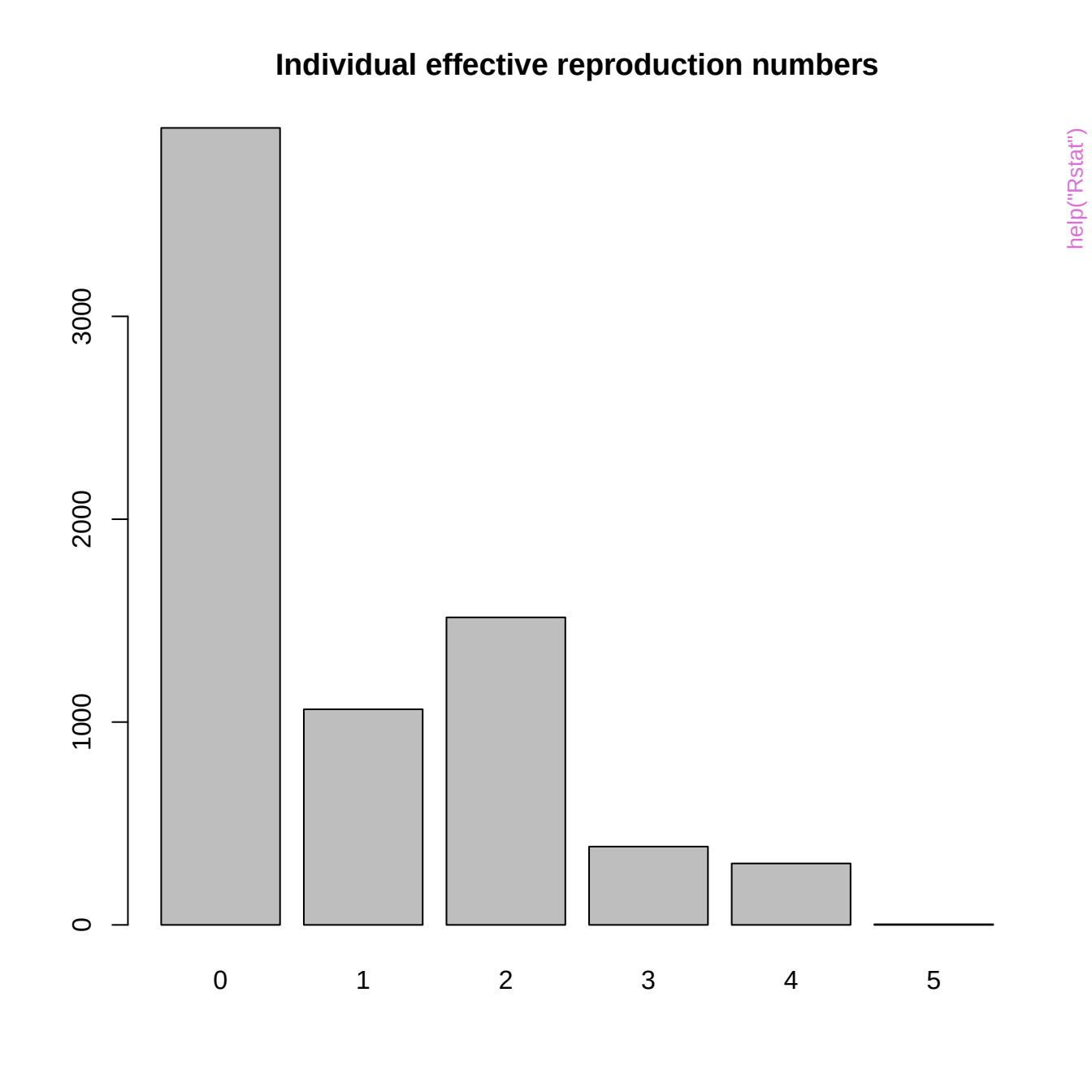
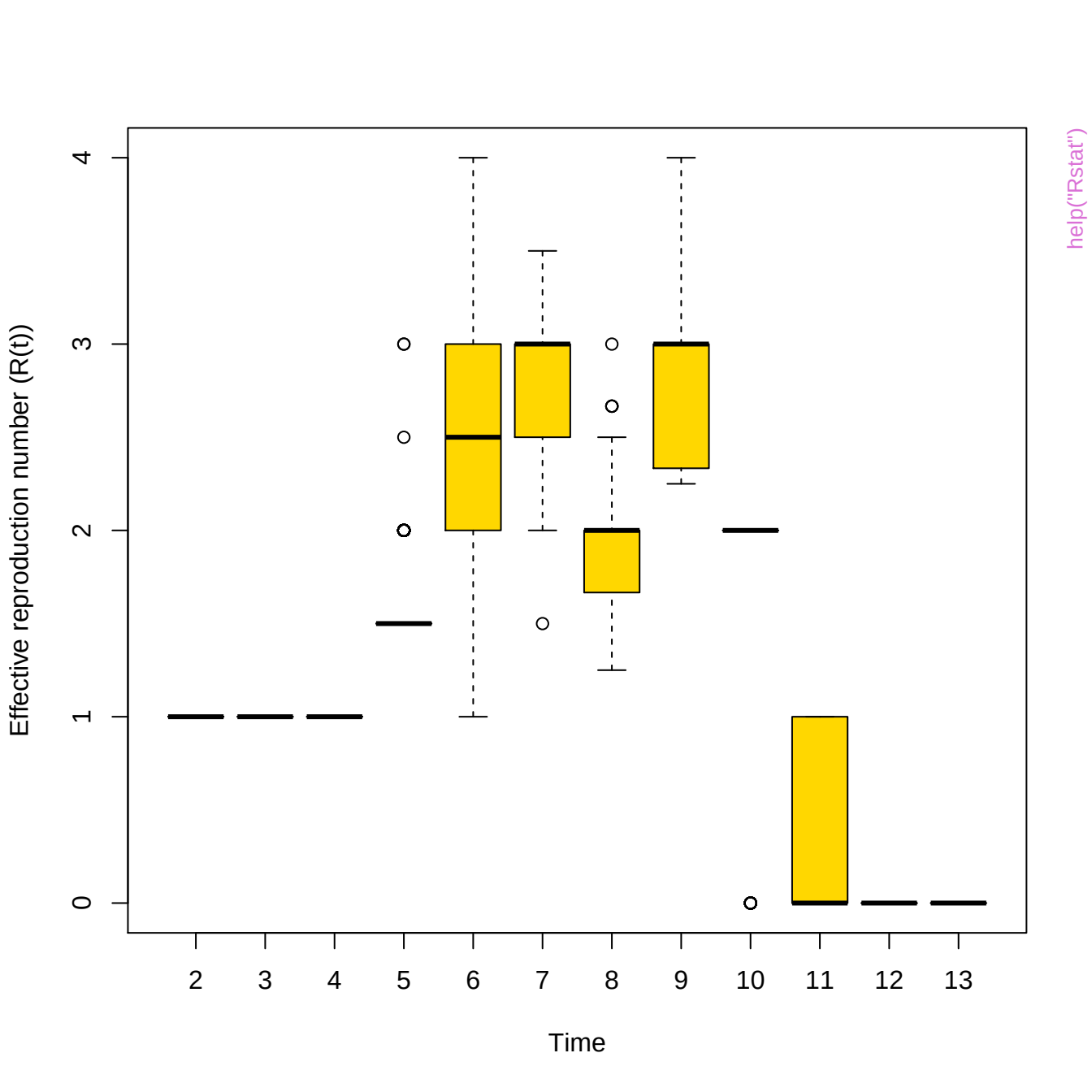
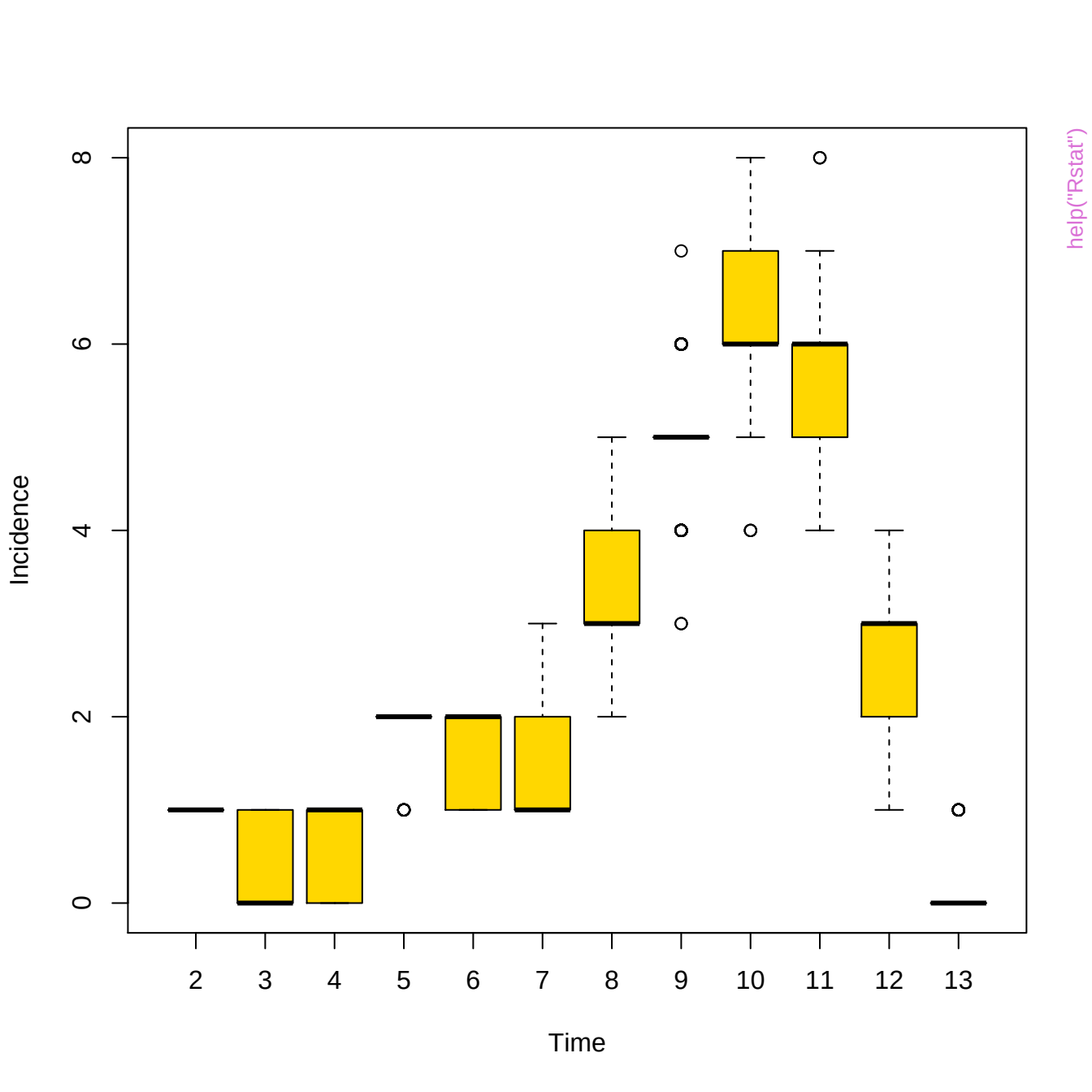
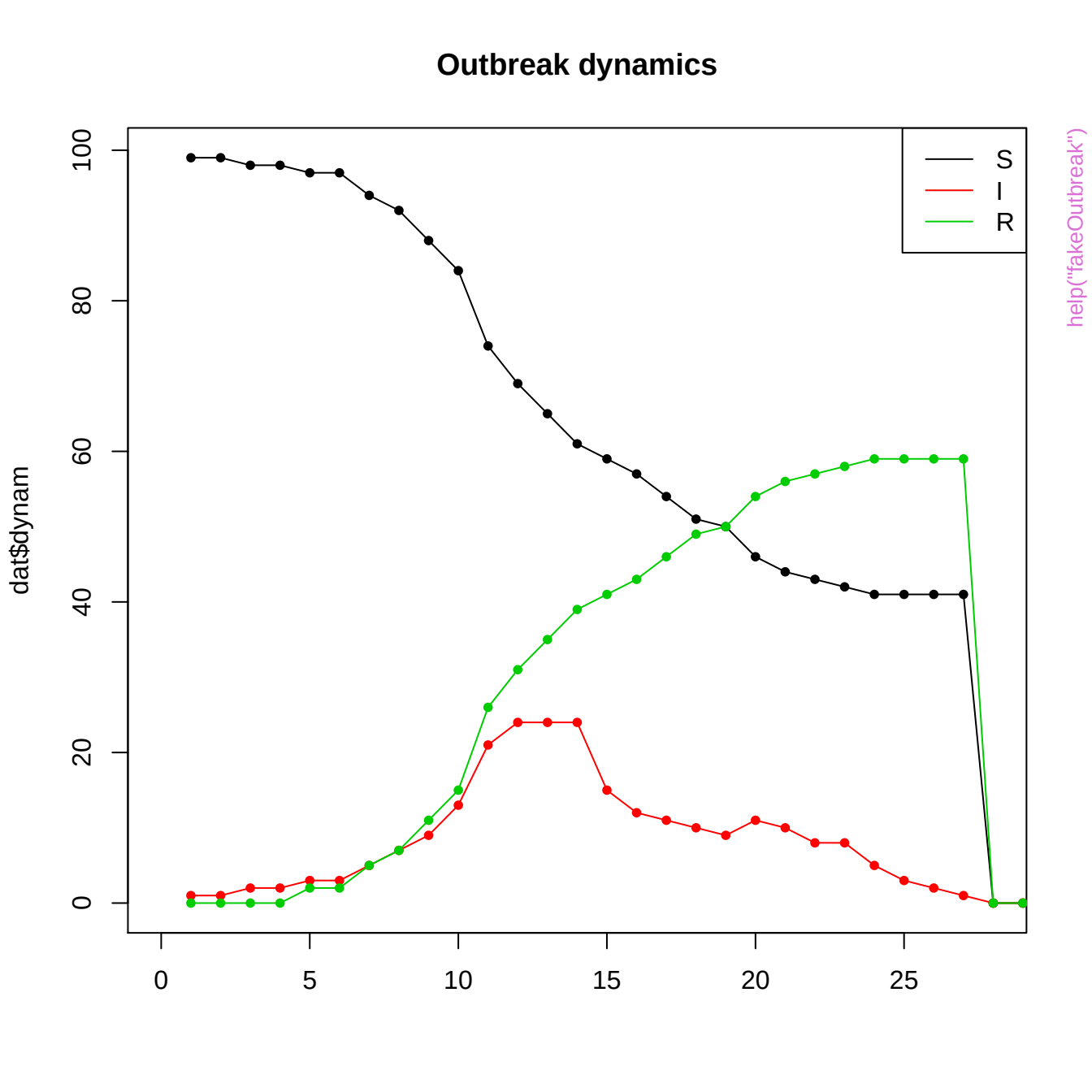

Individual effective reproduction numbers
0
1000
2000
3000
0
1
2
3
4
5
help("Rstat")

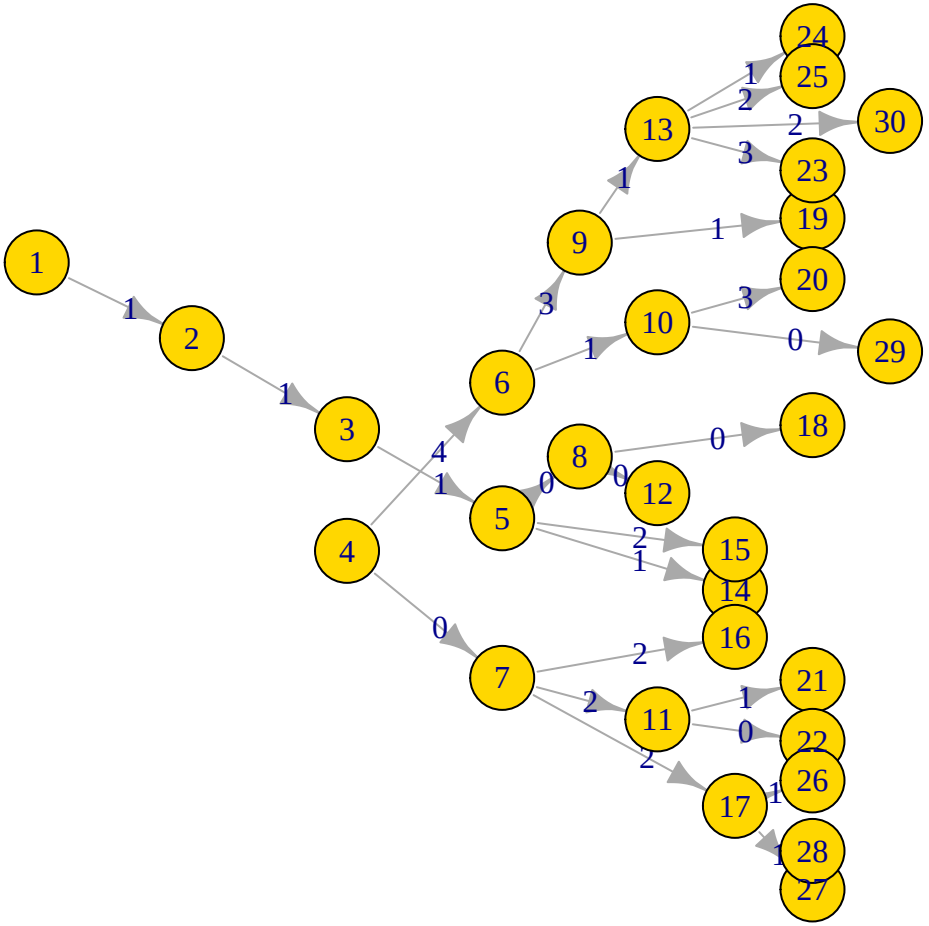

Effective reproduction number (R(t))
0
1
2
3
4
2
3
4
5
6
7
8
9
10
11
12
13
Time
help("Rstat")


Incidence
0
2
4
6
8
Time
2
3
4
5
6
7
8
9
10
11
12
13
help("Rstat")

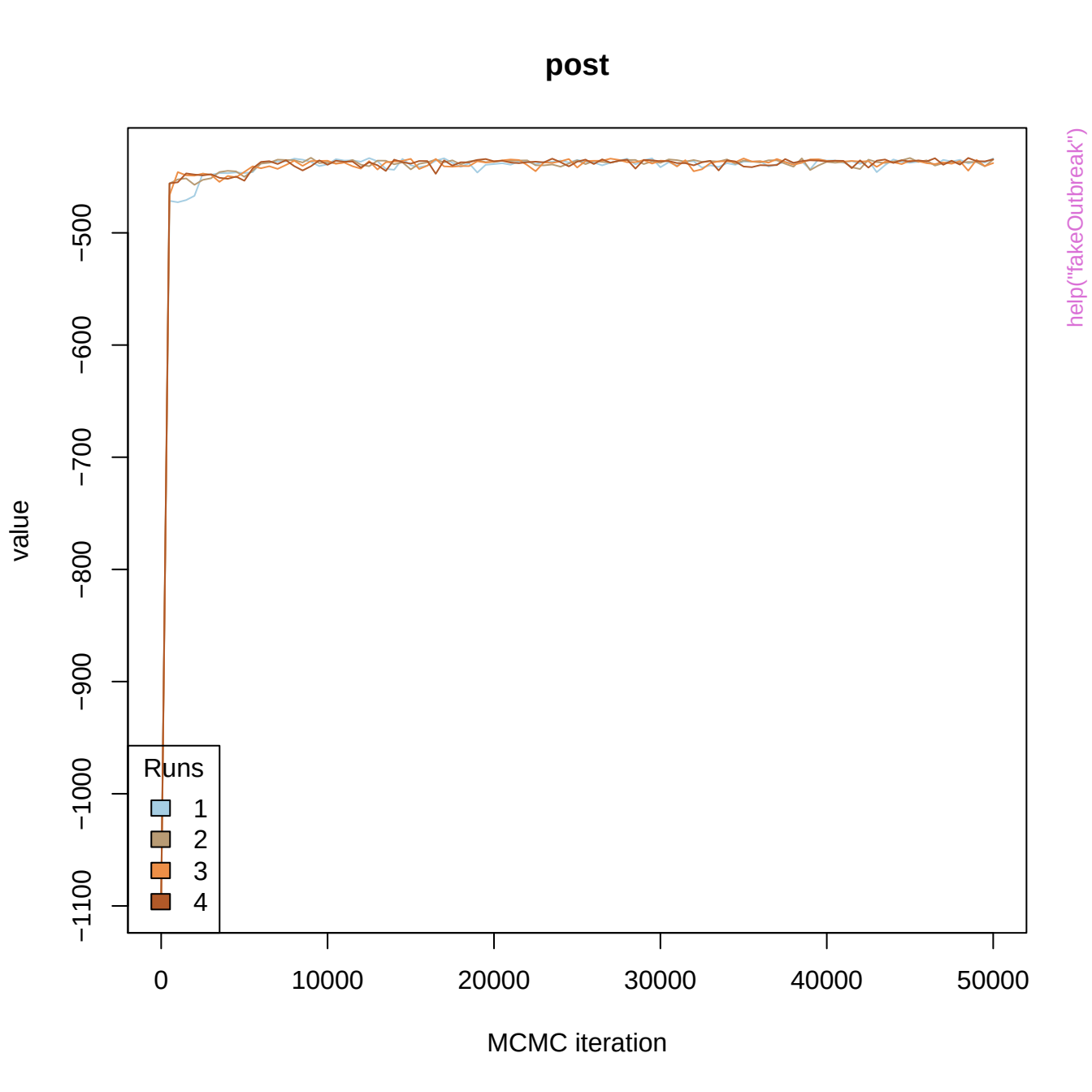

Outbreak dynamics
S
I
R
dat$dynam
0
20
40
60
80
100
0
5
10
15
20
25
help("fakeOutbreak")

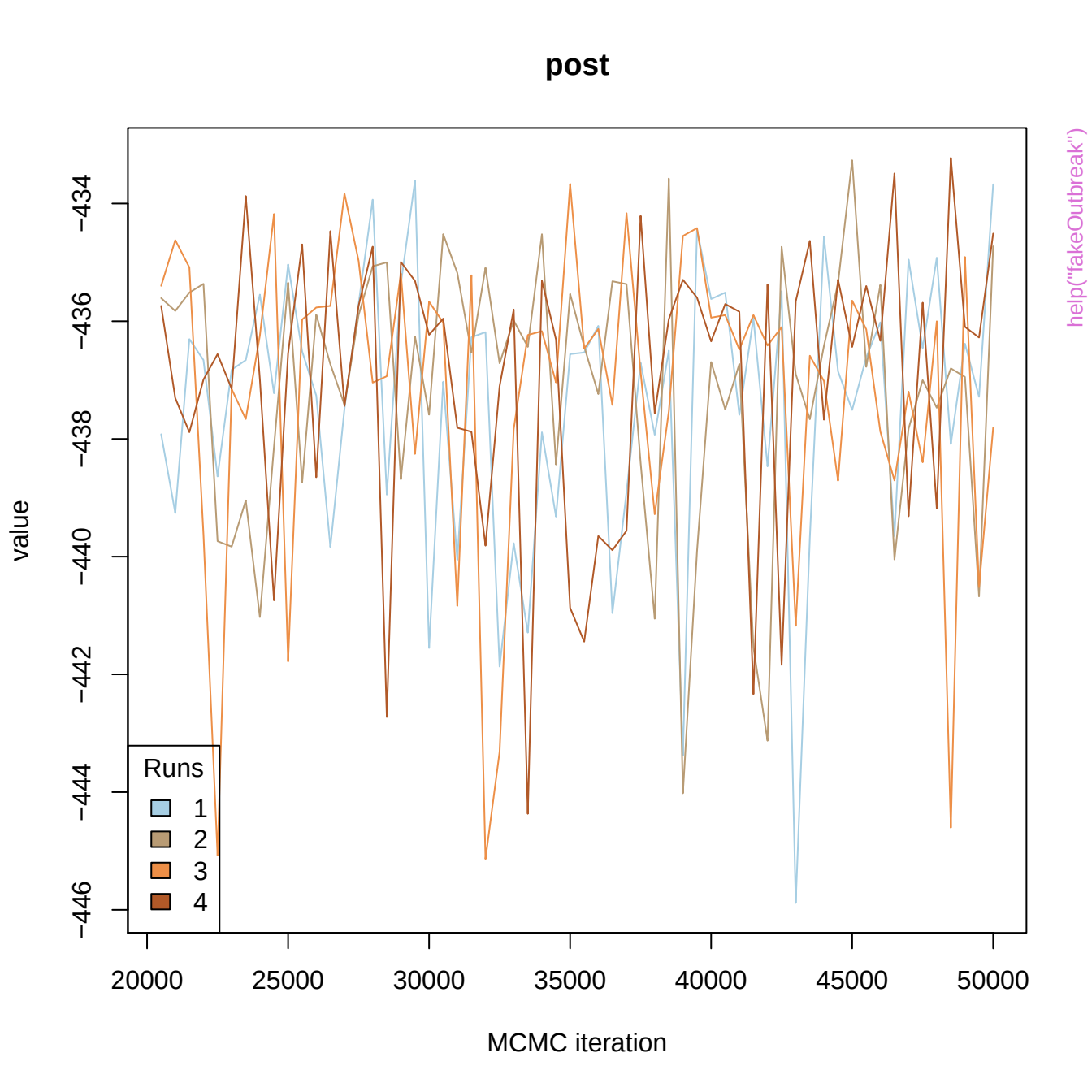
Data − transmission tree

arrow annotations are numbers of mutations

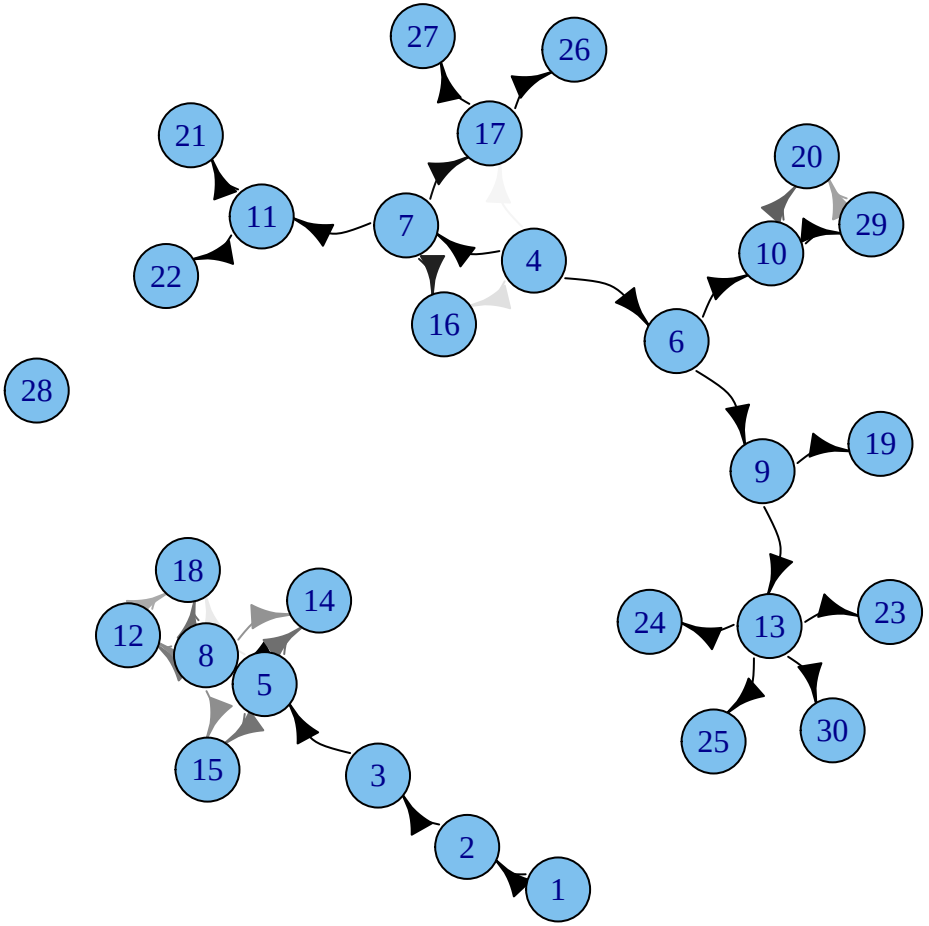


help("fakeOutbreak")


post
value
−500
−600
−700
−800
−900
−1000
−1100
0
10000
20000
30000
40000
50000
MCMC iteration
Runs
1
2
3
4
help("fakeOutbreak")

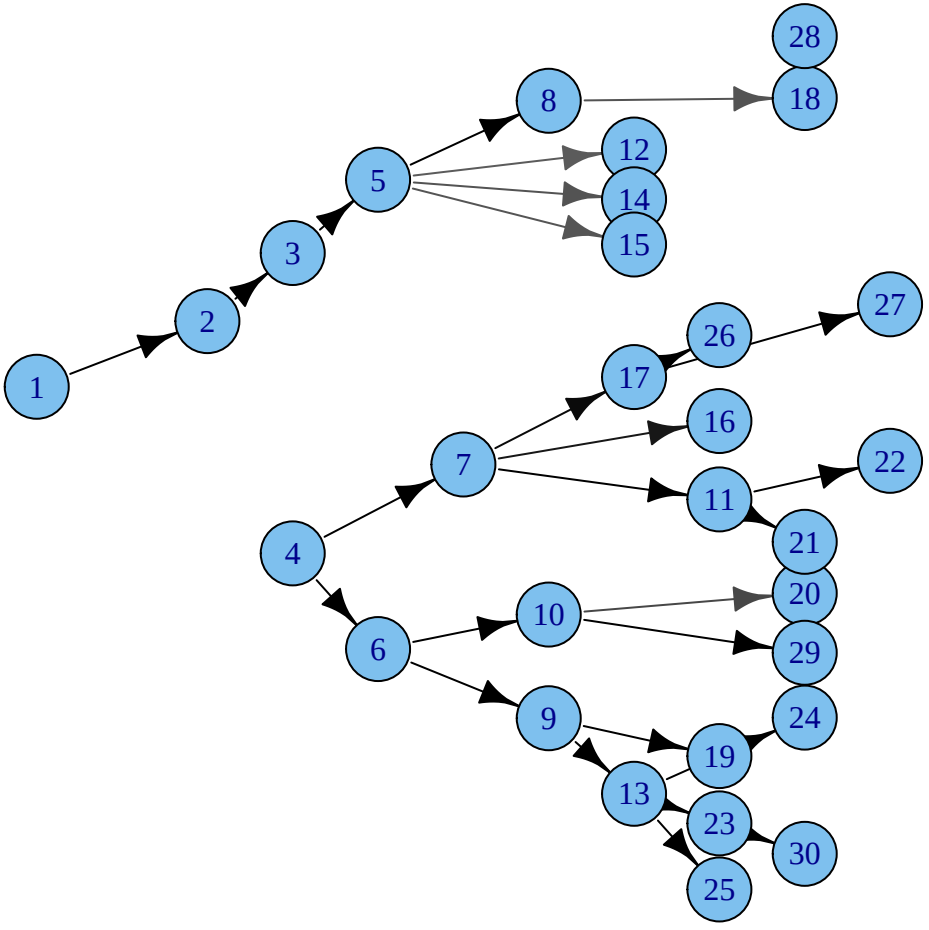

post
value
−434
−436
−438
−440
−442
−444
−446
Runs
1
2
3
4
20000
25000
30000
35000
40000
45000
50000
MCMC iteration
help("fakeOutbreak")

Posterior ancestries



help("fakeOutbreak")

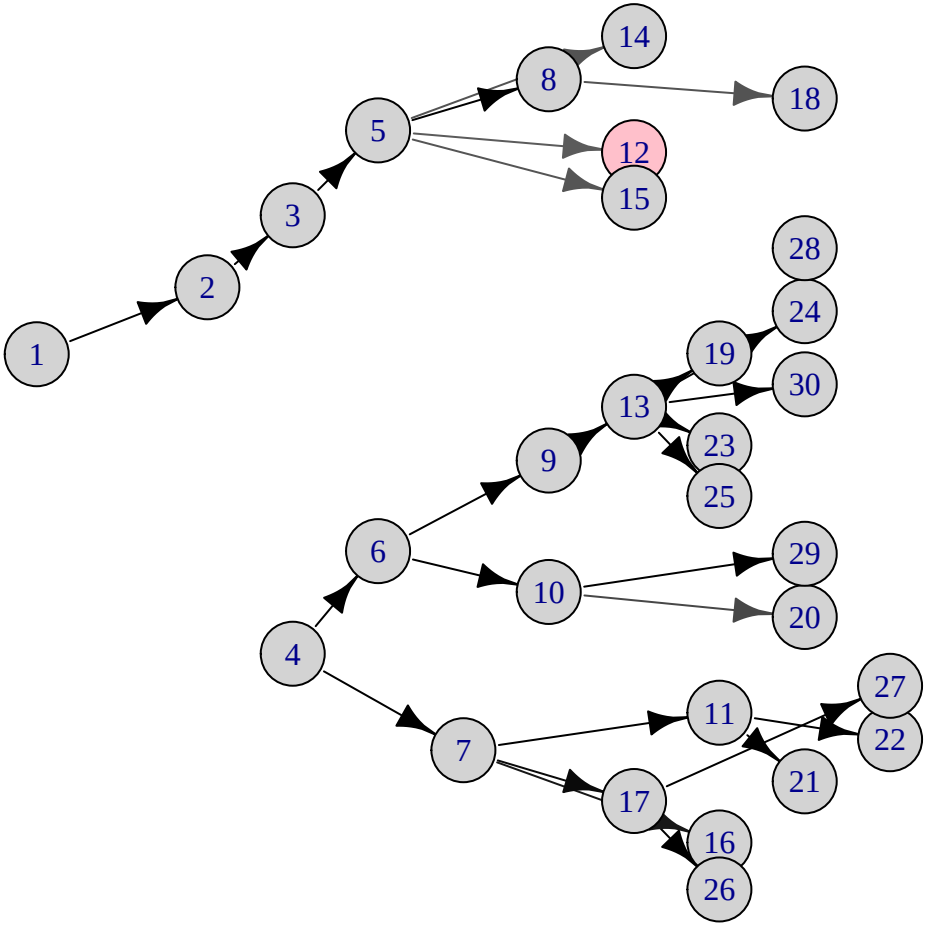
Consensus ancestries



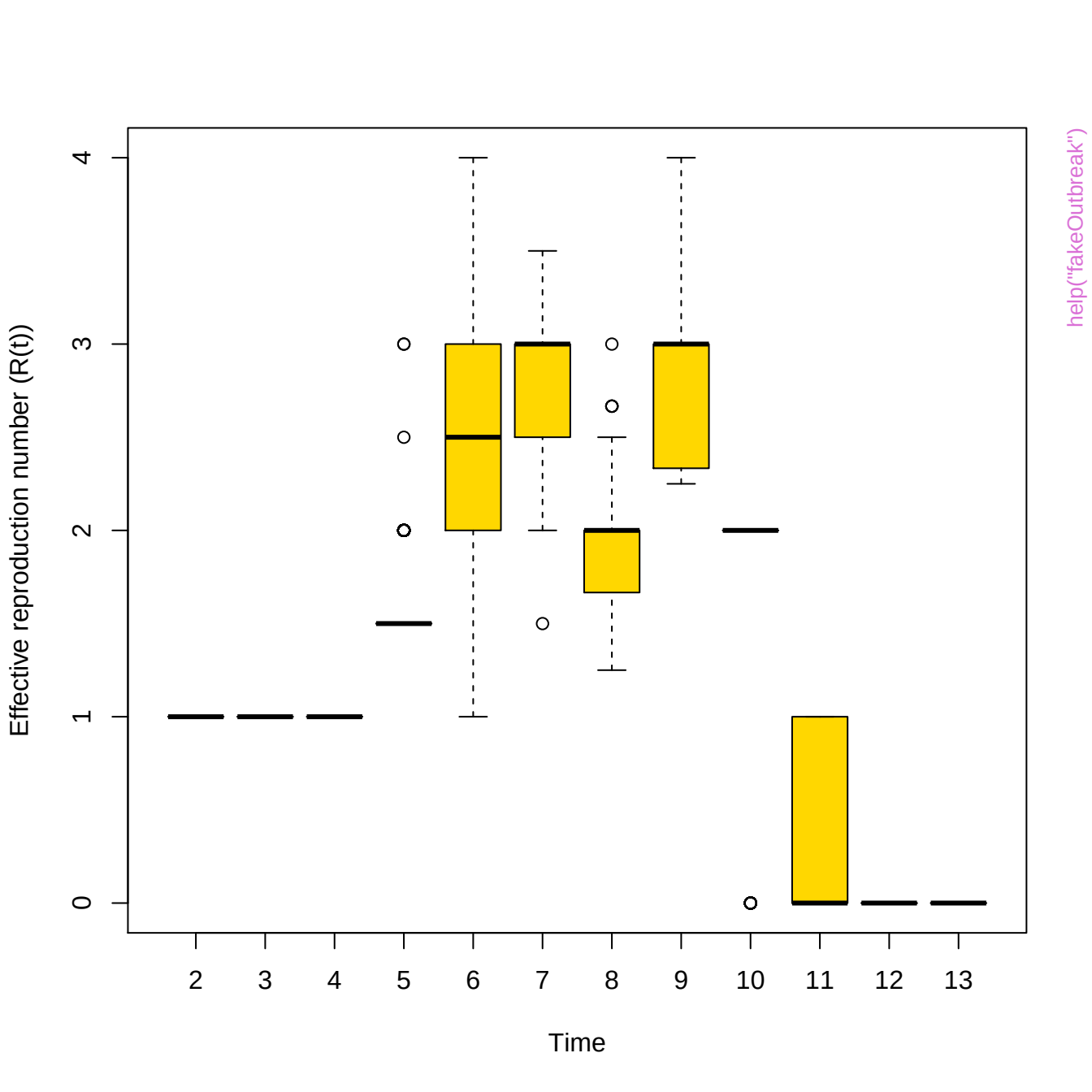
help("fakeOutbreak")

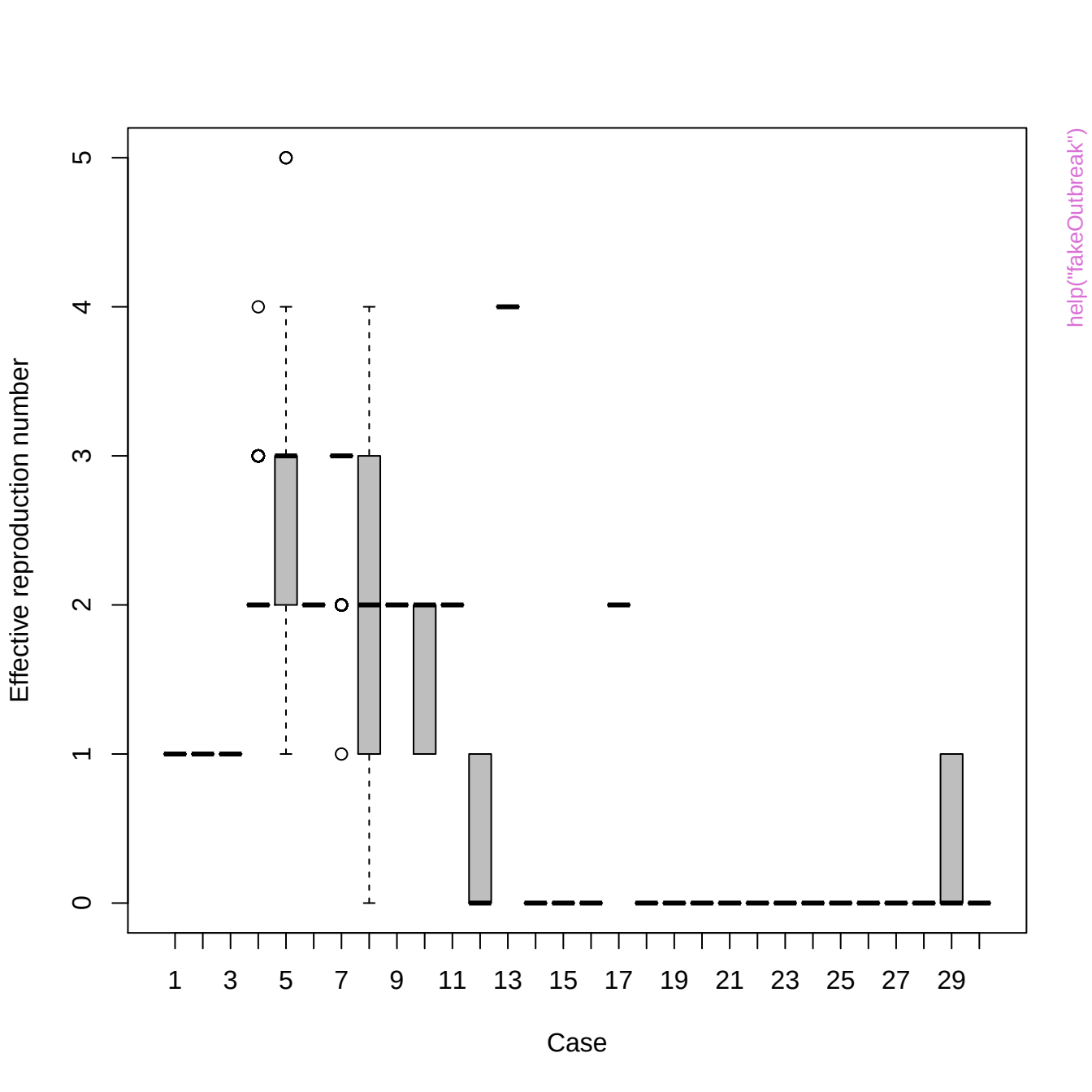
Consensus ancestries

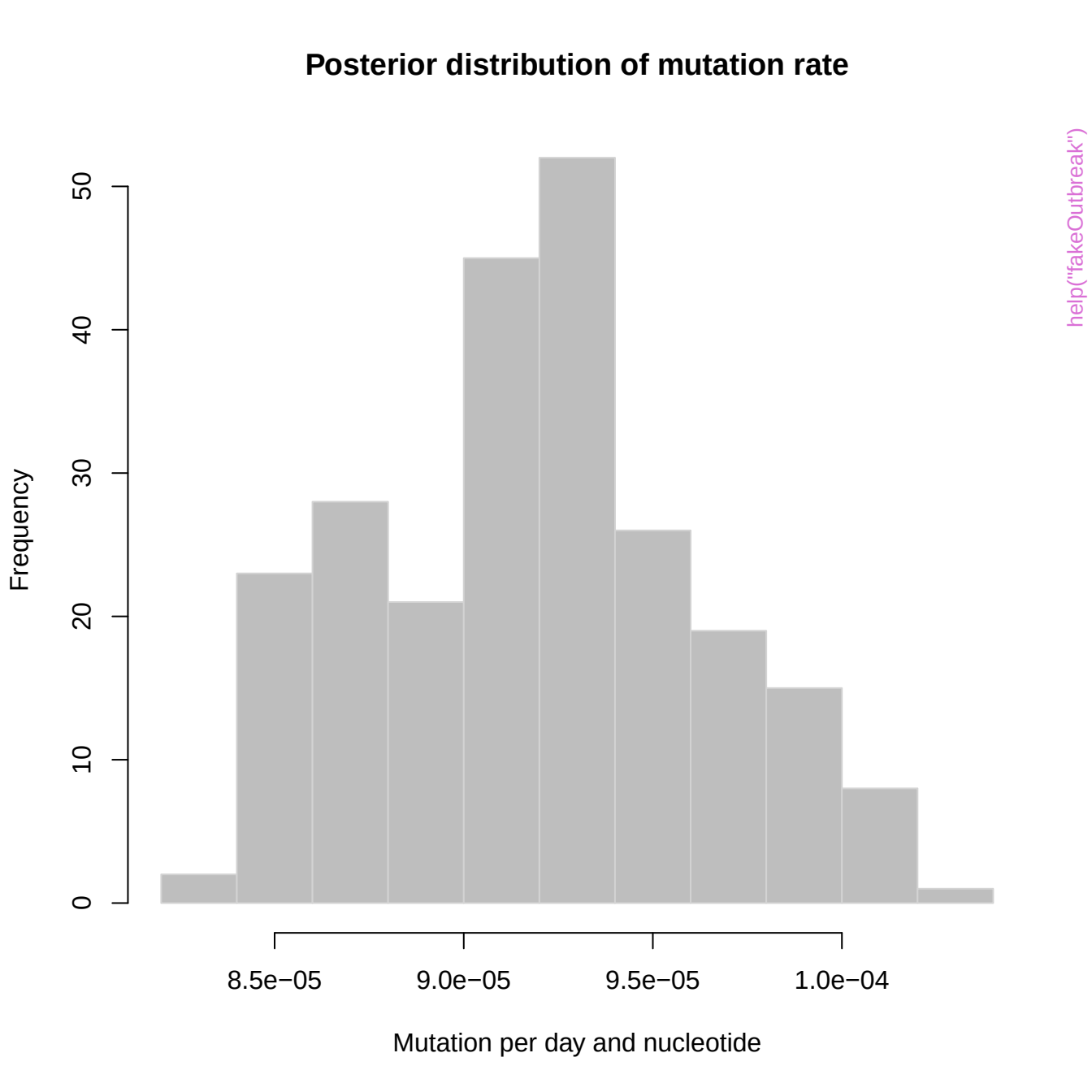
cases with erroneous ancestries in pink

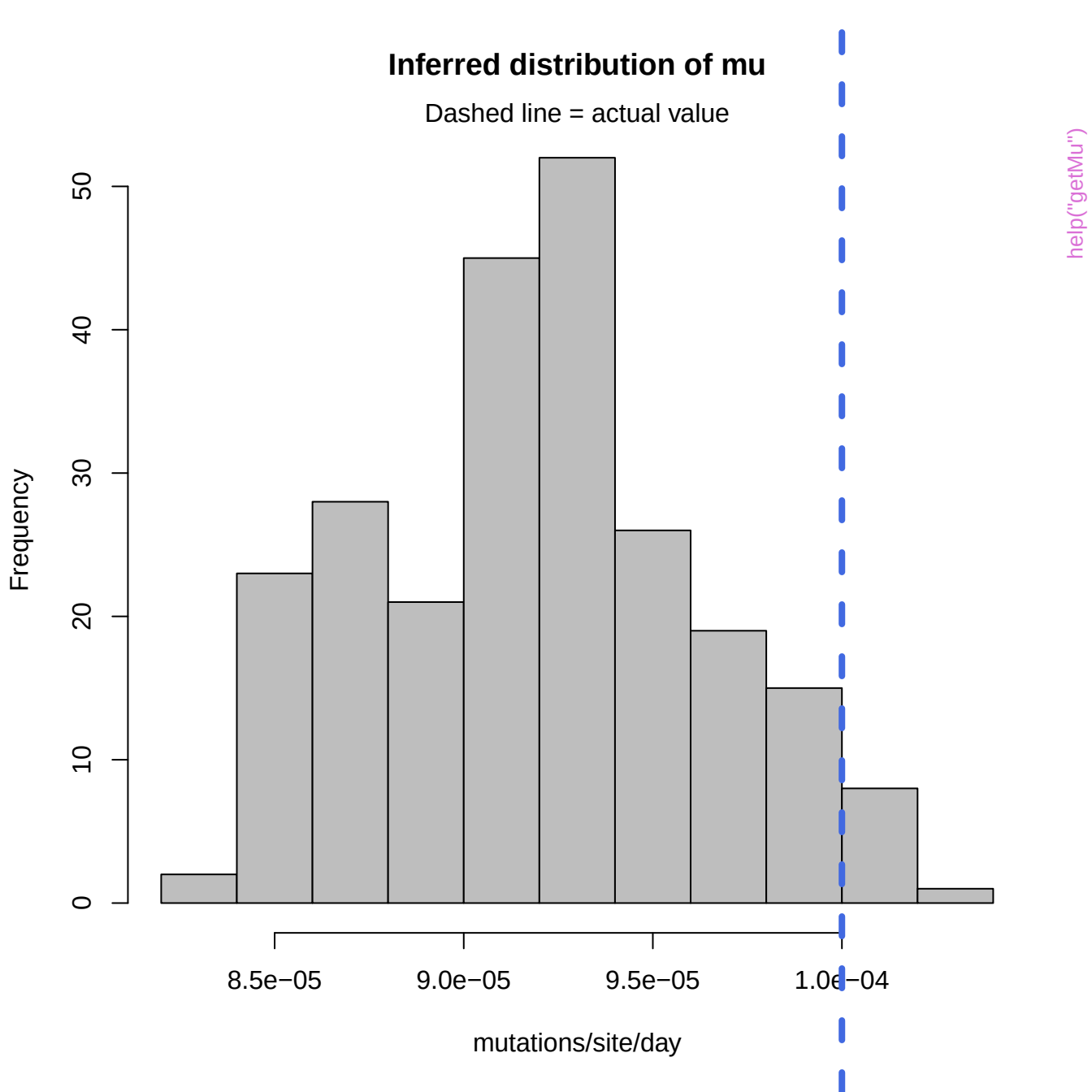


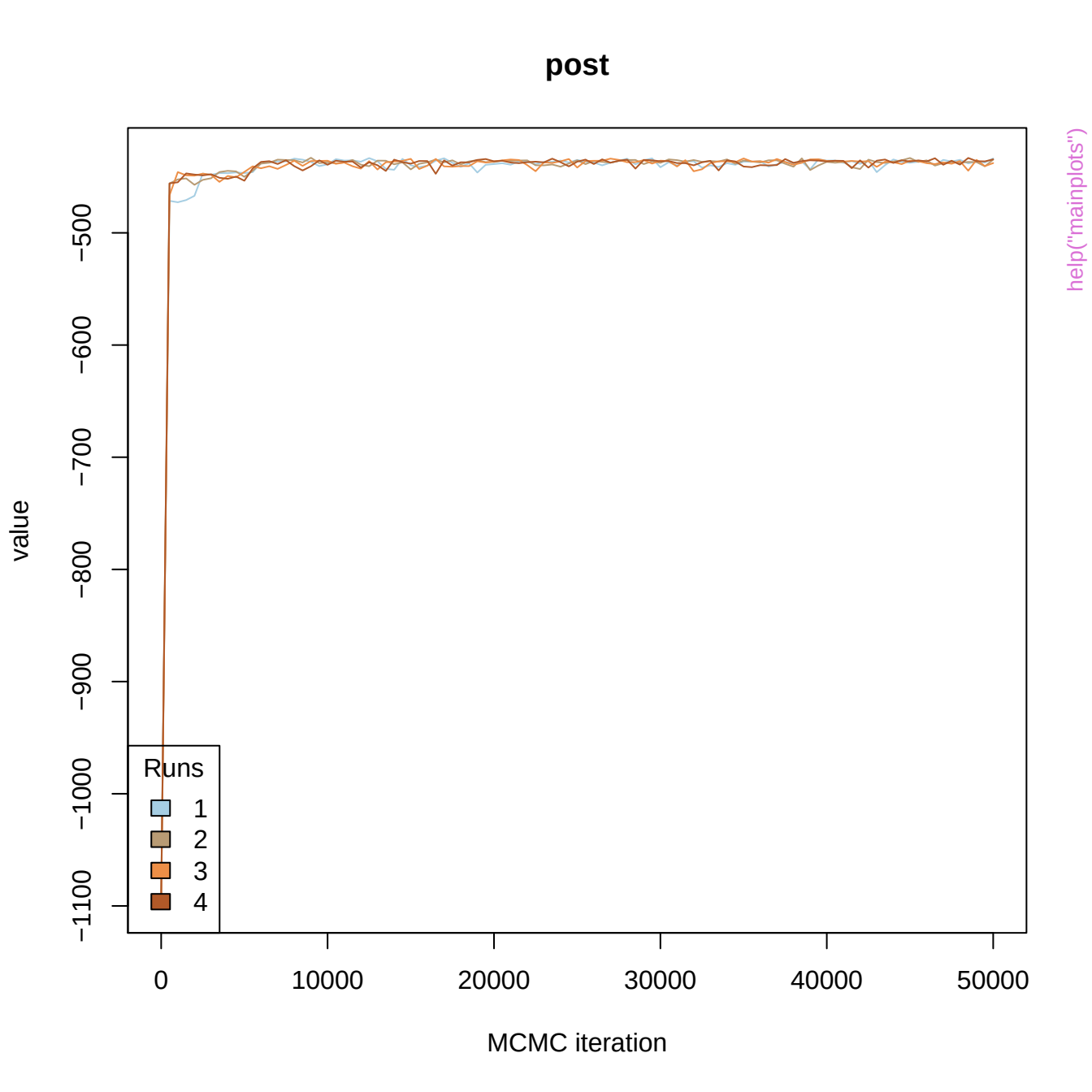
help("fakeOutbreak")

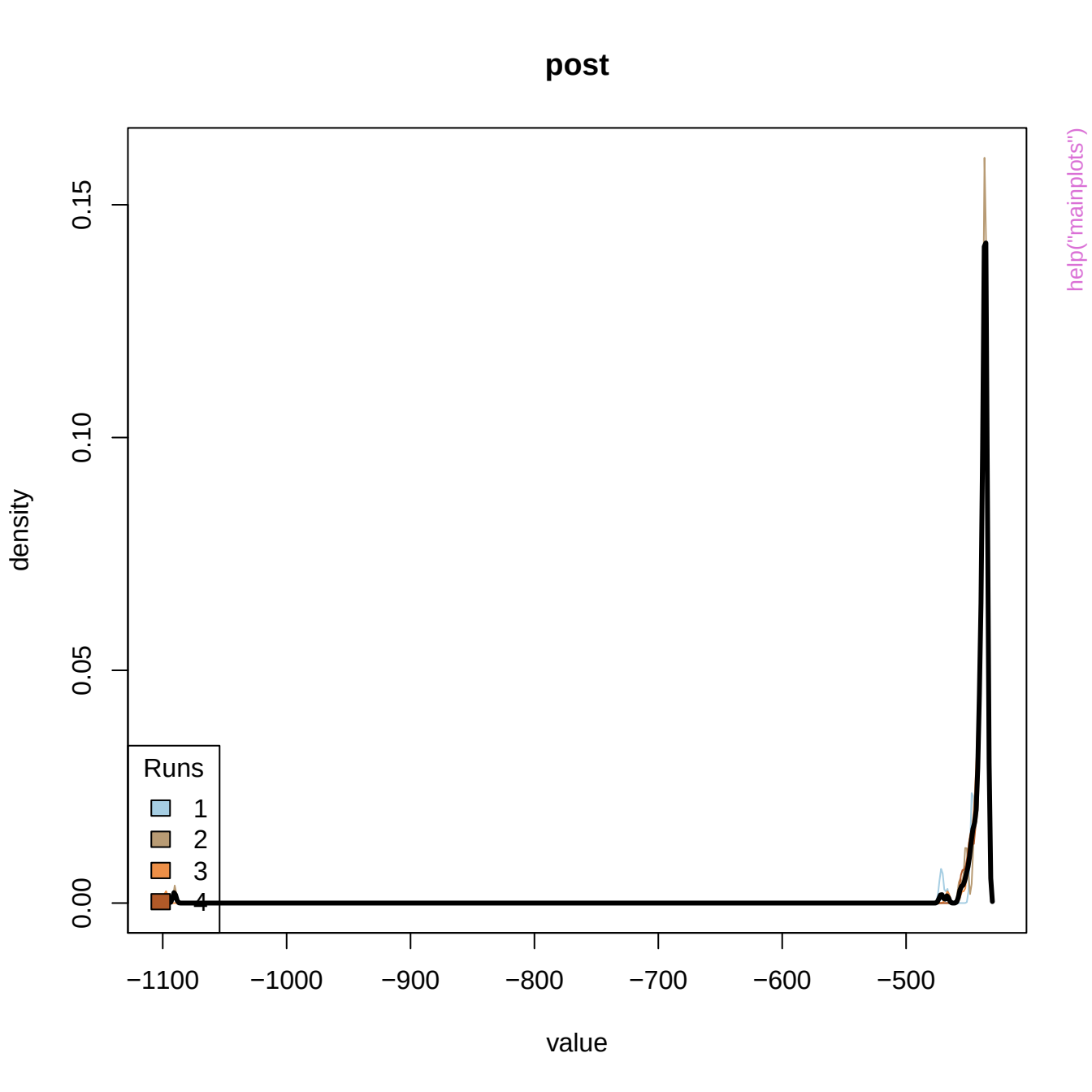

Effective reproduction number (R(t))
0
1
2
3
4
2
3
4
5
6
7
8
9
10
11
12
13
Time
help("fakeOutbreak")

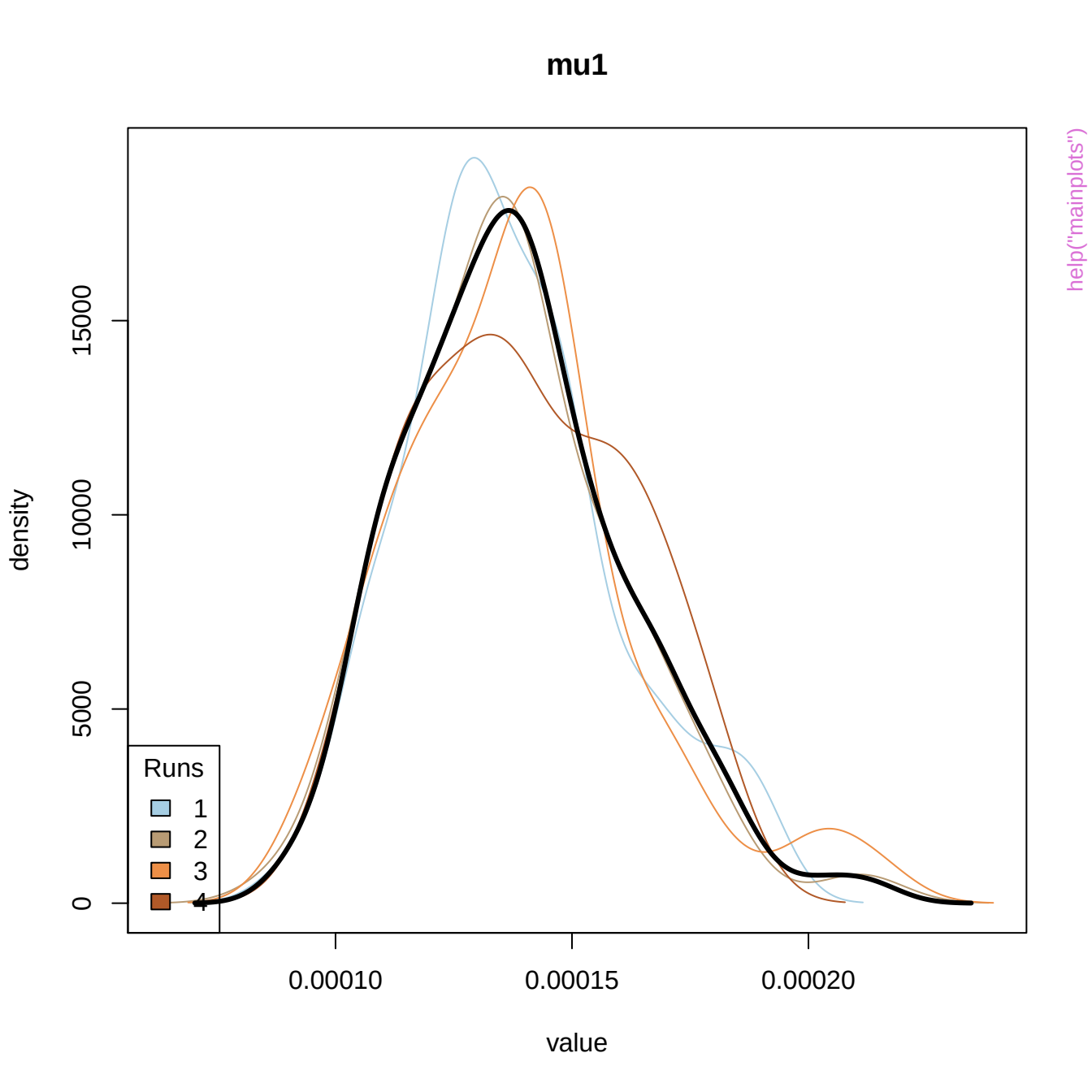

Effective reproduction number
0
1
2
3
4
5
1
3
5
7
9
11
13
15
17
19
21
23
25
27
29
Case
help("fakeOutbreak")


Posterior distribution of mutation rate
Frequency
0
10
20
30
40
50
8.5e−05
9.0e−05
9.5e−05
1.0e−04
Mutation per day and nucleotide
help("fakeOutbreak")

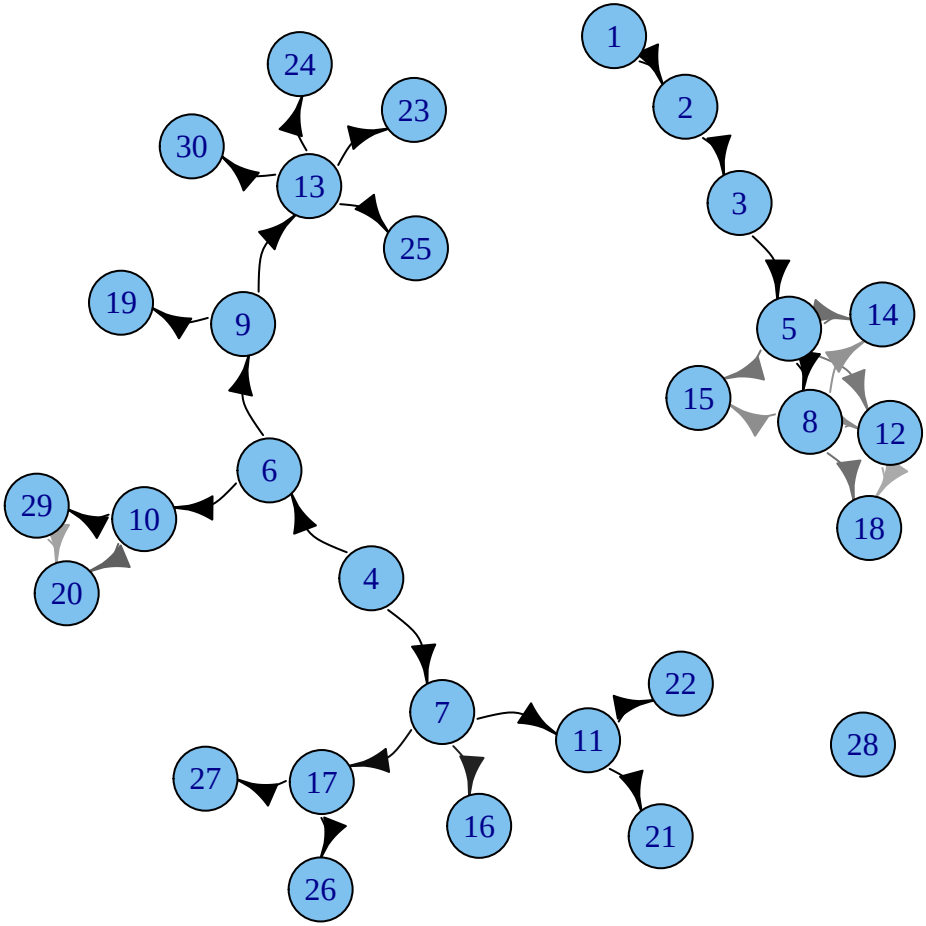

Inferred distribution of mu
Dashed line = actual value
Frequency
0
10
20
30
40
50
8.5e−05
9.0e−05
9.5e−05
1.0e−04
mutations/site/day
help("getMu")


post
value
−500
−600
−700
−800
−900
−1000
−1100
0
10000
20000
30000
40000
50000
MCMC iteration
Runs
1
2
3
4
help("mainplots")

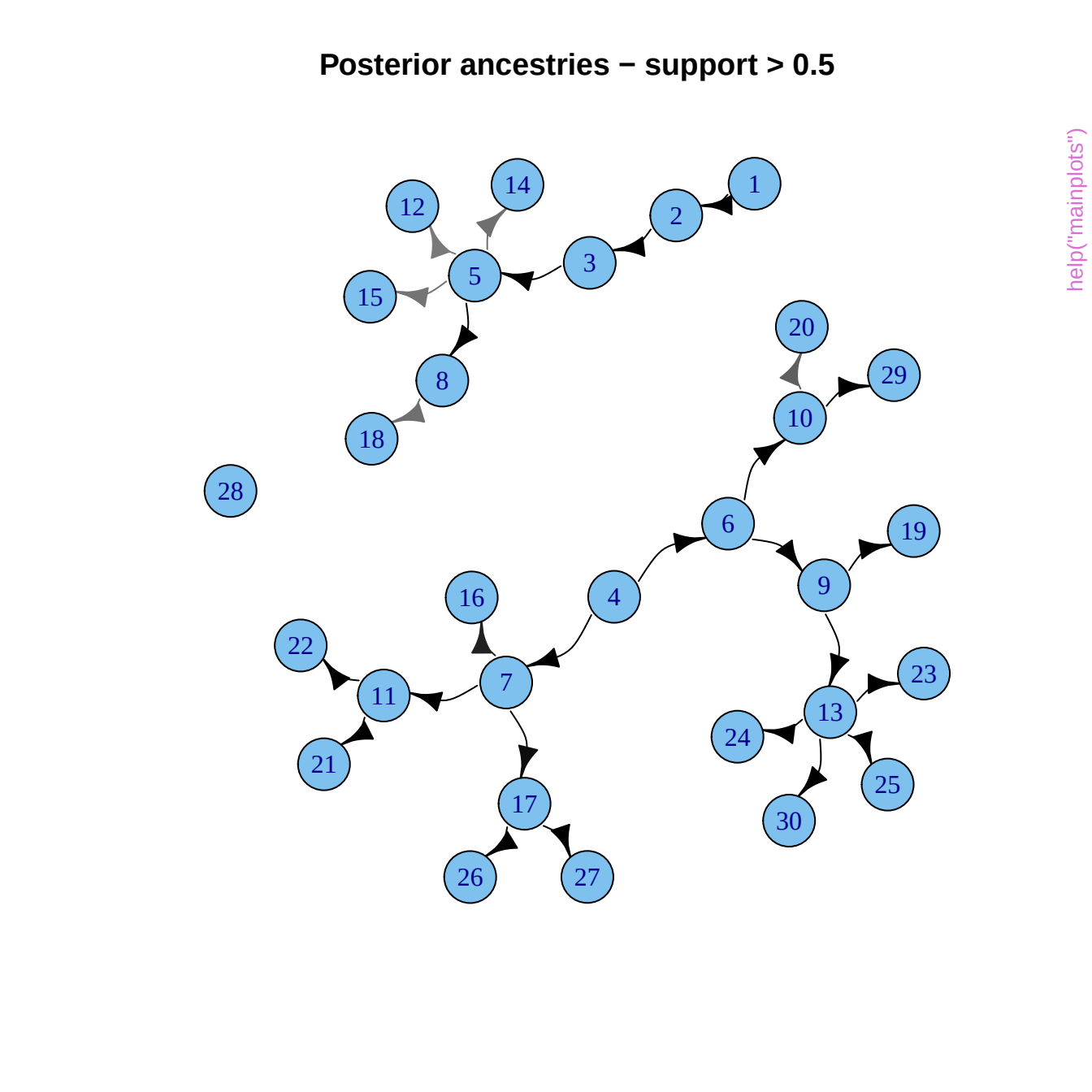

post
density
0.00
0.05
0.10
0.15
Runs
1
2
3
4
−1100
−1000
−900
−800
−700
−600
−500
value
help("mainplots")


mu1
density
0
5000
10000
15000
0.00010
0.00015
0.00020
value
Runs
1
2
3
4
help("mainplots")

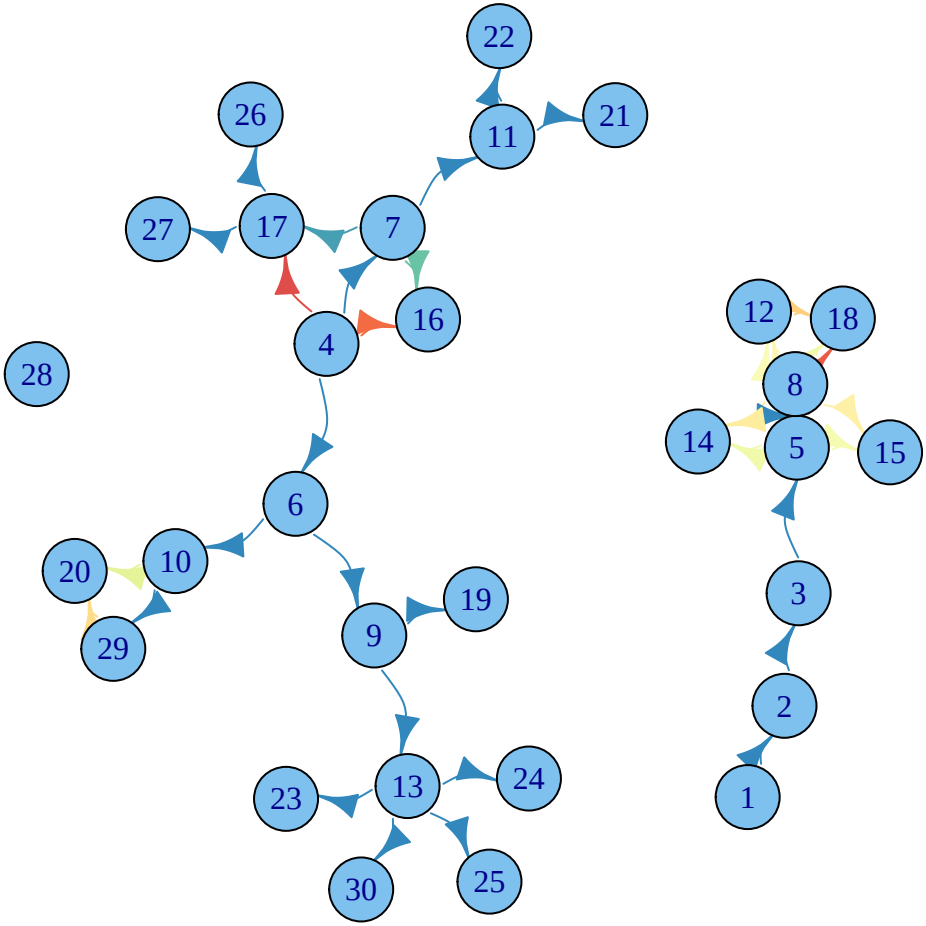
Posterior ancestries



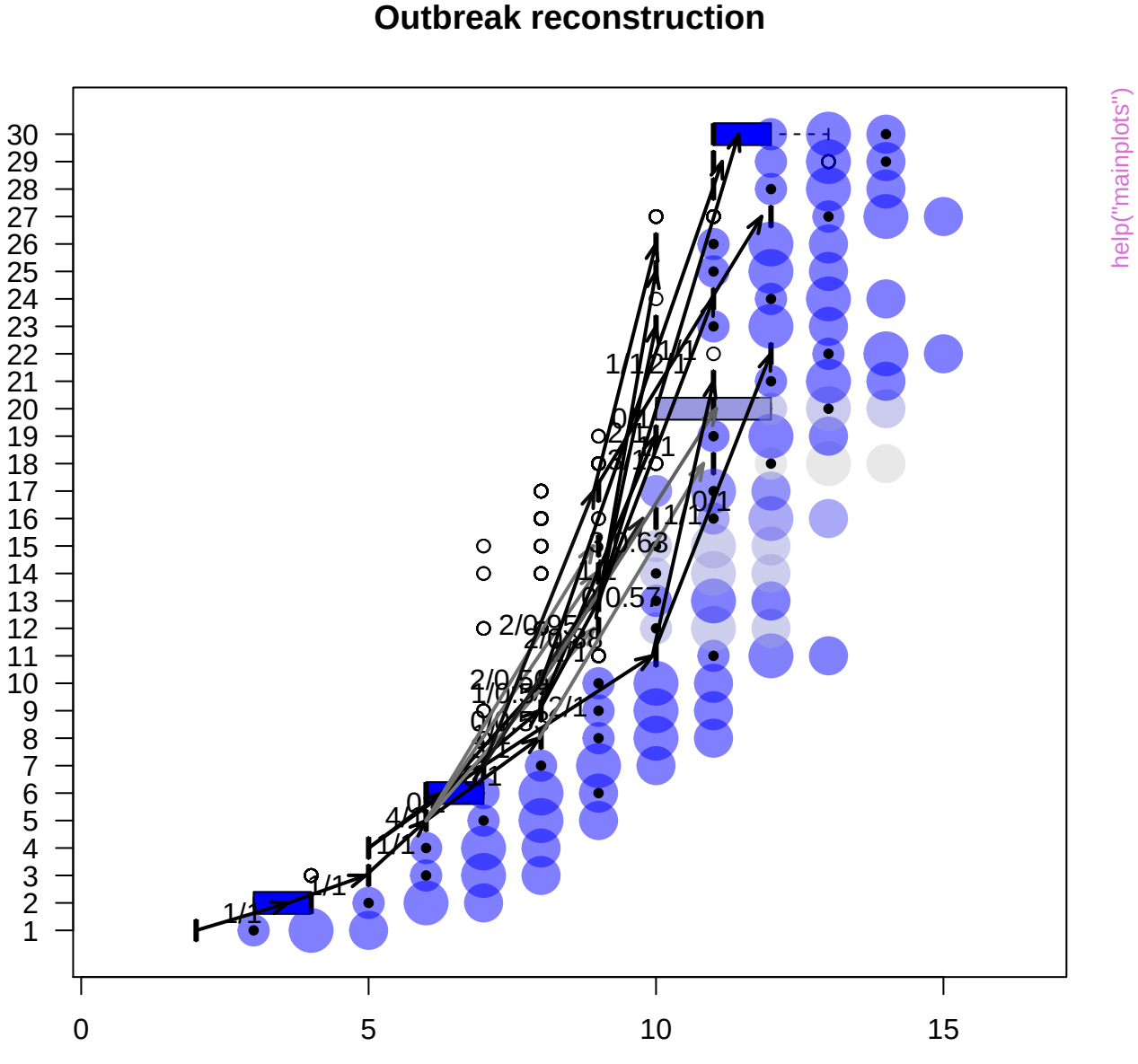
help("mainplots")

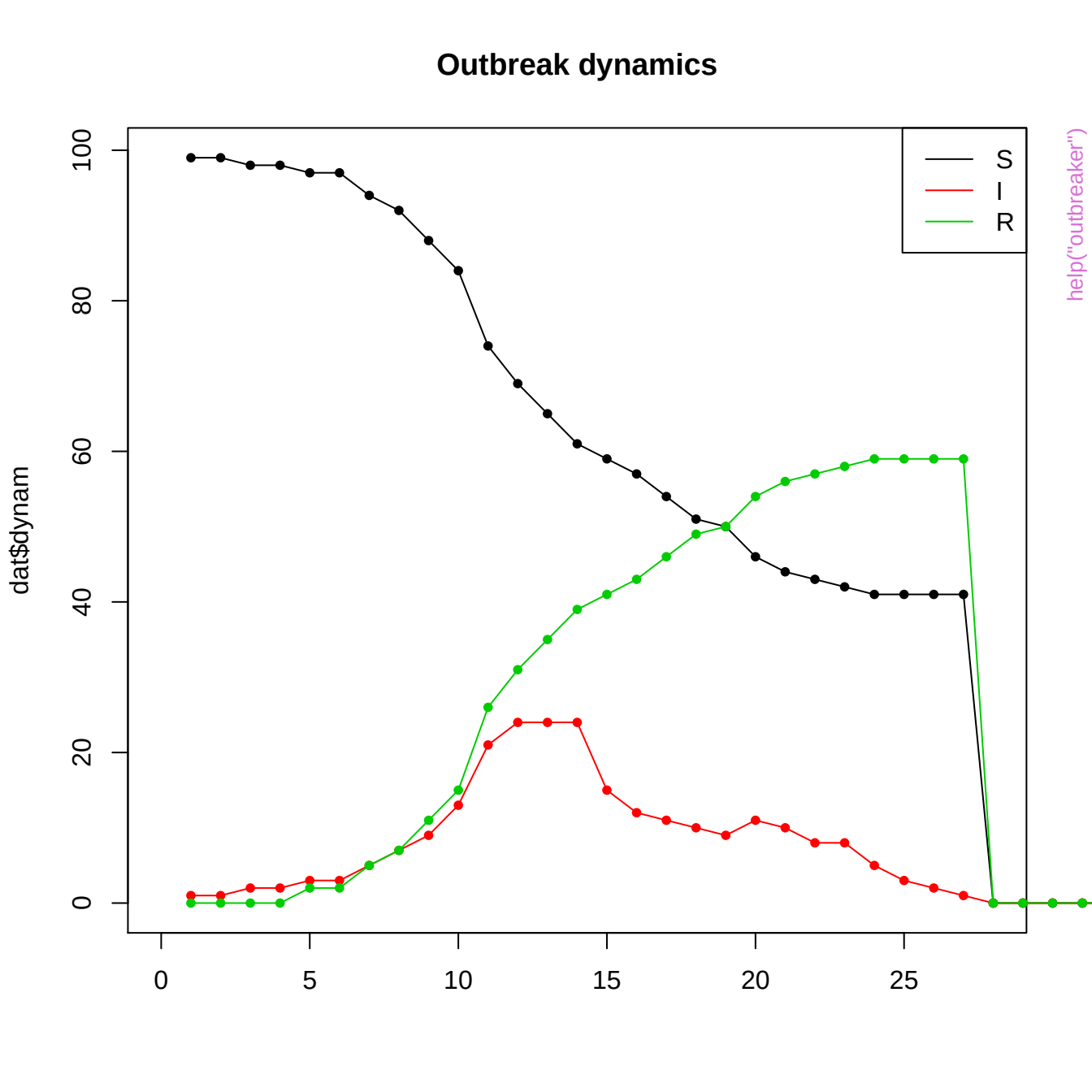

Posterior ancestries − support > 0.5
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
help("mainplots")

Posterior ancestries − support > 0.01



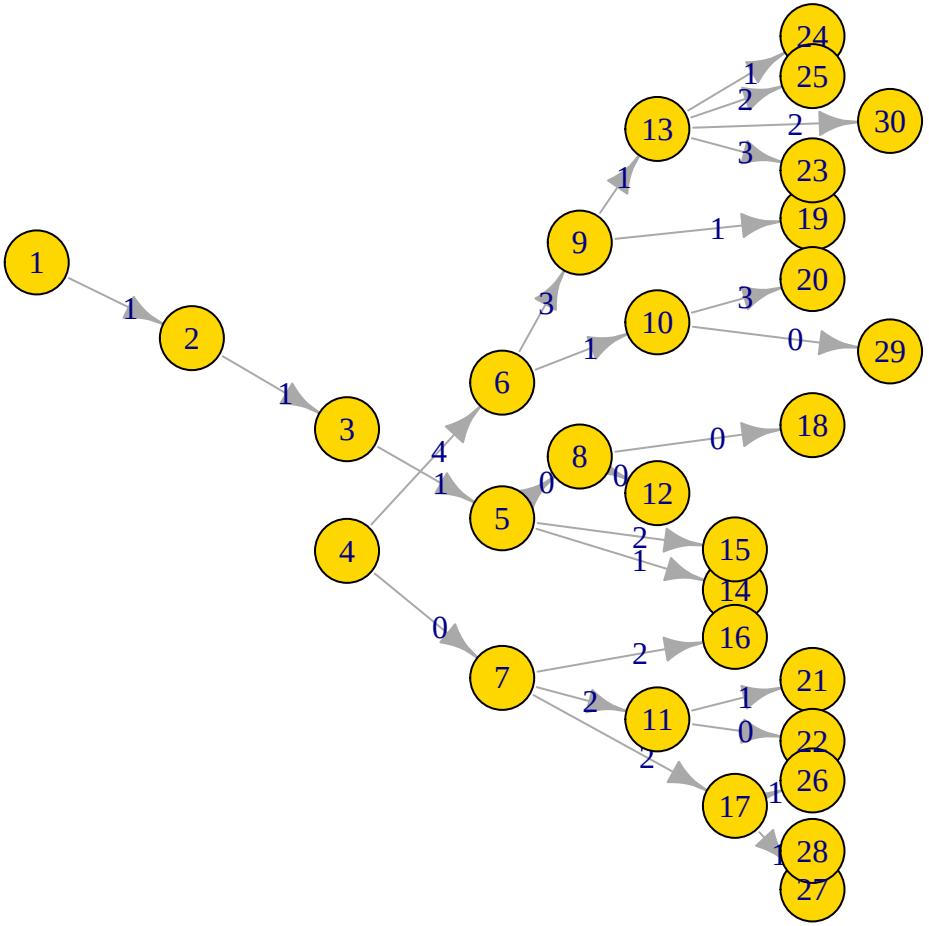
help("mainplots")


Outbreak reconstruction
help("mainplots")
0
5
10
15
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30

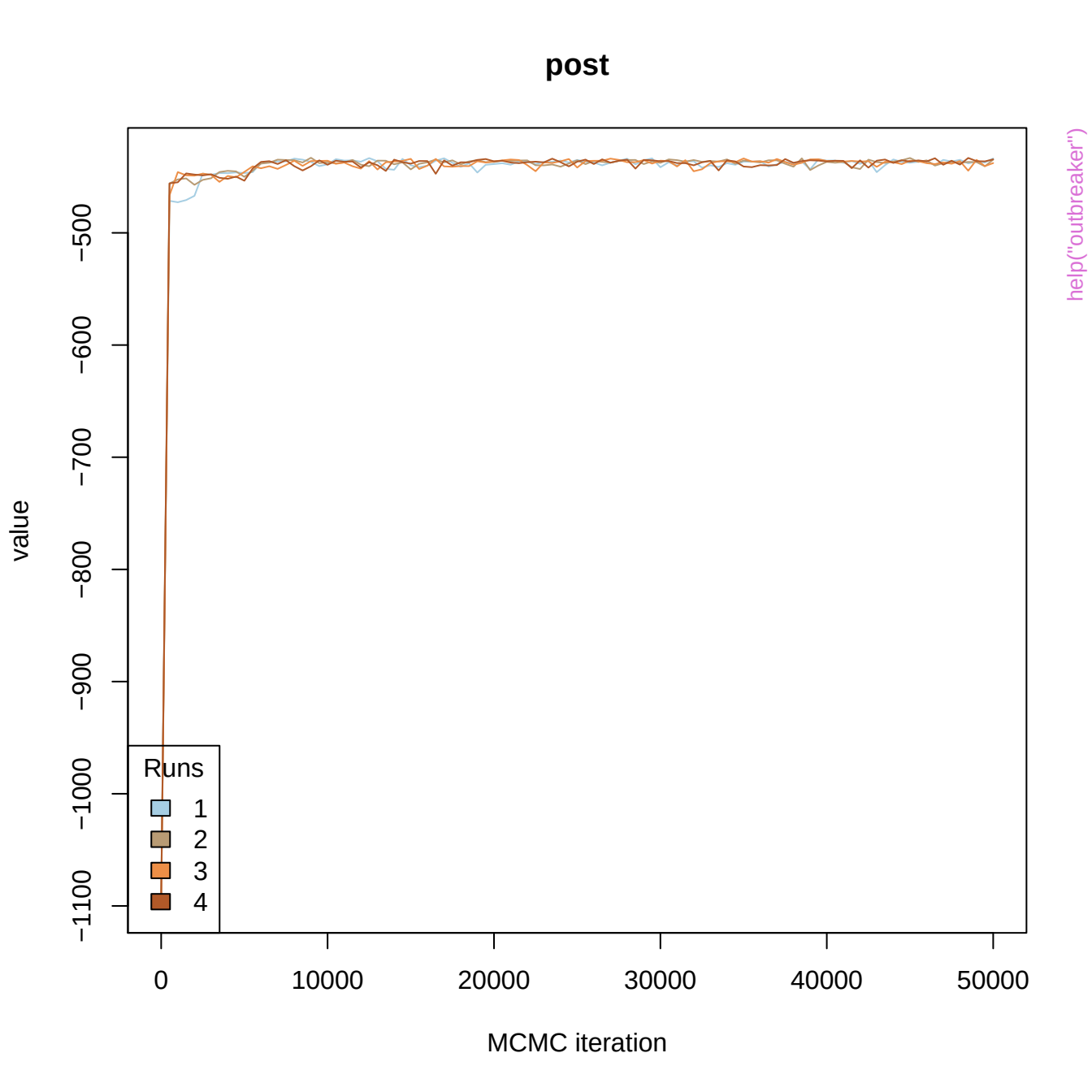

Outbreak dynamics
S
I
R
dat$dynam
0
20
40
60
80
100
0
5
10
15
20
25
help("outbreaker")

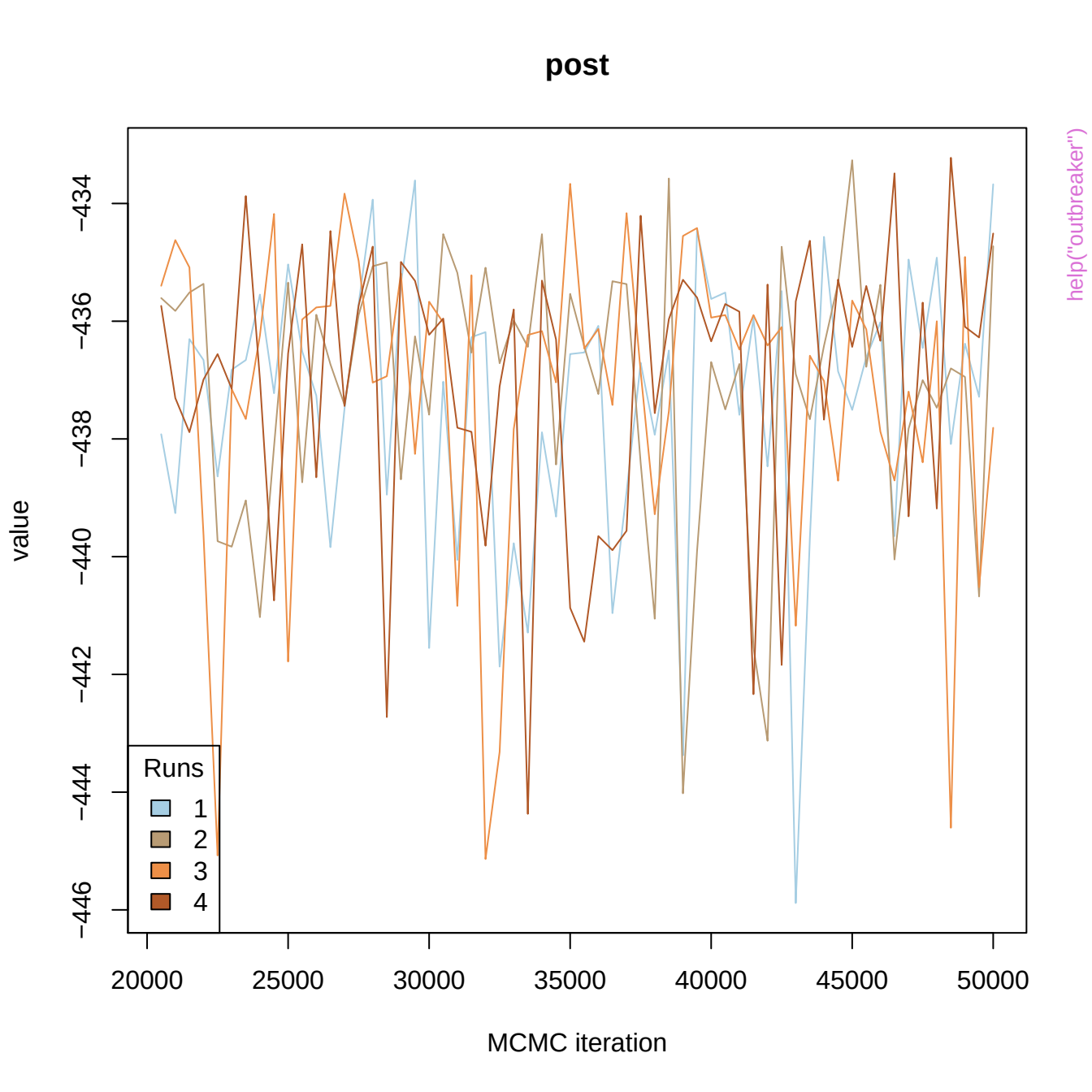
Data − transmission tree

arrow annotations are numbers of mutations

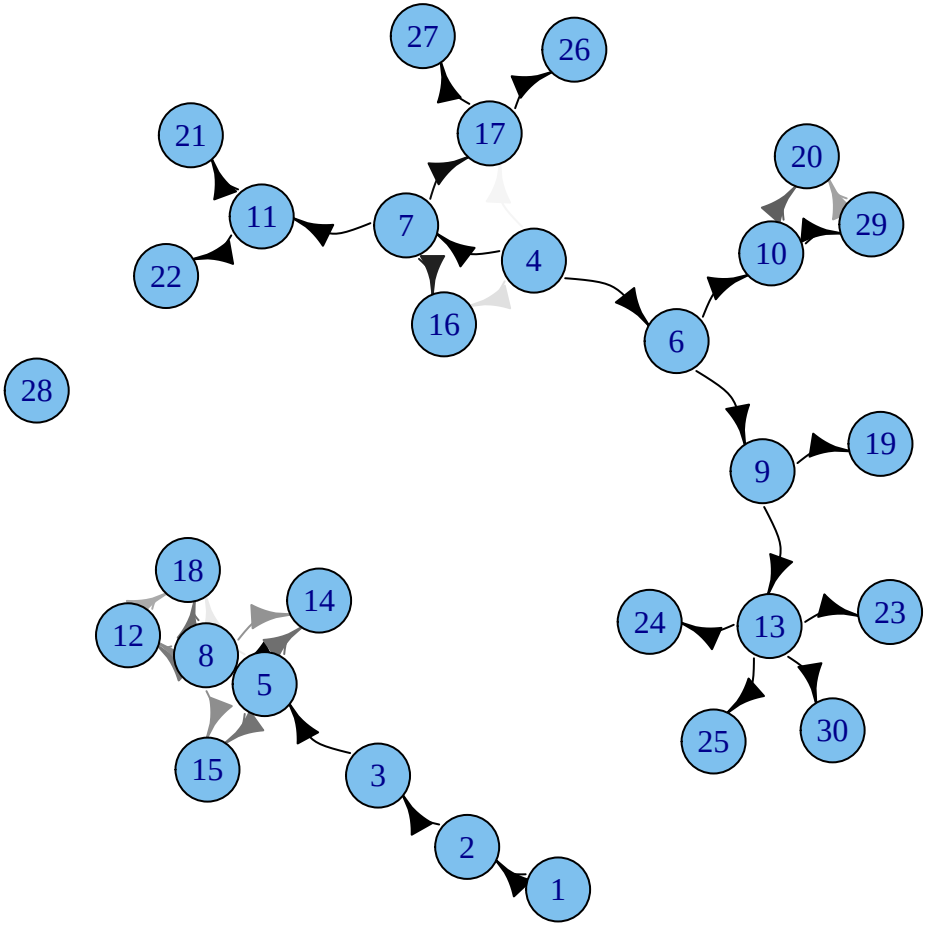


help("outbreaker")


post
value
−500
−600
−700
−800
−900
−1000
−1100
0
10000
20000
30000
40000
50000
MCMC iteration
Runs
1
2
3
4
help("outbreaker")

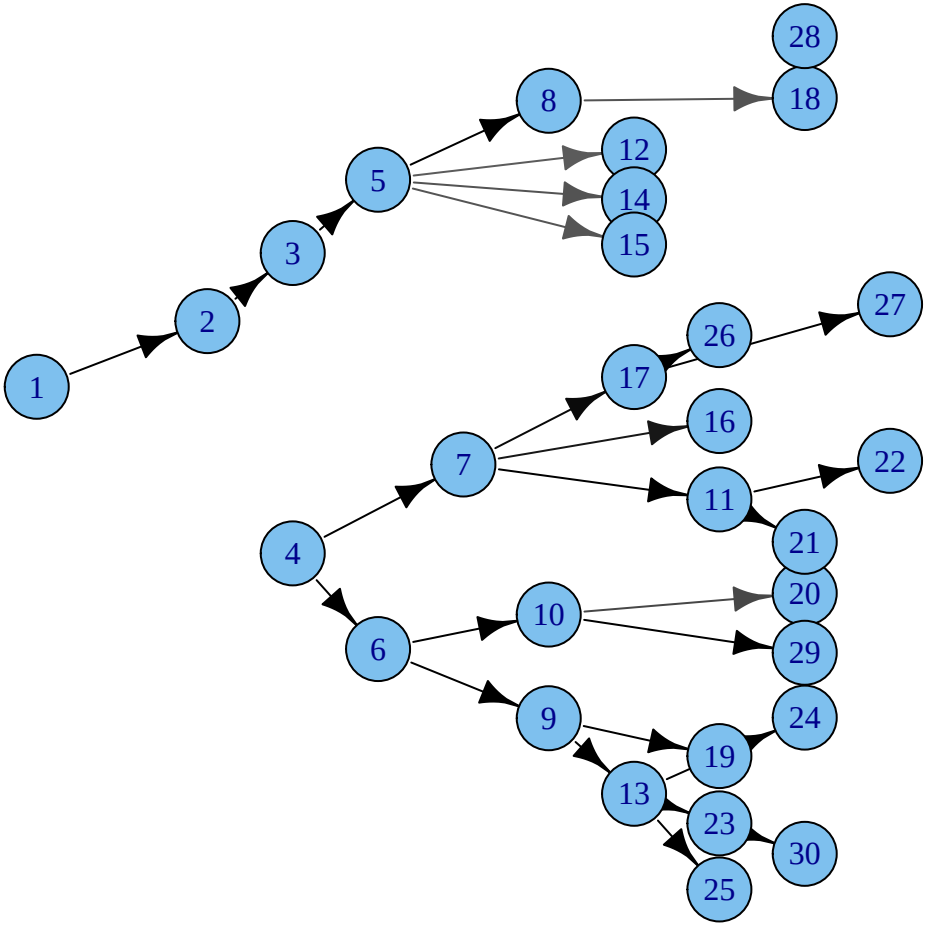

post
value
−434
−436
−438
−440
−442
−444
−446
Runs
1
2
3
4
20000
25000
30000
35000
40000
45000
50000
MCMC iteration
help("outbreaker")

Posterior ancestries



help("outbreaker")

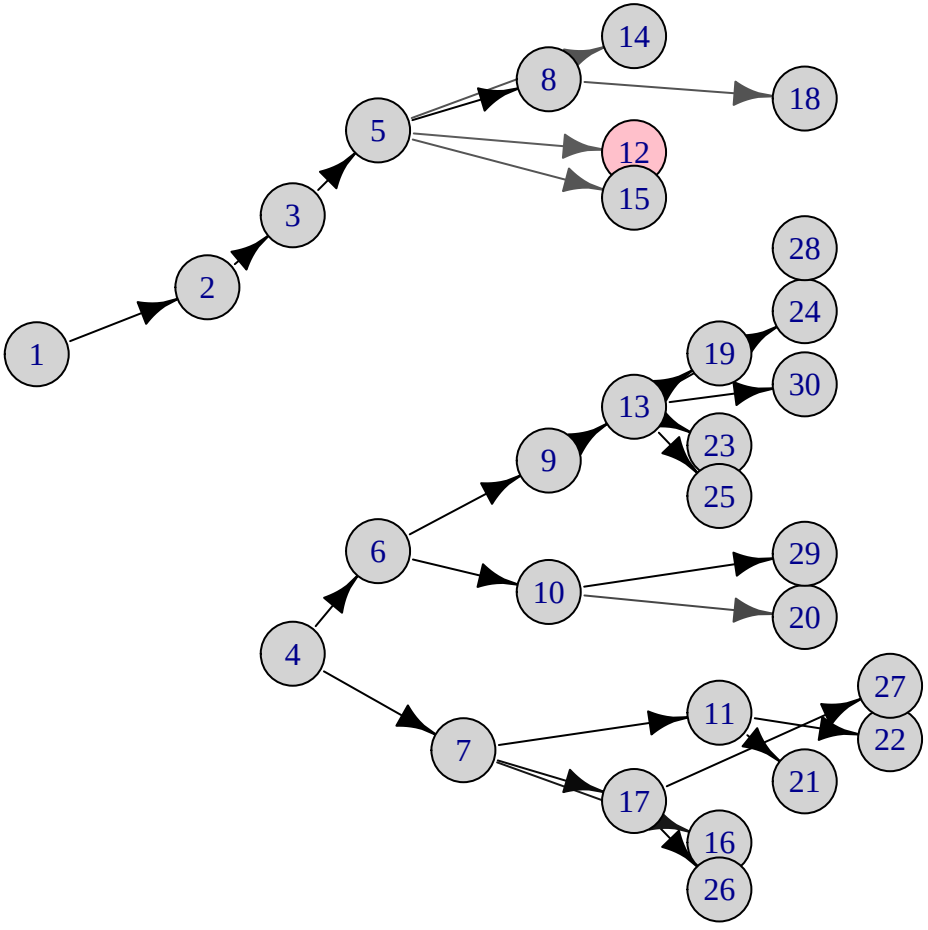
Consensus ancestries



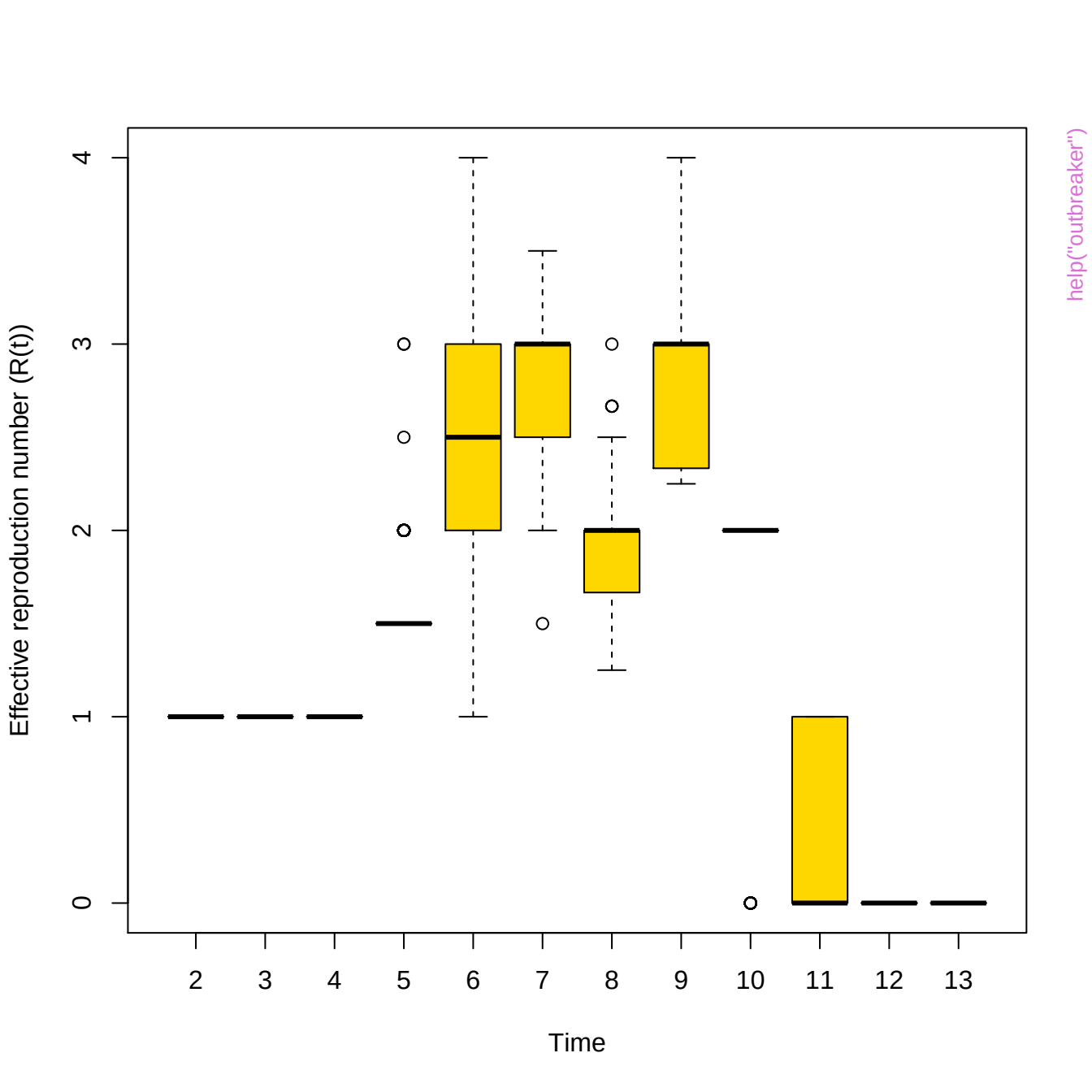
help("outbreaker")

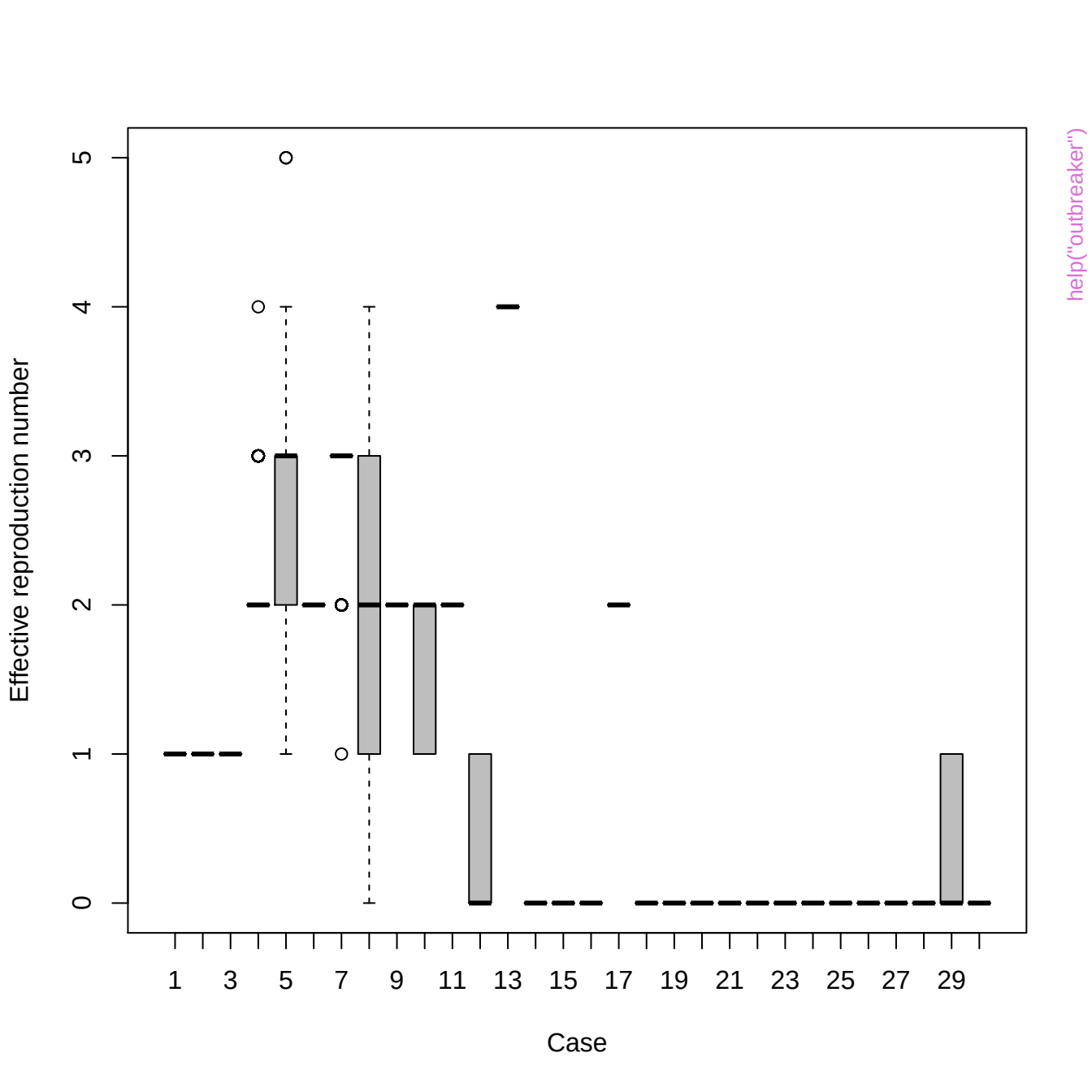
Consensus ancestries

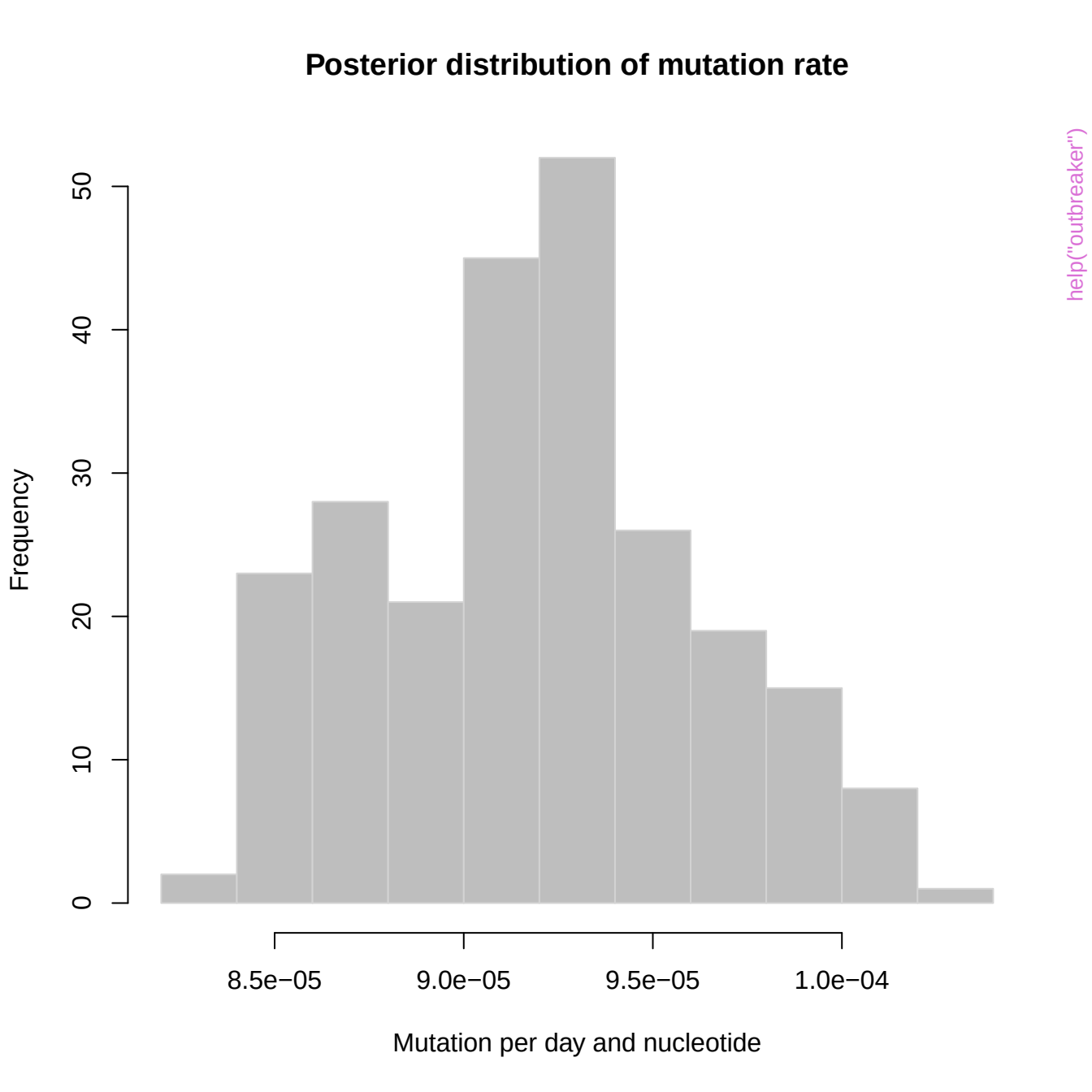
cases with erroneous ancestries in pink



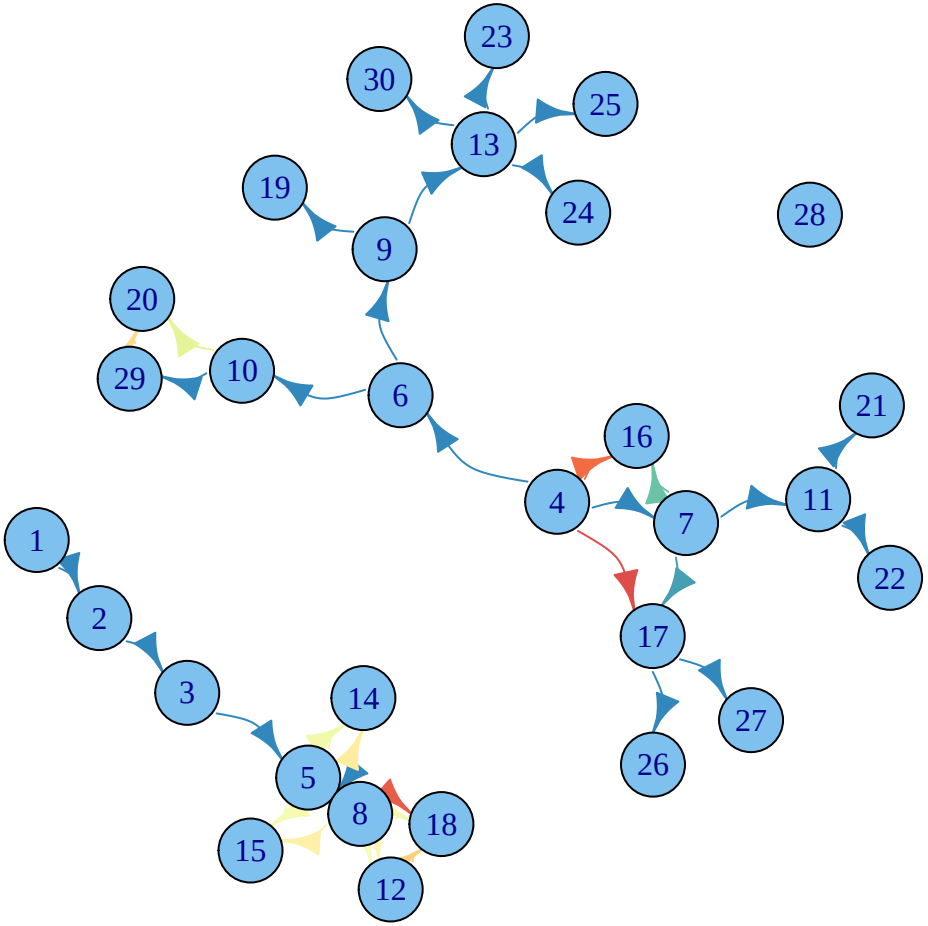
help("outbreaker")


Effective reproduction number (R(t))
0
1
2
3
4
2
3
4
5
6
7
8
9
10
11
12
13
Time
help("outbreaker")


Effective reproduction number
0
1
2
3
4
5
1
3
5
7
9
11
13
15
17
19
21
23
25
27
29
Case
help("outbreaker")

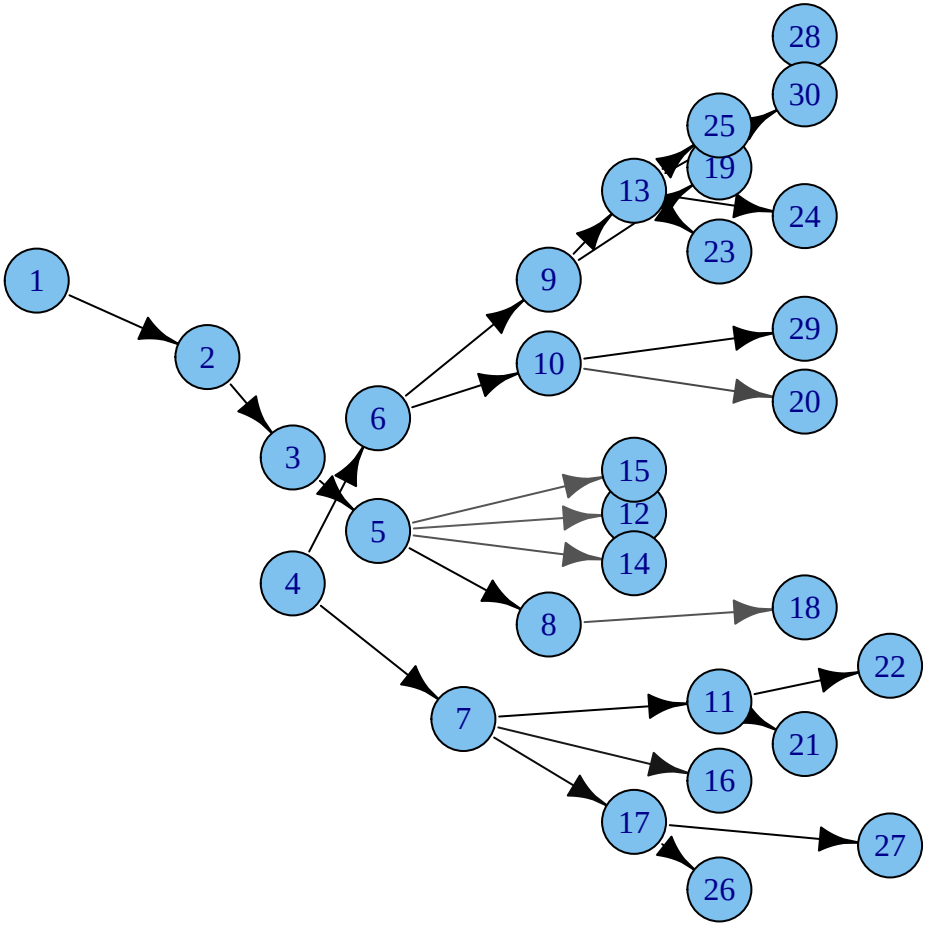

Posterior distribution of mutation rate
Frequency
0
10
20
30
40
50
8.5e−05
9.0e−05
9.5e−05
1.0e−04
Mutation per day and nucleotide
help("outbreaker")

Posterior ancestries − support > 0.01



help("tTree")

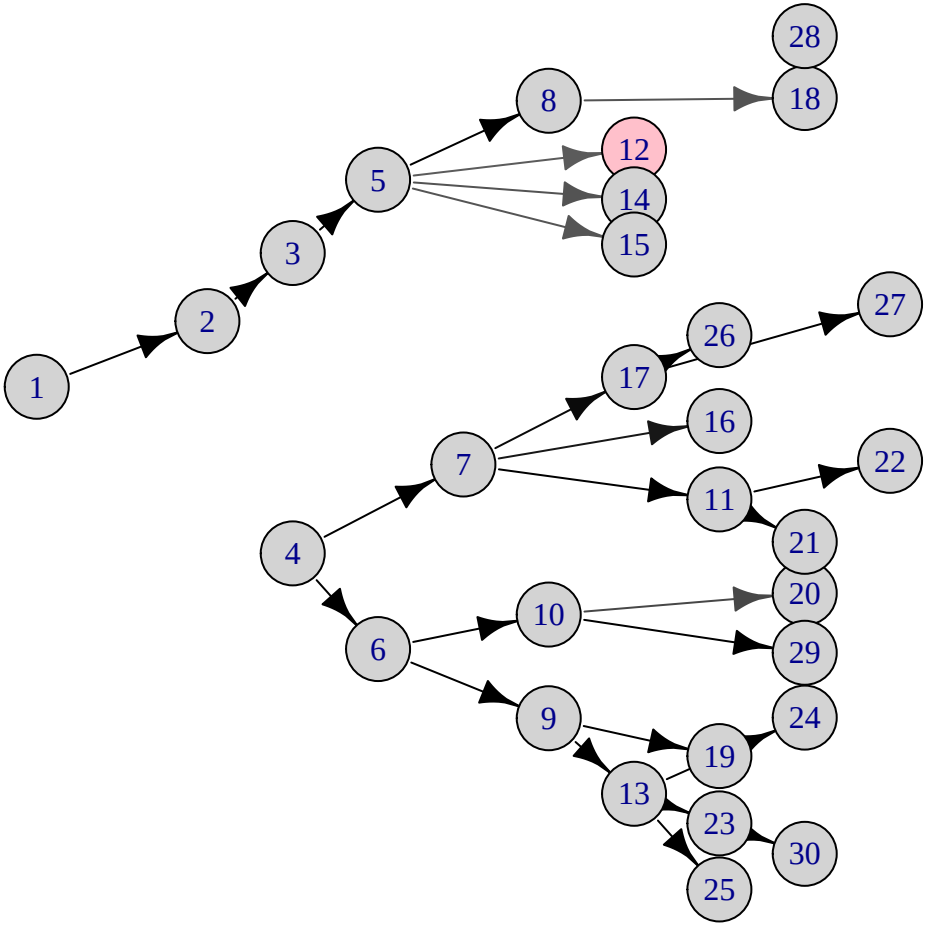
Consensus ancestries



help("tTree")

Consensus ancestries

cases with erroneous ancestries in pink



help("tTree")