Parsimony and perfect phylogeny

Lecture 6.2

The basis of modern biology

- Cell theory
- Mechanism
- [✓ Evolution]

Observations

- Species have great fertility, but not all their offspring survive
- Populations (groups of species) remain approximately the same size
- The resources (food, space, mates) are limited

Inference: there should be a struggle for survival

Observations

- No 2 individuals are completely identical
- Much of this variation is inheritable

Inference: Those who survive pass their traits to the next generation

Darwin's Theory of Evolution explains the mechanism

- Variation: There is variation in every population
- Competition: Organisms compete for limited resources
- Offspring: Organisms produce more offspring than can survive
- Genetics: Organisms pass genetic traits on to their offspring
- Natural Selection: Those organisms with the most beneficial traits are more likely to survive and reproduce.

All life: descent with modification

“*Probably all organic beings which have ever lived on this earth have descended from some one primordial life form. There is grandeur in this view of life that, whilst this planet has gone cycling on according to the fixed law of gravity, from so simple a beginning - endless forms most beautiful and most wonderful have been, and are being evolved*.”

(**Charles Darwin**, The Origin of Species)

Some facts

- The earth with liquid water is more than 3.6 billion years old
- Cellular life has been around for at least half of that period
- Organized multicellular life is at least 800 million years old
- Major life forms now on earth were not at all represented in the past. There were no birds or mammals 250 million years ago
- Major life forms of the past are no longer living. There used to be dinosaurs and Pithecanthropus, and there are none now
- All living forms come from previous living forms. Therefore, all present forms of life arose from ancestral forms that were different. Birds arose from nonbirds and humans from nonhumans

Evolution of molecules: variation

- On the molecular level the variation is achieved by random changes in the DNA:
  - Sequence mutations
  - Genome rearrangements
  - Combinatorics of sexual reproduction
  - Horizontal transfer of transposons
  - Gene duplications

Evolution of molecules: selection

- Selection can be applied only to the molecules with observable function: phenotype – proteins
- Evolutionary molecular "inventions" proven to be useful are preserved:
  - 40% of Human proteins are in Yeast: two species evolved independently, but this successful set of proteins changed minimally
  - Insulin of human and pig is so similar that pig's insulin was used for diabetic patients

Proteins seem to be a collection of distinct "approved" *domains* (amino acid chains which form a particular shape), which are preserved by selection

Phylogeny and evolution

- A *phylogeny* is a tree representation of the evolutionary history of some events
- Phylogeny construction is a popular computational problem in biology and linguistics
- In this course we will construct phylogenetic trees based on sequences (strings)

Use case: binary attributes

	move (active)	using sun energy	seeds	eggs	milk	swim (active)	fly (active)
Elephant	1	0	0	0	1	0	0
Snake	1	0	0	1	0	0	0
Whale	1	0	0	0	1	1	0
Fern	0	1	0	0	0	0	0
Eagle	1	0	0	1	0	0	1
Sunflower	0	1	1	0	0	0	0

Perfect phylogeny – the character evolved only once

- Many morphological traits evolved independently from different ancestors under the same environmental pressures (wings, fins)
- This is called *homoplasy* and is inescapable in real data
- Homoplasy is a poor indicator of evolutionary relationships because similarity does not reflect shared ancestry
- Sets of characters that admit phylogenies without homoplasy are said to be *compatible*
- Phylogenies that avoid homoplasy are called *perfect* and the character compatibility problem is called *the perfect phylogeny problem*

A perfect phylogenetic tree for binary characters

- Let *M* be a binary matrix representing *K* objects in terms of *C* characters or traits, which describe the objects. Each character takes one of 2 possible values: 0 or 1, which is recorded in the corresponding cell of M

- Given M for K objects and C characters, *a perfect phylogenetic tree* for M is a rooted directed tree T:
  - with exactly K leaves – 1 leaf per object
  - each character labels exactly 1 edge
  - for any object, the characters that label the edges along the path from the root to the parent of a corresponding leaf specify all the characters of this object whose value is 1

Parsimony principle

- In science, *parsimony* is preference for the least complex explanation. This is regarded as good when judging hypotheses.
- Occam's razor also states the "principle of parsimony“: *entia non sunt multiplicanda praeter necessitatem*, is the principle that "entities must not be multiplied beyond necessity": i.e. the simplest explanation or strategy tends to be the best one
- Under maximum parsimony, the preferred phylogenetic tree is the tree that requires the smallest number of evolutionary changes.

Parsimony of perfect phylogenetic trees

- The root of the tree represents an ancestral object that has none of the present characters
- Each character changes from 0 state to 1 state exactly once and never changes back from 1 to 0: once acquired, it can not be lost
- In the tree, any leaf below the node with incoming edge labeled by some character always has this character
- If each edge is labeled by each evolutionary event only **once**, the tree has the fewest state changes among all rooted trees for the given set of objects and characters, and thus represents **the most parsimonious tree**

The perfect phylogeny problem

Given matrix M, determine whether there is a phylogenetic tree for M and if yes, build it

Matrix M

C characters

K species

	1	2	3	4	5	6	7
A.	1	0	0	0	1	0	0
B.	1	0	0	1	0	0	0
C.	1	0	0	0	1	1	0
D.	0	1	0	0	0	0	0
E.	1	0	0	1	0	0	1
F.	0	1	1	0	0	0	0

Pre-processing: reorder columns

Solution: from Gusfield Chapter 17.3

	1	2	3	4	5	6	7
A.	1	0	0	0	1	0	0
B.	1	0	0	1	0	0	0
C.	1	0	0	0	1	1	0
D.	0	1	0	0	0	0	0
E.	1	0	0	1	0	0	1
F.	0	1	1	0	0	0	0

Radix sort (descending) of columns as binary numbers

>

	1	5	4	6	2	7	3
A.	1	1	0	0	0	0	0
B.	1	0	1	0	0	0	0
C.	1	1	0	1	0	0	0
D.	0	0	0	0	1	0	0
E.	1	0	1	0	0	1	0
F.	0	0	0	0	1	0	1

The resulting sets of species possessing characters:

A={1,5} B={1,4} C={1,5,6} D={2} E={1,4,7} F={2,3}

The resulting sets of characters that appear in species:

1={A,B,C,E} 5={A,C} 4={B,E} 6={C} 2={D,F} 7={E} 3={F}

Test for perfect phylogeny

The resulting sets of characters appear in objects:

1={A,B,C,E} 5={A,C} 4={B,E} 6={C} 2={D,F} 7={E} 3={F}

Theorem

Matrix M has a perfect phylogenetic tree if and only if any pair of the character sets is either disjoint, or one is a subset of another.

Such sets are called *compatible*

For any two sets *i* and *j*:

Set $i \cap$ Set $j = \emptyset$

or

Set $i \subset$ Set j

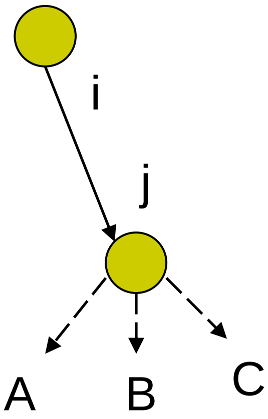
M has a perfect phylogenetic tree if and only if any pair of the character sets is *compatible*

Proof I: **If there is a phylogenetic tree T, then any two character sets are compatible**

- Let ei be the edge of T where character i changes from 0 to 1, and let ej be the similar edge for character j. All the objects that possess character i (or j) are found below these edges. Since in the phylogenetic tree each character labels only 1 edge, there are only

- 4 cases of possible relative topology of ei and ej:
  - (1) ei=ej – the same edge for both characters
  - (2,3) ei is on the path from the root to ej (or vice versa)
  - (4) ei and ej are in separate subtrees (disjoint sets) ■

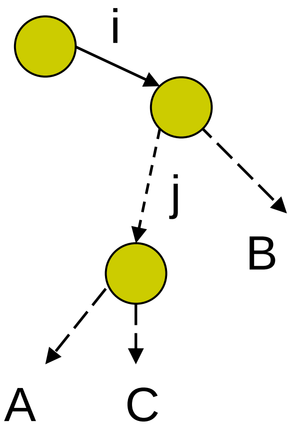
	i	j
A	1	1
B	1	1
C	1	1



Set $i \subset$ Set j

(1)

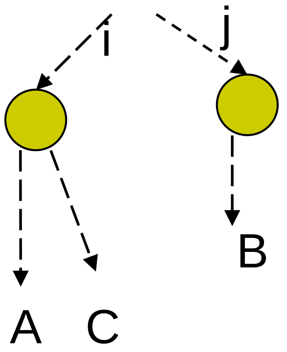
	i	j
A	1	1
B	1	
C	1	1



Set $j \subset$ Set i

(2)

	i	j
A	1	
B		1
C	1	



Set $j \cap$ Set $i = \emptyset$

(3)

M has a perfect phylogenetic tree if and only if any pair of the character sets is *compatible*

Proof II: **If any two character sets are compatible, then there is a phylogenetic tree T**

- Consider objects B and E, and let k be the largest character (the rightmost in M) that they both possess
- We need to proof that if B possesses character i<k, then E also possesses this character, in order to have a perfect phylogenetic tree
- Since Set i ∩ Set j already has common character k (through object B), then Set i ∩ Set j ≠ ∅, and hence Set i is contained in Set j (or vice versa). Therefore, the character i of object E must also be in state 1, and the perfect phylogenetic tree can be constructed ■

k

	1	2	3	4
A.	1	1	0	0
B.	1	0	1	0
C.	1	1	0	1
D.	0	0	0	0
E.	1	0	1	0

Construction in time O(KC)

The resulting sets of objects possessing characters in the sorted matrix M:

A={1,5} B={1,4} C={1,5,6} D={2} E={1,4,7} F={2,3}

1. Consider each ***column*** of M as a binary number. Using radix sort, sort these numbers in non-increasing order
2. Represent each object in a sorted matrix M as a sequence of characters which have state 1
3. Consider each object as a string consisting from this sequence plus sentinel ($)
4. Build *the keyword tree* for all obtained strings. Remove sentinel – you will get a perfect phylogenetic tree

Perfect phylogeny – step 1

	1	2	3	4	5	6	7
A.	1	0	0	0	1	0	0
B.	1	0	0	1	0	0	0
C.	1	0	0	0	1	1	0
D.	0	1	0	0	0	0	0
E.	1	0	0	1	0	0	1
F.	0	1	1	0	0	0	0

Radix sort (decreasing) of columns as binary numbers

	1	5	4	6	2	7	3
A.	1	1	0	0	0	0	0
B.	1	0	1	0	0	0	0
C.	1	1	0	1	0	0	0
D.	0	0	0	0	1	0	0
E.	1	0	1	0	0	1	0
F.	0	0	0	0	1	0	1

The resulting sets of objects possessing characters:

A={1,5} B={1,4} C={1,5,6} D={2} E={1,4,7} F={2,3}

The resulting sets of characters appearing in objects:

1={A,B,C,E} 5={A,C} 4={B,E} 6={C} 2={D,F} 7={E} 3={F}

Perfect phylogeny – step 2

	1	5	4	6	2	7	3
A.	1	1	0	0	0	0	0
B.	1	0	1	0	0	0	0
C.	1	1	0	1	0	0	0
D.	0	0	0	0	1	0	0
E.	1	0	1	0	0	1	0
F.	0	0	0	0	1	0	1

The resulting sets of objects possessing characters:

A={1,5} B={1,4} C={1,5,6} D={2} E={1,4,7} F={2,3}

Perfect phylogeny – step 3

	1	5	4	6	2	7	3
A.	1	1	0	0	0	0	0
B.	1	0	1	0	0	0	0
C.	1	1	0	1	0	0	0
D.	0	0	0	0	1	0	0
E.	1	0	1	0	0	1	0
F.	0	0	0	0	1	0	1

The resulting strings with sentinels:

A=1 5 $

B=1 4 $

C=1 5 6 $

D=2 $

E=1 4 7 $

F=2 3 $

Perfect phylogeny – step 4

The resulting strings with sentinels:

A=1 5 $

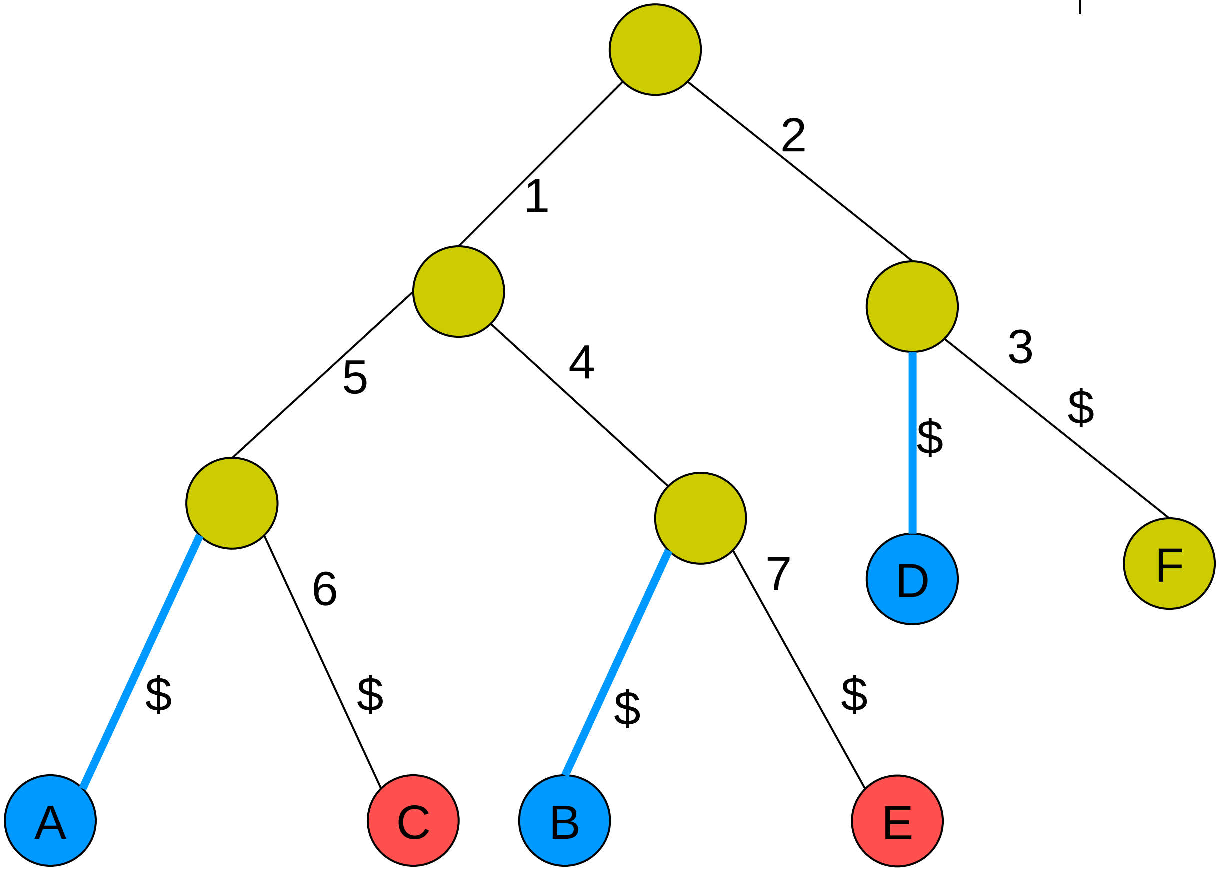
B=1 4 $

C=1 5 6 $

D=2 $

E=1 4 7 $

F=2 3 $



The keyword tree containing all strings

Perfect phylogeny – tree

The resulting strings with sentinels:

A=1 5 $

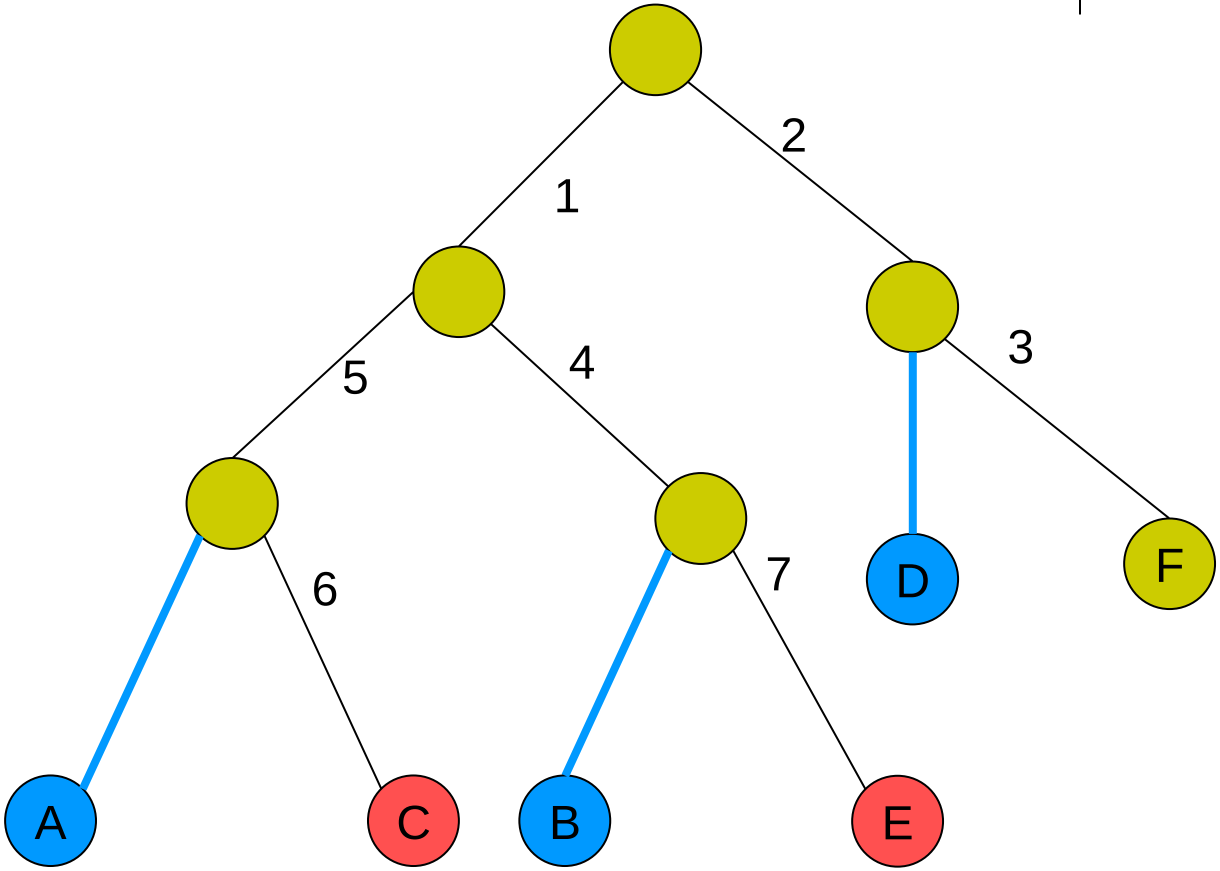
B=1 4 $

C=1 5 6 $

D=2 $

E=1 4 7 $

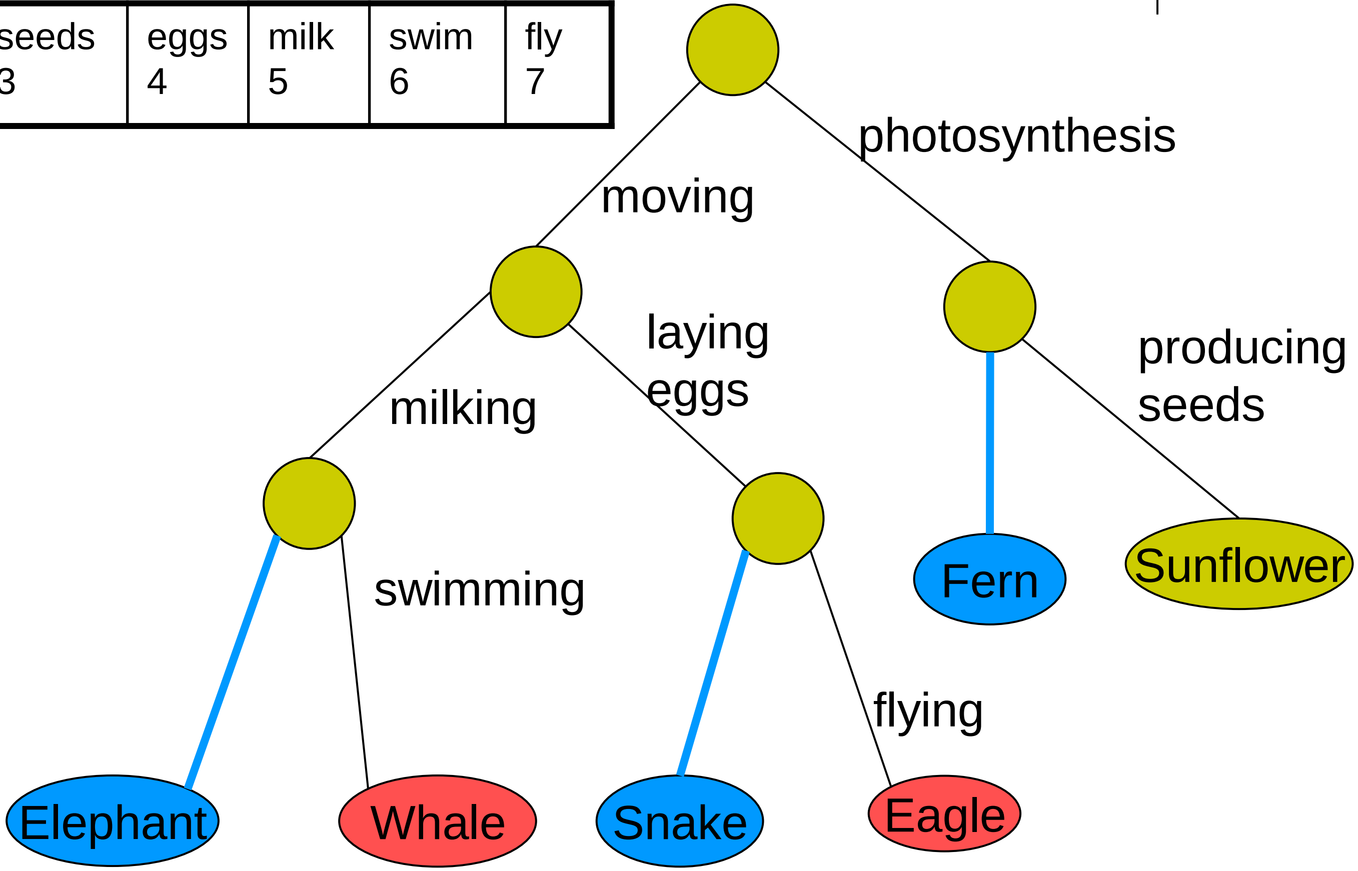
F=2 3 $



Our first phylogenetic tree

move	photosynthesis	seeds	eggs	milk	swim	fly
1	2	3	4	5	6	7

A. Elephant
B. Snake
C. Whale
D. Fern
E. Eagle
F. Sunflower



The source of a binary data

- Morphological traits – not a good choice, since there is a lot of homoplasy – convergent evolution – the same morphological character is acquired more than once and not from the common ancestor
- Biosequences – substrings, special patterns, gaps – better in non-coding regions, since the coding regions do not evolve much with time

Perfect phylogeny for insertions

```
         Ins1      Ins2      Ins3     Ins4
A: RPCVCPKQAVLRQAAQLAQVLQRQI____QQLRRL__AA
B: RPCACP___VLRQVVQ__QALQRQIIQGPQQLRRL__AA
C: KPCLCPKQAAVKQAAHLVQQLYQGQ____KQVRRA__LL
D: KPCVCP___VLRQAAH__QQLYQGQIQGPRQVRRAFRVA
E: KPCVCP___VLRQAAHLVQQLYQGQ____RQVRRLF_AA
```

	Ins 1	Ins 2	Ins 3	Ins 4
A	1	1	0	0
B	0	0	1	0
C	1	1	0	0
D	0	0	1	1
E	0	1	0	0

Exercise:

- Is there a tree?
- If yes, build one