

Why the @#\$% is the GMOD meeting being held here?

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&

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Informatics @ NESCent

Mission

- Support for sponsored science
- “Cyberinfrastructure” to enable evolutionary synthesis
 - Data sharing/exchange and database technology
 - Software development (e.g. hackathons)
 - Training, dissemination and user support

Resources

- IT and bioinformatics staff (currently hiring!)
- Hardware for HPC, software development & web/db services
- Visiting scientists (both technical experts and user)



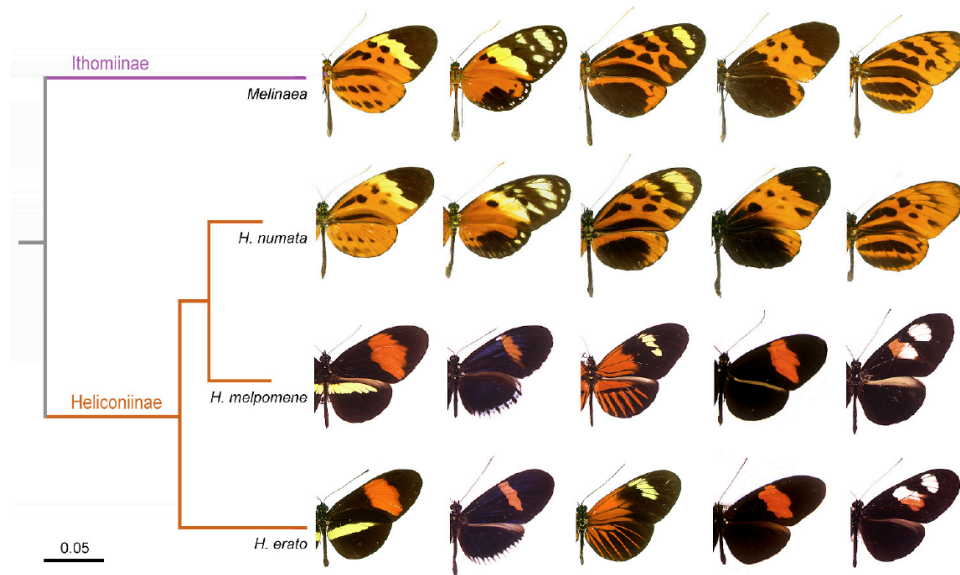
Interspecific phenotypic diversity and model organism developmental genetics

- Questions
 - What zebrafish mutants differ from wild type in the same way that a particular anatomical features distinguishes these groups of fish?
 - Are characters that are phylogenetically correlated among fish species also genetically correlated in zebrafish mutants?
- Can be answered using the Phenotype and Trait Ontology (PATO) as a bridge





Evolutionary model organisms





Types of evolutionary model organisms

Genome model relatives that are convenient for evolution/ecology, or just for comparison

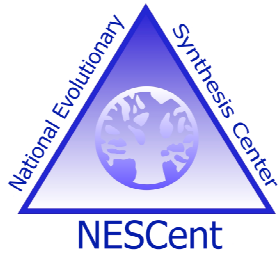
- *Drosophila pseudoobscura*
- *Caenorhabditis briggsae*
- *Arabidopsis lyrata*

Phylogenetically important lineages

- *Ciona intestinalis* (sea squirt)

Historically popular evolutionary models

- *Mimulus spp.* (monkeyflowers)
- *Heliconius spp.*
- *Gasterosteus aculeatus* (sticklebacks)
- *Geospiza spp.* (Darwin's finches)



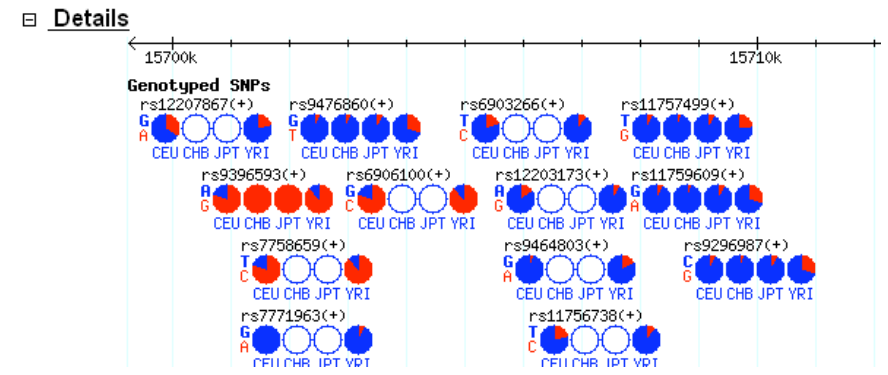
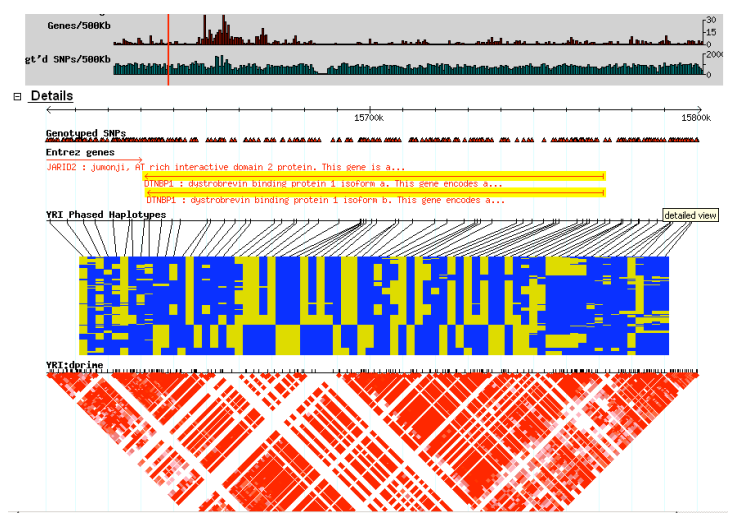
NESCent's interest in GMOD

- A meeting in the middle
 - Model organisms are venturing into comparative genomics and population genetics
 - Evolutionary biologists are acquiring genomic information from their own model systems
- Focus of our initial efforts
 - Chado population module
 - Visualization of phenotypic variation & geographic information
 - User support, training, dissemination



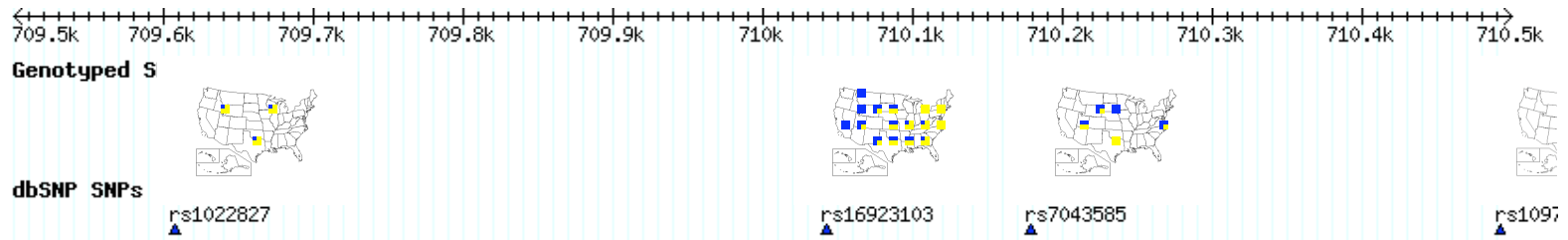
Existing glyphs

- Allele tower
- Pie chart
- Haplotype block
- Pairwise plot (for LD)
- XY plot
- Whiskerplot
- Embedded images



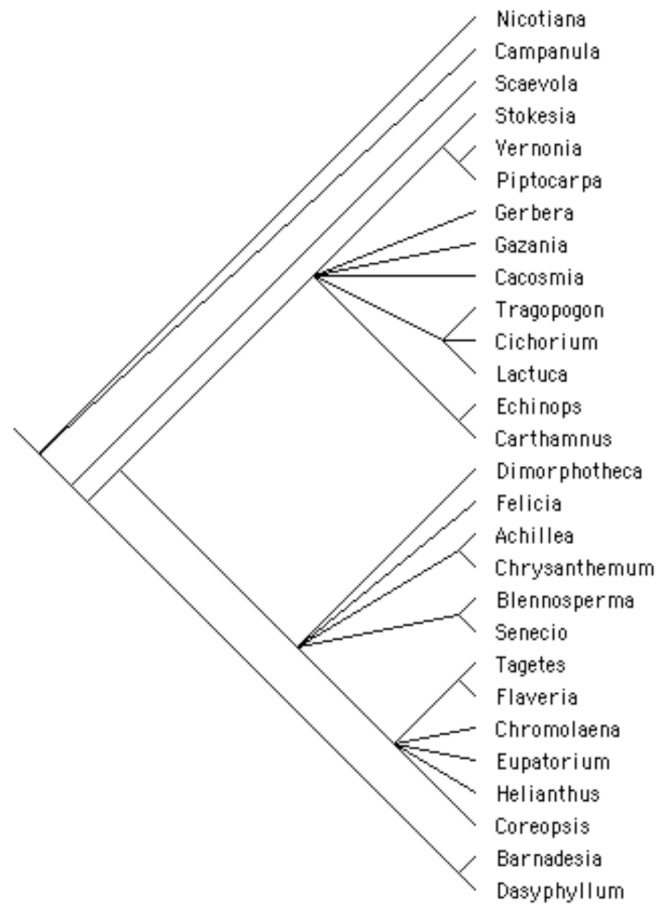


Proposed glyph (Bio::Graphics)





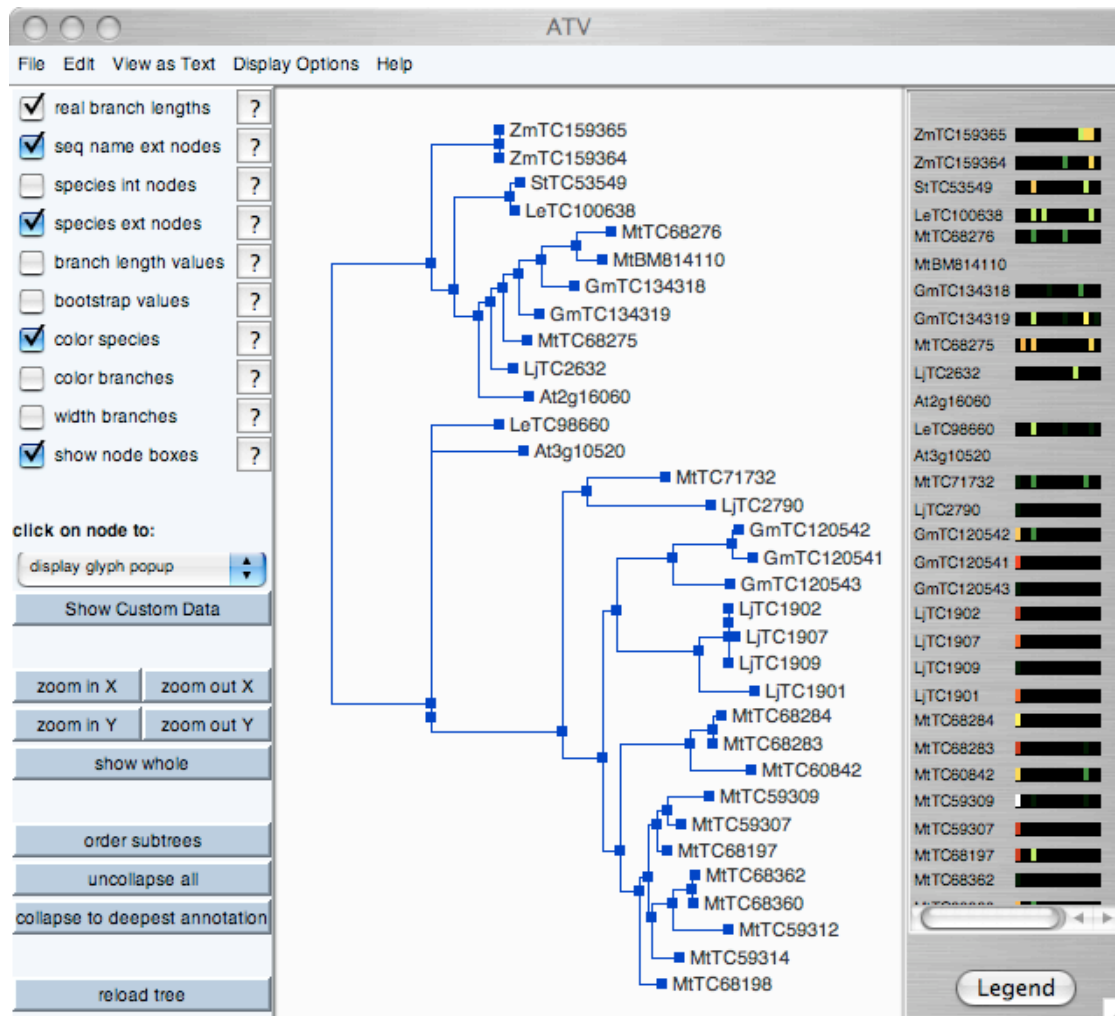
Visualizing phylogenies (old school)





Visualizing phylogenies

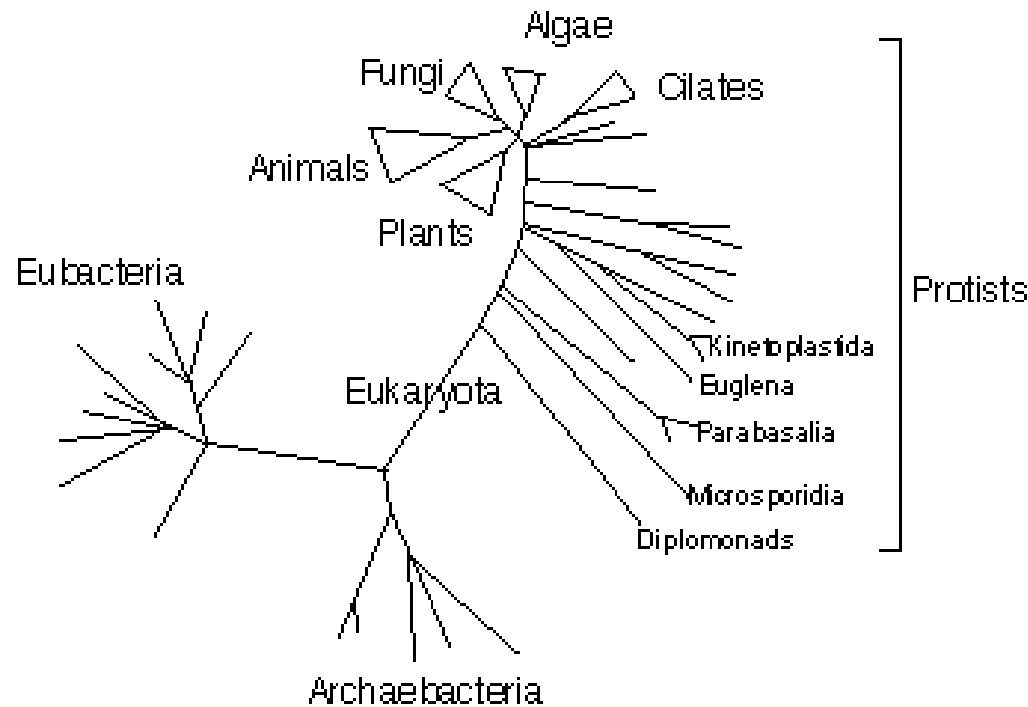
ATV 3.0 (Zmasek & Cannon)





Some closing thoughts

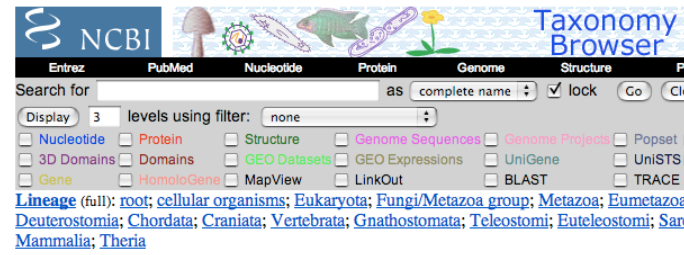
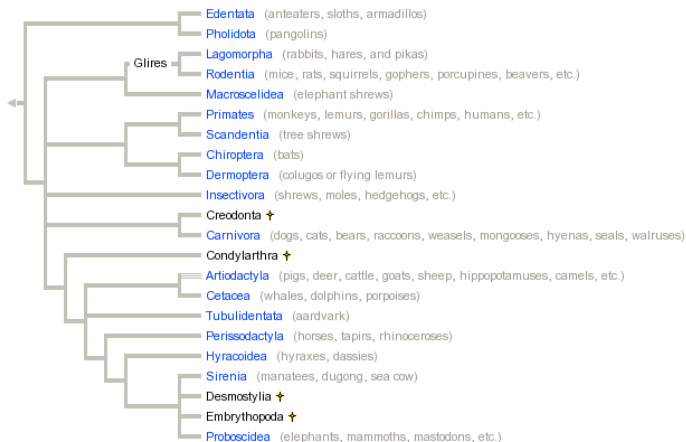
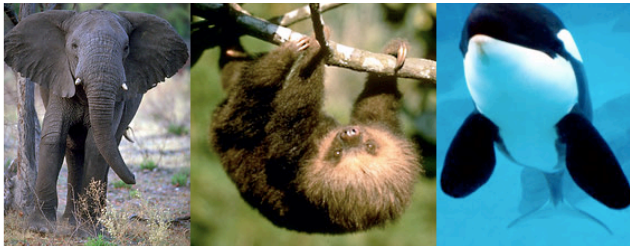
- Are clade-oriented databases sufficient to solve the impending genome glut?





Some closing thoughts

- How important is a machine-readable tree-of-life, and how far are we from that goal?




- o **Eutheria** (placentals) *Click on organism name to get more information.*



- o **Afrotheria**
 - o **Chrysochloridae** (golden moles)
 - **Amblysomus**
 - **Chrysochloris**
 - **Chrysoxpalax**
 - o **Hyracoidea**
 - **Procaviidae** (hyraxes)
 - o **Macroscelidea**
 - **Macroscelididae**
 - o **Proboscidea**
 - **Elephantidae** (elephants)
 - o **Sirenia**
 - **Dugongidae** (dugong and sea cow)
 - **Trichechidae** (manatees)
 - o **Tenrecidae** (tenrecs)
 - **Geogalinae**
 - **Oryzorictinae**
 - **Potamogalinae**
 - **Tenrecinae**



Some closing thoughts

- How important are curated cross-species gene/protein family data?


Tree families database

TF101089

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Descriptions

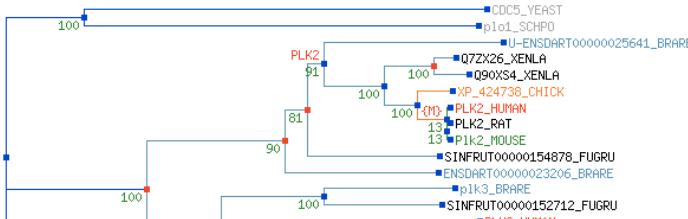
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Accession	TF101089
Symbol	PLK1-3
Family Name	polo-like kinase 1-3
Family Size	seed: 35 / full: 76
Old Accessions	TF314597
Curator	lh3@sanger.ac.uk
Descriptions	PLK1 inactivates WEE1 and MYT1, and activates CDC25C, both by phosphorylation. PLK1 also phosphorylates FBXO5, leading to FBXO5 ubiquitination, and indirectly stabilizing APC complex.
PhIGs Cluster ID	198101
Last Modified	2005-07-26

(Please mail to treefam@sanger.ac.uk if you think this tree is wrong or have any other comments.)

View Curated Seed Tree

[Instructions](#) [ATV](#) [TreeView](#)



CDC5_YEAST

p1o1_SCHPO

U-ENS DART00000025641_BRARE

Q7ZX26_XENLA

Q90XS4_XENLA

XP_424738_CHICK

PLK2_HUMAN

PLK2_RAT

P1K2_MOUSE

SINFRUT00000154878_FUGRU

ENSDART00000023206_BRARE

p1k3_BRARE

SINFRUT00000152712_FUGRU