Visualizing phylogenetic trees, and linking them to databases

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Outline:

- Representing phylogenetic trees for outreach and understanding. A users' perspective.
- How to incorporate a phylogenetic ontology in bioinformatics?

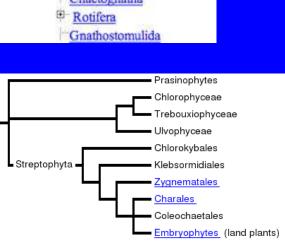
Representing phylogenetic trees for outreach and understanding

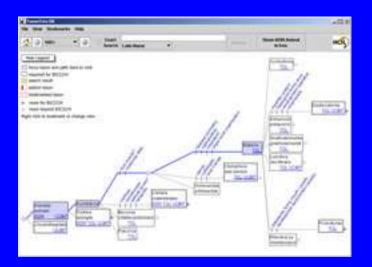
- A users' perspective.
 http://www.sims.berkeley.edu/~rebecca/cipres/compare.htm
- Audiences:
 - middle school
 - high school
 - college students in diversity courses
 - professional users of systematic information
 - systematic biologists

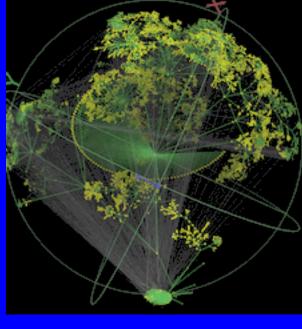
Interim Interview Results, sample of common responses:

- For middle school, start with where humans fit on the tree. Back up to show context for mammals, vertebrates, animals, eukaryotes, whole tree.
- Won't know how to navigate tree from taxon names...won't recognize them. Therefore, will need search tools and other guidance to find relevant parts.
- Will want to use common names
- Will want to use the tree as a way to access taxon information, not just the classification itself.



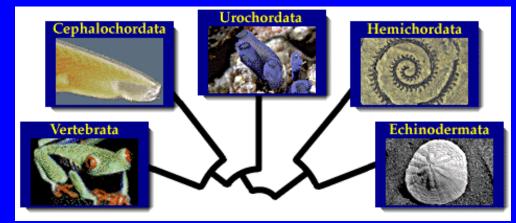






TaxonTree

Walrus -- 3D hyperbolic geometry



UCMP - Evolution site

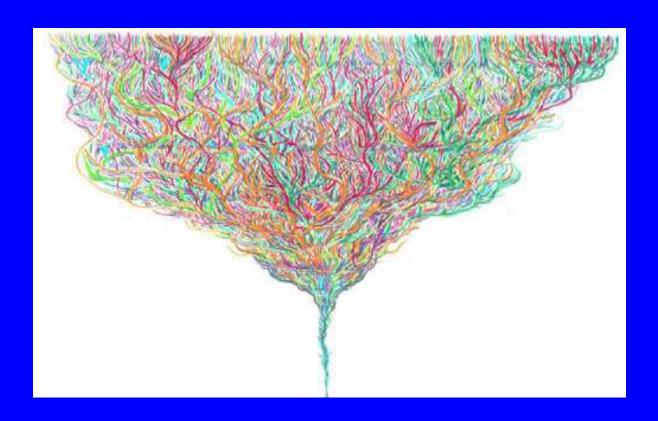
...and my favorite -- the GreenToL hyperbolic tree

Preliminary taxonomy of visualization approaches to nested data structures.

```
matrix
indented text
    whole tree depth first (like this list)
    whole tree breadth first (many dichotomous keys)
    path-plus-breadth lineage browser (BIOT, GenBank, old parts of tol website)
space-filling
    linear: set-based display (Prometheus)
    2-D: "tree"-map
"trees" - branching diagrams
    navigated left-to-right
           static - (Paup and many published trees)
           interactive presentation
                      of fixed views (current tol website)
                      of dynamic views (taxonTree)
    navigated bottom to top
           static - (MacClade)
           dynamic
           hyperbolic (PEG)
    center-to-outside layout
           circle (UCMP Evolution website)
           spiral
           sphere (WALRUS)
```

What is the tree of life?

- It is a single, magnificent genealogy connecting all organisms alive today, and that ever lived.
- Biodiversity is the whole tree of life, not just the named species.
- In fact, even a complete list of named species would be a very poor representation of biodiversity (contra certain recent writers).



Biodiversity Isn't Species

- Biodiversity is the whole tree of life, not just the named species.
- There are lineages smaller and larger than the traditional species level.
- Species are not comparable between lineages in any manner, just an arbitrary cut-off somewhere along a branch in the tree of life.
- Thus only a creationist should think that species are the fundamental units of biodiversity, or that a list of currently named species in some way provides an inventory of biodiversity.

A proliferation of biological databases:

Species-based:

- •identification (e.g., DELTA, LucID, MEKA)
- •monographs/floras/faunas (e.g., Jepson Flora Project)
- •distribution (e.g., BBS, UK Plant Atlas, CalFlora)
- •images (e.g., CalPhoto, FishBASE)
- •taxonomic management (e.g., IPNI, Tropicos)
- basic and applied ecology (USDA FEIS)

Individual-based:

- •specimen-management (e.g., Biota, BRAHMS, SMaSCH)
- •observation records (e.g., CalFlora, FishWatcher)
- ecological inventory (e.g., VegBank, SALVIAS)
- •gene records (e.g., GenBank)



Very few are **Phylogenetic**, so far those are designed for:

- tree storage (TreeBASE)
- •displaying current phylogenetic trees (e.g., Tree of Life, Phylomatic, Apweb).

The Problem:

- Most biological databases remain as essentially a "flat file" with respect to evolution.
- Data are entered with whatever taxon name (usually a species or a genus) happens to be attached to them.
- The only sense of evolutionary relationships is given by a schema of higher-taxon names (say families and phyla) that can be used to group the basic information.
- These higher taxa may or may not be monophyletic, and essentially function as static sorting bins -- there is no way to access or display emergent properties of data at higher evolutionary levels or to discover finer-scale patterns at lower levels.

The Problem, in a nutshell:

- The problem with unification of all these types of databases is that there is low linkage among them, despite high overlap in taxonomic coverage the linkage that exists is via a static taxonomic hierarchy.
- This restricts the analytical potential of databases.

The Solution, in a nutshell:

- Use the ubiquitous nature of the tree of life for linking databases.
- All biological data fall *somewhere* on the tree of life, which is the one thing that can unify them all.

• All biological data fall *somewhere* on the tree of life,

which is the *one thing* that can unify them all.

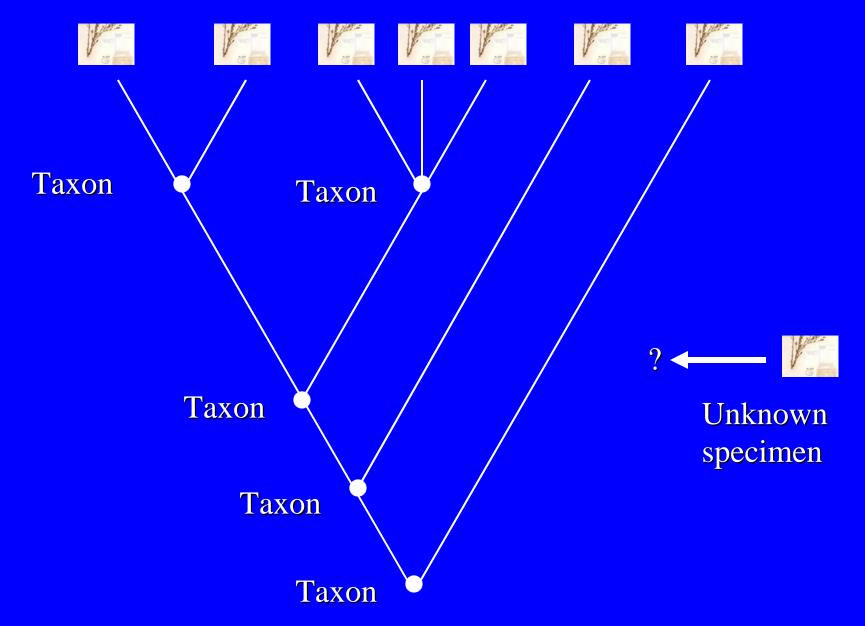


• Seriously, the use of phylogeny-space as the fundamental ontology for biological data, would have the same revolutionary impact as the use of spatial data has had on geography. Instead of Geographic Information Systems (GIS), we would have Phylogenetic Information Systems...

The Tree of Life as information-organizer:

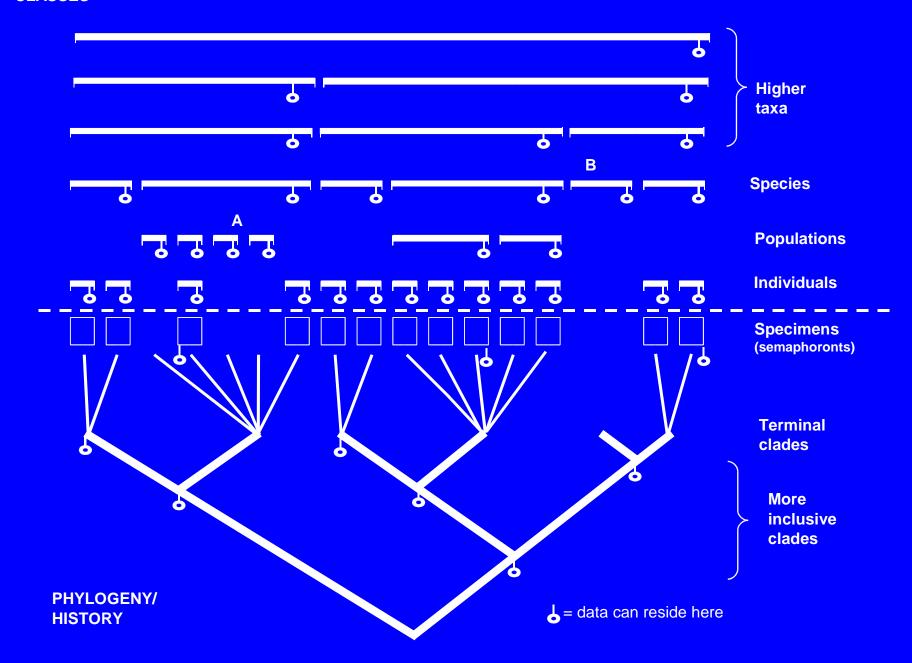
- Of all types of biological relationships, phylogeny provides the best *general purpose* classification. In other words, the single most important thing you can know about an organism is what is it related to.
- Phylogeny can be *the* factor that unites together all disparate biological databases.
- The centerpiece of future biological databases will be phylogenetic classification, a deeply nested hierarchy of nodes linked to all available structural and functional data at each level.

Specimens:



Two distinctions to make:

- Between the phylogeny (which is an inference about *history*) and the named taxa (which are nested classes of *extant* individuals).
 - •The ultimate units of phylogenetic analysis are specimens -- semaphoronts in the terms used by Hennig (these include such items as museum specimens, photomicrographs, and tubes of extracted DNA). Never species or other taxa!

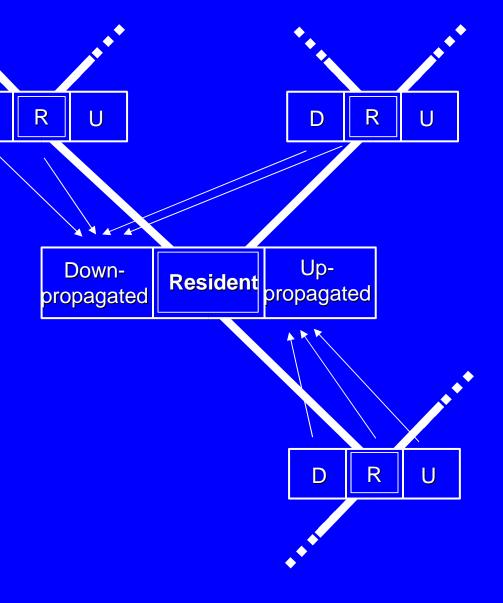


- Semaphoronts are the units bearing the empirical character data, and they are linked together into increasingly more inclusive monophyletic groups, each of which has an hypothesized ancestral node with inferred synapomorphies.
- The important thing to note is that the semaphoronts bear the actual data, and all the higher nodes have *inferred* ancestral states.
- On the other hand, phylogenetic taxa are made up of nested classes of contemporaneous organisms. The taxa can have their own attributes, such as average height and geographic distribution, that are not necessarily the same as the inferred ancestral attribute of the lineage.

Two distinctions to make:

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Between data that are intrinsically resident at a node versus attributes that are inferred from elsewhere on the tree (either above or below).

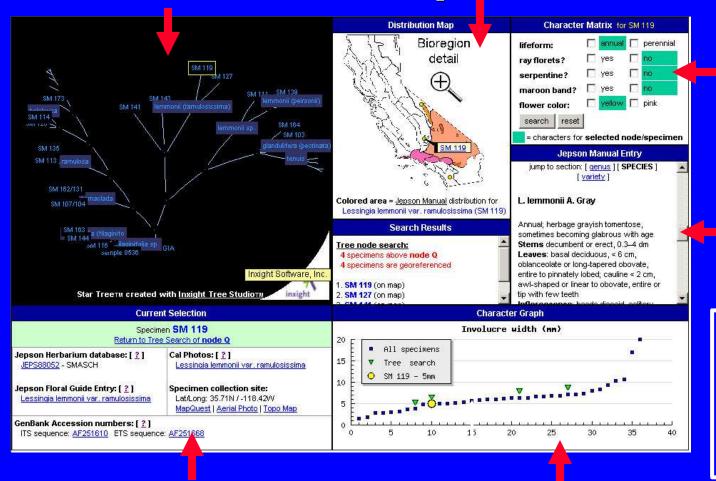


- •Conventional statistical analysis focuses on downpropagated data (summary statistics of individual data points).
- •Phylogenetic methods, including parsimony and maximum likelihood, utilize up and down-propagated methods in calculation of ancestral states.
- •Up-propagated data can also provide predictive insights into organismal traits based on phylogenetic relationships.

PEG: Phylogeny, Ecology, Geography

Tree interface

Map interface



Character Interface

Description from literature

Collaborators:

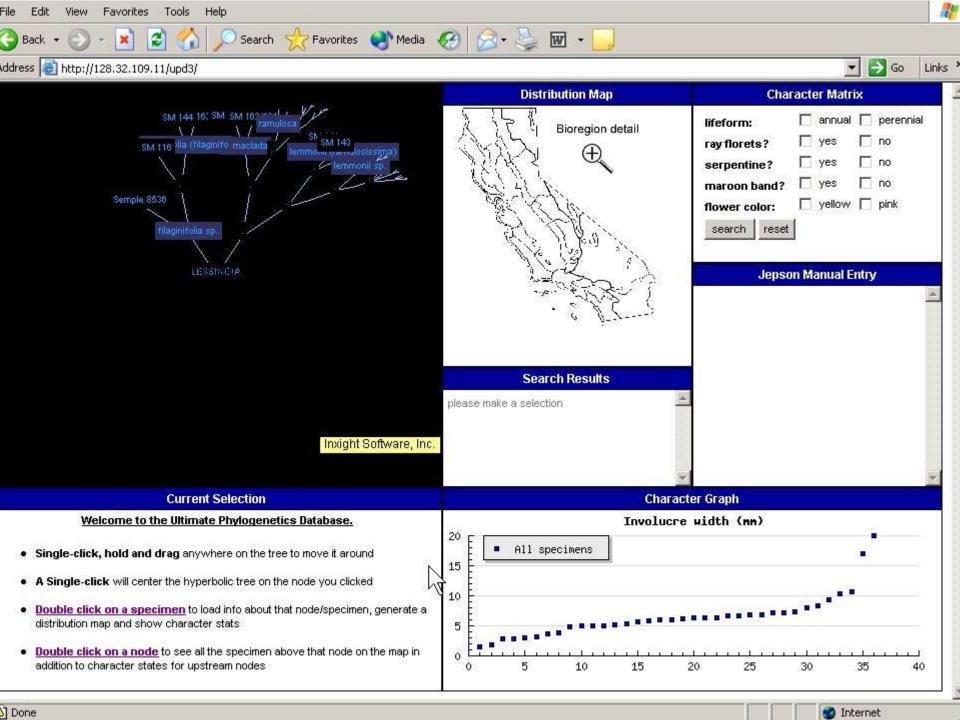
- Brent Mishler
- David Ackerly
- Cam Webb

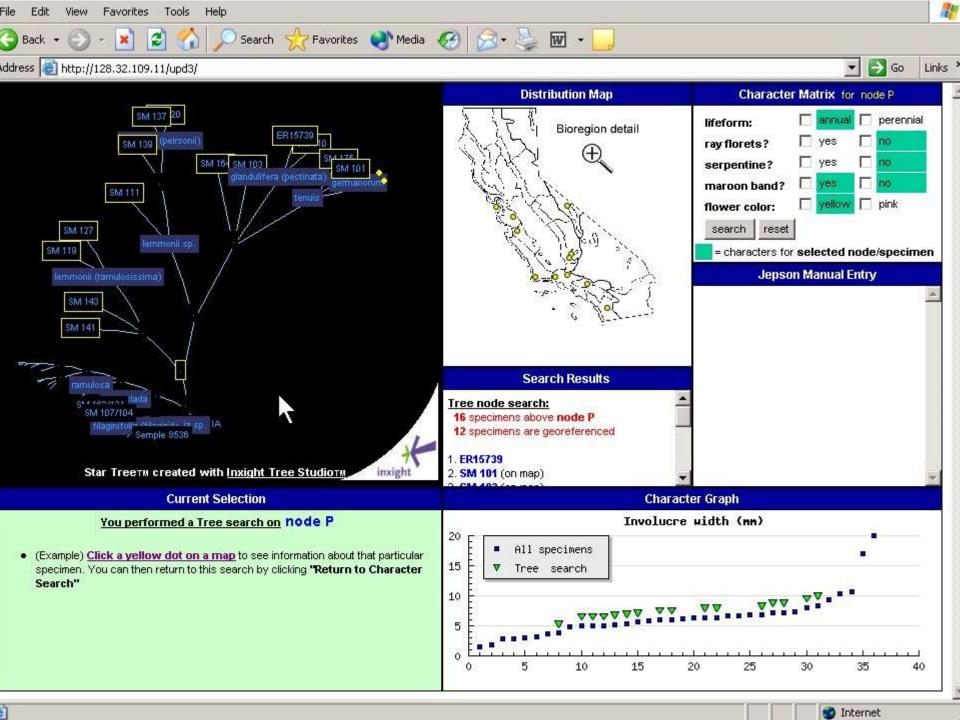
Collection interface (voucher data; photos; Genebank)

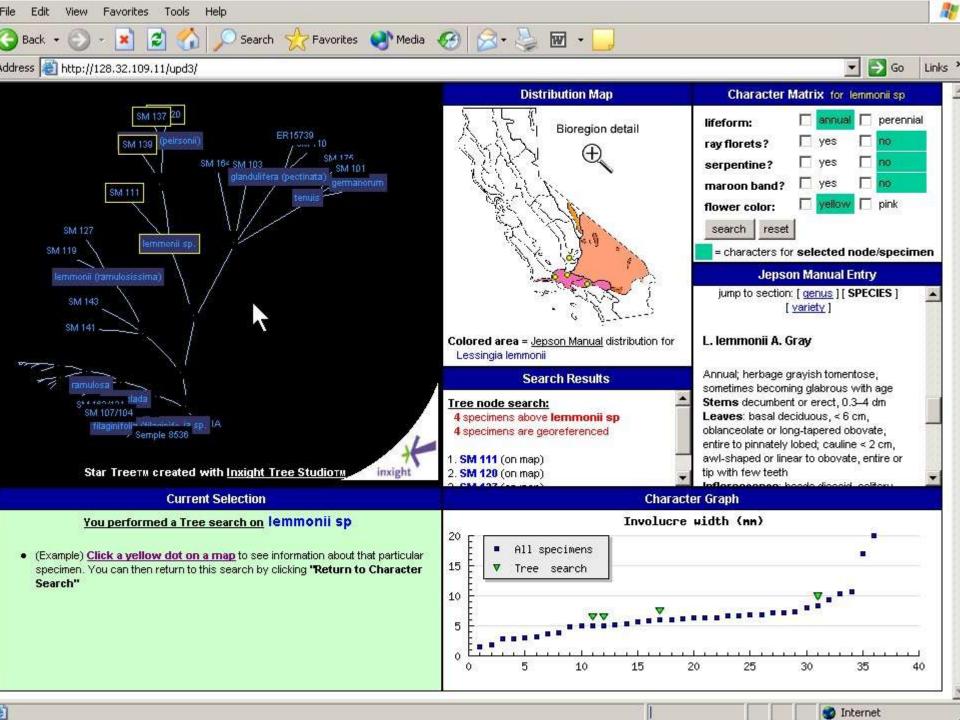
Ecological Interface

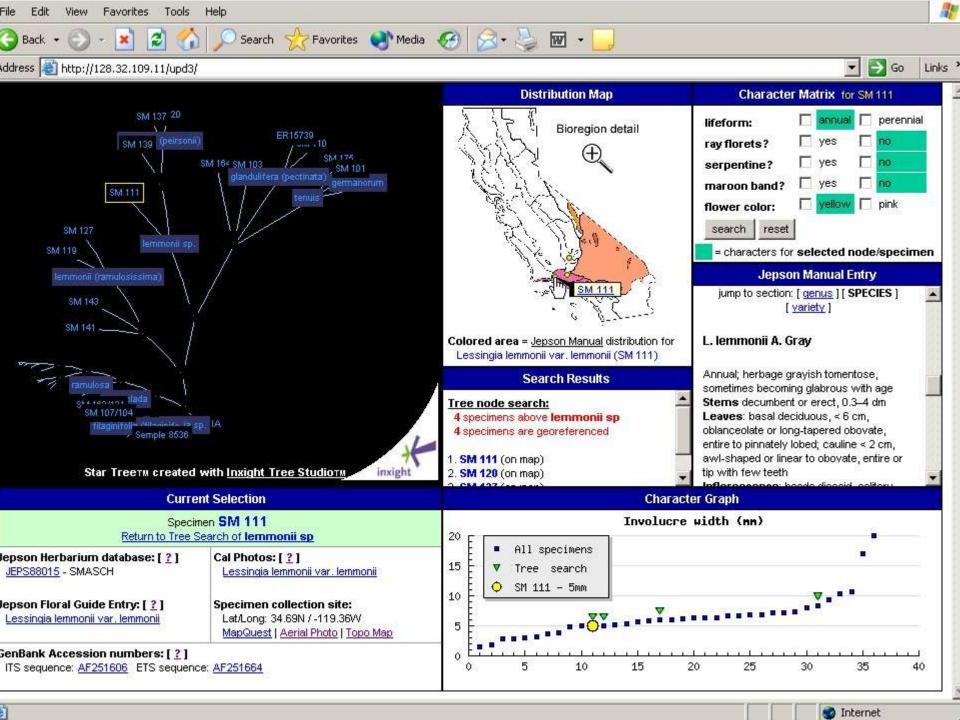
Hyperbolic tree software generously provided by Inxight Software, Inc.

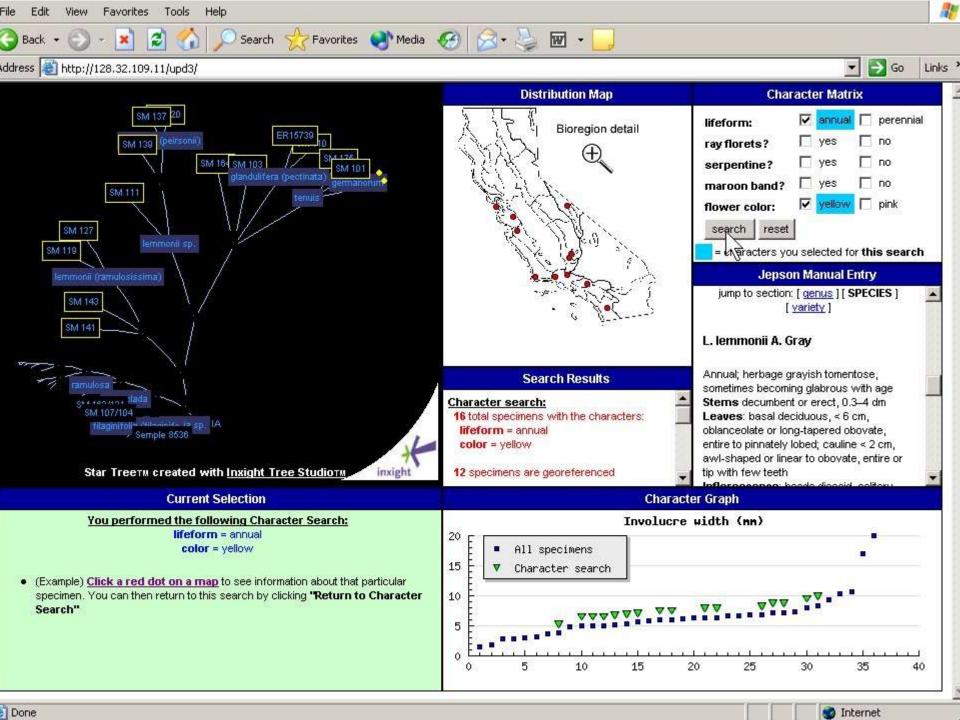
Demo at: http://ucjeps.berkeley.edu/upd/

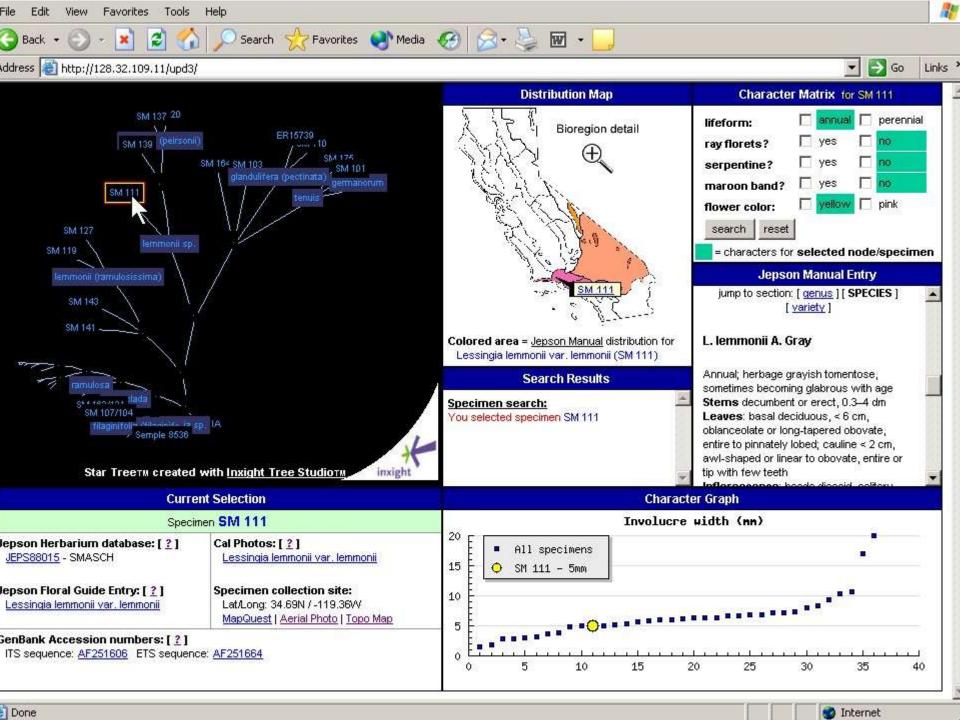


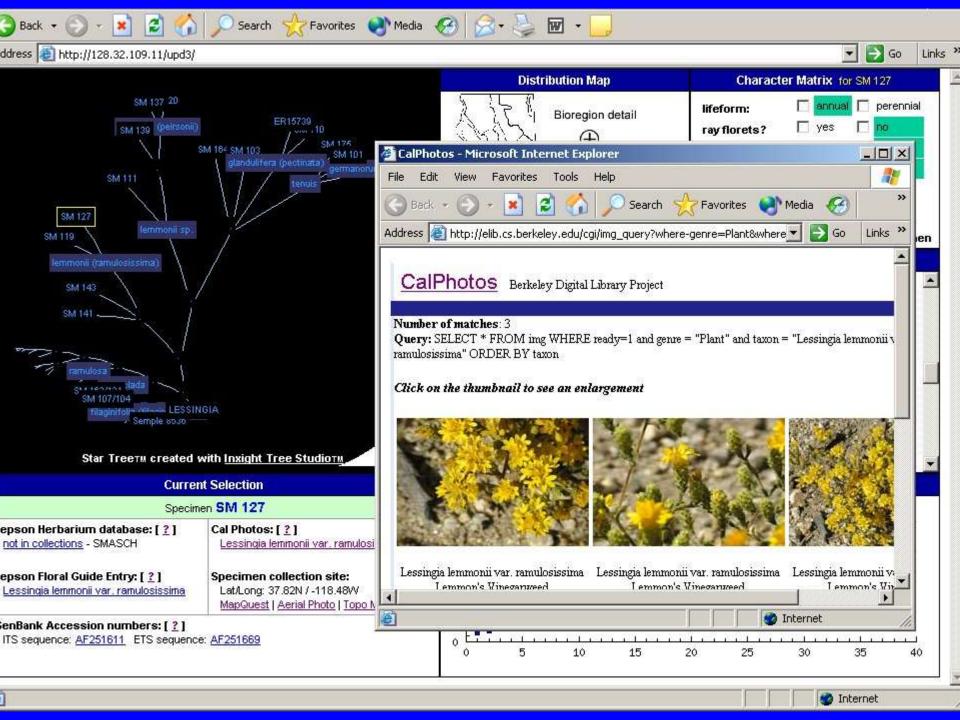


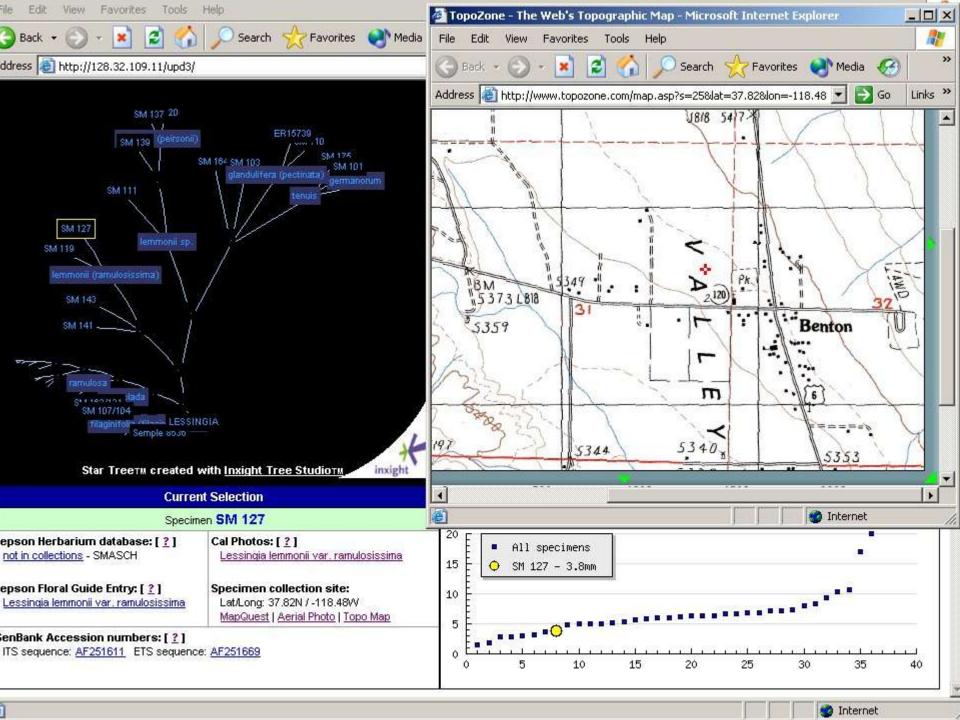


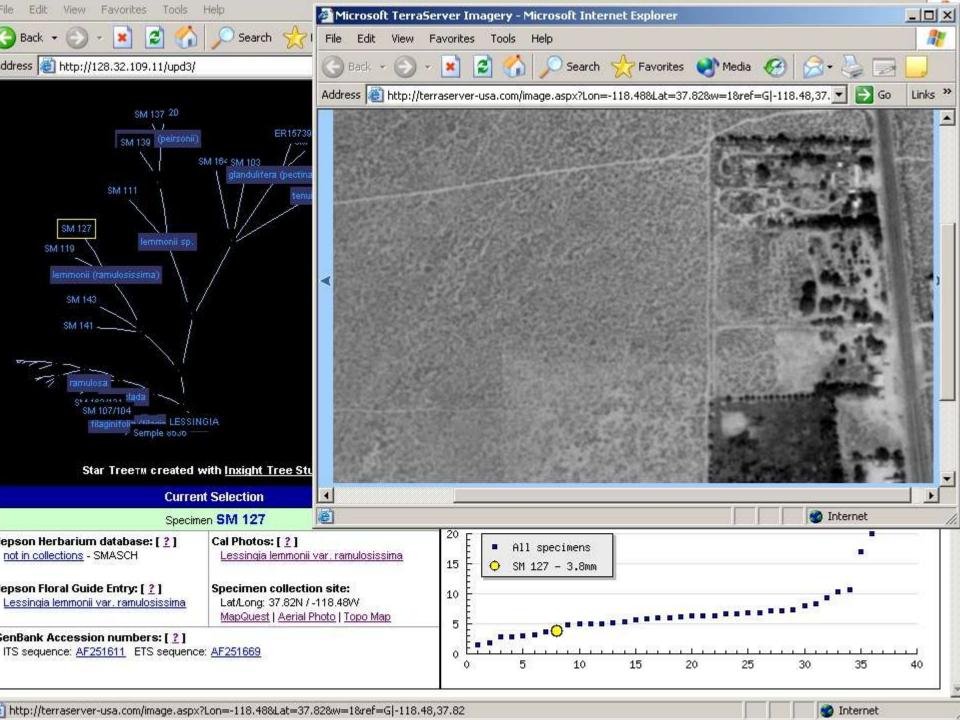


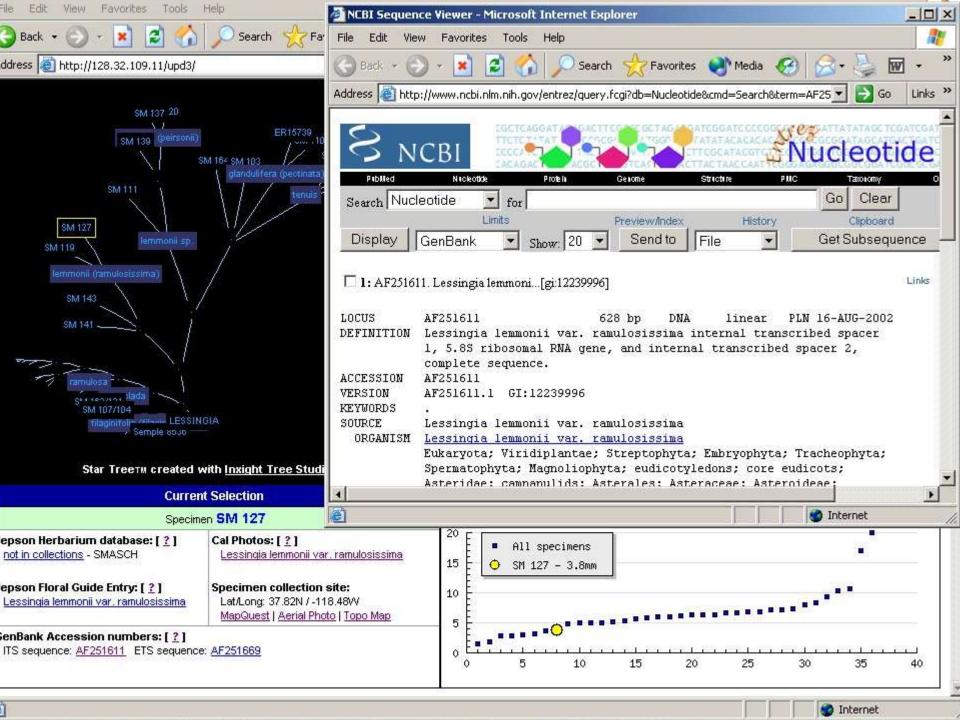












Conclusions

- The PEG database will add a Phylogenetic ontology to existing resources for Ecology and Geography to allow a brand new way of viewing and understanding biological diversity.
- The PEG database will allow a user to query a unified database to search for the clades that occur in a specified geographic region, the morphological, molecular, or ecological variation in specimens distal to a chosen node, or the subset of clades with a particular combination of character states.
- Such a database can be used for such seemingly disparate tasks as herbarium management, geographic inventories, systematic studies, comparative ecology, macroevolutionary comparisons, conservation planning, or identification of unknown plants.