Hands-on Session I: Constructing Trees

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Session Organization

- Goal: To be comfortable building trees from real data
- Lecture:
  - Standard Software Packages
  - Details on Web-based Software
  - Motivating Problem
- Lab:
  - Organized so you can use the DIMACS lab, or your own laptop
  - Welcome to work singly or in groups

Lecture Outline

- Motivating Problem

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- Building Trees Overview

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- Sequence & Tree Formats

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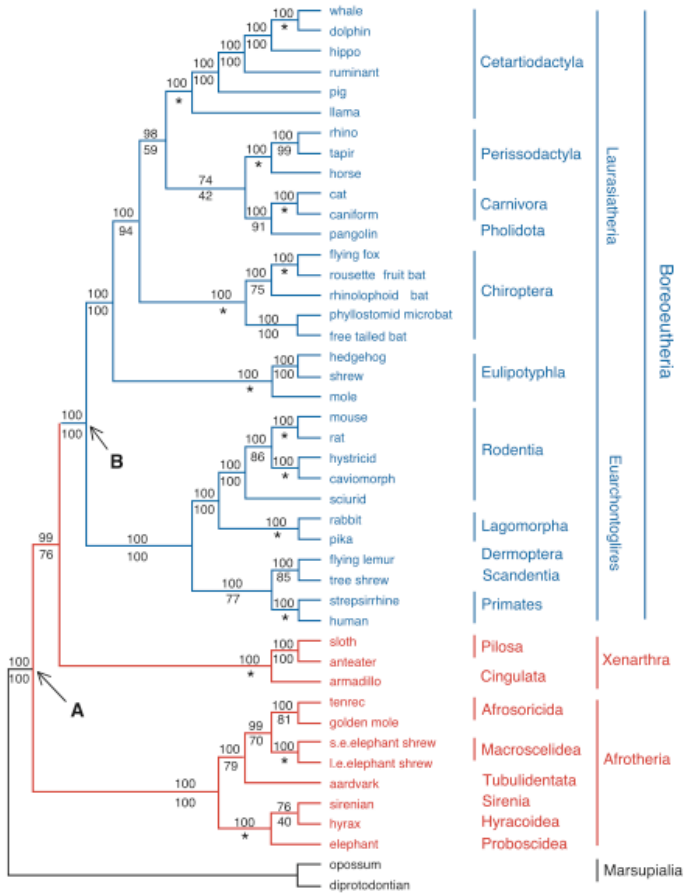
- Motivating Problem
- Building Trees Overview
- Software
- Sequence & Tree Formats
- Analyzing & Visualizing the Results

Motivating Problem: Which co-evolved?

Murphy *et al.*
"Resolution of the Early Placental Mammal Radiation Using Bayesian Phylogenetics,"
Science '01



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- For example: (Hillis *et al.*, *Sys Bio*, 2005), is it better
  - to build trees on each gene sequence and take the consensus, or
  - concatenate the sequences and look at those trees?

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- For example: (Hillis *et al.*, *Sys Bio*, 2005), is it better
  - to build trees on each gene sequence and take the consensus, or
  - concatenate the sequences and look at those trees?
- More tractable:
  - which of these genes co-evolved?
  - focus on several, or try all of them

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We'll focus on the last two today.

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  - General Time Reversible (GTR): assume symmetric substitution matrix (ie A changes to C at the same rate C changes to A).

Models of Evolution

APPENDIX 2. Model parameters for the genes studied by Murphy et al. (2000):

		Base frequencies				Relative substitution rates						Proportion invariant	
Gene	Preferred model	A	C	G	T	AC	AG	AT	CG	CT	GT	sites	Alpha
Preferred model and estimated base frequencies for each gene						Model substitution and rate heterogeneity parameters for each gene							
ADORA3	K2P	0.25	0.25	0.25	0.25	1	3	1	1	3	1	0	
ADRB2	HKY+I+G	0.2	0.33	0.25	0.22	1	5.75	1	1	5.75	1	0.46	1.05
APP	GTR+I+G	0.25	0.24	0.18	0.33	1.6	3.66	0.47	0.72	2.65	1	0	0.78
ATP7A	GTR+I+G	0.33	0.21	0.19	0.19	1.11	5.33	0.68	0.92	4.43	1	0.2	1.56
BDNF	HKY+I+G	0.21	0.33	0.28	0.17	1	4.73	1	1	4.73	1	0.42	0.61
BMI1	GTR+I+G	0.29	0.15	0.16	0.4	2.35	7.08	0.64	1.77	5.71	1	0.14	0.82
CNR1	GTR+I+G	0.18	0.32	0.25	0.24	3.43	14	1.3	2.13	14.6	1	0.53	0.7
CREM	GTR+I+G	0.21	0.24	0.28	0.27	1.68	3.44	0.55	0.8	2.97	1	0.18	1.6
EDG1	HKY+I+G	0.17	0.36	0.27	0.2	1	4.93	1	1	4.93	1	0.44	0.72
PLCB4	GTR+I+G	0.3	0.27	0.19	0.24	0.94	2.77	0.59	0.56	2.33	1	0.04	2.88
PNOC	GTR+I+G	0.23	0.33	0.31	0.12	0.9	2.73	0.86	0.38	4.14	1	0.15	1.09
RAG1	GTR+I+G	0.21	0.3	0.29	0.19	2.04	5.59	1.01	0.67	9.09	1	0.49	1.07
RAG2	HKY+I+G	0.28	0.24	0.22	0.27	1	6	1	1	6	1	0.35	1.63
TYR	GTR+I+G	0.24	0.26	0.25	0.25	2.18	7.86	1.3	0.93	8.76	1	0.32	1.27
ZFX	HKY+I+G	0.35	0.23	0.18	0.23	1	7.94	1	1	7.94	1	0.49	1.24
VWF	HKY+I+G	0.2	0.34	0.28	0.18	1	4.41	1	1	4.41	1	0.15	0.92
BRCA1	GTR+I+G	0.33	0.22	0.23	0.22	1.15	4.38	0.75	1.17	4.75	1	0.04	3.4
IRBP	GTR+I+G	0.21	0.3	0.3	0.18	1.5	4.91	1.34	0.83	5.8	1	0.18	1.04
A2AB	GTR+I+G	0.17	0.34	0.3	0.18	1.02	3.59	0.93	0.62	3.71	1	0.3	1.29
mtRNA	GTR+I+G	0.34	0.2	0.21	0.25	5.86	14	3.85	0.58	29.3	1	0.41	0.53

(From Hillis *et al.* '05.)

Tree Building Software

Some Packages that perform multiple methods:

- Phylogenetic Analysis Using Parsimony (PAUP 4.0): Swofford '02
- Phylogenetic Inference Package (Phylip 3.6): Felsenstein '06
- Molecular Evolutionary Genetic Analysis (MEGA 3.1): Kumar, Tamura, & Nei '04
- SplitsTree 4: Huson & Bryant '06

Tree Building Software

Some specialized software:

- MrBayes 3.1: Bayesan inference of phylogeny, Huelsenbeck *et al.* '05
- Bayesian Evolutionary Analysis Sampling Trees (BEAST): Drummond & Rambaut '03
- Quartet Puzzling: Strimmer & Von Haeseler '96

Software with Web Interface

Web access available for:

- At the Pasteur Institute

  `http://bioweb.pasteur.fr/intro-uk.html`:

  Phylip, Quartet Puzzling, Weighbor, etc.

- SplitsTree (older version: 3.2) at:

  `http://bibiserv.techfak.uni-bielefeld.de/splits/submission.html`

Software for Today:

- Suggested that you use on-line software (quicker to get started, but will run slower)
- Or, you can download most programs to your laptops:
  - most freely available (notable exception: PAUP)
  - newer ones in Java and machine independent
  - most run on Unix (Linux & OS X), some run on Windows

Sequence Formats

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- Phylip:
- FASTA:
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- FASTA:
- Can use the program READSEQ to convert from one to another. And EXTRACTSEQ (EMBOSS) to extract a region.

Sequence Formats

PAUP:

```
#NEXUS

Begin data;
Dimensions ntax=44 nchar=17028;
Format datatype=dna interleave gap=-;
Matrix
Opossum            TGCCTCTTCCGTTCAGTAATGAGGATGGACTACATGGTCTATTTCAGCTT
Diprotodontian     TGCCGCTTCCGCTCAGTTATGAGGATGGACTACATGGTCTATTTCAGCTT
Sloth              TGCAAATTCAGTTCCGTCATGAGAATGGACTACATGGTCTACTTCAGTTT
Armadillo          TGCAAATTCACTTCCGTCATGAGGATGGACTACATGGTGTACTTCAGTTT
Anteater           TGCAAATTCAGTTCCGTTGTGAGGATGGACTACATGGTCTACTTCAGTTT
Hedgehog           TGCCAATTCCGTTCTGTTGTGAGAATGGACTACATGGTGTTCTTCAGCTT
Mole               TGCAAGTTCCGCACAGTCGTGAGGATGGACTACATGGTCTACTTCAGCTT
Shrew              TGCCAGTTCCGCTCTGTGGTGAGGATGGACTACATGGTCTACTTCAGCTT
Tenrecid           TGCAAATTCCGTTCTACTATGAGAATGGACTACATGGTCTACTTCAGCTT
GoldenMole         TGCCAATTTCGTTCCGTAATGAGGATGGACTATATGGTCTACTTCAGCTT
...
```

Sequence Formats

Phylip:

```
 44 17028
Opossum      TGCCTCTTCC GTTCAGTAAT GAGGATGGAC TACATGGTCT ATTTCAGCTT
Diprotodon   TGCCGCTTCC GCTCAGTTAT GAGGATGGAC TACATGGTCT ATTTCAGCTT
Sloth        TGCAAATTCA GTTCCGTCAT GAGAATGGAC TACATGGTCT ACTTCAGTTT
Armadillo    TGCAAATTCA CTTCCGTCAT GAGGATGGAC TACATGGTGT ACTTCAGTTT
Anteater     TGCAAATTCA GTTCCGTTGT GAGGATGGAC TACATGGTCT ACTTCAGTTT
Hedgehog     TGCCAATTCC GTTCTGTTGT GAGAATGGAC TACATGGTGT TCTTCAGCTT
Mole         TGCAAGTTCC GCACAGTCGT GAGGATGGAC TACATGGTCT ACTTCAGCTT
Shrew        TGCCAGTTCC GCTCTGTGGT GAGGATGGAC TACATGGTCT ACTTCAGCTT
Tenrecid     TGCAAATTCC GTTCTACTAT GAGAATGGAC TACATGGTCT ACTTCAGCTT
GoldenMole   TGCCAATTTC GTTCCGTAAT GAGGATGGAC TATATGGTCT ACTTCAGCTT
...
```

Sequence Formats

FASTA:

```
>Opossum, 17028 bases, FC7ADFCB checksum.
TGCCTCTTCCGTTCAGTAATGAGGATGGACTACATGGTCTATTTCAGCTT
TTTCACATGGATCCTCATCCCTTTGGTCATCATGTGTGCCATCTATGTTG
ACATTTTCTATGTCATCCGGAACAAGCTCAGACAGAACTTCTCTGGCTCA
AAAGAGACAGGTGCATTCTATGGGAAGGAGTTCAAGACAGCCAAATCCCT
CTTTCTCATCCTCTTCTTGTTTGCCATATCCTGGCTGCCTTTATCCATCA
TCAACTGTATTTCTTATTTCTTCCCTAAGGCTGAGATA---CCTTCAGTT
TTGCTTGGGTTGGA?ATCCTGCTATCCCAT??????????????????????
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??????????????????????????????????????????????????
??????????????????????????????????????????????????
??????????????????????????CCCGGGTGGTCATTTTGATGGTGTG
...
```

Visualizing Trees

Web access available for:

- Phylip: Felsenstein
- SplitsTree: Bryant & Huson
- Mesquite: Wayne & David Maddison

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  (Then convert sequences into the needed format.)
- Look at the resulting trees– do they support your hypothesis?

Helpful Websites

- Dataset for this tutorial:

  `http://comet.lehman.cuny.edu/stjohn/dimacsTutorial`

- The Pasteur Institute:

  `http://bioweb.pasteur.fr/intro-uk.html`:

- SplitsTree: at:

  `http://bibiserv.techfak.uni-bielefeld.de/splits/submission.html`