

```
1 data(sunfish.tree)
2 data(sunfish.data)
3 ## extract character of interest
4 gw<-setNames(sunfish.data$gape.width,
5   rownames(sunfish.data))
6 ## run penalized-likelihood optimization
7 ## lambda=0.1 is arbitrary
8 fitBM<-multirateBM(sunfish.tree,gw,
9   lambda=0.01)
10 ## print and plot the results
11 print(fitBM)
12 plot(fitBM,ftype="i",fsize=0.8,lwd=6,
13   outline=TRUE)
14
```

14:1 (Top Level) R Script

Console Terminal Background Jobs

R 4.2.2 ~ /

+ lambda=0.01)

Beginning optimization....

Optimization iteration 1. Using "L-BFGS-" optimization method.

Best (penalized) log-likelihood so far: 38.4615

Done optimization.

> ## print and plot the results

> print(fitBM)

Multi-rate Brownian model using multirateBM.

Fitted rates:

Acantharchus_pomotis	Lepomis_gibbosus	Lepomis_microlophus	Lepomis_punctatus
0.060276	0.038039	0.043168	0.048633
Lepomis_miniatus	Lepomis_auritus	Lepomis_marginatus	Lepomis_megalotis
0.042838	0.254773	0.245238	0.306099 ....

lambda penalty term: 0.01

log-likelihood: 40.148315

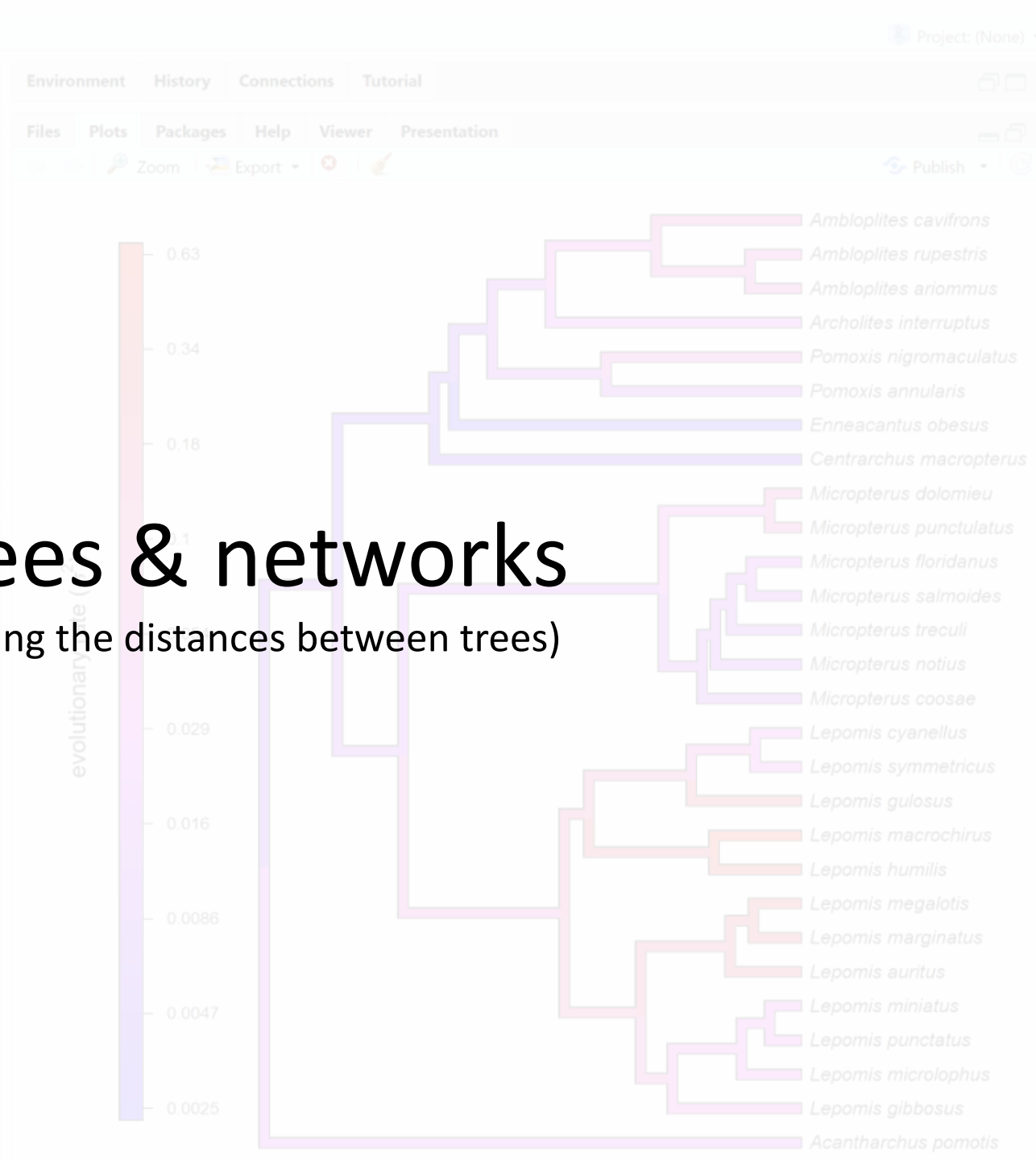
AIC: 31.703369

R thinks it has found a solution.

> plot(fitBM,ftype="i",fsize=0.8,lwd=6,
+ outline=TRUE)
>

# Consensus trees & networks

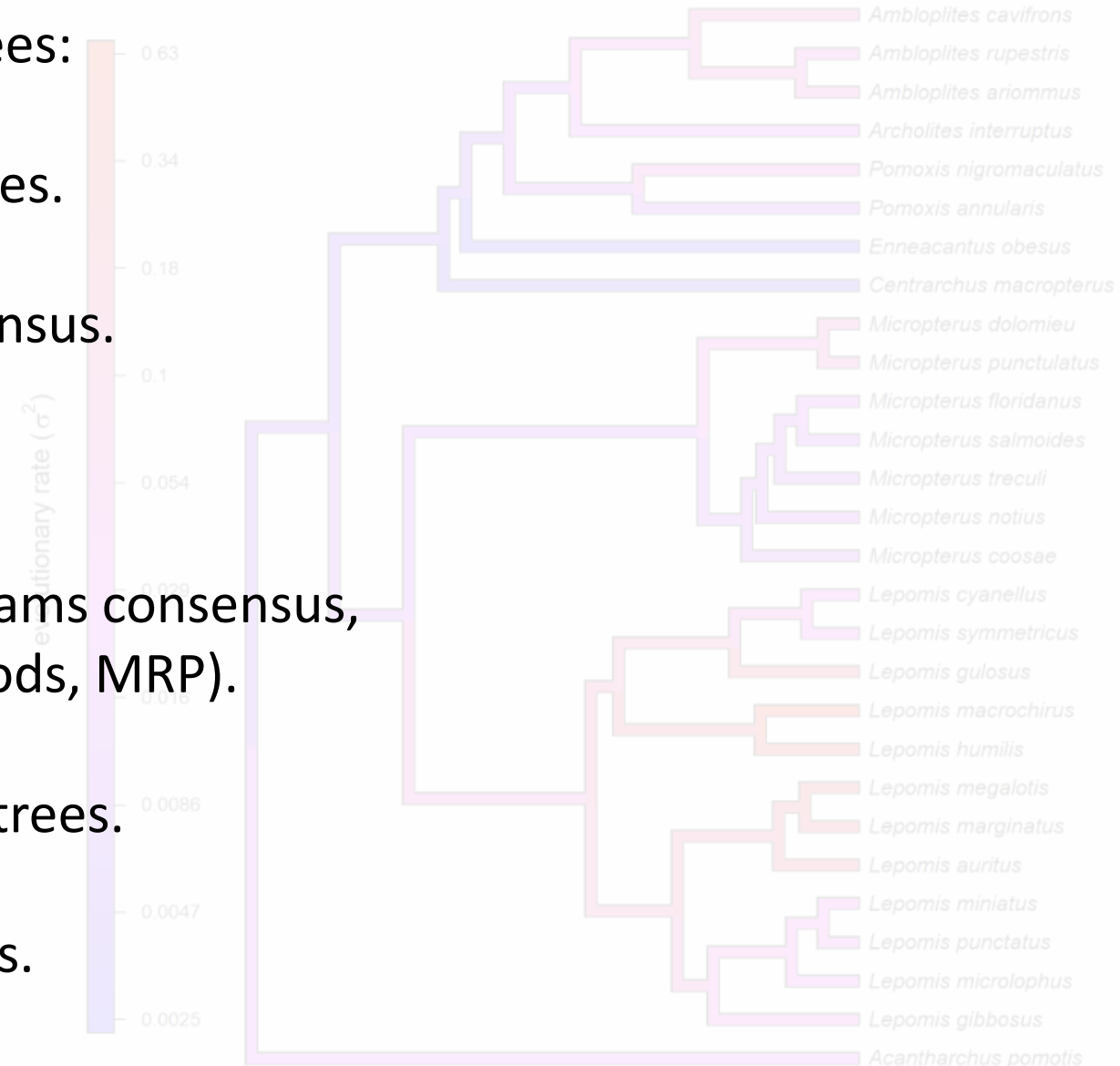
(with a digression on measuring the distances between trees)



# Consensus trees

Types of consensus trees:

1. Strict consensus trees.
2. Majority rule consensus.
3. “X-%” consensus.
4. Other methods (Adams consensus, compatibility methods, MRP).
5. Minimum distance trees.
6. Consensus networks.



```
1 data(sunfish.tree)
2 data(sunfish.data)
3 ## extract character of interest
4 gw<-setNames(sunfish.data$gape.width,
5   rownames(sunfish.data))
6 ## run penalized-likelihood optimization
7 ## lambda=0.1 is arbitrary
8 fitBM<-multirateBM(sunfish.tree,gw,
9   lambda=0.01)
10 ## print and plot the results
11 print(fitBM)
12 plot(fitBM,ftype="i",fsize=0.8,lwd=6,
13   outline=TRUE)
14
```

14:1 (Top Level)

Console Terminal Background Jobs

R 4.2.2 ~ /

```
+ lambda=0.01)
```

Beginning optimization....

Optimization iteration 1. Using "L-BFGS-B" optimization method.

Best (penalized) log-likelihood so far: 38.4615

Done optimization.

```
> ## print and plot the results
```

```
> print(fitBM)
```

Multi-rate Brownian model using multirateBM.

Fitted rates:

```
Acantharchus_pomotis Lepomis_gibbosus Lepomis_microlophus Lepomis_punctatus
```

```
0.060276 0.038039 0.043168 0.048633
```

```
Lepomis_miniatus Lepomis_auritus Lepomis_marginatus Lepomis_megalotis
```

```
0.042838 0.254773 0.22238 0.28689
```

lambda penalty term: 0.01

log-likelihood: 40.148315

AIC: 31.703369

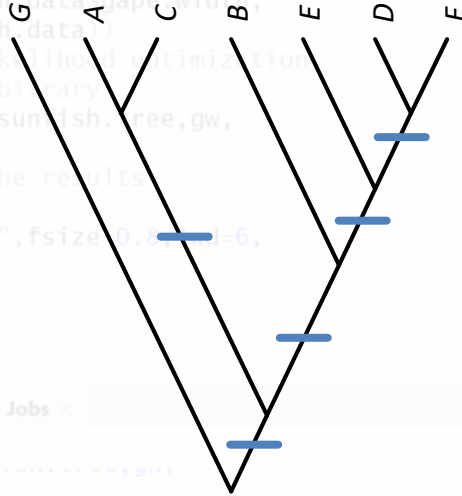
R thinks it has found a solution.

```
> plot(fitBM,ftype="i",fsize=0.8,lwd=6,
```

```
+ outline=TRUE)
```

```
>
```

# Strict consensus tree



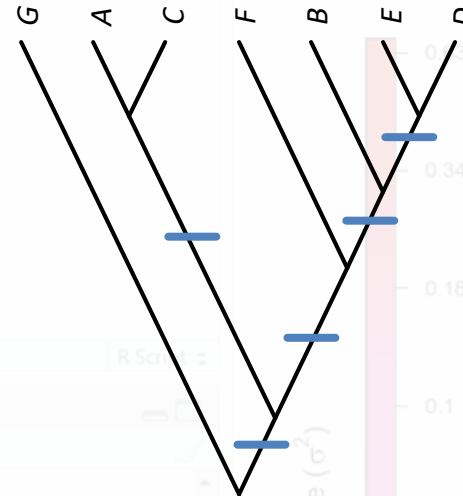
{GACBE|DF}

{GACB|EDF}

{GAC|BEDF}

{G|ACBEDF}

{AC|GBEDF}



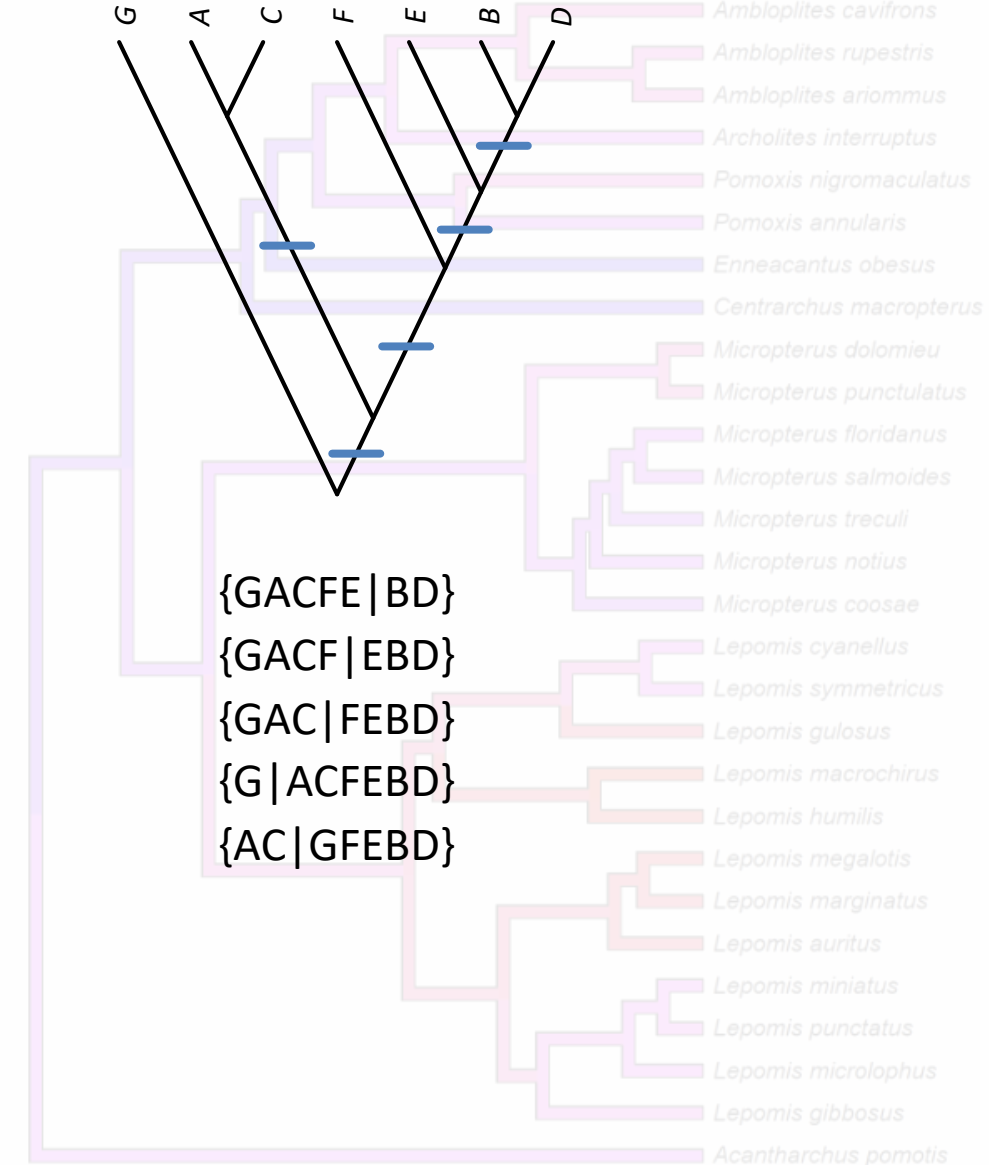
{GACFB|ED}

{GACF|BED}

{GAC|FBED}

{G|ACFBED}

{AC|GFBED}



{GACFE|BD}

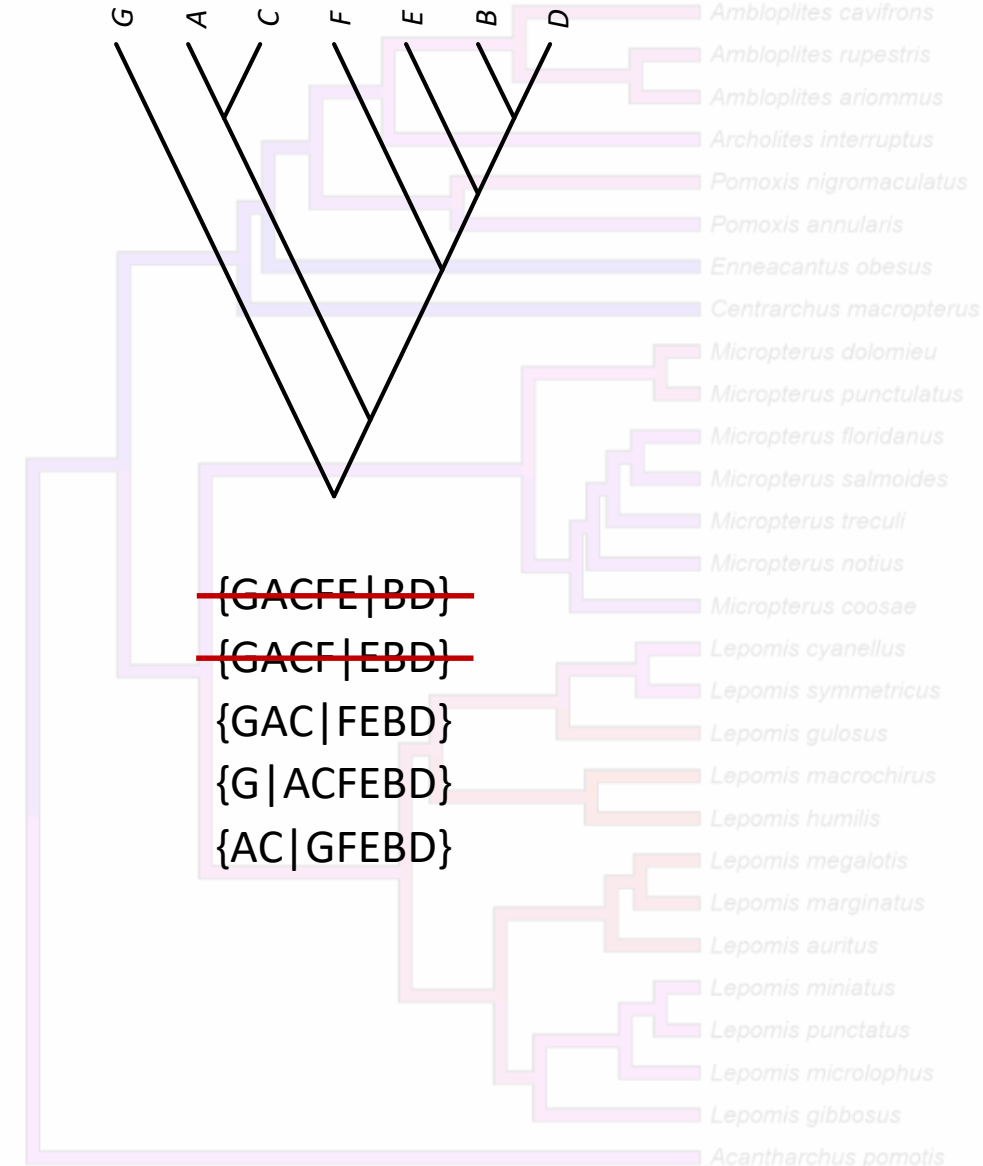
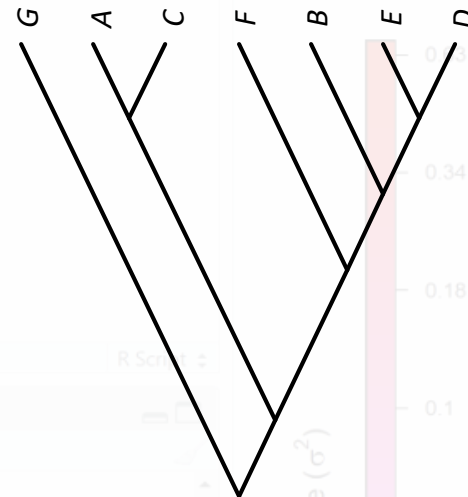
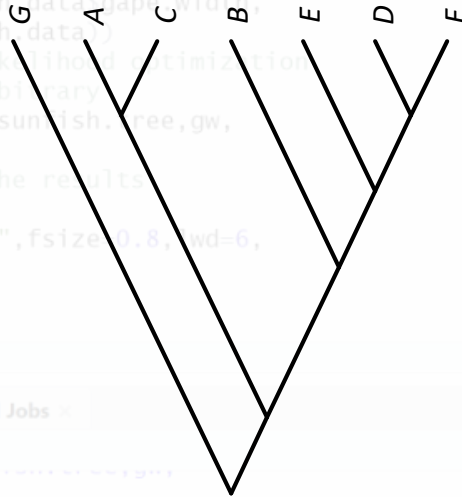
{GACF|EBD}

{GAC|FEBD}

{G|ACFEBD}

{AC|GFEBD}

# Strict consensus tree



~~{GACBE|DF}~~

~~{GACB|EDF}~~

{GAC|BEDF}

{G|ACBEDF}

{AC|GBEDF}

~~{GACFB|ED}~~

~~{GACF|BED}~~

{GAC|FBED}

{G|ACFBED}

{AC|GFBED}

~~{GACFE|BD}~~

~~{GACF|EBD}~~

{GAC|FEBD}

{G|ACFEBD}

{AC|GFEBD}

# Strict consensus tree

```
1 data(sunfish.tree)
2 data(sunfish.data)
3 ## extract character of interest
4 gw<-setNames(sunfish.data$gape.width,
5   rownames(sunfish.data))
6 ## run penalized-likelihood optimization
7 ## lambda=0.1 is arbitrary
8 fitBM<-multirateBM(sunfish.tree,gw,
9   lambda=0.01)
10 ## print and plot the results
11 print(fitBM)
12 plot(fitBM,ftype="i",fsize=0.8,lwd=6,
13   outline=TRUE)
```

{GAC|FBED}  
{G|ACFBED}  
{AC|GFBED}

14:1 (Top Level) ±

Console Terminal Background Jobs

R 4.2.2 ~ /

```
+ lambda=0.01)
```

Beginning optimization....

Optimization iteration 1. Using "L-BFGS-B" method.

Best (penalized) log-likelihood so far: -30.445

Done optimization.

```
> ## print and plot the results
```

```
> print(fitBM)
```

Multi-rate Brownian model using multirateBM.

Fitted rates:

Acantharchus_pomotis	Lepomis_gibbosus	Lepomis_microlophus	Lepomis_punctatus
0.060276	0.038039	0.043168	0.048633

Lepomis_miniatus	Lepomis_auritus	Lepomis_marginatus	Lepomis_megalotis
0.042838	0.254773	0.245238	0.306099 ....

lambda penalty term: 0.01

log-likelihood: 40.148315

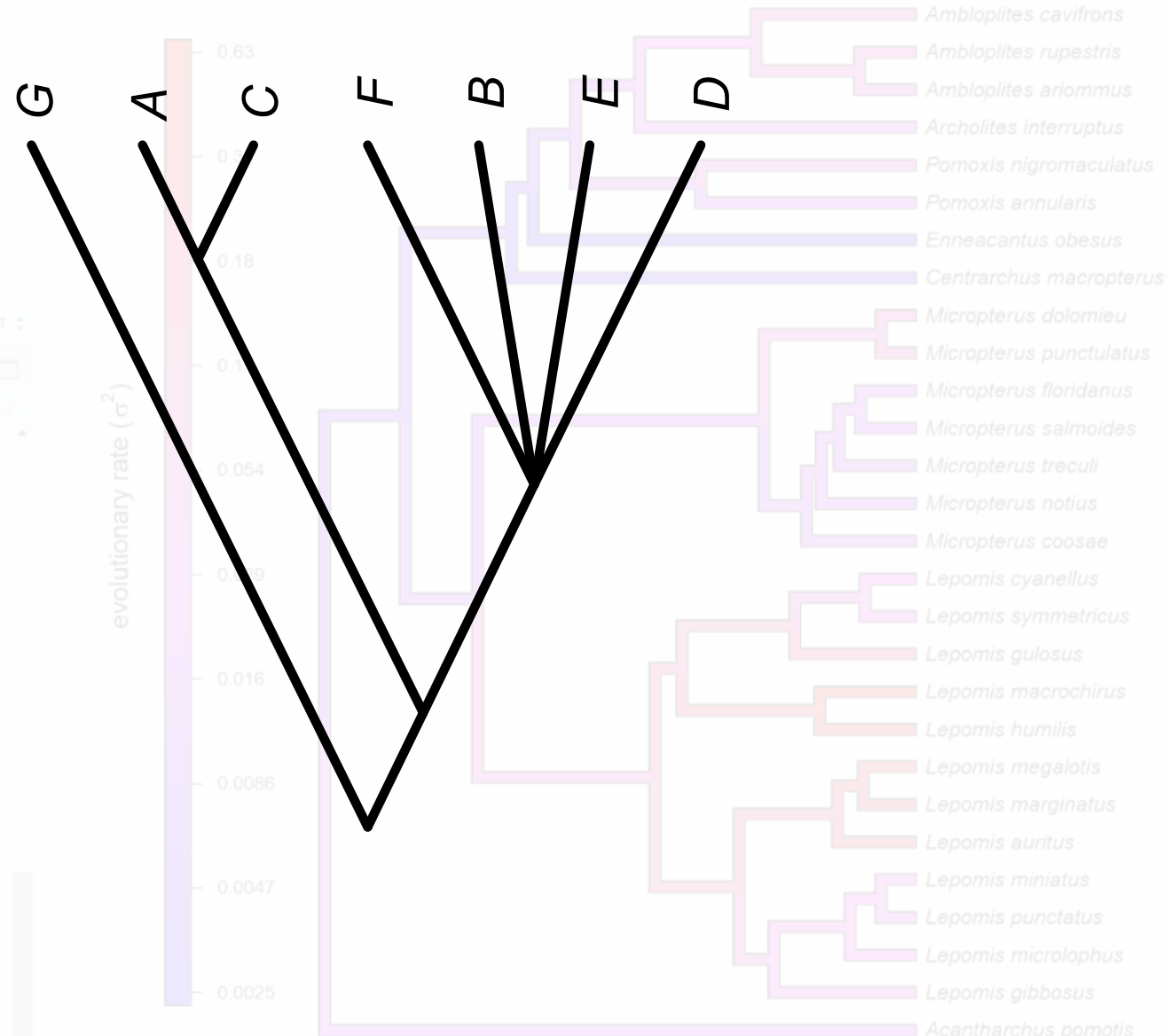
AIC: 31.703369

R thinks it has found a solution.

```
> plot(fitBM,ftype="i",fsize=0.8,lwd=6,
```

```
+   outline=TRUE)
```

```
>
```



# Consensus trees

## Types of consensus trees:

1. Strict consensus trees.

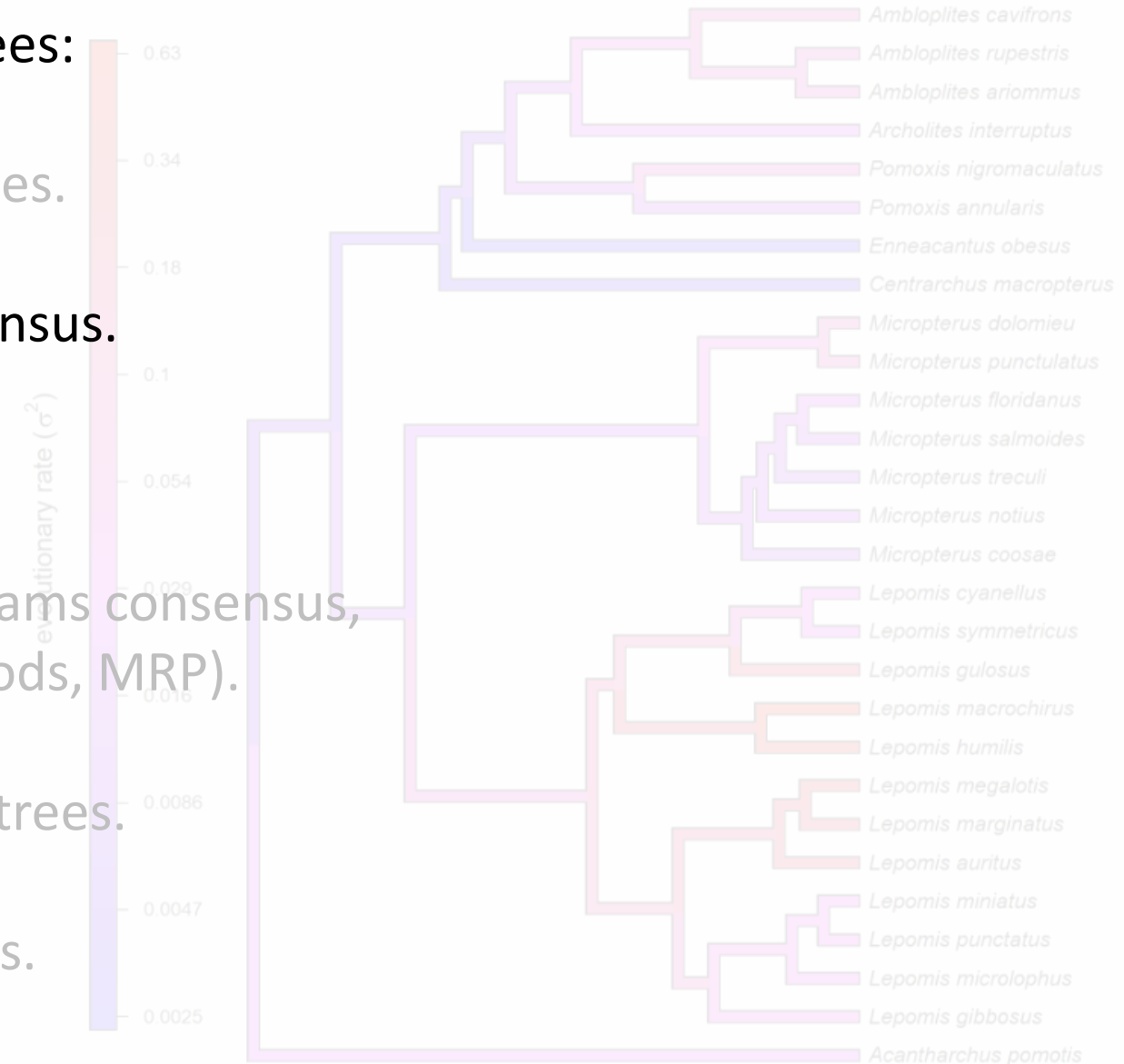
2. Majority rule consensus.

3. “X-” consensus.

4. Other methods (Adams consensus, compatibility methods, MRP).

5. Minimum distance trees.

6. Consensus networks.



```
1 data(sunfish.tree)
2 data(sunfish.data)
3 ## extract character of interest
4 gw<-setNames(sunfish.data$gape.width,
5   rownames(sunfish.data))
6 ## run penalized-likelihood optimization
7 ## lambda=0.1 is arbitrary
8 fitBM<-multirateBM(sunfish.tree,gw,
9   lambda=0.01)
10 ## print and plot the results
11 print(fitBM)
12 plot(fitBM,ftype="i",fsize=0.8,lwd=6,
13   outline=TRUE)
14
```

14:1 (Top Level)

Console Terminal Background Jobs

```
R 4.2.2 ~ /
+ lambda=0.01)
Beginning optimization....
Optimization iteration 1. Using "L-BFGS-B" optimization method.
Best (penalized) log-likelihood so far: 38.4615
Done optimization.
> ## print and plot the results
> print(fitBM)
Multi-rate Brownian model using multirateBM.

Fitted rates:
Acantharchus_pomotis Lepomis_gibbosus Lepomis_microlophus Lepomis_punctatus
0.060276 0.038039 0.043168 0.048633
Lepomis_miniatus Lepomis_auritus Lepomis_marginatus Lepomis_megalotis
0.042838 0.254773 0.25238 0.306999

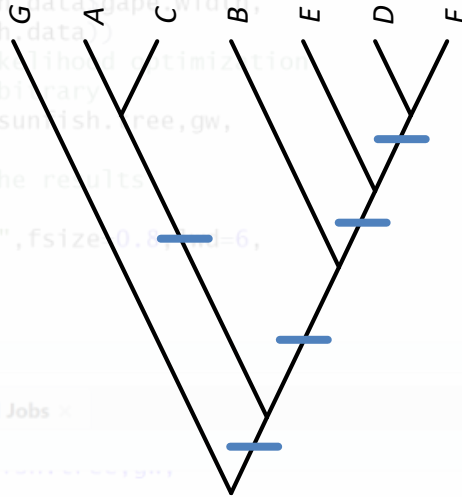
lambda penalty term: 0.01
log-likelihood: 40.148315
AIC: 31.703369

R thinks it has found a solution.

> plot(fitBM,ftype="i",fsize=0.8,lwd=6,
+   outline=TRUE)
>
```



# Majority rule consensus tree



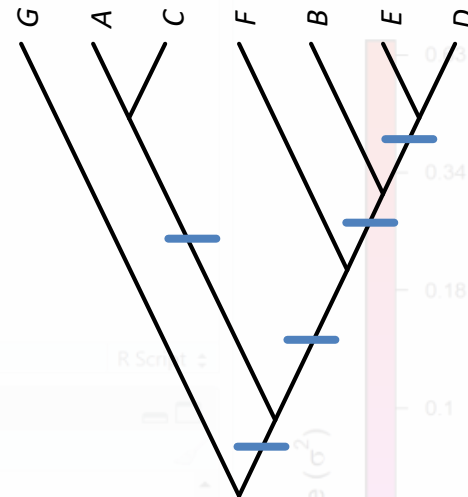
{GACBE | DF} ✗

{GACB | EDF} ✗

{GAC | BEDF} ✓

{G | ACBEDF} ✓

{AC | GBEDF} ✓



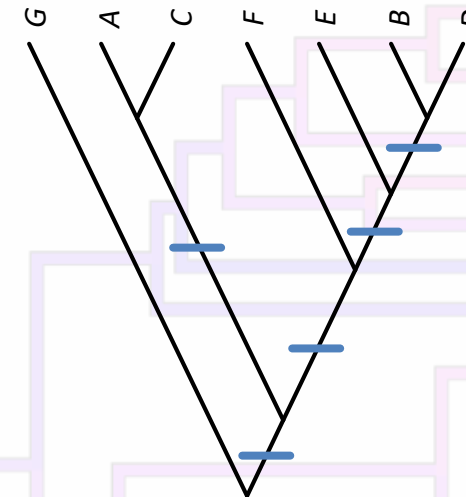
{GACFB | ED} ✗

{GACF | BED} ✓

{GAC | FBED} ✓

{G | ACFBED} ✓

{AC | GFBED} ✓



{GACFE | BD} ✗

{GACF | EBD} ✓

{GAC | FEBD} ✓

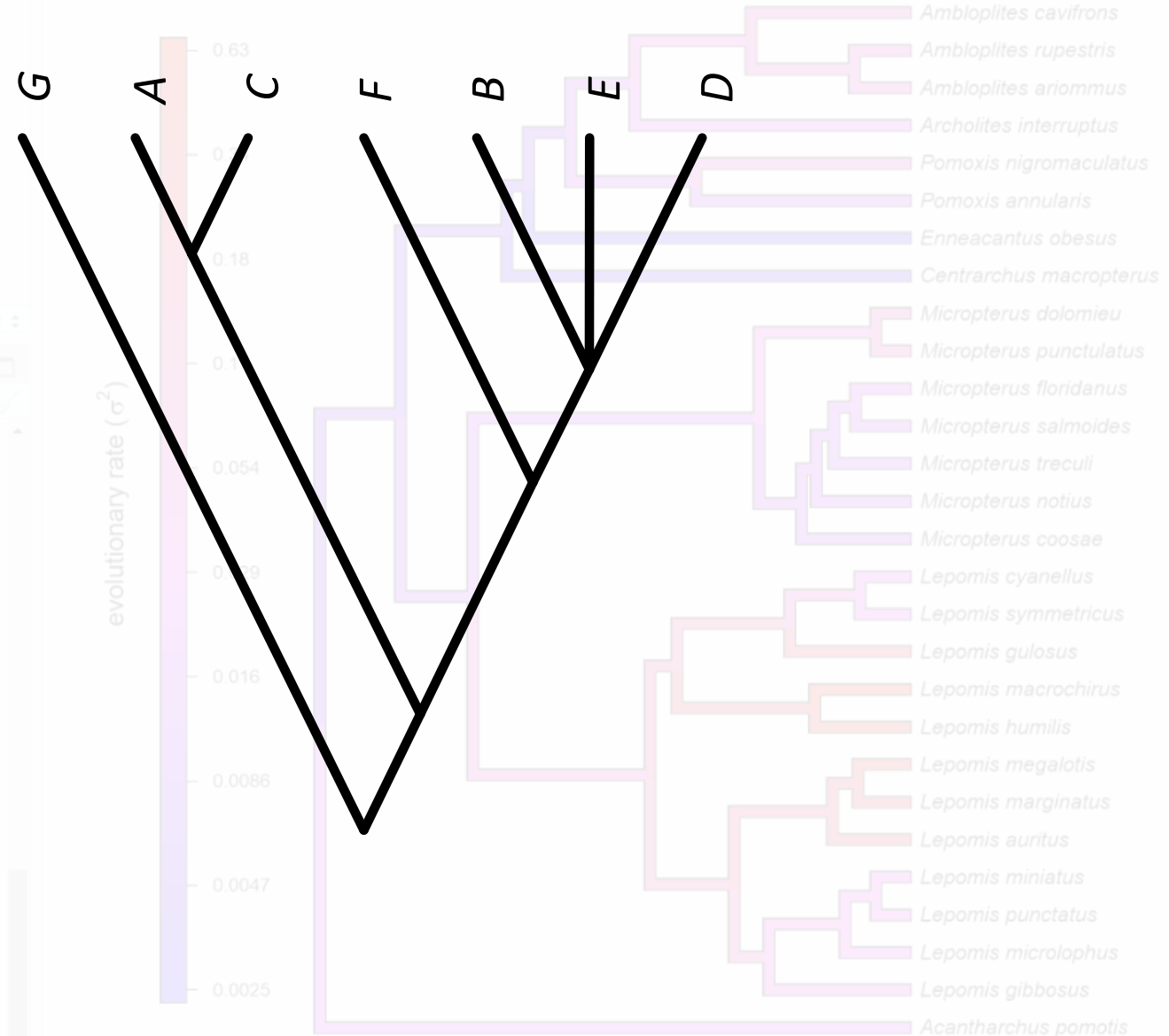
{G | ACFEBD} ✓

{AC | GFEBD} ✓

Ambloplites cavifrons  
Ambloplites rupestris  
Ambloplites ariommus  
Archolites interruptus  
Pomoxis nigromaculatus  
Pomoxis annularis  
Enneacanthus obesus  
Centrarchus macropterus  
Micropterus dolomieu  
Micropterus punctulatus  
Micropterus floridanus  
Micropterus salmoides  
Micropterus treculi  
Micropterus notius  
Micropterus coosae  
Lepomis cyanellus  
Lepomis symmetricus  
Lepomis gulosus  
Lepomis macrochirus  
Lepomis humilis  
Lepomis megalotis  
Lepomis marginatus  
Lepomis auritus  
Lepomis miniatus  
Lepomis punctatus  
Lepomis microlophus  
Lepomis gibbosus  
Acantharchus pomotis

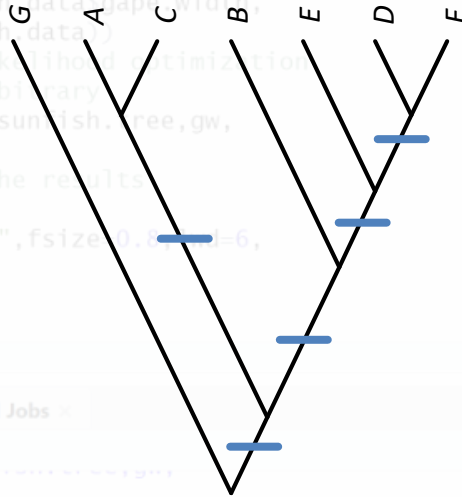
# Majority rule consensus tree

{GACF|BED}  
{GAC|FBED}  
{G|ACFBED}  
{AC|GFBED}





# Majority rule consensus tree



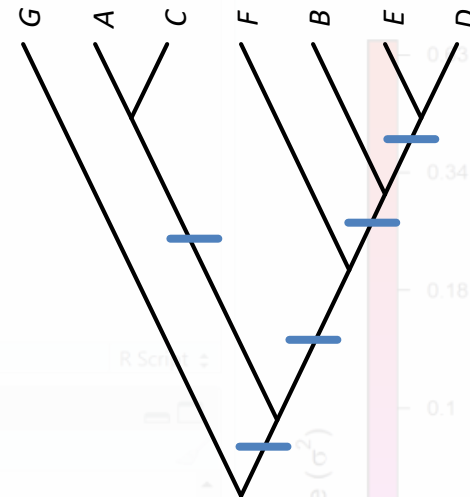
{GACBE|DF} ✗

{GACB|EDF} ✗

{GAC|BEDF} ✓

{G|ACBEDF} ✓

{AC|GBEDF} ✓



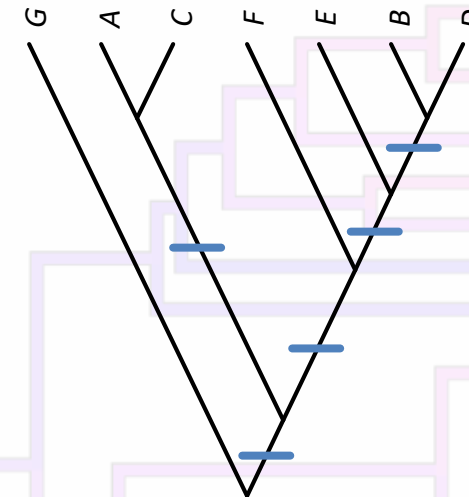
{GACFB|ED} ✗

67% {GACF|BED} ✓

100% {GAC|FBED} ✓

100% {G|ACFBED} ✓

100% {AC|GFBED} ✓



{GACFE|BD} ✗

{GACF|EBD} ✓

{GAC|FEBD} ✓

{G|ACFEBD} ✓

{AC|GFEBD} ✓

- Ambloplites cavifrons
- Ambloplites rupestris
- Ambloplites ariommus
- Archolites interruptus
- Pomoxis nigromaculatus
- Pomoxis annularis
- Enneacanthus obesus
- Centrarchus macropterus
- Micropterus dolomieu
- Micropterus punctulatus
- Micropterus floridanus
- Micropterus salmoides
- Micropterus treculi
- Micropterus notius
- Micropterus coosae
- Lepomis cyanellus
- Lepomis symmetricus
- Lepomis gulosus
- Lepomis macrochirus
- Lepomis humilis
- Lepomis megalotis
- Lepomis marginatus
- Lepomis auritus
- Lepomis miniatus
- Lepomis punctatus
- Lepomis microlophus
- Lepomis gibbosus
- Acantharchus pomotis

# Majority rule consensus tree

67%

{GACF|BED}

100%

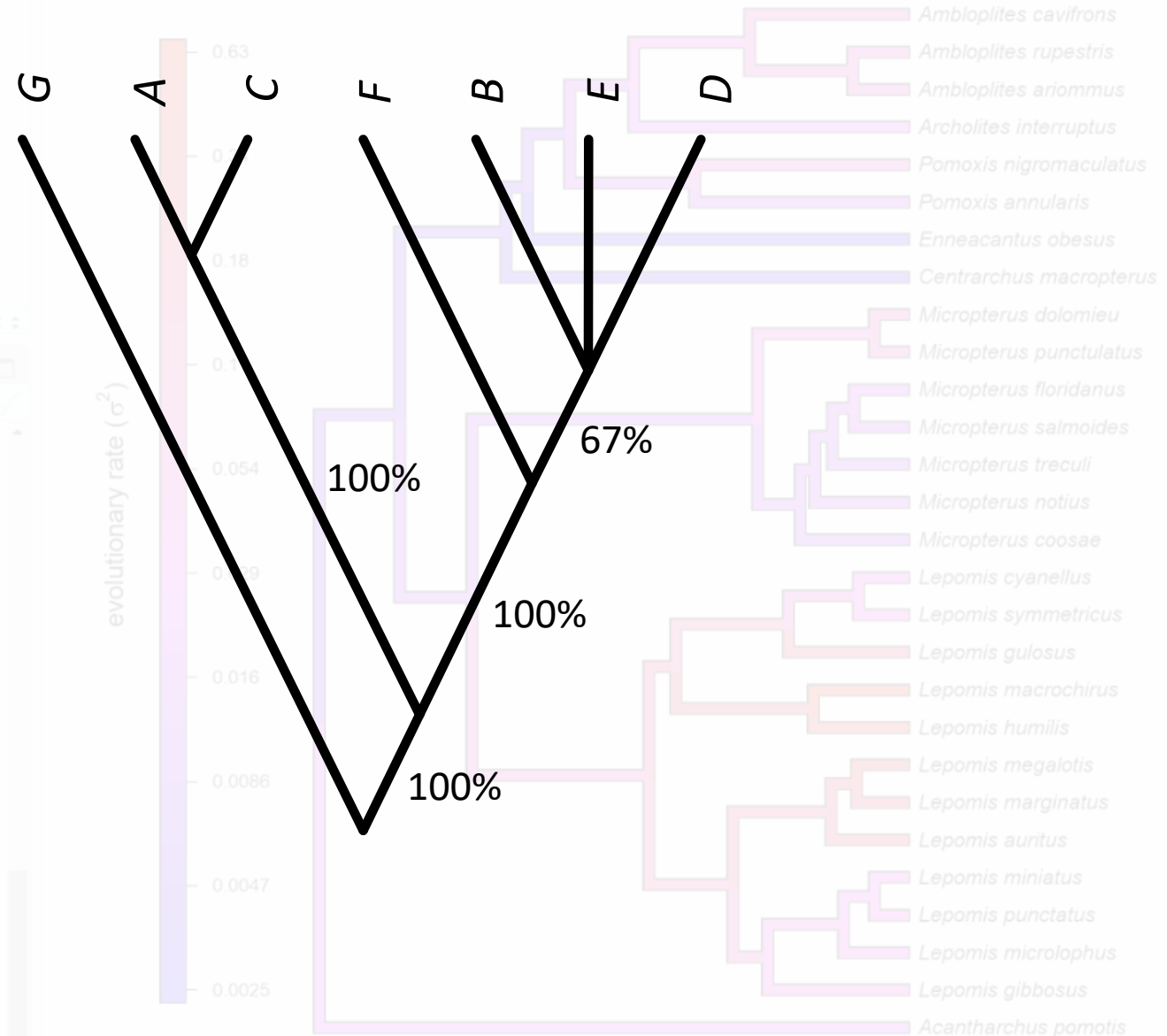
{GAC|FBED}

100%

{G|ACFBED}

100%

{AC|GFBED}



# Consensus trees

## Types of consensus trees:

1. Strict consensus trees.

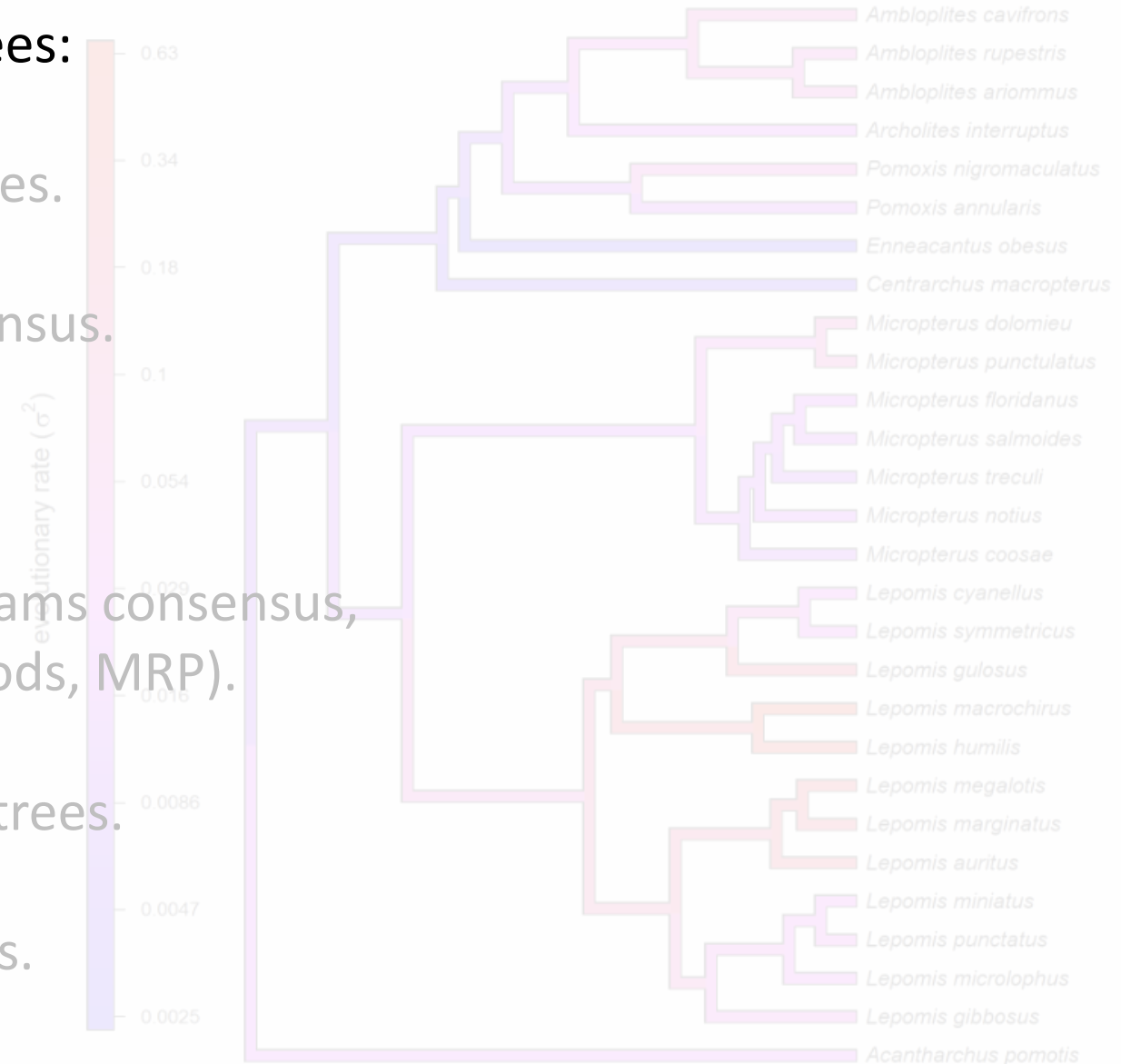
2. Majority rule consensus.

3. “X-%” consensus.

4. Other methods (Adams consensus, compatibility methods, MRP).

5. Minimum distance trees.

6. Consensus networks.



```
1 data(sunfish.tree)
2 data(sunfish.data)
3 ## extract character of interest
4 gw<-setNames(sunfish.data$gape.width,
5   rownames(sunfish.data))
6 ## run penalized-likelihood optimization
7 ## lambda=0.1 is arbitrary
8 fitBM<-multirateBM(sunfish.tree,gw,
9   lambda=0.01)
10 ## print and plot the results
11 print(fitBM)
12 plot(fitBM,ftype="i",fsize=0.8,lwd=6,
13   outline=TRUE)
14
```

14:1 (Top Level)

Console Terminal Background Jobs

```
R 4.2.2 ~ /
+ lambda=0.01)
Beginning optimization....
Optimization iteration 1. Using "L-BFGS-B" optimization method.
Best (penalized) log-likelihood so far: 38.4615
Done optimization.
> ## print and plot the results
> print(fitBM)
Multi-rate Brownian model using multirateBM.

Fitted rates:
Acantharchus_pomotis Lepomis_gibbosus Lepomis_microlophus Lepomis_punctatus
0.060276 0.038039 0.043168 0.048633
Lepomis_miniatus Lepomis_auritus Lepomis_marginatus Lepomis_megalotis
0.042838 0.254773 0.25238 0.306999

lambda penalty term: 0.01
log-likelihood: 40.148315
AIC: 31.703369

R thinks it has found a solution.

> plot(fitBM,ftype="i",fsize=0.8,lwd=6,
+   outline=TRUE)
>
```

# Percentage rule consensus trees

67%

{GACF|BED}

100%

{GAC|FBED}

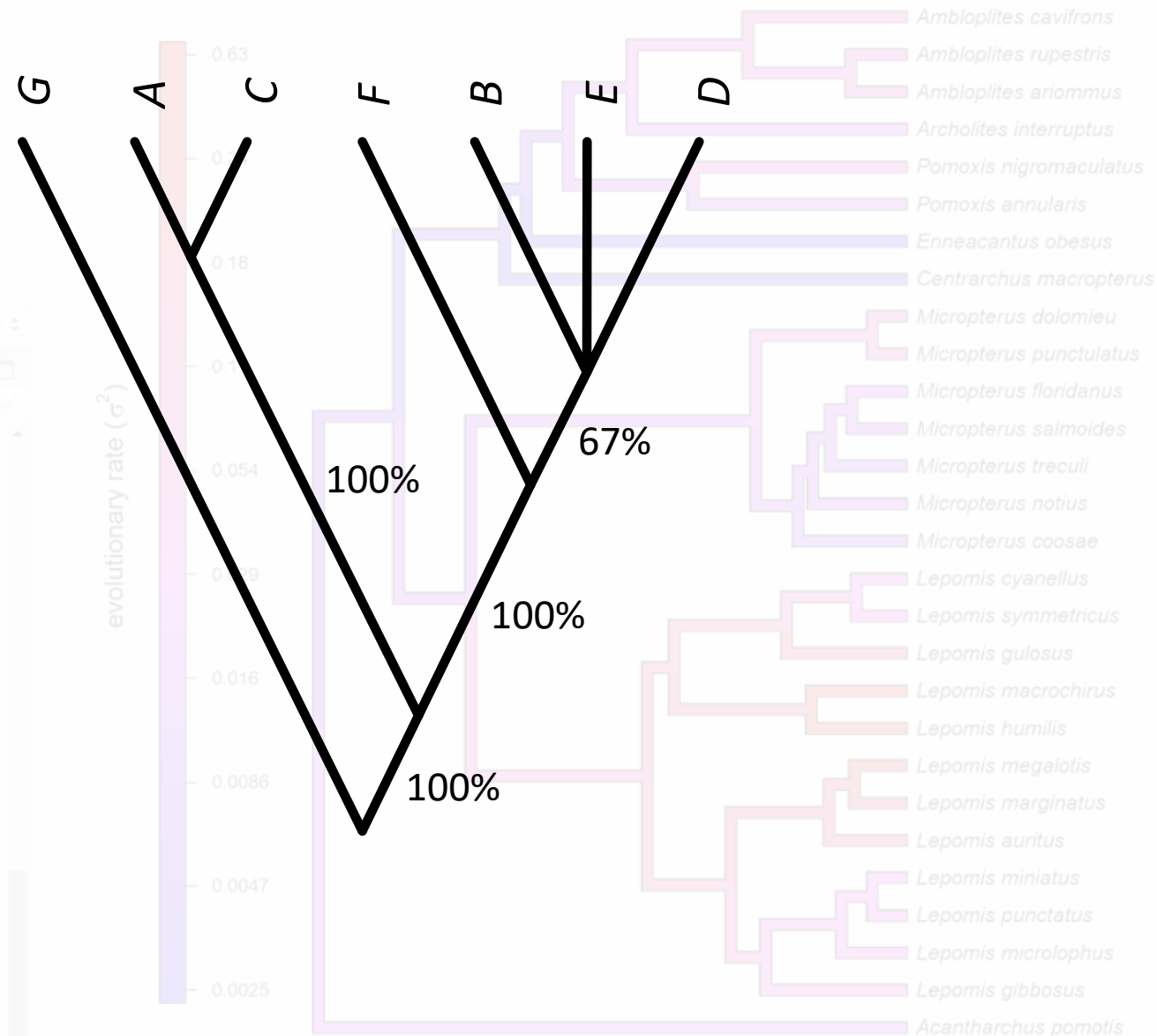
100%

{G|ACFBED}

100%

{AC|GFBED}

65%



# Percentage rule consensus trees

67%

{GACF|BED}

100%

{GAC|FBED}

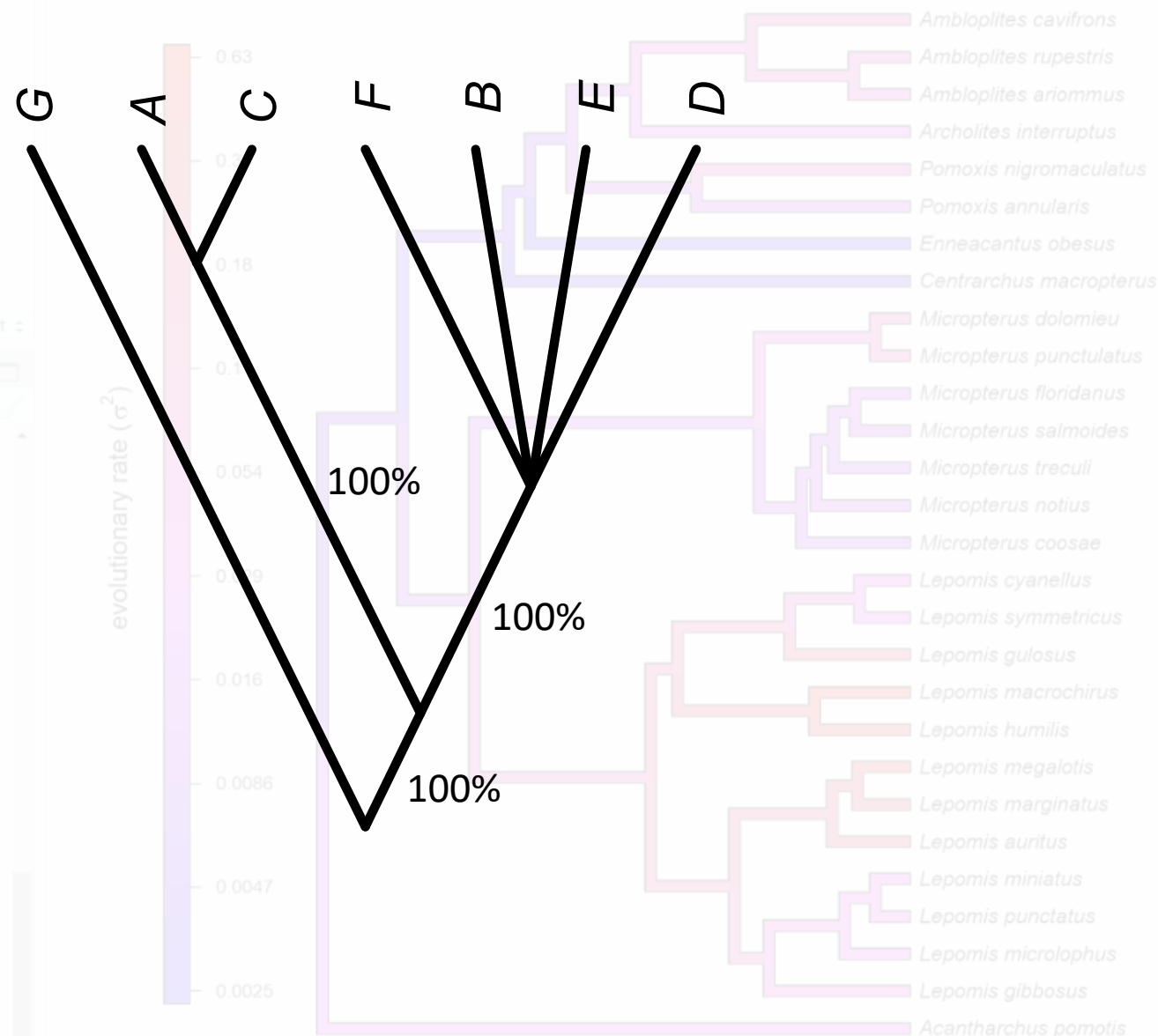
100%

{G|ACFBED}

100%

{AC|GFBED}

80%



# Consensus trees

## Types of consensus trees:

1. Strict consensus trees.

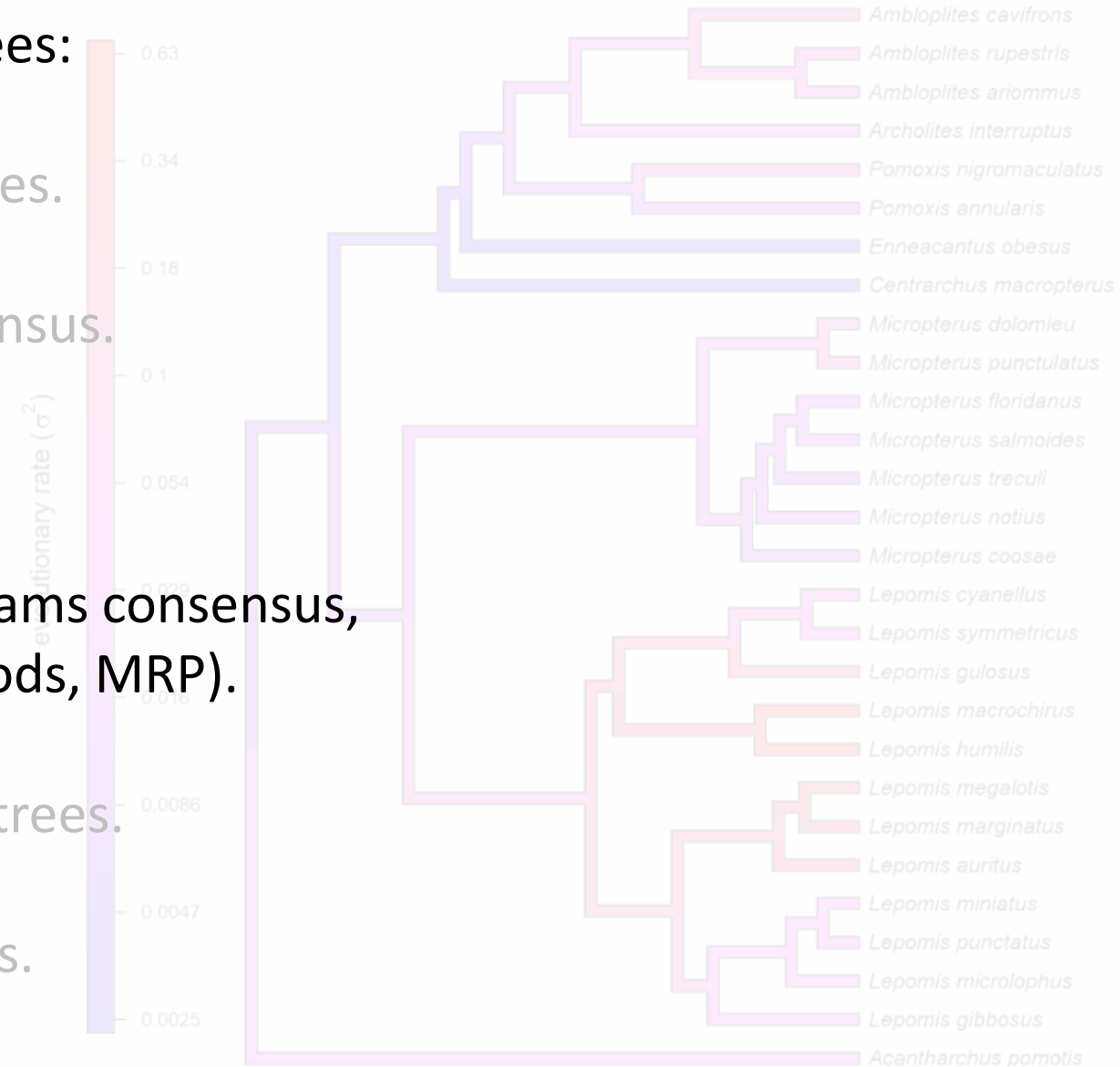
2. Majority rule consensus.

3. “X-%” consensus.

4. Other methods (Adams consensus, compatibility methods, MRP).

5. Minimum distance trees.

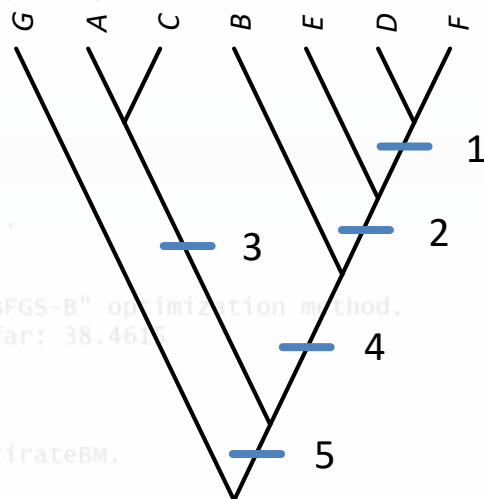
6. Consensus networks.



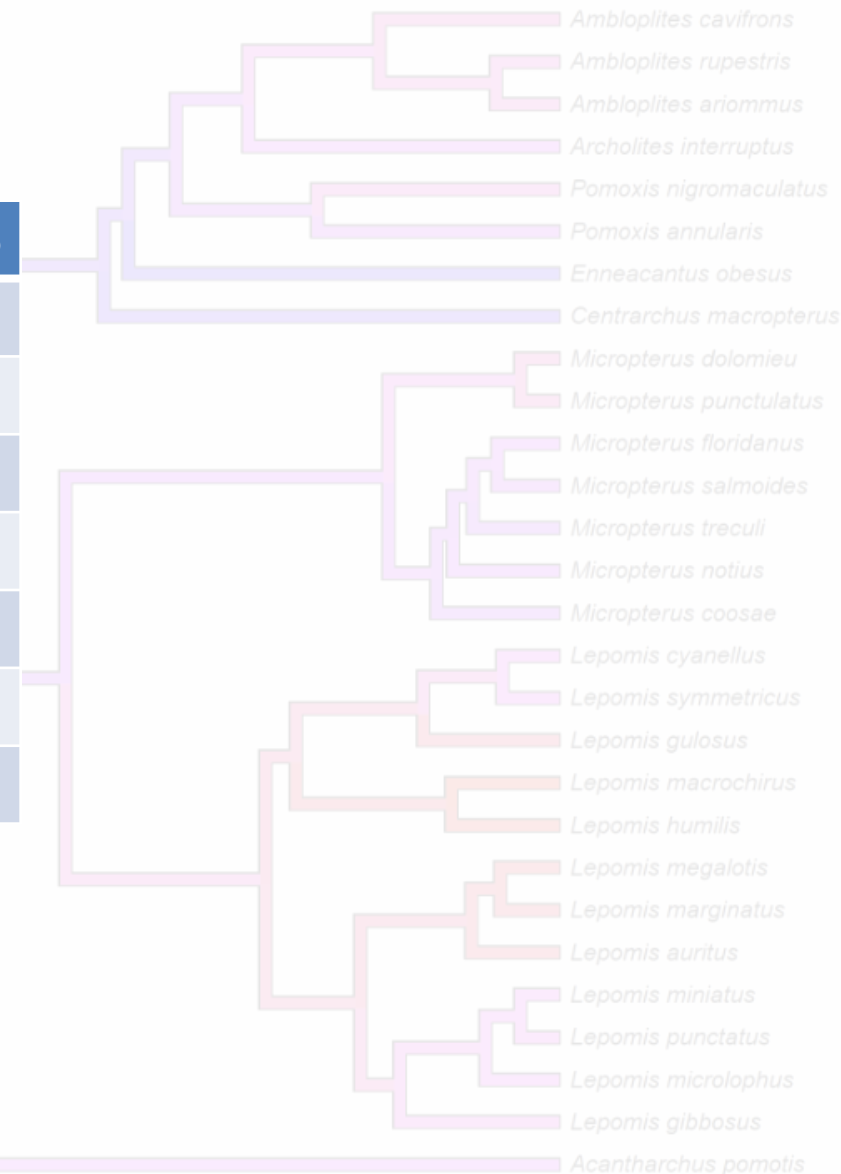


# MRP consensus trees

MRP = matrix representation parsimony

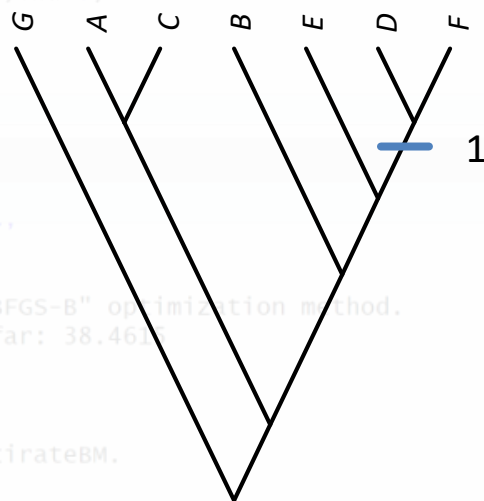


Species	1	2	3	4	5
A					
B					
C					
D					
E					
F					
G					

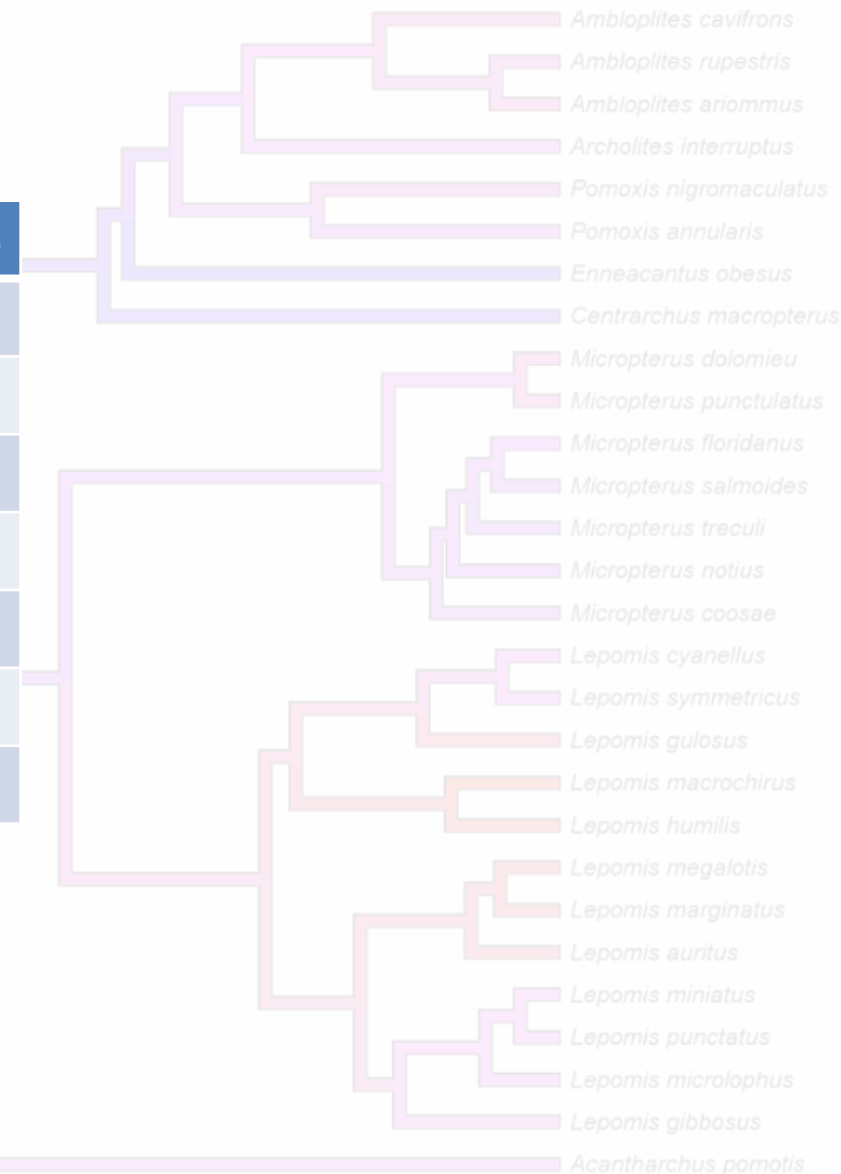


# MRP consensus trees

MRP = matrix representation parsimony

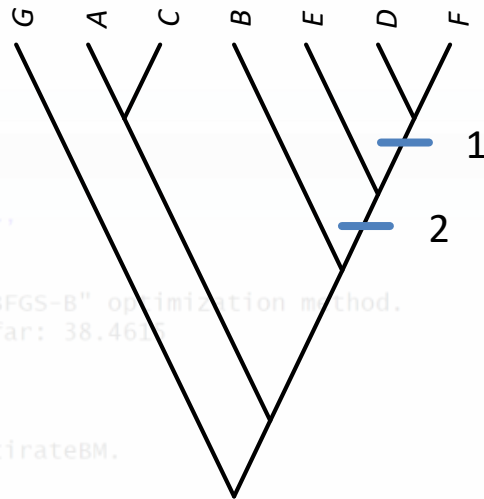


Species	1	2	3	4	5
A	0				
B	0				
C	0				
D	1				
E	0				
F	1				
G	0				

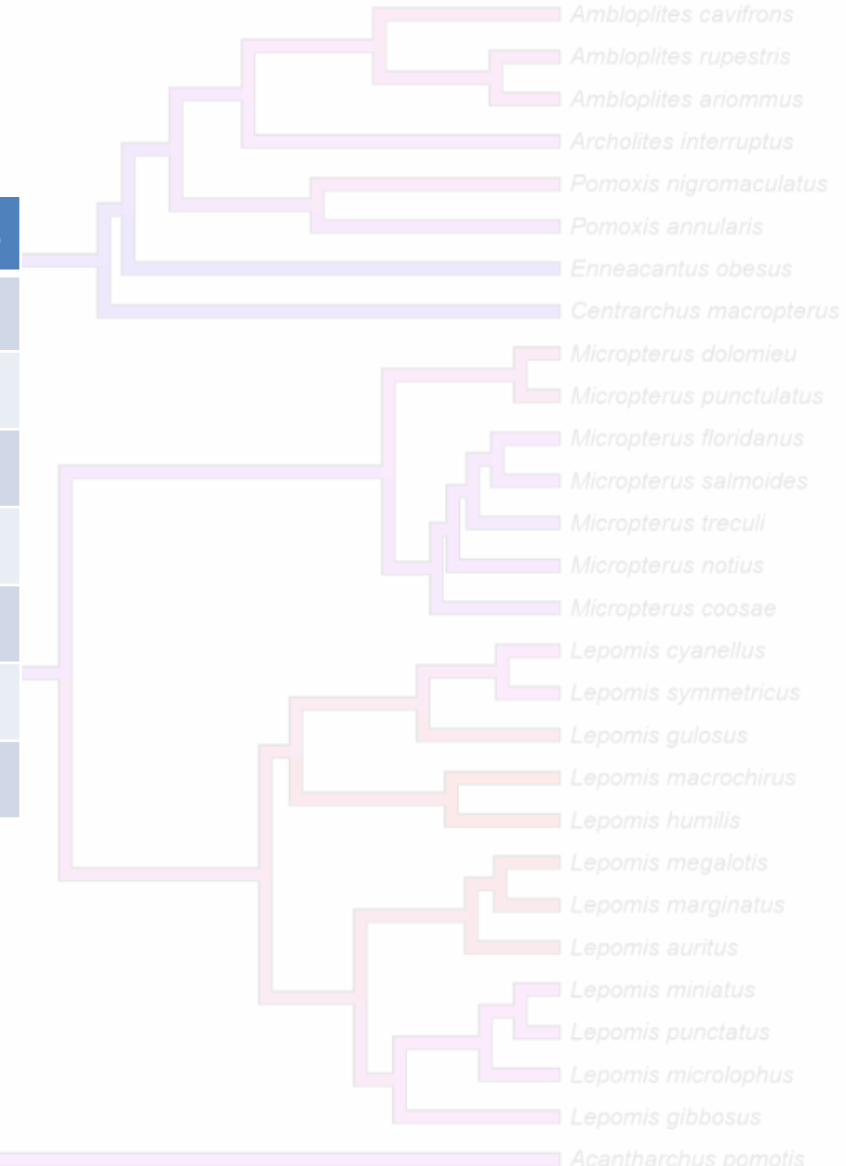


# MRP consensus trees

MRP = matrix representation parsimony

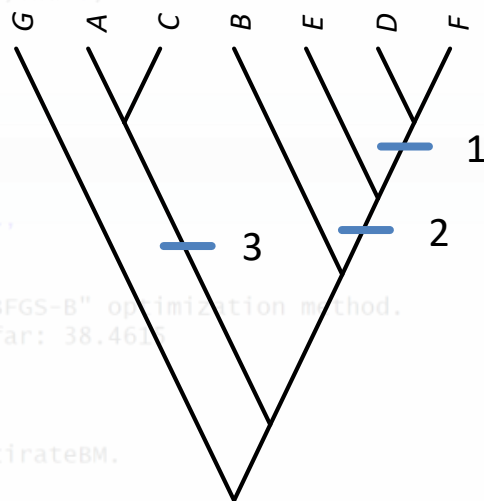


Species	1	2	3	4	5
A	0	0			
B	0	0			
C	0	0			
D	1	1			
E	0	1			
F	1	1			
G	0	0			

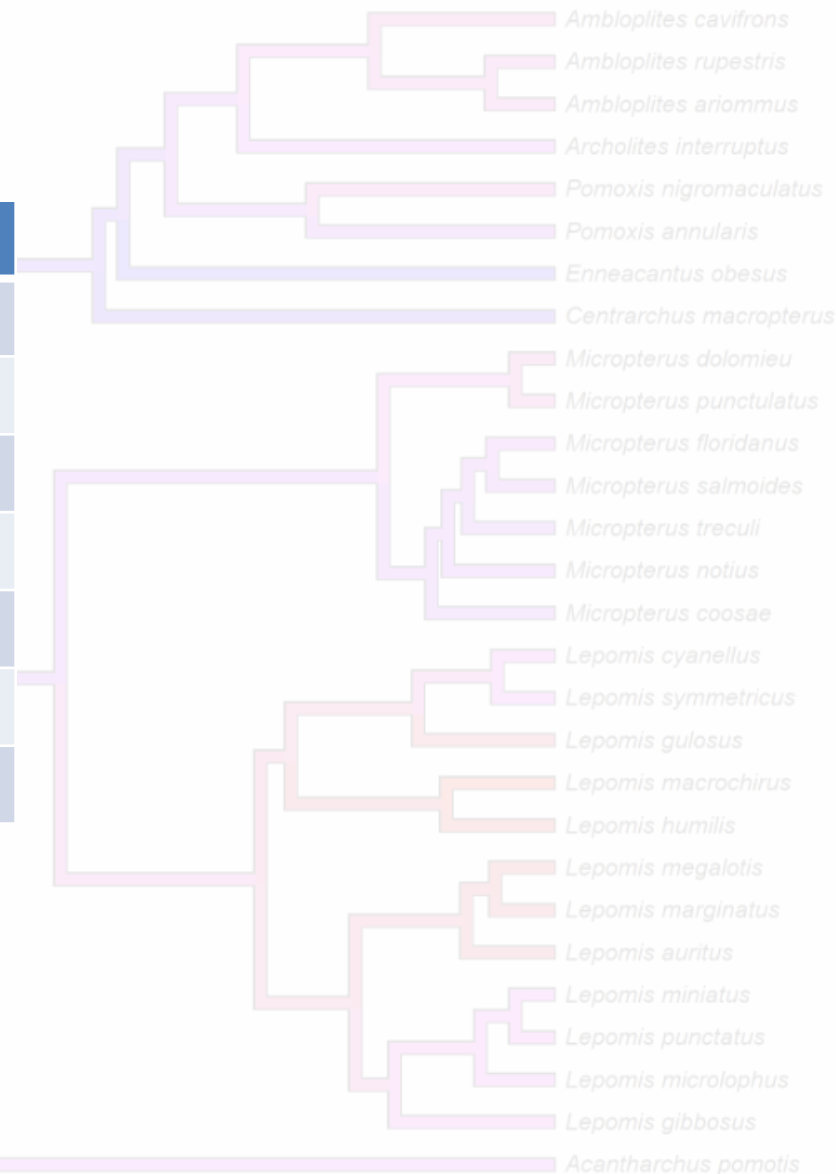


# MRP consensus trees

MRP = matrix representation parsimony

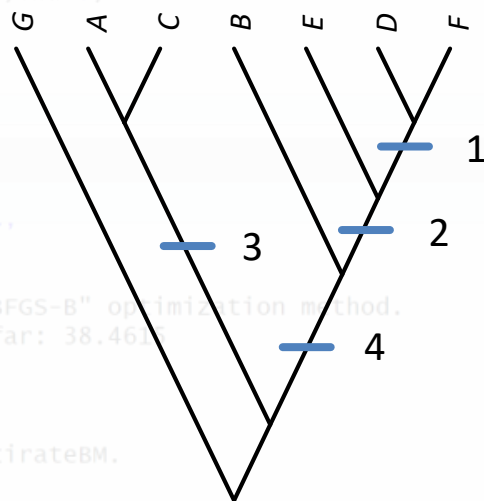


Species	1	2	3	4	5
A	0	0	1		
B	0	0	0		
C	0	0	1		
D	1	1	0		
E	0	1	0		
F	1	1	0		
G	0	0	0		

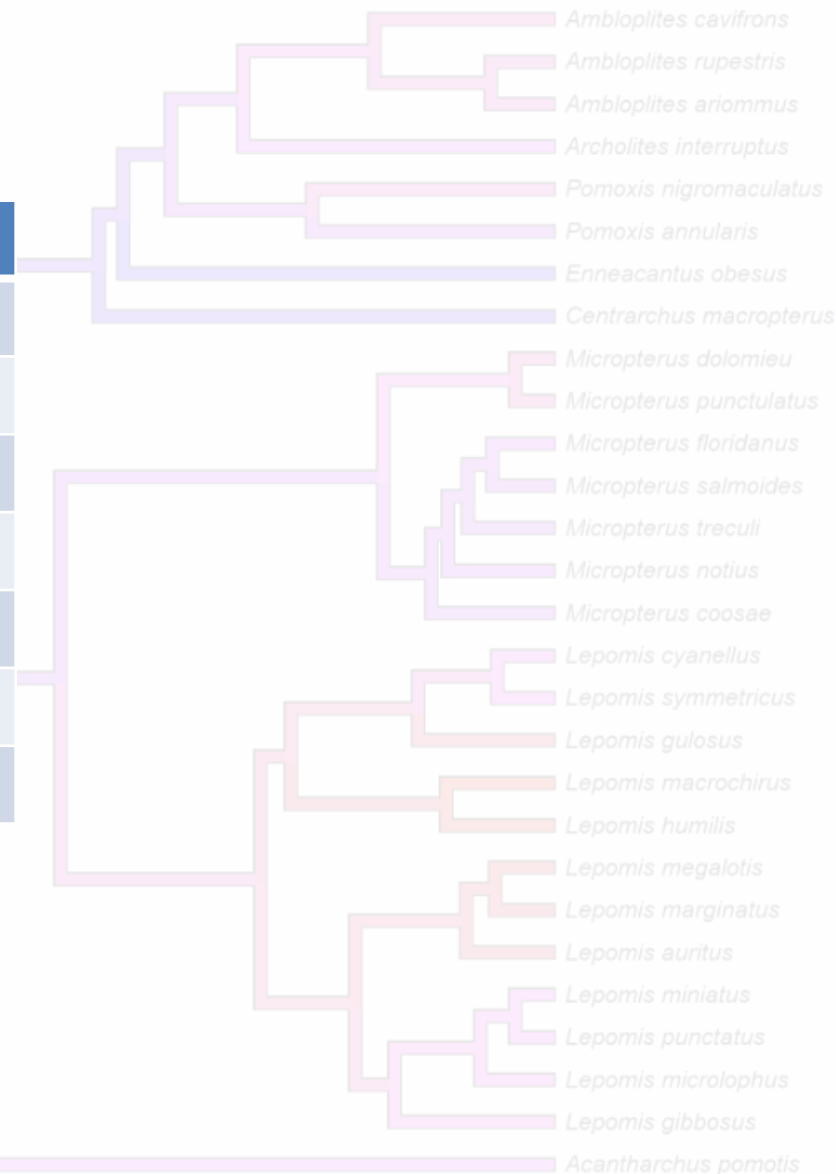


# MRP consensus trees

MRP = matrix representation parsimony

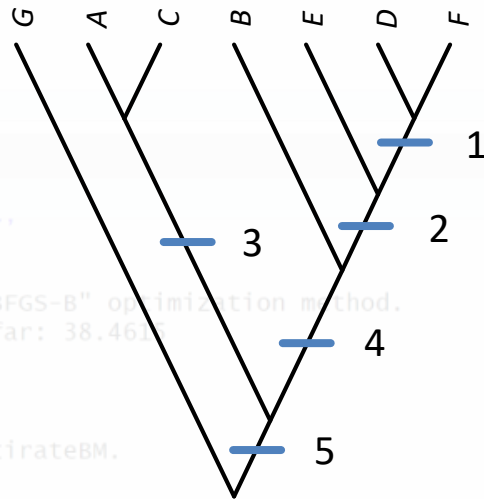


Species	1	2	3	4	5
A	0	0	1	0	
B	0	0	0	1	
C	0	0	1	0	
D	1	1	0	1	
E	0	1	0	1	
F	1	1	0	1	
G	0	0	0	0	



# MRP consensus trees

MRP = matrix representation parsimony

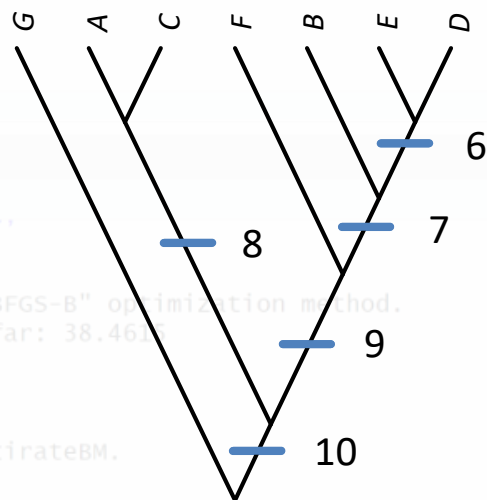


Species	1	2	3	4	5
A	0	0	1	0	1
B	0	0	0	1	1
C	0	0	1	0	1
D	1	1	0	1	1
E	0	1	0	1	1
F	1	1	0	1	1
G	0	0	0	0	0

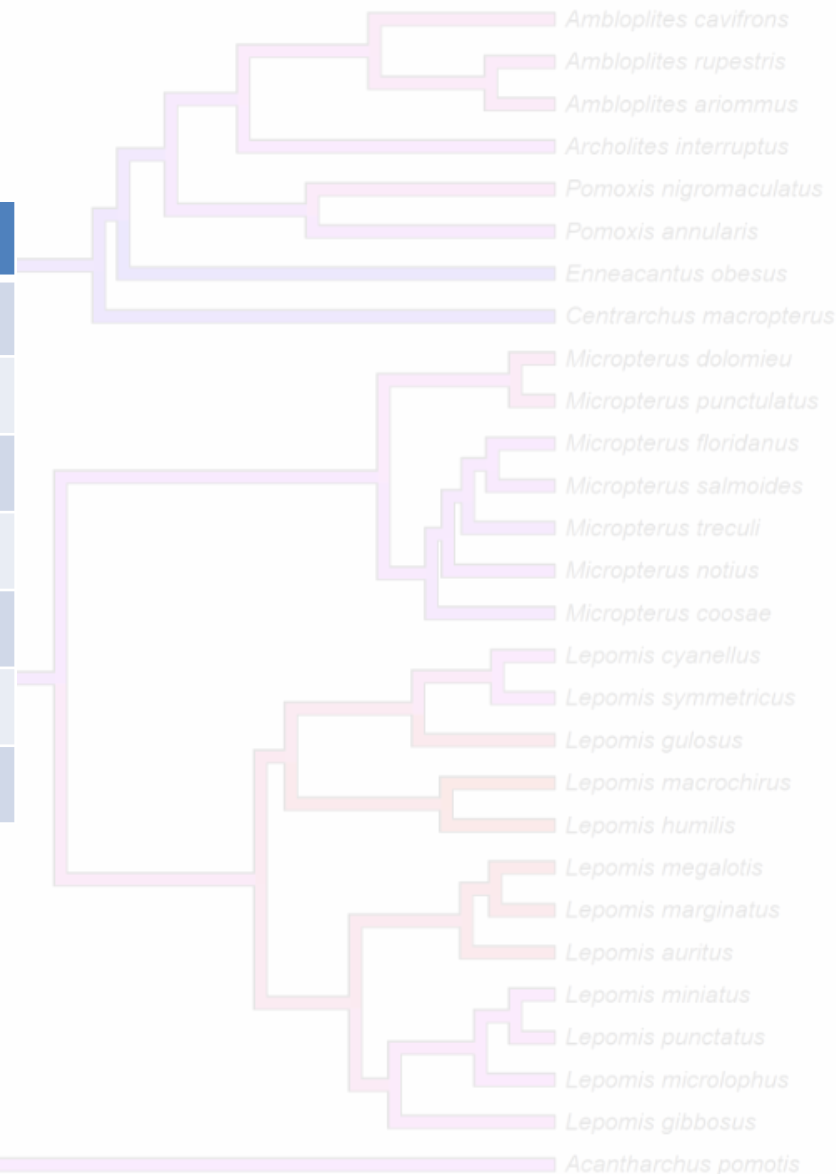


# MRP consensus trees

MRP = matrix representation parsimony

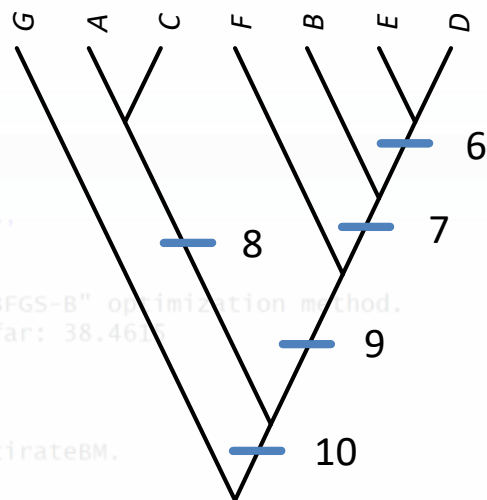


Species	1	2	3	4	5
A	0	0	1	0	1
B	0	0	0	1	1
C	0	0	1	0	1
D	1	1	0	1	1
E	0	1	0	1	1
F	1	1	0	1	1
G	0	0	0	0	0

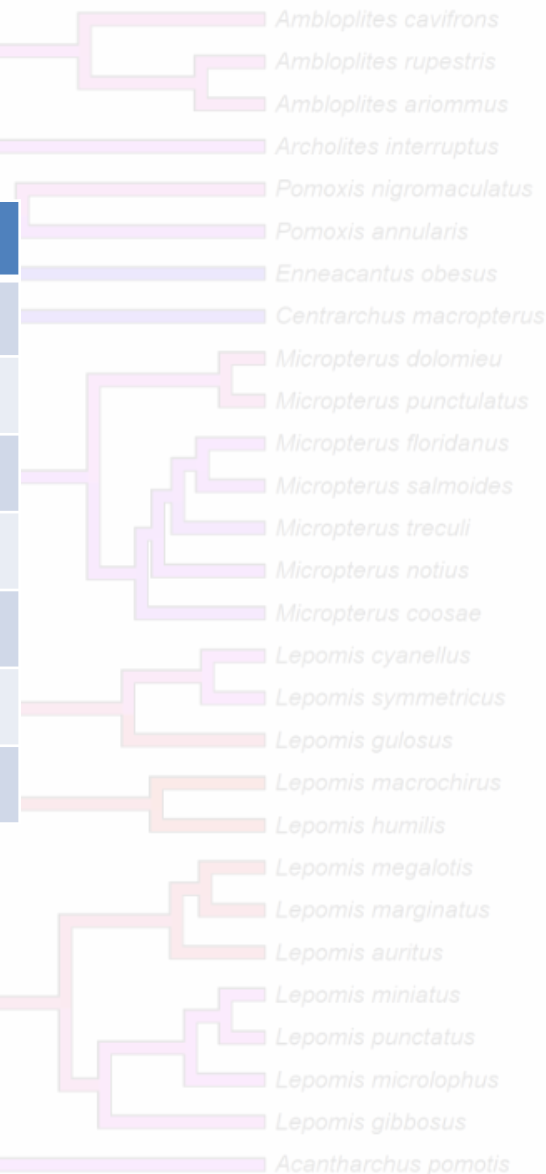


# MRP consensus trees

MRP = matrix representation parsimony

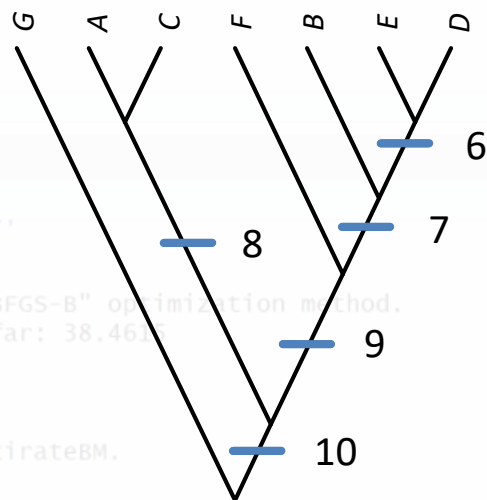


Species	1	2	3	4	5	6	7	8	9	10
A	0	0	1	0	1					
B	0	0	0	1	1					
C	0	0	1	0	1					
D	1	1	0	1	1					
E	0	1	0	1	1					
F	1	1	0	1	1					
G	0	0	0	0	0					

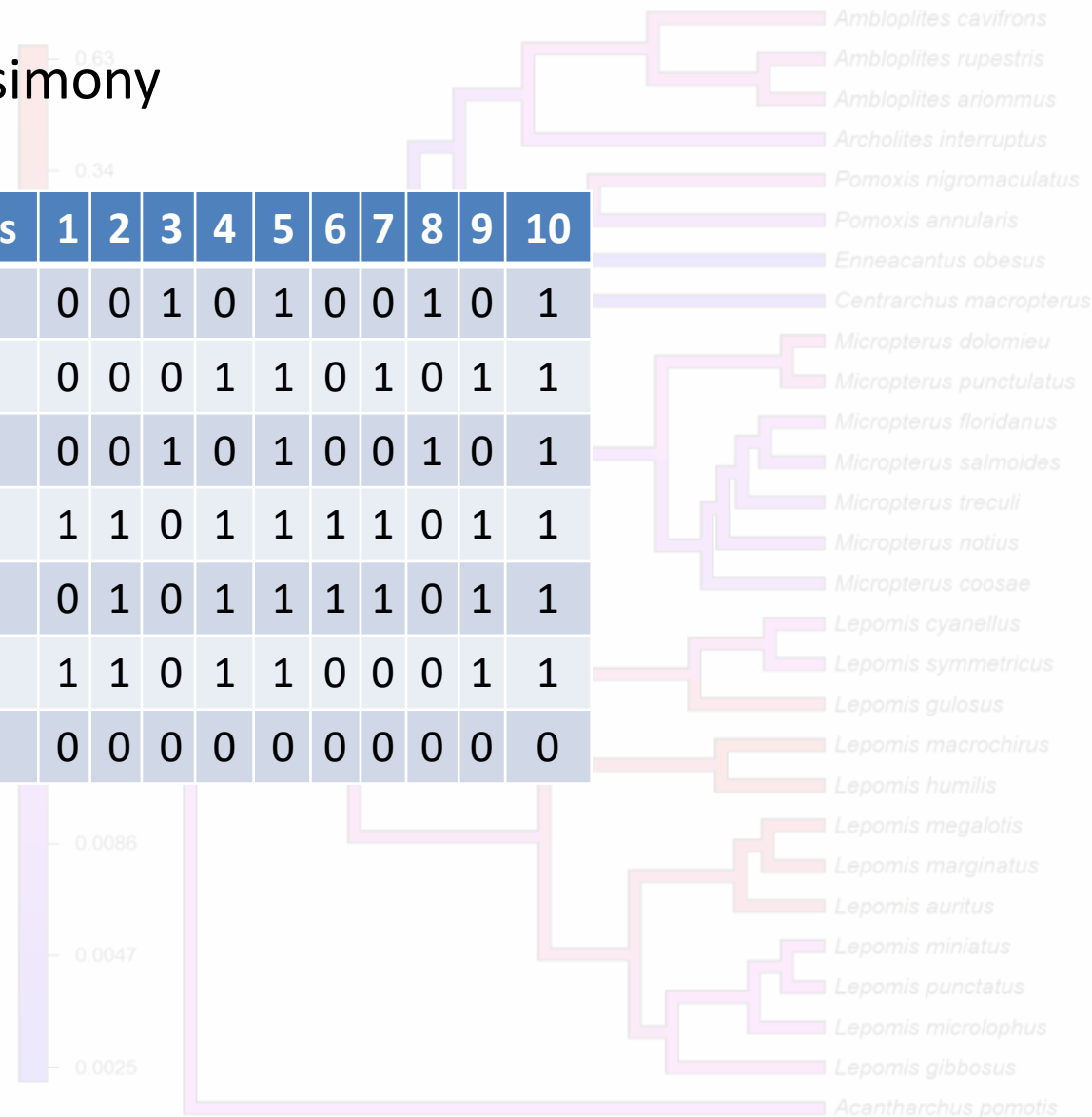


# MRP consensus trees

MRP = matrix representation parsimony



Species	1	2	3	4	5	6	7	8	9	10
A	0	0	1	0	1	0	0	1	0	1
B	0	0	0	1	1	0	1	0	1	1
C	0	0	1	0	1	0	0	1	0	1
D	1	1	0	1	1	1	1	0	1	1
E	0	1	0	1	1	1	1	0	1	1
F	1	1	0	1	1	0	0	0	1	1
G	0	0	0	0	0	0	0	0	0	0



# Consensus trees

## Types of consensus trees:

1. Strict consensus trees.

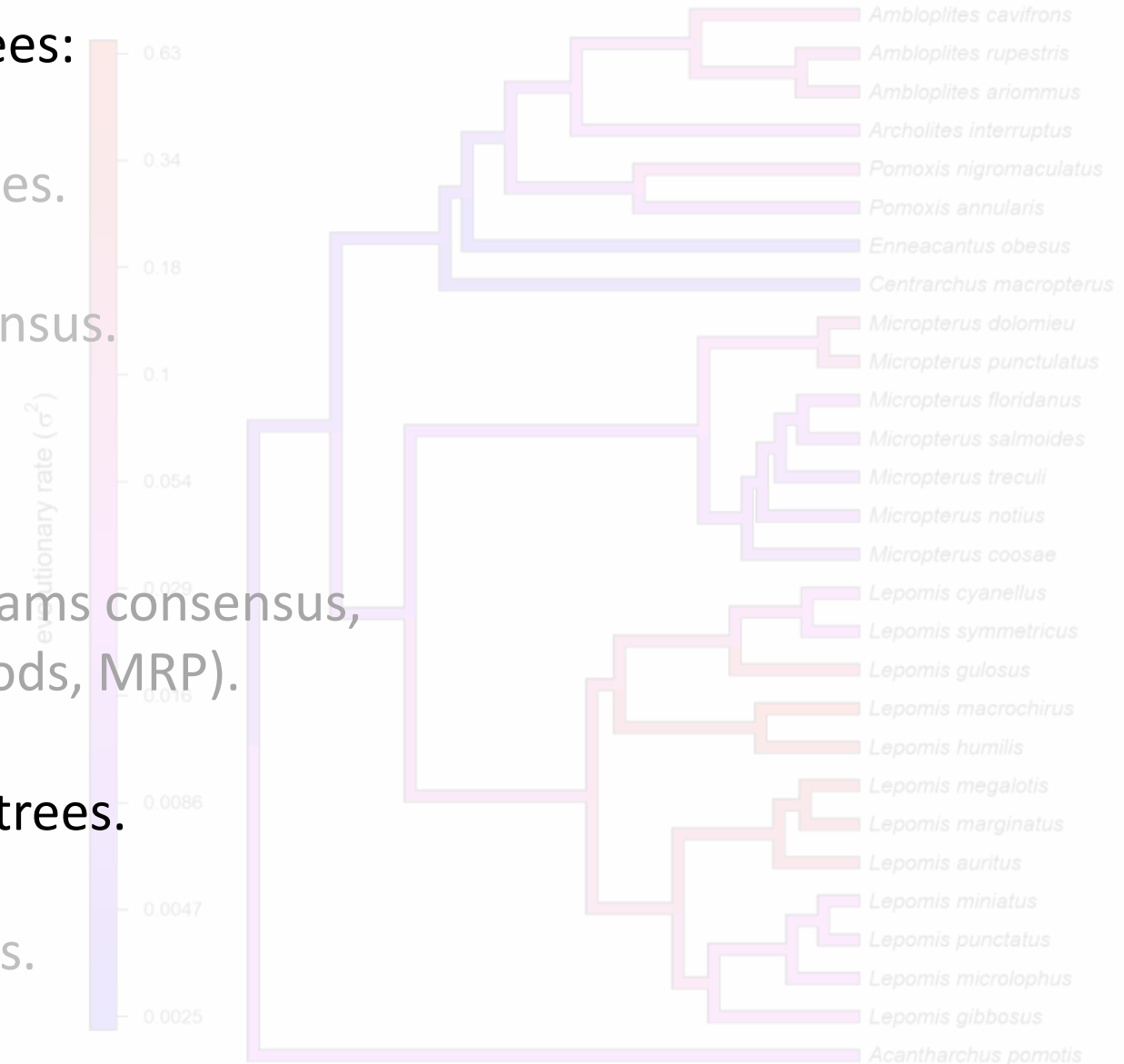
2. Majority rule consensus.

3. “X-%” consensus.

4. Other methods (Adams consensus, compatibility methods, MRP).

5. Minimum distance trees.

6. Consensus networks.



```
1 data(sunfish.tree)
2 data(sunfish.data)
3 ## extract character of interest
4 gw<-setNames(sunfish.data$gape.width,
5   rownames(sunfish.data))
6 ## run penalized-likelihood optimization
7 ## lambda=0.1 is arbitrary
8 fitBM<-multirateBM(sunfish.tree,gw,
9   lambda=0.01)
10 ## print and plot the results
11 print(fitBM)
12 plot(fitBM,ftype="i",fsize=0.8,lwd=6,
13   outline=TRUE)
14
```

14:1 (Top Level)

```
Console Terminal Background Jobs
R 4.2.2 ~ /
+ lambda=0.01)
Beginning optimization....
Optimization iteration 1. Using "L-BFGS-B" optimization method.
Best (penalized) log-likelihood so far: 38.4615
Done optimization.
> ## print and plot the results
> print(fitBM)
Multi-rate Brownian model using multirateBM.
```

```
Fitted rates:
Acantharchus_pomotis Lepomis_gibbosus Lepomis_microlophus Lepomis_punctatus
0.060276 0.038039 0.043168 0.048633
Lepomis_miniatus Lepomis_auritus Lepomis_marginatus Lepomis_megalotis
0.042838 0.254773 0.22238 0.206000

lambda penalty term: 0.01
log-likelihood: 40.148315
AIC: 31.703369
```

R thinks it has found a solution.

```
> plot(fitBM,ftype="i",fsize=0.8,lwd=6,
+   outline=TRUE)
>
```

Untitled1\*

```
1 data(sunfish.tree)
2 data(sunfish.data)
3 ## extract character of interest
4 gw<-setNames(sunfish.data$gape.wid
5   rownames(sunfish.data))
6 ## run penalized-likelihood optimi
7 ## lambda=0.1 is arbitrary
8 fitBM<-multirateBM(sunfish.tree,gw
9   lambda=0.01)
10 ## print and plot the results
11 print(fitBM)
12 plot(fitBM,ftype="i",fsize=0.8,lwd
13   outline=TRUE)
14
```

14.1 (Top Level)

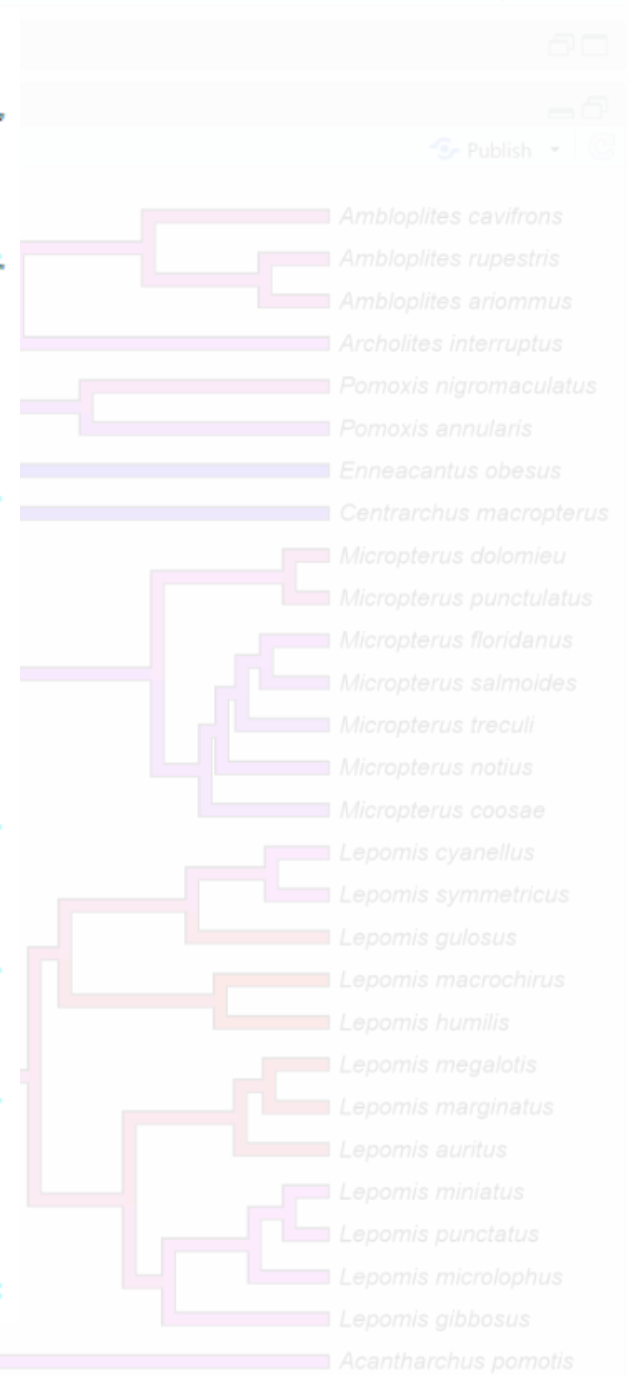
Console Terminal Background Jobs

```
R 4.2.2 ~ /
+ lambda=0.01)
Beginning optimization....
Optimization iteration 1. Using "L-BFGS-
Best (penalized) log-likelihood so far:
Done optimization.
> ## print and plot the results
> print(fitBM)
Multi-rate Brownian model using multirat

Fitted rates:
Acantharchus_pomotis Lepomis_gibbosus L
0.060276 0.038039
Lepomis_miniatius Lepomis_auritus Lepomi
0.042838 0.254773

lambda penalty term: 0.01
log-likelihood: 40.148315
AIC: 31.703369

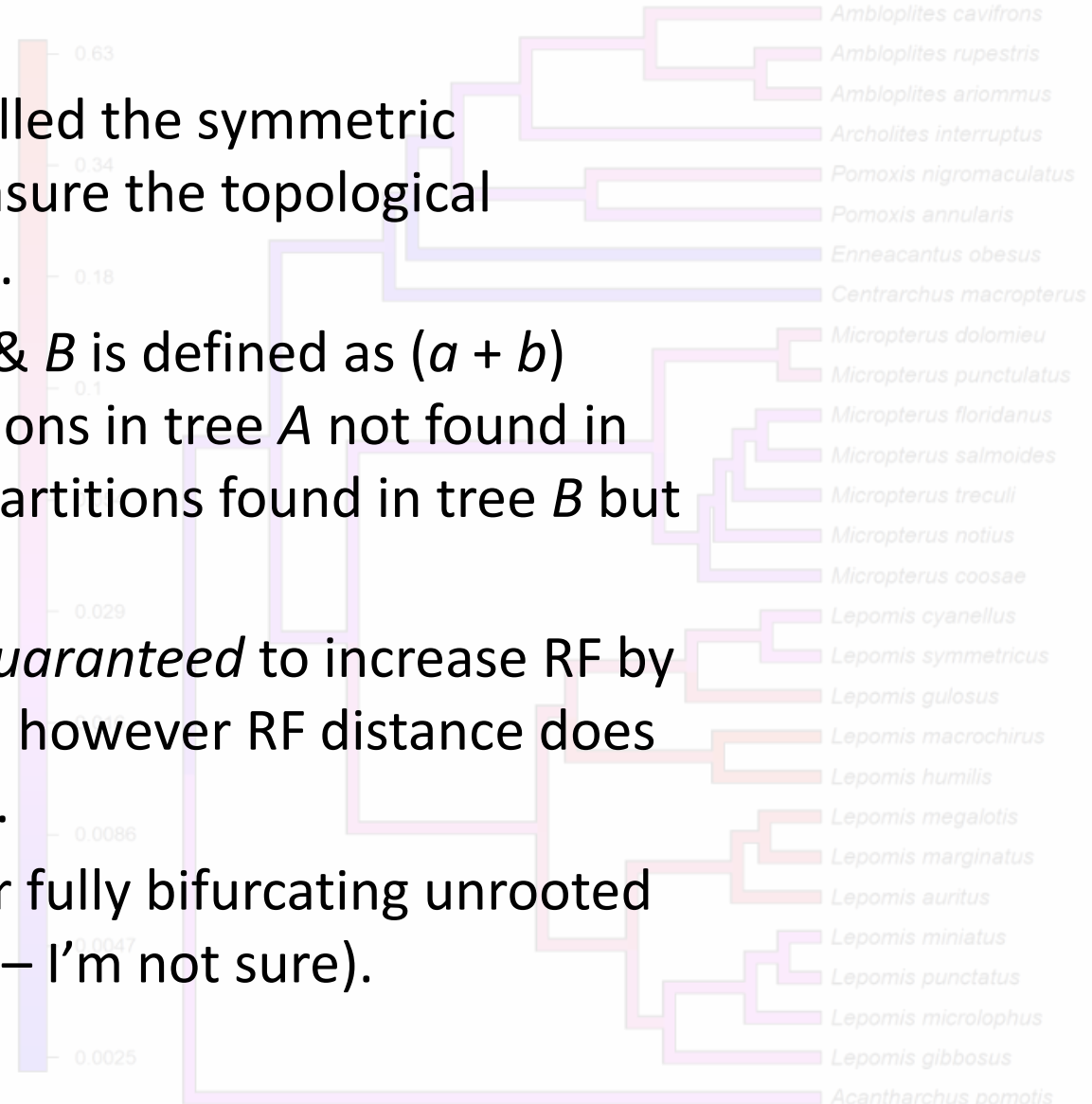
R thinks it has found a solution.
> plot(fitBM,ftype="i",fsize=0.8,lwd=6,
+   outline=TRUE)
>
```





# Digression on tree topology distance

- [Robinson-Foulds distance](#) (also called the symmetric difference metric) is a way to measure the topological dissimilarity of phylogenetic trees.
- The RF distance between trees  $A$  &  $B$  is defined as  $(a + b)$  where  $a$  is the number of bipartitions in tree  $A$  not found in tree  $B$ ; and  $b$  is the number of bipartitions found in tree  $B$  but not  $A$ .
- One NNI on a bifurcating tree is *guaranteed* to increase RF by  $a$  and  $b$  by  $+1$  (and thus RF by  $+2$ ); however RF distance does not necessarily  $= 2 \times$  NNI distance.
- $(a + b) = 2a = 2b$  is true at least for fully bifurcating unrooted trees (and may be true in general – I'm not sure).





```
1 data(sunfish.tree)
2 data(sunfish.data)
3 ## extract character of interest
4 gw<-setNames(sunfish.data$gapc
5   rownames(sunfish.data))
6 ## run penalized-likelihood of
7 ## lambda=0.1 is arbitrary
8 fitBM<-multirateBM(sunfish.tr
9   lambda=0.01)
10 ## print and plot the results
11 print(fitBM)
12 plot(fitBM,ftype="i",fsize=0.8
13   outline=TRUE)
14
```

R 4.2.2 ~ / ~  
+ lambda=0.01)  
Beginning optimization....  
Optimization iteration 1. Using "L-  
Best (penalized) log-likelihood so  
Done optimization.

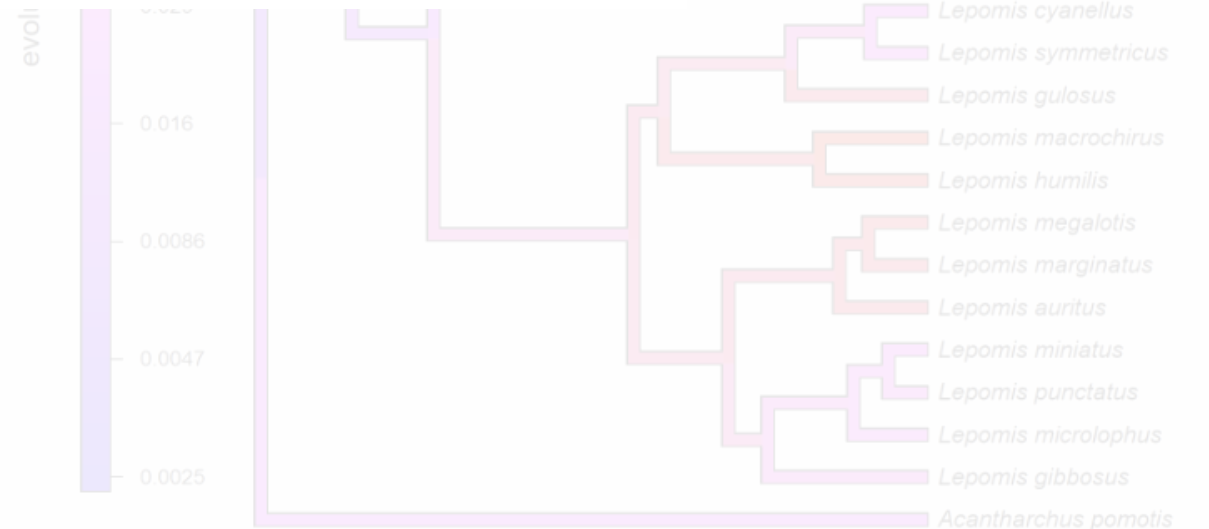
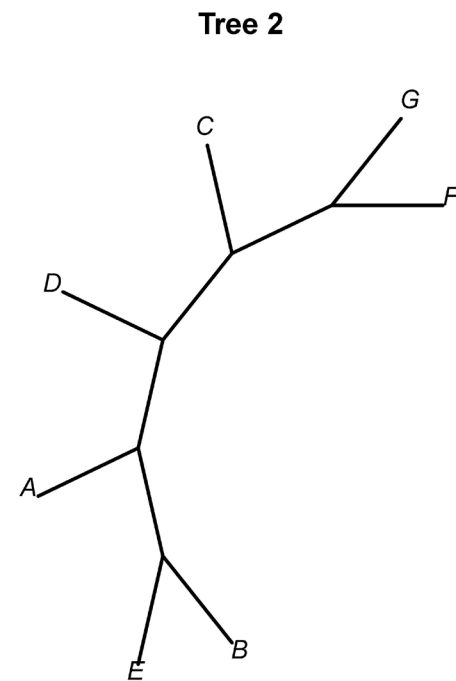
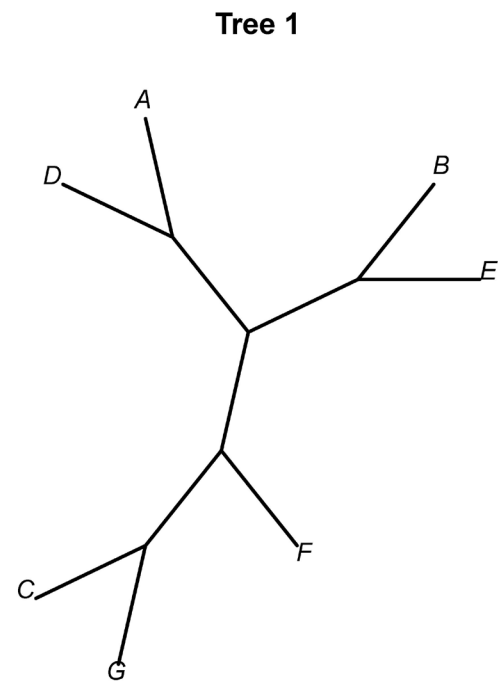
> ## print and plot the results  
> print(fitBM)  
Multi-rate Brownian model using multirateBM.

Fitted rates:  
Acantharchus\_pomotis Lepomis\_gibbosus Lepomis\_microlophus Lepomis\_punctatus  
0.060276 0.038039 0.043168 0.048633  
Lepomis\_miniatus Lepomis\_auritus Lepomis\_marginatus Lepomis\_megalotis  
0.042838 0.254773 0.245238 0.306099 ....

lambda penalty term: 0.01  
log-likelihood: 40.148315  
AIC: 31.703369

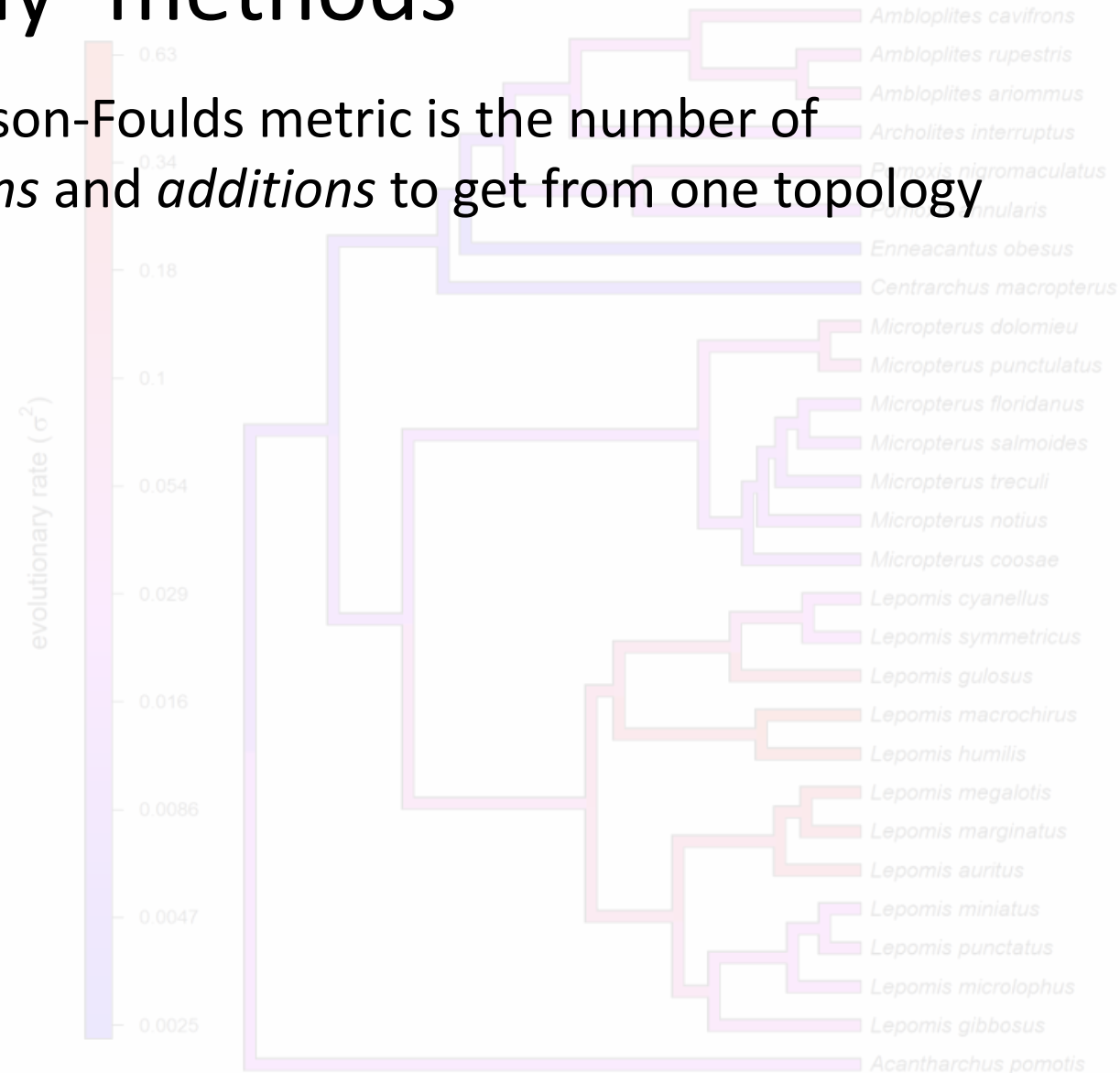
R thinks it has found a solution.

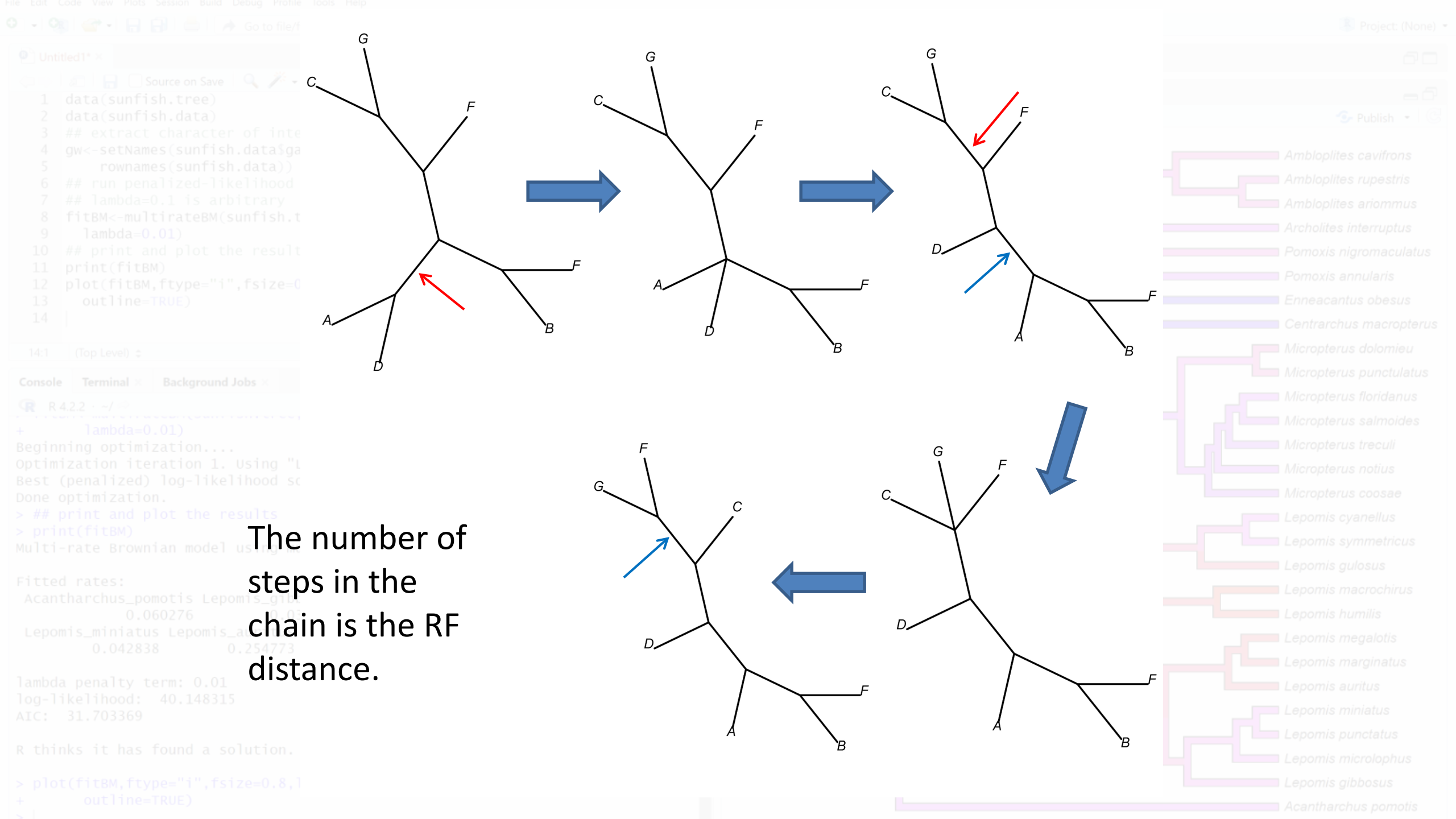
> plot(fitBM,ftype="i",fsize=0.8,lwd=6,  
+ outline=TRUE)  
>



# Obvious shortcoming in 'topology only' methods

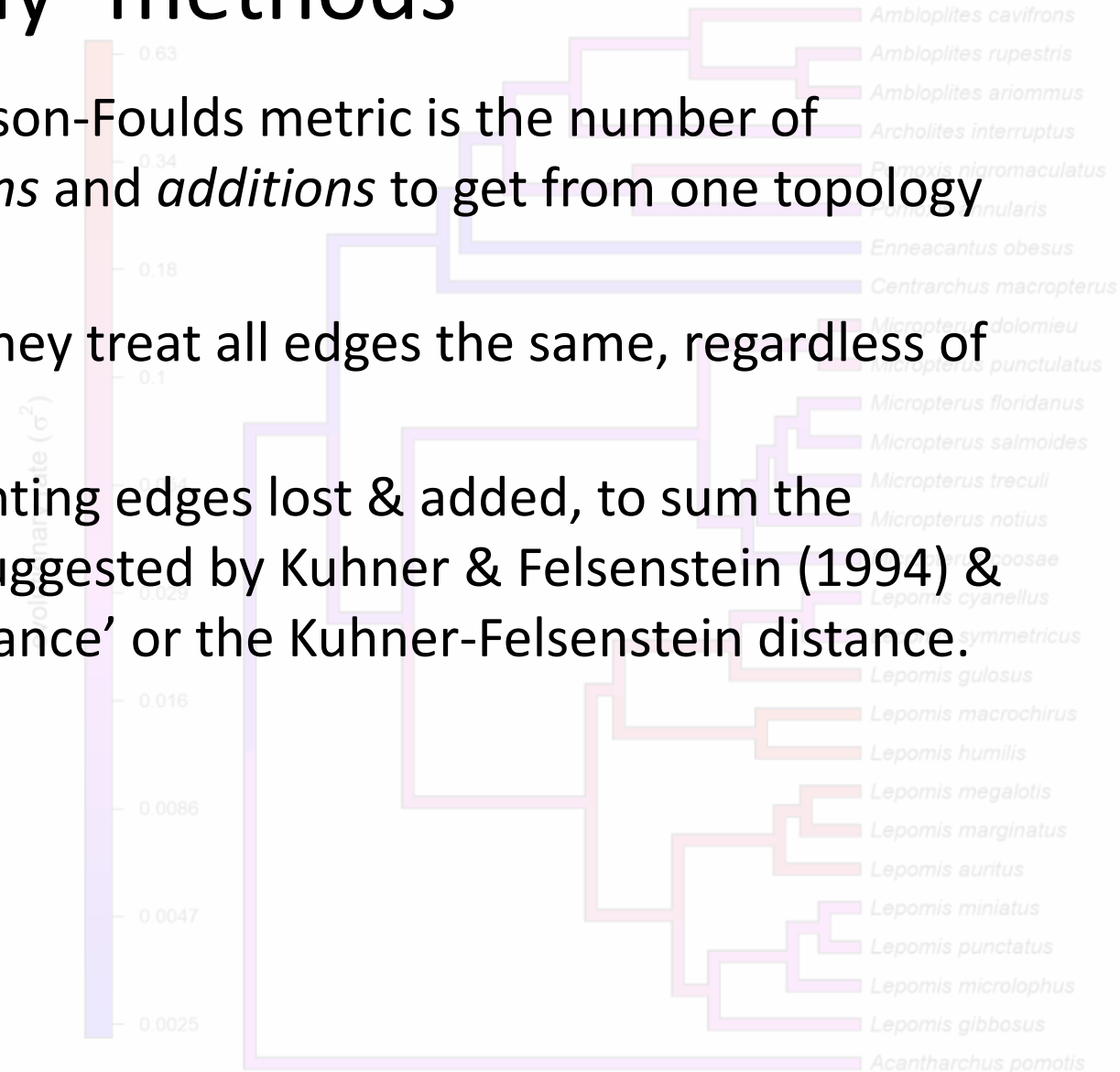
- An alternative interpretation of the Robinson-Foulds metric is the number of changes is the number of edge *contractions* and *additions* to get from one topology to the other.





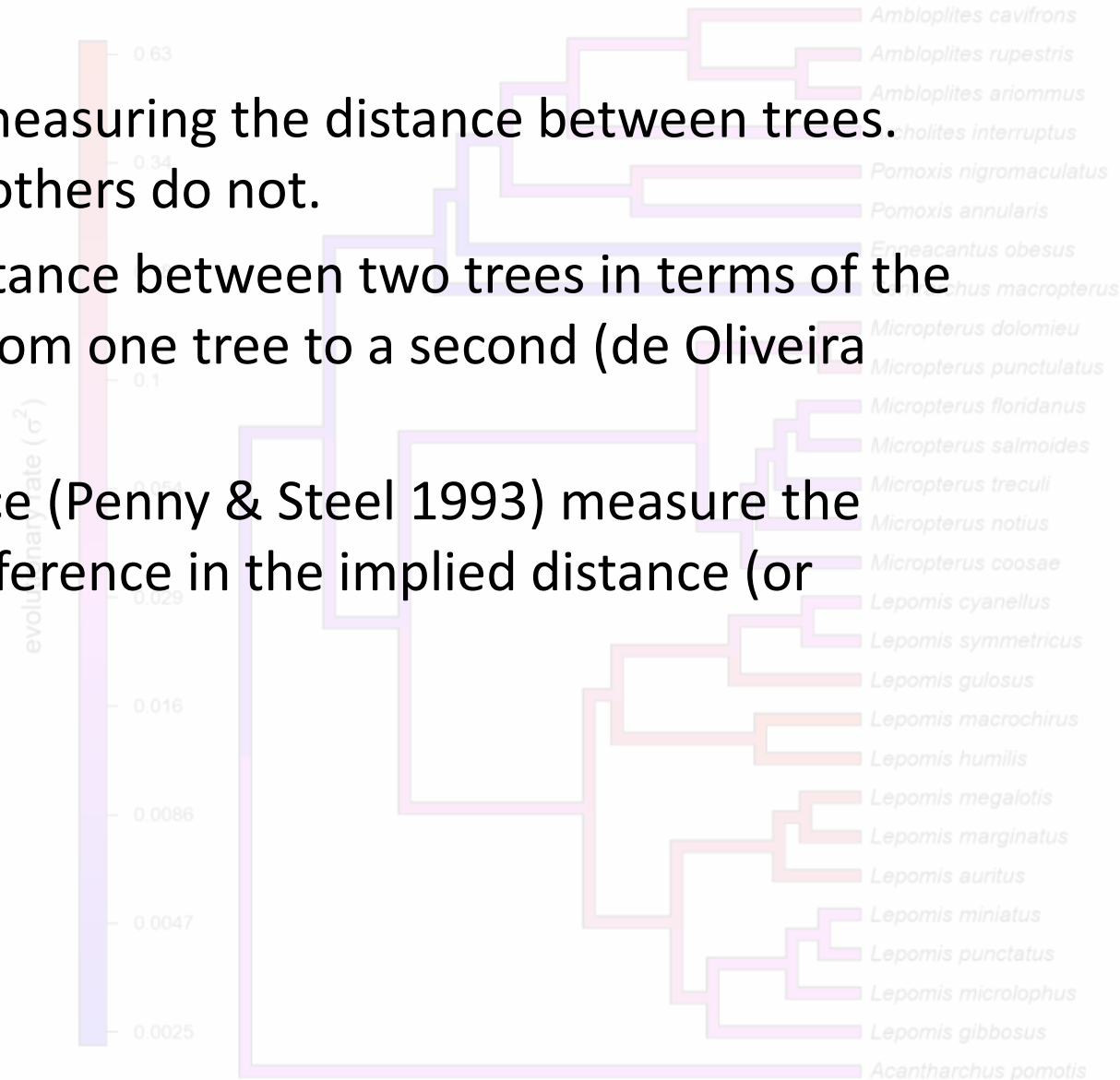
# Obvious shortcoming in 'topology only' methods

- An alternative interpretation of the Robinson-Foulds metric is the number of changes is the number of edge *contractions* and *additions* to get from one topology to the other.
- A disadvantage of these methods is that they treat all edges the same, regardless of their length.
- One other approach is instead of just counting edges lost & added, to sum the length of these edges. This method was suggested by Kuhner & Felsenstein (1994) & is sometimes called the 'branch score distance' or the Kuhner-Felsenstein distance.



# Other tree distance measures

- There are a variety of other methods for measuring the distance between trees. Some take branch lengths into account & others do not.
- SPR distance measures the topological distance between two trees in terms of the number of SPR events required to move from one tree to a second (de Oliveira Martins 2008).
- Path difference or weighted path difference (Penny & Steel 1993) measure the difference between trees based on the difference in the implied distance (or weighted distances) between species.



Untitled1\* ×

Source on Save

```
1 data(sunfish.tree)
2 data(sunfish.data)
3 ## extract character of interest
4 gw<-setNames(sunfish.data$gape
5   rownames(sunfish.data))
6 ## run penalized-likelihood op
7 ## lambda=0.1 is arbitrary
8 fitBM<-multirateBM(sunfish.tre
9   lambda=0.01)
10 ## print and plot the results
11 print(fitBM)
12 plot(fitBM,ftype="i",fsize=0.8
13   outline=TRUE)
14
```

14:1 (Top Level)

Console Terminal Background Jobs

R 4.2.2 ~ /

```
+ lambda=0.01)
Beginning optimization....
Optimization iteration 1. Using "L-B
Best (penalized) log-likelihood so f
Done optimization.
> ## print and plot the results
> print(fitBM)
Multi-rate Brownian model using mult
```

Fitted rates:

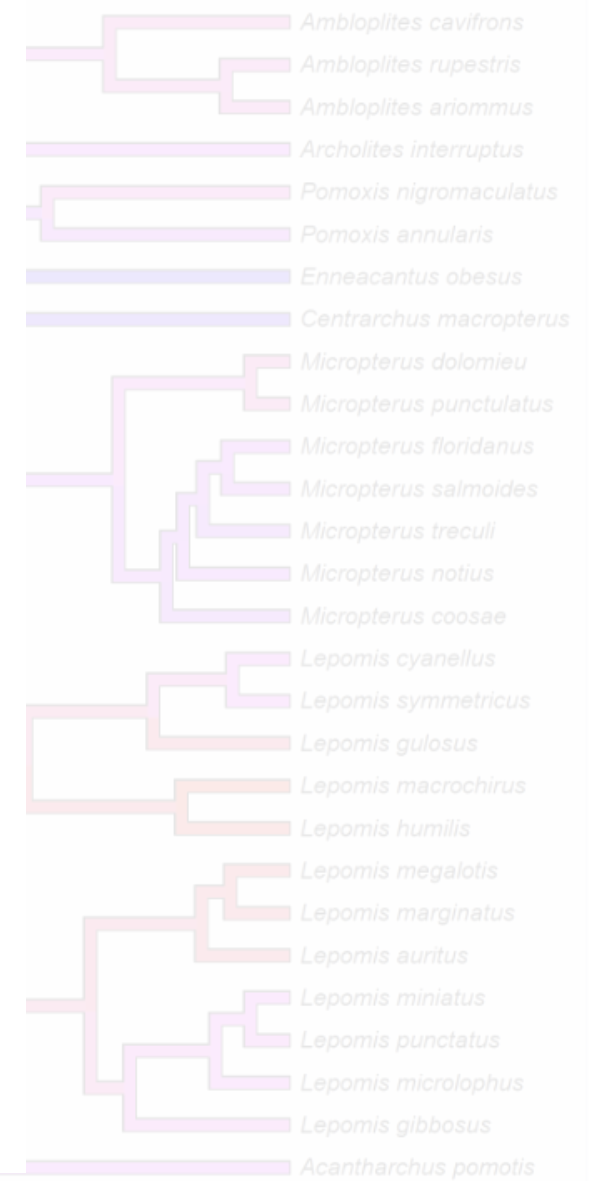
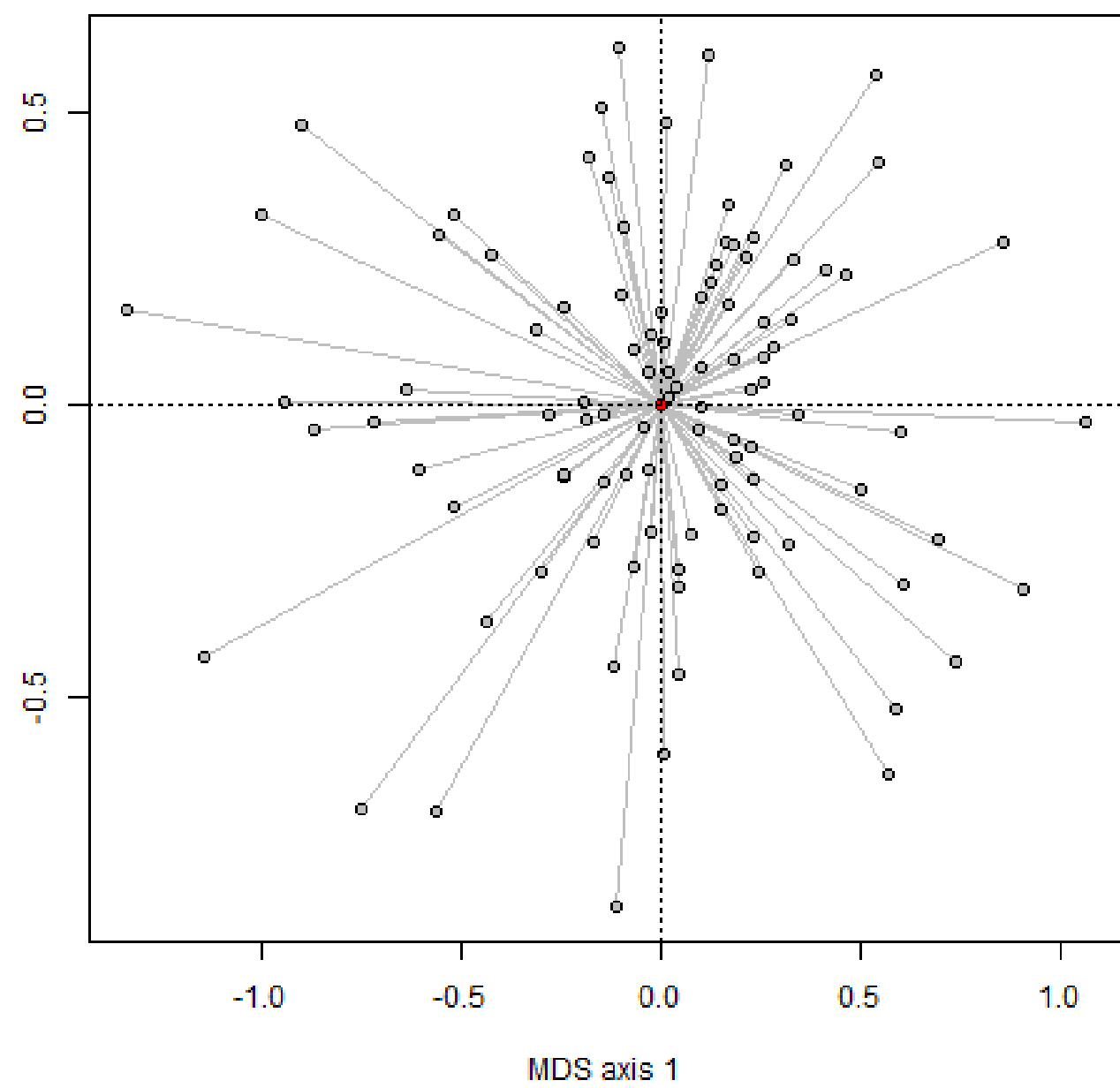
Acantharchus_pomotis	Lepomis_gibbosus
0.060276	0.0380
Lepomis_miniatus	Lepomis_auritus
0.042838	0.254773

lambda penalty term: 0.01  
log-likelihood: 40.148315  
AIC: 31.703369

R thinks it has found a solution.

```
> plot(fitBM,ftype="i",fsize=0.8,lwd
+   outline=TRUE)
>
```

MDS axis 2





Untitled1\*

```
1 data(sunfish.tree)
2 data(sunfish.data)
3 ## extract character of interest
4 gw<-setNames(sunfish.data$gape.wid
5   rownames(sunfish.data))
6 ## run penalized-likelihood optimi
7 ## lambda=0.1 is arbitrary
8 fitBM<-multirateBM(sunfish.tree,gw
9   lambda=0.01)
10 ## print and plot the results
11 print(fitBM)
12 plot(fitBM,ftype="i",fsize=0.8,lwd
13   outline=TRUE)
14
```

14.1 (Top Level)

Console Terminal Background Jobs

R 4.2.2 ~/

```
+ lambda=0.01)
Beginning optimization....
```

```
Optimization iteration 1. Using "L-BFGS-
Best (penalized) log-likelihood so far:
Done optimization.
```

```
> ## print and plot the results
> print(fitBM)
Multi-rate Brownian model using multirat
```

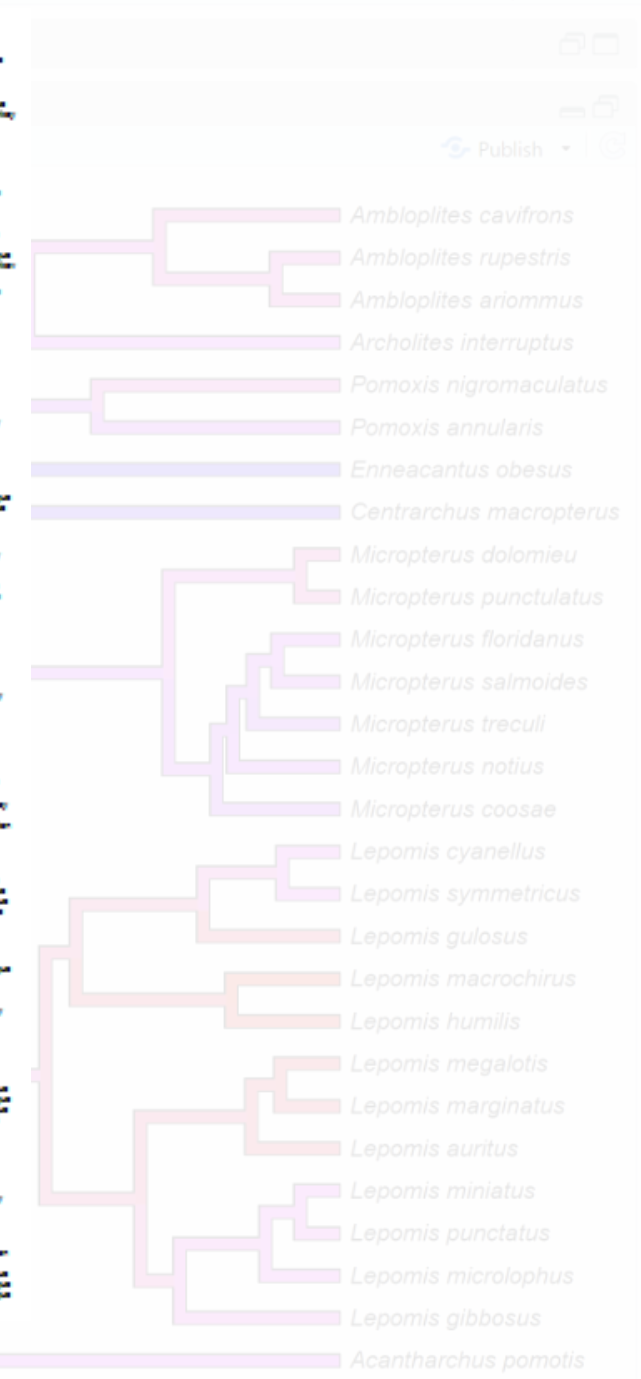
Fitted rates:

```
Acantharchus_pomotis Lepomis_gibbosus L
0.060276 0.038039
Lepomis_miniatius Lepomis_auritus Lepomi
0.042838 0.254773
```

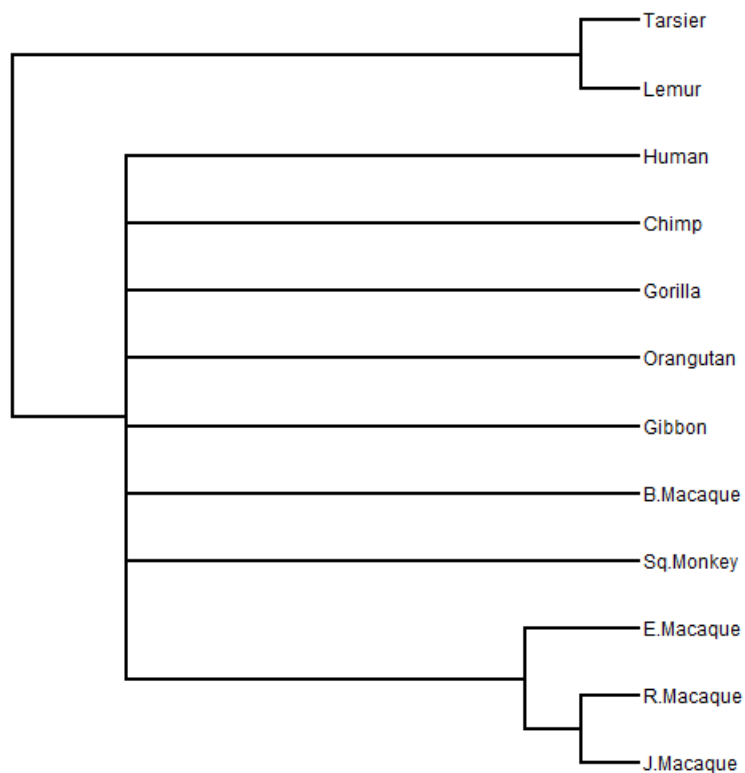
```
lambda penalty term: 0.01
log-likelihood: 40.148315
AIC: 31.703369
```

R thinks it has found a solution.

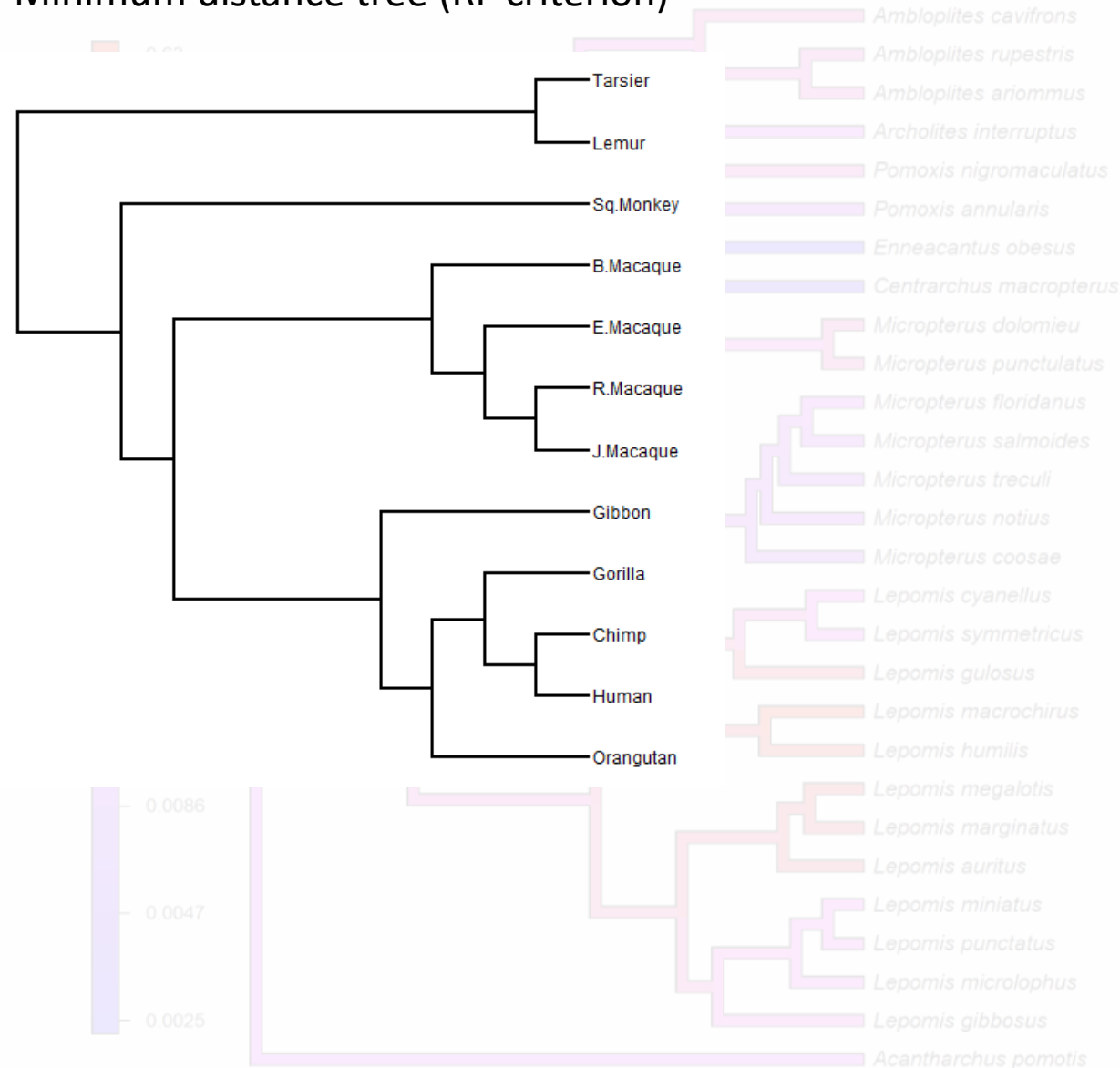
```
> plot(fitBM,ftype="i",fsize=0.8,lwd=6,
+   outline=TRUE)
>
```

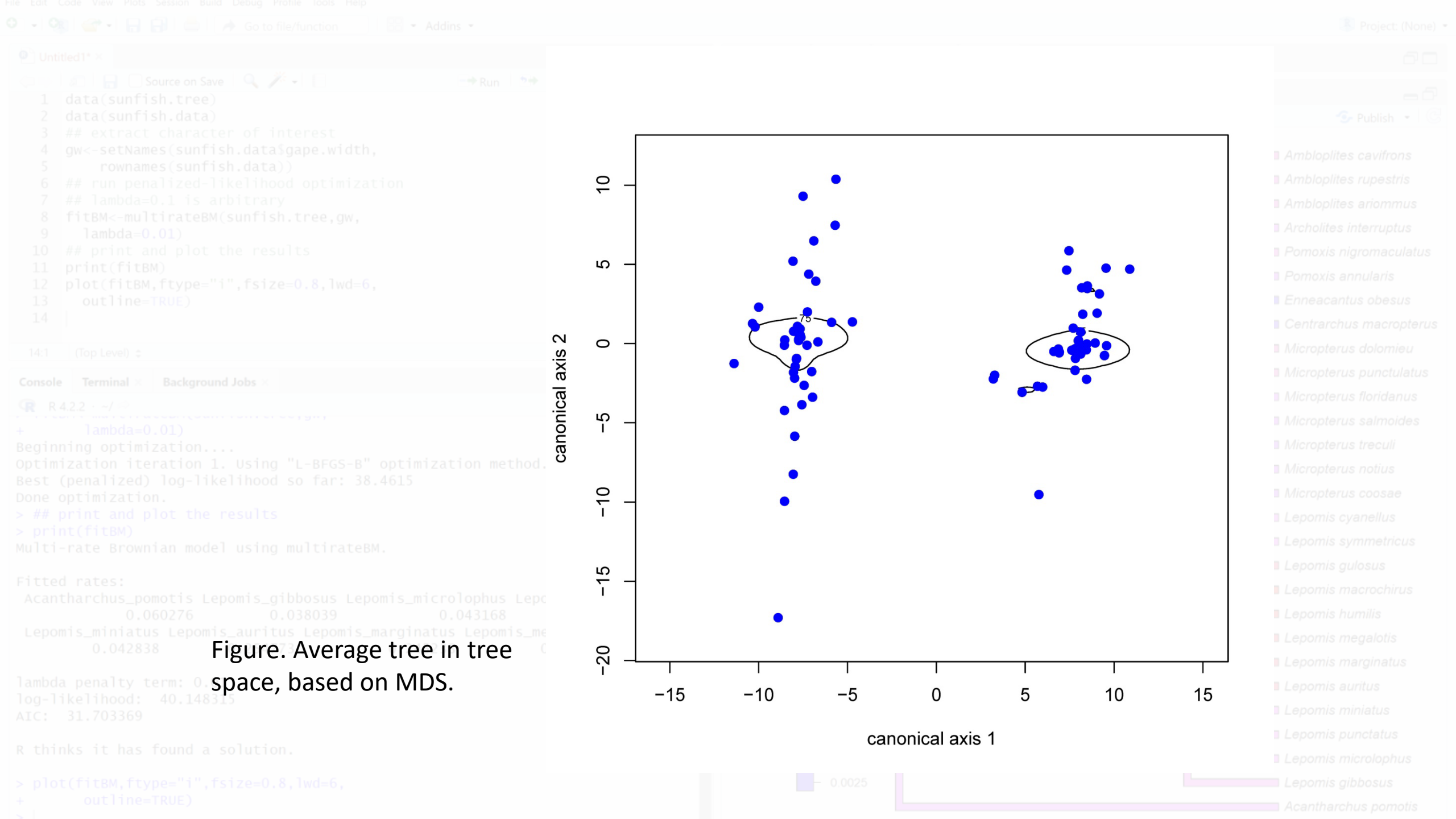


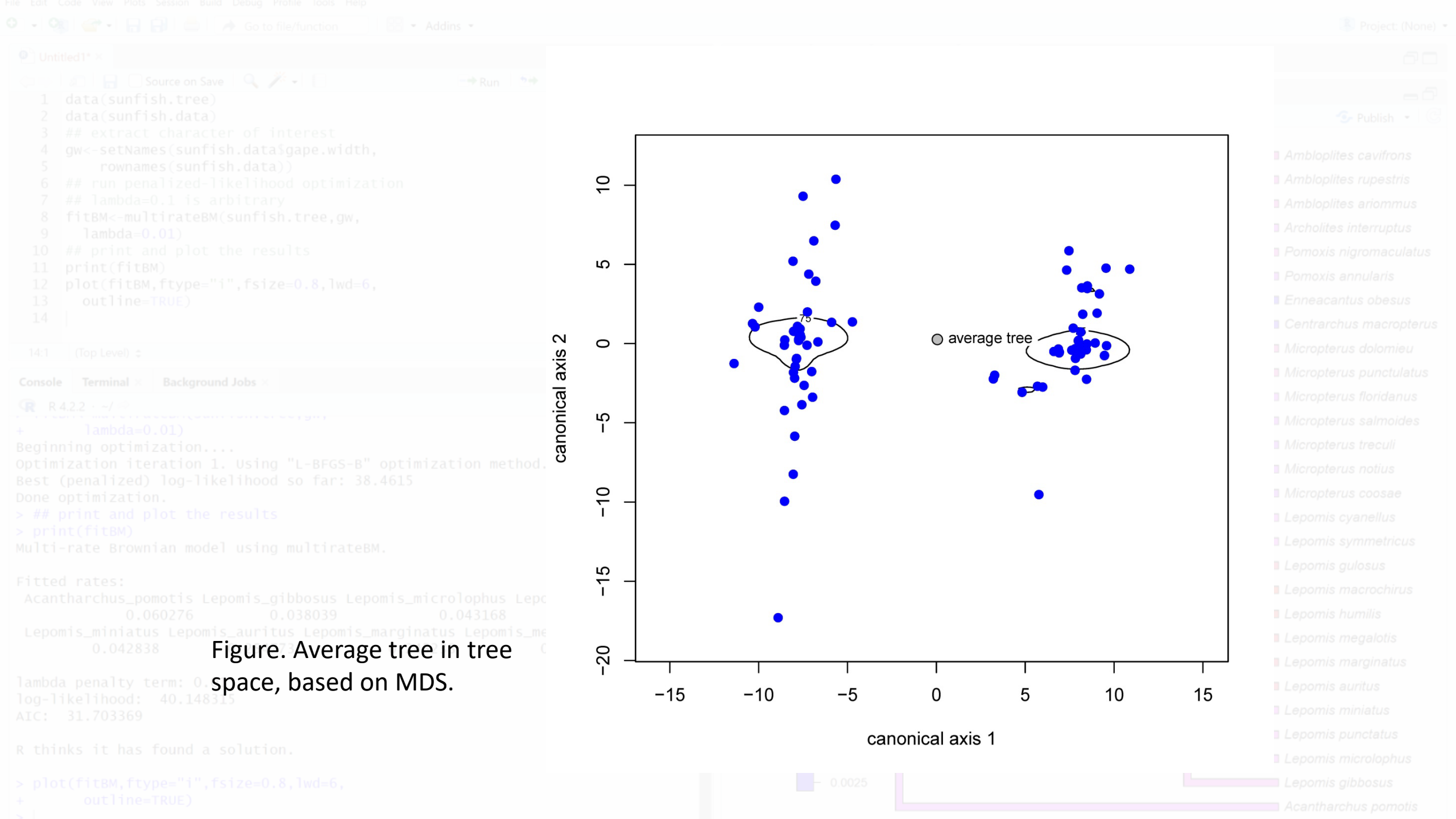
## Majority-rule consensus tree



## Minimum distance tree (RF criterion)







# Consensus trees

## Types of consensus trees:

1. Strict consensus trees.

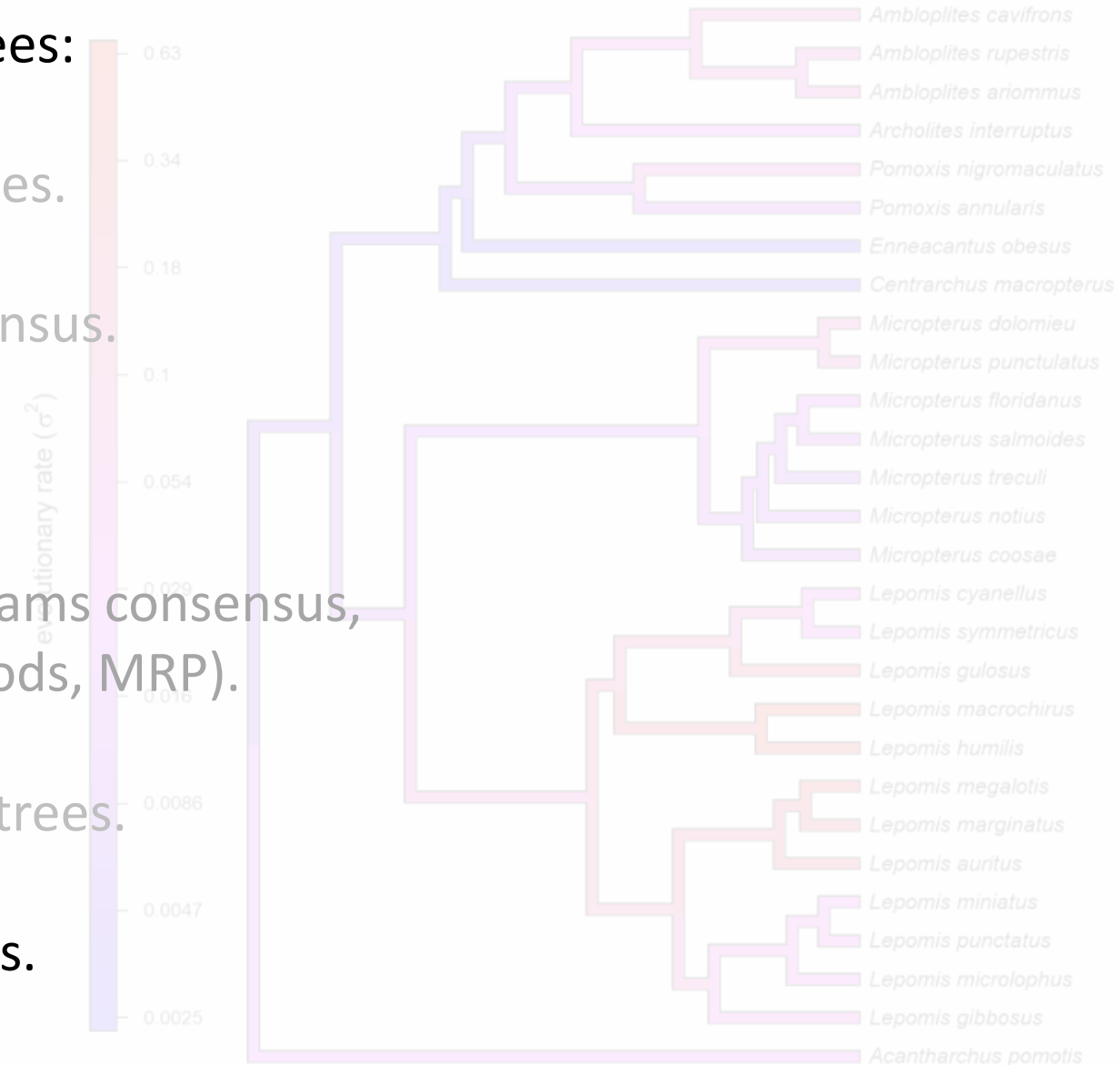
2. Majority rule consensus.

3. “X-” consensus.

4. Other methods (Adams consensus, compatibility methods, MRP).

5. Minimum distance trees.

6. Consensus networks.



```
1 data(sunfish.tree)
2 data(sunfish.data)
3 ## extract character of interest
4 gw<-setNames(sunfish.data$gape.width,
5   rownames(sunfish.data))
6 ## run penalized-likelihood optimization
7 ## lambda=0.1 is arbitrary
8 fitBM<-multirateBM(sunfish.tree,gw,
9   lambda=0.01)
10 ## print and plot the results
11 print(fitBM)
12 plot(fitBM,ftype="i",fsize=0.8,lwd=6,
13   outline=TRUE)
14
```

14:1 (Top Level)

Console Terminal Background Jobs

```
R 4.2.2 ~ /
+ lambda=0.01)
Beginning optimization....
Optimization iteration 1. Using "L-BFGS-B" optimization method.
Best (penalized) log-likelihood so far: 38.4615
Done optimization.
> ## print and plot the results
> print(fitBM)
Multi-rate Brownian model using multirateBM.

Fitted rates:
Acantharchus_pomotis Lepomis_gibbosus Lepomis_microlophus Lepomis_punctatus
0.060276 0.038039 0.043168 0.048633
Lepomis_miniatus Lepomis_auritus Lepomis_marginatus Lepomis_megalotis
0.042838 0.254773 0.25238 0.306999

lambda penalty term: 0.01
log-likelihood: 40.148315
AIC: 31.703369

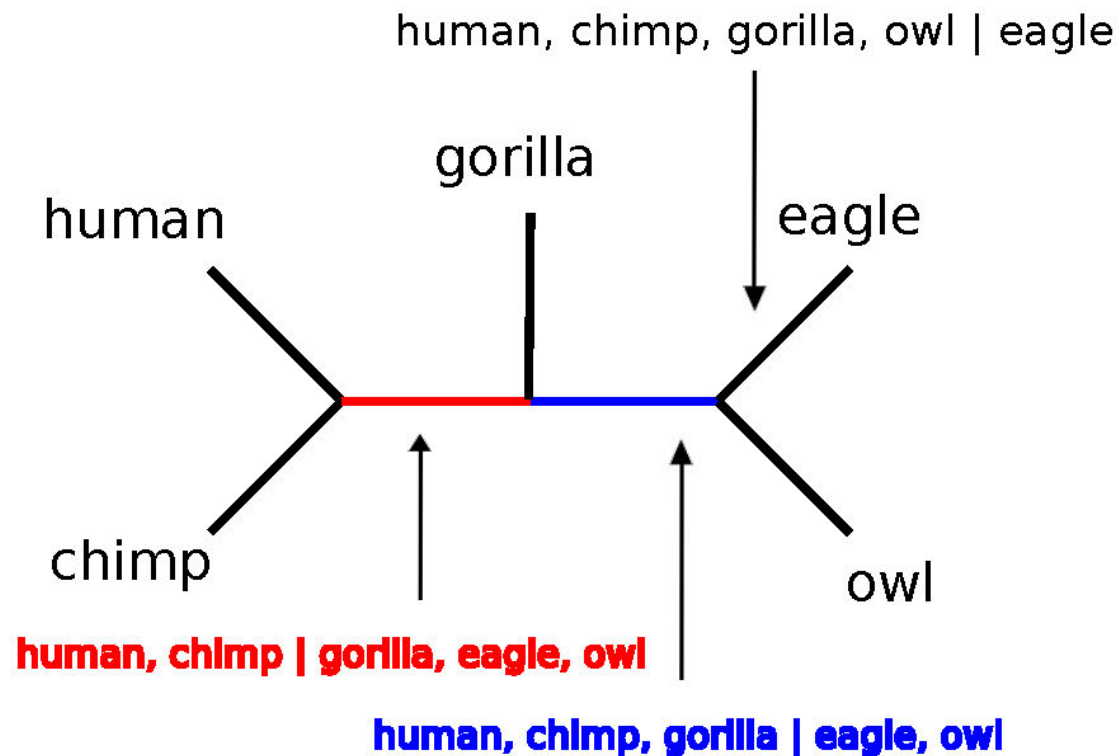
R thinks it has found a solution.

> plot(fitBM,ftype="i",fsize=0.8,lwd=6,
+   outline=TRUE)
>
```



# Splits (Definition)

- ▶ A split is a bipartition of the taxa (labels, species) into two sets
- ▶ A bipartition of one taxa vs. the rest is known as a trivial split
- ▶ A split corresponds to an edge in a phylogenetic tree, removing the edge from a tree creates two sub-trees
- ▶ A tree only contains compatible splits



Project: (None)

Publish

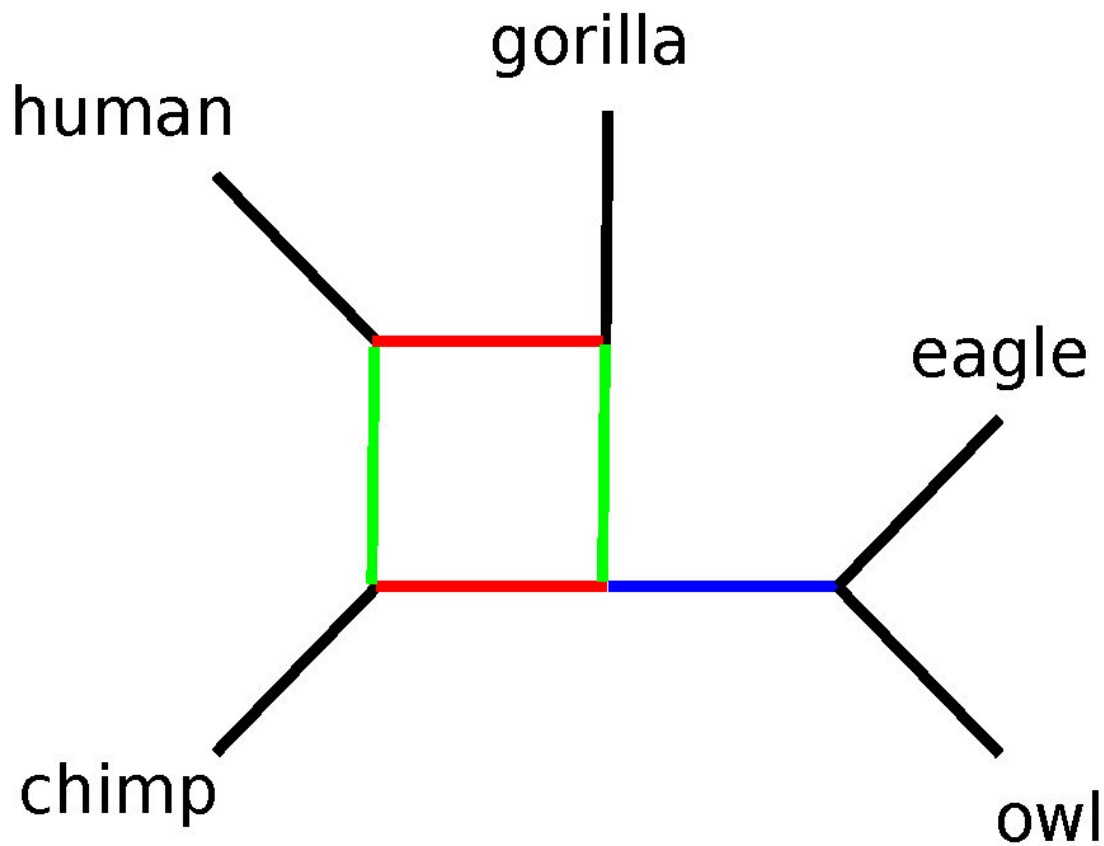
- Ambloplites cavifrons
- Ambloplites rupestris
- Ambloplites ariommus
- Archolites interruptus
- Pomoxis nigromaculatus
- Pomoxis annularis
- Enneacantus obesus
- Centrarchus macropterus
- Micropterus dolomieu
- Micropterus punctulatus
- Micropterus floridanus
- Micropterus salmoides
- Micropterus treculi
- Micropterus notius
- Micropterus coosae
- Lepomis cyanellus
- Lepomis symmetricus
- Lepomis gulosus
- Lepomis macrochirus
- Lepomis humilis
- Lepomis megalotis
- Lepomis marginatus
- Lepomis auritus
- Lepomis miniatus
- Lepomis punctatus
- Lepomis microlophus
- Lepomis gibbosus
- Acantharchus pomotis



# Incompatible Splits

Some collections of splits fit not on a tree but on a splits graph.

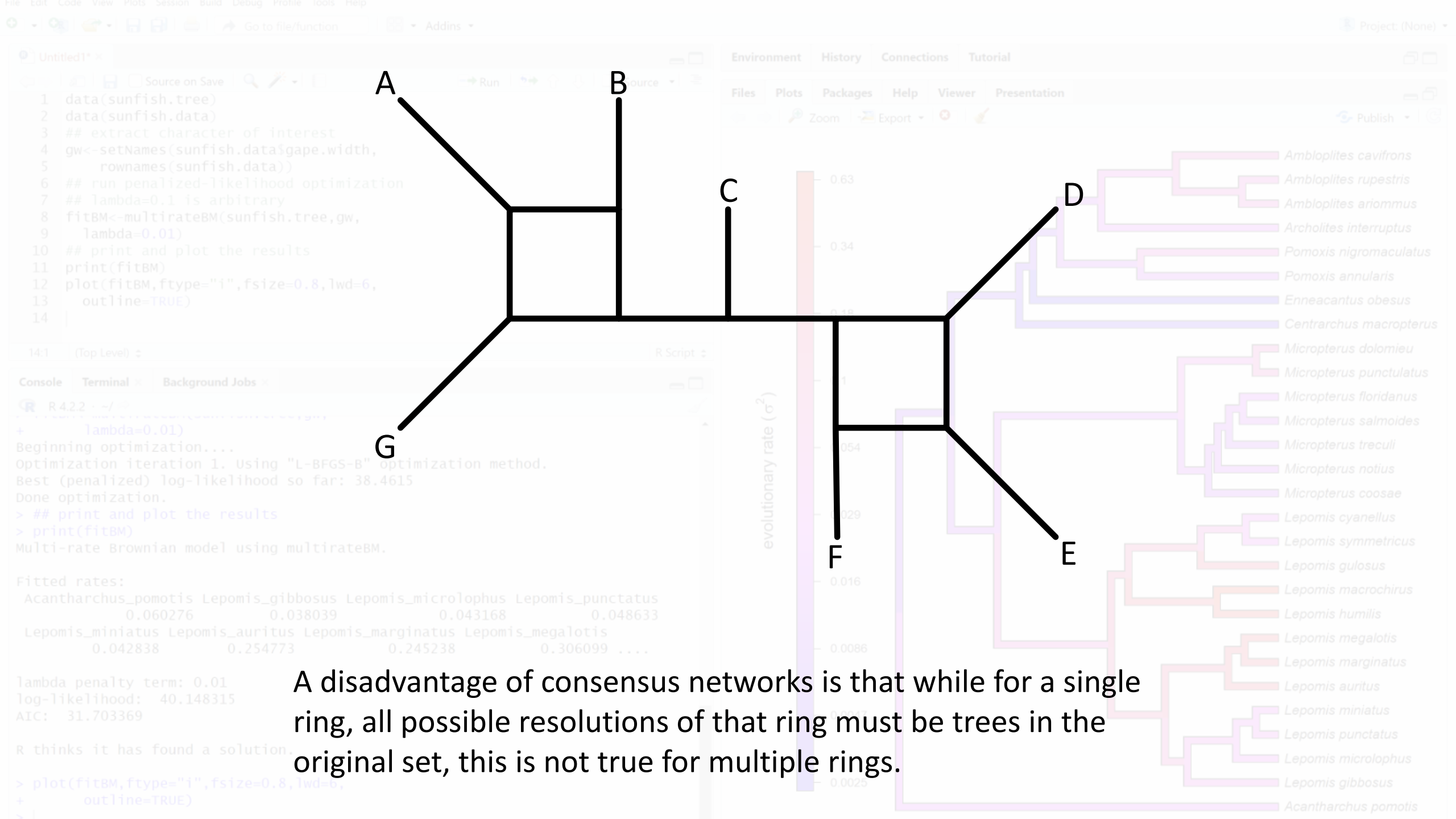
**human, chimp | gorilla, eagle, owl**  
**human, gorilla | chimp, eagle, owl**



Project: (None)

Publish

- Ambloplites cavifrons
- Ambloplites rupestris
- Ambloplites ariommus
- Archolites interruptus
- Pomoxis nigromaculatus
- Pomoxis annularis
- Enneacantus obesus
- Centrarchus macropterus
- Micropterus dolomieu
- Micropterus punctulatus
- Micropterus floridanus
- Micropterus salmoides
- Micropterus treculi
- Micropterus notius
- Micropterus coosae
- Lepomis cyanellus
- Lepomis symmetricus
- Lepomis gulosus
- Lepomis macrochirus
- Lepomis humilis
- Lepomis megalotis
- Lepomis marginatus
- Lepomis auritus
- Lepomis miniatus
- Lepomis punctatus
- Lepomis microlophus
- Lepomis gibbosus
- Acantharchus pomotis



A disadvantage of consensus networks is that while for a single ring, all possible resolutions of that ring must be trees in the original set, this is not true for multiple rings.

