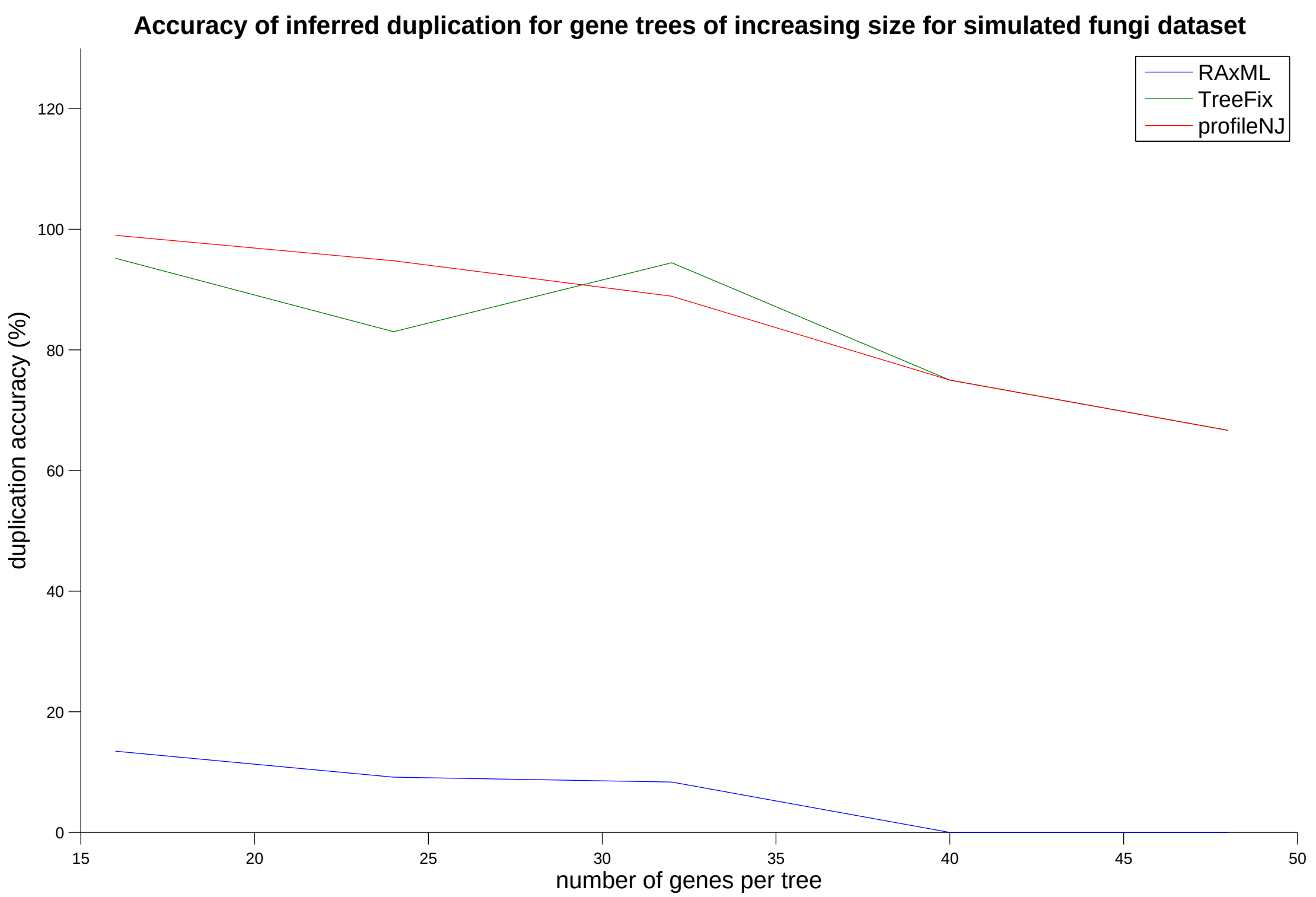
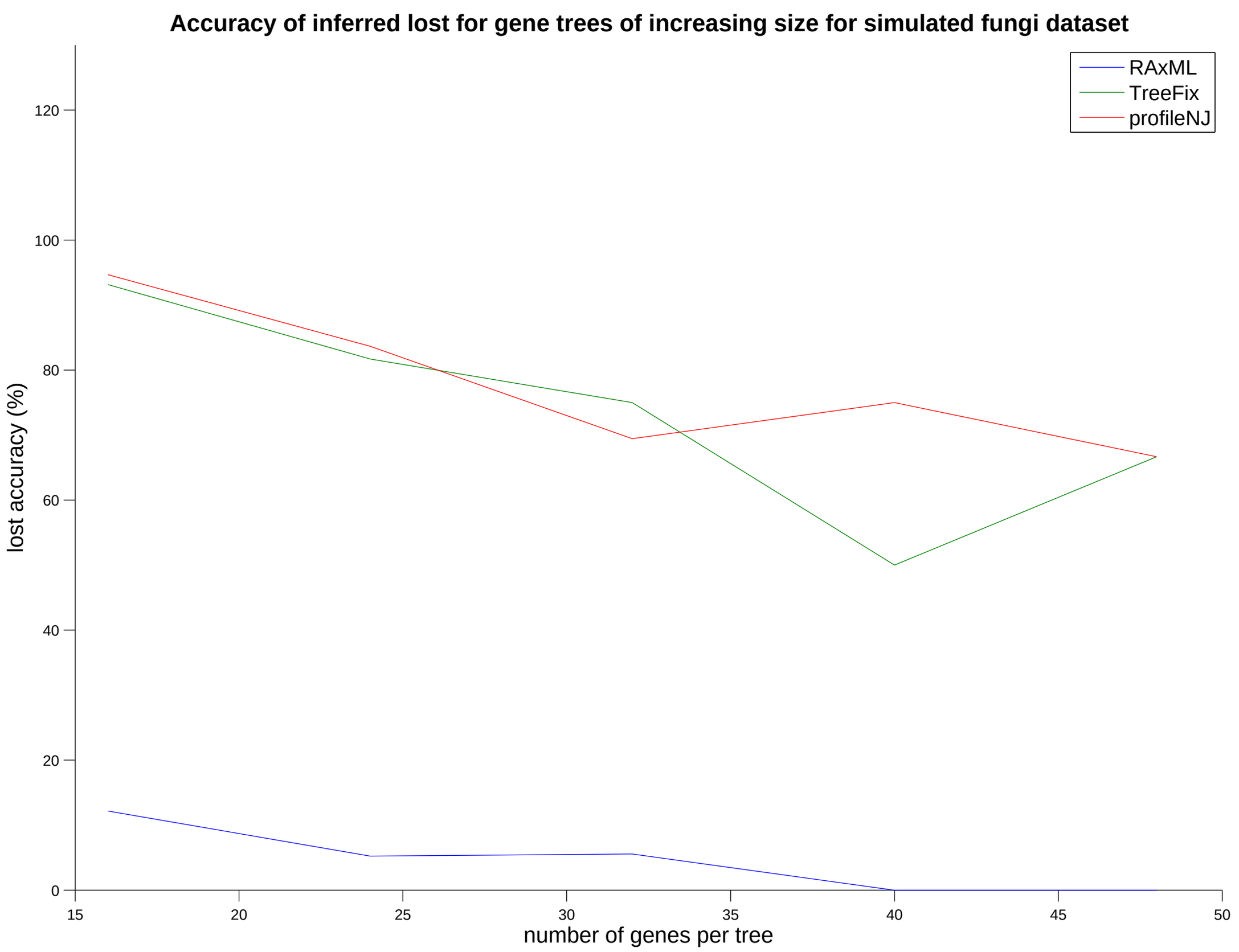
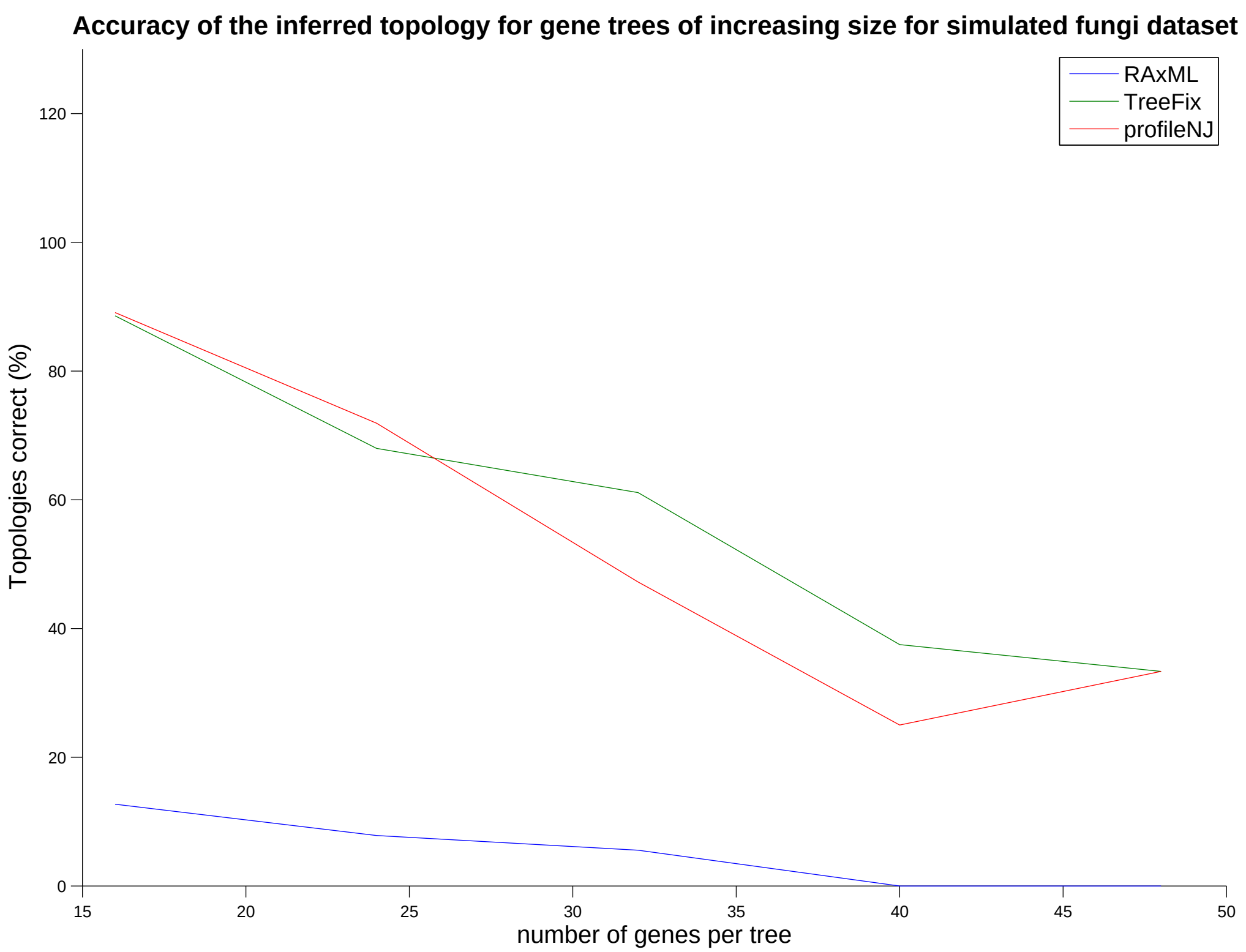
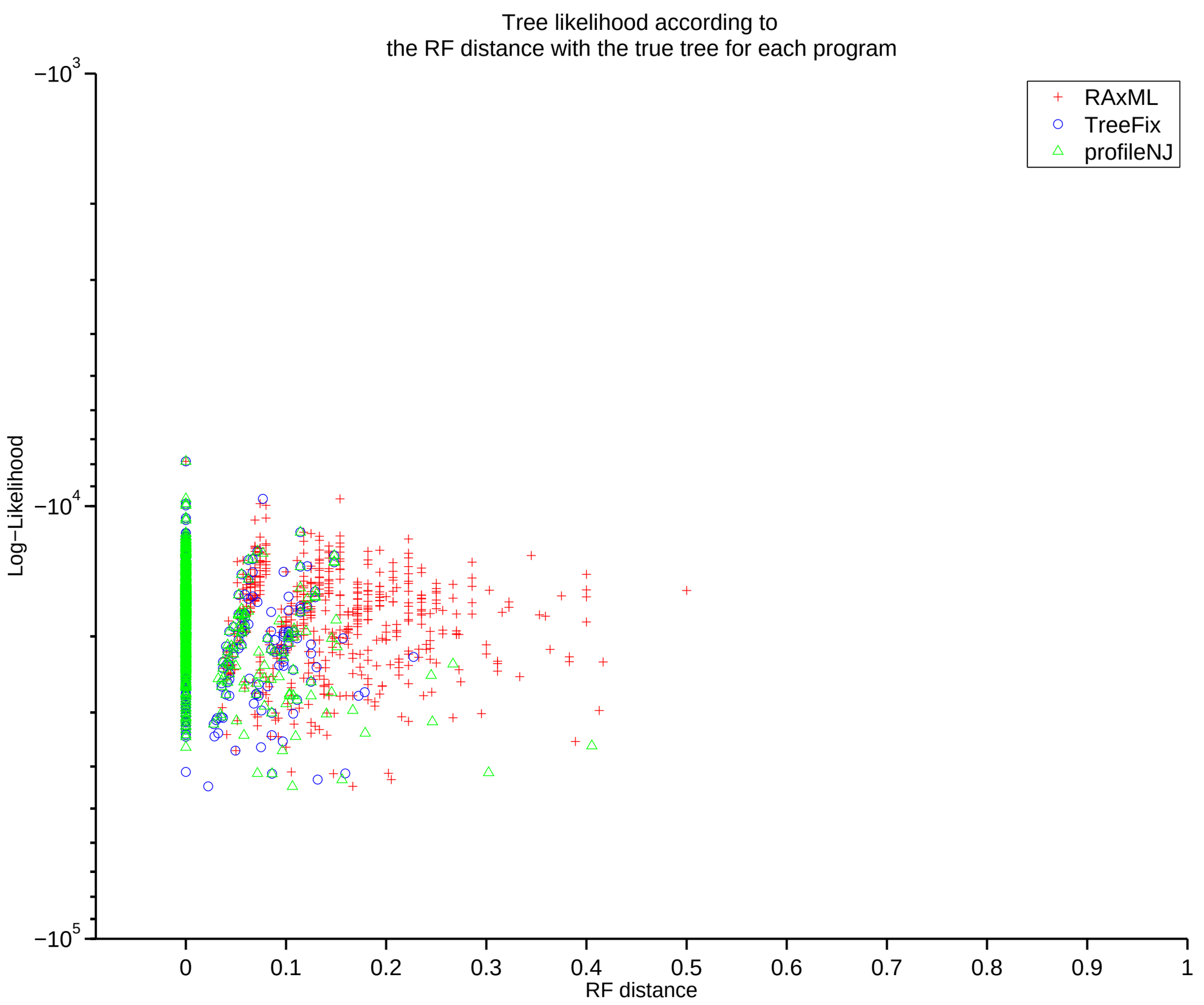
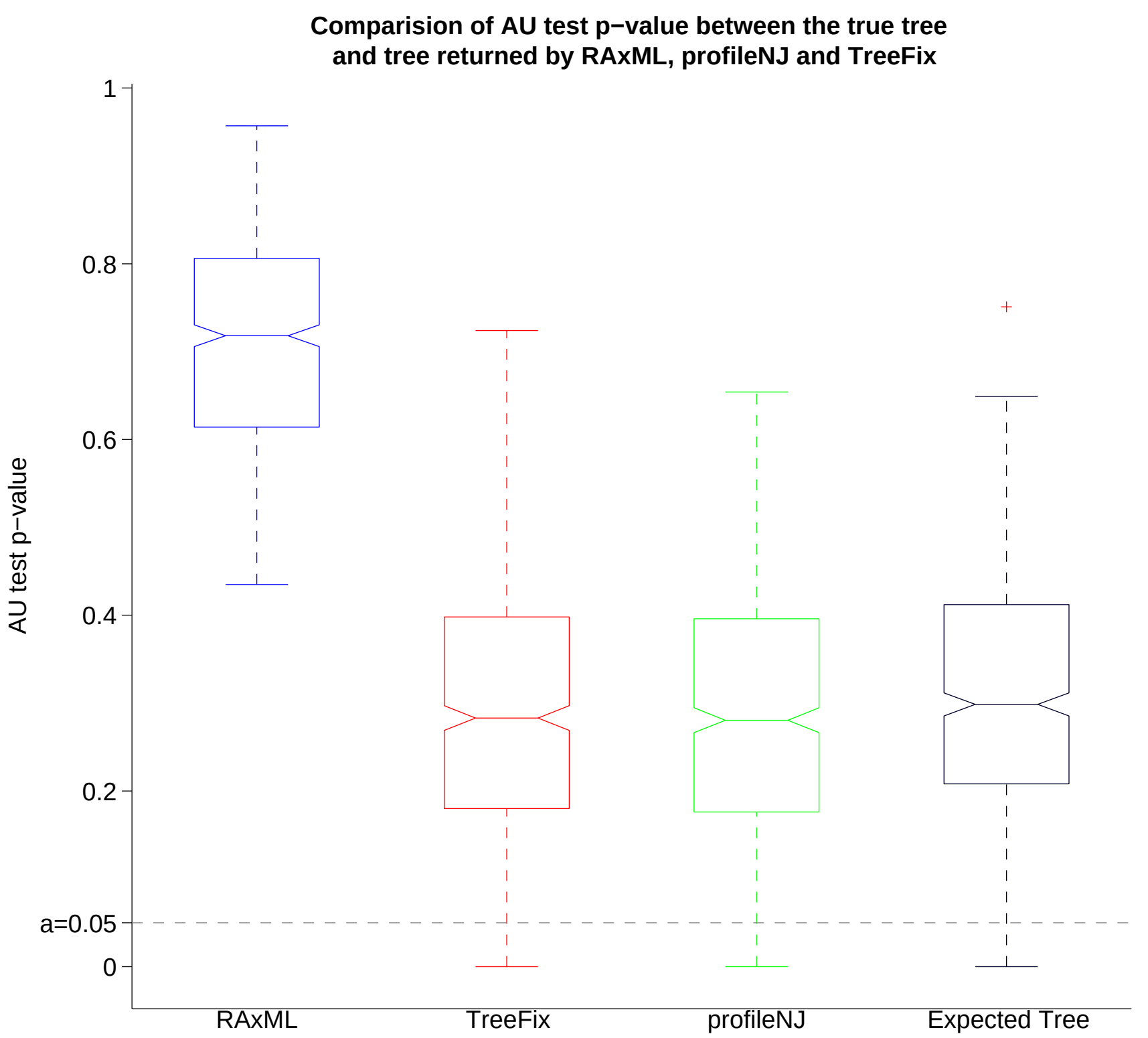
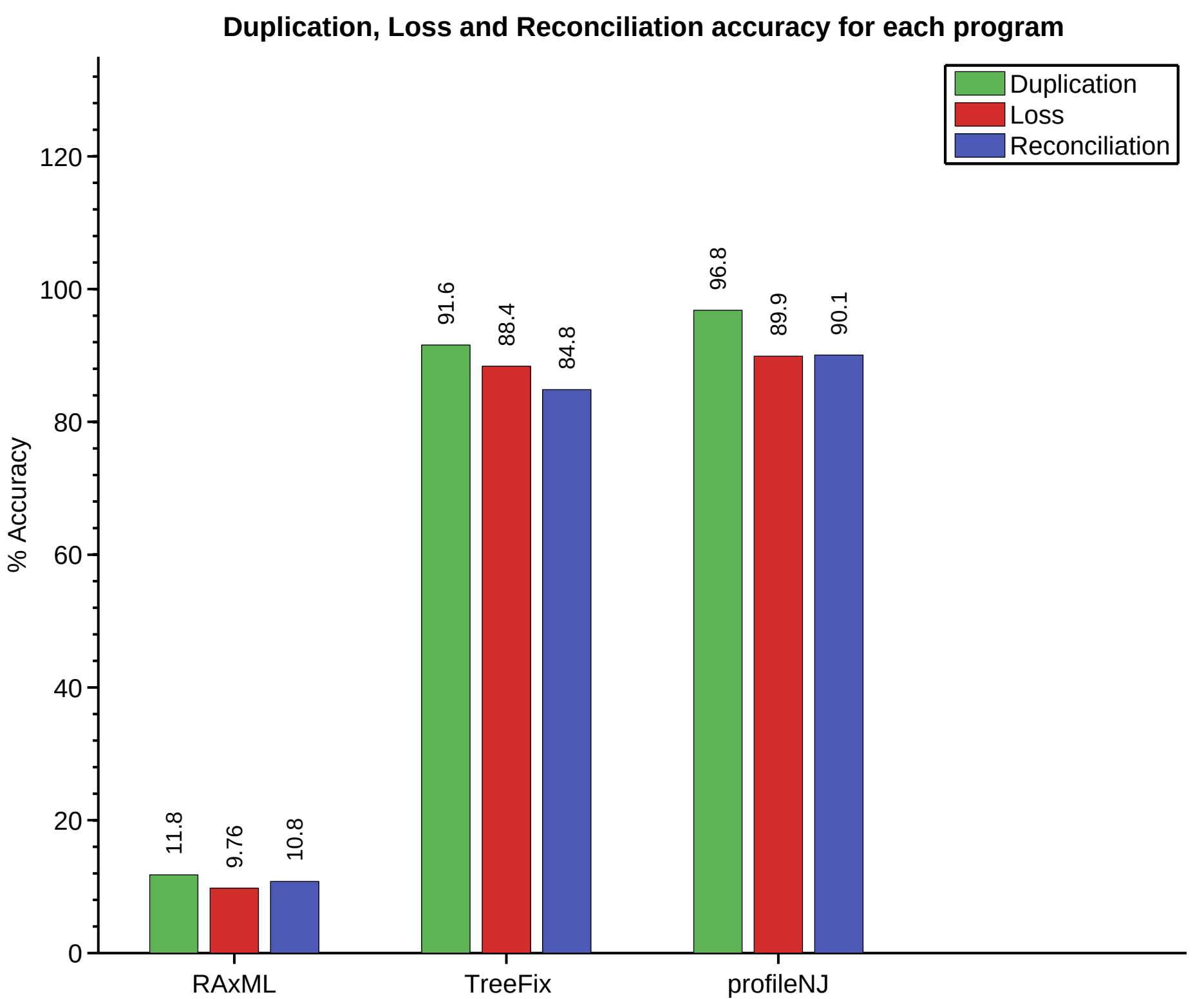

Accuracy of inferred duplication for gene trees of increasing size for simulated fungi dataset
RAxML
TreeFix
profileNJ
duplication accuracy (%)
0
20
40
60
80
100
120
15
20
25
30
35
40
45
50
number of genes per tree

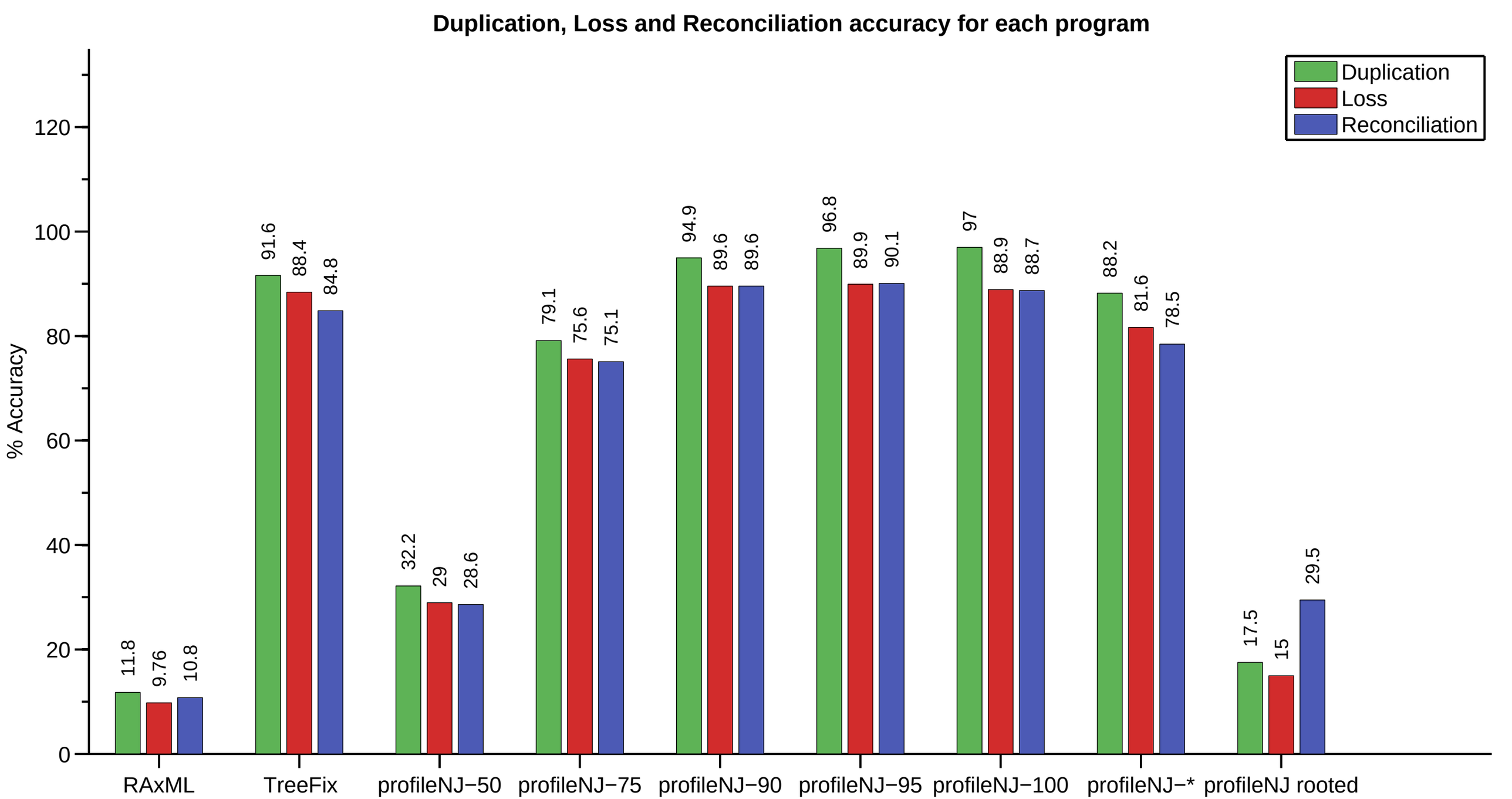

Accuracy of inferred lost for gene trees of increasing size for simulated fungi dataset
RAxML
TreeFix
profileNJ
lost accuracy (%)
120
100
80
60
40
20
0
15
20
25
30
35
40
45
50
number of genes per tree

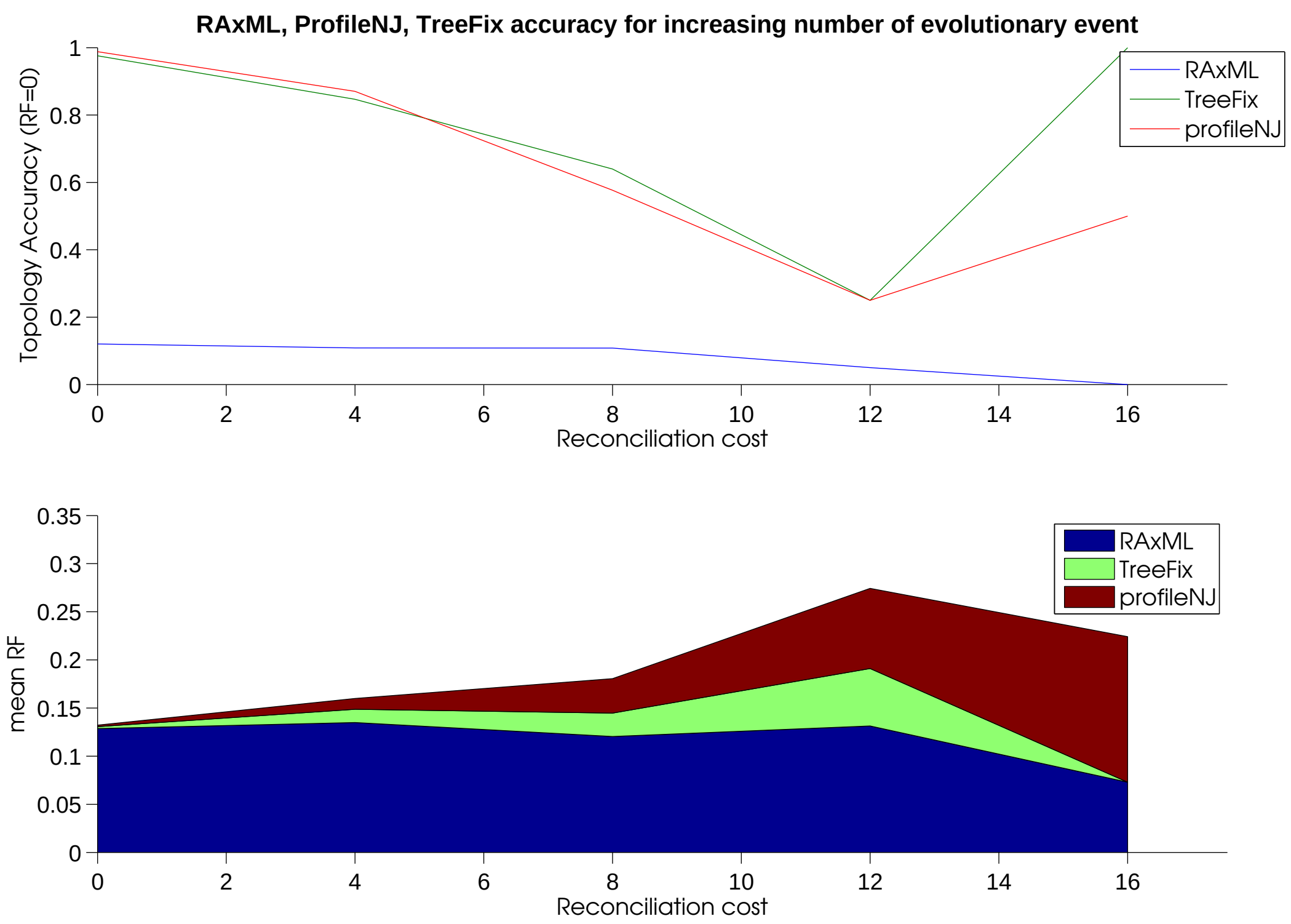

Accuracy of the inferred topology for gene trees of increasing size for simulated fungi dataset
RAxML
TreeFix
profileNJ
Topologies correct (%)
0
20
40
60
80
100
120
15
20
25
30
35
40
45
50
number of genes per tree

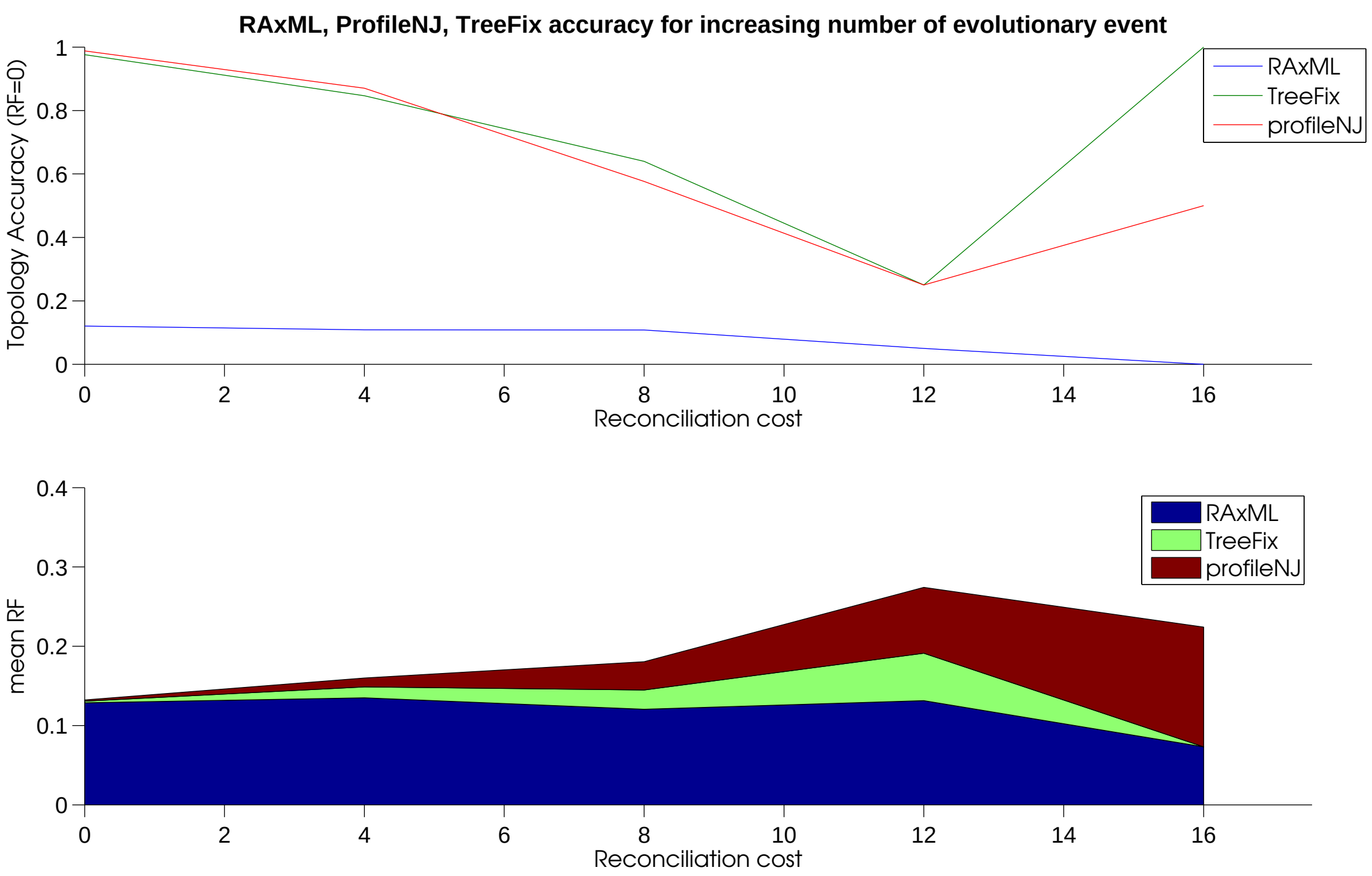

Tree likelihood according to
the RF distance with the true tree for each program
RAxML
TreeFix
profileNJ
Log−Likelihood
−10^3
−10^4
−10^5
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
RF distance

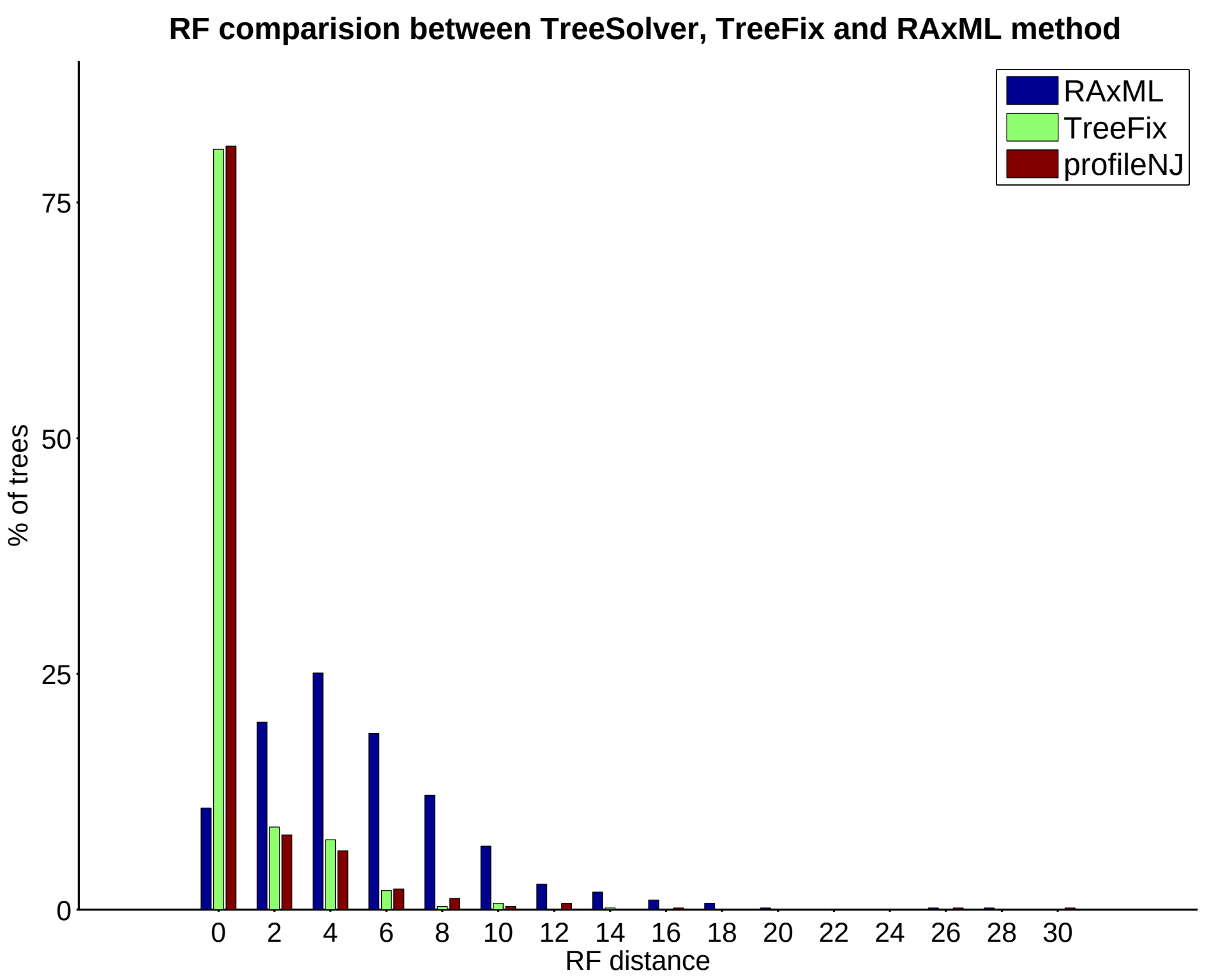

Comparision of AU test p−value between the true tree
and tree returned by RAxML, profileNJ and TreeFix
AU test p−value
1
0.8
0.6
0.4
0.2
a=0.05
0
RAxML
TreeFix
profileNJ
Expected Tree

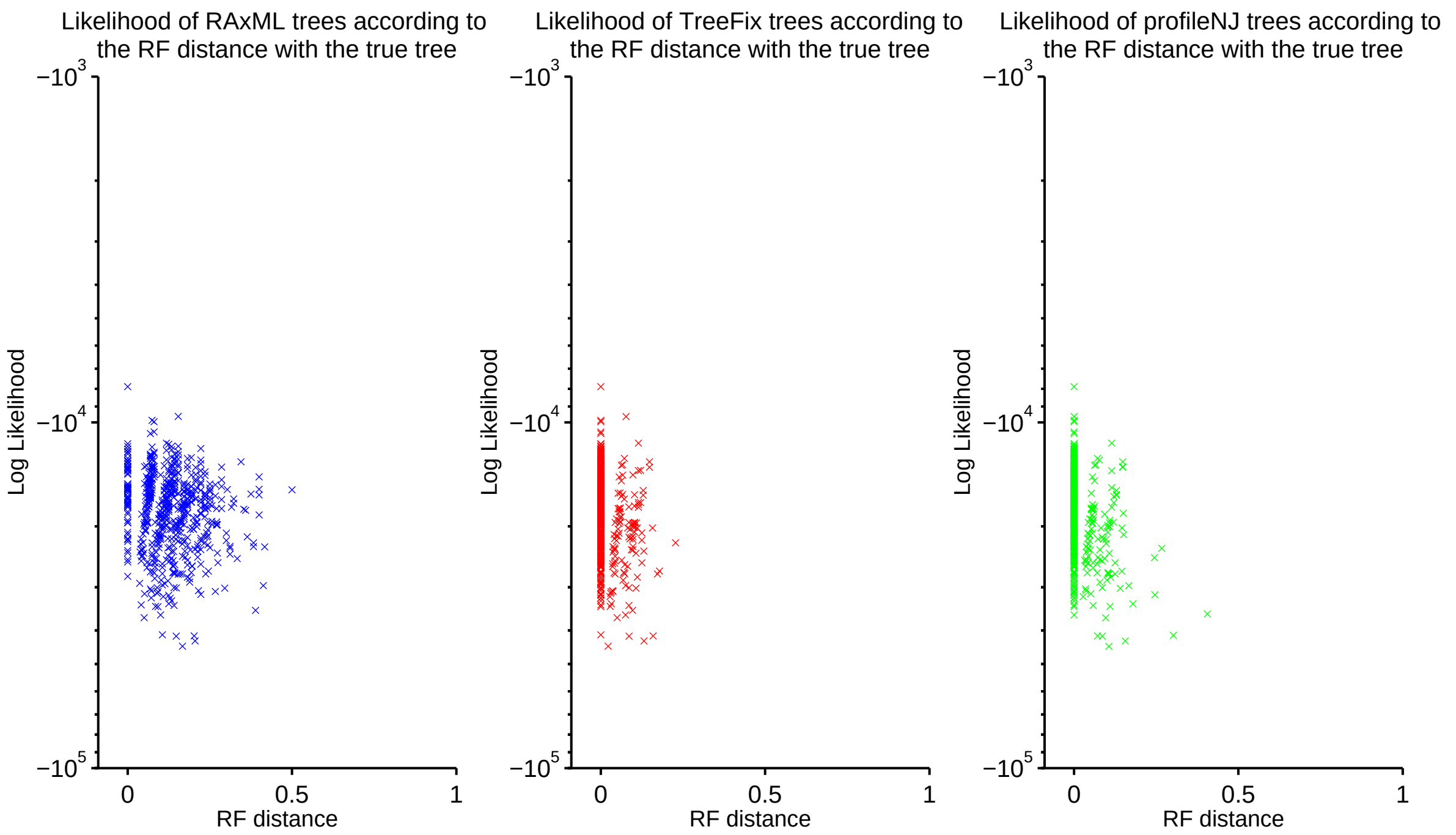

Duplication, Loss and Reconciliation accuracy for each program
Duplication
Loss
Reconciliation
% Accuracy
0
20
40
60
80
100
120
11.8
9.76
10.8
91.6
88.4
84.8
96.8
89.9
90.1
RAxML
TreeFix
profileNJ

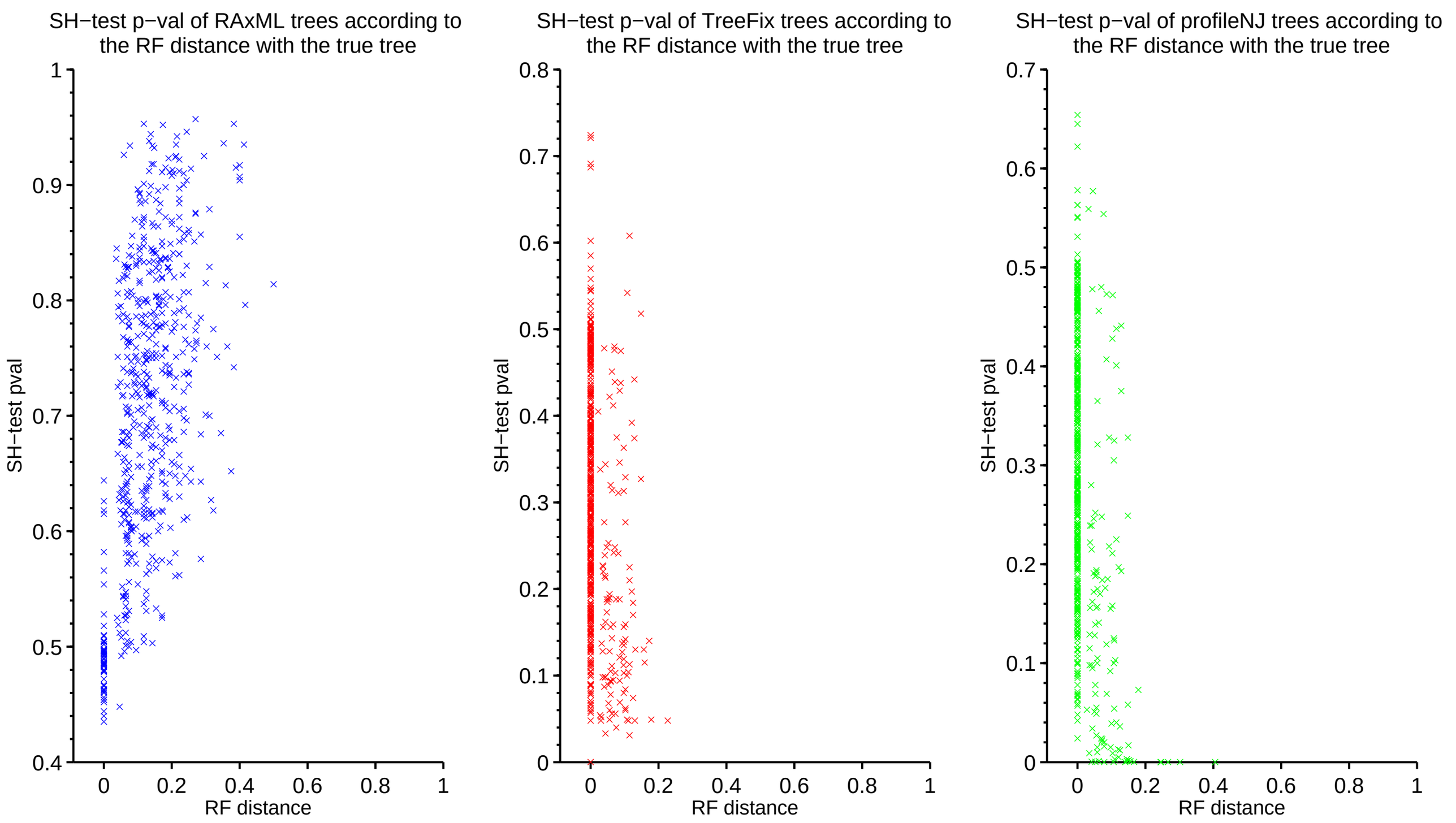

Duplication, Loss and Reconciliation accuracy for each program
Duplication
Loss
Reconciliation
% Accuracy
0
20
40
60
80
100
120
11.8
9.76
10.8
91.6
88.4
84.8
32.2
29
28.6
79.1
75.6
75.1
94.9
89.6
89.6
96.8
89.9
90.1
97
88.9
88.7
88.2
81.6
78.5
17.5
15
29.5
RAxML
TreeFix
profileNJ−50
profileNJ−75
profileNJ−90
profileNJ−95
profileNJ−100
profileNJ−*
profileNJ rooted

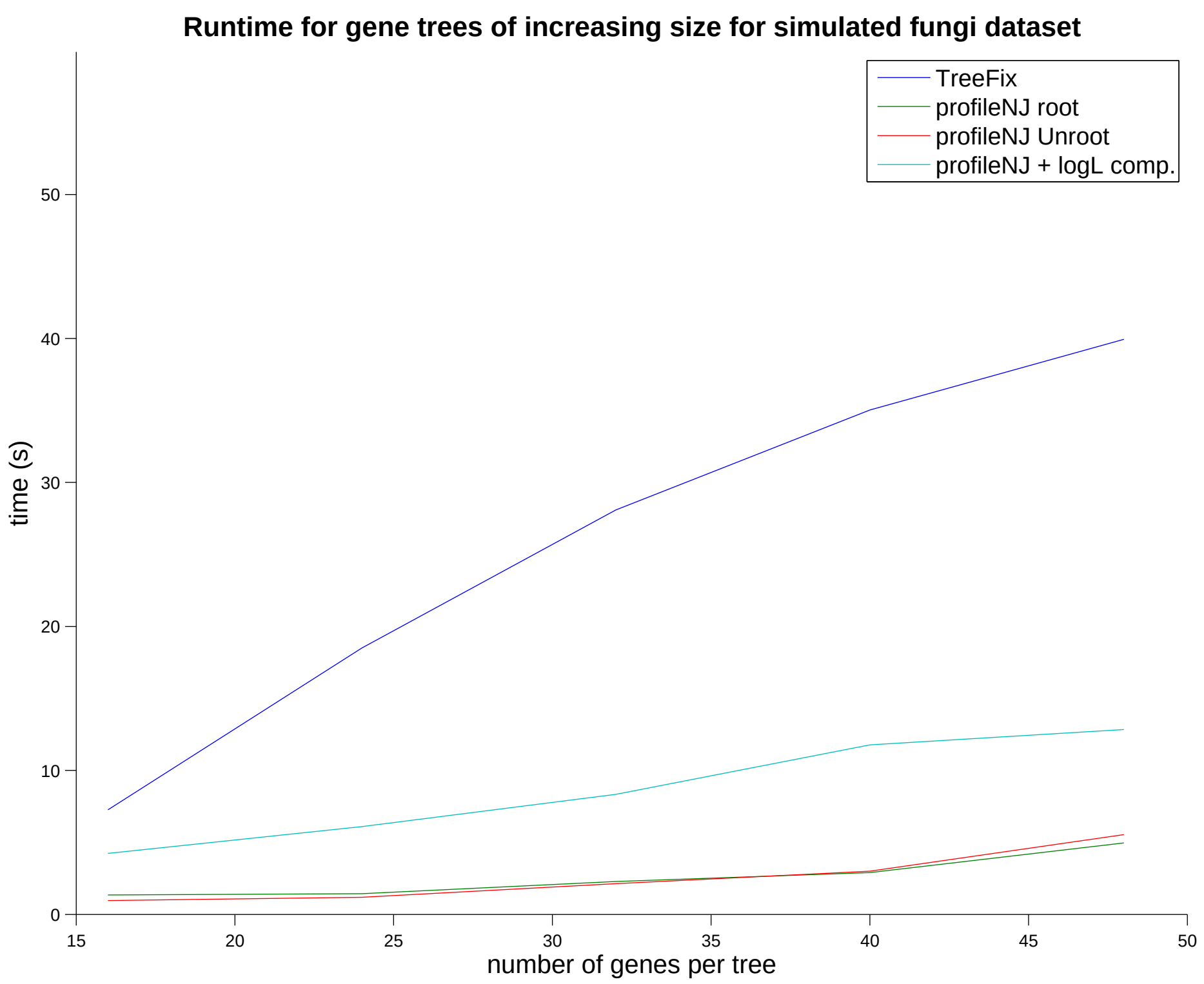

RAxML, ProfileNJ, TreeFix accuracy for increasing number of evolutionary event
Topology Accuracy (RF=0)
1
0.8
0.6
0.4
0.2
0
0
2
4
6
8
10
12
14
16
Reconciliation cost
RAxML
TreeFix
profileNJ
mean RF
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
0
2
4
6
8
10
12
14
16
Reconciliation cost
RAxML
TreeFix
profileNJ


RAxML, ProfileNJ, TreeFix accuracy for increasing number of evolutionary event
Topology Accuracy (RF=0)
1
0.8
0.6
0.4
0.2
0
0
2
4
6
8
10
12
14
16
Reconciliation cost
RAxML
TreeFix
profileNJ
mean RF
0.4
0.3
0.2
0.1
0
0
2
4
6
8
10
12
14
16
Reconciliation cost
RAxML
TreeFix
profileNJ


RF comparision between TreeSolver, TreeFix and RAxML method
RAxML
TreeFix
profileNJ
% of trees
0
25
50
75
0
2
4
6
8
10
12
14
16
18
20
22
24
26
28
30
RF distance


Likelihood of RAxML trees according to the RF distance with the true tree
Likelihood of TreeFix trees according to the RF distance with the true tree
Likelihood of profileNJ trees according to the RF distance with the true tree
Log Likelihood
−10^3
−10^4
−10^5
0
0.5
1
RF distance


SH−test p−val of RAxML trees according to the RF distance with the true tree
SH−test pval
RF distance
1
0.9
0.8
0.7
0.6
0.5
0.4
0
0.2
0.4
0.6
0.8
1
SH−test p−val of TreeFix trees according to the RF distance with the true tree
SH−test pval
RF distance
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
0.2
0.4
0.6
0.8
1
SH−test p−val of profileNJ trees according to the RF distance with the true tree
SH−test pval
RF distance
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
0.2
0.4
0.6
0.8
1


Runtime for gene trees of increasing size for simulated fungi dataset
TreeFix
profileNJ root
profileNJ Unroot
profileNJ + logL comp.
time (s)
0
10
20
30
40
50
15
20
25
30
35
40
45
50
number of genes per tree