

Introduction to Phylogenetics  
Week 1

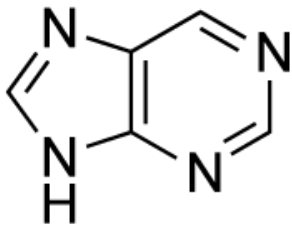
Basic Concepts of  
Molecular Evolution

# I. Basic Concepts

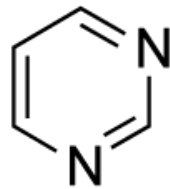
- Most life uses DNA as its genetic template
- Some viruses use RNA as the genetic template
- Evolution rate – Depends a great deal on generation time, fidelity of enzymes, fecundity and environmental stressors

# I. Basic Concepts

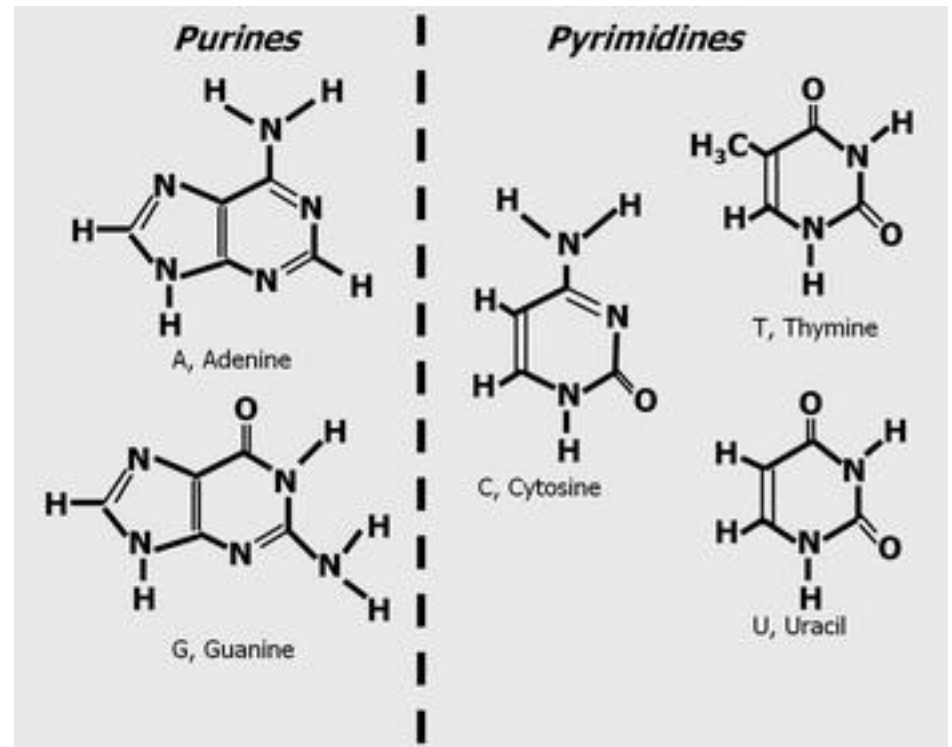
- Purines are A or G and pyrimidines are T or C (or U)



purine (R)

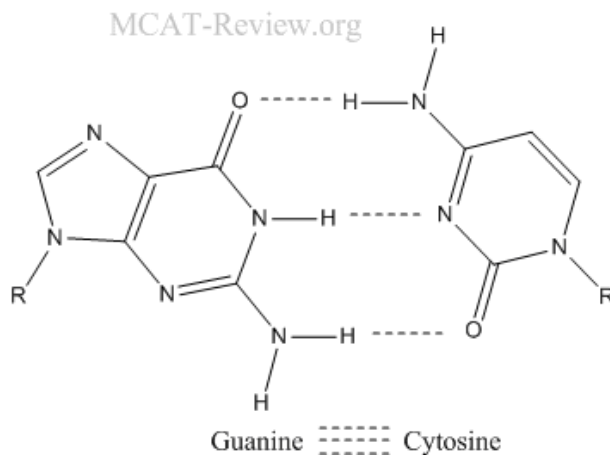
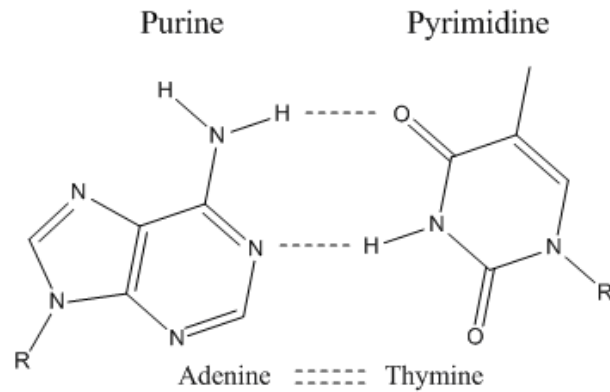


pyrimidine (Y)



# I. Basic Concepts

- $A=T$  and  $G \cong C$



Kind of a big deal when it comes to evolution

# I. Basic Concepts

- Because of purine: pyrimidine base pairing, transitions are more likely to occur than transversions
  - Transitions (4): A  $\leftrightarrow$  G, C  $\leftrightarrow$  T
  - Transversions (8): A  $\leftrightarrow$  C, A  $\leftrightarrow$  T, G  $\leftrightarrow$  C, G  $\leftrightarrow$  T

**Kind of a big deal when it  
comes to evolution**

# I. Basic Concepts

- Genetic code is degenerate

|                     |   | Second base of codon             |                   |                       |                    |   |                     |
|---------------------|---|----------------------------------|-------------------|-----------------------|--------------------|---|---------------------|
|                     |   | U                                | C                 | A                     | G                  |   |                     |
| First base of codon | U | UUU Phenylalanine phe            | UCU Serine ser    | UAU Tyrosine tyr      | UGU Cysteine cys   | U | Third base of codon |
|                     |   | UUC                              | UCC               | UAC                   | UGC                | C |                     |
|                     |   | UUA Leucine leu                  | UCA               | UAA STOP codon        | UGA STOP codon     | A |                     |
|                     |   | UUG                              | UCG               | UAG                   | UGG Tryptophan trp | G |                     |
|                     | C | CUU Leucine leu                  | CCU Proline pro   | CAU Histidine his     | CGU Arginine arg   | U |                     |
|                     |   | CUC                              | CCC               | CAC                   | CGC                | C |                     |
|                     |   | CUA                              | CCA               | CAA Glutamine gin     | CGA                | A |                     |
|                     |   | CUG                              | CCG               | CAG                   | CGG                | G |                     |
|                     | A | AUU Isoleucine ile               | ACU Threonine thr | AAU Asparagine asn    | AGU Serine ser     | U |                     |
|                     |   | AUC                              | ACC               | AAC                   | AGC                | C |                     |
|                     |   | AUA                              | ACA               | AAA Lysine lys        | AGA Arginine arg   | A |                     |
|                     |   | AUG Methionine met (start codon) | ACG               | AAG                   | AGG                | G |                     |
|                     | G | GUU Valine val                   | GCU Alanine ala   | GAU Aspartic acid asp | GGU Glycine gly    | U |                     |
|                     |   | GUC                              | GCC               | GAC                   | GGC                | C |                     |
|                     |   | GUA                              | GCA               | GAA Glutamic acid glu | GGA                | A |                     |
|                     |   | GUG                              | GCG               | GAG                   | GGG                | G |                     |

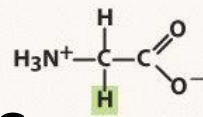
Only change in AA:

30% at 3<sup>rd</sup> base  
100% at 2<sup>nd</sup> base  
96% at 1<sup>st</sup> base

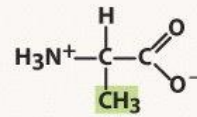
# I. Basic Concepts

- AAs can have similar chemistry

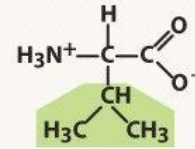
## Nonpolar side chains



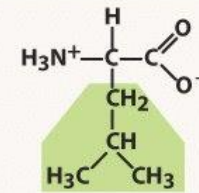
Glycine (G)  
Gly



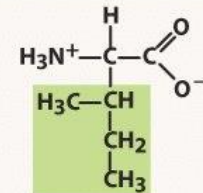
Alanine (A)  
Ala



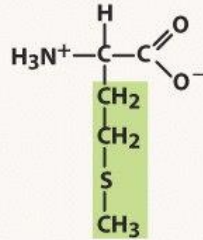
Valine (V)  
Val



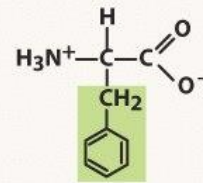
Leucine (L)  
Leu



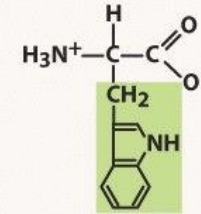
Isoleucine (I)  
Ile



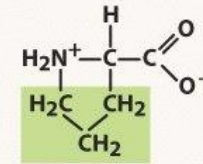
Methionine (M)  
Met



Phenylalanine (F)  
Phe

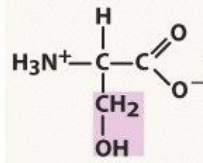


Tryptophan (W)  
Trp

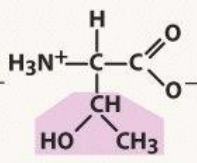


Proline (P)  
Pro

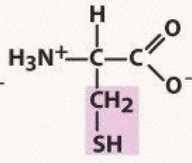
## Polar side chains



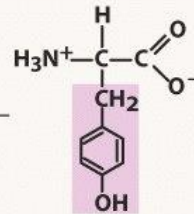
Serine (S)  
Ser



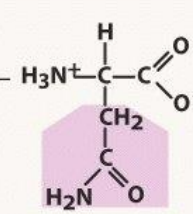
Threonine (T)  
Thr



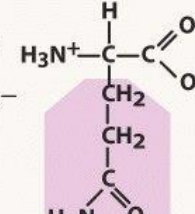
Cysteine (C)  
Cys



Tyrosine (Y)  
Tyr



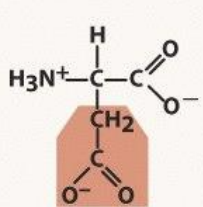
Asparagine (N)  
Asn



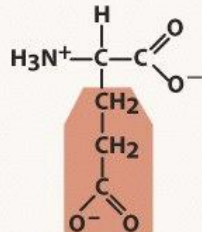
Glutamine (Q)  
Gln

## Electrically charged side chains

### Acidic

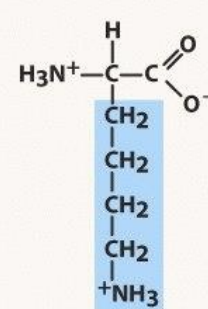


Aspartate (D)  
Asp

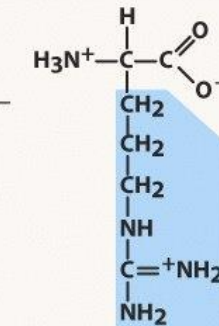


Glutamate (E)  
Glu

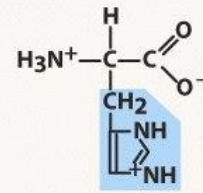
### Basic



Lysine (K)  
Lys



Arginine (R)  
Arg



Histidine (H)  
His

# I. Basic Concepts

- Synonymous mutation – silent mutation
  - Generally under neutral selection
  - Can affect RNA stability
  - Can affect tRNA usage
- Non-synonymous mutation – non-silent
  - change in amino acid coding

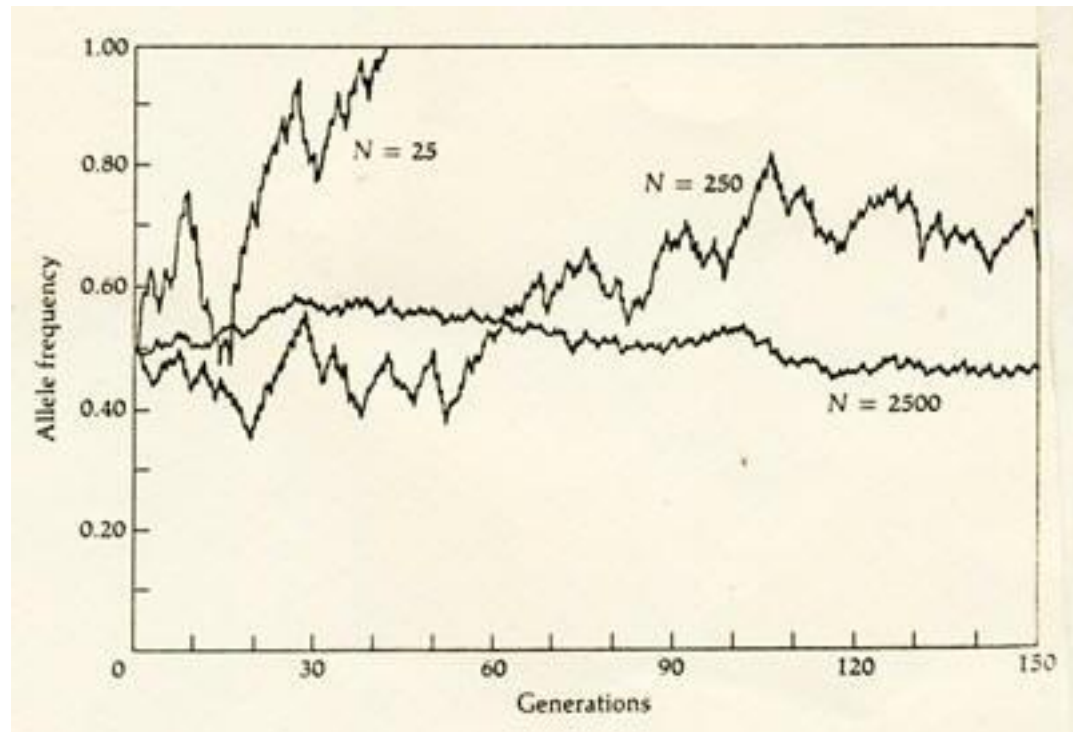


# I. Basic Concepts

- Gene duplication
- Orthologs
  - High selection pressure
- Paralogs
  - Relaxed selection pressure
  - Increased mutation rate
  - Evolution unique functions

## II. Population genetics

- Mutations – polymorphisms in offspring
- Fixation rate – rate where polymorphisms reach 100%



## II. Population genetics

- Many genetic changes are maintained as polymorphisms in a population
- Cannot calculate rate of fixation

$$\frac{1}{2N} \approx 2Nm = m$$

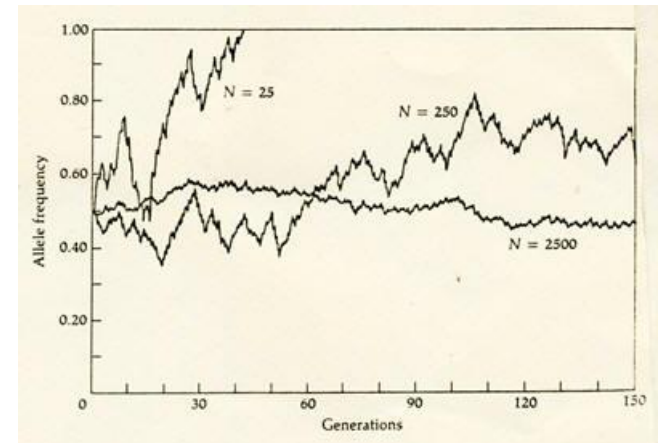
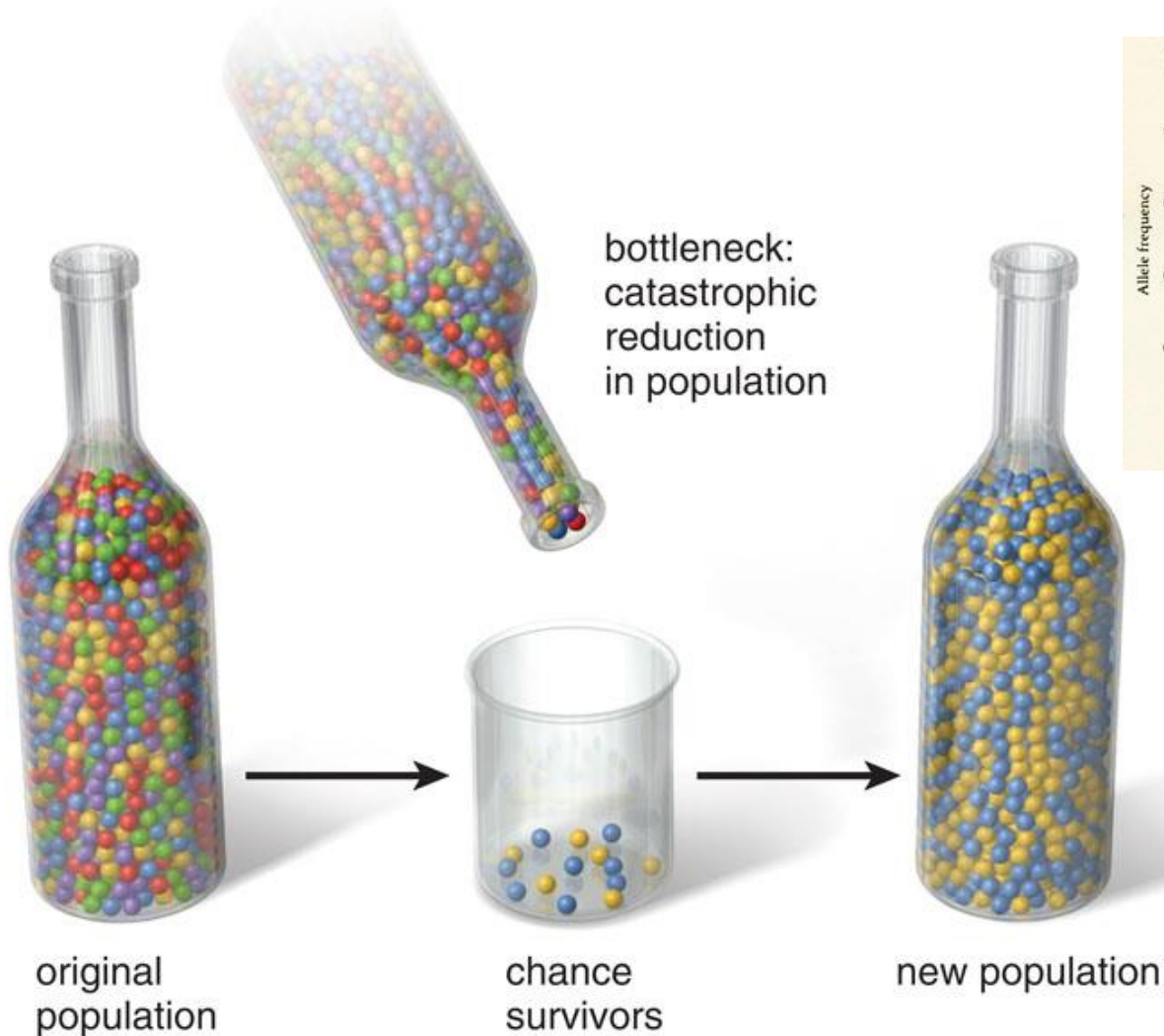
- Can use difference in genetic structure as equivalent to genetic differences

## II. Population genetics

- Rate of population change
  - Underlying mutation rate
  - Generation time
  - Impact of allele on fitness
    - Positive selection
    - Negative selection
    - Balancing selection
  - Population size

# II. Population genetics: Bottlenecks

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Coalescent event

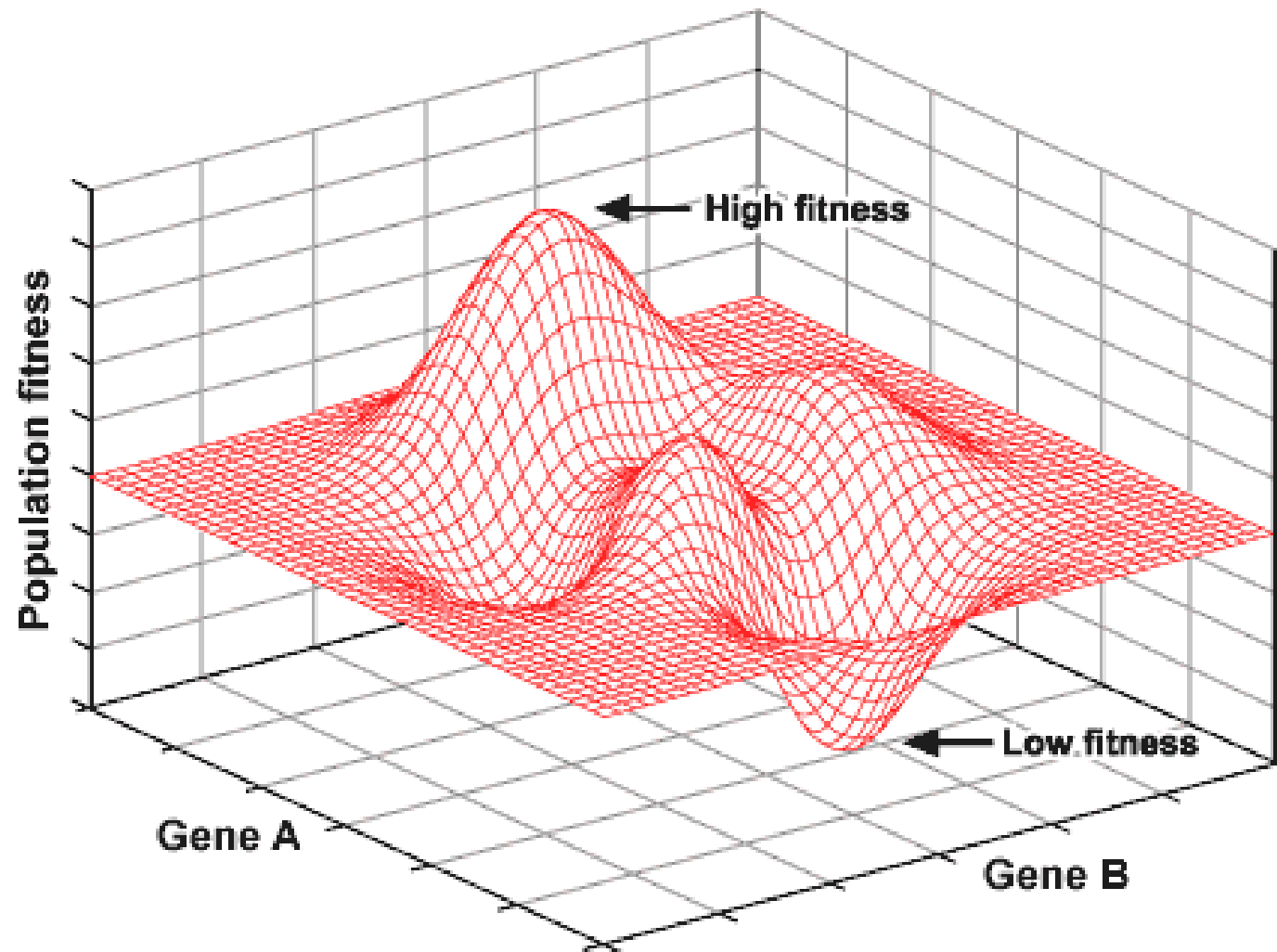
# III. Evolutionary Models

- Deterministic
  - Chance events (other than environmental) do not dramatically effect allele frequencies
  - Change dependent positive/negative selection
  - Needs large population
- Stochastic
  - Random fluctuations determine allele frequency
  - Change cannot be determined by mutation rate
  - More important in small populations
  - Genetic drift (random sampling more important)

# III. Evolutionary Models

- Evolution is likely a combination of deterministic and stochastic effects
  - Mutations result in genetic variation that natural selection acts as dominant force
- Adaptive evolution – positive selective pressure on mutations
- Neutral theory – stochastic fixation of neutral/nearly neutral mutations
  - Assumes many organisms well adapted to current conditions
  - Positive selection only affects few individuals within greater population

# III. Evolutionary Models

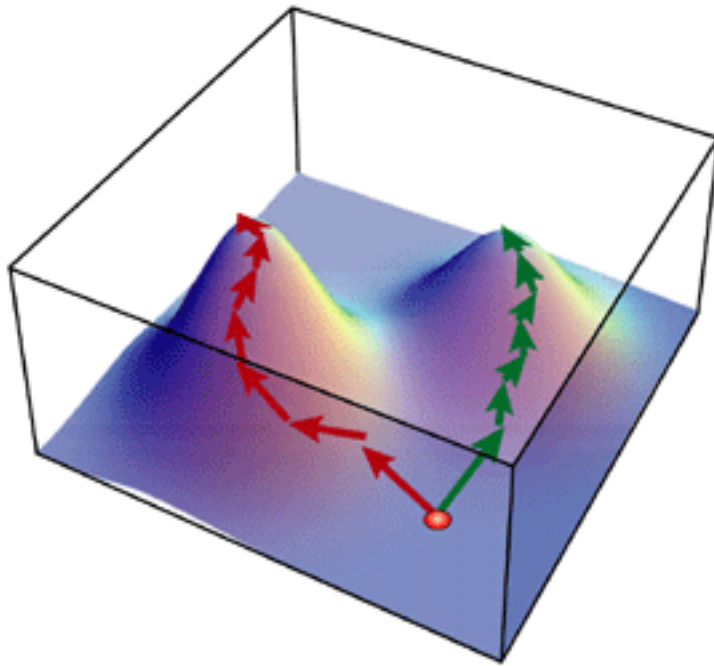




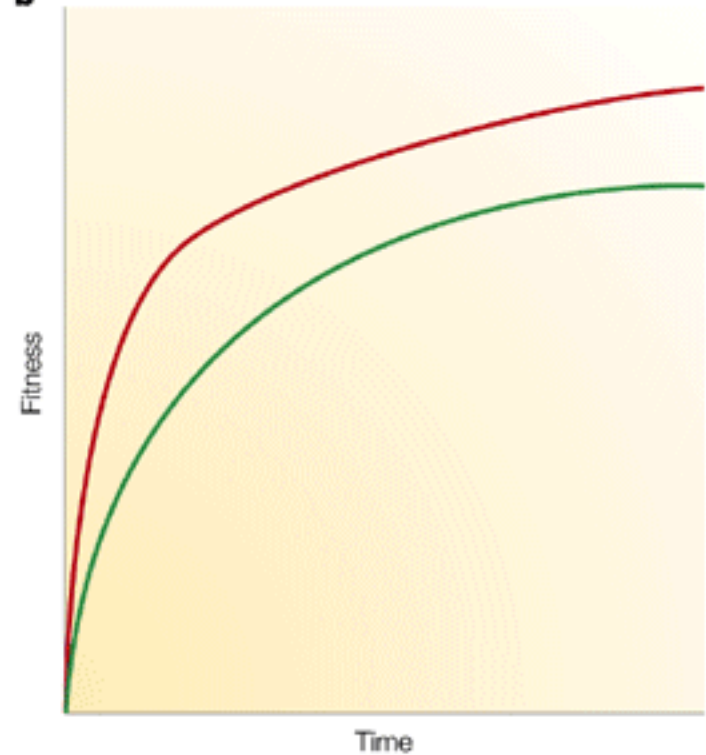
# III. Evolutionary Models

- Adaptive landscapes

**a**



**b**



# III. Phylogeny

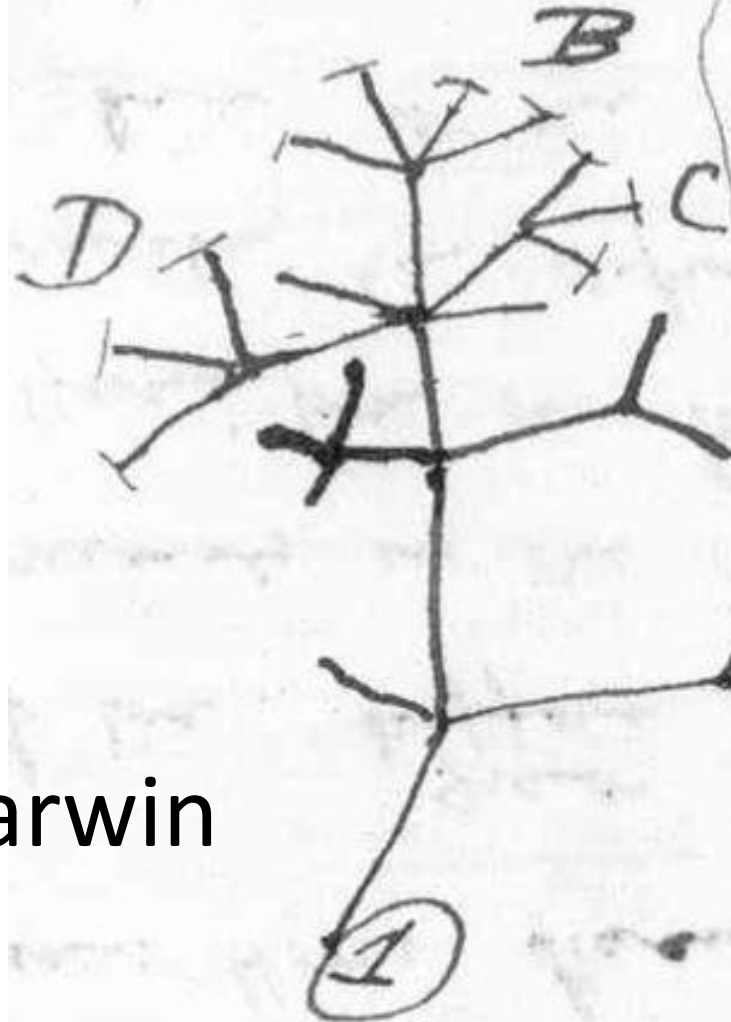
Carl Linnaeus - Father of modern taxonomy

Began classifying plants based on structure – published *Systema Naturae* in 1735



# III. Phylogeny

I think



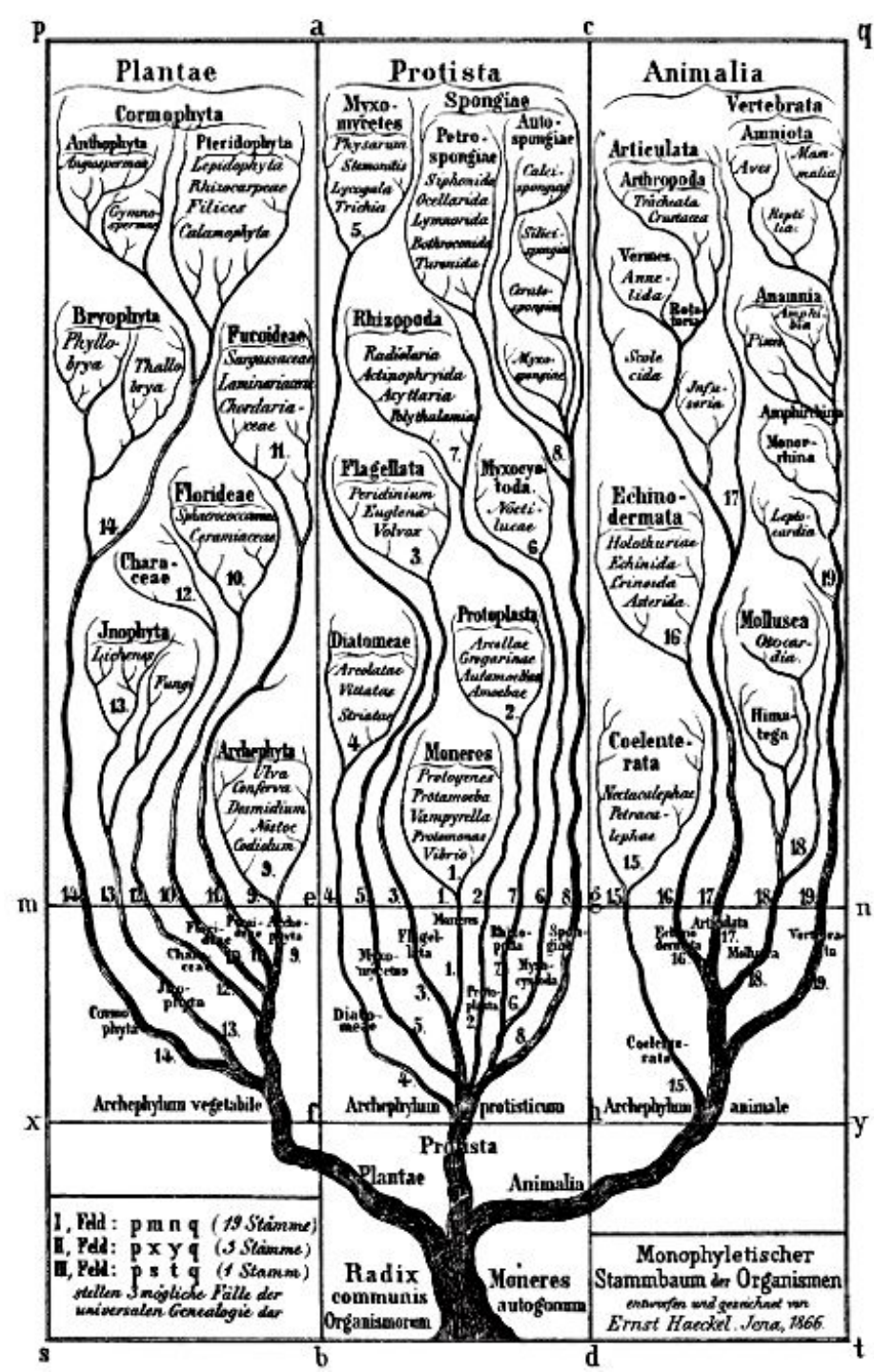
36  
Can never be that we  
know that there are  
more living species in  
the world than there  
were (as is) - 1837  
as the world is  
as the world is

Charles Darwin

c. 1837

# III. Phylogeny

Haeckle - First to include microorganisms within a tree  
Created the group – Monera  
Five-kingdom Tree of Life



# IV. Molecular Phylogeny

- Determine relationships between genes/gene fragments
- Homologous regions need to be aligned (program)
- Missing sequence data must be trimmed (program)
- Determine appropriate evolutionary model to use (program)
- Generate phylogenetic tree (program)
- Test tree (program)



# IV. Molecular Phylogeny

|                     |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    |             |
|---------------------|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|-------------|
| Nucleotide position | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 |             |
| Microbe 1           | A | C | U | G | A | C | U | C | A | U  | A  | G  | A  | U  | C  | 4/15 = 0.27 |
| Microbe 2           | A | G | U | G | A | G | U | C | A | G  | A  | C  | A  | U  | C  | 4/15 = 0.27 |
| Microbe 3           | U | C | U | G | G | G | U | C | A | G  | A  | C  | A  | U  | C  | 5/15 = 0.33 |
| Microbe 4           | U | G | U | G | G | U | C | C | A | U  | A  | C  | A  | U  | C  | 4/15 = 0.27 |
|                     |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    | 5/15 = 0.33 |
|                     |   |   |   |   |   |   |   |   |   |    |    |    |    |    |    | 3/15 = 0.20 |

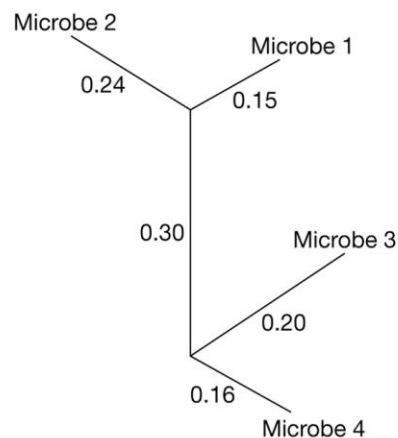
(a) Sequence alignment and analysis

| Microbe | 1   | 2    | 3    | 4    |
|---------|-----|------|------|------|
| 1       | 1.0 | 0.27 | 0.27 | 0.33 |
| 2       |     | 1.0  | 0.27 | 0.33 |
| 3       |     |      | 1.0  | 0.20 |
| 4       |     |      |      | 1.0  |

(b) Calculated evolutionary distance

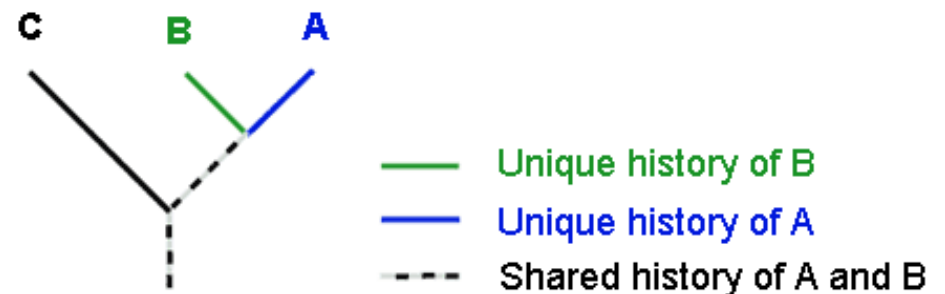
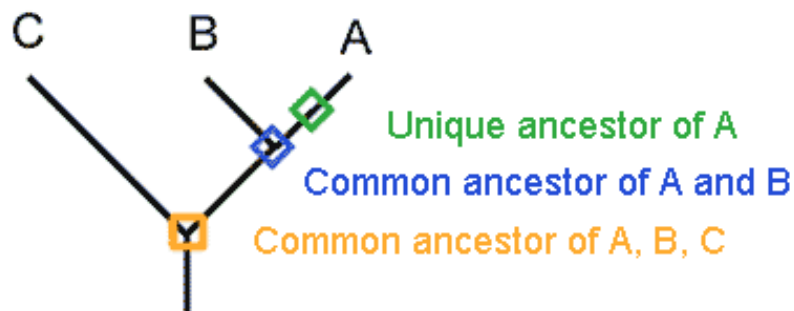
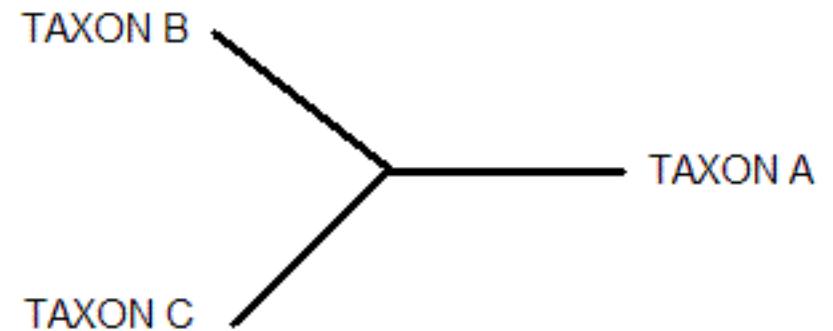
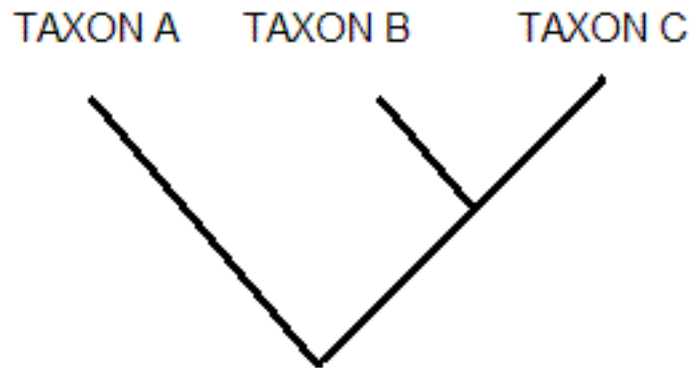
| Microbe | 1   | 2    | 3    | 4    |
|---------|-----|------|------|------|
| 1       | 1.0 | 0.32 | 0.32 | 0.44 |
| 2       |     | 1.0  | 0.32 | 0.44 |
| 3       |     |      | 1.0  | 0.26 |
| 4       |     |      |      | 1.0  |

(c) Corrected evolutionary distance

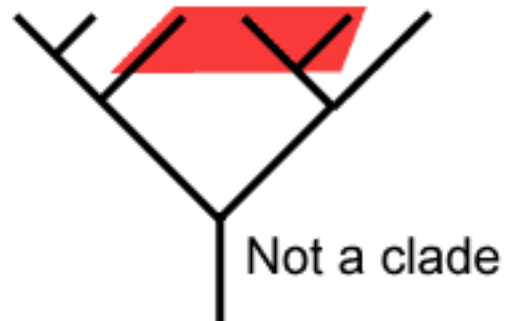
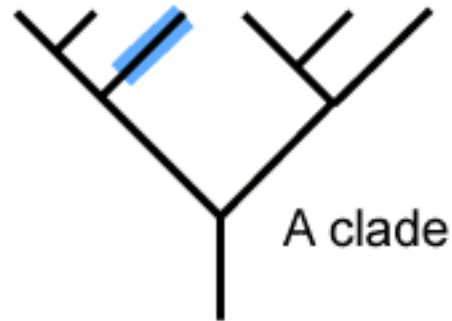
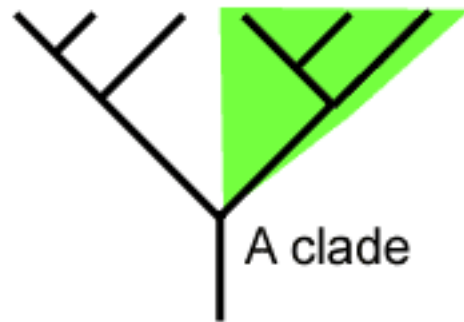


(d) Phylogenetic tree

# IV. Molecular Phylogeny

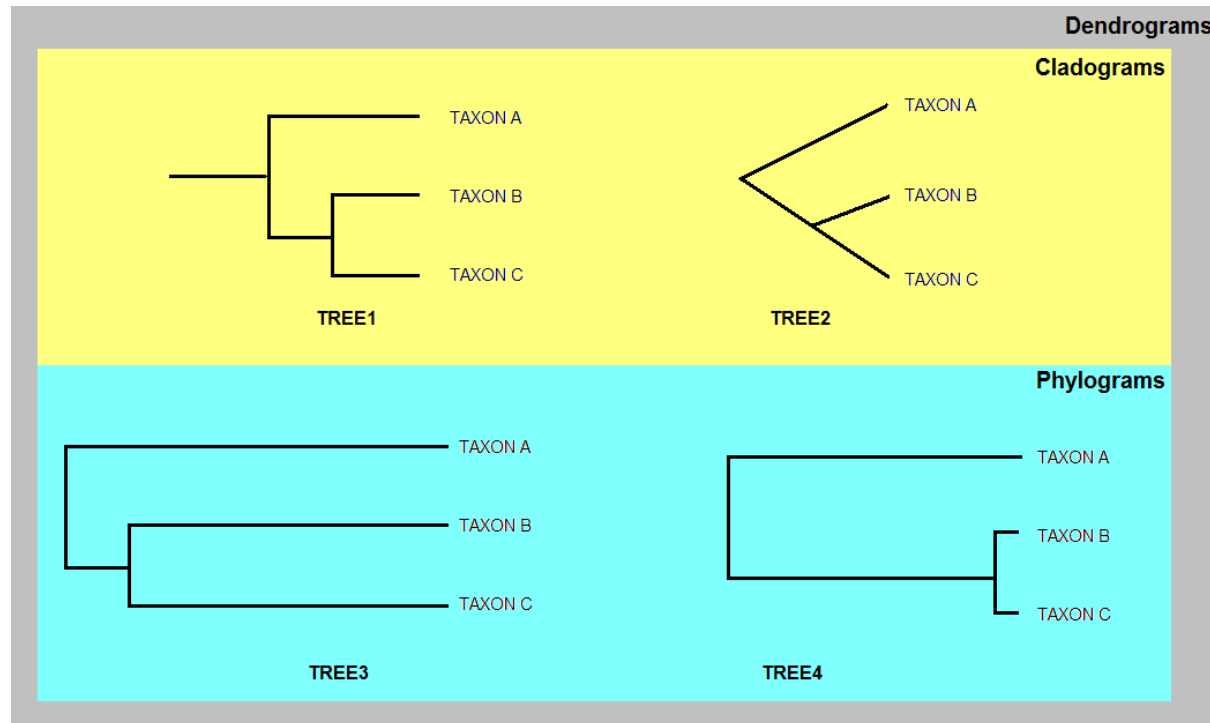


# IV. Molecular Phylogeny

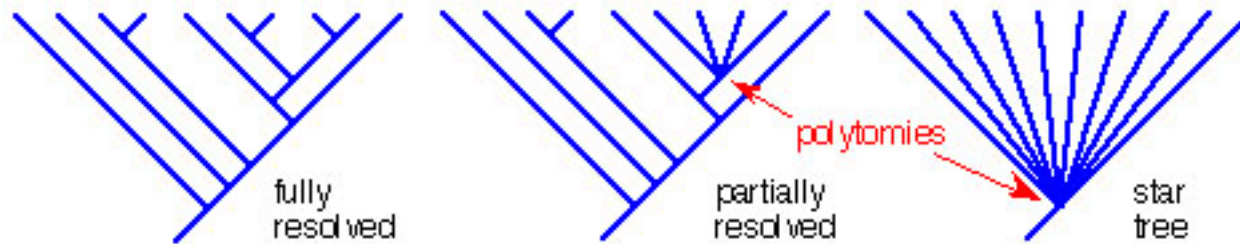


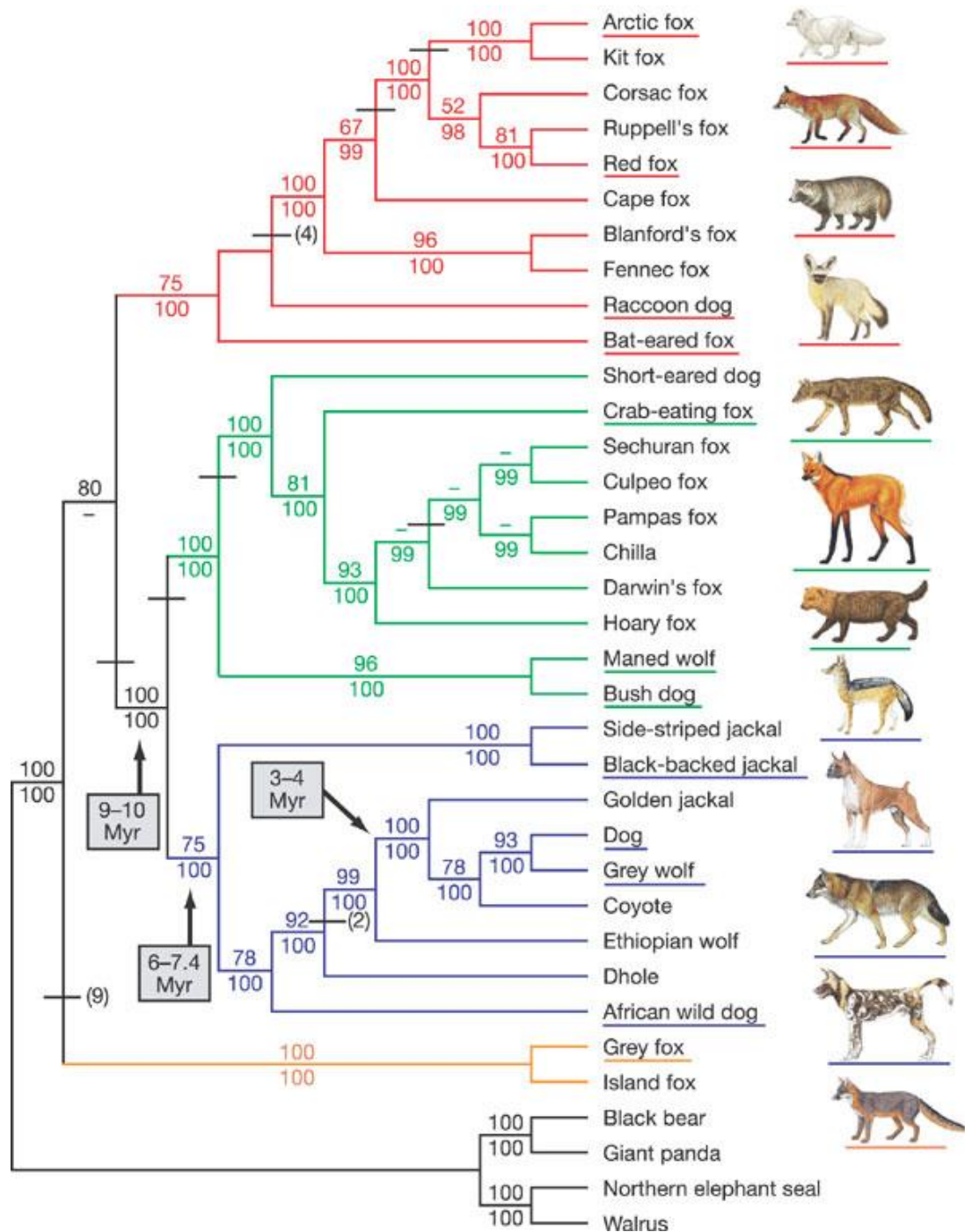


# IV. Molecular Phylogeny

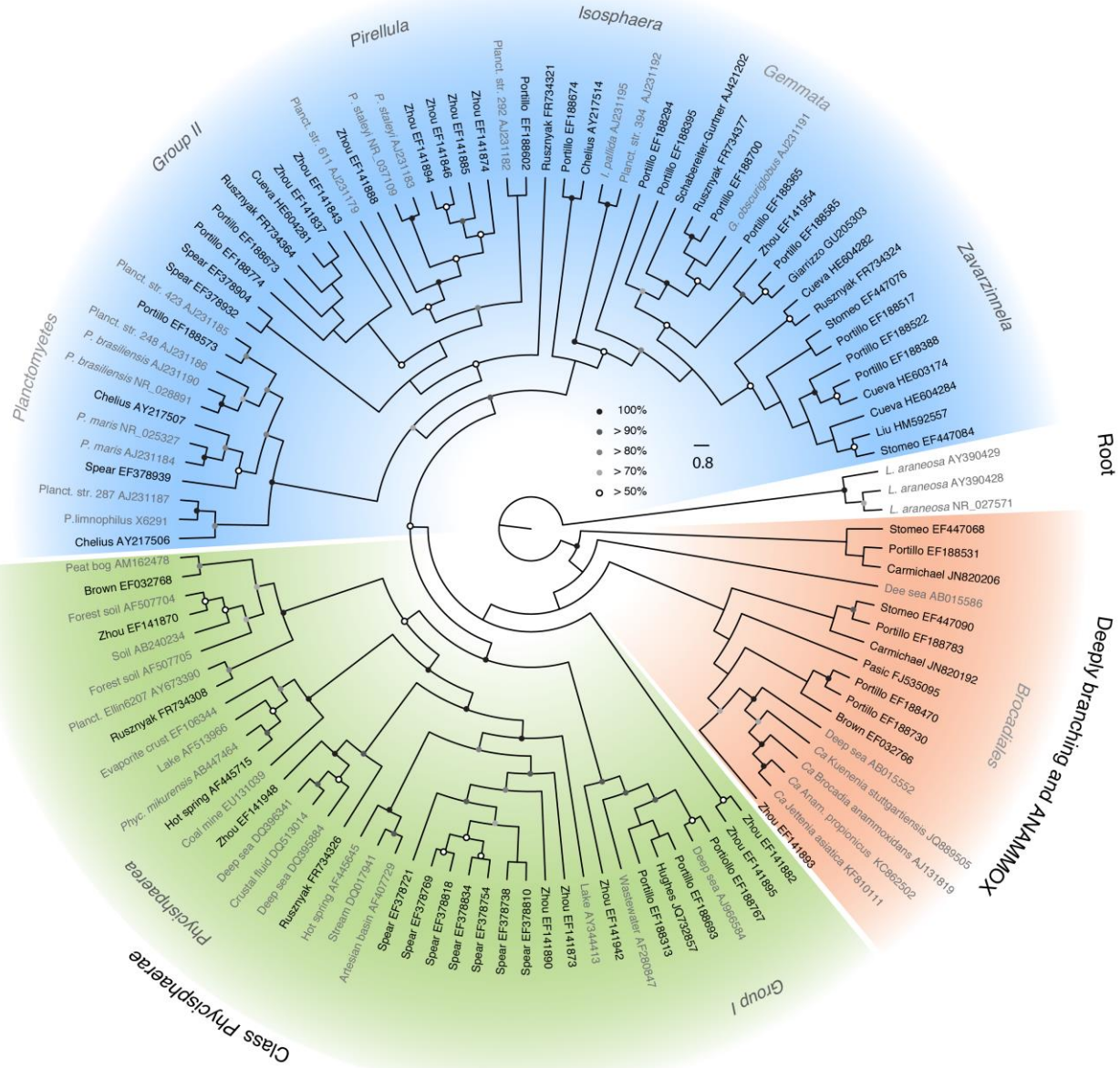


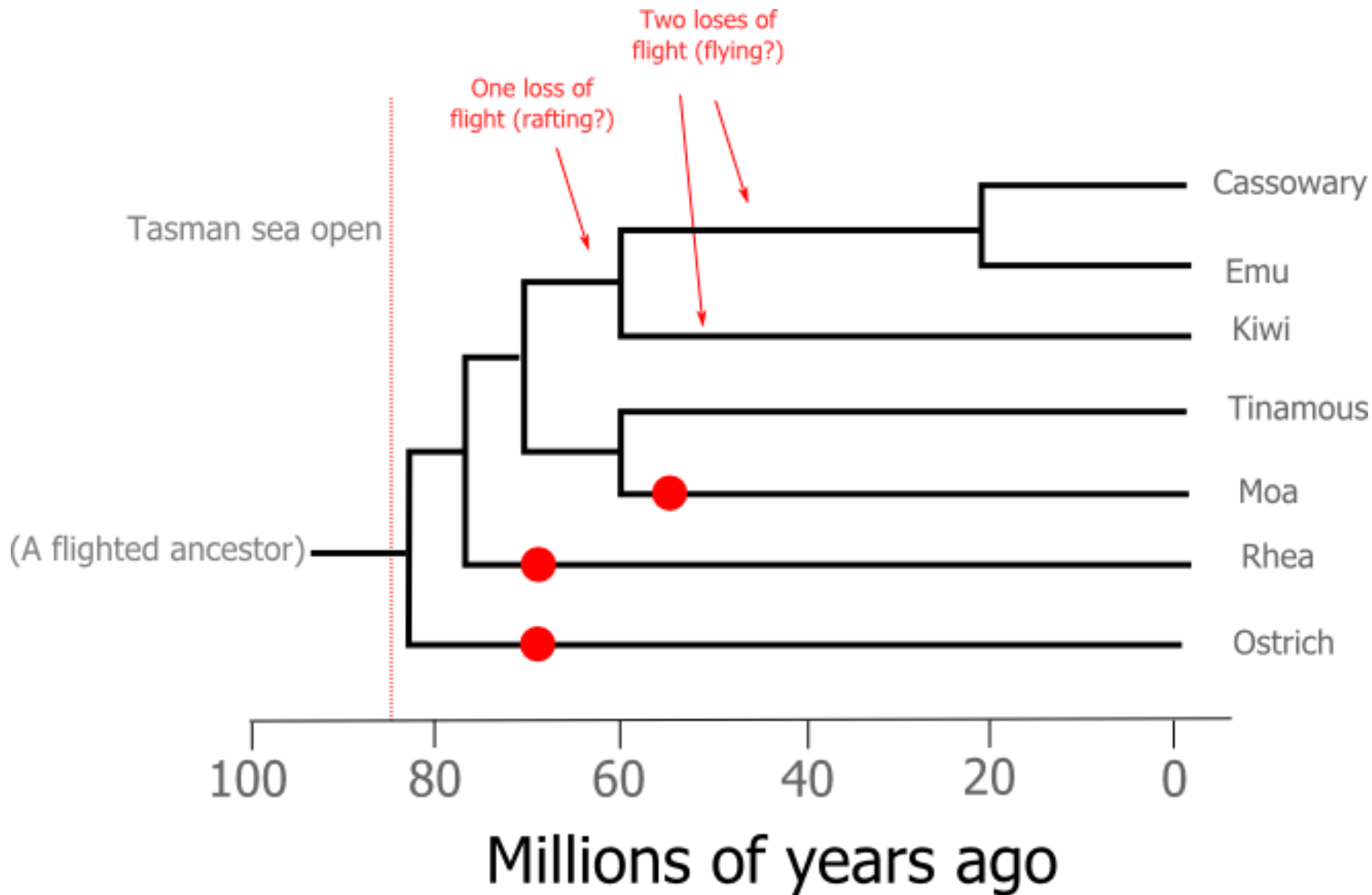
# IV. Molecular Phylogeny





Class *Planctomycea*





# I. Definitions

- Synonymous mutation
- Non-synonymous mutation
- Transition
- Transversion
- Indels
- Positive selection
- Neutral selection
- Neutral theory
- Stochastic effects
- Allee effects