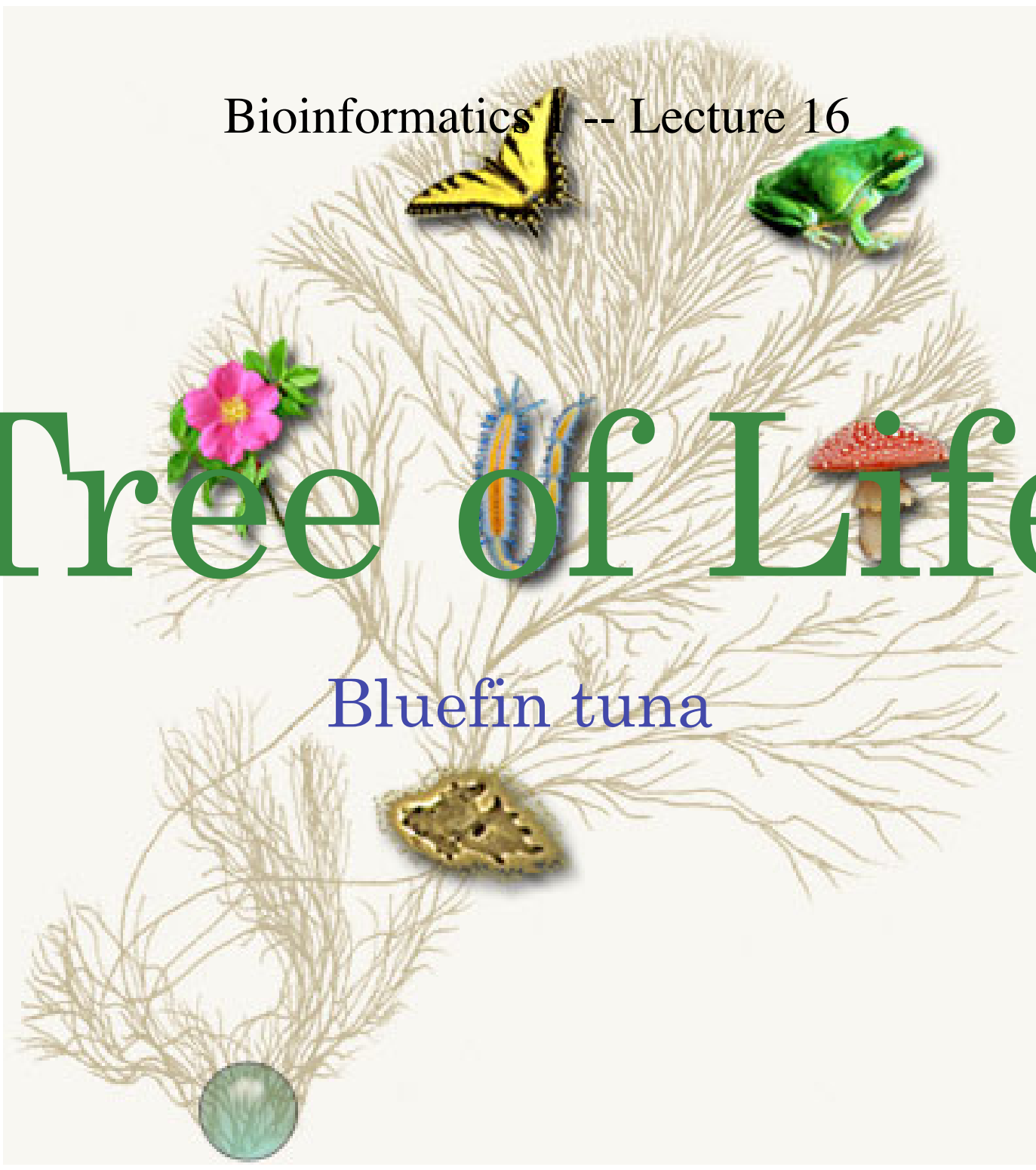
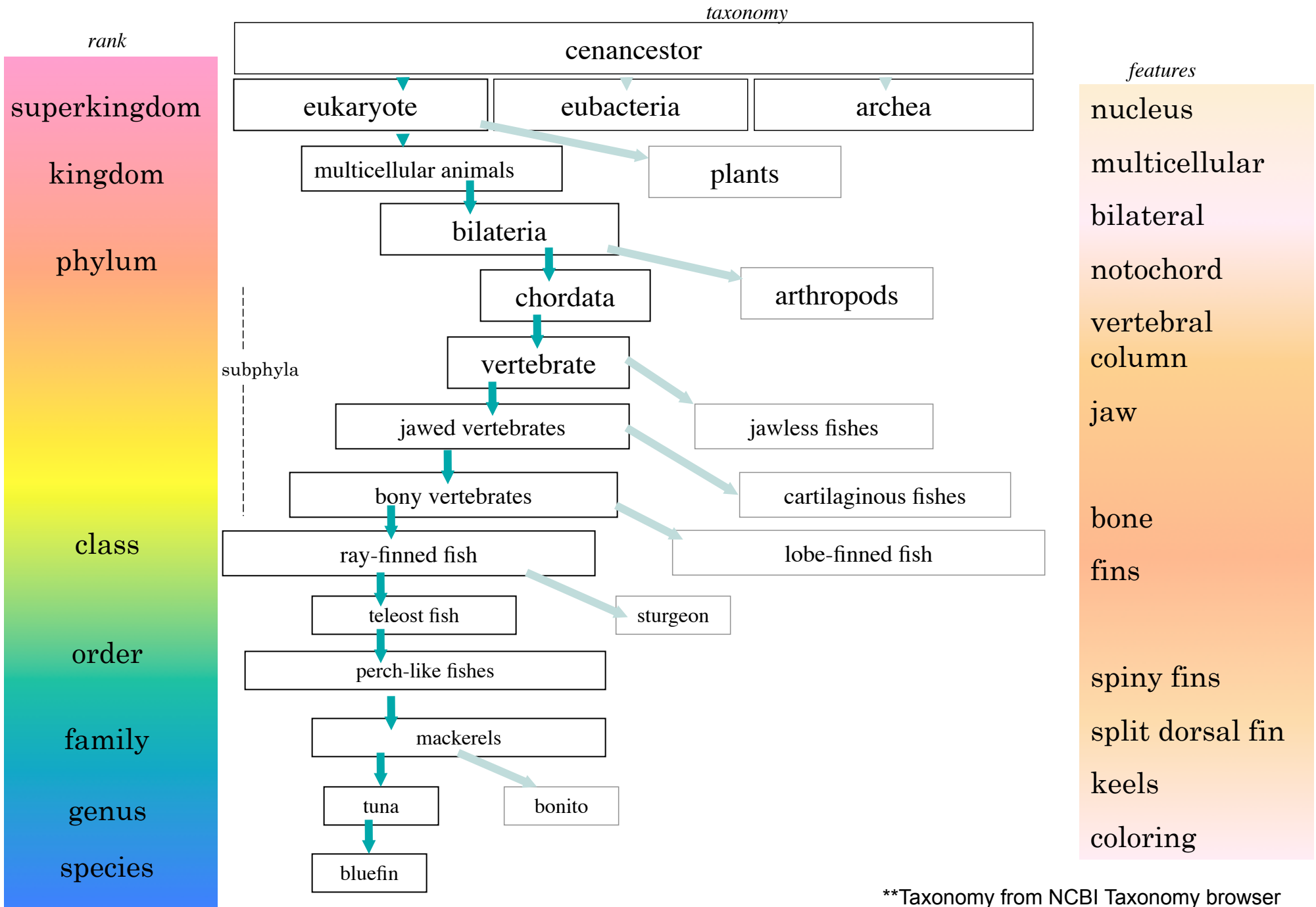


Tree of Life

Bluefin tuna

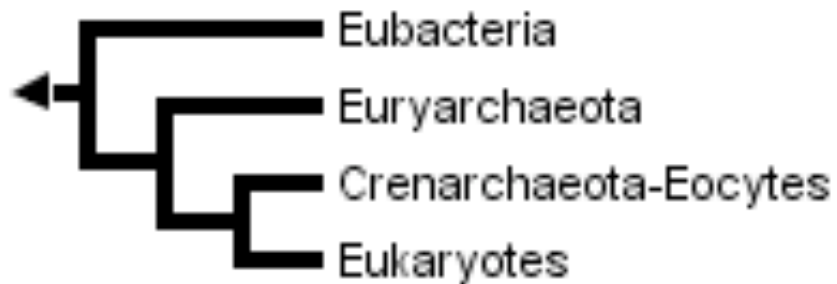
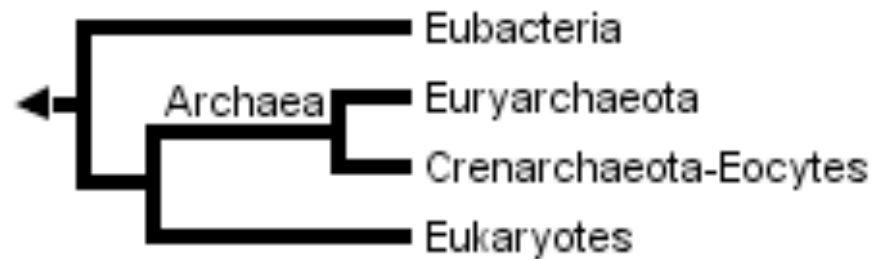


Location of bluefin tuna in tree of life



**Taxonomy from NCBI Taxonomy browser

tolweb.org/tree

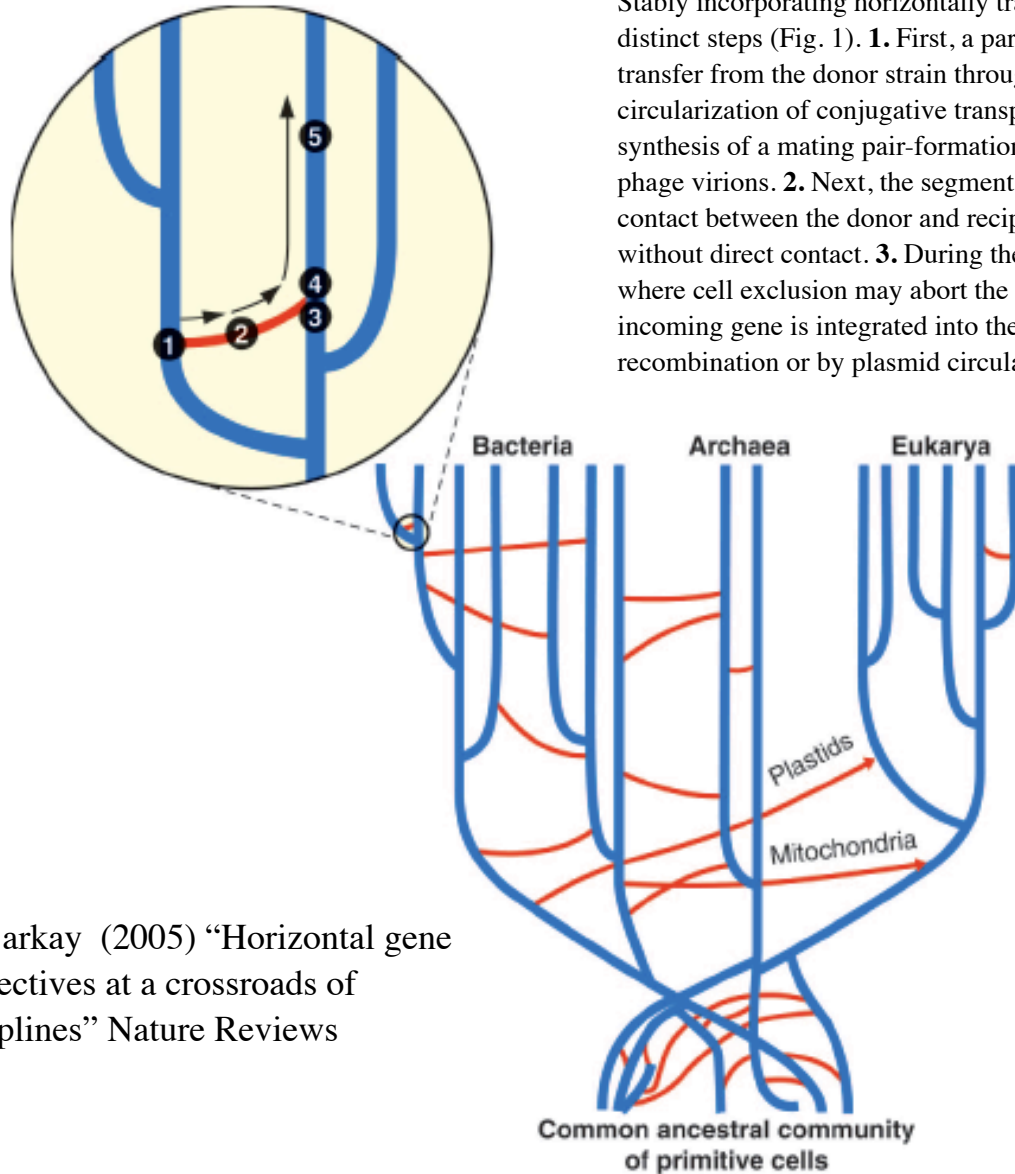


Earliest branching... still controversial.

Life is not strictly a tree -- horizontal gene transfer

Discrete Steps Needed for Stability of Gene Transfer

Stably incorporating horizontally transferred genes into a recipient genome involves five distinct steps (Fig. 1). **1.** First, a particular segment of DNA or RNA is prepared for transfer from the donor strain through one of several processes, including excision and circularization of conjugative transposons, initiation of conjugal plasmid transfer by synthesis of a mating pair-formation protein complex, or packaging of nucleic acids into phage virions. **2.** Next, the segment is transferred either by conjugation, which requires contact between the donor and recipient cells, or by transformation and transduction without direct contact. **3.** During the third step, genetic material enters the recipient cell, where cell exclusion may abort the transfer. **4.** Otherwise, during the fourth step, the incoming gene is integrated into the recipient genome by legitimate or sitespecific recombination or by plasmid circularization and complementary strand



synthesis. Barriers to transfer during this step come from restriction modification systems, failure to integrate and replicate within the new host genome, and incompatibility with resident plasmids. **5.** In the final step, transferred genes are replicated as part of the recipient genome and transmitted to daughter cells in stable fashion over successive generations. Researchers from different disciplines tend to focus on specific stages within this five-step sequence. Thus, evolutionary biologists who examine microbial genomes for evidence of past transfers tend to look at HGTs from the perspective of step five. Molecular biologists are more likely to examine the details of the transfer events, while microbial ecologists look more broadly when they describe the magnitude and diversity of the mobile gene pool, sometimes called the mobilome.

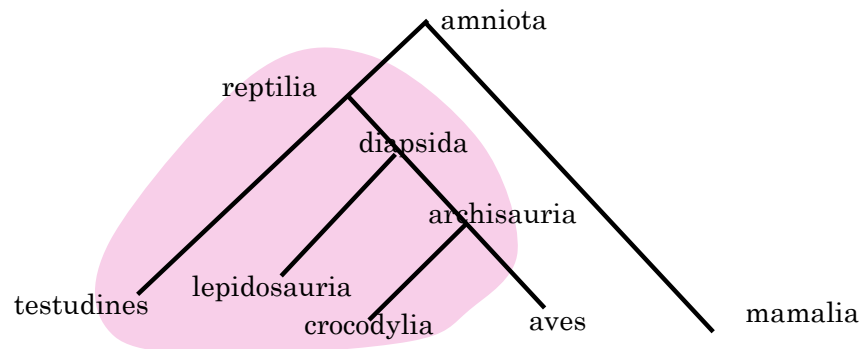
BF Smets, T Barkay (2005) "Horizontal gene transfer: perspectives at a crossroads of scientific disciplines" Nature Reviews Microbiology.

In class exercise: explore taxonomy browser

- NCBI
- TaxBrowser
 - Find homo sapiens starting from the root
 - Where do the following first appear
 - two eyes
 - jaw
 - four limbs
 - five fingers
 - no tail

Classification is not phylogeny ...not always

- **Paraphyly** (paraphyletic) -- a taxonomic classification that does not contain all of the descendents of the common ancestor. “Reptile” is paraphyletic because does not include birds which diverged after the common ancestor.
- **Monophyletic** -- a classification that includes all descendents of a common ancestor.

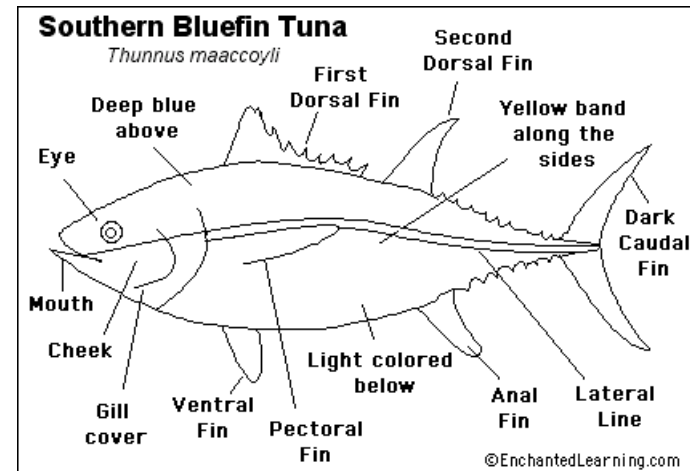


Atlantic bluefin tuna: *thunnus thynnus*

Kingom	Phylum	Class	Order	Family	Genus	Species
ANIMALIA	CHORDATA	ACTINOPTERYGII	PERCIFORMES	SCOMBRIDAE	THUNNUS	THYNNUS
animal	notochord	ray-finned fishes	perch-like	mackerels	tuna	bluefin

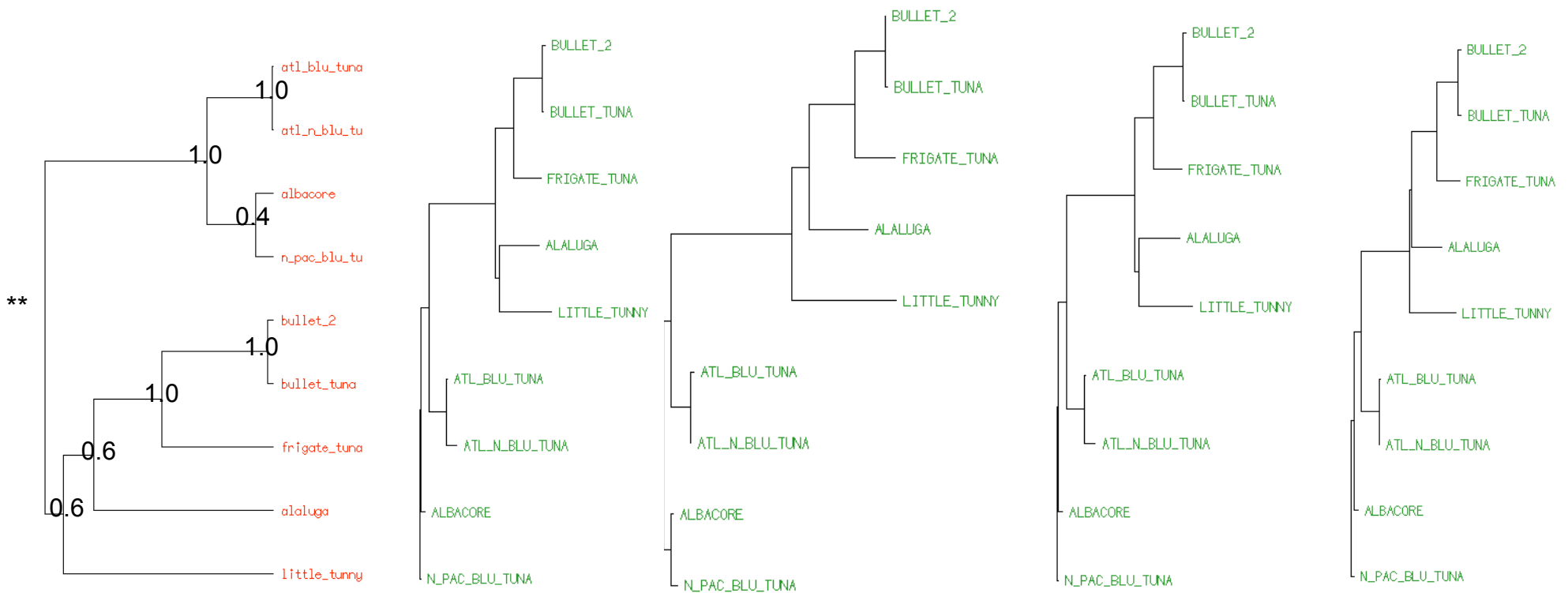


[Critically Endangered \(IUCN 2.3\)](#)



<http://www.iucnredlist.org/search>

Bluefin tuna trees

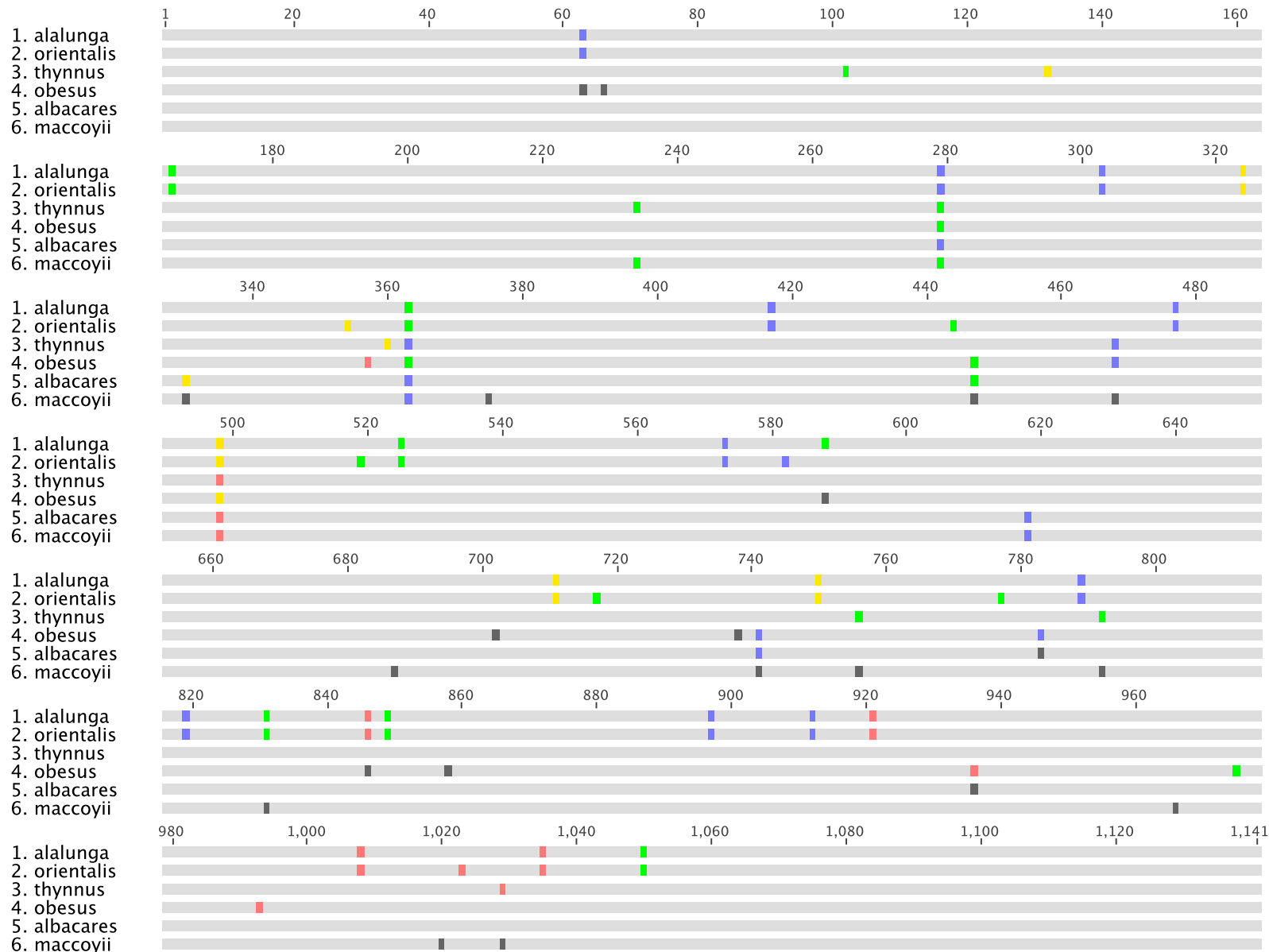


The classification “bluefin” is paraphyletic, since the common ancestor of N. Atlantic Bluefin and Pacific Bluefin includes a non-bluefin tuna, the albacore.

**Unrooted trees. Bootstrap value for root not possible.

Tuna MSA

Mitochondrial cytochrome B (DNA) -- one of the most widely sequenced genes



Are there enough differences here?

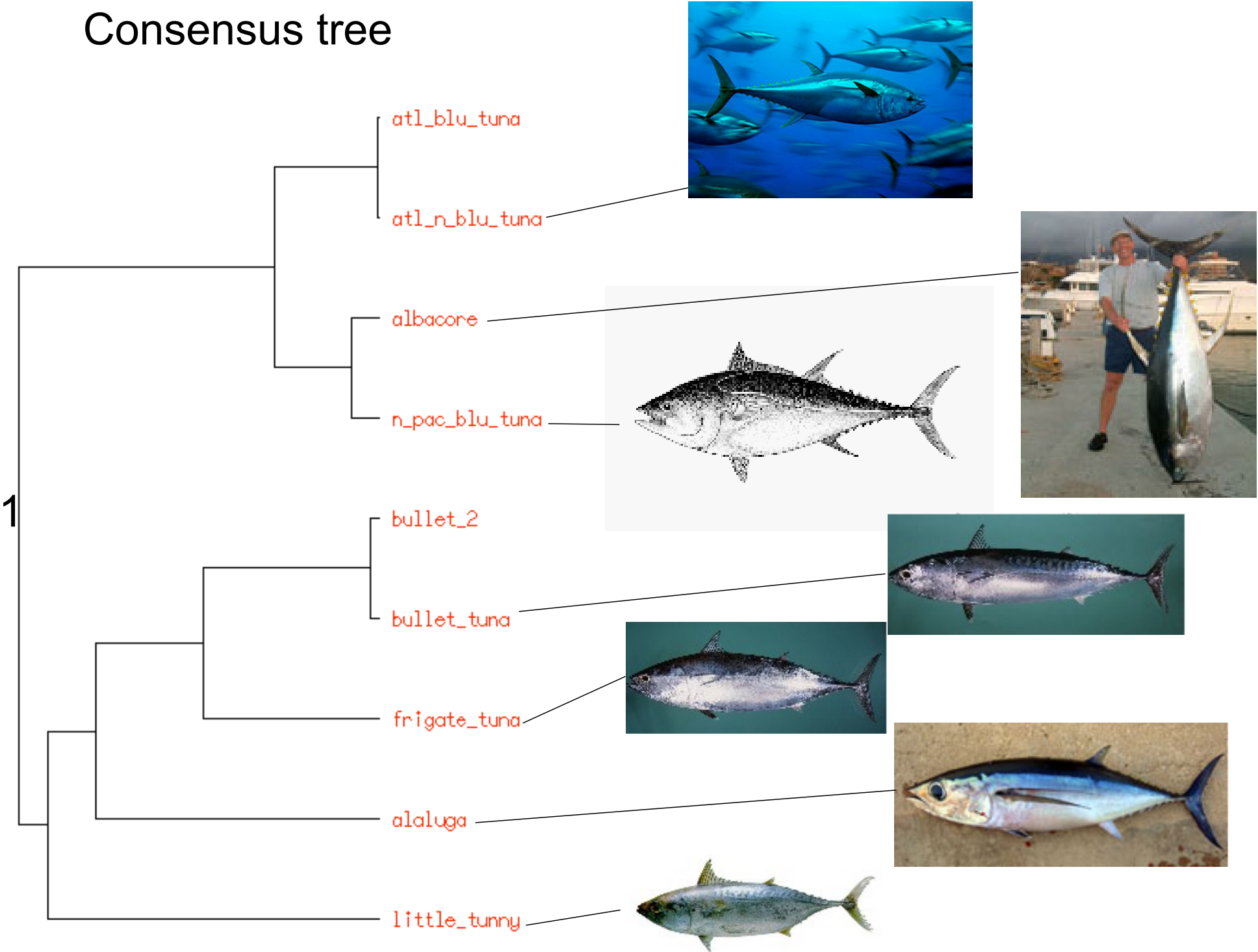
What to do with **low** p-distance MSAs

- Save the length of the alignment.
- Then, delete identity columns
- Generate tree using QP with ML.
- Search tree space using NNI; determine branch lengths using Least Squares.
- Bootstrap. Report the consensus tree with bootstrap values.

What to do with **high p-** distance MSAs

- Prune, trim to produce a representative set of columns.
- Generate tree using NJ.
- Get branch lengths using FM or LS.
- Sum patristic distances. Sum sequence weights. Sum profile
- Generate a HMM*.
- Add sequences by aligning to the HMM. Repeat steps 1-5.

Consensus tree



Install PHYLIP