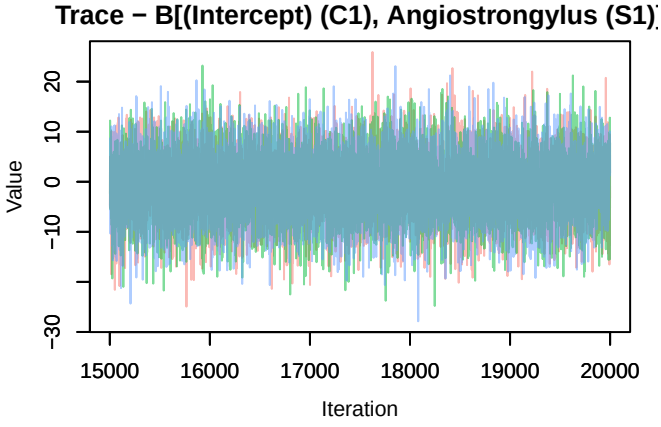
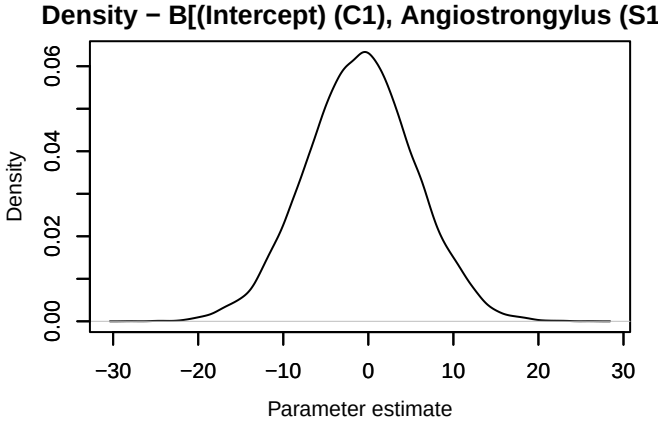
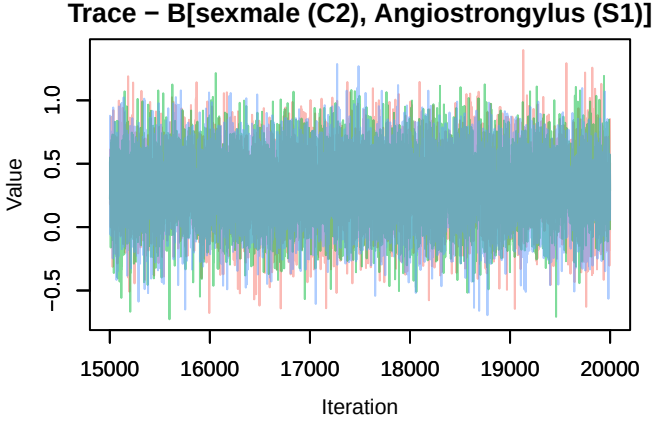
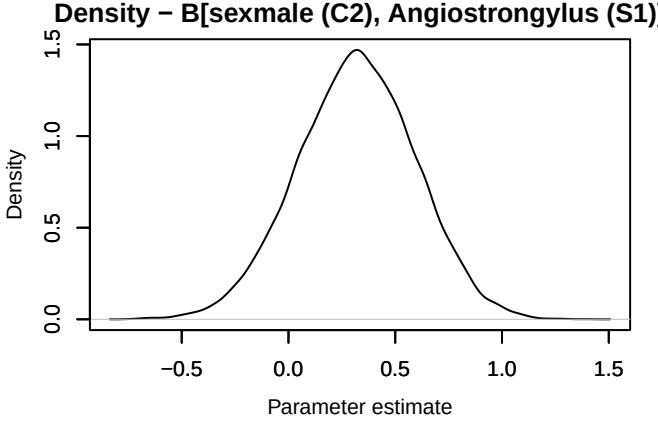
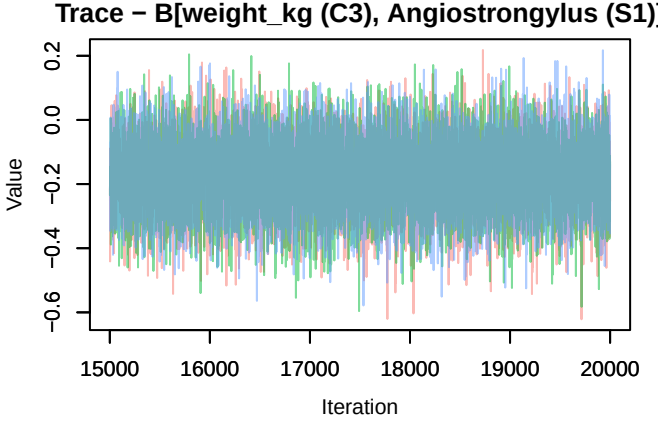
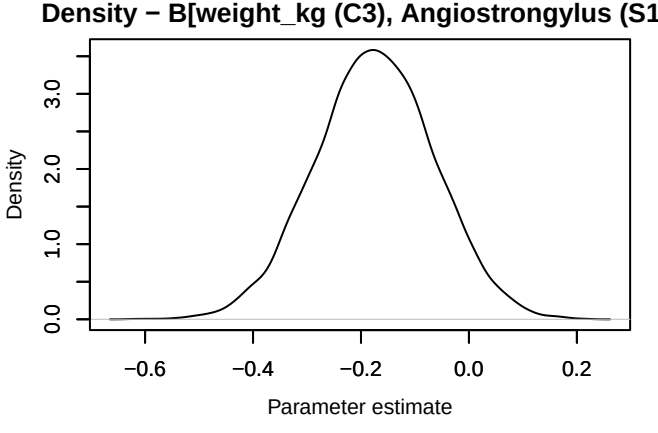

Trace − B[(Intercept) (C1), Angiostrongylus (S1)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−30
−10
0
10
20

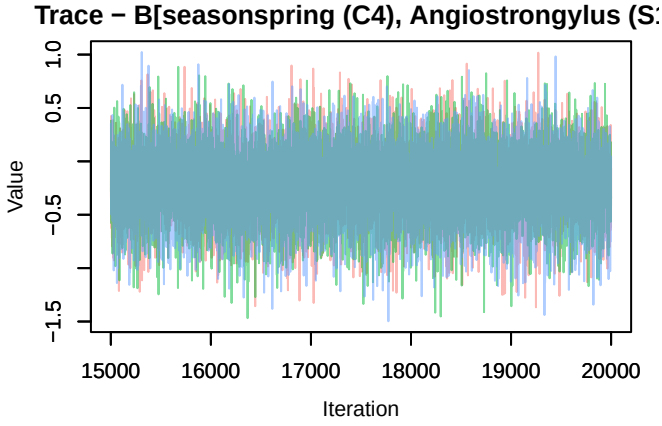

Density − B[(Intercept) (C1), Angiostrongylus (S1
Density
Parameter estimate
0.00
0.02
0.04
0.06
−30
−20
−10
0
10
20
30

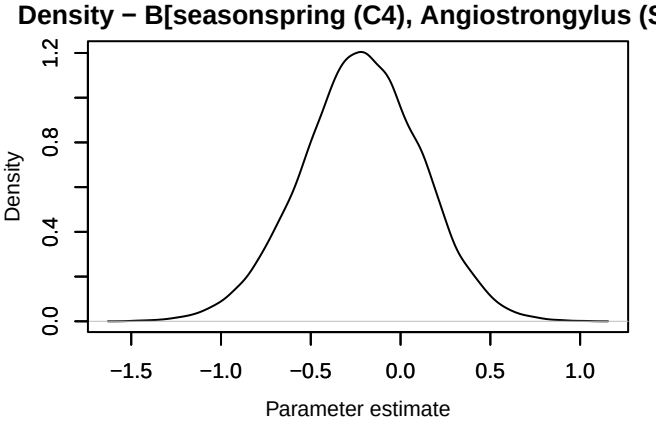

Trace − B[sexmale (C2), Angiostrongylus (S1)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−0.5
0.0
0.5
1.0

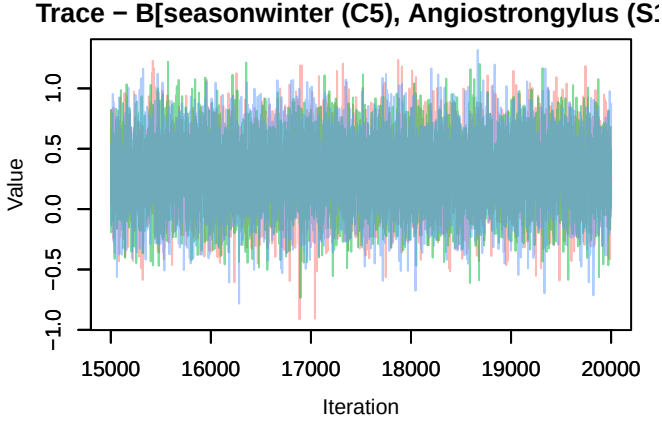

Density − B[sexmale (C2), Angiostrongylus (S1)
Density
Parameter estimate
0.0
0.5
1.0
1.5
−0.5
0.0
0.5
1.0
1.5

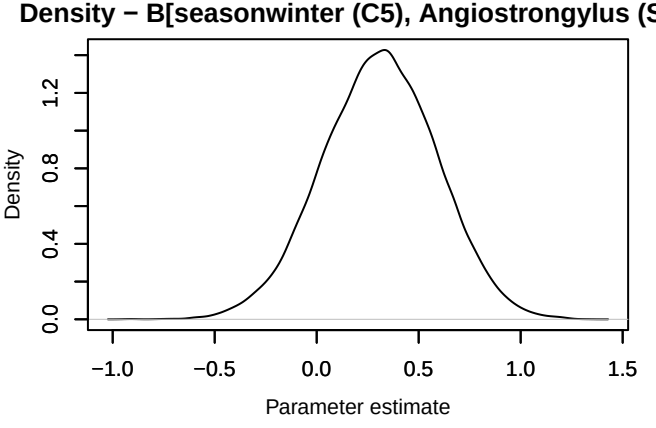

Trace − B[weight_kg (C3), Angiostrongylus (S1)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−0.6
−0.4
−0.2
0.0
0.2

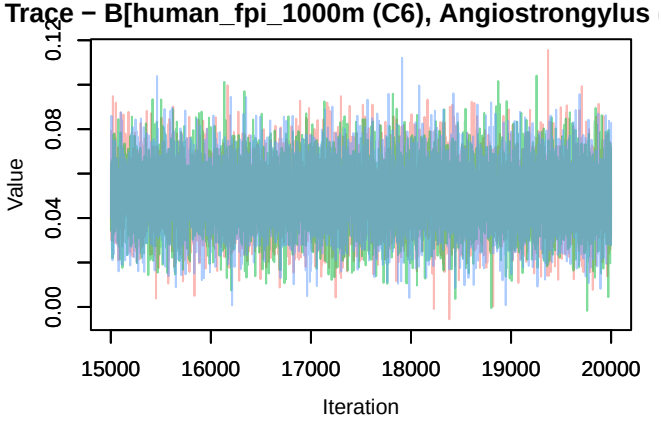

Density − B[weight_kg (C3), Angiostrongylus (S1
Density
Parameter estimate
0.0
1.0
2.0
3.0
−0.6
−0.4
−0.2
0.0
0.2

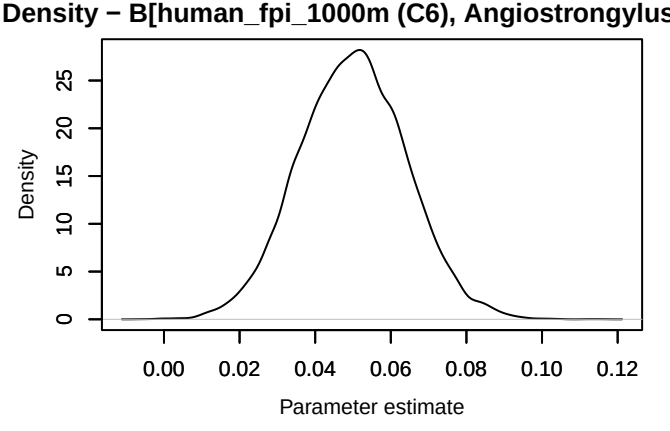

Trace − B[seasonspring (C4), Angiostrongylus (S
Value
Iteration
15000
16000
17000
18000
19000
20000
1.0
0.5
−0.5
−1.5

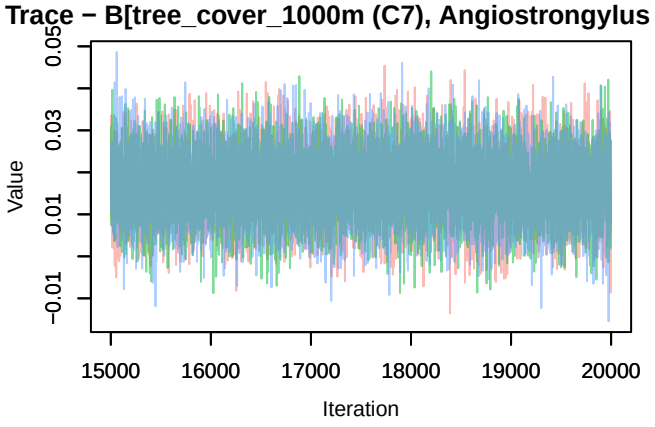

Density − B[seasonspring (C4), Angiostrongylus (S
Density
Parameter estimate
1.2
0.8
0.4
0.0
−1.5
−1.0
−0.5
0.0
0.5
1.0

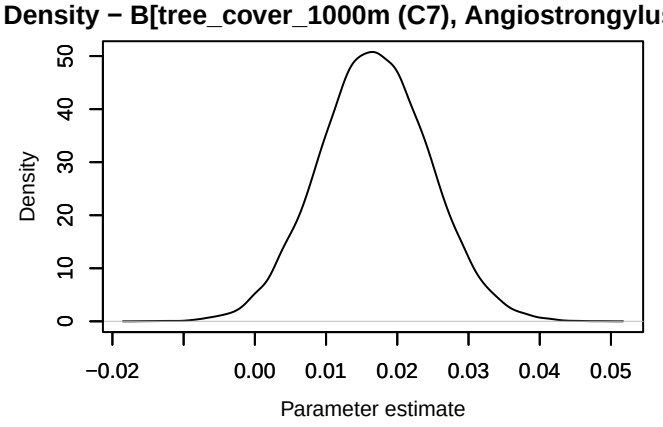

Trace − B[seasonwinter (C5), Angiostrongylus (S
Value
Iteration
15000
16000
17000
18000
19000
20000
1.0
0.5
0.0
−0.5
−1.0

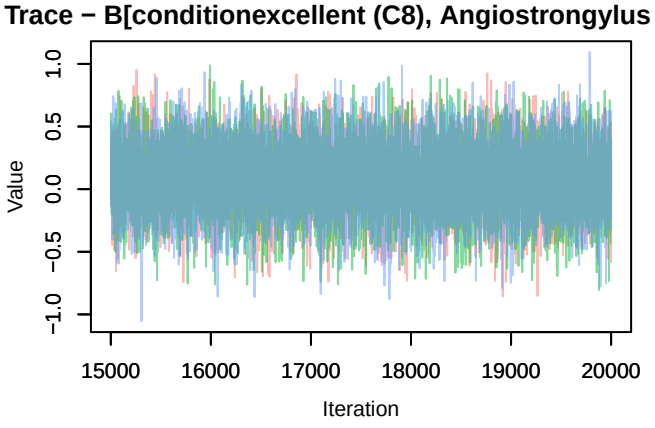

Density − B[seasonwinter (C5), Angiostrongylus (S
Density
Parameter estimate
1.2
0.8
0.4
0.0
−1.0
−0.5
0.0
0.5
1.0
1.5

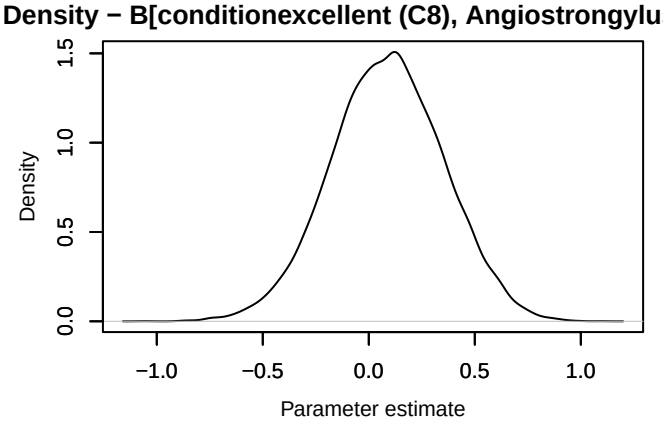

Trace − B[human_fpi_1000m (C6), Angiostrongylus
Value
Iteration
15000
16000
17000
18000
19000
20000
0.12
0.08
0.04
0.00

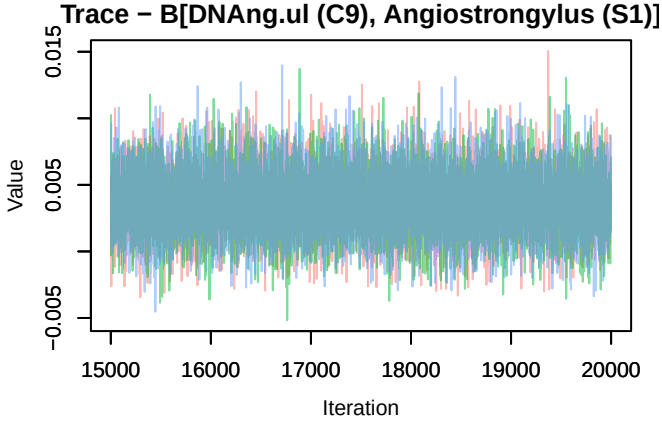

Density − B[human_fpi_1000m (C6), Angiostrongylus
Density
Parameter estimate
25
20
15
10
5
0
0.00
0.02
0.04
0.06
0.08
0.10
0.12

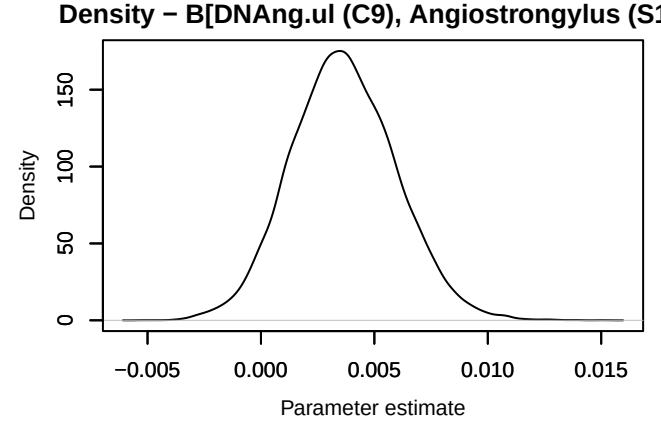

Trace − B[tree_cover_1000m (C7), Angiostrongylus
Value
0.05
0.03
0.01
−0.01
15000
16000
17000
18000
19000
20000
Iteration

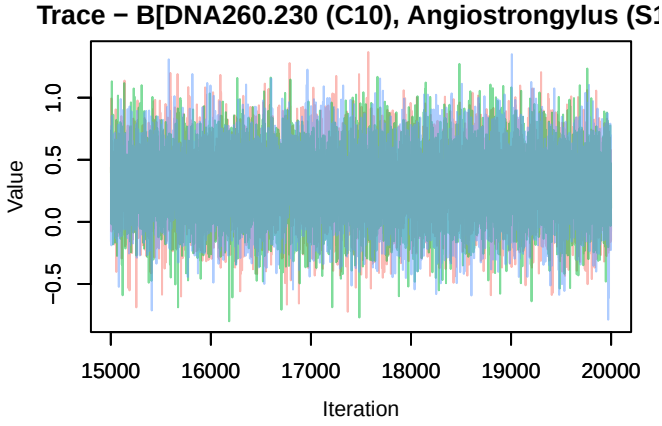

Density − B[tree_cover_1000m (C7), Angiostrongylus
Density
50
40
30
20
10
0
−0.02
0.00
0.01
0.02
0.03
0.04
0.05
Parameter estimate

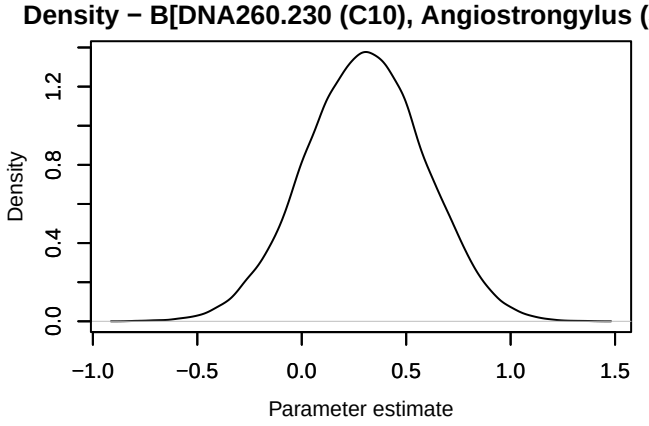

Trace − B[conditionexcellent (C8), Angiostrongylus
Value
1.0
0.5
0.0
−0.5
−1.0
15000
16000
17000
18000
19000
20000
Iteration

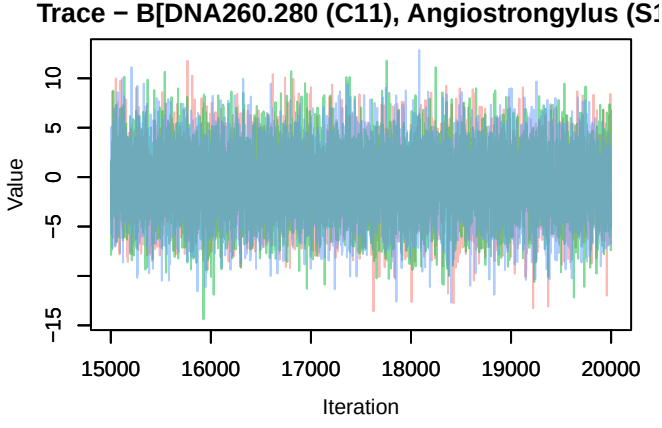

Density − B[conditionexcellent (C8), Angiostrongylus
Density
1.5
1.0
0.5
0.0
−1.0
−0.5
0.0
0.5
1.0
Parameter estimate

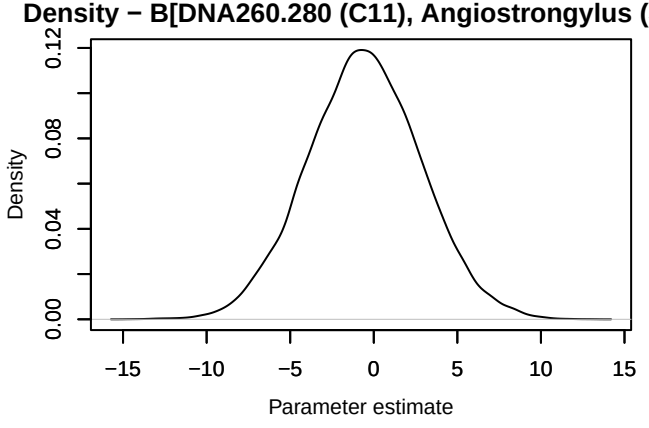

Trace − B[DNAng.ul (C9), Angiostrongylus (S1)]
Value
0.015
0.005
−0.005
15000
16000
17000
18000
19000
20000
Iteration

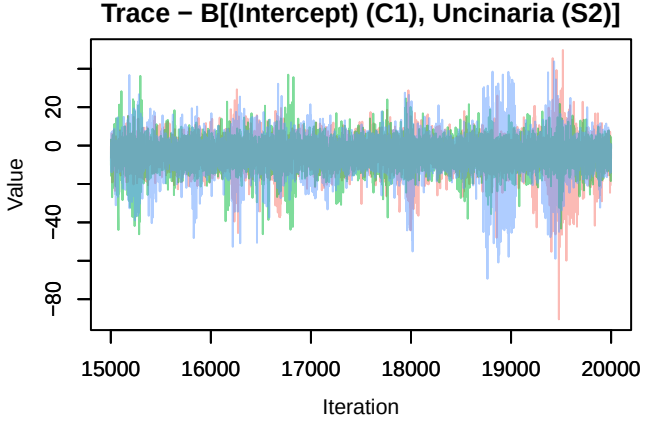

Density − B[DNAng.ul (C9), Angiostrongylus (S1
Density
150
100
50
0
−0.005
0.000
0.005
0.010
0.015
Parameter estimate

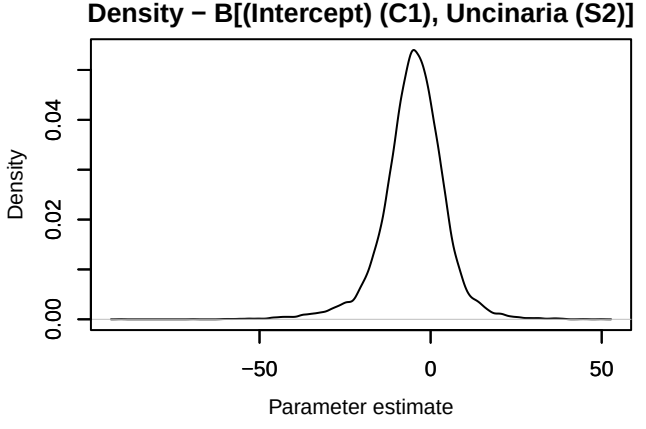

Trace − B[DNA260.230 (C10), Angiostrongylus (S1
Value
1.0
0.5
0.0
−0.5
15000
16000
17000
18000
19000
20000
Iteration

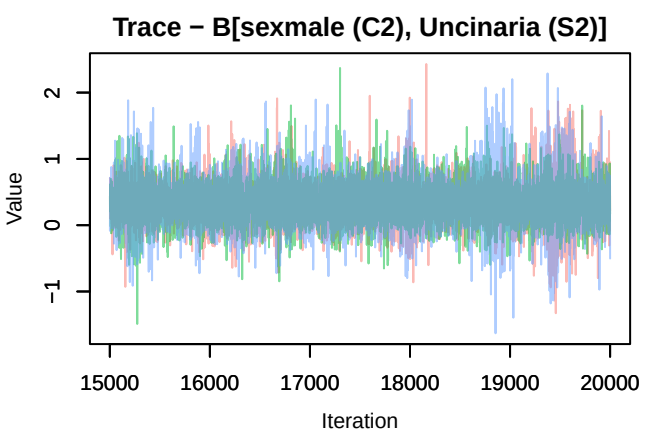

Density − B[DNA260.230 (C10), Angiostrongylus (S
Density
1.2
0.8
0.4
0.0
−1.0
−0.5
0.0
0.5
1.0
1.5
Parameter estimate

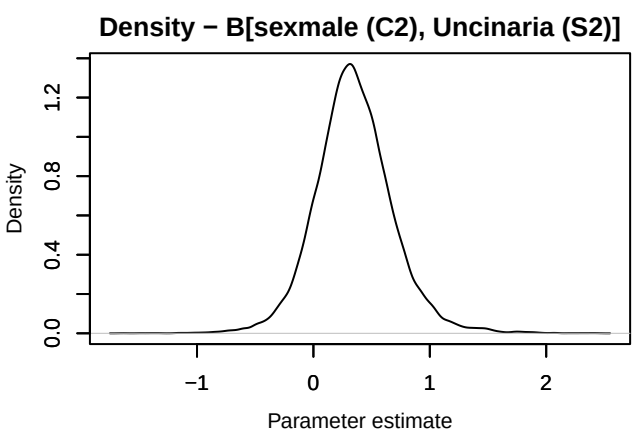

Trace − B[DNA260.280 (C11), Angiostrongylus (S1
Value
10
5
0
−5
−15
15000
16000
17000
18000
19000
20000
Iteration

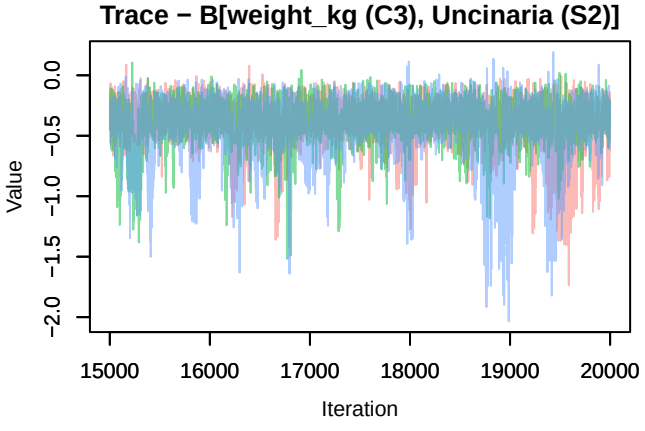

Density − B[DNA260.280 (C11), Angiostrongylus (S
Density
0.12
0.08
0.04
0.00
−15
−10
−5
0
5
10
15
Parameter estimate

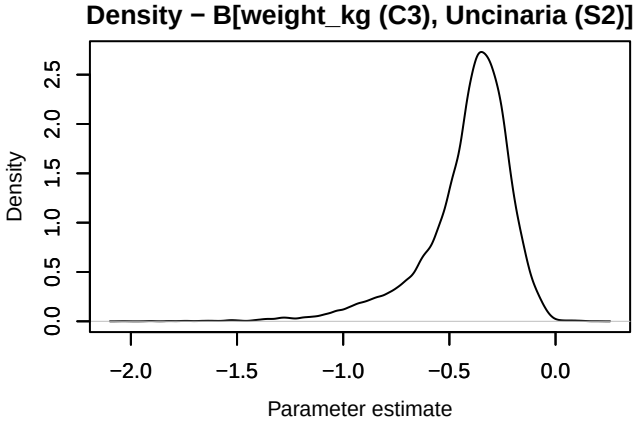

Trace − B[(Intercept) (C1), Uncinaria (S2)]
Value
20
0
−40
−80
15000
16000
17000
18000
19000
20000
Iteration

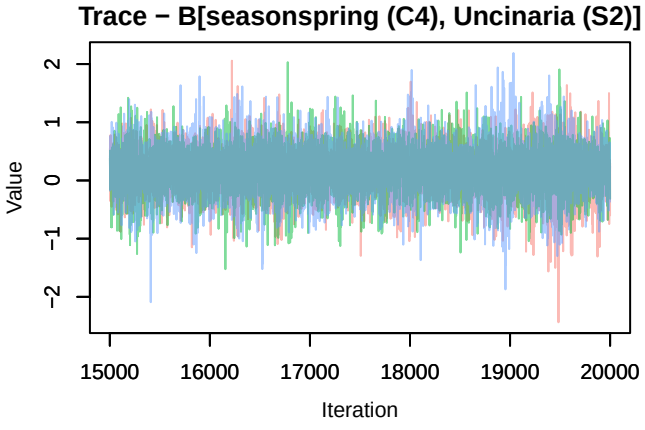

Density − B[(Intercept) (C1), Uncinaria (S2)]
Density
0.04
0.02
0.00
−50
0
50
Parameter estimate

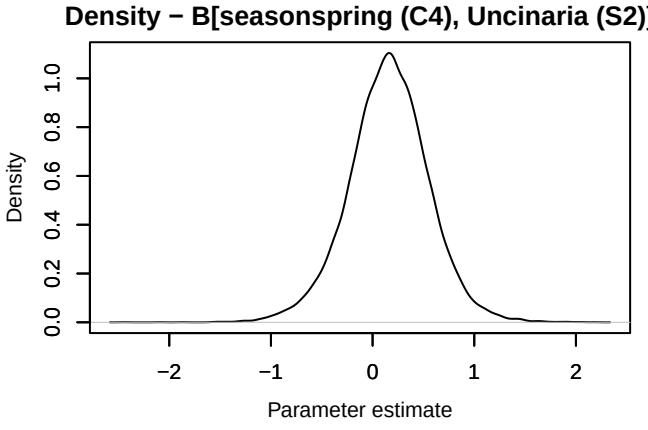

Trace − B[sexmale (C2), Uncinaria (S2)]
Value
Iteration
15000
16000
17000
18000
19000
20000

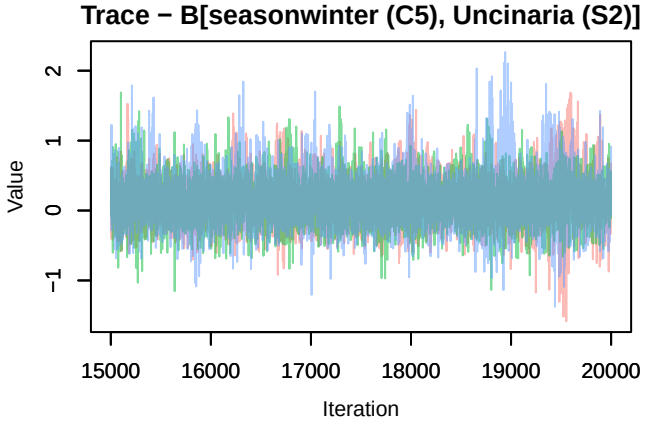

Density − B[sexmale (C2), Uncinaria (S2)]
Density
Parameter estimate

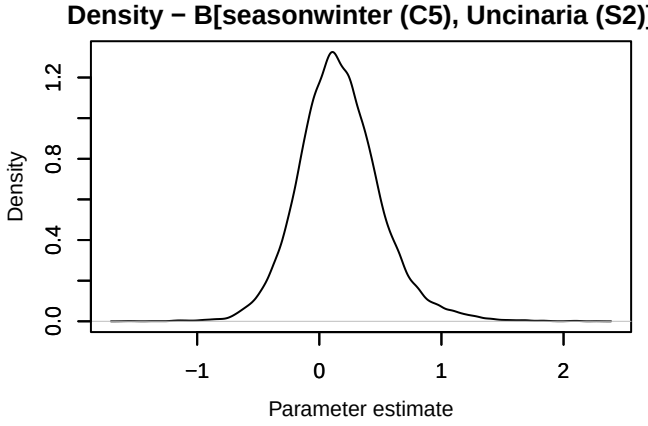

Trace − B[weight_kg (C3), Uncinaria (S2)]
Value
Iteration
15000
16000
17000
18000
19000
20000

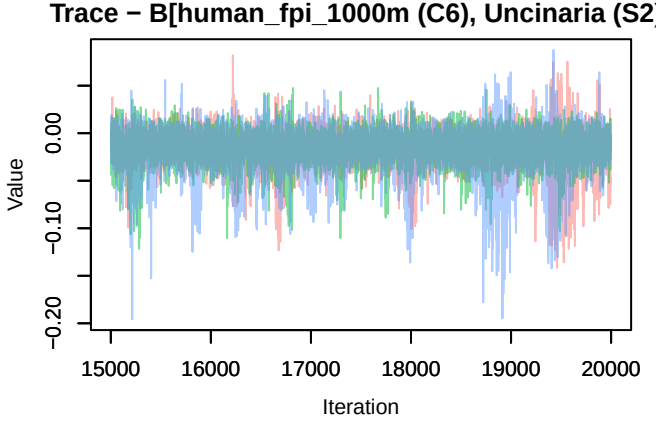

Density − B[weight_kg (C3), Uncinaria (S2)]
Density
Parameter estimate

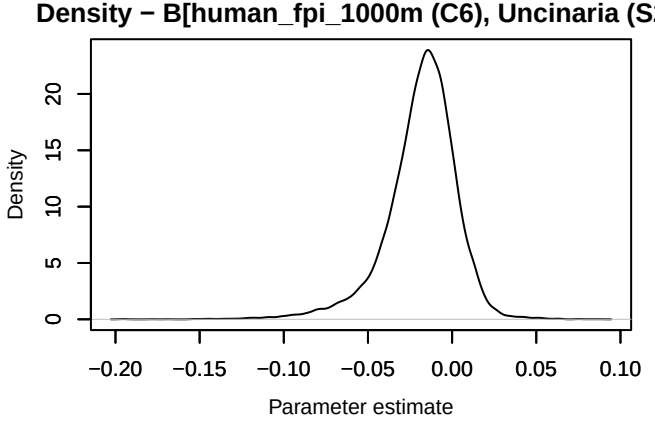

Trace − B[seasonspring (C4), Uncinaria (S2)]
Value
Iteration
15000
16000
17000
18000
19000
20000

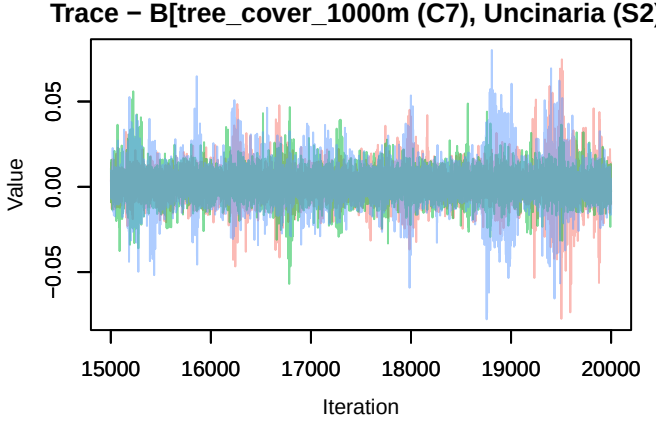

Density − B[seasonspring (C4), Uncinaria (S2)]
Density
Parameter estimate

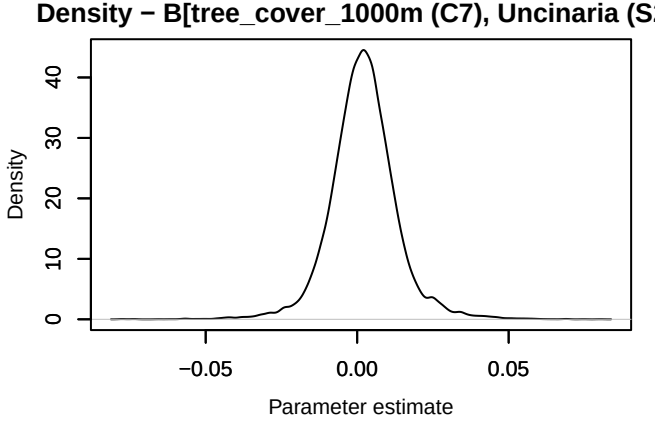

Trace − B[seasonwinter (C5), Uncinaria (S2)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−1
0
1
2

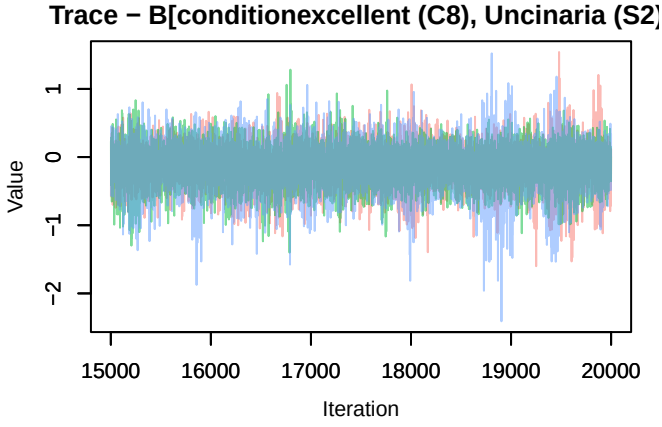

Density − B[seasonwinter (C5), Uncinaria (S2)]
Density
Parameter estimate
0.0
0.4
0.8
1.2
−1
0
1
2

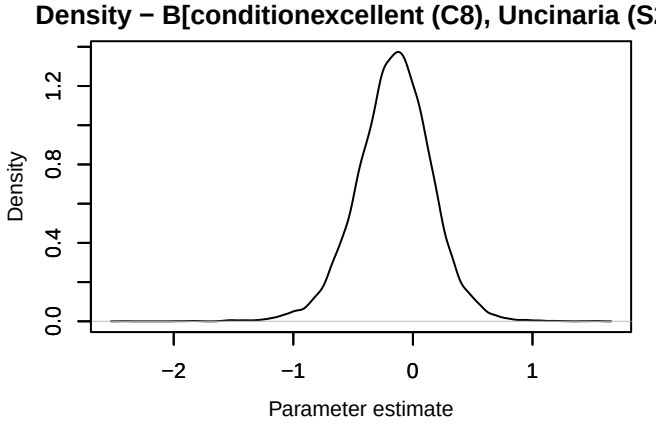

Trace − B[human_fpi_1000m (C6), Uncinaria (S2)
Value
Iteration
15000
16000
17000
18000
19000
20000
−0.20
−0.10
0.00

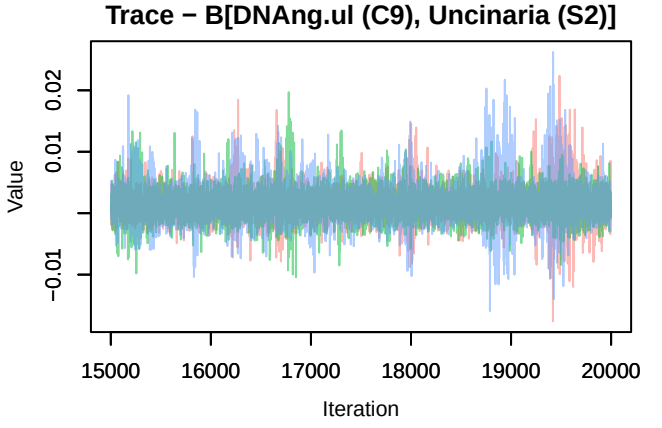

Density − B[human_fpi_1000m (C6), Uncinaria (S2
Density
Parameter estimate
0
5
10
15
20
−0.20
−0.15
−0.10
−0.05
0.00
0.05
0.10

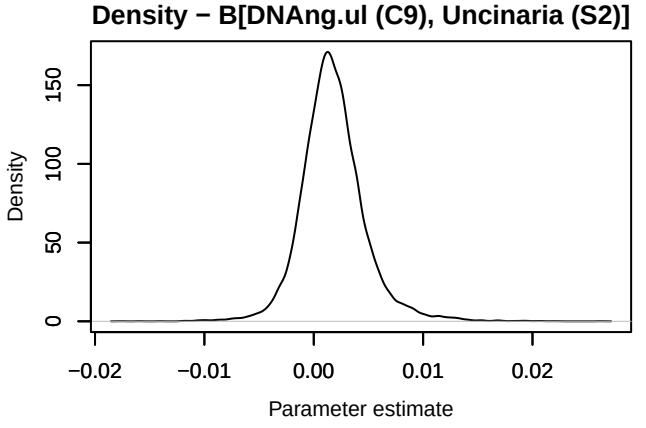

Trace − B[tree_cover_1000m (C7), Uncinaria (S2)
Value
Iteration
15000
16000
17000
18000
19000
20000
−0.05
0.00
0.05

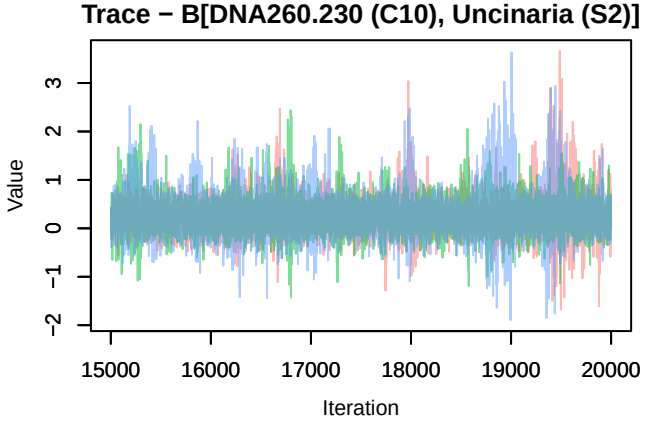

Density − B[tree_cover_1000m (C7), Uncinaria (S2
Density
Parameter estimate
0
10
20
30
40
−0.05
0.00
0.05

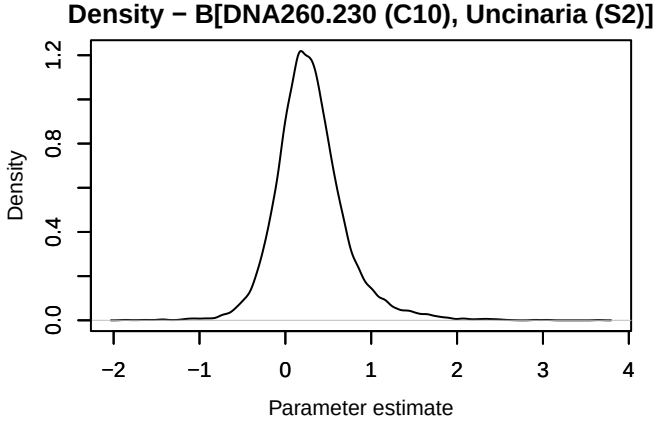

Trace − B[conditionexcellent (C8), Uncinaria (S2)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−2
−1
0
1

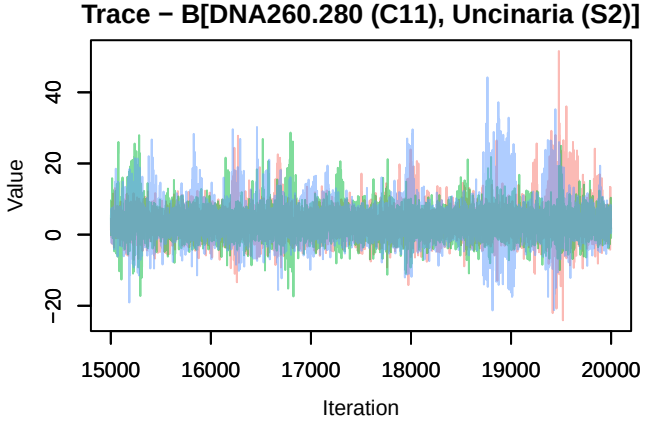

Density − B[conditionexcellent (C8), Uncinaria (S2)]
Density
Parameter estimate
0.0
0.4
0.8
1.2
−2
−1
0
1

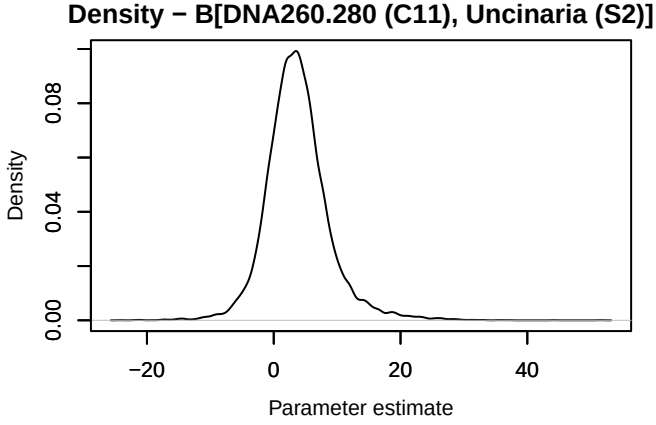

Trace − B[DNAng.ul (C9), Uncinaria (S2)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−0.01
0.01
0.02

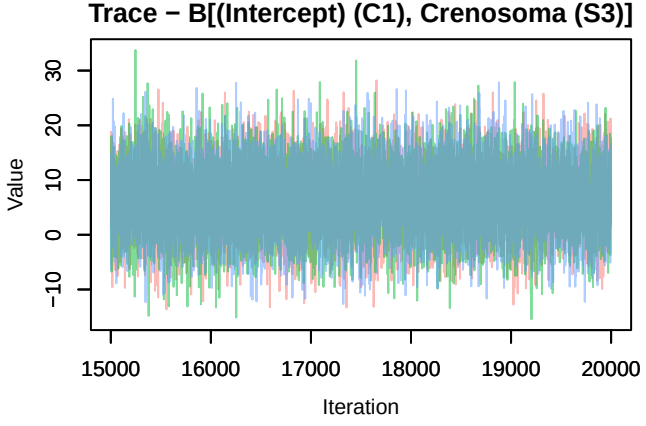

Density − B[DNAng.ul (C9), Uncinaria (S2)]
Density
Parameter estimate
0
50
100
150
−0.02
−0.01
0.00
0.01
0.02

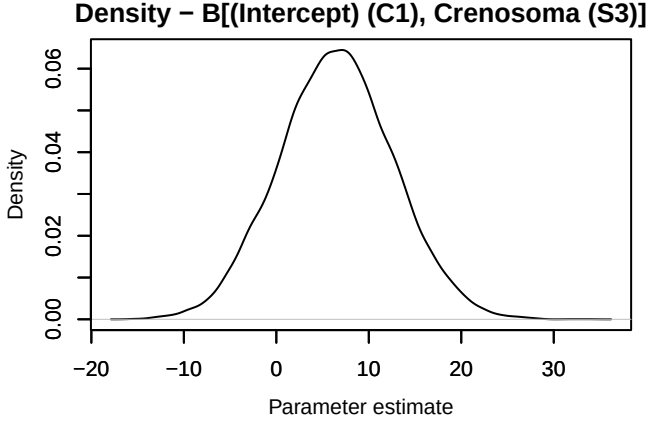

Trace − B[DNA260.230 (C10), Uncinaria (S2)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−2
−1
0
1
2
3

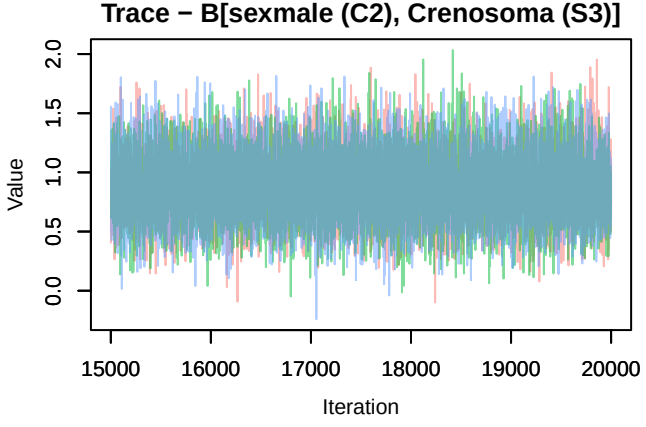

Density − B[DNA260.230 (C10), Uncinaria (S2)]
Density
Parameter estimate
0.0
0.4
0.8
1.2
−2
−1
0
1
2
3
4

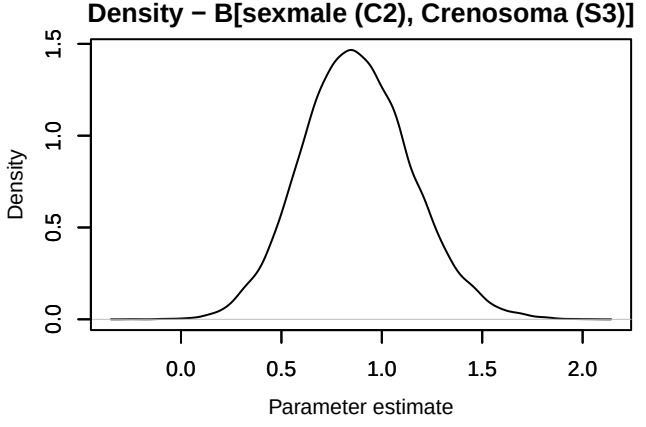

Trace − B[DNA260.280 (C11), Uncinaria (S2)]
Value
40
20
0
−20
15000
16000
17000
18000
19000
20000
Iteration

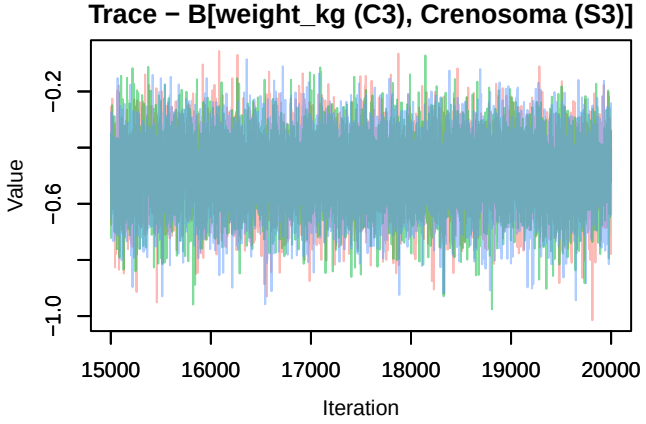

Density − B[DNA260.280 (C11), Uncinaria (S2)]
Density
0.08
0.04
0.00
−20
0
20
40
Parameter estimate

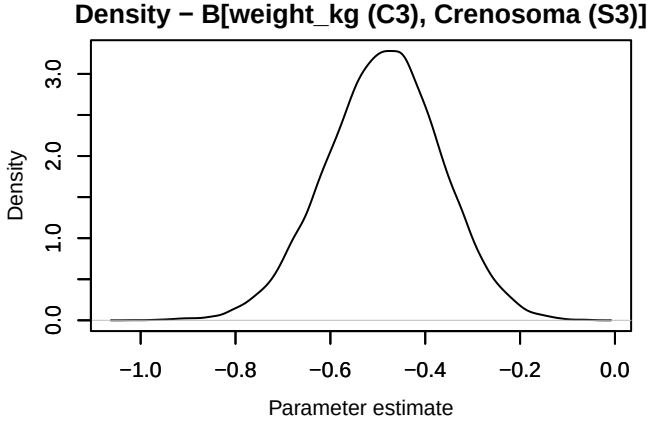

Trace − B[(Intercept) (C1), Crenosoma (S3)]
Value
30
20
10
0
−10
15000
16000
17000
18000
19000
20000
Iteration

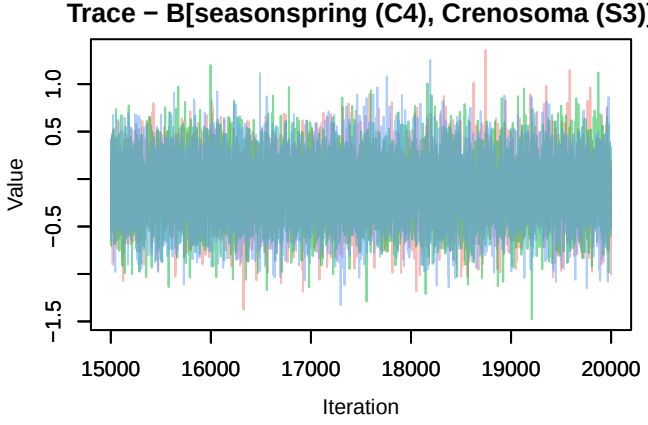

Density − B[(Intercept) (C1), Crenosoma (S3)]
Density
0.06
0.04
0.02
0.00
−20
−10
0
10
20
30
Parameter estimate

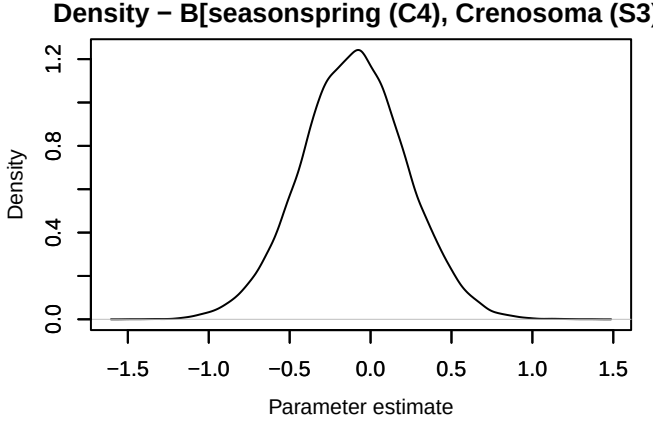

Trace − B[sexmale (C2), Crenosoma (S3)]
Value
2.0
1.5
1.0
0.5
0.0
15000
16000
17000
18000
19000
20000
Iteration

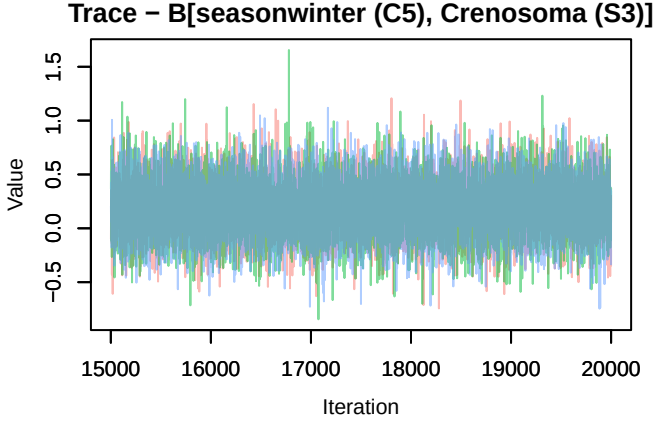

Density − B[sexmale (C2), Crenosoma (S3)]
Density
1.5
1.0
0.5
0.0
0.0
0.5
1.0
1.5
2.0
Parameter estimate

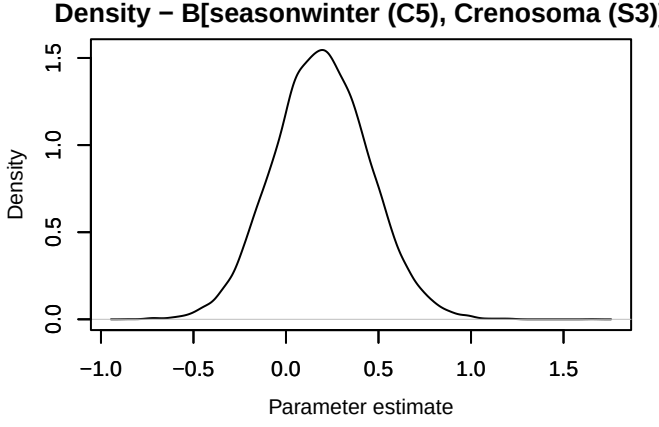

Trace − B[weight_kg (C3), Crenosoma (S3)]
Value
−0.2
−0.6
−1.0
15000
16000
17000
18000
19000
20000
Iteration

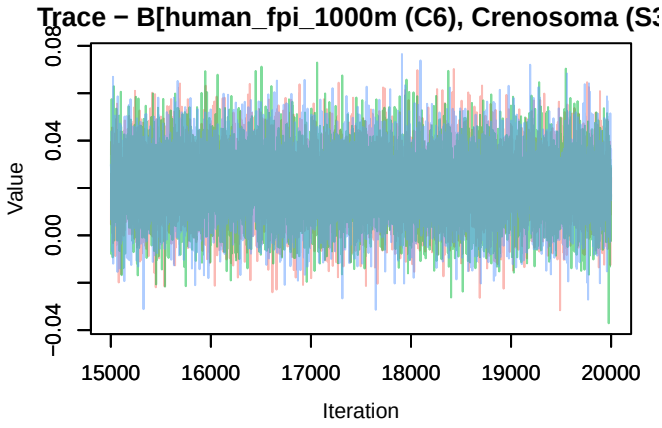

Density − B[weight_kg (C3), Crenosoma (S3)]
Density
3.0
2.0
1.0
0.0
−1.0
−0.8
−0.6
−0.4
−0.2
0.0
Parameter estimate

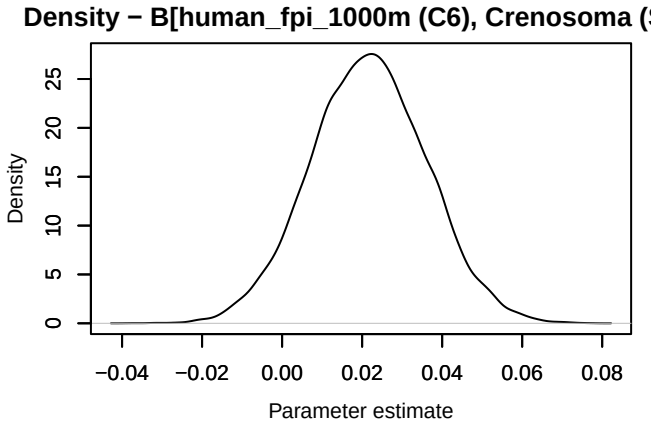

Trace − B[seasonspring (C4), Crenosoma (S3)]
Value
1.0
0.5
−0.5
−1.5
15000
16000
17000
18000
19000
20000
Iteration

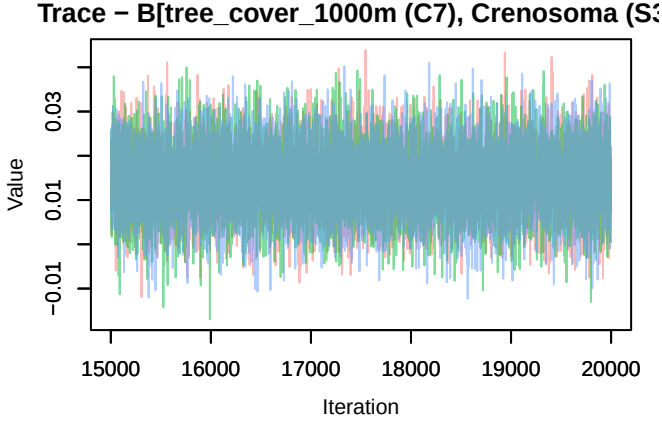

Density − B[seasonspring (C4), Crenosoma (S3)
Density
1.2
0.8
0.4
0.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Parameter estimate

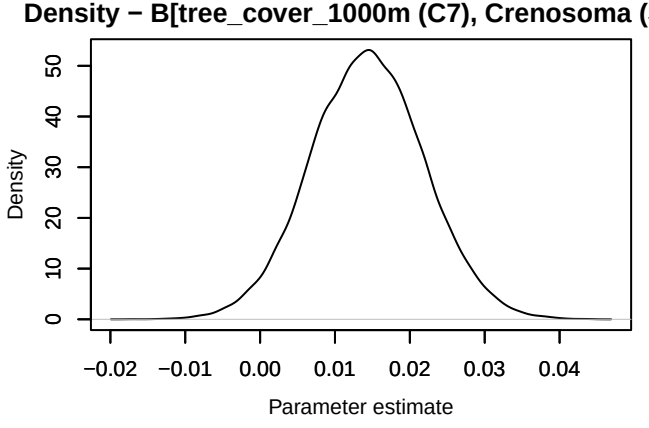

Trace − B[seasonwinter (C5), Crenosoma (S3)]
Value
1.5
1.0
0.5
0.0
−0.5
15000
16000
17000
18000
19000
20000
Iteration

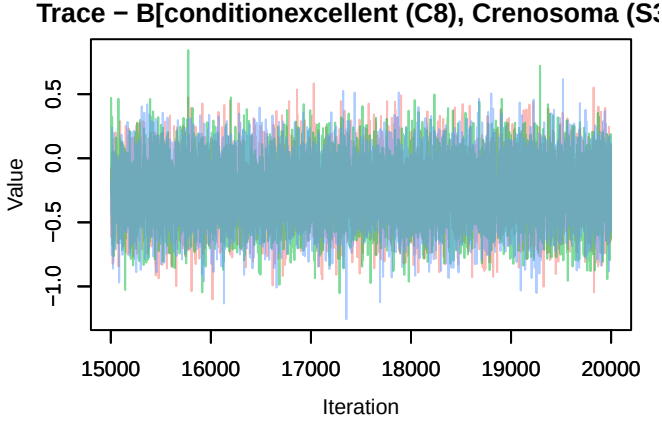

Density − B[seasonwinter (C5), Crenosoma (S3)
Density
1.5
1.0
0.5
0.0
−1.0
−0.5
0.0
0.5
1.0
1.5
Parameter estimate

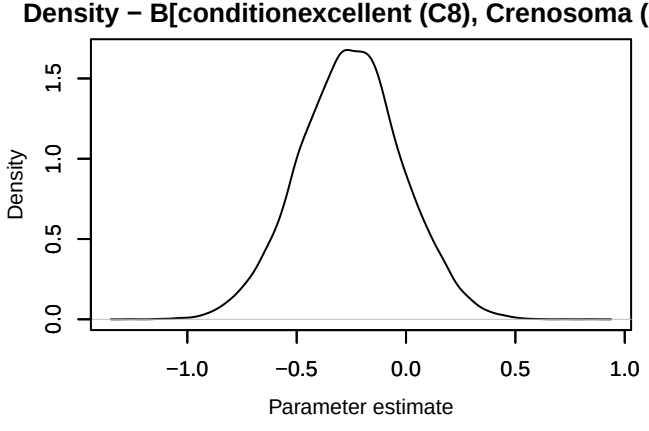

Trace − B[human_fpi_1000m (C6), Crenosoma (S3
Value
0.08
0.04
0.00
−0.04
15000
16000
17000
18000
19000
20000
Iteration

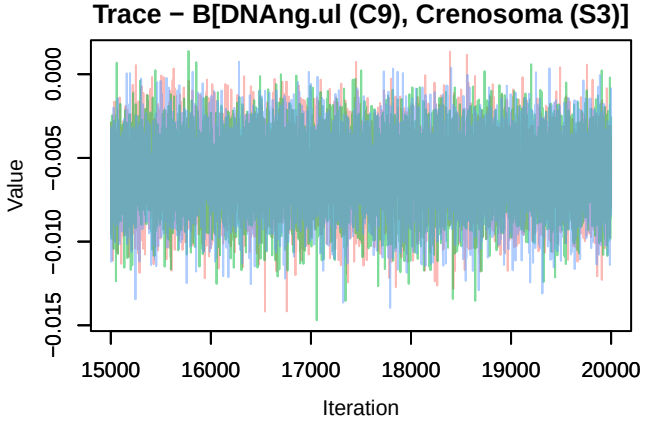

Density − B[human_fpi_1000m (C6), Crenosoma (S
Density
25
20
15
10
5
0
−0.04
−0.02
0.00
0.02
0.04
0.06
0.08
Parameter estimate

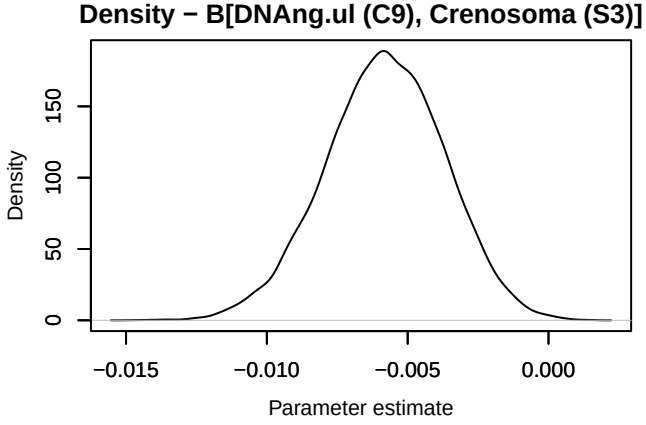

Trace − B[tree_cover_1000m (C7), Crenosoma (S3
Value
0.03
0.01
−0.01
15000
16000
17000
18000
19000
20000
Iteration

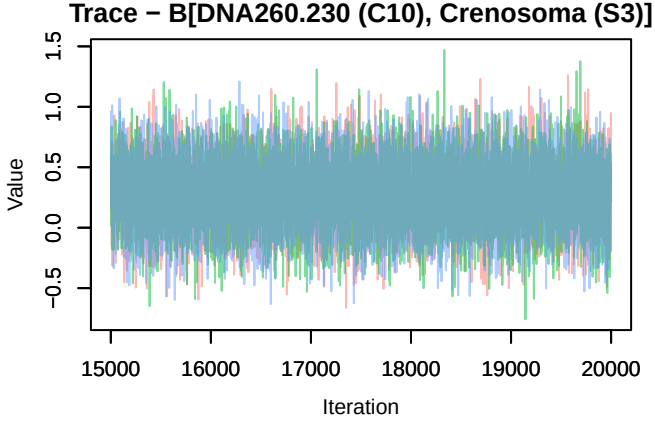

Density − B[tree_cover_1000m (C7), Crenosoma (S
Density
50
40
30
20
10
0
−0.02
−0.01
0.00
0.01
0.02
0.03
0.04
Parameter estimate

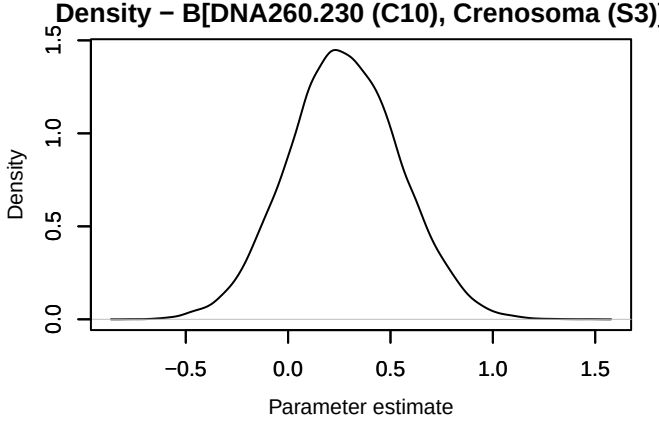

Trace − B[conditionexcellent (C8), Crenosoma (S3
Value
0.5
0.0
−0.5
−1.0
15000
16000
17000
18000
19000
20000
Iteration

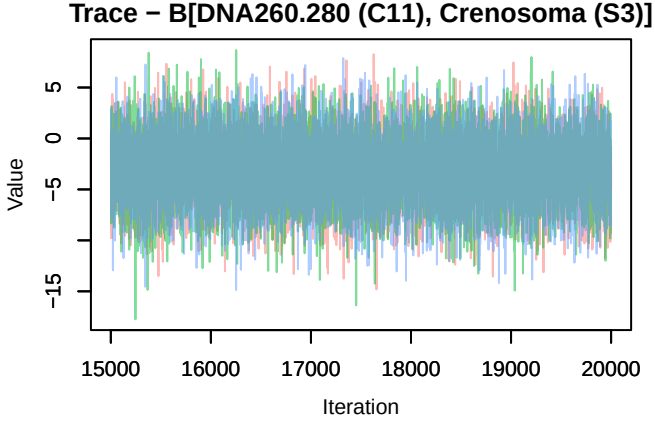

Density − B[conditionexcellent (C8), Crenosoma (S
Density
1.5
1.0
0.5
0.0
−1.0
−0.5
0.0
0.5
1.0
Parameter estimate

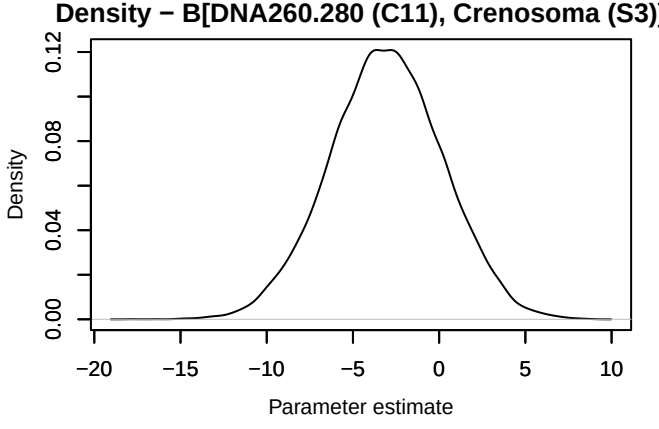

Trace − B[DNAng.ul (C9), Crenosoma (S3)]
Value
0.000
−0.005
−0.010
−0.015
15000
16000
17000
18000
19000
20000
Iteration

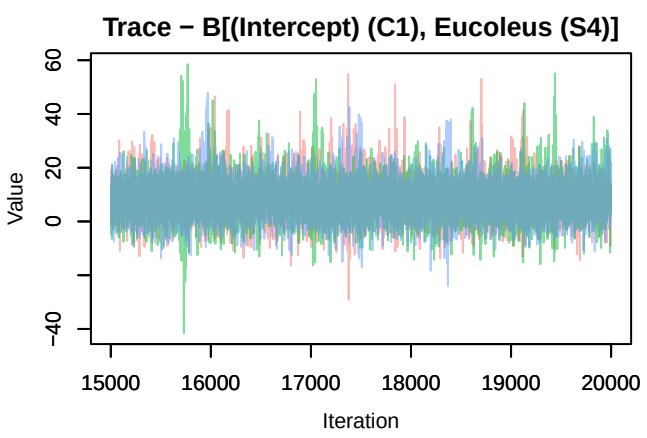

Density − B[DNAng.ul (C9), Crenosoma (S3)]
Density
150
100
50
0
−0.015
−0.010
−0.005
0.000
Parameter estimate

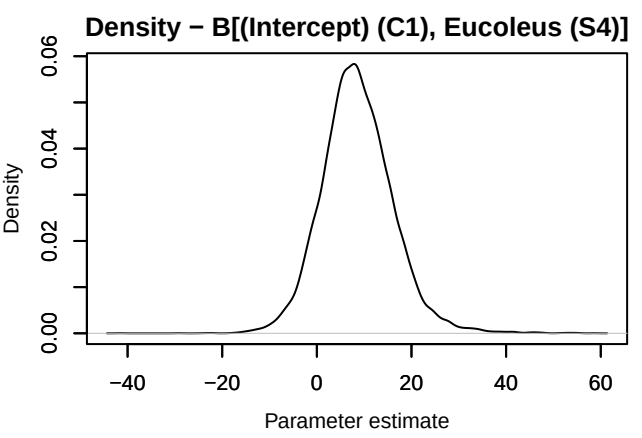

Trace − B[DNA260.230 (C10), Crenosoma (S3)]
Value
1.5
1.0
0.5
0.0
−0.5
15000
16000
17000
18000
19000
20000
Iteration

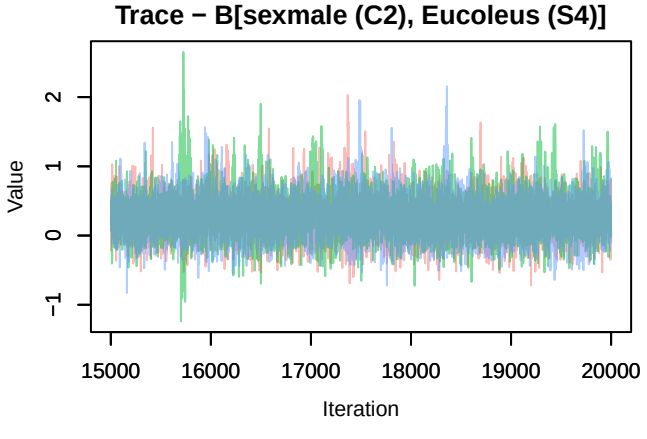

Density − B[DNA260.230 (C10), Crenosoma (S3)]
Density
1.5
1.0
0.5
0.0
−0.5
0.0
0.5
1.0
1.5
Parameter estimate

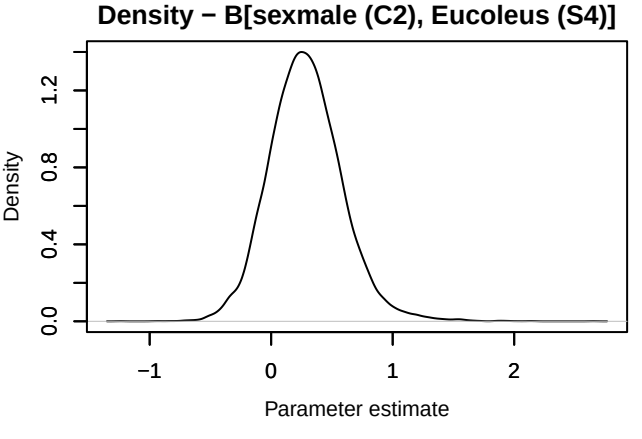

Trace − B[DNA260.280 (C11), Crenosoma (S3)]
Value
5
0
−5
−15
15000
16000
17000
18000
19000
20000
Iteration

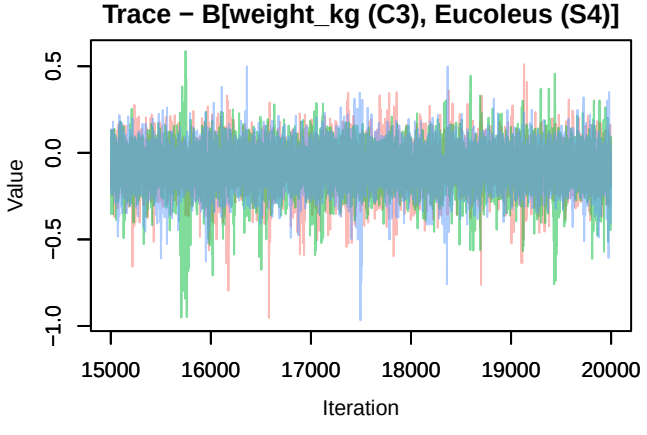

Density − B[DNA260.280 (C11), Crenosoma (S3)]
Density
0.12
0.08
0.04
0.00
−20
−15
−10
−5
0
5
10
Parameter estimate

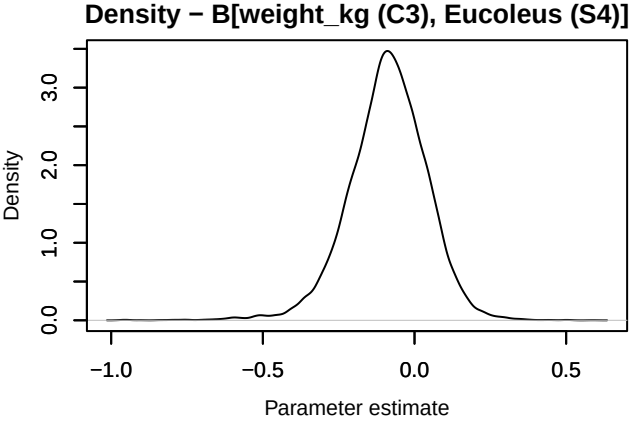

Trace − B[(Intercept) (C1), Eucoleus (S4)]
Value
60
40
20
0
−40
15000
16000
17000
18000
19000
20000
Iteration

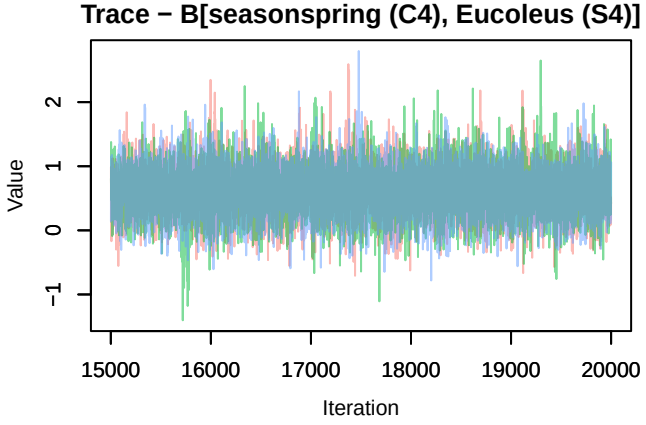

Density − B[(Intercept) (C1), Eucoleus (S4)]
Density
0.06
0.04
0.02
0.00
−40
−20
0
20
40
60
Parameter estimate

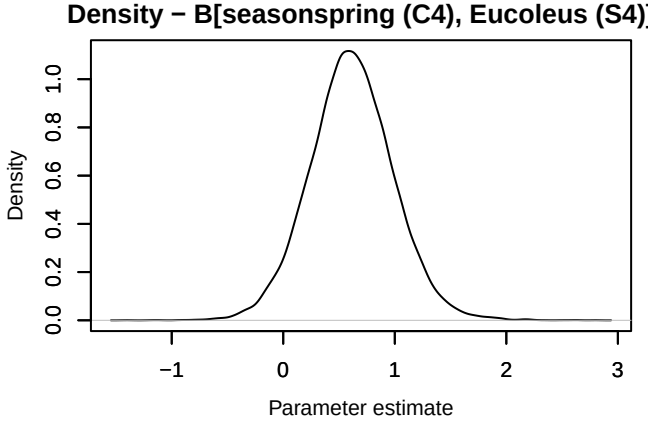

Trace − B[sexmale (C2), Eucoleus (S4)]
Value
2
1
0
−1
15000
16000
17000
18000
19000
20000
Iteration

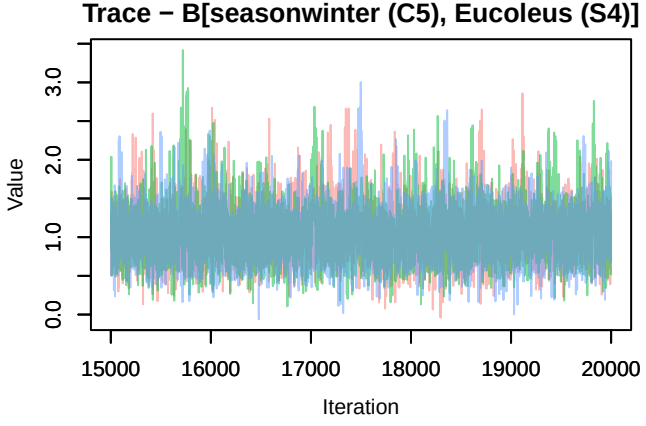

Density − B[sexmale (C2), Eucoleus (S4)]
Density
1.2
0.8
0.4
0.0
−1
0
1
2
Parameter estimate

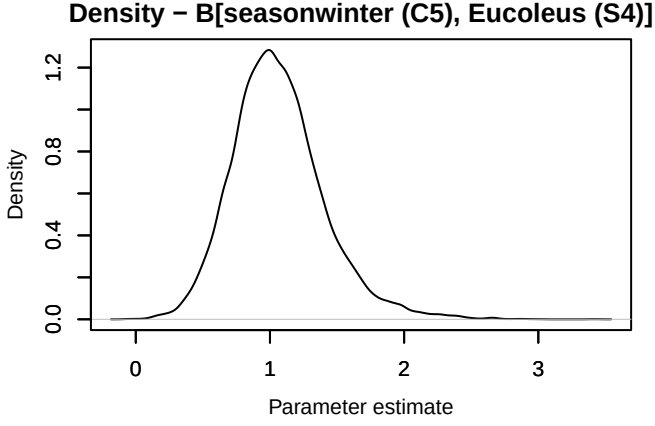

Trace − B[weight_kg (C3), Eucoleus (S4)]
Value
0.5
0.0
−0.5
−1.0
15000
16000
17000
18000
19000
20000
Iteration

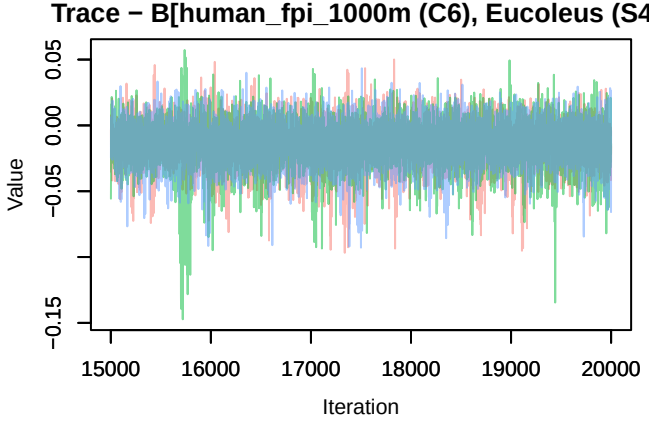

Density − B[weight_kg (C3), Eucoleus (S4)]
Density
3.0
2.0
1.0
0.0
−1.0
−0.5
0.0
0.5
Parameter estimate

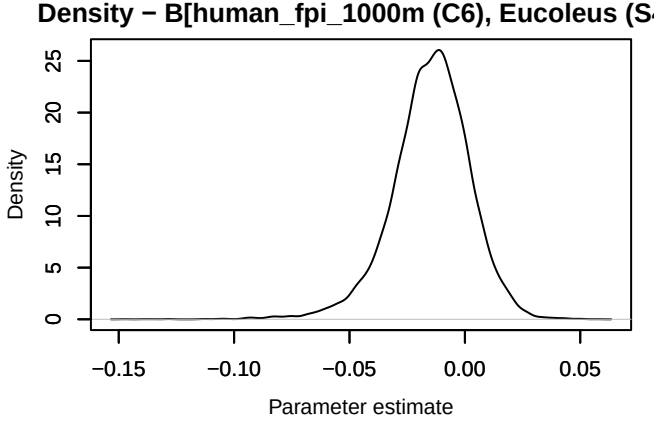

Trace − B[seasonspring (C4), Eucoleus (S4)]
Value
Iteration
15000
16000
17000
18000
19000
20000

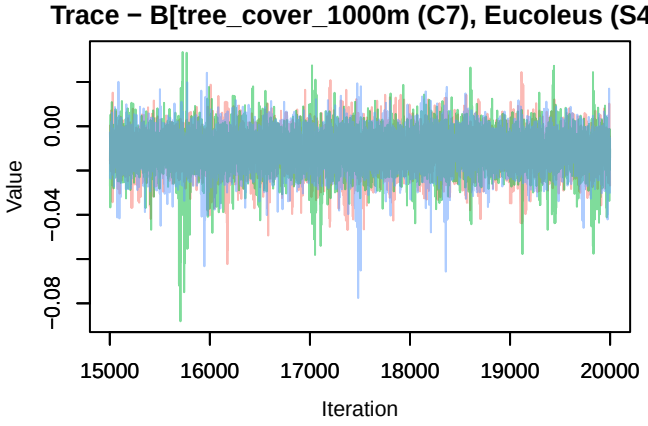

Density − B[seasonspring (C4), Eucoleus (S4)]
Density
Parameter estimate

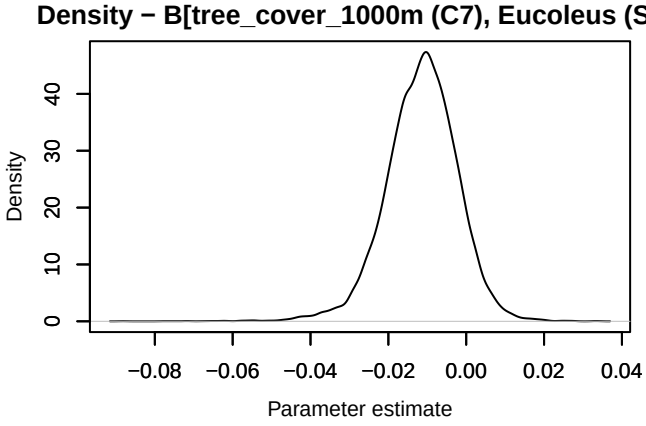

Trace − B[seasonwinter (C5), Eucoleus (S4)]
Value
Iteration
15000
16000
17000
18000
19000
20000

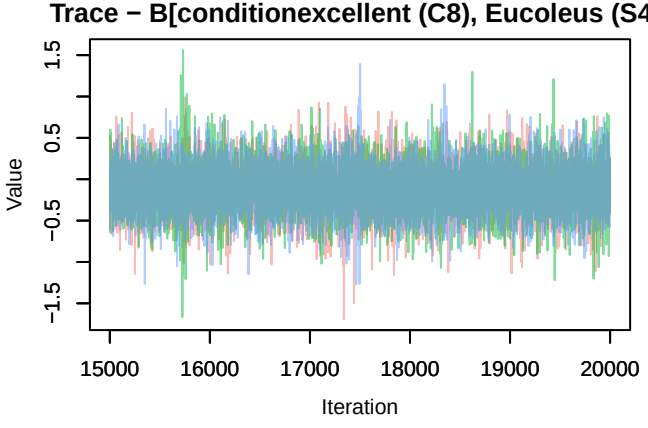

Density − B[seasonwinter (C5), Eucoleus (S4)]
Density
Parameter estimate

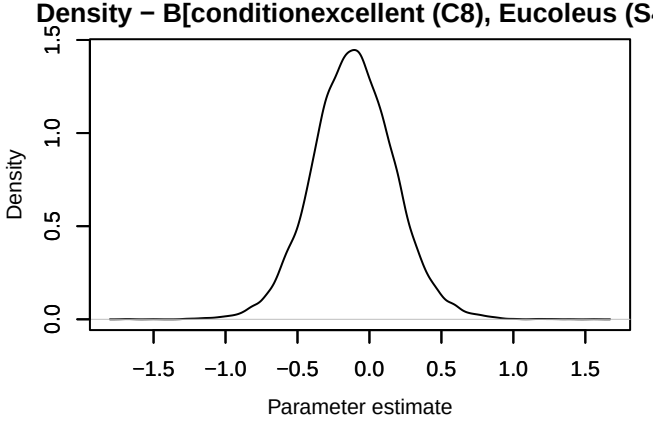

Trace − B[human_fpi_1000m (C6), Eucoleus (S4
Value
Iteration
15000
16000
17000
18000
19000
20000

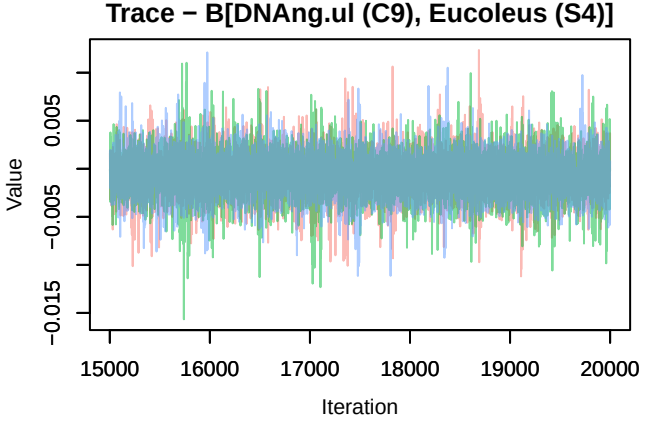

Density − B[human_fpi_1000m (C6), Eucoleus (S4
Density
Parameter estimate

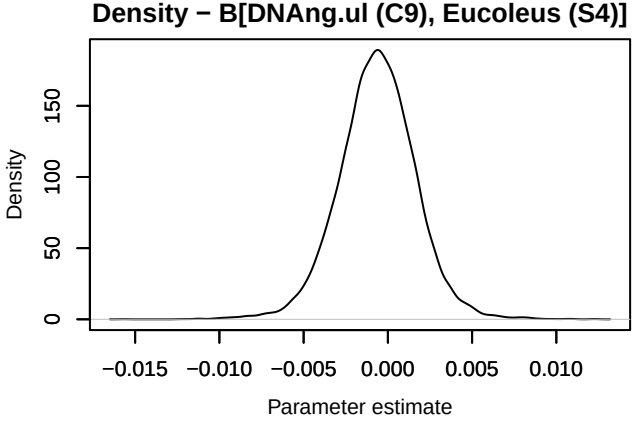

Trace − B[tree_cover_1000m (C7), Eucoleus (S4)
Value
0.00
−0.04
−0.08
15000
16000
17000
18000
19000
20000
Iteration

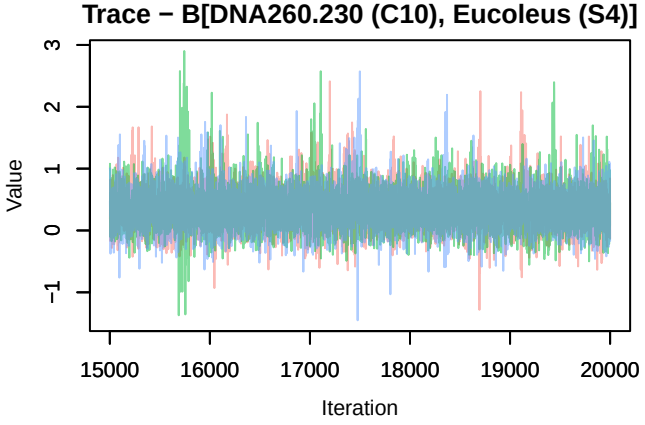

Density − B[tree_cover_1000m (C7), Eucoleus (S4
Density
0
10
20
30
40
−0.08
−0.06
−0.04
−0.02
0.00
0.02
0.04
Parameter estimate

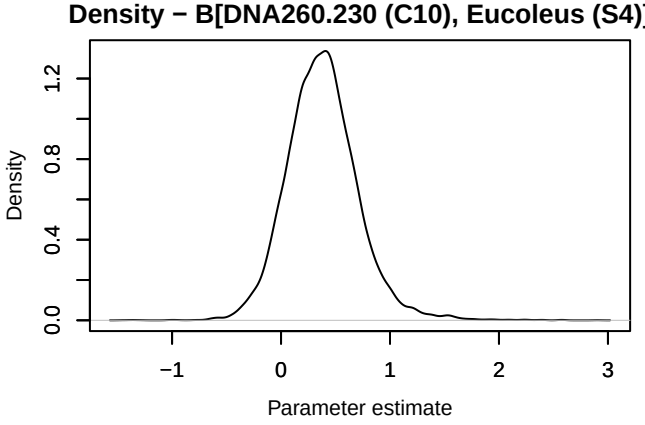

Trace − B[conditionexcellent (C8), Eucoleus (S4)
Value
1.5
0.5
−0.5
−1.5
15000
16000
17000
18000
19000
20000
Iteration

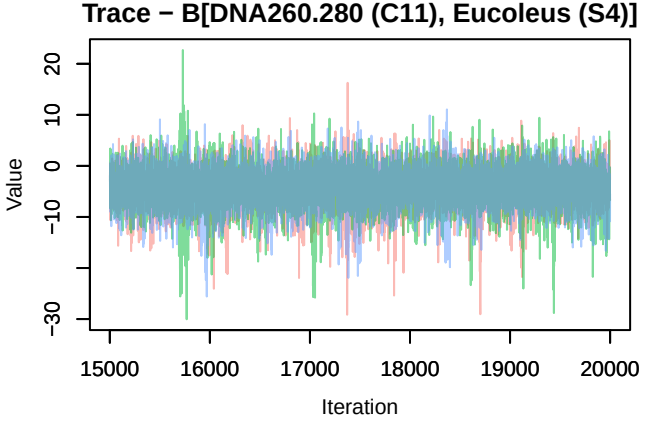

Density − B[conditionexcellent (C8), Eucoleus (S4
Density
0.0
0.5
1.0
1.5
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Parameter estimate

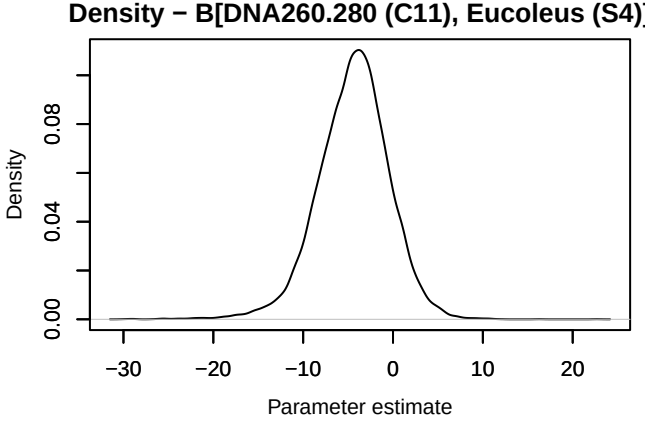

Trace − B[DNAng.ul (C9), Eucoleus (S4)]
Value
0.005
−0.005
−0.015
15000
16000
17000
18000
19000
20000
Iteration

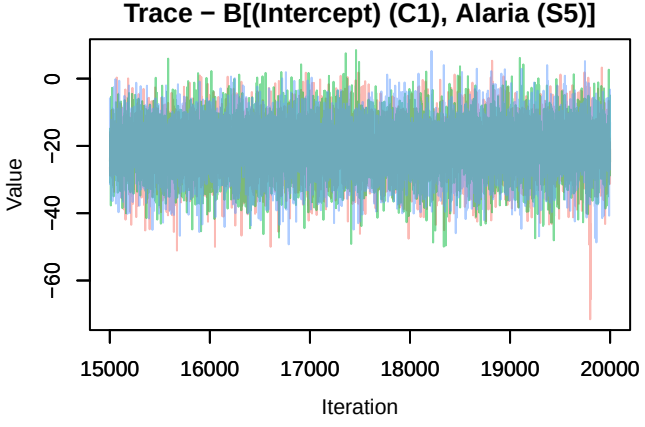

Density − B[DNAng.ul (C9), Eucoleus (S4)]
Density
0
50
100
150
−0.015
−0.010
−0.005
0.000
0.005
0.010
Parameter estimate

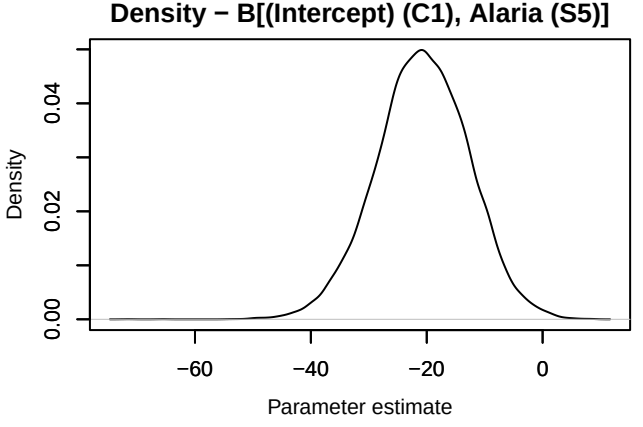

Trace − B[DNA260.230 (C10), Eucoleus (S4)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−1
0
1
2
3

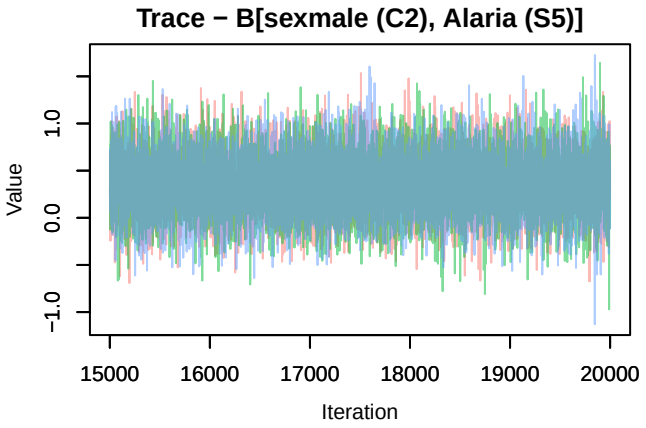

Density − B[DNA260.230 (C10), Eucoleus (S4)]
Density
Parameter estimate
0.0
0.4
0.8
1.2
−1
0
1
2
3

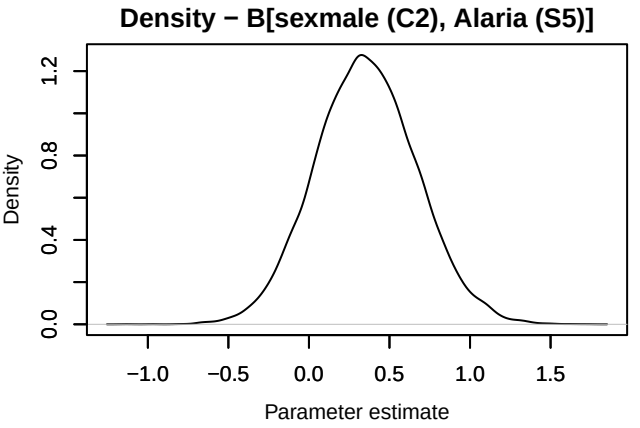

Trace − B[DNA260.280 (C11), Eucoleus (S4)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−30
−10
0
10
20

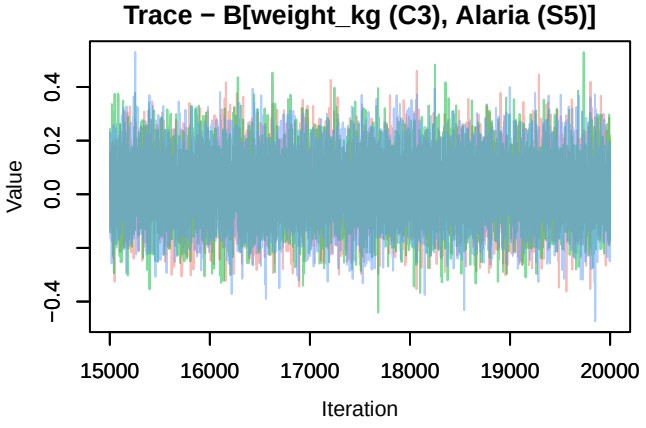

Density − B[DNA260.280 (C11), Eucoleus (S4)]
Density
Parameter estimate
0.00
0.04
0.08
−30
−20
−10
0
10
20

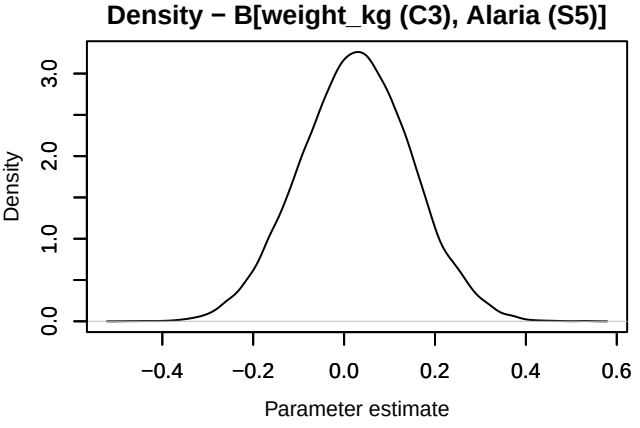

Trace − B[(Intercept) (C1), Alaria (S5)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−60
−40
−20
0

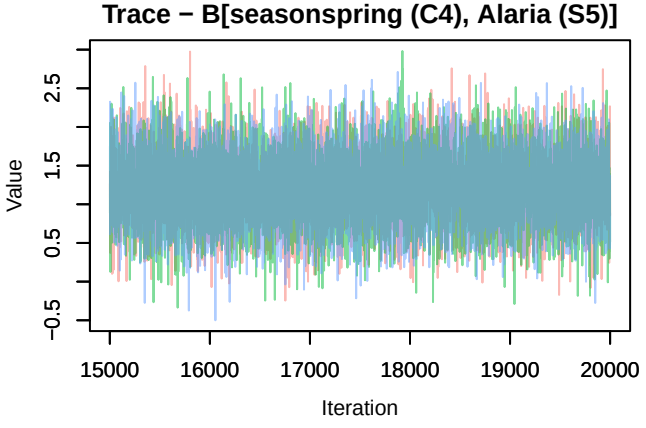

Density − B[(Intercept) (C1), Alaria (S5)]
Density
Parameter estimate
0.00
0.02
0.04
−60
−40
−20
0

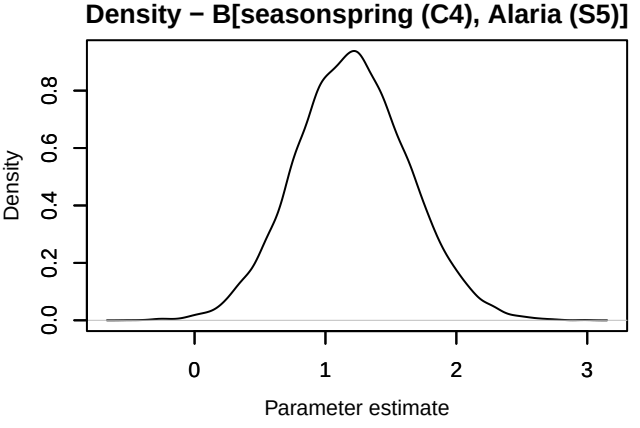

Trace − B[sexmale (C2), Alaria (S5)]
Value
1.0
0.0
−1.0
15000
16000
17000
18000
19000
20000
Iteration

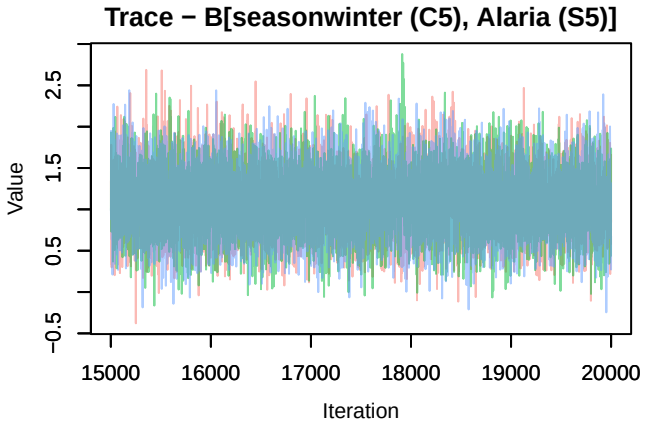

Density − B[sexmale (C2), Alaria (S5)]
Density
1.2
0.8
0.4
0.0
−1.0
−0.5
0.0
0.5
1.0
1.5
Parameter estimate

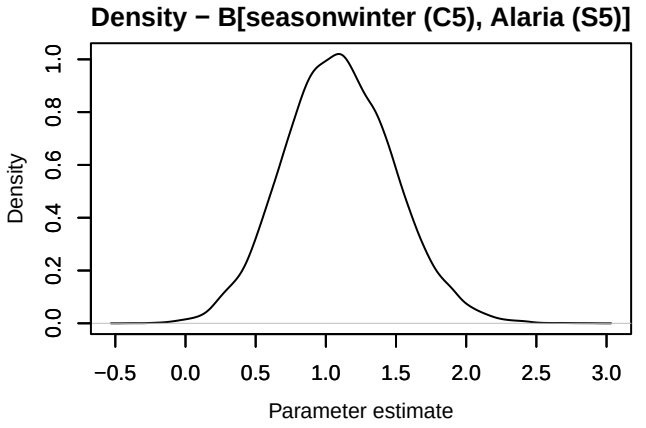

Trace − B[weight_kg (C3), Alaria (S5)]
Value
0.4
0.2
0.0
−0.4
15000
16000
17000
18000
19000
20000
Iteration

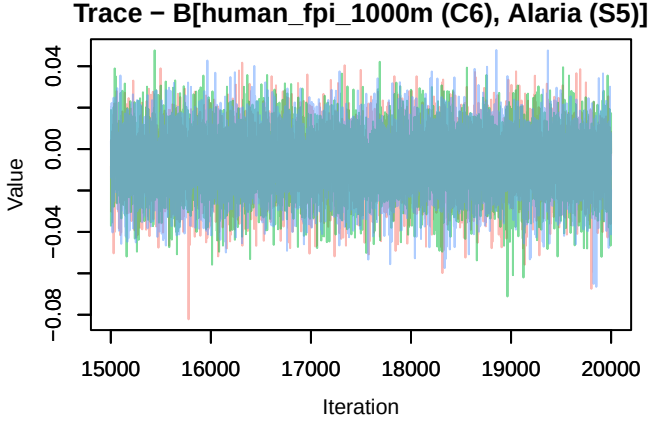

Density − B[weight_kg (C3), Alaria (S5)]
Density
3.0
2.0
1.0
0.0
−0.4
−0.2
0.0
0.2
0.4
0.6
Parameter estimate

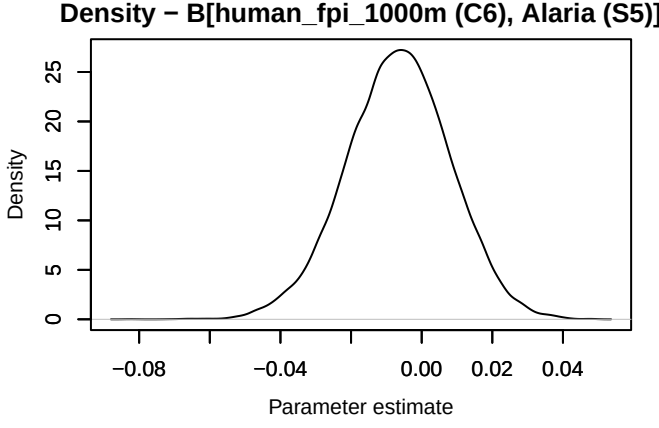

Trace − B[seasonspring (C4), Alaria (S5)]
Value
2.5
1.5
0.5
−0.5
15000
16000
17000
18000
19000
20000
Iteration

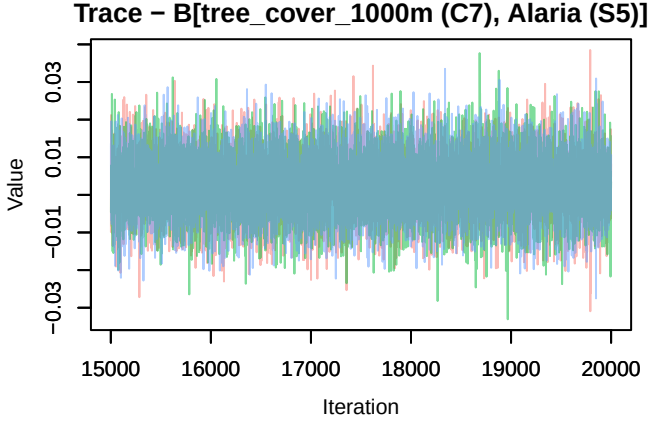

Density − B[seasonspring (C4), Alaria (S5)]
Density
0.8
0.6
0.4
0.2
0.0
0
1
2
3
Parameter estimate

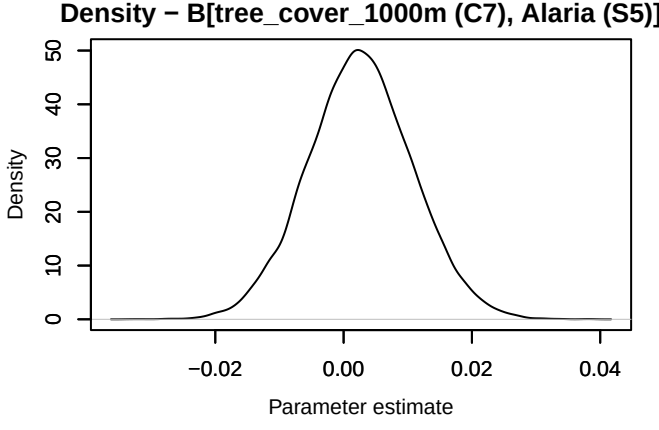

Trace − B[seasonwinter (C5), Alaria (S5)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−0.5
0.5
1.5
2.5

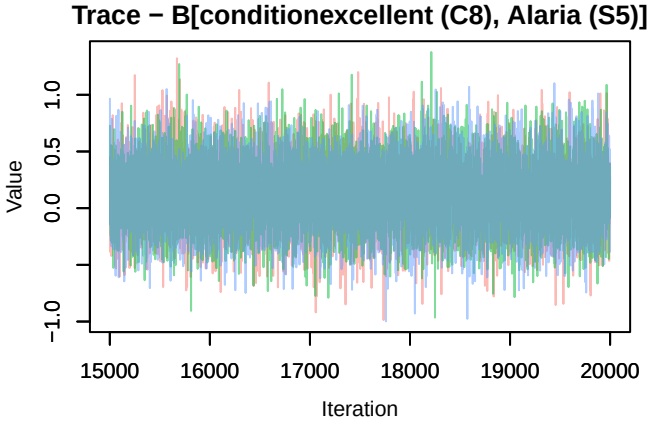

Density − B[seasonwinter (C5), Alaria (S5)]
Density
Parameter estimate
0.0
0.2
0.4
0.6
0.8
1.0
−0.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0

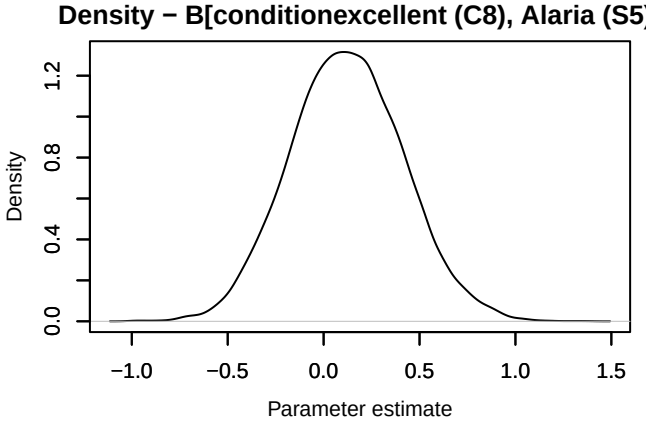

Trace − B[human_fpi_1000m (C6), Alaria (S5)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−0.08
−0.04
0.00
0.04

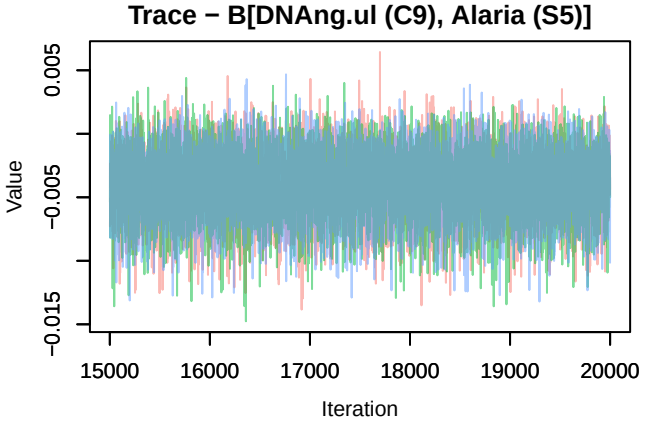

Density − B[human_fpi_1000m (C6), Alaria (S5)]
Density
Parameter estimate
0
5
10
15
20
25
−0.08
−0.04
0.00
0.02
0.04

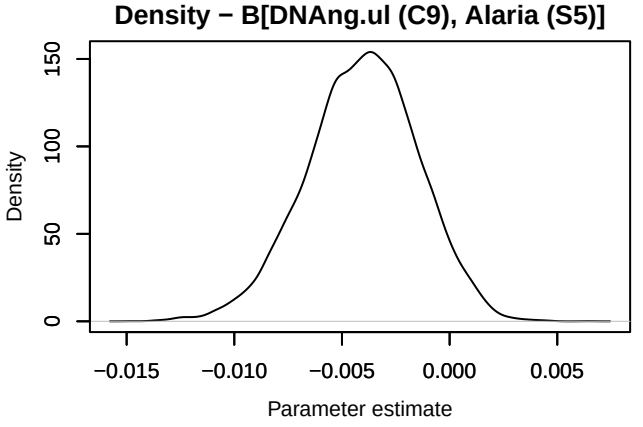

Trace − B[tree_cover_1000m (C7), Alaria (S5)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−0.03
−0.01
0.01
0.03

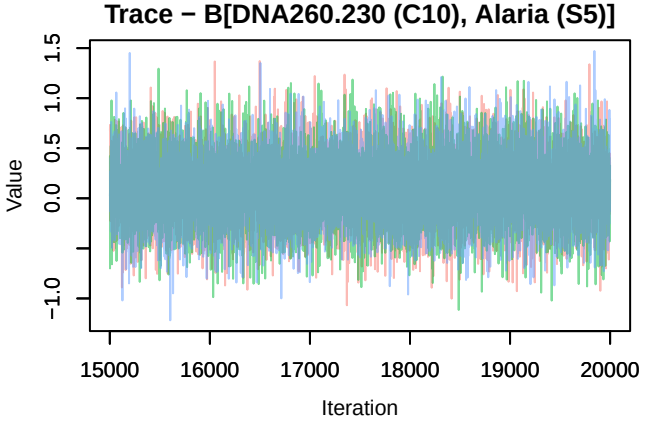

Density − B[tree_cover_1000m (C7), Alaria (S5)]
Density
Parameter estimate
0
10
20
30
40
50
−0.02
0.00
0.02
0.04

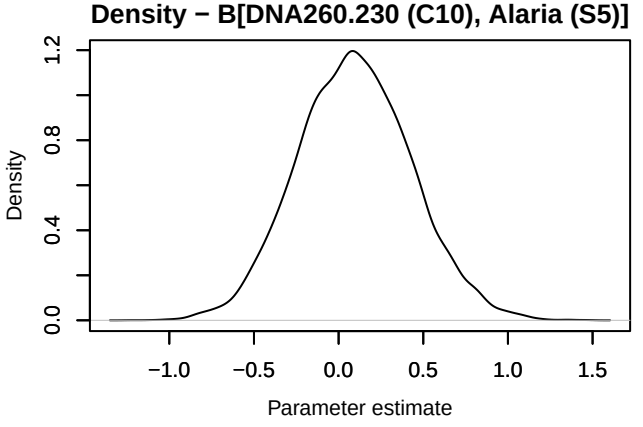

Trace − B[conditionexcellent (C8), Alaria (S5)]
Value
1.0
0.5
0.0
−1.0
15000
16000
17000
18000
19000
20000
Iteration

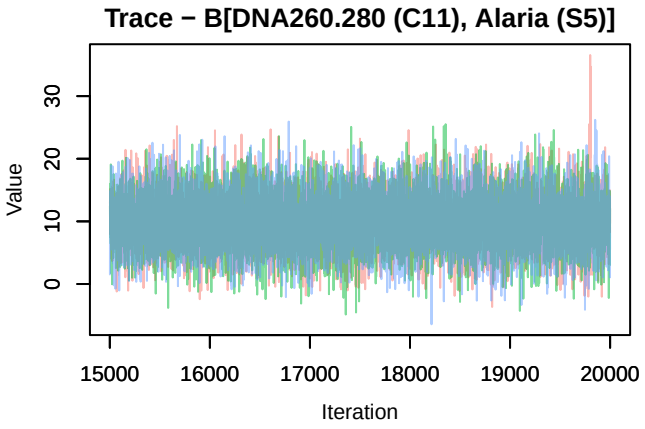

Density − B[conditionexcellent (C8), Alaria (S5)]
Density
1.2
0.8
0.4
0.0
−1.0
−0.5
0.0
0.5
1.0
1.5
Parameter estimate

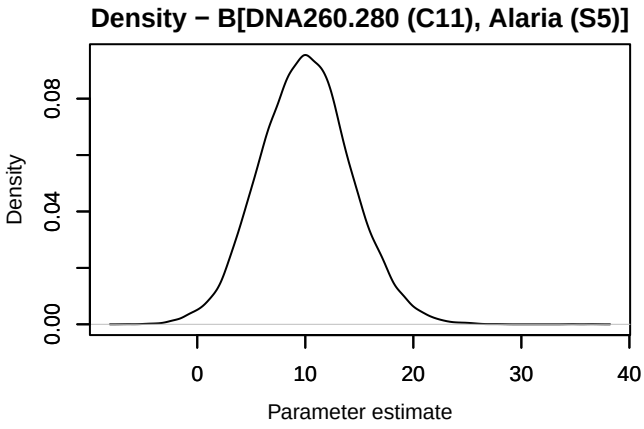

Trace − B[DNAng.ul (C9), Alaria (S5)]
Value
0.005
−0.005
−0.015
15000
16000
17000
18000
19000
20000
Iteration

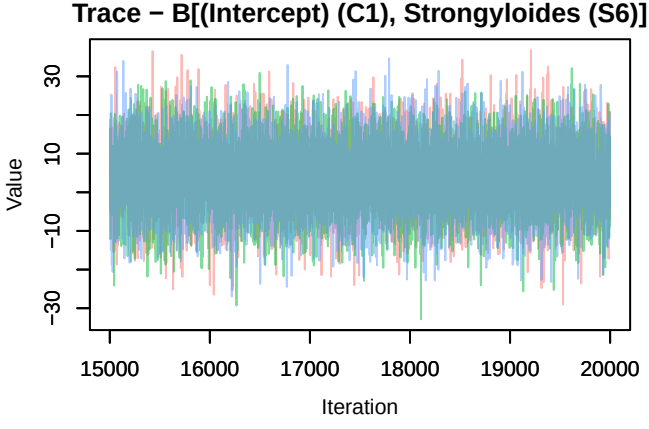

Density − B[DNAng.ul (C9), Alaria (S5)]
Density
150
100
50
0
−0.015
−0.010
−0.005
0.000
0.005
Parameter estimate

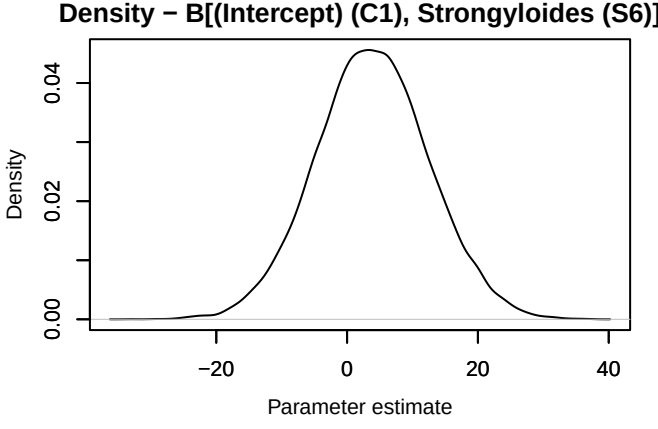

Trace − B[DNA260.230 (C10), Alaria (S5)]
Value
1.5
1.0
0.5
0.0
−1.0
15000
16000
17000
18000
19000
20000
Iteration

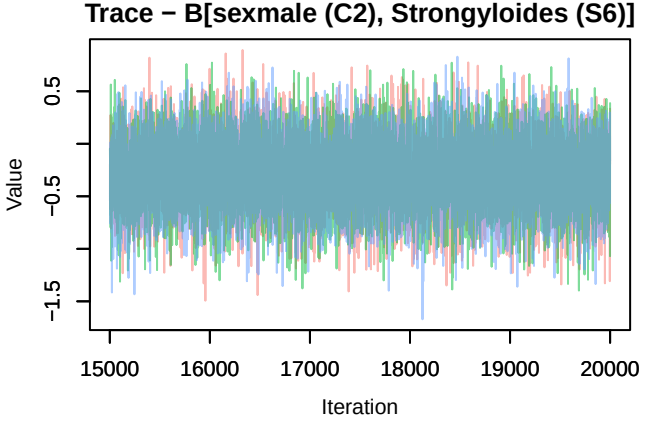

Density − B[DNA260.230 (C10), Alaria (S5)]
Density
1.2
0.8
0.4
0.0
−1.0
−0.5
0.0
0.5
1.0
1.5
Parameter estimate

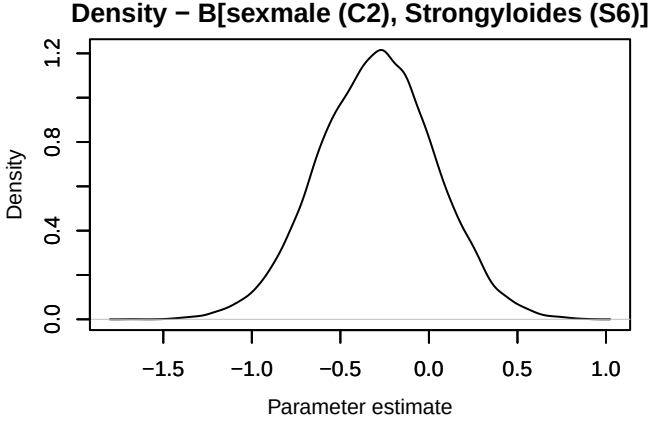

Trace − B[DNA260.280 (C11), Alaria (S5)]
Value
30
20
10
0
15000
16000
17000
18000
19000
20000
Iteration

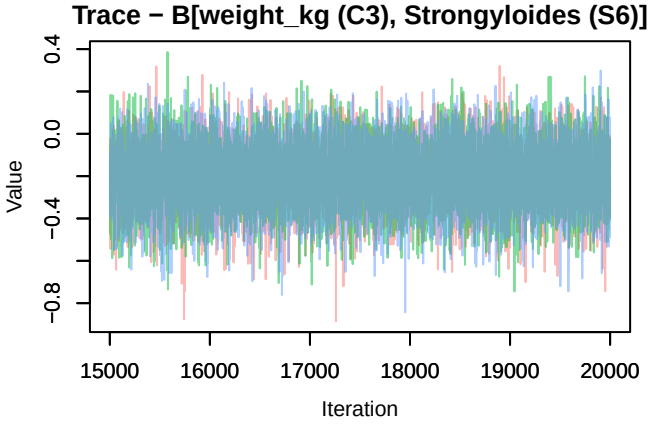

Density − B[DNA260.280 (C11), Alaria (S5)]
Density
0.08
0.04
0.00
0
10
20
30
40
Parameter estimate

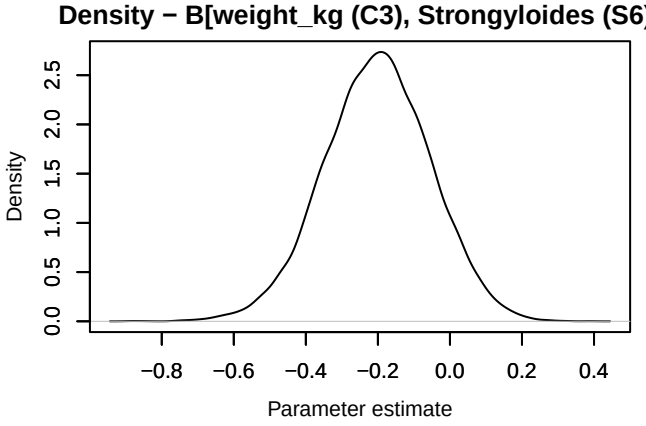

Trace − B[(Intercept) (C1), Strongyloides (S6)]
Value
30
10
−10
−30
15000
16000
17000
18000
19000
20000
Iteration

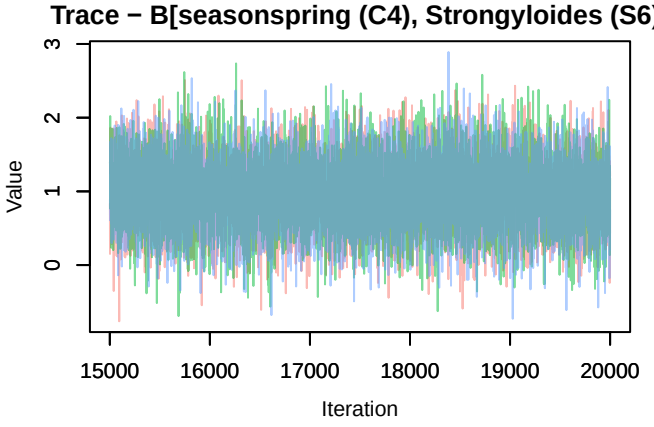

Density − B[(Intercept) (C1), Strongyloides (S6)]
Density
0.04
0.02
0.00
−20
0
20
40
Parameter estimate

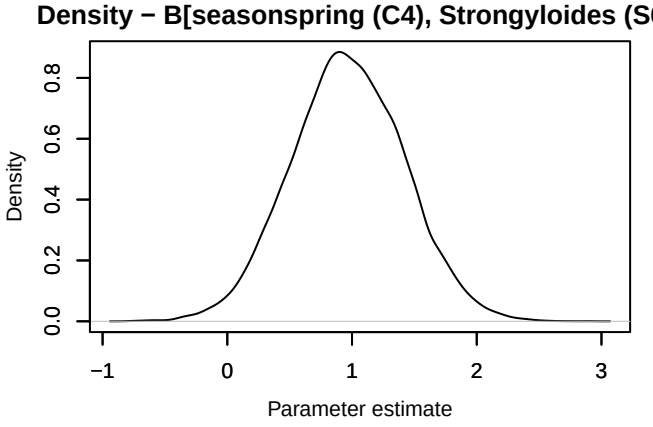

Trace − B[sexmale (C2), Strongyloides (S6)]
Value
0.5
−0.5
−1.5
15000
16000
17000
18000
19000
20000
Iteration

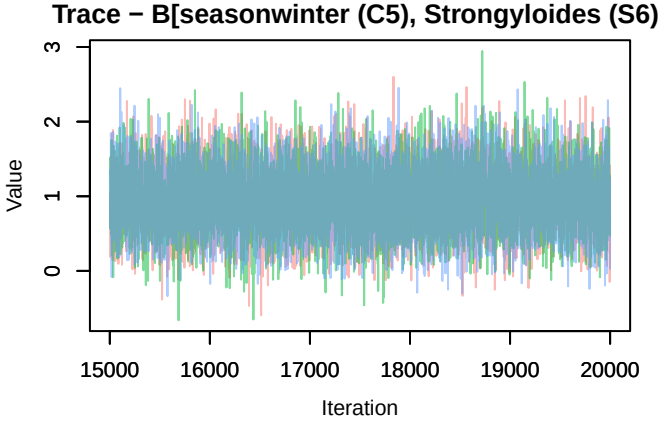

Density − B[sexmale (C2), Strongyloides (S6)]
Density
1.2
0.8
0.4
0.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
Parameter estimate

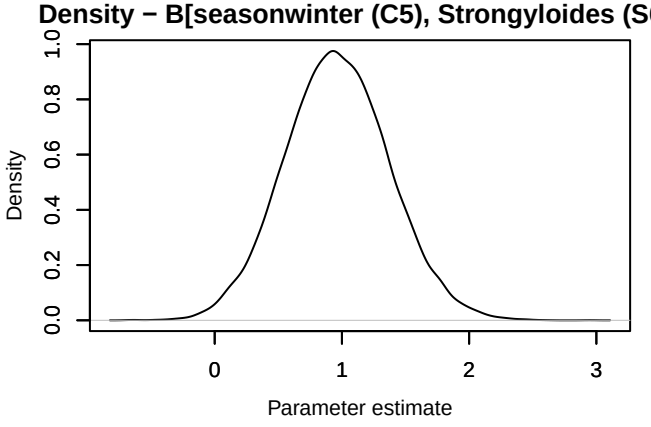

Trace − B[weight_kg (C3), Strongyloides (S6)]
Value
0.4
0.0
−0.4
−0.8
15000
16000
17000
18000
19000
20000
Iteration

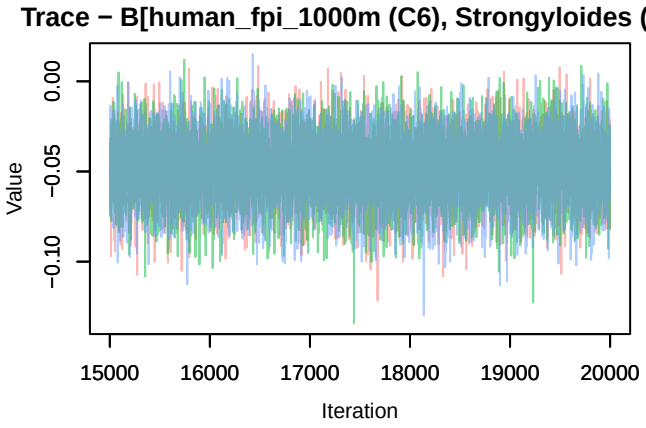

Density − B[weight_kg (C3), Strongyloides (S6)]
Density
2.5
2.0
1.5
1.0
0.5
0.0
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
Parameter estimate

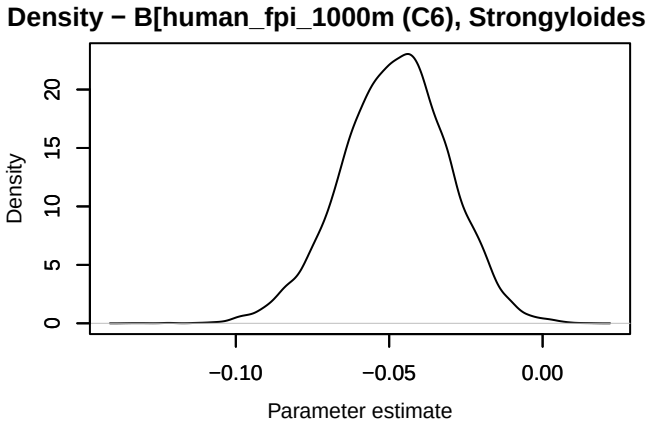

Trace − B[seasonspring (C4), Strongyloides (S6)
Value
3
2
1
0
15000
16000
17000
18000
19000
20000
Iteration

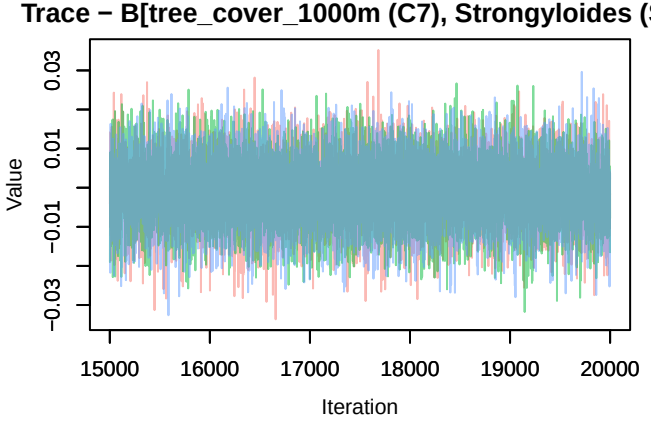

Density − B[seasonspring (C4), Strongyloides (S6
Density
0.8
0.6
0.4
0.2
0.0
−1
0
1
2
3
Parameter estimate

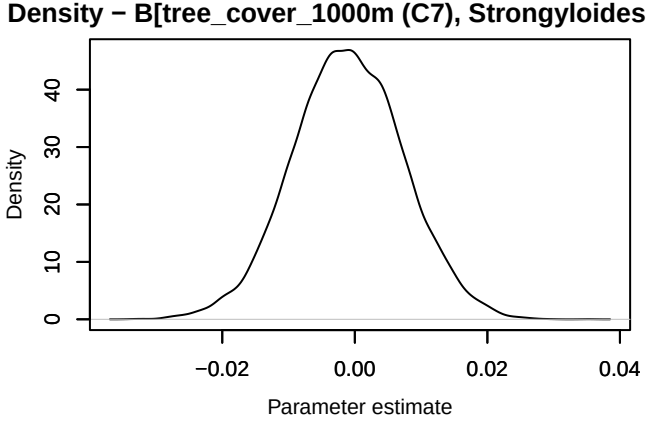

Trace − B[seasonwinter (C5), Strongyloides (S6)
Value
3
2
1
0
15000
16000
17000
18000
19000
20000
Iteration

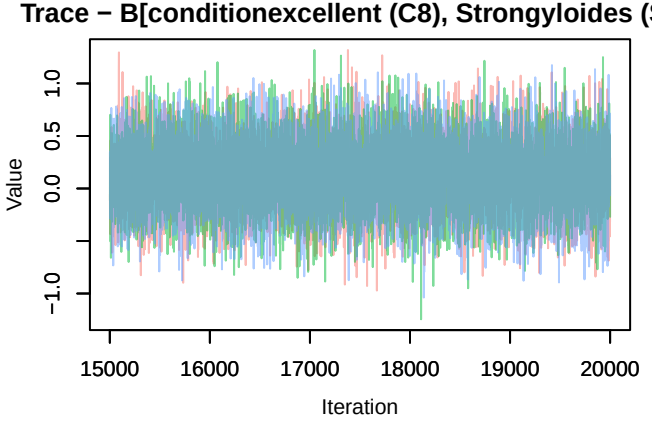

Density − B[seasonwinter (C5), Strongyloides (S6
Density
1.0
0.8
0.6
0.4
0.2
0.0
0
1
2
3
Parameter estimate

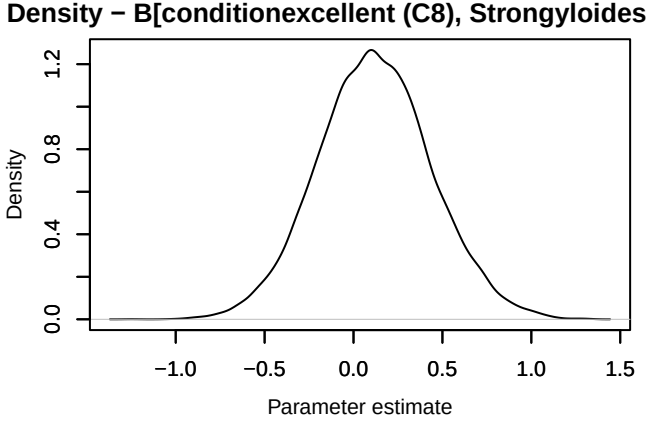

Trace − B[human_fpi_1000m (C6), Strongyloides (S
Value
0.00
−0.05
−0.10
15000
16000
17000
18000
19000
20000
Iteration

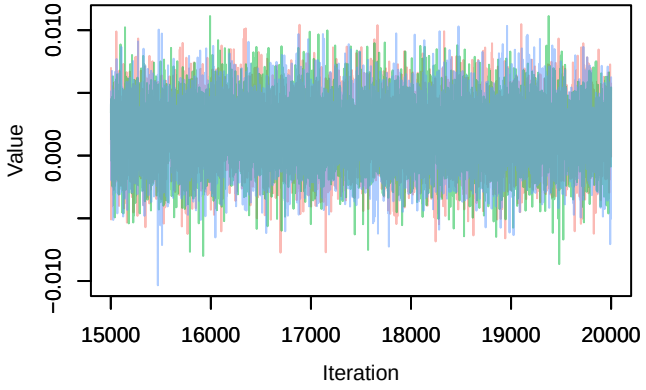

Density − B[human_fpi_1000m (C6), Strongyloides (
Density
0
5
10
15
20
−0.10
−0.05
0.00
Parameter estimate

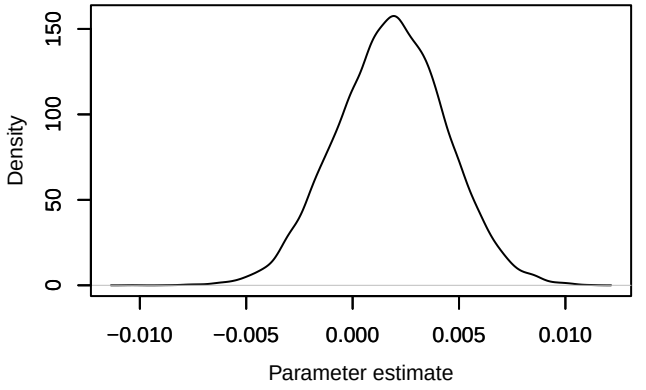

Trace − B[tree_cover_1000m (C7), Strongyloides (S
Value
0.03
0.01
−0.01
−0.03
15000
16000
17000
18000
19000
20000
Iteration

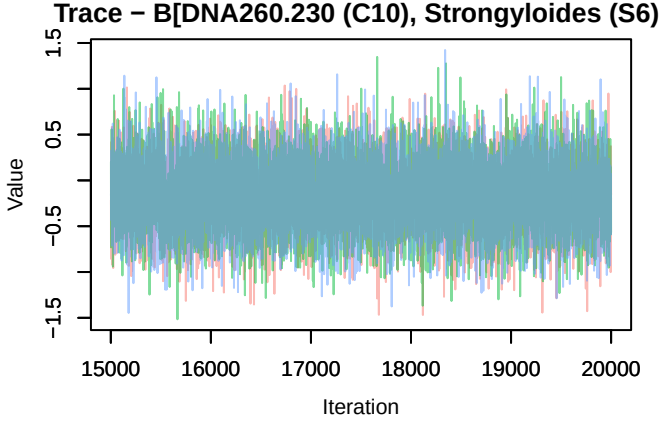

Density − B[tree_cover_1000m (C7), Strongyloides (
Density
0
10
20
30
40
−0.02
0.00
0.02
0.04
Parameter estimate

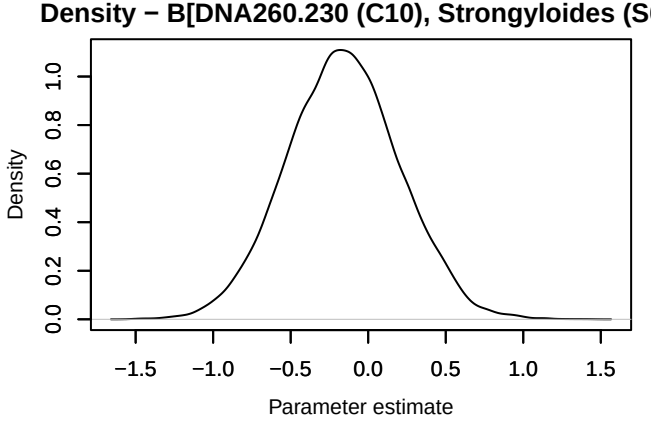

Trace − B[conditionexcellent (C8), Strongyloides (S
Value
1.0
0.5
0.0
−1.0
15000
16000
17000
18000
19000
20000
Iteration

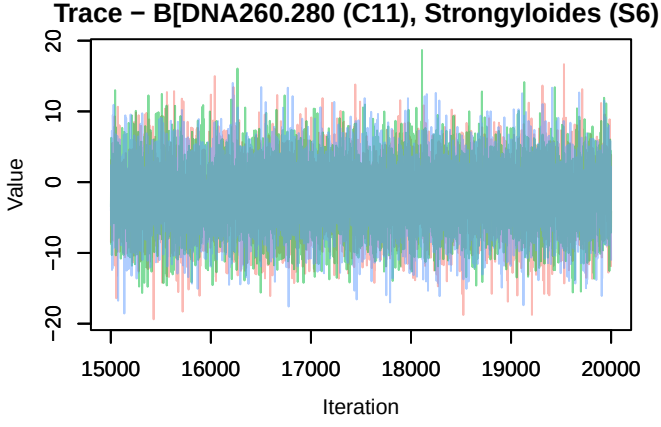

Density − B[conditionexcellent (C8), Strongyloides (
Density
0.0
0.4
0.8
1.2
−1.0
−0.5
0.0
0.5
1.0
1.5
Parameter estimate

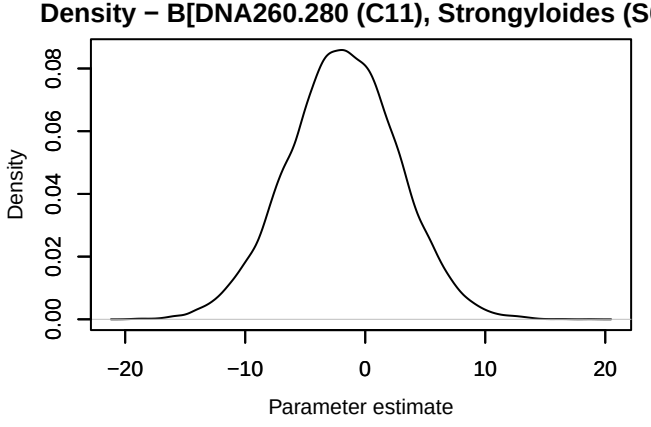

Trace − B[DNAng.ul (C9), Strongyloides (S6)]
Value
0.010
0.000
−0.010
15000
16000
17000
18000
19000
20000
Iteration

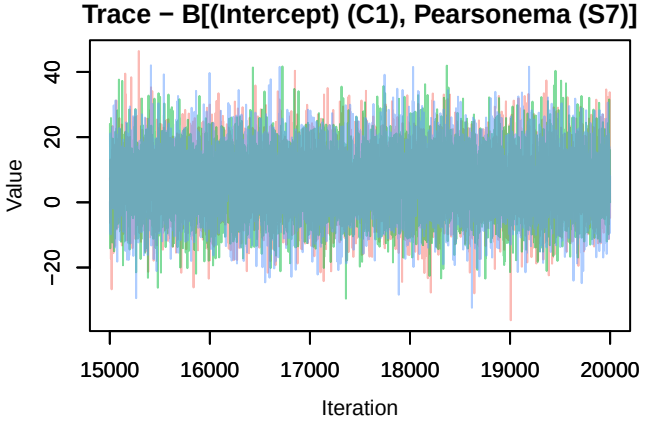

Density − B[DNAng.ul (C9), Strongyloides (S6)]
Density
150
100
50
0
−0.010
−0.005
0.000
0.005
0.010
Parameter estimate

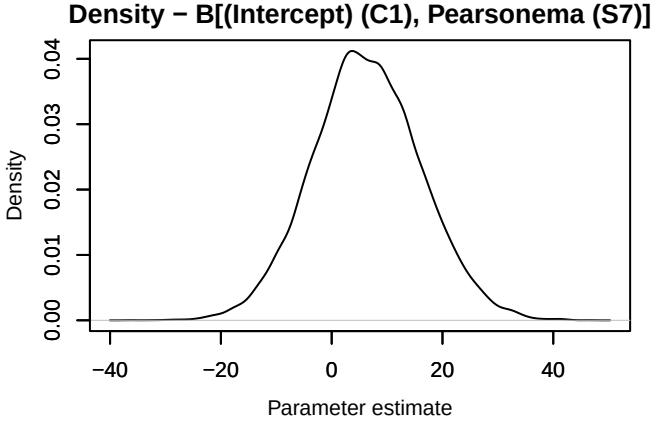

Trace − B[DNA260.230 (C10), Strongyloides (S6)
Value
1.5
0.5
−0.5
−1.5
15000
16000
17000
18000
19000
20000
Iteration

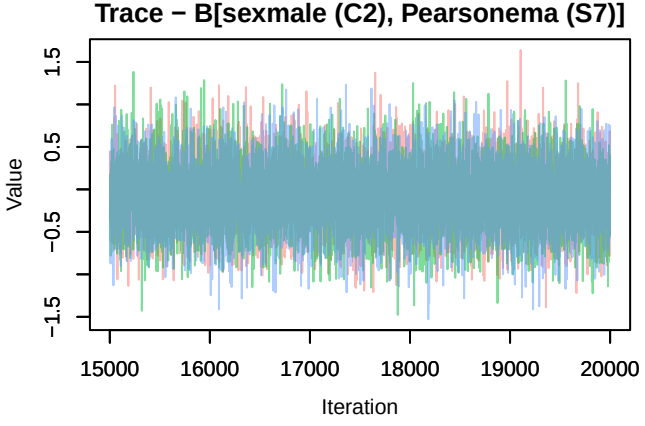

Density − B[DNA260.230 (C10), Strongyloides (S6
Density
1.0
0.8
0.6
0.4
0.2
0.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Parameter estimate

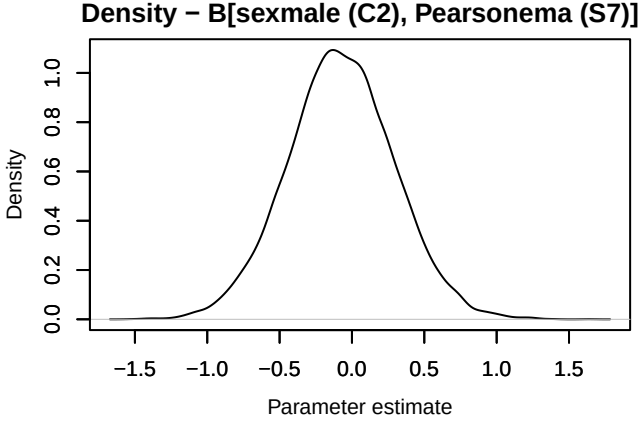

Trace − B[DNA260.280 (C11), Strongyloides (S6)
Value
20
10
0
−10
−20
15000
16000
17000
18000
19000
20000
Iteration

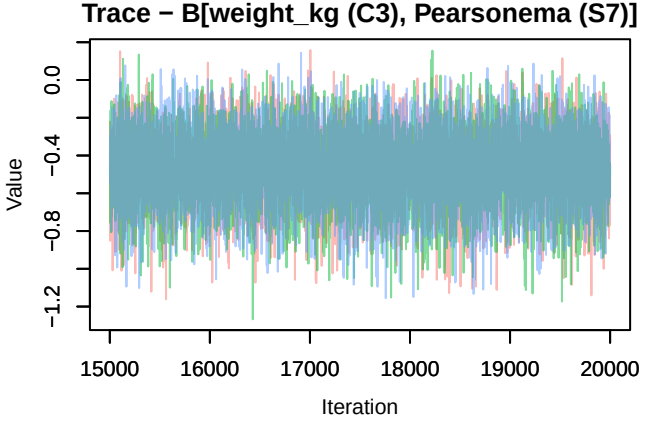

Density − B[DNA260.280 (C11), Strongyloides (S6
Density
0.08
0.06
0.04
0.02
0.00
−20
−10
0
10
20
Parameter estimate

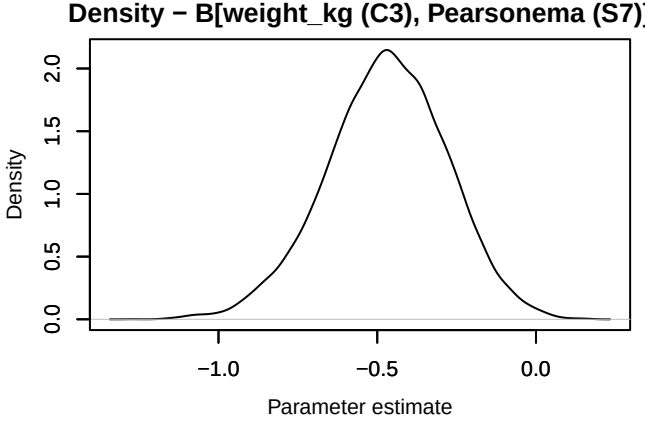

Trace − B[(Intercept) (C1), Pearsonema (S7)]
Value
40
20
0
−20
15000
16000
17000
18000
19000
20000
Iteration

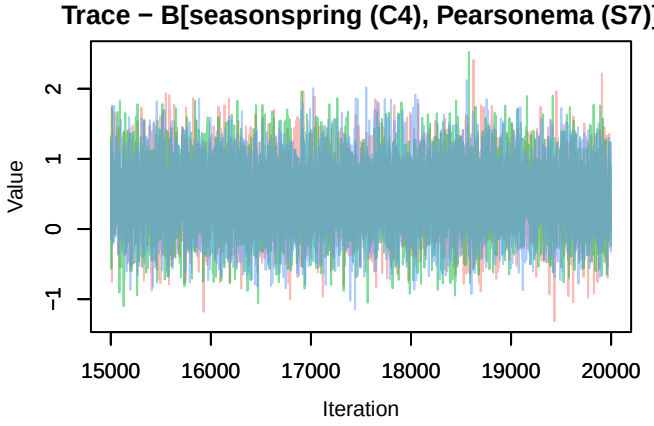

Density − B[(Intercept) (C1), Pearsonema (S7)]
Density
0.04
0.03
0.02
0.01
0.00
−40
−20
0
20
40
Parameter estimate

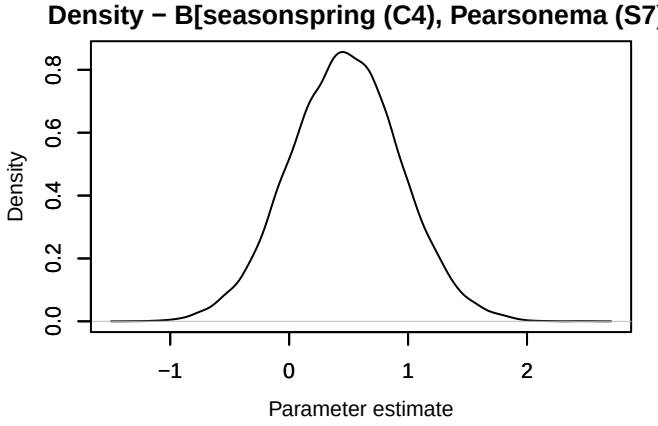

Trace − B[sexmale (C2), Pearsonema (S7)]
Value
1.5
0.5
−0.5
−1.5
15000
16000
17000
18000
19000
20000
Iteration

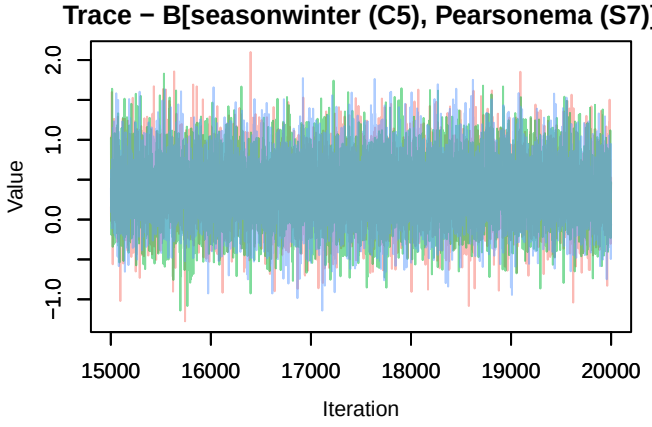

Density − B[sexmale (C2), Pearsonema (S7)]
Density
1.0
0.8
0.6
0.4
0.2
0.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Parameter estimate

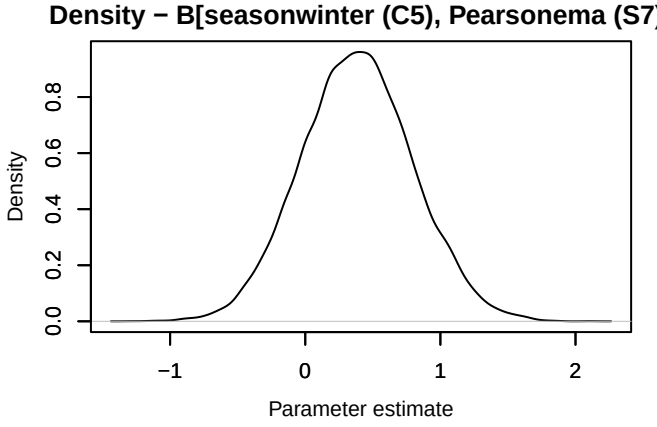

Trace − B[weight_kg (C3), Pearsonema (S7)]
Value
0.0
−0.4
−0.8
−1.2
15000
16000
17000
18000
19000
20000
Iteration

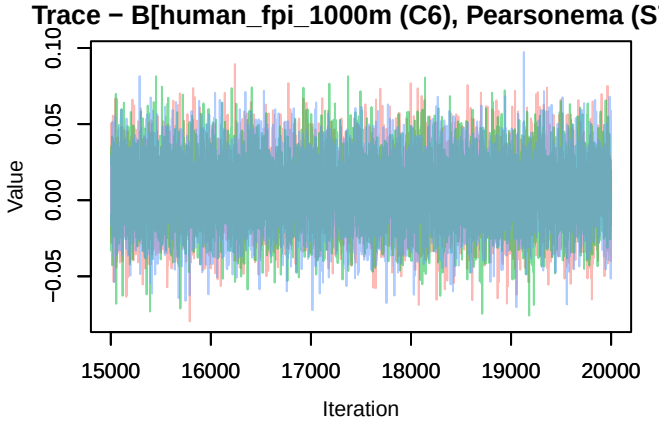

Density − B[weight_kg (C3), Pearsonema (S7)]
Density
2.0
1.5
1.0
0.5
0.0
−1.0
−0.5
0.0
Parameter estimate

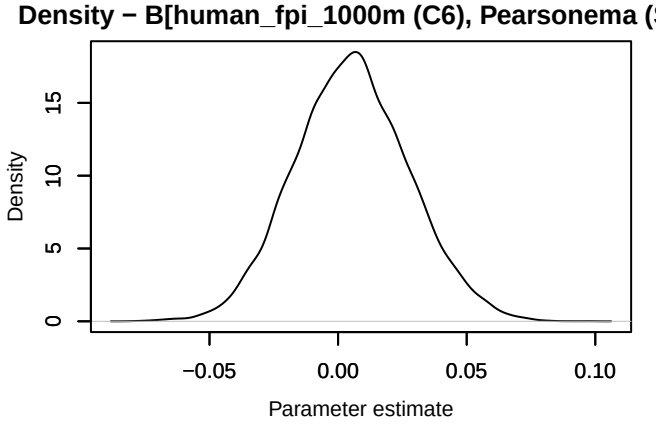

Trace − B[seasonspring (C4), Pearsonema (S7)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−1
0
1
2

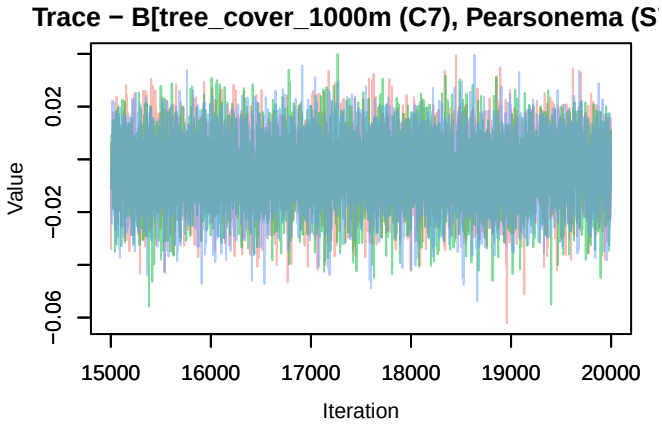

Density − B[seasonspring (C4), Pearsonema (S7
Density
Parameter estimate
0.0
0.2
0.4
0.6
0.8
−1
0
1
2

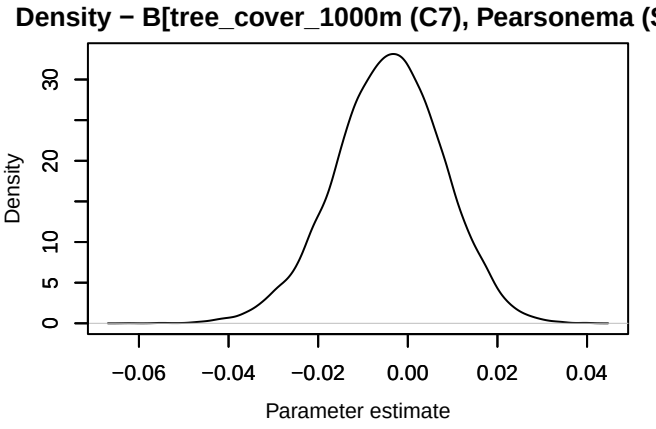

Trace − B[seasonwinter (C5), Pearsonema (S7)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−1.0
0.0
1.0
2.0

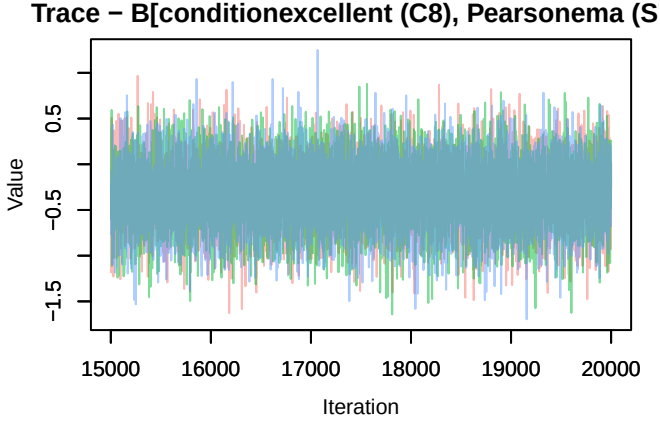

Density − B[seasonwinter (C5), Pearsonema (S7
Density
Parameter estimate
0.0
0.2
0.4
0.6
0.8
−1
0
1
2

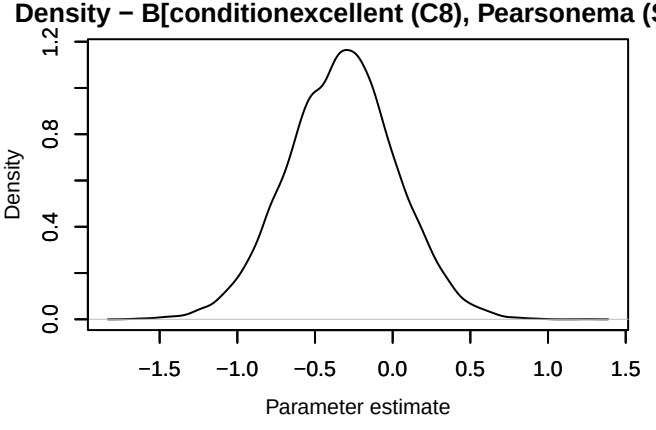

Trace − B[human_fpi_1000m (C6), Pearsonema (S
Value
Iteration
15000
16000
17000
18000
19000
20000
−0.05
0.00
0.05
0.10

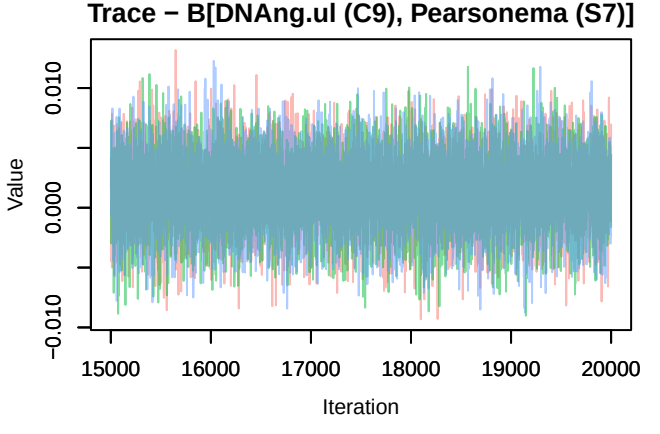

Density − B[human_fpi_1000m (C6), Pearsonema (S
Density
Parameter estimate
0
5
10
15
−0.05
0.00
0.05
0.10

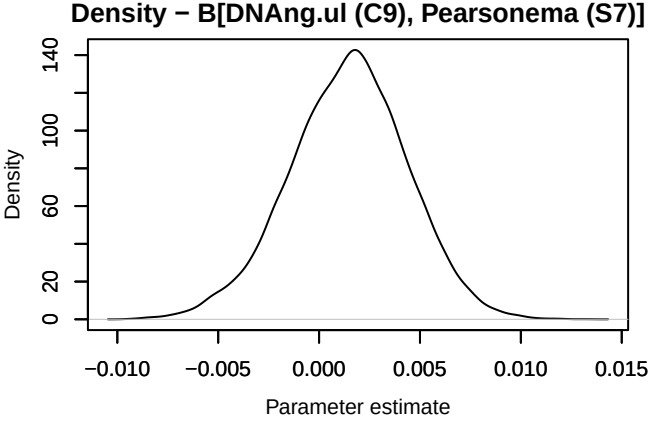

Trace − B[tree_cover_1000m (C7), Pearsonema (S
Value
0.02
−0.02
−0.06
15000
16000
17000
18000
19000
20000
Iteration

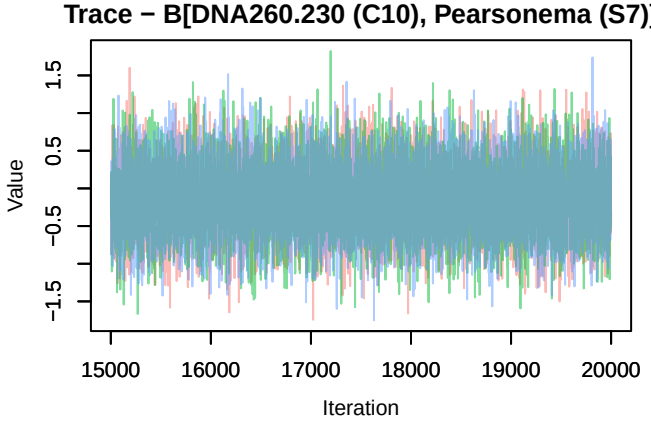

Density − B[tree_cover_1000m (C7), Pearsonema (S
Density
0
5
10
20
30
−0.06
−0.04
−0.02
0.00
0.02
0.04
Parameter estimate

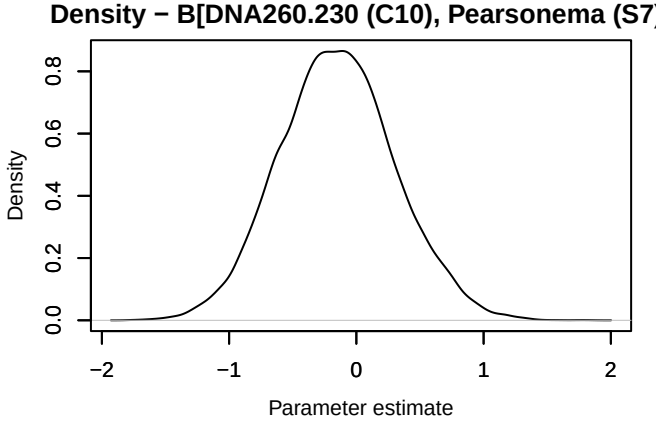

Trace − B[conditionexcellent (C8), Pearsonema (S
Value
0.5
−0.5
−1.5
15000
16000
17000
18000
19000
20000
Iteration

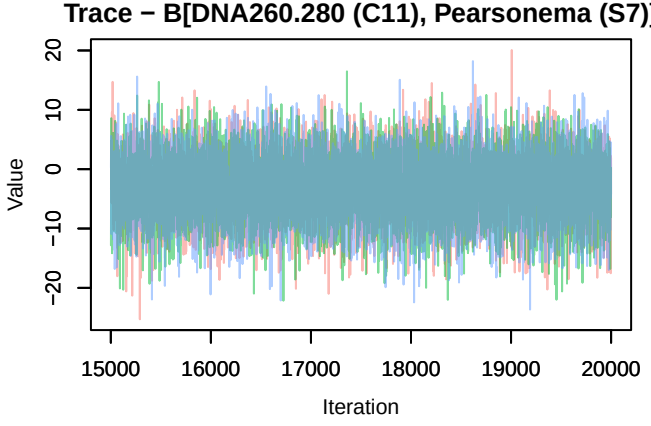

Density − B[conditionexcellent (C8), Pearsonema (S
Density
0.0
0.4
0.8
1.2
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Parameter estimate

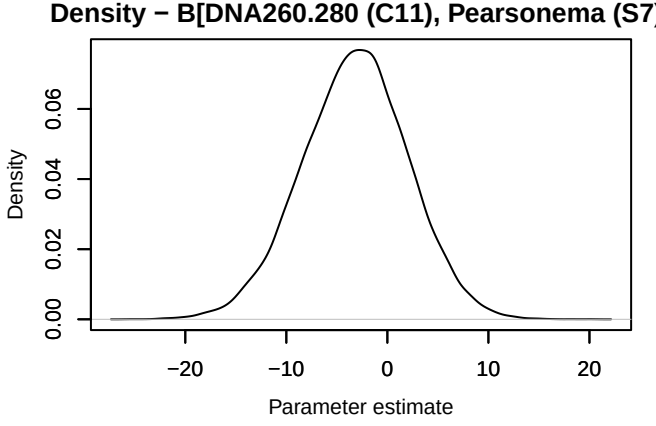

Trace − B[DNAng.ul (C9), Pearsonema (S7)]
Value
0.010
0.000
−0.010
15000
16000
17000
18000
19000
20000
Iteration

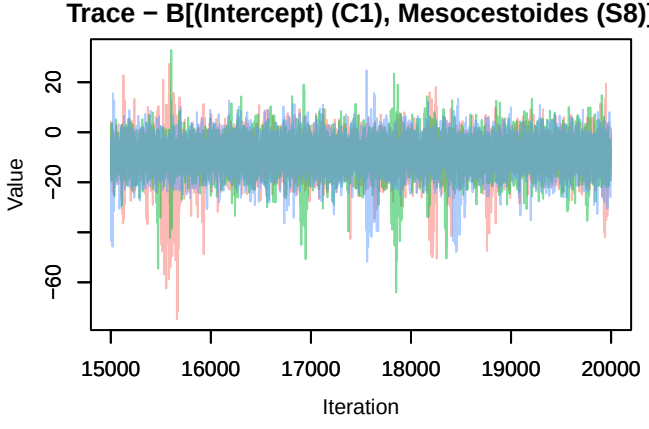

Density − B[DNAng.ul (C9), Pearsonema (S7)]
Density
0
20
60
100
140
−0.010
−0.005
0.000
0.005
0.010
0.015
Parameter estimate

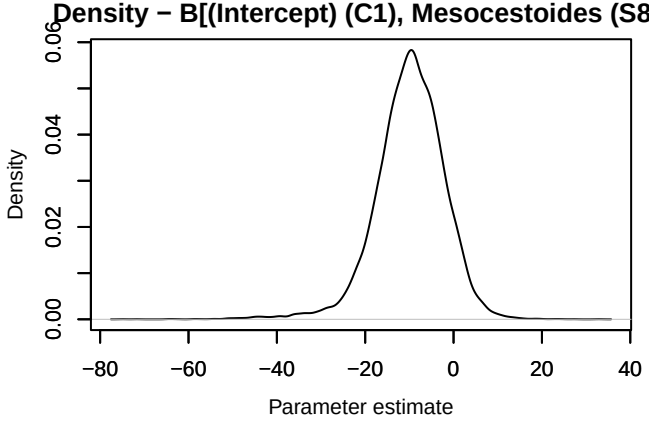

Trace − B[DNA260.230 (C10), Pearsonema (S7)]
Value
1.5
0.5
−0.5
−1.5
15000
16000
17000
18000
19000
20000
Iteration

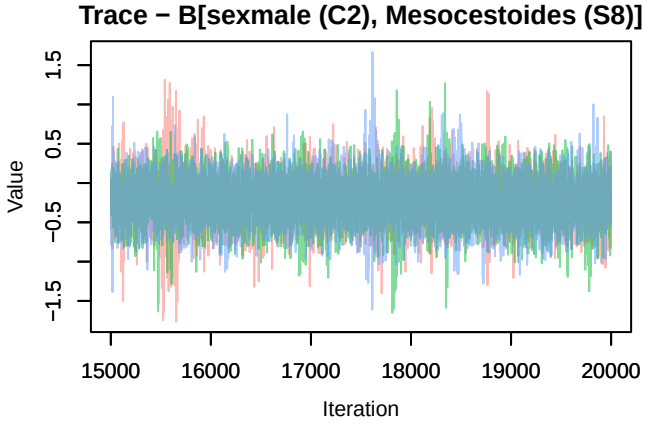

Density − B[DNA260.230 (C10), Pearsonema (S7)]
Density
0.8
0.6
0.4
0.2
0.0
−2
−1
0
1
2
Parameter estimate

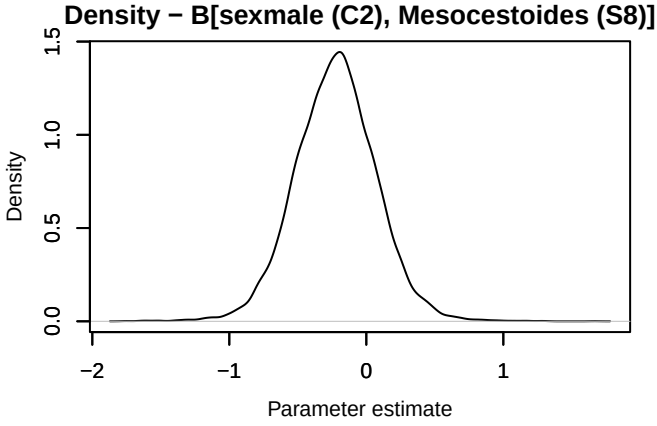

Trace − B[DNA260.280 (C11), Pearsonema (S7)]
Value
20
10
0
−10
−20
15000
16000
17000
18000
19000
20000
Iteration

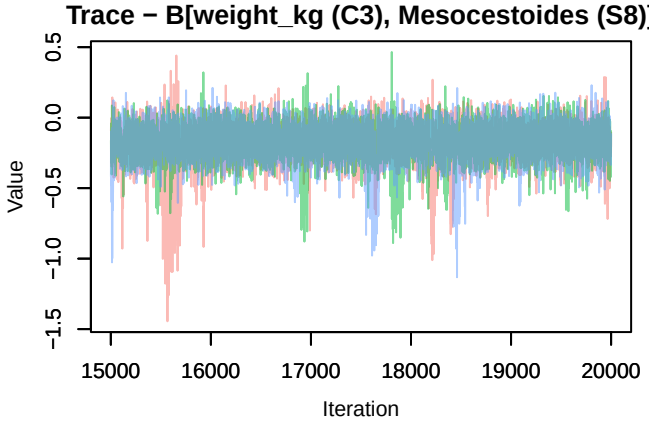

Density − B[DNA260.280 (C11), Pearsonema (S7)]
Density
0.06
0.04
0.02
0.00
−20
−10
0
10
20
Parameter estimate

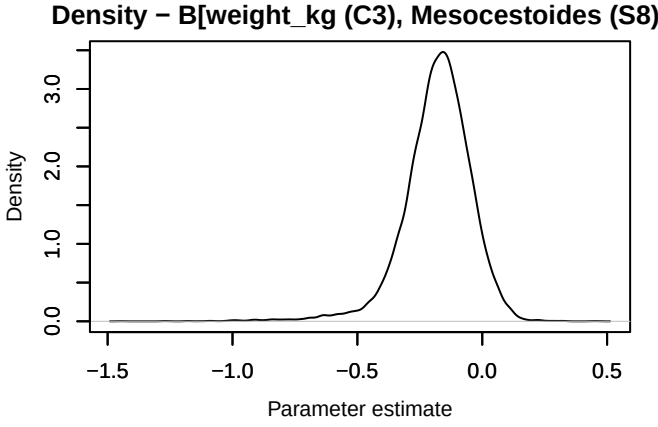

Trace − B[(Intercept) (C1), Mesocestoides (S8)]
Value
20
0
−20
−60
15000
16000
17000
18000
19000
20000
Iteration

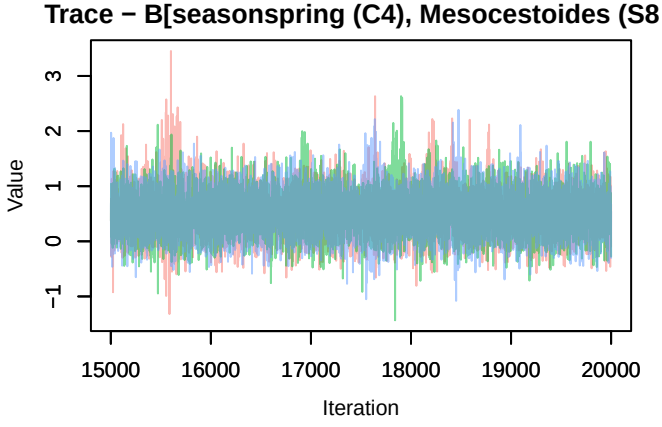

Density − B[(Intercept) (C1), Mesocestoides (S8)]
Density
0.06
0.04
0.02
0.00
−80
−60
−40
−20
0
20
40
Parameter estimate

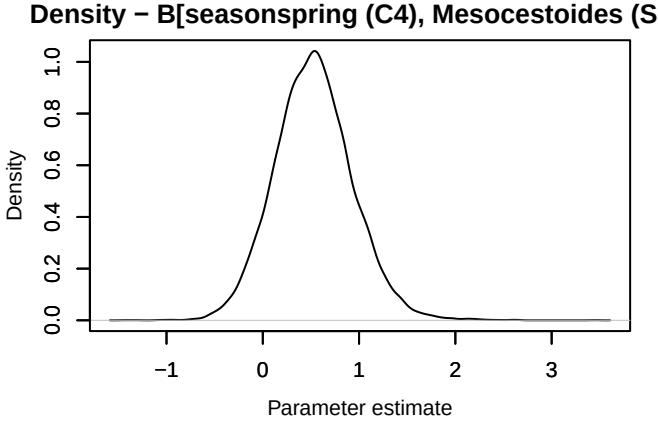

Trace − B[sexmale (C2), Mesocestoides (S8)]
Value
Iteration

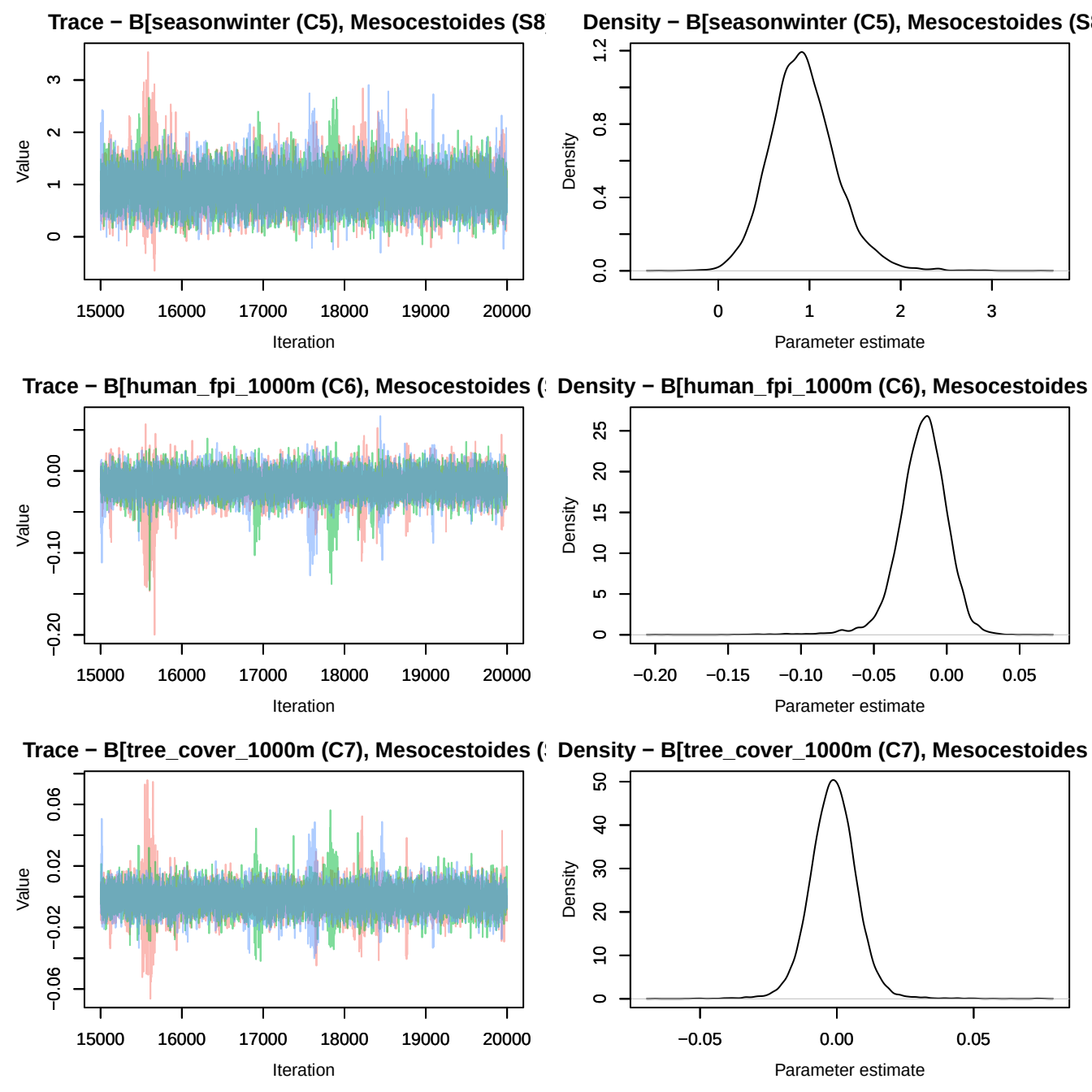

Density − B[sexmale (C2), Mesocestoides (S8)]
Density
Parameter estimate

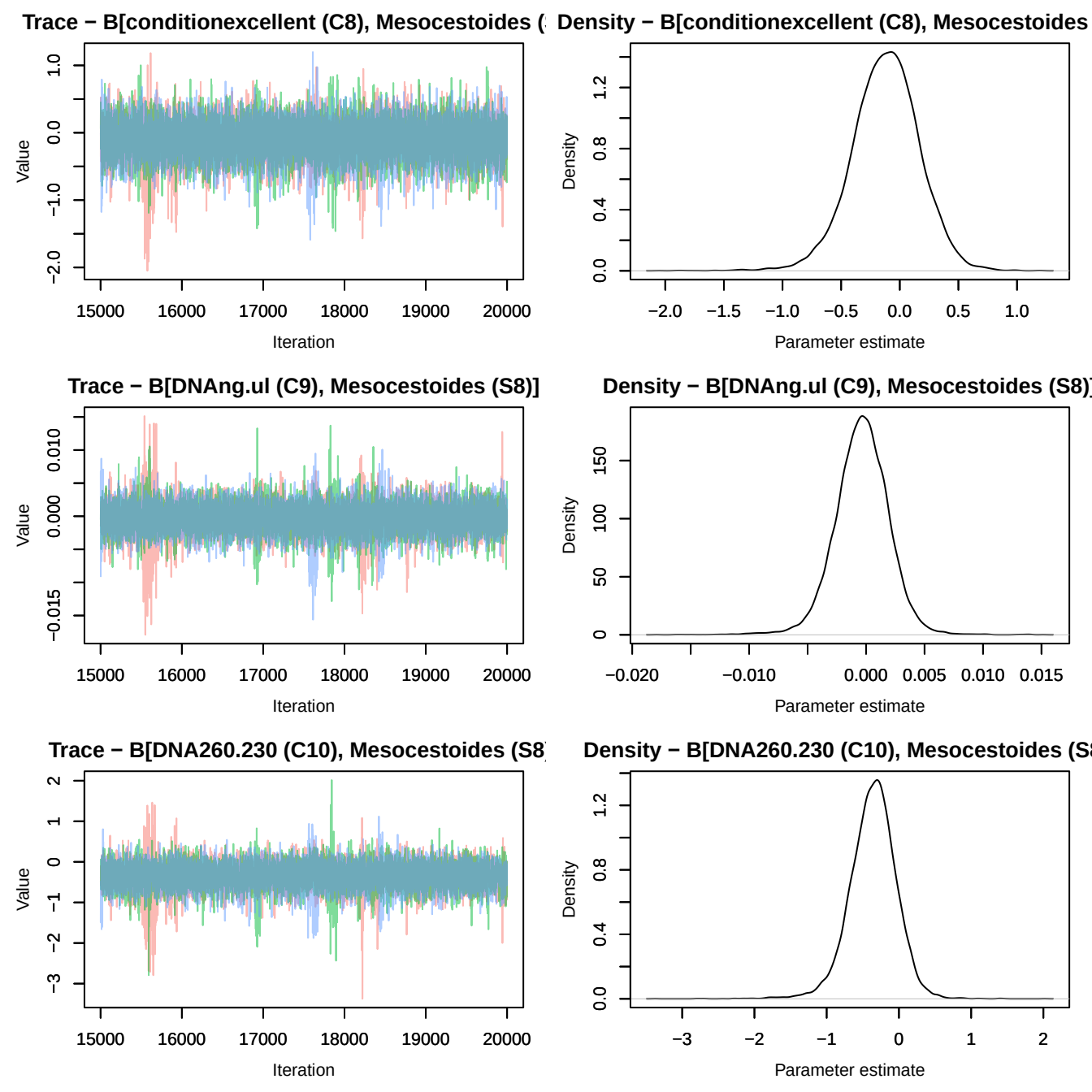

Trace − B[weight_kg (C3), Mesocestoides (S8)]
Value
Iteration

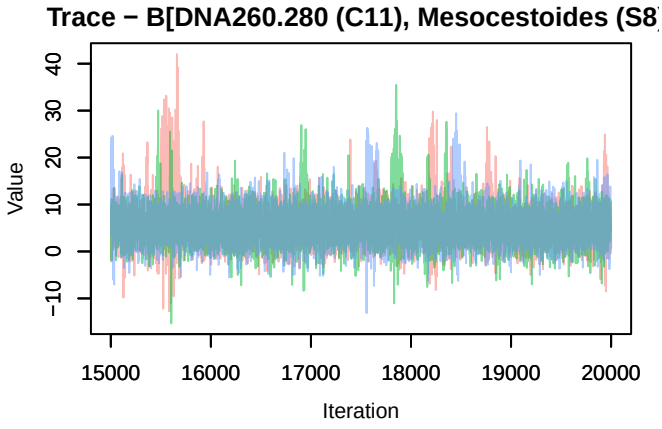

Density − B[weight_kg (C3), Mesocestoides (S8)
Density
Parameter estimate

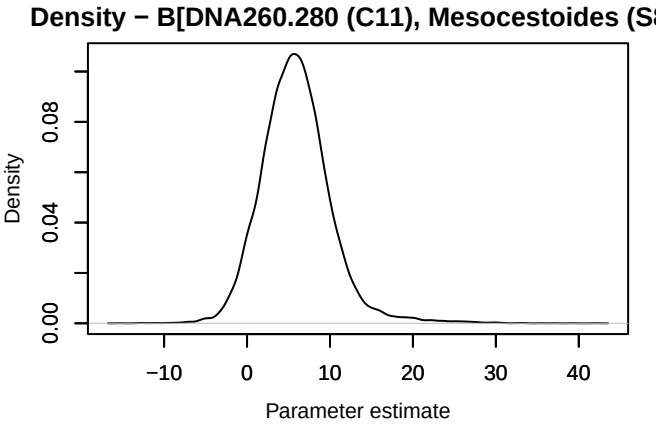

Trace − B[seasonspring (C4), Mesocestoides (S8
Value
Iteration

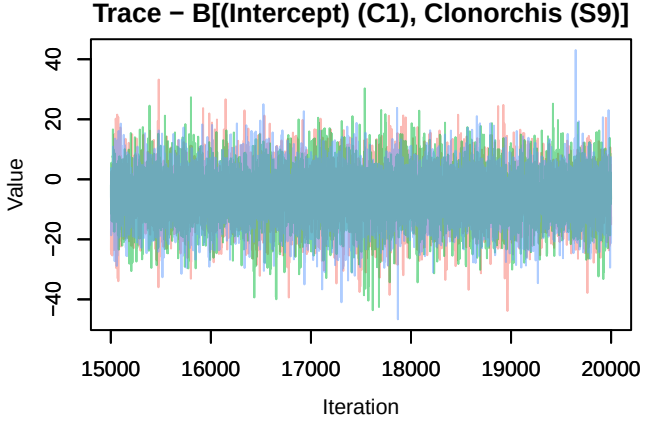

Density − B[seasonspring (C4), Mesocestoides (S
Density
Parameter estimate

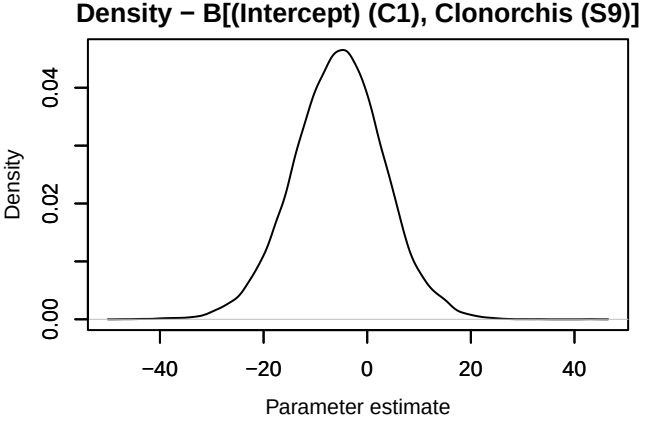

Trace − B[seasonwinter (C5), Mesocestoides (S8
Value
Iteration
Density − B[seasonwinter (C5), Mesocestoides (S
Density
Parameter estimate
Trace − B[human_fpi_1000m (C6), Mesocestoides (
Value
Iteration
Density − B[human_fpi_1000m (C6), Mesocestoides
Density
Parameter estimate
Trace − B[tree_cover_1000m (C7), Mesocestoides (
Value
Iteration
Density − B[tree_cover_1000m (C7), Mesocestoides
Density
Parameter estimate

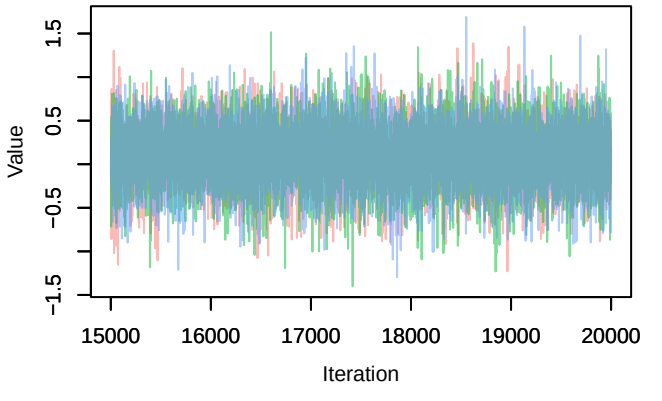

Trace − B[conditionexcellent (C8), Mesocestoides (
Density − B[conditionexcellent (C8), Mesocestoides
Value
Iteration
Density
Parameter estimate
Trace − B[DNAng.ul (C9), Mesocestoides (S8)]
Density − B[DNAng.ul (C9), Mesocestoides (S8)]
Value
Iteration
Density
Parameter estimate
Trace − B[DNA260.230 (C10), Mesocestoides (S8
Density − B[DNA260.230 (C10), Mesocestoides (S8
Value
Iteration
Density
Parameter estimate

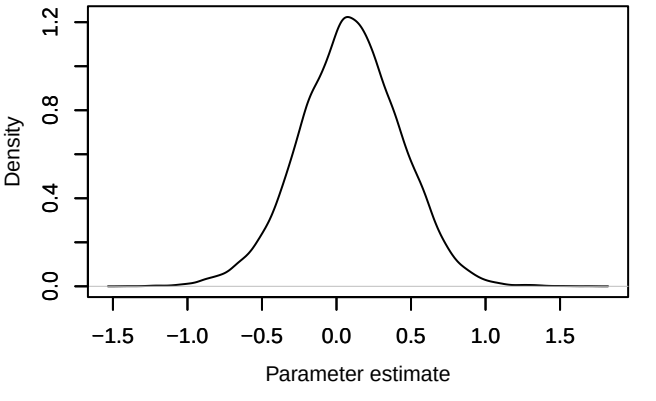

Trace − B[DNA260.280 (C11), Mesocestoides (S8
Value
40
30
20
10
0
−10
15000
16000
17000
18000
19000
20000
Iteration

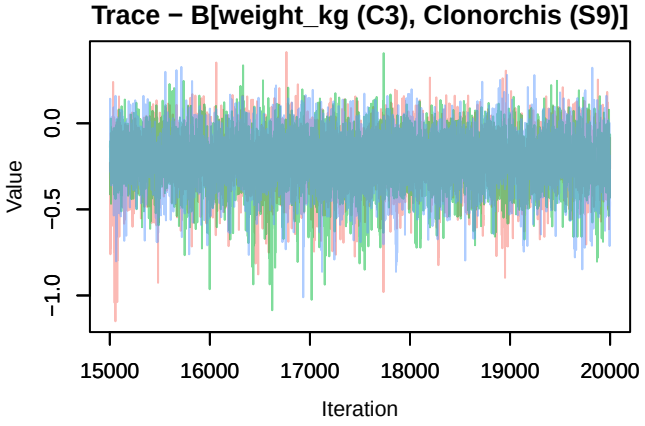

Density − B[DNA260.280 (C11), Mesocestoides (S
Density
0.08
0.04
0.00
−10
0
10
20
30
40
Parameter estimate

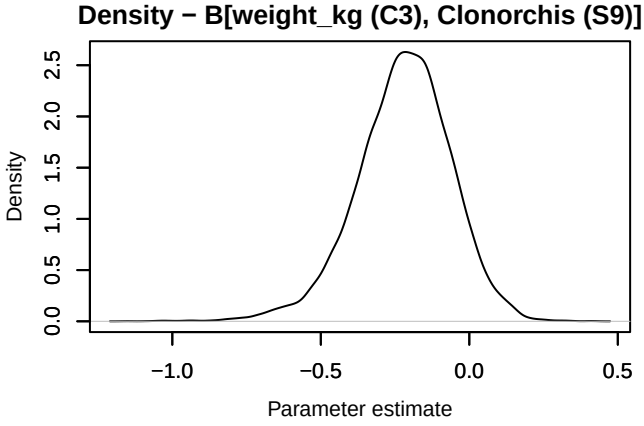

Trace − B[(Intercept) (C1), Clonorchis (S9)]
Value
40
20
0
−20
−40
15000
16000
17000
18000
19000
20000
Iteration

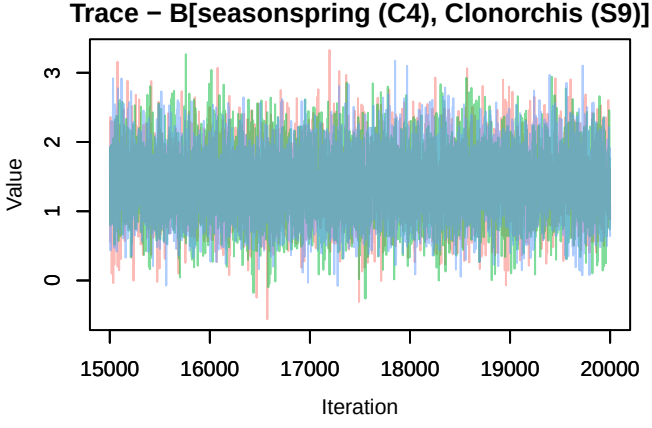

Density − B[(Intercept) (C1), Clonorchis (S9)]
Density
0.04
0.02
0.00
−40
−20
0
20
40
Parameter estimate

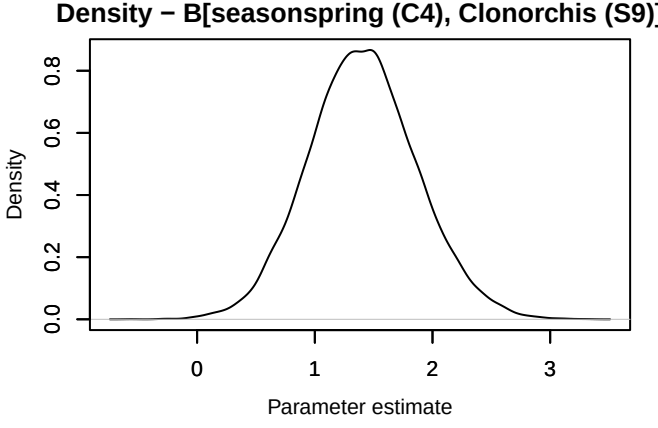

Trace − B[sexmale (C2), Clonorchis (S9)]
Value
1.5
0.5
−0.5
−1.5
15000
16000
17000
18000
19000
20000
Iteration

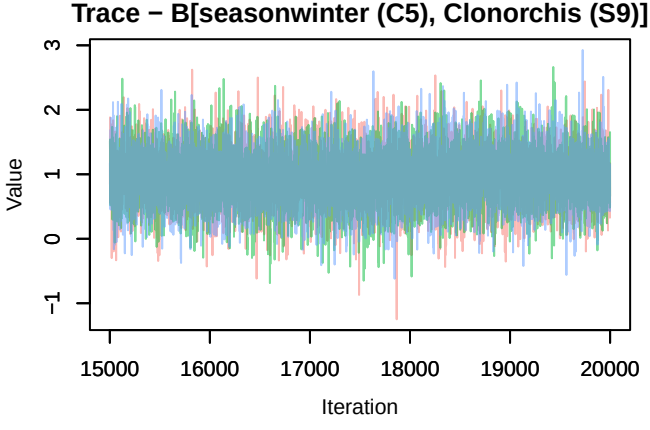

Density − B[sexmale (C2), Clonorchis (S9)]
Density
1.2
0.8
0.4
0.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Parameter estimate

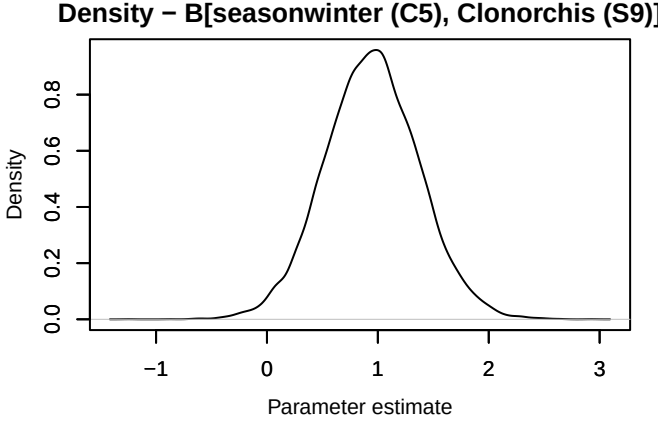

Trace − B[weight_kg (C3), Clonorchis (S9)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−1.0
−0.5
0.0

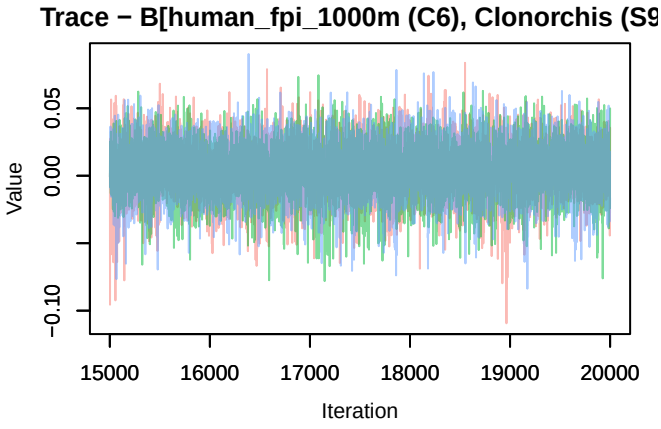

Density − B[weight_kg (C3), Clonorchis (S9)]
Density
Parameter estimate
0.0
0.5
1.0
1.5
2.0
2.5
−1.0
−0.5
0.0
0.5

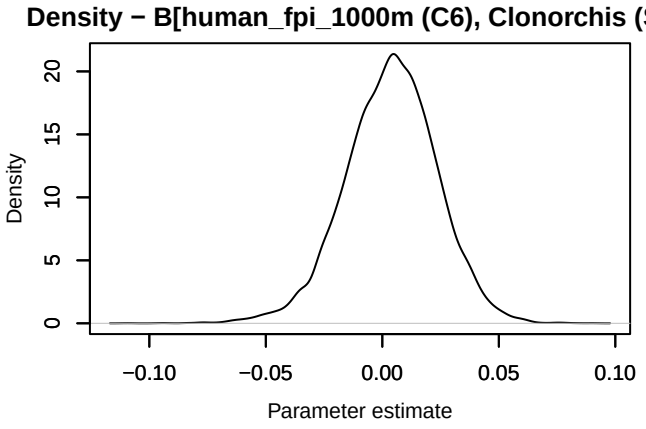

Trace − B[seasonspring (C4), Clonorchis (S9)]
Value
Iteration
15000
16000
17000
18000
19000
20000
0
1
2
3

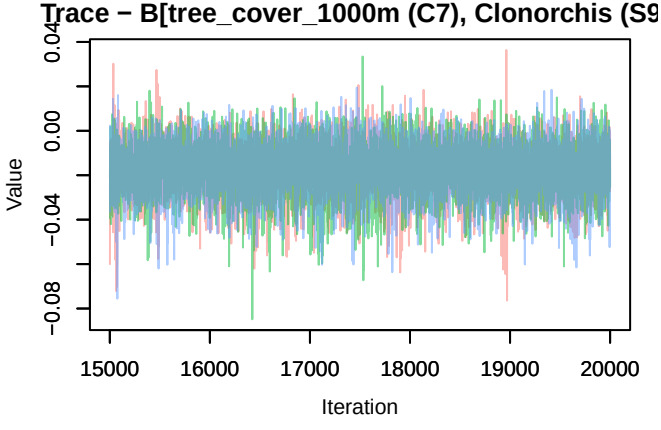

Density − B[seasonspring (C4), Clonorchis (S9)]
Density
Parameter estimate
0.0
0.2
0.4
0.6
0.8
0
1
2
3

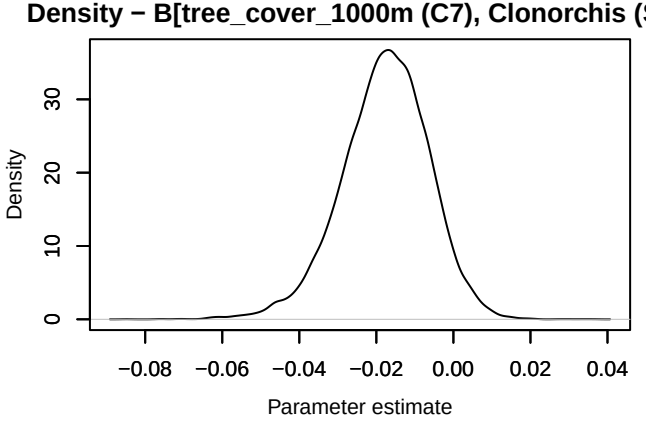

Trace − B[seasonwinter (C5), Clonorchis (S9)]
Value
Iteration
15000
16000
17000
18000
19000
20000
−1
0
1
2
3

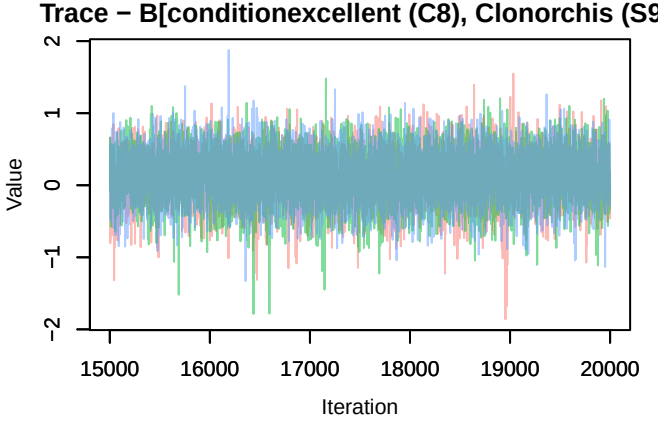

Density − B[seasonwinter (C5), Clonorchis (S9)]
Density
Parameter estimate
0.0
0.2
0.4
0.6
0.8
−1
0
1
2
3

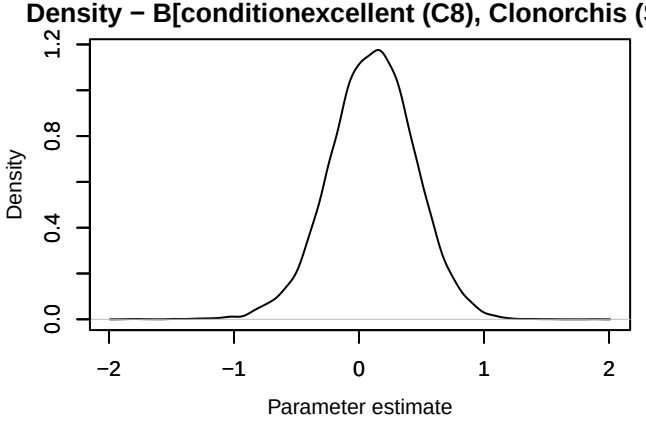

Trace − B[human_fpi_1000m (C6), Clonorchis (S9
Value
0.05
0.00
−0.10
15000
16000
17000
18000
19000
20000
Iteration

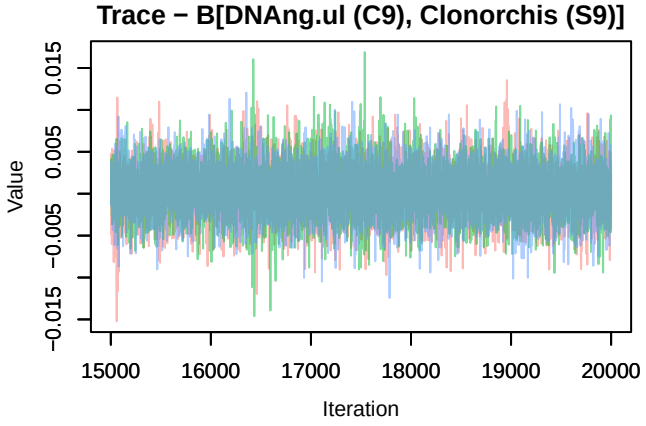

Density − B[human_fpi_1000m (C6), Clonorchis (S
Density
20
15
10
5
0
−0.10
−0.05
0.00
0.05
0.10
Parameter estimate

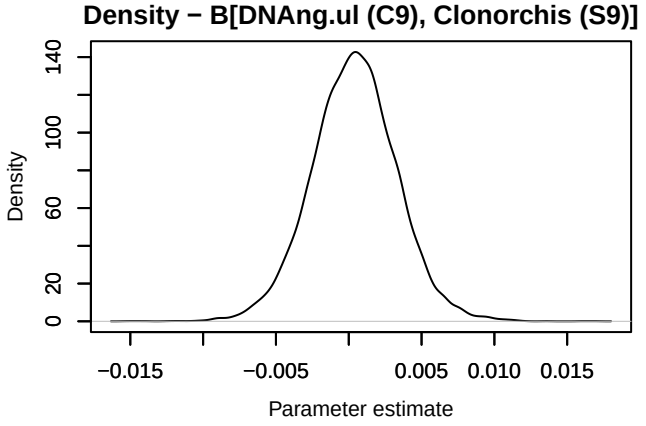

Trace − B[tree_cover_1000m (C7), Clonorchis (S9
Value
0.04
0.00
−0.04
−0.08
15000
16000
17000
18000
19000
20000
Iteration

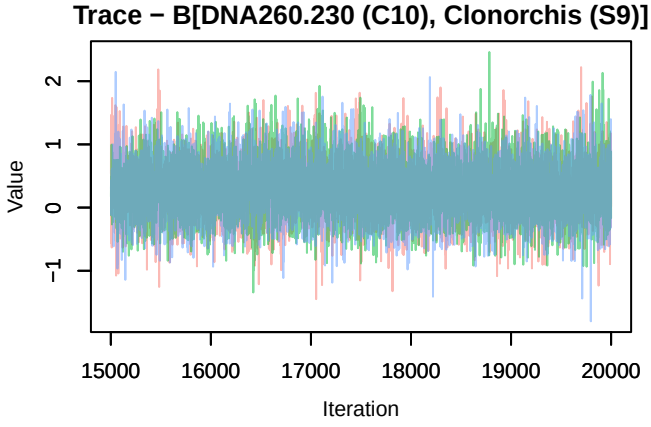

Density − B[tree_cover_1000m (C7), Clonorchis (S
Density
30
20
10
0
−0.08
−0.06
−0.04
−0.02
0.00
0.02
0.04
Parameter estimate

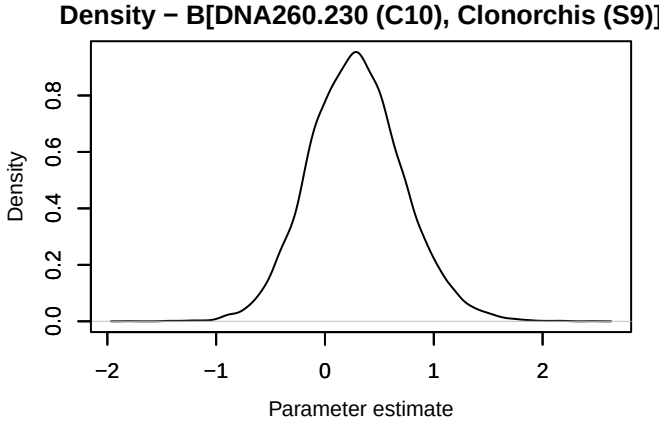

Trace − B[conditionexcellent (C8), Clonorchis (S9
Value
2
1
0
−1
−2
15000
16000
17000
18000
19000
20000
Iteration

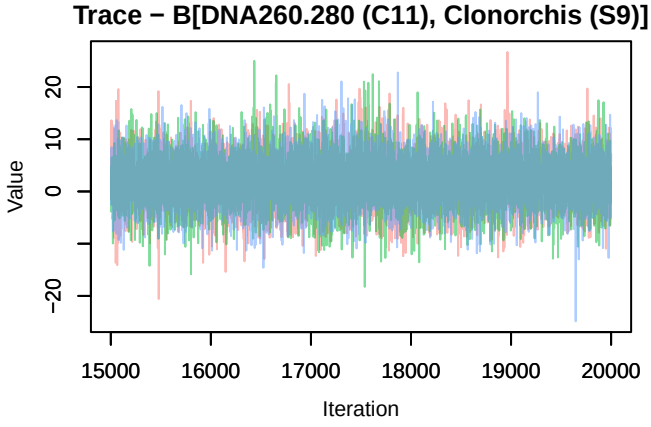

Density − B[conditionexcellent (C8), Clonorchis (S
Density
1.2
0.8
0.4
0.0
−2
−1
0
1
2
Parameter estimate

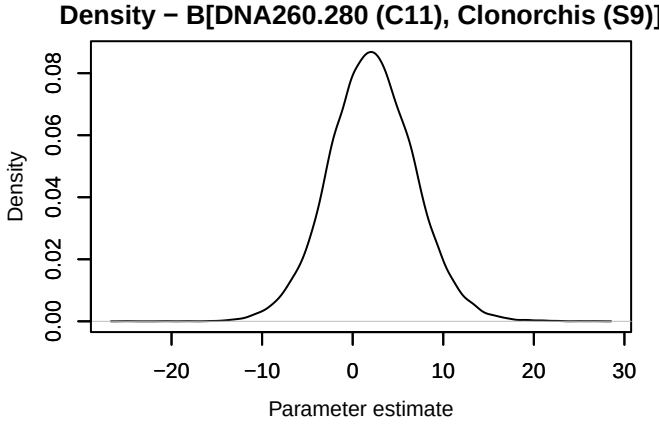

Trace − B[DNAng.ul (C9), Clonorchis (S9)]
Value
0.015
0.005
−0.005
−0.015
15000
16000
17000
18000
19000
20000
Iteration

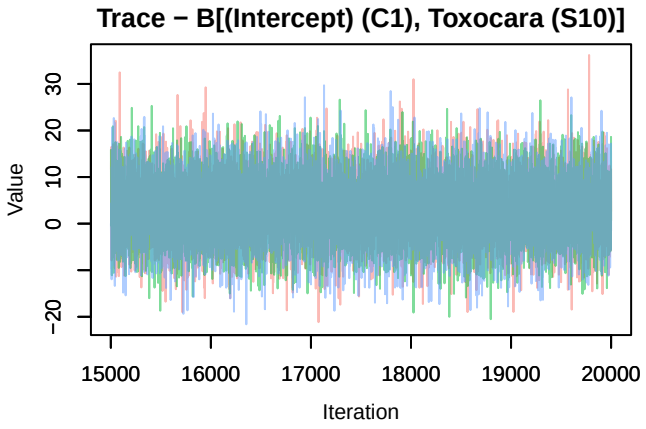

Density − B[DNAng.ul (C9), Clonorchis (S9)]
Density
140
100
60
20
0
−0.015
−0.005
0.005
0.010
0.015
Parameter estimate

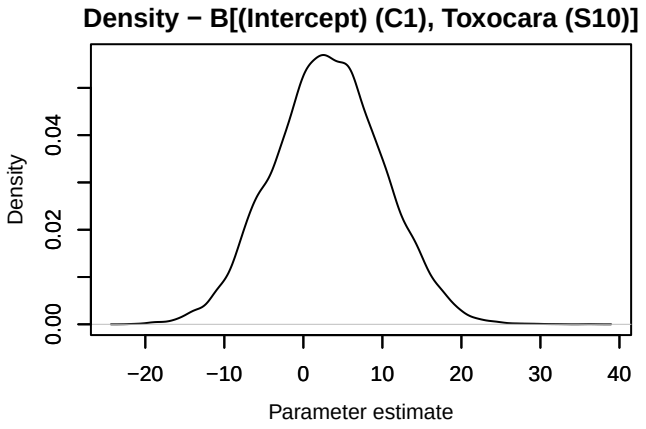

Trace − B[DNA260.230 (C10), Clonorchis (S9)]
Value
2
1
0
−1
15000
16000
17000
18000
19000
20000
Iteration

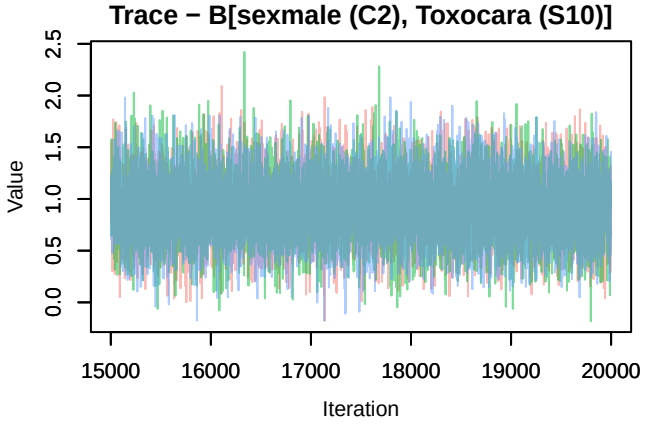

Density − B[DNA260.230 (C10), Clonorchis (S9)]
Density
0.8
0.6
0.4
0.2
0.0
−2
−1
0
1
2
Parameter estimate

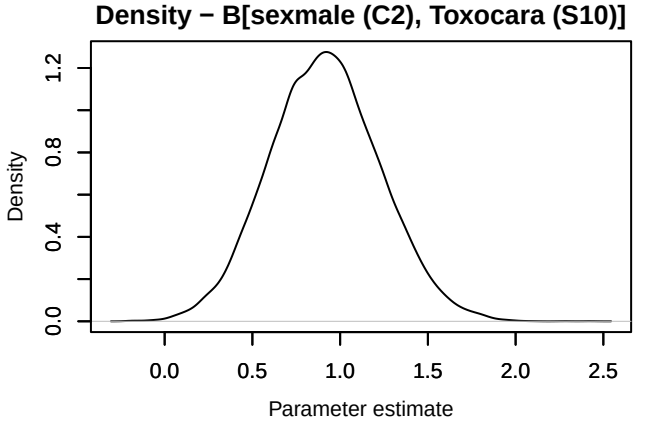

Trace − B[DNA260.280 (C11), Clonorchis (S9)]
Value
20
10
0
−20
15000
16000
17000
18000
19000
20000
Iteration

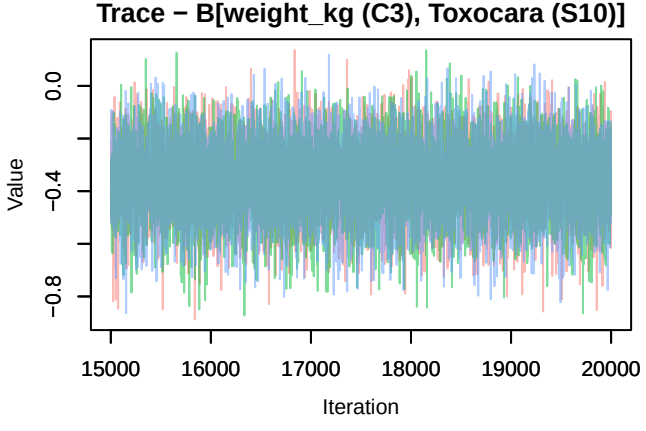

Density − B[DNA260.280 (C11), Clonorchis (S9)]
Density
0.08
0.06
0.04
0.02
0.00
−20
−10
0
10
20
30
Parameter estimate

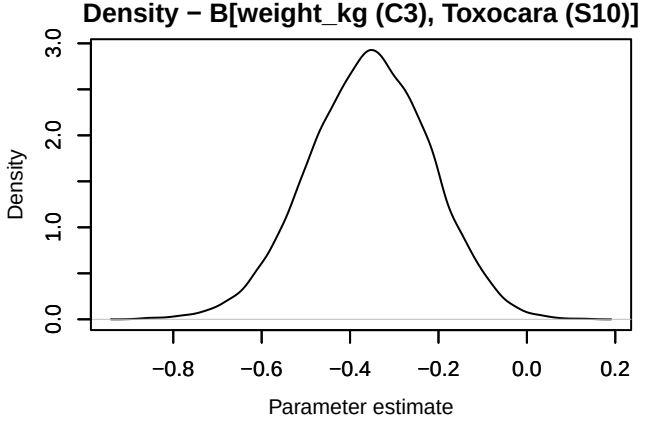

Trace − B[(Intercept) (C1), Toxocara (S10)]
Value
30
20
10
0
−20
15000
16000
17000
18000
19000
20000
Iteration

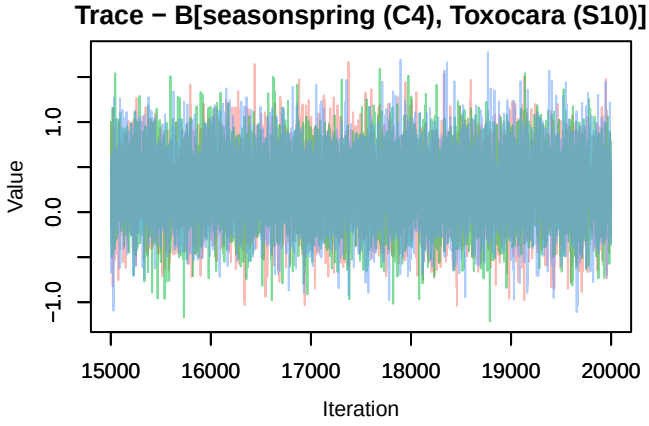

Density − B[(Intercept) (C1), Toxocara (S10)]
Density
0.04
0.02
0.00
−20
−10
0
10
20
30
40
Parameter estimate

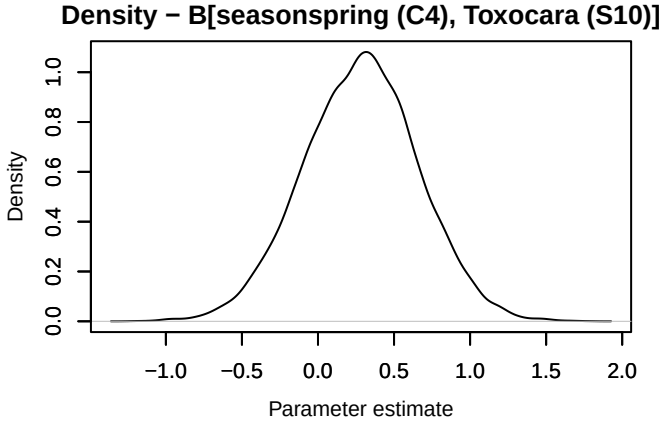

Trace − B[sexmale (C2), Toxocara (S10)]
Value
2.5
2.0
1.5
1.0
0.5
0.0
15000
16000
17000
18000
19000
20000
Iteration

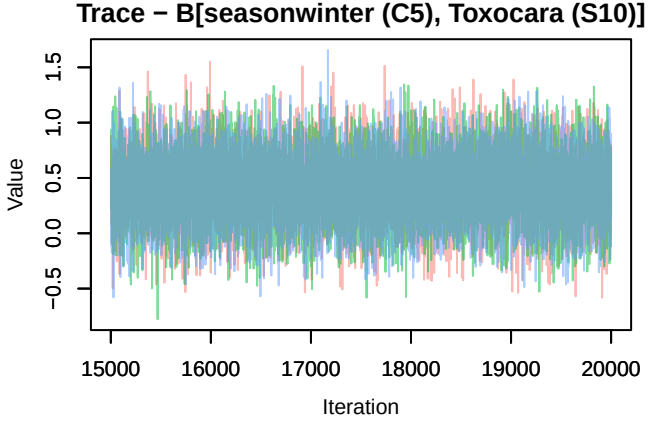

Density − B[sexmale (C2), Toxocara (S10)]
Density
1.2
0.8
0.4
0.0
0.0
0.5
1.0
1.5
2.0
2.5
Parameter estimate

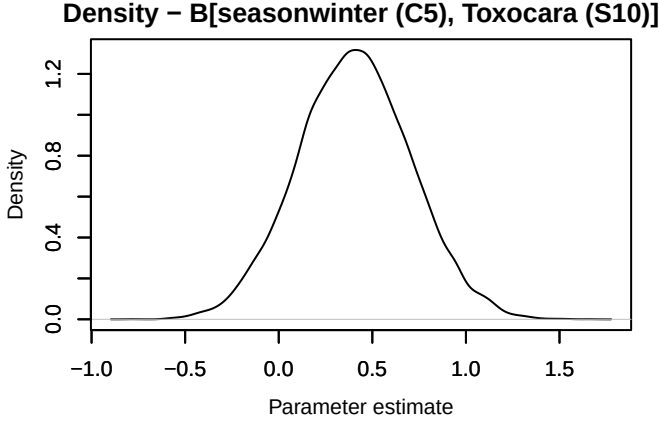

Trace − B[weight_kg (C3), Toxocara (S10)]
Value
0.0
−0.4
−0.8
15000
16000
17000
18000
19000
20000
Iteration

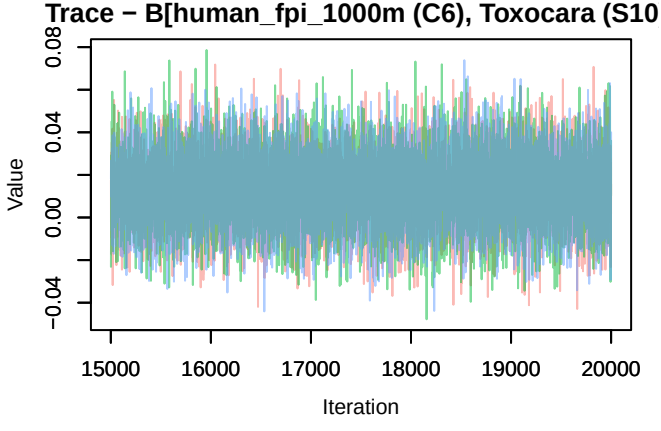

Density − B[weight_kg (C3), Toxocara (S10)]
Density
3.0
2.0
1.0
0.0
−0.8
−0.6
−0.4
−0.2
0.0
0.2
Parameter estimate

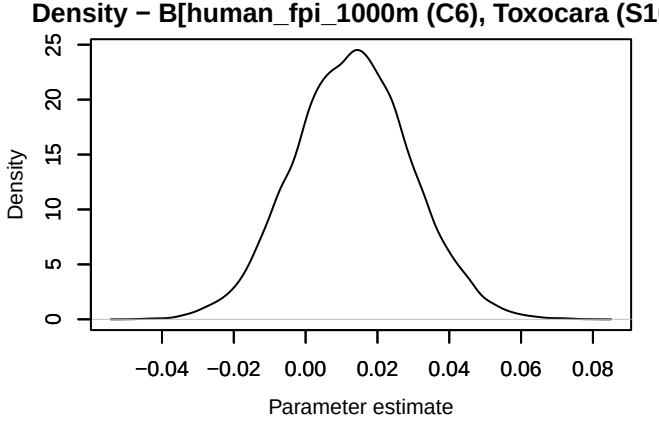

Trace − B[seasonspring (C4), Toxocara (S10)]
Value
1.0
0.0
−1.0
15000
16000
17000
18000
19000
20000
Iteration

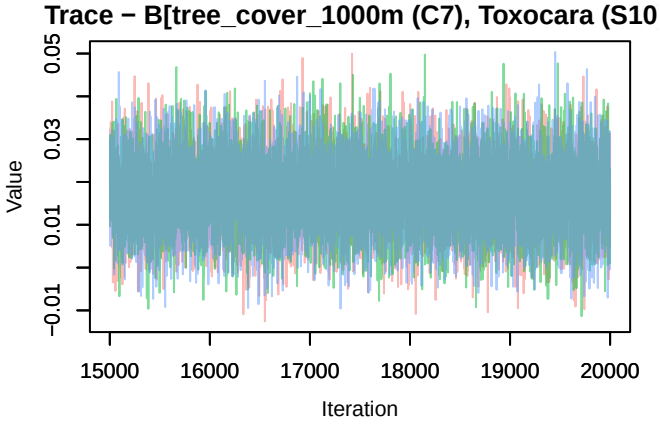

Density − B[seasonspring (C4), Toxocara (S10)]
Density
1.0
0.8
0.6
0.4
0.2
0.0
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
Parameter estimate

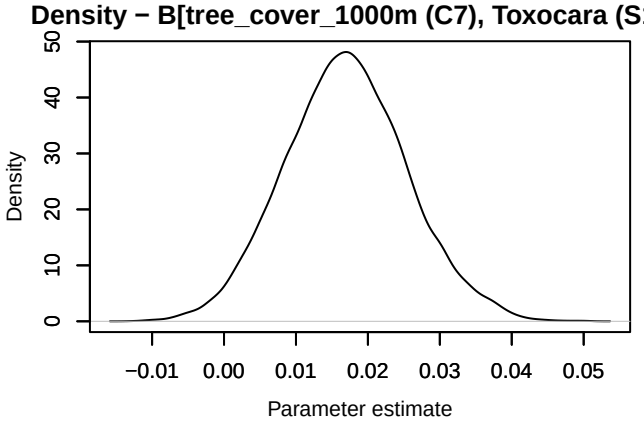

Trace − B[seasonwinter (C5), Toxocara (S10)]
Value
1.5
1.0
0.5
0.0
−0.5
15000
16000
17000
18000
19000
20000
Iteration

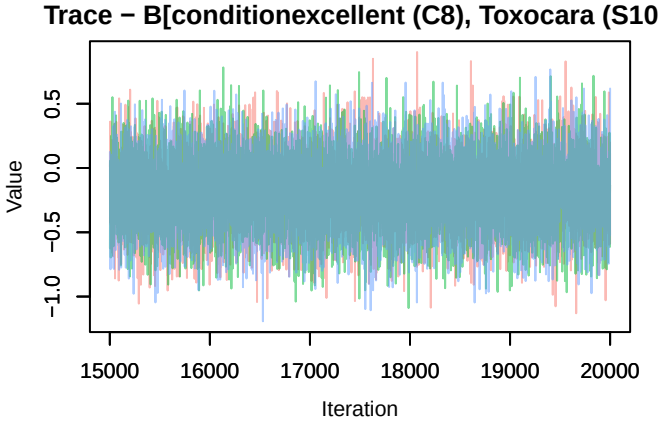

Density − B[seasonwinter (C5), Toxocara (S10)]
Density
1.2
0.8
0.4
0.0
−1.0
−0.5
0.0
0.5
1.0
1.5
Parameter estimate

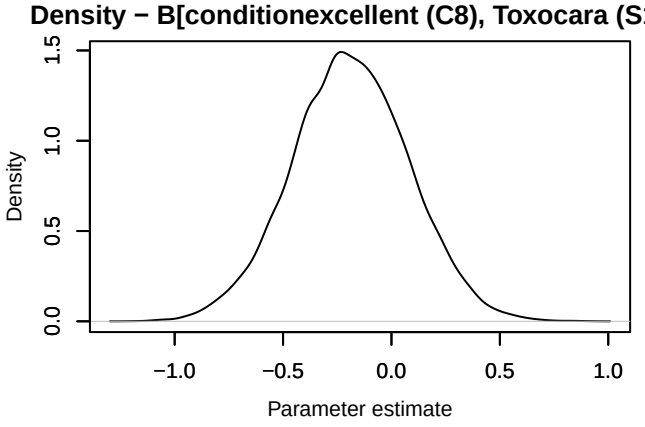

Trace − B[human_fpi_1000m (C6), Toxocara (S10
Value
0.08
0.04
0.00
−0.04
15000
16000
17000
18000
19000
20000
Iteration

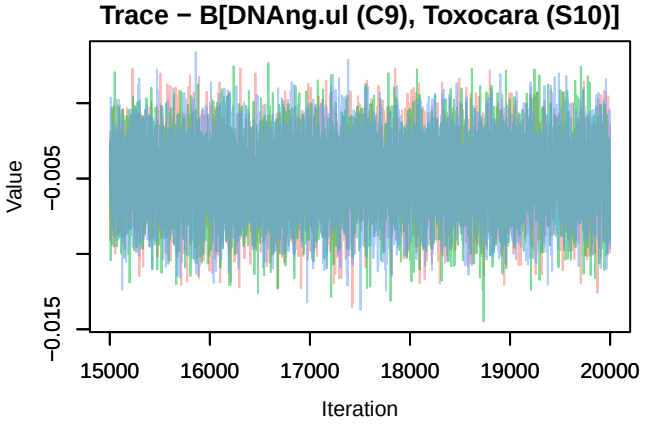

Density − B[human_fpi_1000m (C6), Toxocara (S1
Density
25
20
15
10
5
0
−0.04
−0.02
0.00
0.02
0.04
0.06
0.08
Parameter estimate

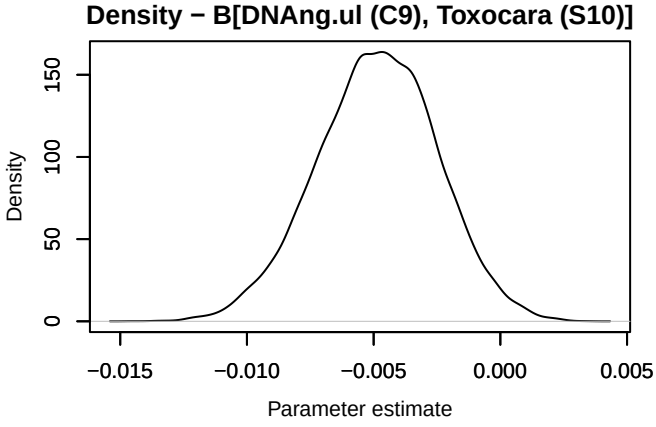

Trace − B[tree_cover_1000m (C7), Toxocara (S10
Value
0.05
0.03
0.01
−0.01
15000
16000
17000
18000
19000
20000
Iteration

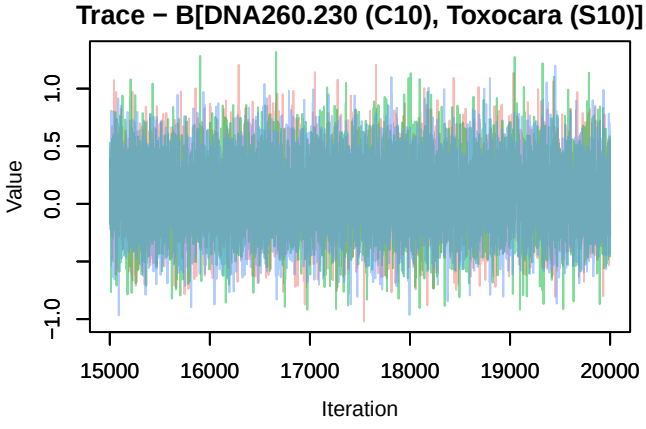

Density − B[tree_cover_1000m (C7), Toxocara (S1
Density
50
40
30
20
10
0
−0.01
0.00
0.01
0.02
0.03
0.04
0.05
Parameter estimate

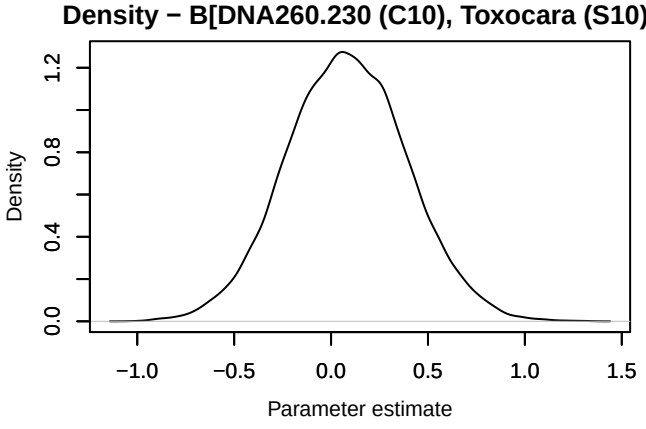

Trace − B[conditionexcellent (C8), Toxocara (S10
Value
0.5
0.0
−0.5
−1.0
15000
16000
17000
18000
19000
20000
Iteration

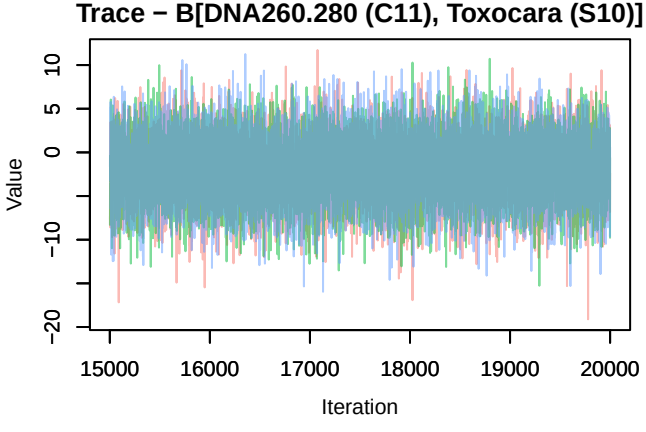

Density − B[conditionexcellent (C8), Toxocara (S1
Density
1.5
1.0
0.5
0.0
−1.0
−0.5
0.0
0.5
1.0
Parameter estimate

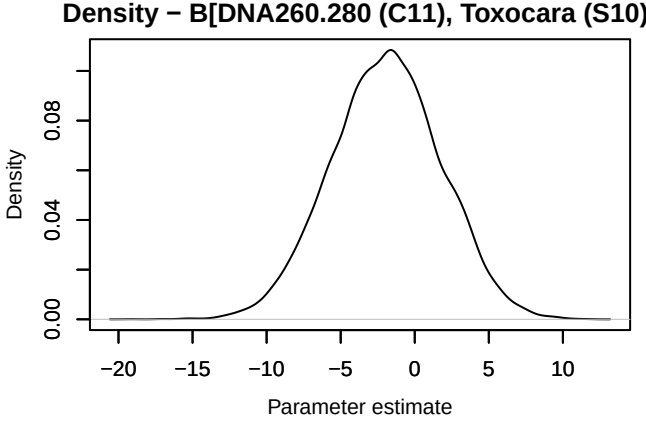

Trace − B[DNAng.ul (C9), Toxocara (S10)]
Value
−0.005
−0.015
15000
16000
17000
18000
19000
20000
Iteration


Density − B[DNAng.ul (C9), Toxocara (S10)]
Density
150
100
50
0
−0.015
−0.010
−0.005
0.000
0.005
Parameter estimate


Trace − B[DNA260.230 (C10), Toxocara (S10)]
Value
1.0
0.5
0.0
−1.0
15000
16000
17000
18000
19000
20000
Iteration


Density − B[DNA260.230 (C10), Toxocara (S10)]
Density
1.2
0.8
0.4
0.0
−1.0
−0.5
0.0
0.5
1.0
1.5
Parameter estimate


Trace − B[DNA260.280 (C11), Toxocara (S10)]
Value
10
5
0
−10
−20
15000
16000
17000
18000
19000
20000
Iteration


Density − B[DNA260.280 (C11), Toxocara (S10)]
Density
0.08
0.04
0.00
−20
−15
−10
−5
0
5
10
Parameter estimate