EEOB563 – Assignment #5

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F84 is not available in raxml, so I'm using F81. The trees are not the same (see following tanglegram), they also have different log-likelihood scores:

```
1  Raxml:  -54568.308901
2  FastMe: -54674.432495
```
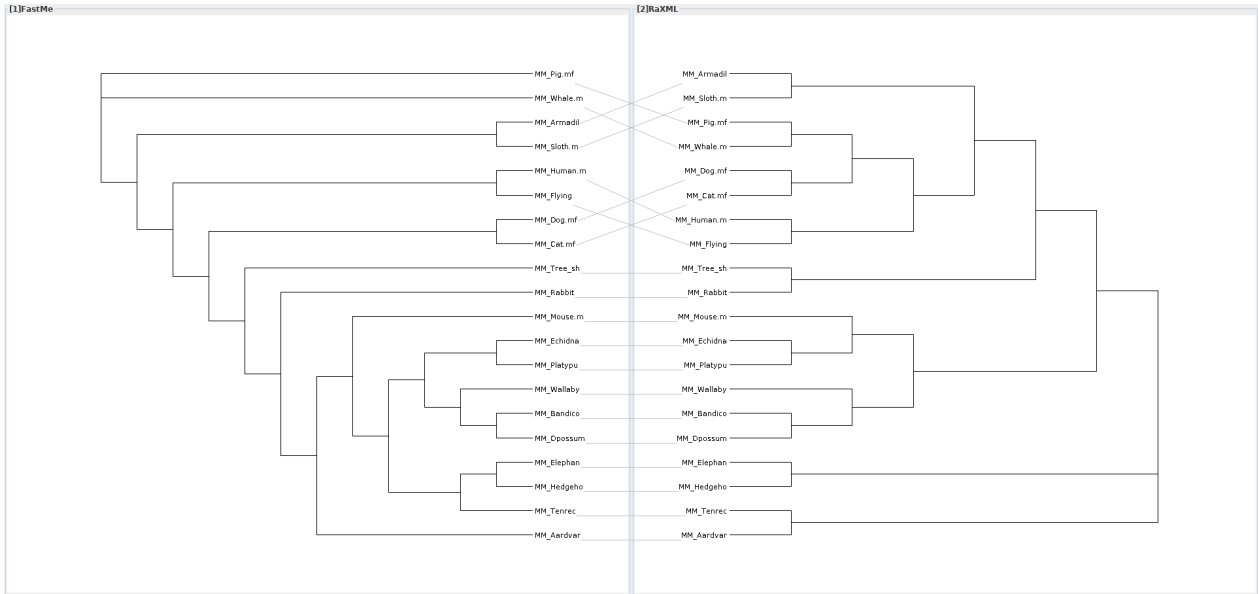

Figure 1: Tanglegram made with Dendroscope (zoom in)

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These are the two commands I used:

```
1  raxml-ng --search --msa ../alignment.phy --model model_codons --prefix codons --seed
       12 --brlen scaled
2  raxml-ng --search --msa ../alignment.phy --model model_genes --prefix genes --seed 12
        --brlen scaled
```

The two models looked like this:

```
1  model_codons:
2    GTR+G+FO, COBX=1-4482/3
3
4  model_genes:
5    GTR+G+FO, cob=1-1248
6    GTR+G+FO, cox1=1249-2808
7    GTR+G+FO, cox2=2809-3543
8    GTR+G+FO, cox3=3544-4482
```

These are the log-likelihoods for the best tree:

```
1  Codons: -45373.634679
2  Genes:  -45270.430490
```

They are much better than the original tree BUT the evolution models I used are different so I'm not sure if it's directly comparable.

Anyway, here is the difference between the Gene partitioned tree and the original RaXML tree, they are very similar except for the rabbit:
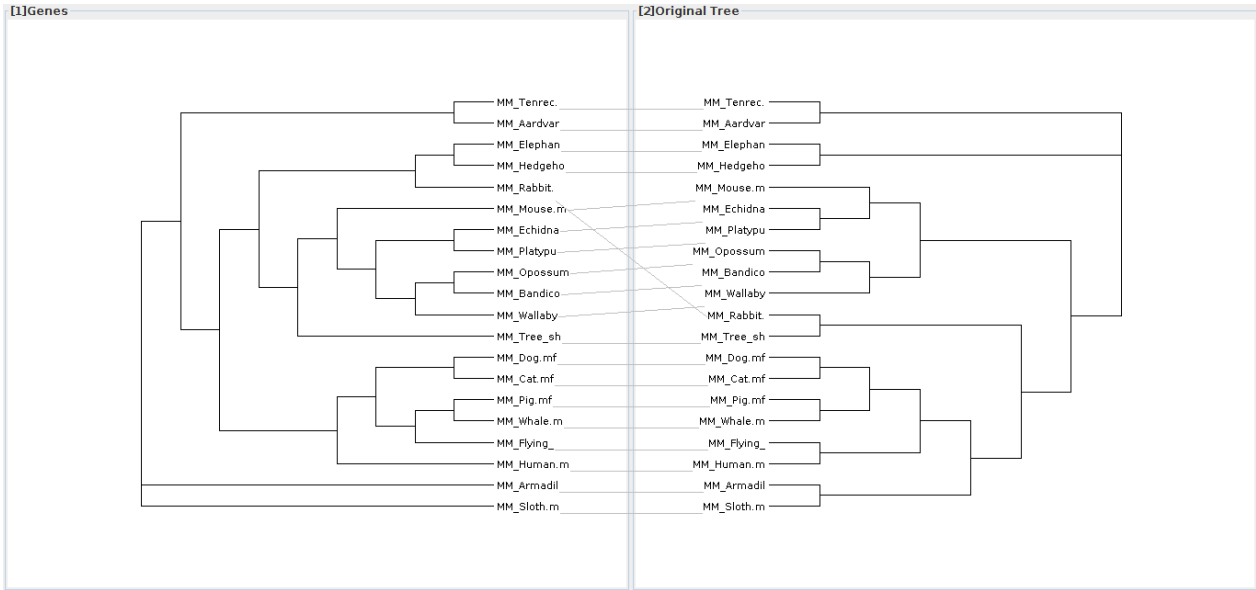
Figure 2: Tanglegram made with Dendroscope (zoom in)

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I had expected a runtime of $\geq$ 10 hours from what the others have told me, I don't remember the runtimes from the lab anymore. In reality, it only took about 6:30 hours though, so I was lucky. This is my slurm script:

```
1   #!/bin/bash
2
3   #SBATCH --time=10:30:00   # walltime limit (HH:MM:SS)
4   #SBATCH --nodes=1    # number of nodes
5   #SBATCH --ntasks-per-node=16   # 16 processor core(s) per node
6   #SBATCH --job-name="5.5_assignment"
7   #SBATCH --mail-user=dpsaroud@iastate.edu   # email address
8   #SBATCH --mail-type=BEGIN
9   #SBATCH --mail-type=END
10  #SBATCH --mail-type=FAIL
11
12  # LOAD MODULES, INSERT CODE, AND RUN YOUR PROGRAMS HERE#!/bin/bash
13  cd /home/dpsaroud/EEOB563/assignments/5/5
14
15  /home/dpsaroud/bin/raxml-ng --all --msa ../alignment.phy --model GTR+G --seed 12 --
         threads 16 --bs-metric fbp --bs-trees 1000
```

Here is the tree, finally the tree is further away from the animals:
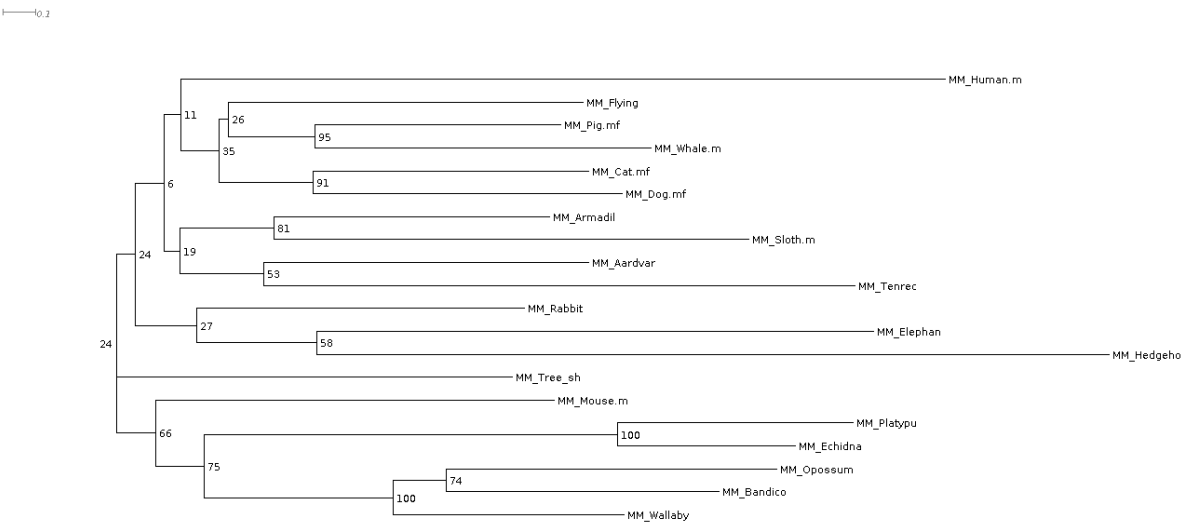
Figure 3: ML tree with bootstrap support values