



Goals

- Goals
- Data
- Products
- Challenges
- Responses

"The goal of AmphibiaTree is no less than a comprehensive tree of all amphibians.

...We envision not simply a skeletal branchwork, but also a tree heavy with foliage and inflorescence, rich in hue and texture."



Steering Committee

Goals

Data

Products

Challenges

Responses

University of Texas, Austin

- David Cannatella
- David Hillis

University of California, Berkeley

- Marvalee Wake
- David Wake
- Harvard University
 - Jim Hanken
- University of Kansas
 - Linda Trueb
 - Rafe Brown



Data and Analysis

Goals

Data

Products

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Responses

Integration of Datasets

- Biodiversity, Genomics, Evolutionary Morphology, Paleontology, Development
- Computational Biology
 - Tree Visualization
 - Visualization of Morphology

Genomic Analysis

• Secondary structure, gene order, etc.



Products

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- Phylogenies
- Web Resources
 - AmphibiaWeb (David Wake)
 - Tree of Life (W. & D. Maddison)
 - Human Resources
 - Training of students through exchanges
 - Community workshops



AmphibiaWeb





AmphibiaWeb

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Data

Products

Challenges

Responses



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Tree of Life

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- Adopt a data portal approach to web sites, in which the relevant data and information are queried from diverse databases (e.g., Tree of Life, AmphibiaWeb, and HerpNET) and displayed to fill the specific needs of the user.
- Use the Tree of Life database (www.tol.org) as the repository for new information about amphibian phylogeny.



Challenges

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- A sense of ownership of individual taxonomic groups
- Community perception about the concentration of resources
- Isolation of individual researchers from the larger community.



Responses

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- Community Workshops: Offer opportunities for training, exchange of ideas, and connection-building.
- Cooperation and Collaboration: Share resources and expertise.
- Open Source Phylogeny: Encourage an approach that promotes integrative data collection rather than a focus on one taxon.



Community Workshops

- Goals
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- Norman, OK May 2004
 Austin, TX Dec 2004
 Advanced Phylogenetics
 - Morphological Applysis
 - Morphological Analysis
- Tampa, FL June 2005Stellenbosch July 2005



Cooperation and Collaboration

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Example: Sequence Give-Away

- Researchers can collect sequence data at no cost if they are willing to sample genes and taxa in a way that promotes a robust phylogeny.
- Data are co-owned, but the researcher has the first right of publication.
- Co-authorship is not expected, and consultation about analysis is available.



Open Source Software

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- Open Source software is free in the sense of "liberated" rather than "costs nothing."
- All aspects of the software development and deployment are open to improvement.
- Open Source overturns intellectual property constraints. Intellectual "property" is something to be distributed rather than guarded.



Open Source Phylogeny

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- A phylogeny is akin to an operating system or software application. It should be a powerful tool for promoting comparative biology.
- Our phylogenies will be better if contributions (data and theory) are welcomed from all contributors, instead of a self-selected group.
- A taxon is not "owned" by a single research group. That is, the Tree of Amphibia should not be simply a compilation of smaller trees produced by individual groups.
- Rather, the goal (a robust phylogeny) is best realized by collaborative integration and synthesis of diverse datasets.

