Untitled

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5/16/2024

The models under comparison have the following order:

1. Predictors included, distributional
2. Predictors included, non-distributional
3. Predictors not included, distributional
4. Predictors not included, non-distributional

```
loo.objects <- readRDS('model.comparisons.RDS')

dominant.compare <- loo.objects[[1]]
dominant.stack <- loo.objects[[2]]
rhythm.compare <- loo.objects[[3]]
rhythm.stack <- loo.objects[[4]]
```

Raw ELPD values

Dominant frequency

```
dominant.compare
```

```
##        elpd_diff se_diff
## model1    0.0       0.0
## model3   -0.9       2.9
## model4 -133.8      25.4
## model2 -134.0      26.1
```

The distributional model with predictors included has the highest ELPD value, but it is not substantially higher than the null distributional model (e.g., more than 2 std. errors higher).

Rhythm

```
rhythm.compare
```

```
##        elpd_diff se_diff
## model3    0.0       0.0
## model1   -2.3       2.7
## model4 -199.5      27.2
## model2 -200.2      27.2
```

The null distributional model has the highest ELPD value, but it is not substantially higher than the distributional model with predictors (e.g., more than 2 std. errors higher).

Stack

Dominant frequency

In terms of stacking weight, we see that the distributional models with predictors has the majority of the stacking weight, but the null distributional model still has a substantial amount of stacking weight.

```
dominant.stack
```

```
## Method: stacking
## ------
##        weight
## model1 0.612
## model2 0.012
## model3 0.376
## model4 0.000
```

Rhythm

In terms of stacking weight, we see that the null distributional model outperforms the distributional model with predictors but the full distributional model has a not insignificant portion of the stacking weight.

```
rhythm.stack
```

```
## Method: stacking
## ------
##        weight
## model1 0.186
## model2 0.014
## model3 0.800
## model4 0.000
```