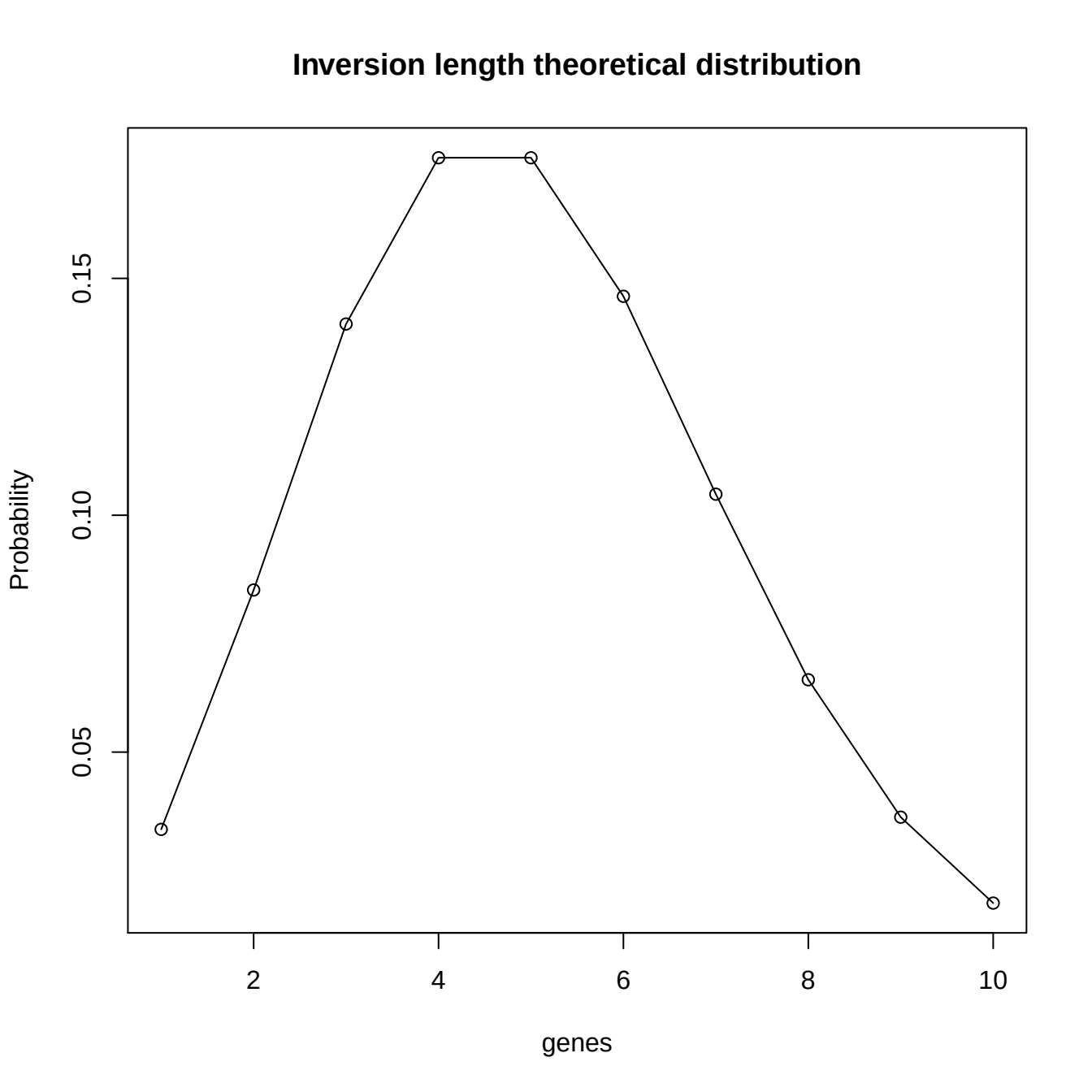
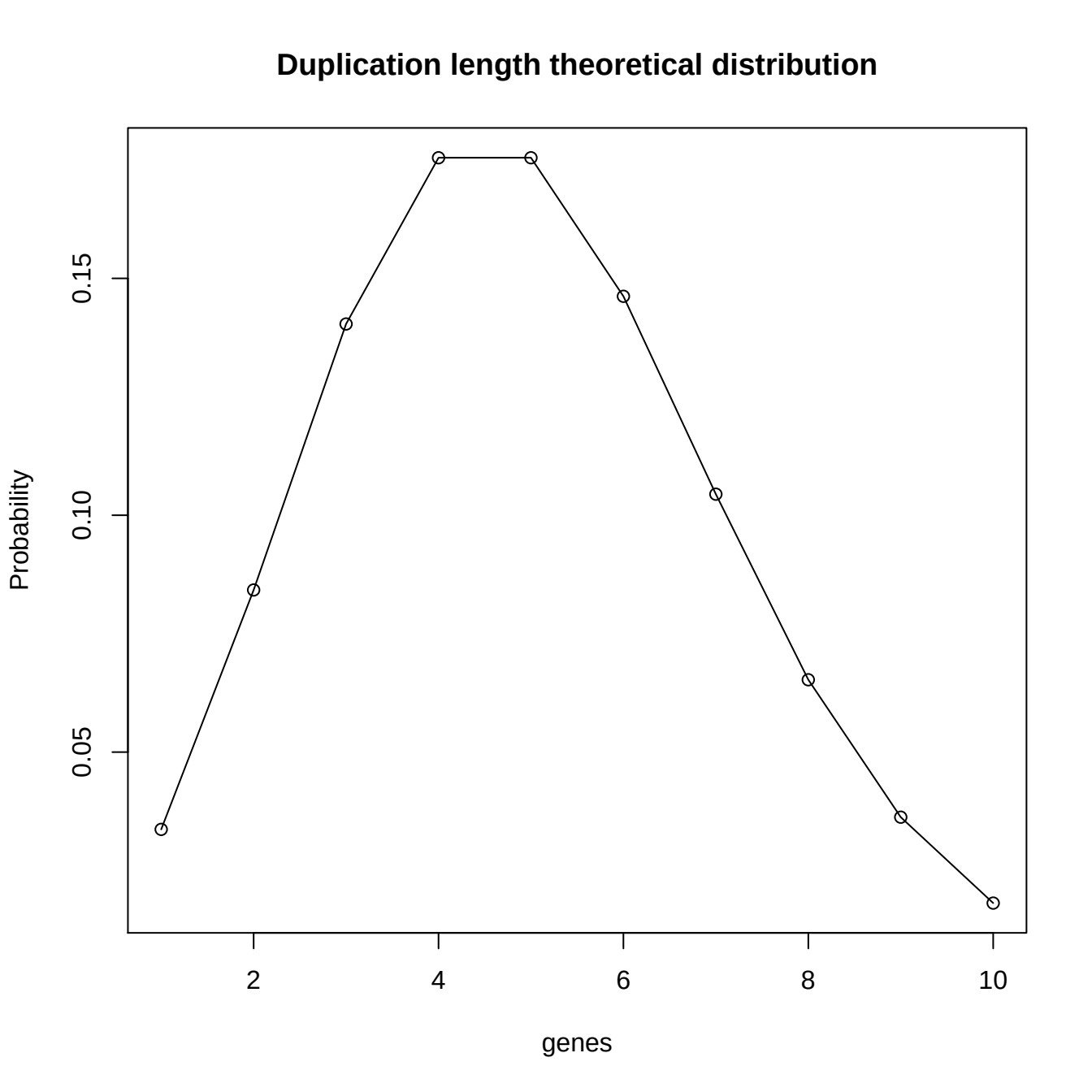
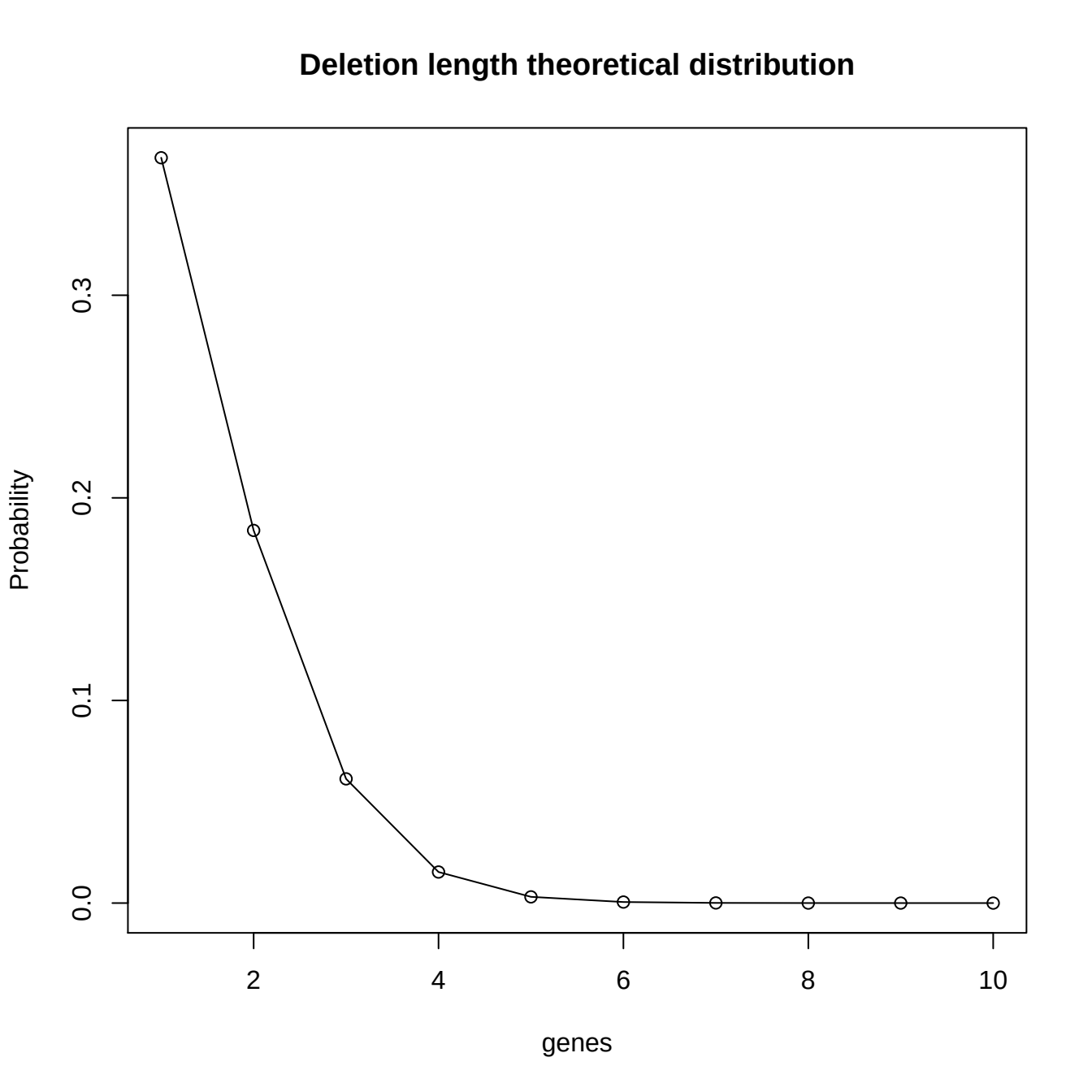
Parameters

genes	100
chr	4
nSpecies	5
averageEvents	5
minimalEventsOnBranch	1
averageInversionLength	5
averageDuplicationLength	5
averageDeletionLength	1
probInversion	0.6
probTranslocation	0.25
probDuplication	0
probDeletion	0
probFusion	0.05
probFission	0.05
probWGD	0.05
averageDeletionRateWGD	1
outDirectory	results_example
phyChroFormat	FALSE
nSimulations	10
seed	0
save	TRUE


Inversion length theoretical distribution
Probability
0.05
0.10
0.15
2
4
6
8
10
genes


Duplication length theoretical distribution
Probability
0.05
0.10
0.15
2
4
6
8
10
genes


Deletion length theoretical distribution
Probability
0.0
0.1
0.2
0.3
2
4
6
8
10
genes