

# phylogenetic\_model\_comparison

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In this notebook, we carry out model comparison for different models of rhythm evolution. We compare the following models:

```
model.types <- c('BM_UV_nondist',  
                 'BM_UV_dist',  
                 'OU_UV_nondist',  
                 'OU_UV_dist')
```

```
loos <- readRDS('frequency_loos.RDS')  
loo_model_weights(loos)
```

```
## Method: stacking  
## -----  
##           weight  
## model1 0.013  
## model2 0.001  
## model3 0.000  
## model4 0.987
```

We see that model 4 (a distributional OU model) is the best fit to the data, with > 90% of the stacking weight.

We validate this result for models fitted only on mammals within the phylogeny:

```
loos <- readRDS('frequency_loos_mammals.RDS')  
loo_model_weights(loos)
```

```
## Method: stacking  
## -----  
##           weight  
## model1 0.000  
## model2 0.022  
## model3 0.053  
## model4 0.925
```

as well as birds:

```
loos <- readRDS('frequency_loos_birds.RDS')  
loo_model_weights(loos)
```

```
## Method: stacking  
## -----  
##           weight  
## model1 0.000  
## model2 0.000  
## model3 0.000
```

## model4 1.000