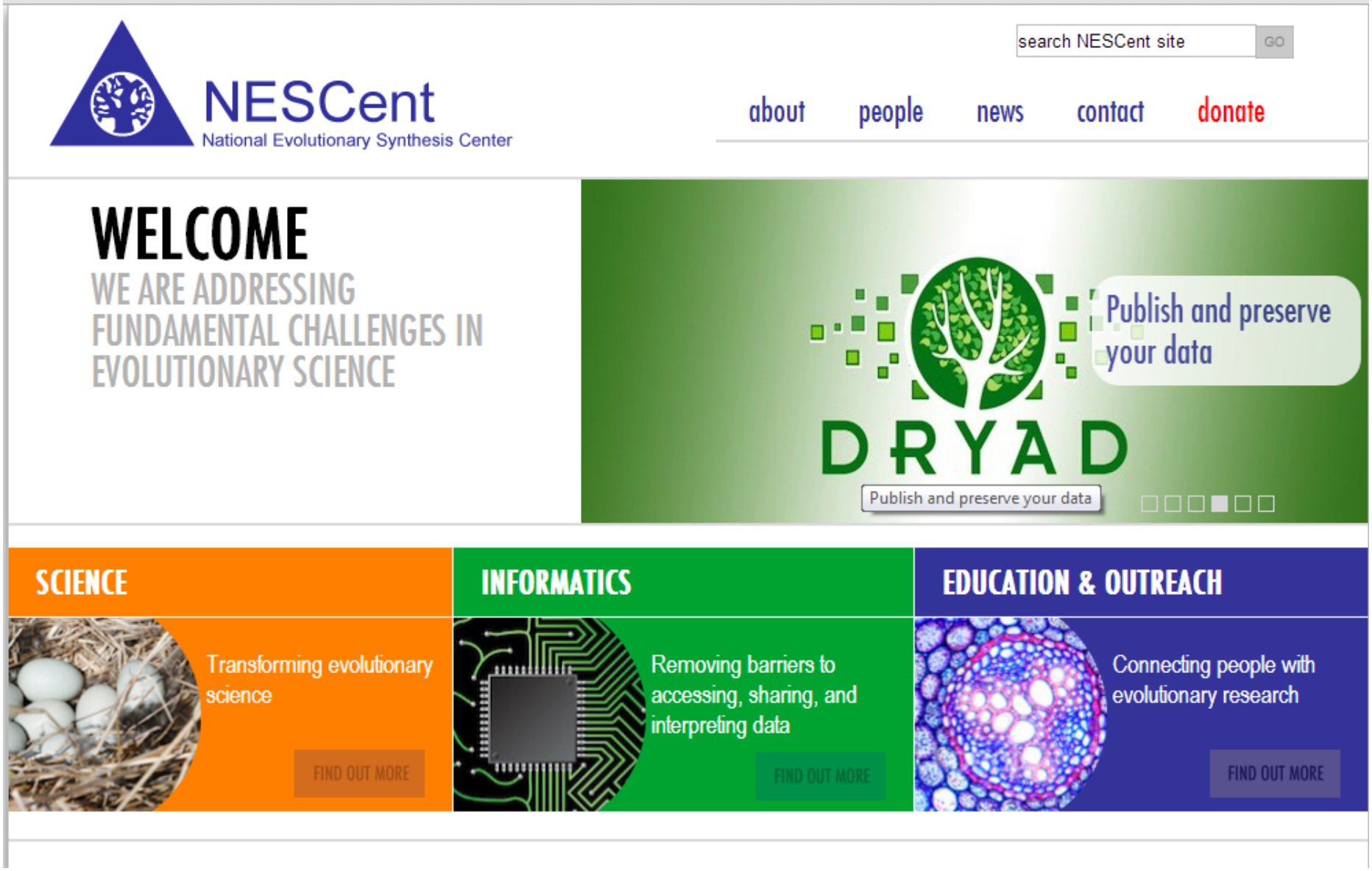
What is phyloinformatics?

- "An information system that is queried using the hieratical relationships of life"
  - Cracraft 2002

- "Informatics of managing, querying, and manipulating phylogenetic data"
  - NESCent, PhyloWS

NESCent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National Evolutionary Synthesis Center
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Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

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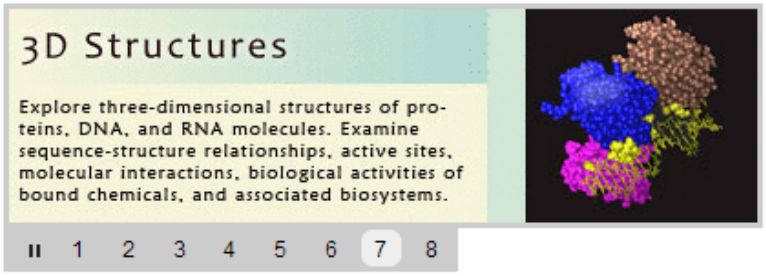
Get Started

- Tools: Analyze data using NCBI software
- Downloads: Get NCBI data or software
- How-To's: Learn how to accomplish specific tasks at NCBI
- Submissions: Submit data to GenBank or other NCBI databases



Popular Resources

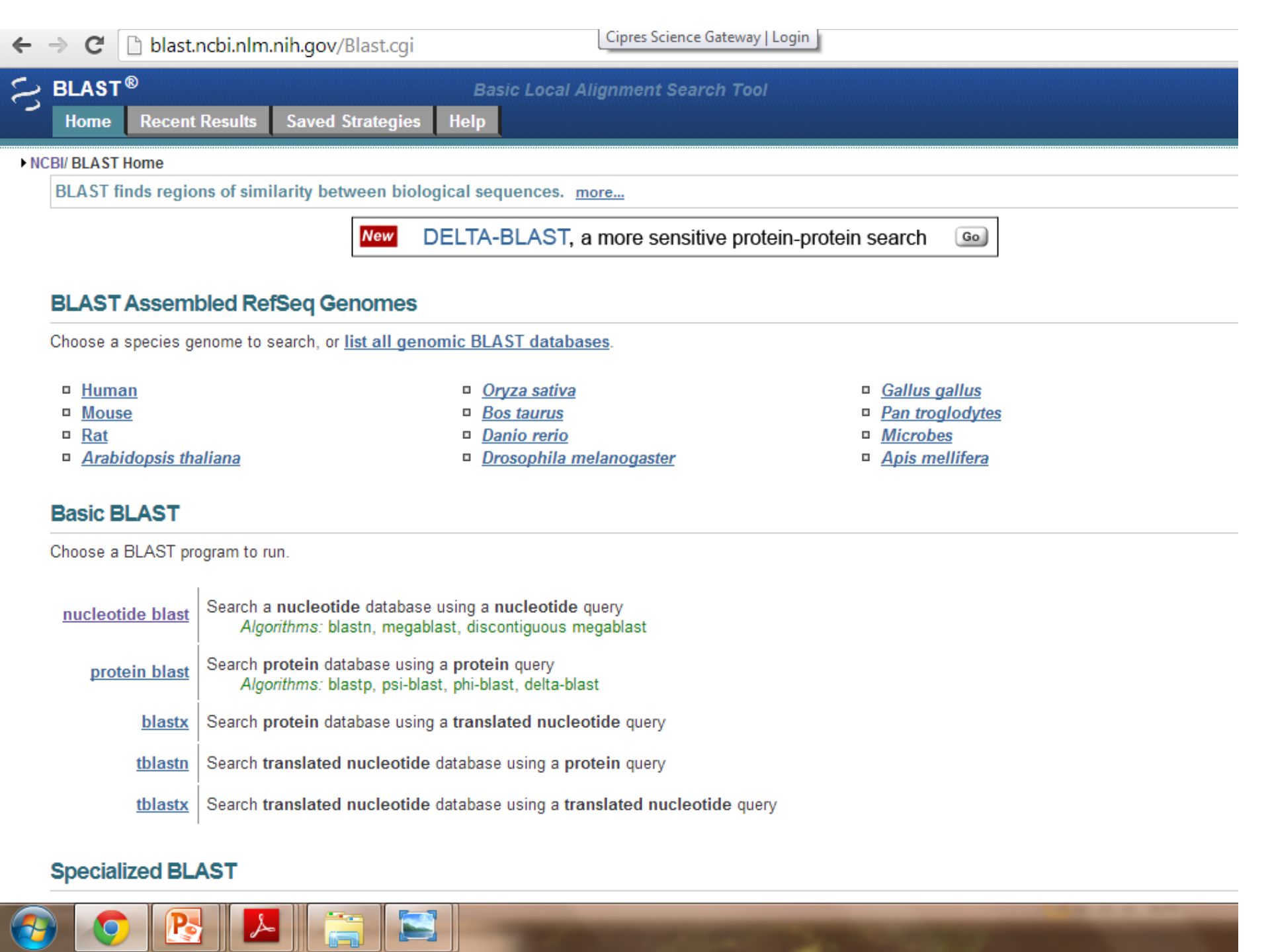
PubMed
Bookshelf
PubMed Central
PubMed Health
BLAST
Nucleotide
Genome
SNP
Gene
Protein
PubChem

NCBI Announcem

RefSeq release 61 n

The complete RefSe
contains 41,958,567

A new NCBI Insights
of NCBI Data for scie


blast.ncbi.nlm.nih.gov/Blast.cgi
Cipres Science Gateway | Login
BLAST®
Basic Local Alignment Search Tool
Home
Recent Results
Saved Strategies
Help
NCBI/ BLAST Home
BLAST finds regions of similarity between biological sequences. more...
New
DELTA-BLAST, a more sensitive protein-protein search
Go
BLAST Assembled RefSeq Genomes
Choose a species genome to search, or list all genomic BLAST databases.
Human
Mouse
Rat
Arabidopsis thaliana
Oryza sativa
Bos taurus
Danio rerio
Drosophila melanogaster
Gallus gallus
Pan troglodytes
Microbes
Apis mellifera
Basic BLAST
Choose a BLAST program to run.
nucleotide blast
Search a nucleotide database using a nucleotide query
Algorithms: blastn, megablast, discontiguous megablast
protein blast
Search protein database using a protein query
Algorithms: blastp, psi-blast, phi-blast, delta-blast
blastx
Search protein database using a translated nucleotide query
tblastn
Search translated nucleotide database using a protein query
tblastx
Search translated nucleotide database using a translated nucleotide query
Specialized BLAST

Lineage (full): root; cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gna
Neopterygii; Teleostei; Elopocephala; Clupeocephala; Otocephala; Ostariophysi; Otophysi; Cypriniphysi; Cypriniformes; Cyprinoidea; Cyprinidae

- **Barbus** (barbels) *Click on organism name to get more information.*
  - **Barbus ablabes**
  - **Barbus cf. aboinensis BOLD:AAI7638**
  - **Barbus albanicus**
  - **Barbus andrewi** (Cape whitefish)
  - **Barbus anoplus** (chubbyhead barb)
  - **Barbus antinorii** (Algerian barb)
  - **Barbus apoensis**
  - **Barbus balcanicus**
  - **Barbus barbus** (barbel)
    - **Barbus barbus barbus**
  - **Barbus barbus x Barbus meridionalis**
  - **Barbus bigornei**
  - **Barbus biscarensis** (Algerian barb)
    - **Barbus biscarensis amguidensis** (Algerian barb)
    - **Barbus biscarensis biscarensis** (Algerian barb)
  - **Barbus borysthenicus**
  - **Barbus brachycephalus** (Aral barbel)
  - **Barbus bynni**
    - **Barbus bynni bynni**

www.phylo.org/portal2/login!input.action

CIPRES SCIENCE GATEWAY

iPlant Collaborative

XSEDE Extreme Science and Engineering Discovery Environment

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Missing results?
Send us the job handle, and we may be able to help.

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- Known Issues
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- Enabled Publications

The CIPRES Science Gateway now offers BEAST, as well as really fast RAxML and MrBayes codes.

First Time Users: Please review the XSEDE Primer and our Fair Use Policy.

CIPRES Login:

*Username:

*Password:

Login Reset

Forgot Password?

iPlant users login here:

iPlant Collaborative
Empowering A New Plant Biology

What is this?

Not registered yet?

Register | Proceed without Registering

Status: XSEDE submissions working normally.

CIPRES Gateway News

Command Change Issues for MB 3.2.1
8/23/2013

CIPRES now has a Google Group.
6/13/2013

Supported Publications (Jun): Coral-dwelling Gobies Radiated More Recently Than Host Corals, more...
7/1/2013

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Main Page

Contents [hide]

Welcome to the GARLI support wiki!

What is GARLI?

GARLI is a program that performs phylogenetic inference using the maximum-likelihood criterion. Several sequence types are supported, incl
support for partitioned models and morphology-like datatypes. It is usable on all operating systems, and is written and maintained by Derrick
garli.support{at}gmail{dot}com).

Obtaining GARLI

Current Version

- **GARLI 2.0 has been released (April 2011)! You can download it at the GARLI page on Google Code: http://garli.go**
  GARLI 2.0 is first "official" release including partitioned models. It is a merging of official release 1.0 and beta version GARLI-PART 0.97.
  backwards compatible with all configuration files and datasets that were used with either Version 1.0 or GARLI-PART 0.97. See this page

Older Versions

- The previous version 1.0 (Dec 09) can still be found on Google Code: http://garli.googlecode.com

http://evolution.genetics.washington.edu/phylip/software.html

Search “phylogenetic software” in Google

Owing to other pressures on my time, I cannot devote time to searching for new programs, so **their authors are begged to (please submission form instead**. That form will be found at the "Submitting" link below. If you are upset that your program is not include much trouble for you to fill out the submission form, then I will not listen to you. This list of software is now aging and its links are more and more outdated. I will make attempts to fix them when I can. If anyone else wants to help with this, let me know.

Here are 392 phylogeny packages and 54 free web servers, (almost) all that I know about. It is an attempt to be completely comprehensive. I have not made any attempt to exclude standard of quality or importance. Updates to these pages are made roughly monthly. Here is a "waiting list" of new programs waiting to have their full entries constructed. Many of th on the web, and some of the older ones are also available from ftp server machines.

The programs listed below include both free and non-free ones; in some cases I do not know whether a program is free. I have listed as free those that I knew were free; for the othe

BioEdit v7.2.3

last update 9/24/2013

Tom Hall
Ibis Biosciences
Thomas.Hall@abbott.com

To the RNaseP Database
Download

Back to BioEdit Main Page

BioEdit is a mouse-driven, easy-to-use sequence alignment editor and sequence analysis program designed and written by a graduate student who knows how frustrating and time consuming it can be to rely upon word-processors and command-line programs for sequence manipulation. BioEdit is intended to supply a single program that can handle most simple sequence and alignment editing and manipulation functions that researchers are likely to do on a daily basis, as well as a few basic sequences analyses.

BioEdit offers a variety of useful features:

- Four modes of manual alignment: select and slide, dynamic grab and drag, gap insert and delete by mouse click, and on-screen typing which behaves like a text editor.
- In-color alignment and editing with separate nucleic acid and amino acid color tables and full control over background colors.
- Plasmid drawing interface for automated creation of plasmid vector graphic from a DNA sequence. Easily mark positions, add features with arrows and curved boxes, and mark restriction enzyme cut sites. Also show detail of polylinker and draw moveable arrows and shapes with drawing tools.
- Dynamic information-based alignment shading.
- Point-and-click color table editing
- Display and print ABI chromatograms with professional-looking output.
- Group sequences into groups or families.
- Lock alignment of grouped sequences for synchronized hand alignment adjustments.
- Annotate sequences with graphical features with dynamic view in alignment windows including feature annotation information tooltips.
- Lock sequences to prevent accidental edits.
- Specify characters to be considered valid for calculations in amino acid and nucleotide sequences.
- Sort sequences by name, LOCUS, DEFINITION, ACCESSION, PID/NID, REFERENCES, COMMENTS or by residue frequency in a selected column.

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DOI:10.1093/sysbio/syt001
Advance Access publication January 9, 2013

Continental Diversification of an African Catfish Radiation (Mochokidae: *Synodontis*)

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Associate Editor: Thomas Near

chains). Convergence of individual runs was assessed using TRACER version 1.5 (Rambaut and Drummond 2009) and any remaining burn-in discarded prior to tree construction. Branch support was determined by Bayesian Posterior Probabilities (BPPs) and was further evaluated by Maximum Likelihood (ML) bootstrap (BS) support. ML analyses were implemented using the parallel version of the program GARLI 2.0 (Zwickl 2006) on the Linux cluster applying the data partitions from PartitionFinder and running 1000 BS replicates.

Bayesian inferences (BI). ML analyses were run using GARLI and GARLI-PART (Genetic Algorithm for Rapid Likelihood Inference, ver. 0.97; Zwickl, 2006), which provides considerable advantages over PAUP in terms of computational efficiency and allows partitioning of the data. It uses a genetic algorithm that finds the tree topology, branch lengths and model parameters that maximise ln(L) simultaneously (Zwickl, 2006). BI analysis was performed using MrBayes version 3.0b4 (Huelsenbeck and Ronquist, 2001). With the two probabilistic methods, the choice of an adequate sequence evolution model remains a crucial issue. The search for the optimal model of nucleotide substitution was conducted using MrModeltest 2.0 (Nylander, 2004) based on the Akaike Information Criterion (AIC) values (Posada and Buckley, 2004).

In our Bayesian analysis, we explored different data partitioning strategies on the combined data set to improve the fit of the substitution model to the data. Four partitioning strategies were used. In the first approach (four partitions: 4P), we ascertained the best-fit model and model parameters based on the AIC values for each codon position for Cyt *b* and for the unpartitioned gene rps7. Within the MrBayes analysis, each codon position of the Cyt *b* was given a separate (unlinked) model. We ran a second MrBayes analysis with the dataset divided into three partitions (3P) corresponding to first and second positions *versus* the third for Cyt *b* gene, while the rps7 was unpartitioned. A third strategy consisted of dividing the dataset into two partitions corresponding to the two genes (2P), and in the fourth strategy, the data were unpartitioned (0P). Searches were conducted using the default parameters, starting with random trees, including three heated and one cold chain for 5,000,000 generations in which parameters and trees were sampled every 100 generations. The log likelihood was plotted against

Lets start working with the our sequences

Open up the GeneStudio project within the phyloinformatics folder

Additional resources

Converting files into other formats

http://www.phylogeny.fr/version2_cgi/data_converter.cgi

Models of evolution

https://code.google.com/p/jmodeltest2/

RAxML

http://embnet.vital-it.ch/raxml-bb/index.php