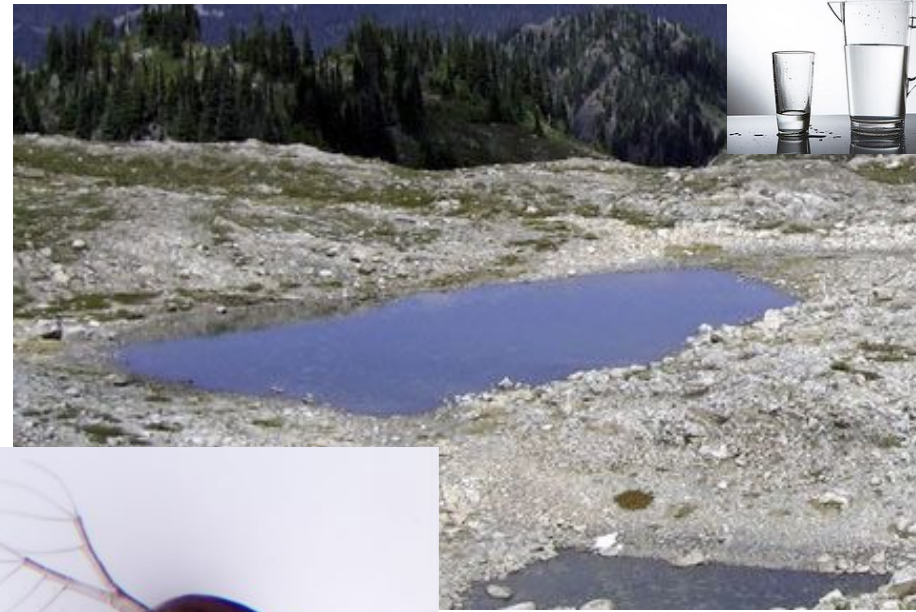


Phylogenetic Inference of Daphnia Genotypes with Varying Degrees of Tolerance to UVR exposure



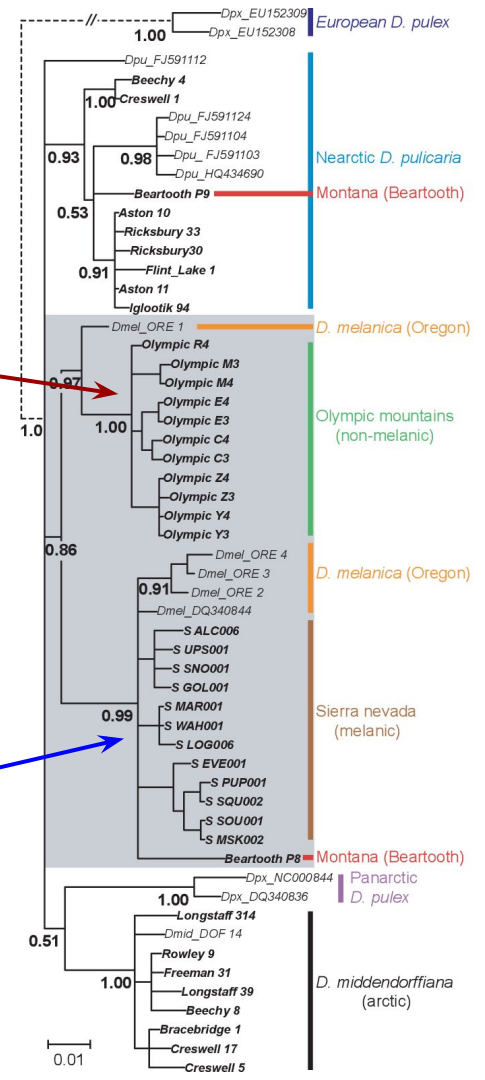
Elizabeth Brooks, Pfrender Lab

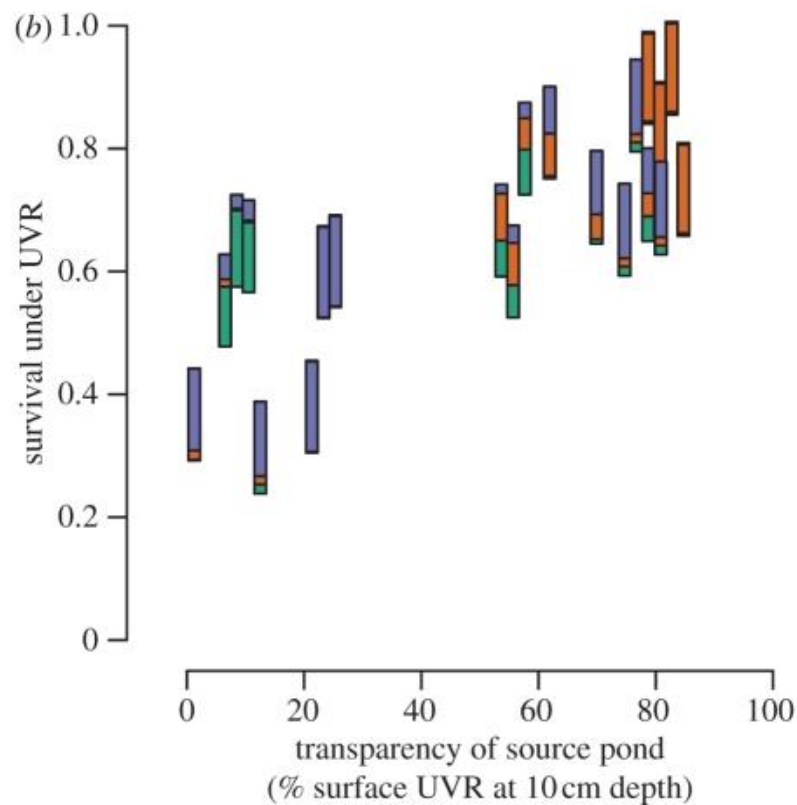
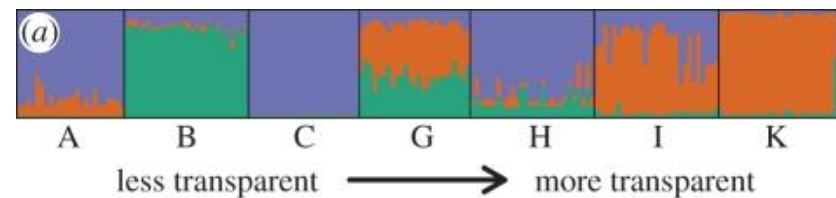
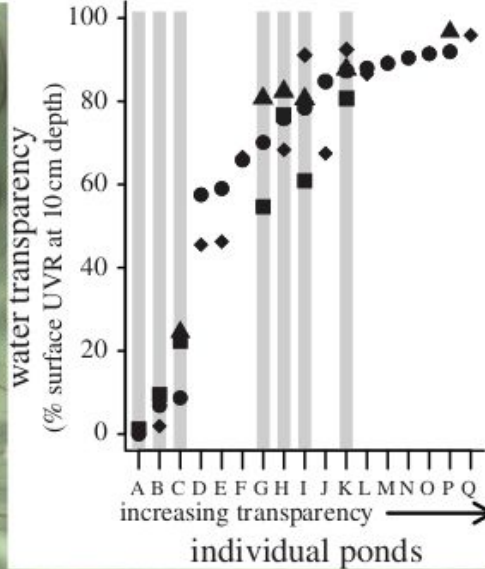
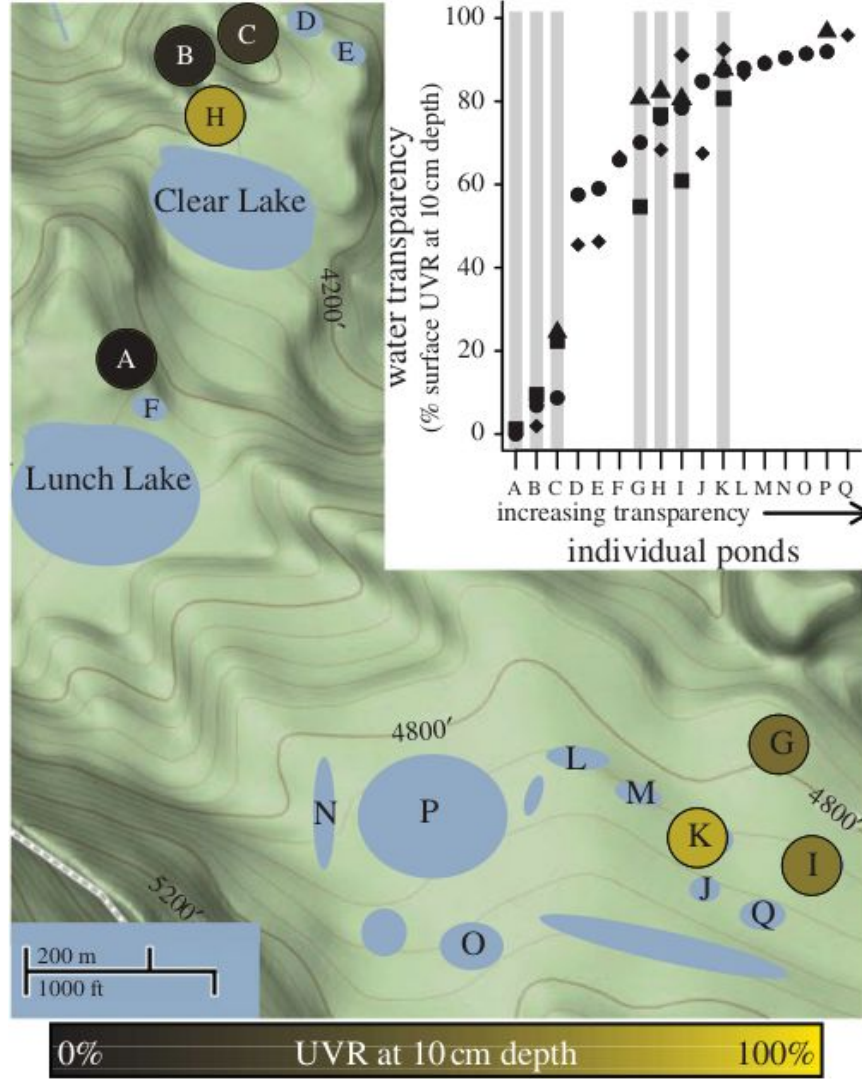


Daphnia melanica with varying tolerance to UV radiation

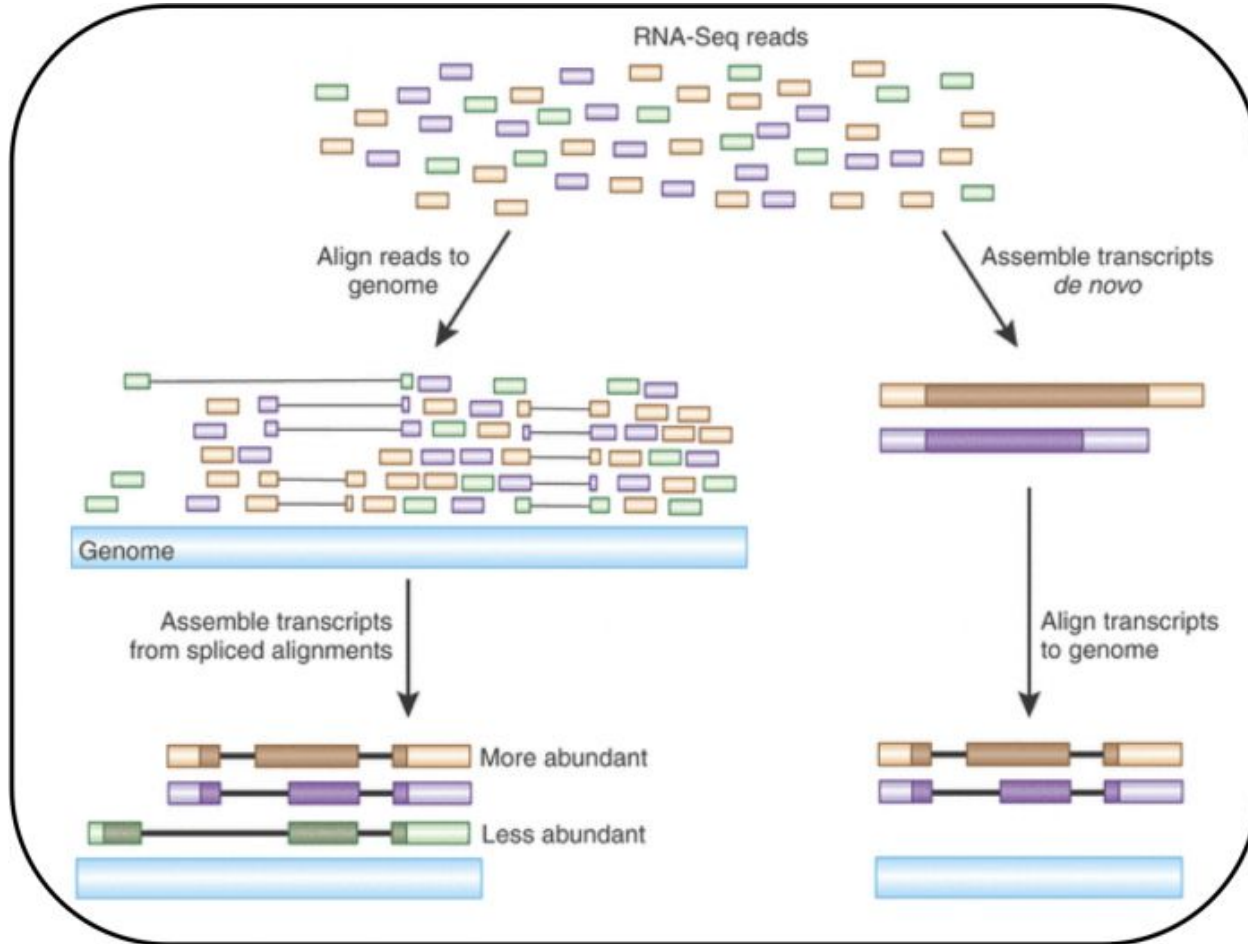
Lab Clonal Genotypes

Olympic E05	Tolerant
Olympic Y05	Tolerant
Olympic Y023	Not Tolerant
Olympic R2	Not Tolerant
Sierra	Tolerant
PA	Not Tolerant





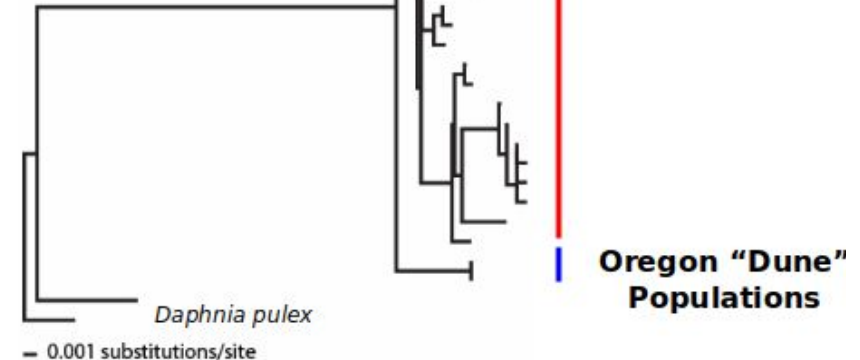
Alignment Based Methods



Reciprocal Best Hits Approach: RBHB

RBH to PA42 Reference Genome

Olympic E05	12868	69.78%
Olympic Y05	12919	70.06%
Olympic Y023	12934	70.14%
Olympic R2	12883	69.86%
Sierra	13220	71.69%
PA	13451	72.94%

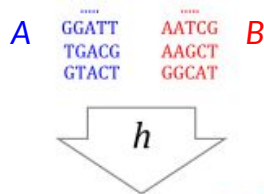


How do divergent adaptive phenotypes arise in naturally subdivided populations of Daphnia?

- Step 1.** Prepare sets of DNA or RNA sequences for each species
- Step 2.** Estimate Jaccard distances between species DNA or RNA sequences using MinHash sketches
- Step 3.** Infer dendrograms from pairwise distance matrix using neighbor-joining (NJ) or hierarchical clustering (UPGMA)

Alignment-Free Methods

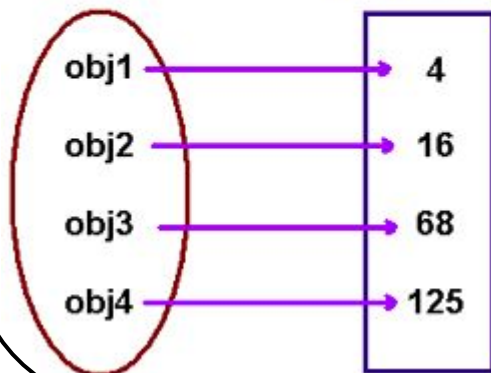
Step 1: Generate Sketch



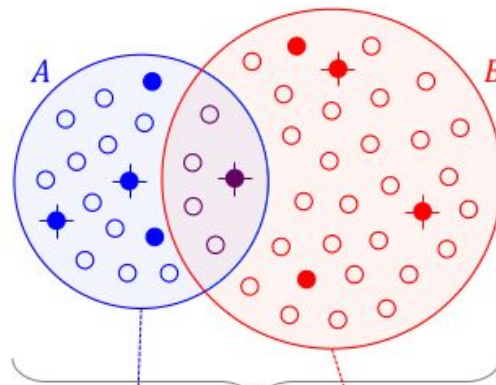
OBJECT → INTEGER

DATA

HASH CODES



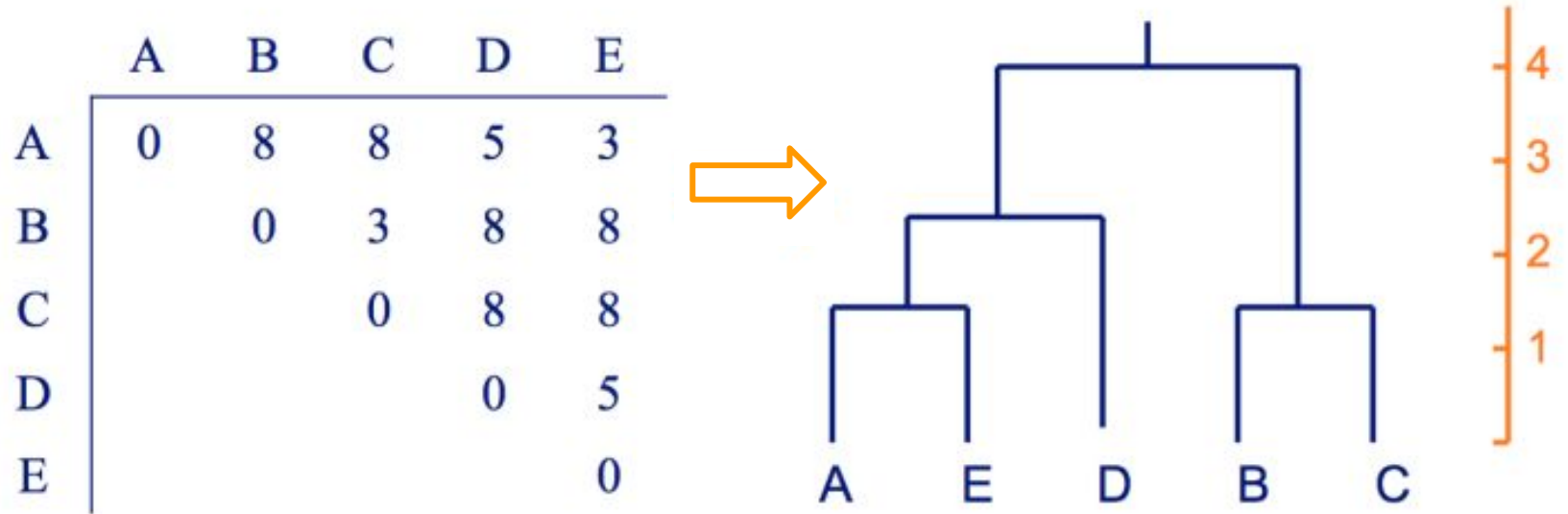
Step 2: Calculate Distance



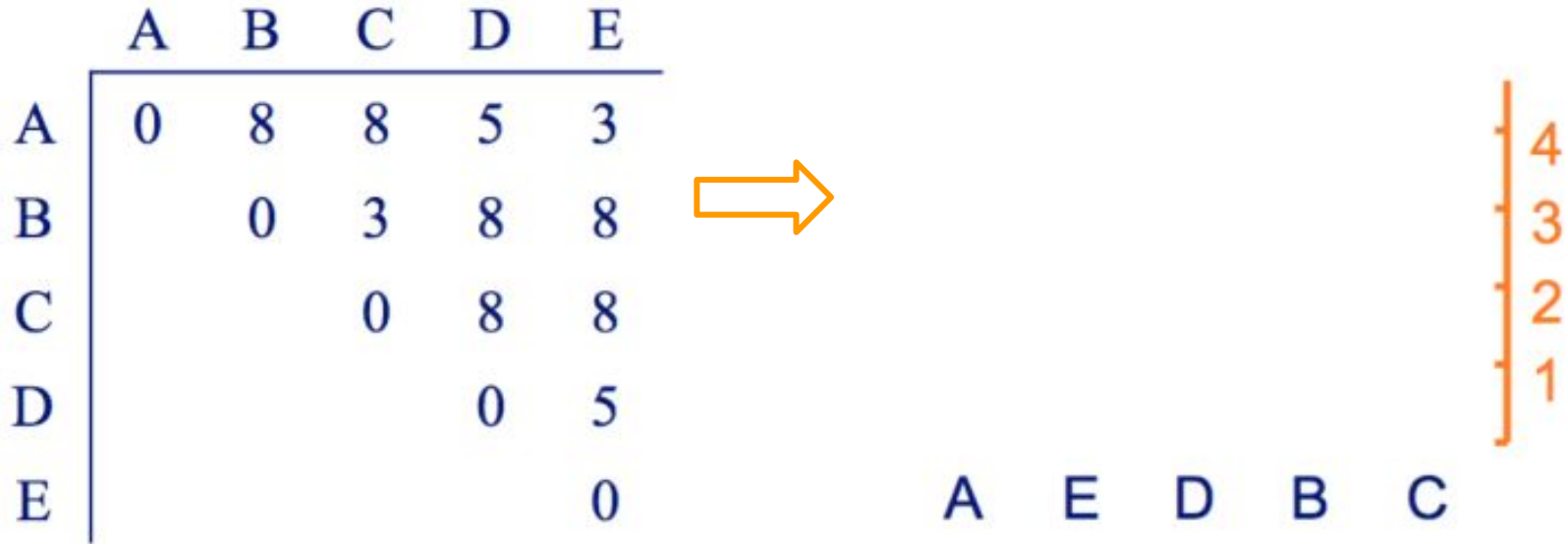
$S(A)$	$S(A \cup B)$	$S(B)$
42	42	66
64	64	82
82	66	87
128	82	104
139	87	127

$$J(A, B) = \frac{|A \cap B|}{|A \cup B|} \approx \frac{|S(A \cup B) \cap S(A) \cap S(B)|}{|S(A \cup B)|}$$

Alignment-Free Methods: Distance Matrix

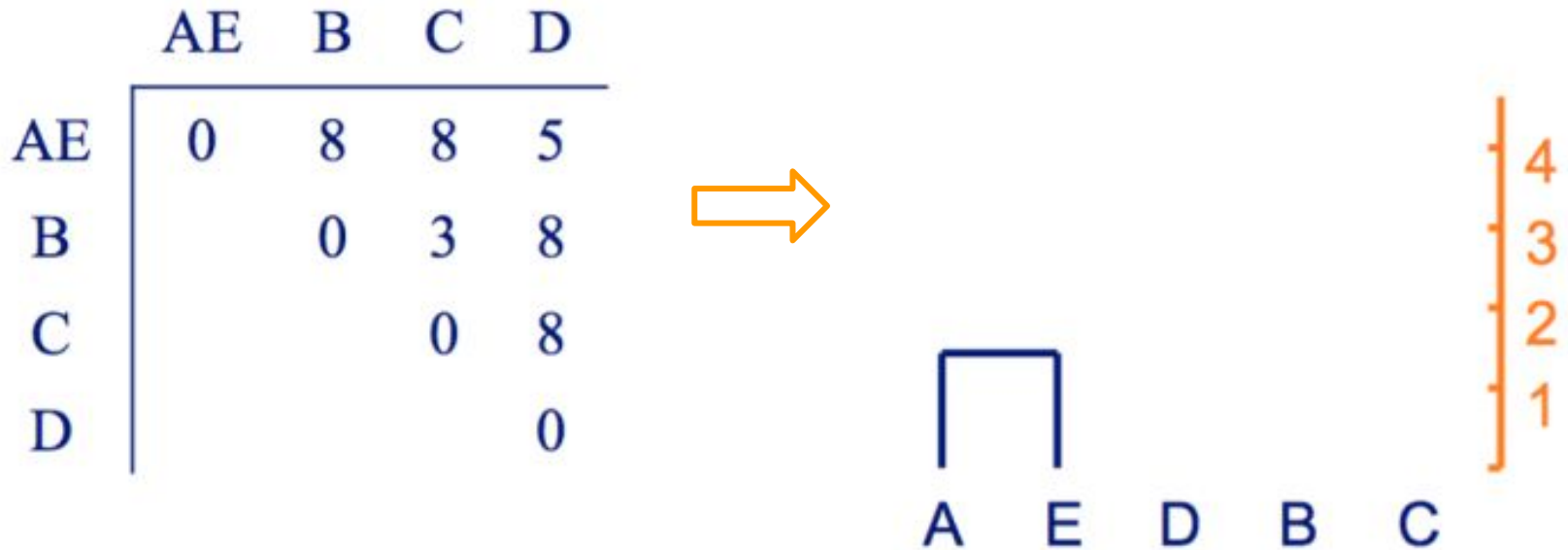


Molecular Clock Approach: UPGMA



Step 1: Pick the two most similar taxa clusters and merge them

Molecular Clock Approach: UPGMA



Step 1: Pick the two most similar taxa clusters and merge them

Step 2: Create a new node in the tree for the merged cluster

Molecular Clock Approach: UPGMA

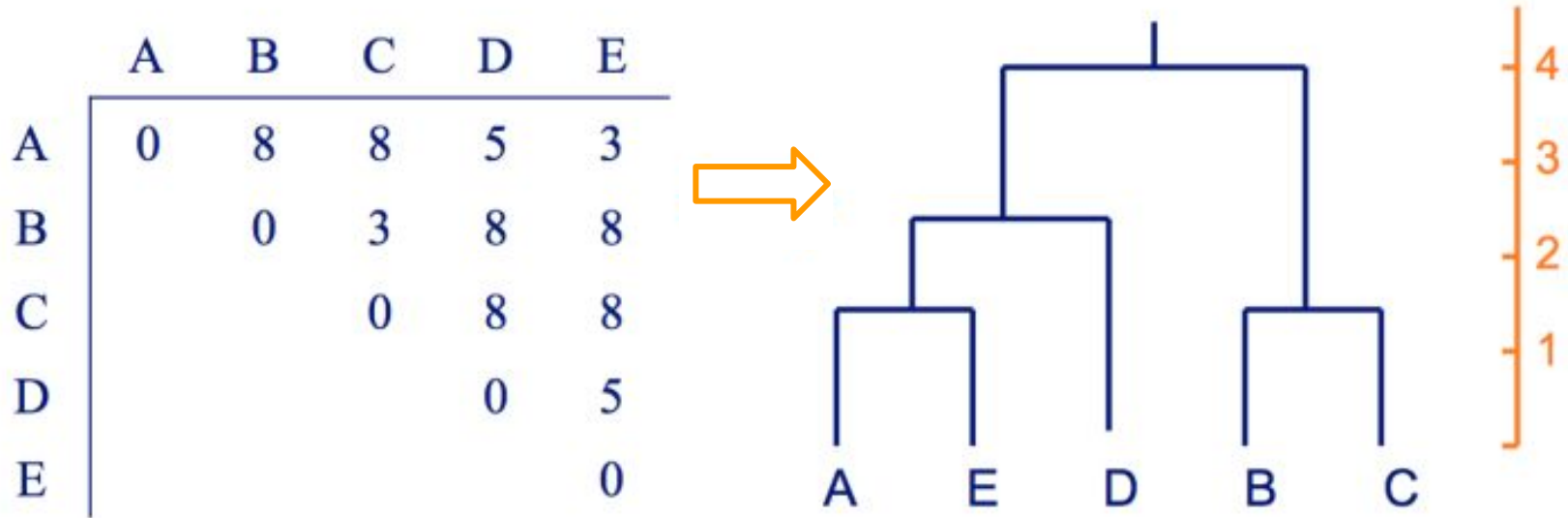
	AE	BC	D
AE	0	8	5
BC		0	8
D			0



	AED	BC
AED	0	8
BC		0



Molecular Clock Approach: UPGMA



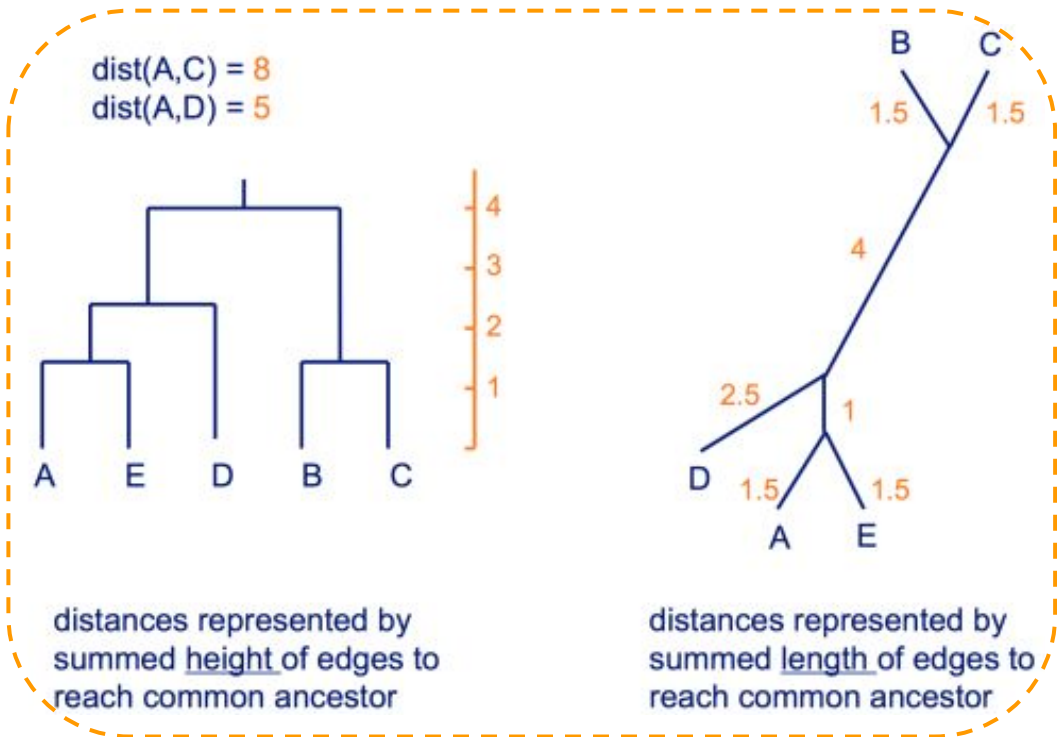
Step 1: Pick the two most similar taxa clusters and merge them

Step 2: Create a new node in the tree for the merged cluster



Minimum Evolution Approach: NJ

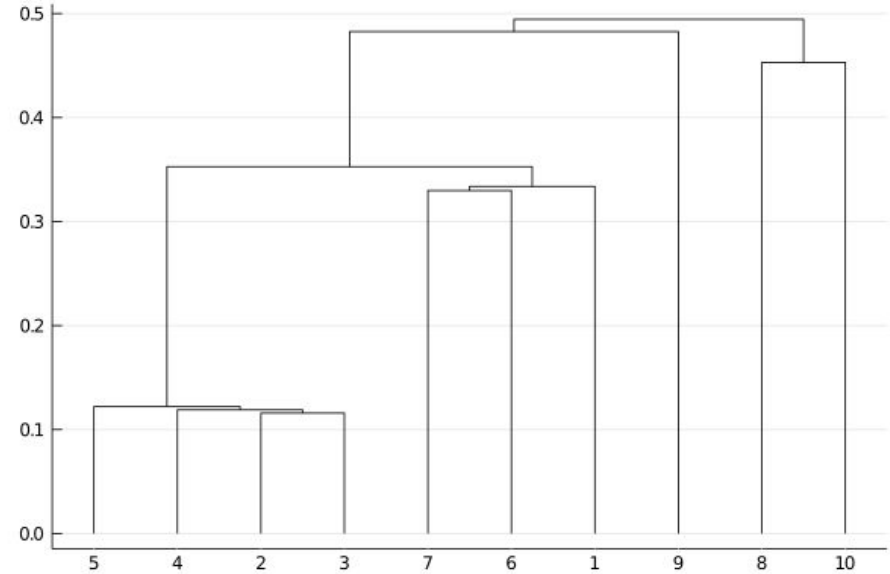
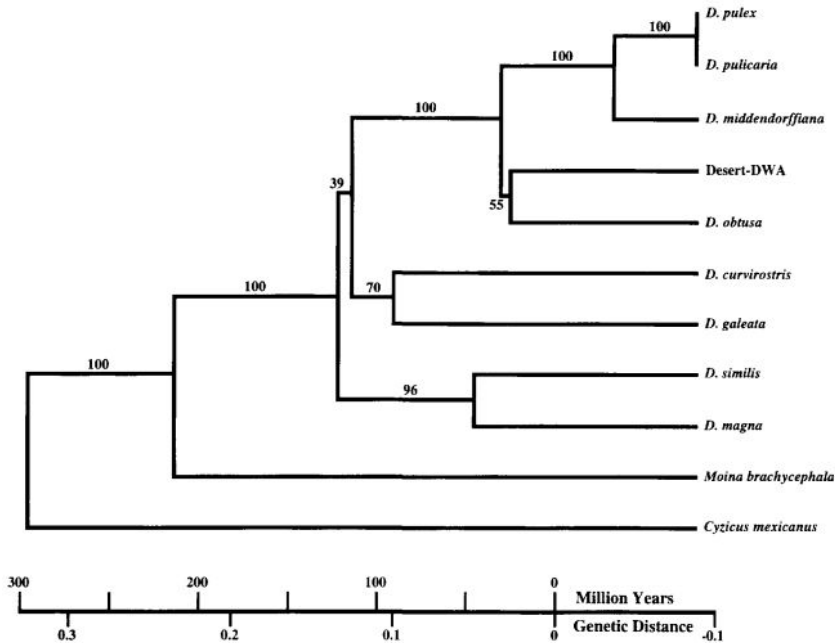
	A	B	C	D	E
A	0	8	8	5	3
B		0	3	8	8
C			0	8	8
D				0	5
E					0



Step 1: Select branch lengths by least-squares

Step 2: Choose the topology with the lowest total branch lengths

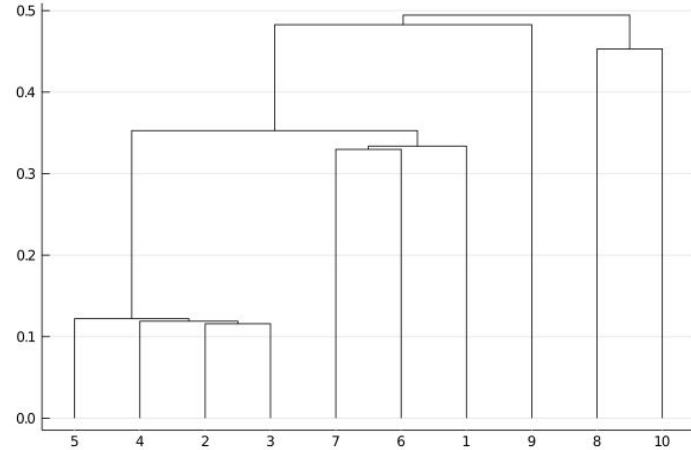
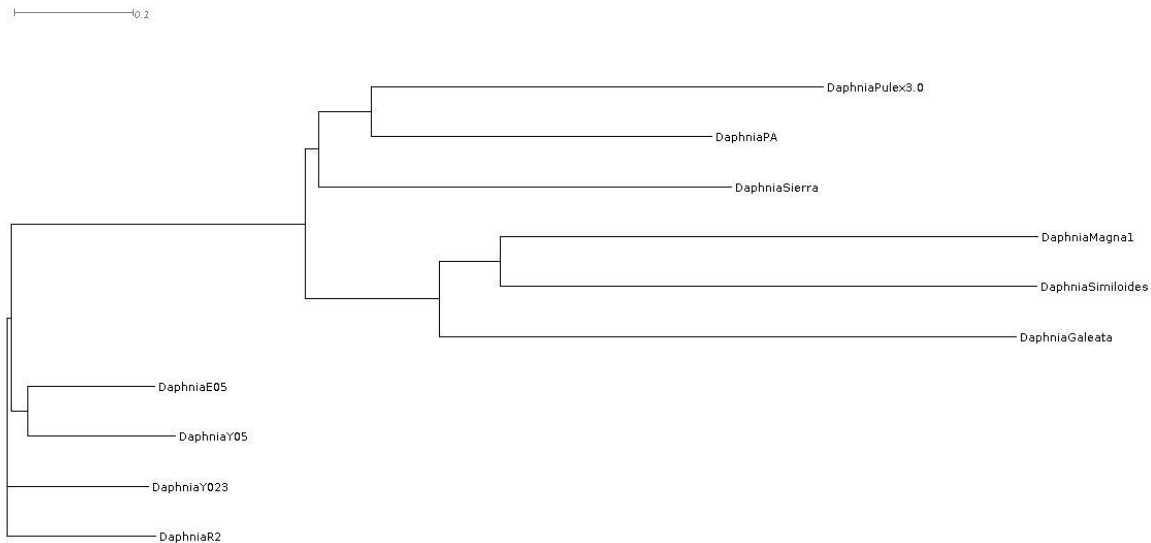
UPGMA Daphnia RNA Sequences



Daphnia Genotypes

- | | |
|------------------|--------------------|
| 1. Pulex 3.0 | 6. Pulex PA |
| 2. Melanica E05 | 7. Melanica Sierra |
| 3. Melanica Y05 | 8. Magna 1 |
| 4. Melanica Y023 | 9. Galeata |
| 5. Melanica R2 | 10. Similoides |

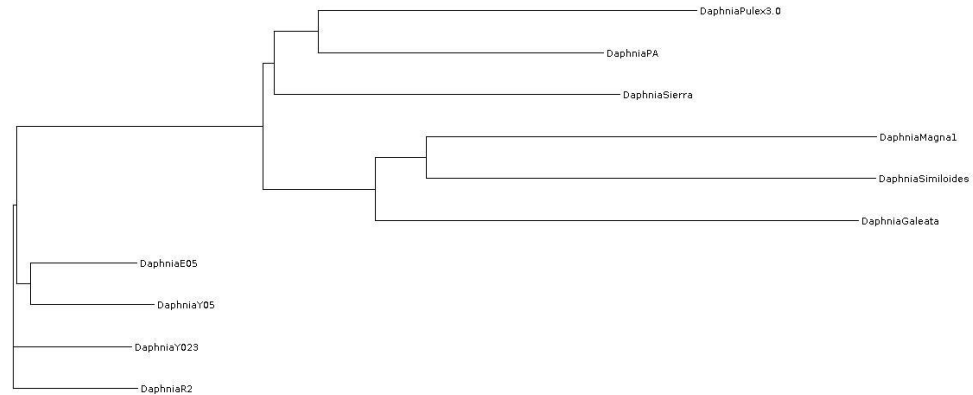
NJ vs UPGMA: Daphnia RNA Sequences



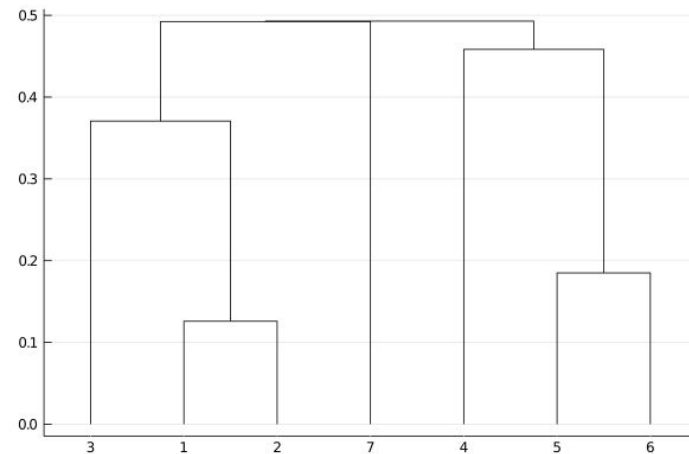
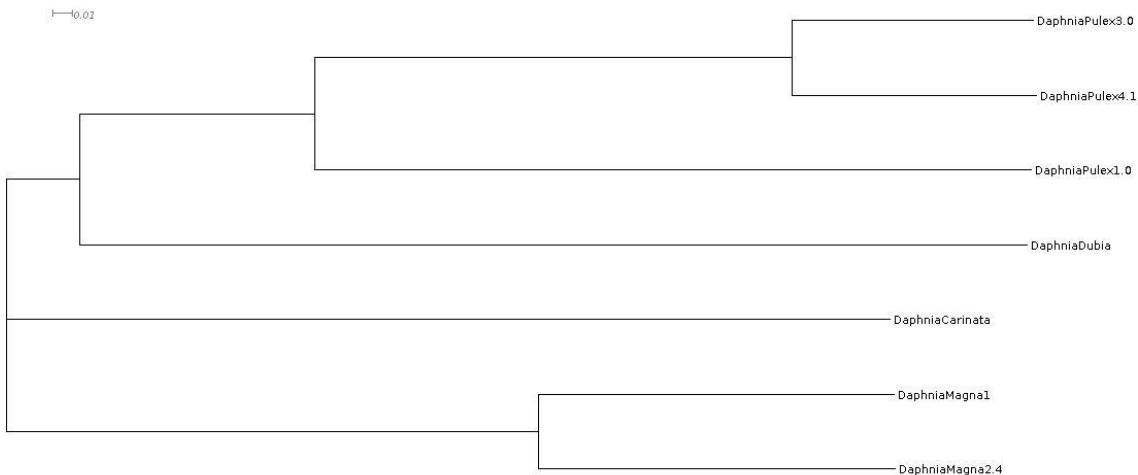
Daphnia Genotypes

- | | | | |
|----|---------------|-----|-----------------|
| 1. | Pulex 3.0 | 6. | Pulex PA |
| 2. | Melanica E05 | 7. | Melanica Sierra |
| 3. | Melanica Y05 | 8. | Magna 1 |
| 4. | Melanica Y023 | 9. | Galeata |
| 5. | Melanica R2 | 10. | Similoides |

A horizontal number line with a starting point at 0 and an ending point at 0.02. A tick mark is placed at the midpoint, labeled 0.01.



NJ vs UPGMA: Daphnia DNA Sequences



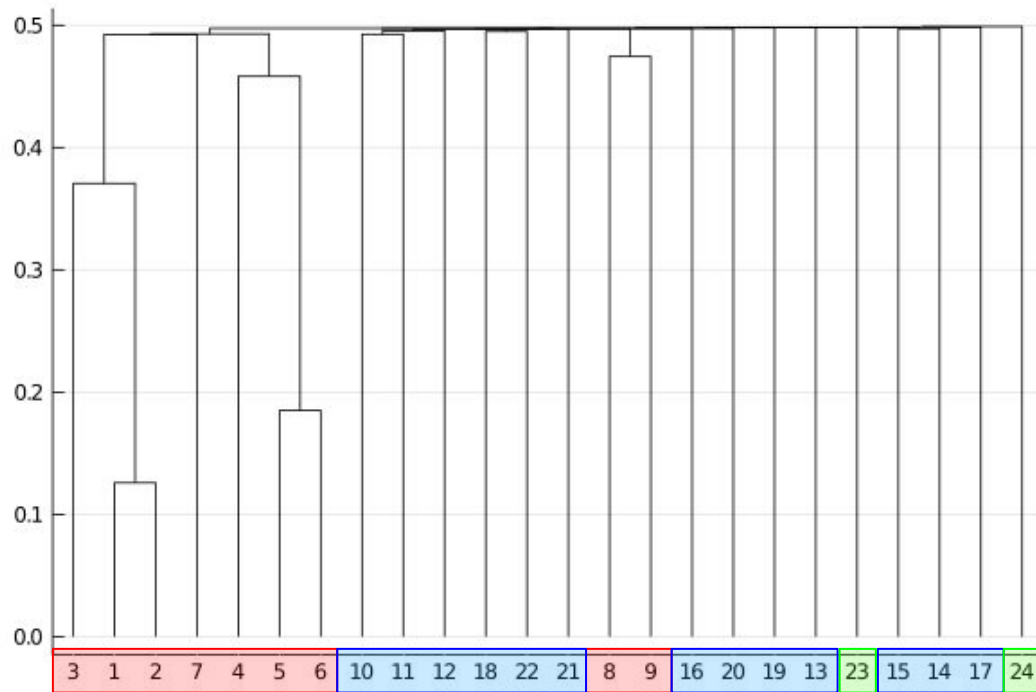
Daphnia Genotypes

- | | | | |
|----|-----------|----|-----------|
| 1. | Pulex 3.0 | 6. | Magna 2.4 |
| 2. | Pulex 4.1 | 7. | Dubia |
| 3. | Pulex 1.0 | | |
| 4. | Carinata | | |
| 5. | Magna 1 | | |

UPGMA Arthropod DNA Sequences

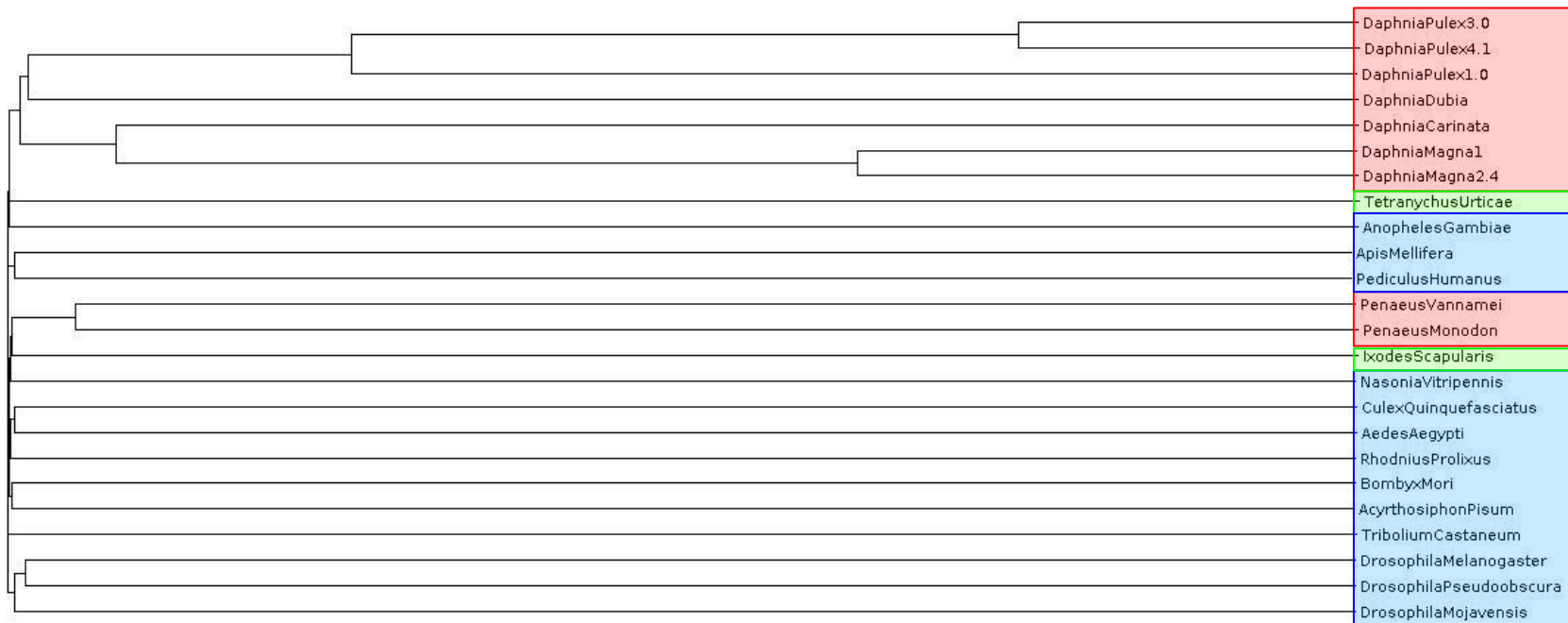
Species include:

1. *Daphnia pulex* 3.0 (common water flea)
2. *Daphnia pulex* 4.1 (common water flea)
3. *Daphnia pulex* 1.0 (common water flea)
4. *Daphnia carinata* (crustaceans)
5. *Daphnia magna* 1 (crustaceans)
6. *Daphnia magna* 2.4 (crustaceans)
7. *Daphnia dubia* (crustaceans)
8. *Penaeus vannamei* (Pacific white shrimp)
9. *Penaeus monodon* (black tiger shrimp)
10. *Drosophila melanogaster* (fruit fly)
11. *Drosophila pseudoobscura* (flies)
12. *Drosophila mojavensis* (flies)
13. *Anopheles gambiae* (African malaria mosquito)
14. *Culex quinquefasciatus* (southern house mosquito)
15. *Aedes aegypti* (yellow fever mosquito)
16. *Bombyx mori* (domestic silkworm)
17. *Tribolium castaneum* (red flour beetle)
18. *Apis mellifera* (honey bee)
19. *Nasonia vitripennis* (jewel wasp)
20. *Rhodnius prolixus* (bugs)
21. *Acyrtosiphon pisum* (pea aphid)
22. *Pediculus humanus* (human body louse)
23. *Ixodes scapularis* (black-legged tick)
24. *Tetranychus urticae* (two-spotted spider mite)



NJ Arthropod DNA Sequences

0.02



OrthoMCL vs NJ: Arthropod DNA Sequences

