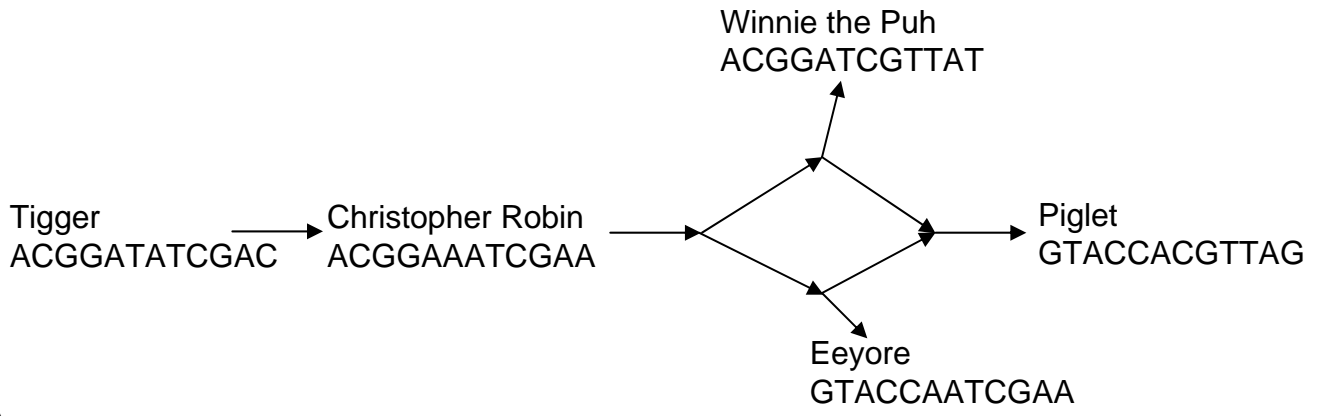
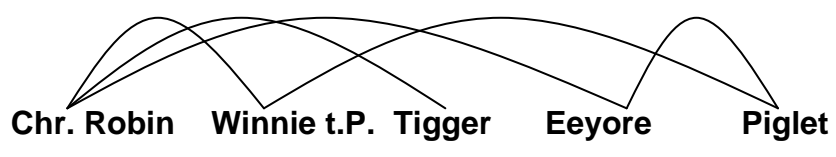


Answers to exercises of Chapter 11 (Phylogenetic Networks)

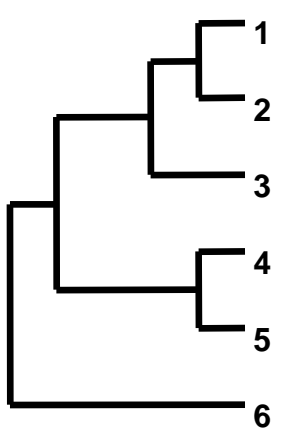
1)



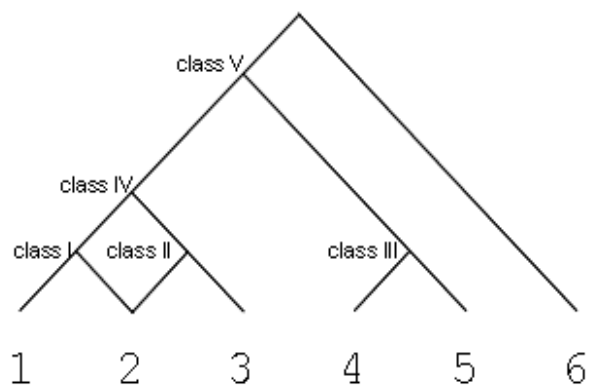
2)

	1	2	3	4	5	6	class 1	class 2	class 3	class 4	class 5
1	-	0.1	0.3	0.4	0.4	0.4	0.1	0.2	0.4	0.2	0.3
2		-	0.1	0.4	0.4	0.5	0.1	0.1	-	-	-
3			-	0.4	0.4	0.4	0.2	0.4	0.4	0.3	0.4
4				-	0.3	0.6	0.4	0.4	0.3	0.4	0.4
5					-	0.4	0.5	0.5	0.5	0.4	0.4
6						-	-	0.2	0.4	0.5	0.5
class 1								-	0.4	0.2	0.3
class 2									-	0.6	0.5
class 3										0.2	0.2
class 4										-	0.2
class 5											-

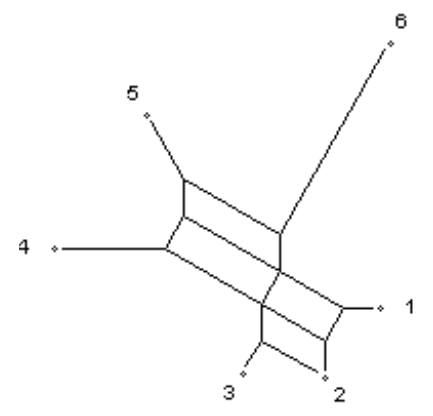
UPGMA



Pyramidal Clustering Model



Split Decomposition



3)

Distance-, character-, and likelihood-based tree reconstruction methodologies. Neighbor joining (NJ) and unweighted pair-group method with arithmetic means (UPGMA) are distance based methods; character based methods are exhaustive and heuristic parsimony programs with the Parsimony Ratchet algorithm, trying to overcome the problem of speed; and Maximum likelihood and Bayesian analysis are the likelihood based tree reconstruction methodologies.

Disadvantage of tree reconstruction methods:

- do not reflect reticulate evolution
- do not reflect noise in data (due to data errors, biased sampling, etc.)
- cannot reflect hybridization events
- only depict hierarchical structures
- cannot depict divergence of recent relationships
- cannot depict multiple descendants from a common ancestor
- assume ancestral taxa to be extinct

4)

Hybridization, reticulate evolution, polyploidization, homologous character evolution, and others

5)

Split decomposition network, reflecting deviations from the tree-like structure, visualizing complexity in phylogenetic data; however, it cannot prove existence of recombination and lateral gene transfer.