

Reported Information:

All trees are binary: both in the network and yielded by UPGMA reconstruction. The distance reported is false positive distance, which is always equal to the false negative distance.

Test Results:

1. Ultrametric tree
1 contact edge – yielding 3 distinct trees in the network
Edge transmission factor: 0.5
Character transmission factor: 0.5
1 in 4 character will be transmitted on average.
Sequence length $k = 300$

Average distance from UPGMA tree to trees in the network: (2.0 , 1.7 , 2.4)

UPGMA correctly returned one of the network trees in 3 out of 10 runs

2. Ultrametric tree
1 contact edge – yielding 3 distinct trees in the network
Edge transmission factor: 0.5
Character transmission factor: 0.5
1 in 4 character will be transmitted on average.
Sequence length $k = 600$

Average distance from UPGMA tree to trees in the network: (2.4 , 1.8 , 1.4)

UPGMA correctly returned one of the network trees in 3 out of 10 runs.

3. Non-ultrametric tree
Edge stddev. from ultrametric: 0.3 (0.2? double-check)
1 contact edge – yielding 3 distinct trees in the network
Edge transmission factor: 0.5
Character transmission factor: 0.5
1 in 4 character will be transmitted on average.
Sequence length $k = 300$

Average distance from UPGMA tree to trees in the network: (4.0 , 6.7 , 7.2)

UPGMA never returns one of the network trees.

4. Non-ultrametric tree
Edge stddev. from ultrametric: 0.3 (0.2? double check)
1 contact edge – yielding 3 distinct trees in the network
Edge transmission factor: 0.5
Character transmission factor: 0.5
1 in 4 character will be transmitted on average.
Sequence length $k = 600$

Average distance from UPGMA tree to trees in the network: (3.0 , 7.6 , 7.5)
UPGMA never returns one of the network trees.

5. Ultrametric tree
No contact edges
Sequence length $k = 300$

Average distance from UPGMA tree to true tree: (1.1)
UPGMA correctly returned the true tree in 3 out of 10 runs.

6. Ultrametric tree
No contact edges.
Sequence length $k = 600$

Average distance from UPGMA tree to trees in the network: (0.7)
UPGMA correctly returned the true tree in 5 out of 10 runs.

7. Non-ultrametric tree
Edge stddev. from ultrametric: 0.3 (0.2? double-check)
No contact edges.
Sequence length $k = 300$

Average distance from UPGMA tree to trees in the network: (2.2)
UPGMA correctly returns the true tree in 1 out of 10 runs.

8. Non-ultrametric tree
Edge stddev. from ultrametric: 0.3 (0.2? double check)
No contact edges.
Sequence length $k = 600$

Average distance from UPGMA tree to trees in the network: (4.6)
UPGMA never returns the true tree.