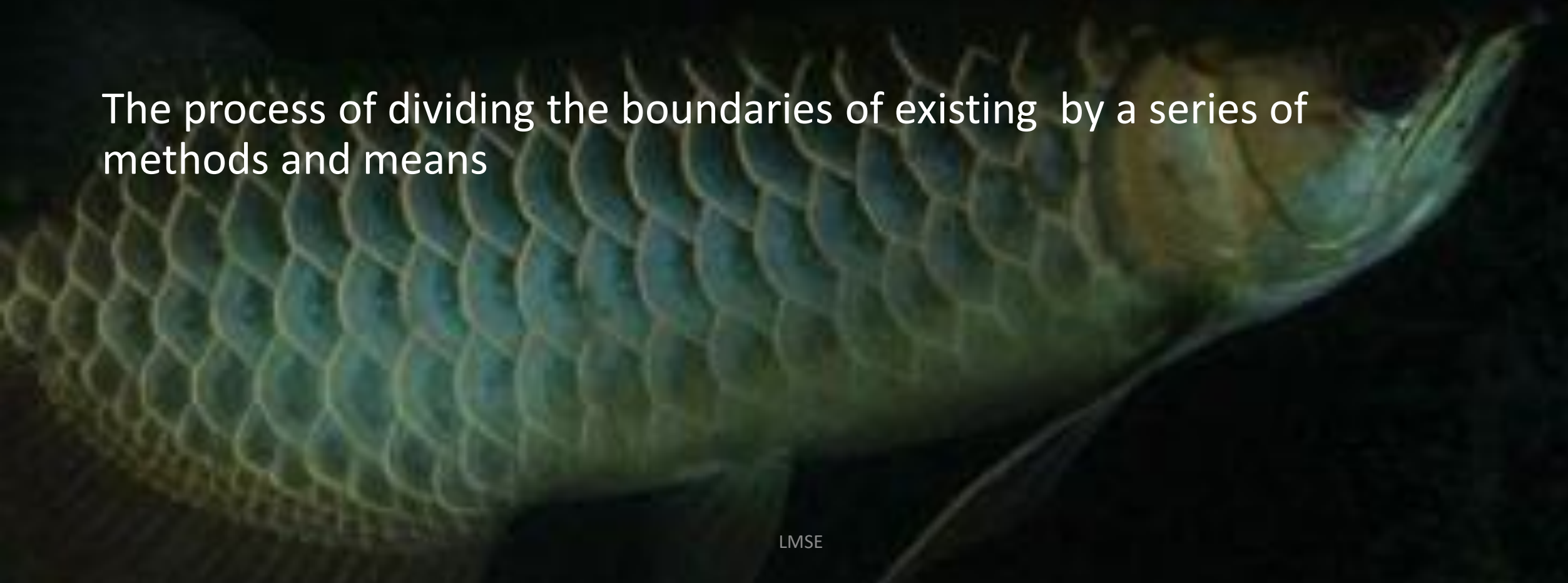


species delimitation

what is the species delimitation?

The process of dividing the boundaries of existing by a series of methods and means



BFD(Bayes factor delimitation)

- A method of species delimitation in a Bayesian framework using SNP data and the programs SNAPP and BEAST.
- MLE(marginal likelihood estimate) value

The advantage of BFD

- **One advantage** of BFD over other species ,delimitation approaches is the ability to integrate over species trees during the species delimitation procedure, which removes the constraint of specifying a guide tree that represents the true species relationships.
- **Another advantage** is the ability to compare models that contain different numbers of species.
- **disadvantage**
the user needs to predefine the number of species and sample assignments, and this prevents the method from searching among all possible species assignments.



model

three sample,

modle1 A B C D

modle2 A C B D

modle3 A BC D

modle4 ABC D

modle5 A B C D


```
huw@rocky: ~/Documents/cesky-krumlov/BFDstar-tutorial/runA
File Edit View Search Terminal Help
Step      theta      likelihood      contribution      ESS
0          1          -689.959        -207.5882         7.3537
1          0.7278      -783.28         -163.0258         3.2729
2          0.5123      -712.4686       -125.3681         2.8007
3          0.3459      -707.6063       -92.6481          8.4624
4          0.2217      -708.9683       -63.4489          15.3821
5          0.1326      -711.6711       -43.1487          8.1671
6          0.0722      -715.4402       -27.208           28.9048
7          0.0343      -743.3929       -15.9101          10.1209
8          0.0132      -785.3403       -7.7228           8.3383
9          0.0034      -795.7847       -2.4576           12.4234
10         0.0003      -783.5203       -0.2647           12.1521
11         0          -807.7434       0                 15.0655

marginal L estimate = -748.7911131431778

Total wall time: 51 seconds
Done
```





modle

$$BF=2*(MLE1-MLE2)$$

A negative BF value indicates support in favor of model1.

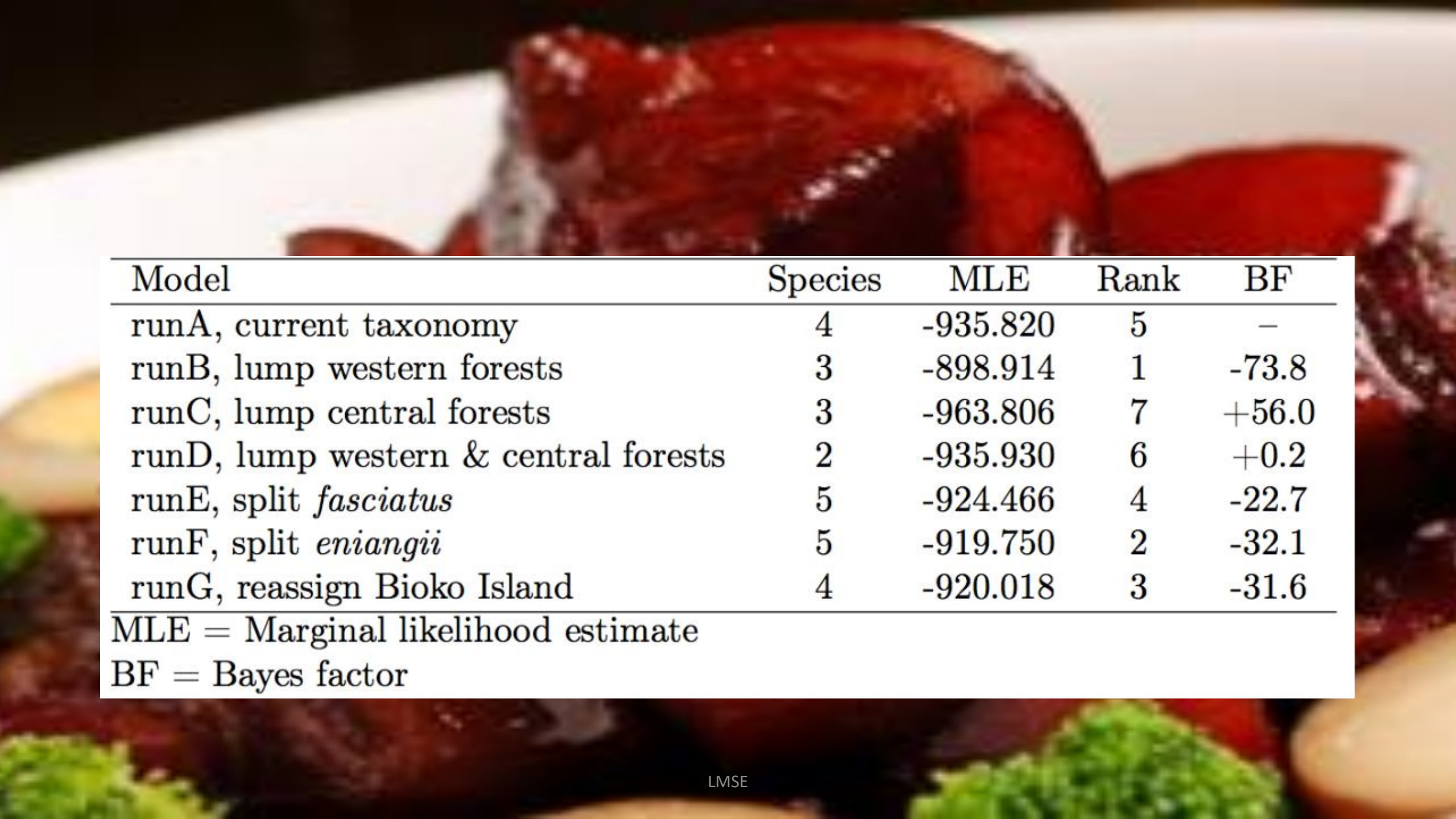
A positive BF value indicates support in favor of model 2.

$0 < \ln(BF) < 1$ is not worth more than bare mention ($1 < BF < 2.7$)

$1 < \ln(BF) < 3$ is positive evidence ($2.7 < BF < 20$)

$3 < \ln(BF) < 5$ is strong support ($20 < BF < 148$)

$5 < \ln(BF)$ is decisive ($148 < BF$)



Model	Species	MLE	Rank	BF
runA, current taxonomy	4	-935.820	5	—
runB, lump western forests	3	-898.914	1	-73.8
runC, lump central forests	3	-963.806	7	+56.0
runD, lump western & central forests	2	-935.930	6	+0.2
runE, split <i>fasciatus</i>	5	-924.466	4	-22.7
runF, split <i>eniangii</i>	5	-919.750	2	-32.1
runG, reassign Bioko Island	4	-920.018	3	-31.6

MLE = Marginal likelihood estimate

BF = Bayes factor



What do we need in BFD analysis?

- 1. **programs**: We will be using the free, open-source software package, BEAST (Bayesian Evolutionary Analysis Sampling Trees; <http://beast2.org>), for estimating species trees. For this tutorial, you will need to use BEAST version 2.1 or better. The distribution comes with the BEAUTi, including SNAPP.
- 2. **data**: the data should be in binary format(necessary for SNAPP)

THANK YOU

