();
numWeights = numChars / percent;

j = 0;
while (j < numWeights)
weight = random(max = range);
col = random(max = numChars) + 1;
weights weight:col;
j++;
endwhile;
end;

set maxtrees = 1 nreps = 5;
while (true)
set criterion=parsimony;
hsearch start = stepwise swap = tbr;
range = 3;

weights reset;

set criterion=likelihood;
hsearch start = current swap = tbr;
endwhile;
end ;

```

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

### 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>



<http://dna.cs.byu.edu/psoda>

