The following appendix accompanies the article

Do pingers reduce interactions between bottlenose dolphins and nets? Experimental evidence from artisanal fisheries around the Balearic Islands

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Appendix 1. Statistical analysis: model building and outputs

Presence/absence of evidence of dolphins interacting with net:

First, a simple model with just the experimental conditions (here I is the 1/0 response variable representing the presence (1) or absence (0) of evidence of dolphins interacting with the net):

```
>summary(mod)
Call:
glm(formula = I ~ factor(PINGER_TREATMENT_CODE), family = binomial)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.4172  -0.3880  -0.2967  -0.2967   2.5080

Coefficients:
                             Estimate Std. Error z value Pr(>|z|)
(Intercept)                   -2.3979     0.3015  -7.953 1.82e-15 ***
factor(PINGER_TREATMENT_CODE)2  -0.1507     0.3843  -0.392   0.6949
factor(PINGER_TREATMENT_CODE)3  -0.7030     0.3515  -2.000   0.0455 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 488.32  on 1148  degrees of freedom
Residual deviance: 482.78  on 1146  degrees of freedom
AIC: 488.78

Number of Fisher Scoring iterations: 5
```

But we notice large variation between vessels within treatments, so fit a model with a fixed vessel effect:

```
>mod2 <- glm(formula = I ~ factor(VESSEL) + factor(PINGER_TREATMENT_CODE), family = binomial)
```

We find that VESSEL is highly significant:

```
> anova(mod2,test='Chi')
Analysis of Deviance Table

Model: binomial, link: logit

Response: I

Terms added sequentially (first to last)

Df Deviance Resid. Df Resid. Dev P(>|Chi|)
NULL                                    1148     488.32
factor(VESSEL)                  59   126.58      1089     361.74  7.73e-07
factor(PINGER_TREATMENT_CODE)    1     0.72      1088     361.02      0.40
> extractAIC(mod2)
[1]  61.0000 483.0167
```

And that this model fits significantly better:

```
> anova(mod,mod2,test='Chi')
Analysis of Deviance Table

Model 1: I ~ factor(PINGER_TREATMENT_CODE)
Model 2: I ~ factor(VESSEL) + factor(PINGER_TREATMENT_CODE)
  Resid. Df Resid. Dev   Df Deviance P(>|Chi|)
1      1146     482.78
2      1088     361.02   58   121.77 1.986e-06
```

However, because we are interested in the effect of treatment across vessels *in general* then perhaps a mixed model would be better:

```
>summary(mod3)
Call:
lmer(I ~ factor(PINGER_TREATMENT_CODE) + (1 | VESSEL), family = binomial)

Generalized linear mixed model fit using Laplace
Formula: I ~ factor(PINGER_TREATMENT_CODE) + (1 | VESSEL)
   Data: Pinger_month_edit
 Family: binomial(logit link)
   AIC   BIC logLik deviance
 463.7 483.9 -227.8    455.7
Random effects:
 Groups  Name        Variance Std.Dev.
 VESSEL (Intercept) 1.6799   1.2961
number of obs: 1148, groups: VESSEL, 60

Estimated scale (compare to  1 )  0.834157

Fixed effects:
                             Estimate Std. Error z value Pr(>|z|)
(Intercept)                   -2.5755     0.6227  -4.136 3.54e-05 ***
factor(PINGER_TREATMENT_CODE)2  -0.1974     0.7930  -0.249   0.8034
factor(PINGER_TREATMENT_CODE)3  -1.1910     0.7019  -1.697   0.0897 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:
                           (Intr) f(PINGER_TREATMENT_CODE)2
f(PINGER_TREATMENT_CODE)2 -0.785
f(PINGER_TREATMENT_CODE)3 -0.887  0.700
```

This is a much better fit (AIC 463.7 vs 488.78) than first model, with no VESSEL term:

```
> logLik(mod3)
`log Lik.' -227.867 (df=4)
> logLik(mod)
`log Lik.' -241.3919 (df=3)
> 2*(-227.867-(-241.3919))
[1] 27.0498
> pchisq(27.0498,1,lower=FALSE)
[1] 1.982807e-07
```

Previous work has shown strong seasonal variation in depredation rates, so I introduce month as a factor:

```
> mod5 <- lmer(I ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE) + (1 | VESSEL), family = binomial)
> summary(mod5)
Generalized linear mixed model fit using Laplace
Formula: I ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE) + (1 | VESSEL)
   Data: Pinger
 Family: binomial(logit link)
   AIC BIC logLik deviance
 431.6 477 -206.8    413.6
Random effects:
 Groups  Name        Variance Std.Dev.
 VESSEL (Intercept) 1.651    1.2849
number of obs: 1148, groups: VESSEL, 60

Estimated scale (compare to  1 )  0.7858615

Fixed effects:
                             Estimate Std. Error z value Pr(>|z|)
(Intercept)                   -4.8030     1.2637  -3.801 0.000144 ***
factor(MONTH)8                 2.7855     1.2102   2.302 0.021356 *
factor(MONTH)9                 2.0615     1.2312   1.674 0.094051 .
factor(MONTH)10                3.0042     1.2123   2.478 0.013210 *
factor(MONTH)11                3.3178     1.2548   2.644 0.008193 **
```

```
factor(MONTH)12                   5.4189     1.2956   4.182 2.88e-05 ***
factor(PINGER_TREATMENT_CODE)2  -0.5834     0.8044  -0.725 0.468242
factor(PINGER_TREATMENT_CODE)3  -1.7245     0.7171  -2.405 0.016181 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:
                      (Intr) f(MONTH)8 f(MONTH)9 f(MONTH)10 f(MONTH)11 f(MONTH)12 f(PINGER_TREATMENT_CODE)2
fct(MONTH)8           -0.836
fct(MONTH)9           -0.844  0.903
fc(MONTH)10           -0.853  0.915     0.933
fc(MONTH)11           -0.820  0.890     0.896     0.915
fc(MONTH)12           -0.785  0.860     0.866     0.889      0.885
f(PINGER_TREATMENT_CODE)2 -0.320 -0.069    -0.067    -0.070     -0.075     -0.088
f(PINGER_TREATMENT_CODE)3 -0.352 -0.081    -0.076    -0.088     -0.115     -0.134      0.692
```

We find that MONTH is highly significant. Pinger treatment 3 (active pingers) is also significant. Model fit is significantly improved:

```
> anova(mod3,mod5)
Data: Pinger
Models:
mod3: I ~ factor(PINGER_TREATMENT_CODE) + (1 | VESSEL)
mod5: I ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE) + (1 | VESSEL)
     Df     AIC     BIC  logLik  Chisq Chi Df Pr(>Chisq)
mod3  4  463.70  483.88 -227.85
mod5  9  431.59  477.00 -206.79 42.111      5  5.592e-08 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Incorporating pinger make into the model (term labelled PINGER_COMBO) as well as treatment shows one make significant at treatment 3 (active pingers):

```
> mod6 <- lmer(I ~ factor(MONTH) + factor(PINGER_COMBO) + (1 | VESSEL), family = binomial, data=Pinger)
> summary(mod6)
Generalized linear mixed model fit using Laplace
Formula: I ~ factor(MONTH) + factor(PINGER_COMBO) + (1 | VESSEL)
   Data: Pinger
 Family: binomial(logit link)
   AIC BIC logLik deviance
 435.4 501 -204.7    409.4
Random effects:
 Groups  Name        Variance Std.Dev.
 VESSEL (Intercept) 1.4266   1.1944
number of obs: 1148, groups: VESSEL, 60

Estimated scale (compare to  1 )  0.7956322

Fixed effects:
                     Estimate Std. Error z value Pr(>|z|)
(Intercept)           -4.82230    1.25156  -3.853 0.000117 ***
factor(MONTH)8         2.80906    1.20956   2.322 0.020212 *
factor(MONTH)9         2.09007    1.22713   1.703 0.088528 .
factor(MONTH)10        3.04686    1.21046   2.517 0.011832 *
factor(MONTH)11        3.33970    1.25512   2.661 0.007794 **
factor(MONTH)12        5.46546    1.29364   4.225 2.39e-05 ***
factor(PINGER_COMBO)21 -0.93992    1.05770  -0.889 0.374194
factor(PINGER_COMBO)22  0.03378    1.00385   0.034 0.973155
factor(PINGER_COMBO)23 -0.88053    1.01762  -0.865 0.386880
factor(PINGER_COMBO)31 -2.75997    1.01163  -2.728 0.006367 **
factor(PINGER_COMBO)32 -1.19237    0.77748  -1.534 0.125123
factor(PINGER_COMBO)33 -1.53525    0.79452  -1.932 0.053324 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

But does not improve fit over just treatment:

```
> anova(mod5,mod6)
Data: Pinger
Models:
mod5: I ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE) + (1 | VESSEL)
mod6: I ~ factor(MONTH) + factor(PINGER_COMBO) + (1 | VESSEL)
     Df     AIC     BIC  logLik Chisq Chi Df Pr(>Chisq)
mod5  9  431.59  477.00 -206.79
mod6 13  435.38  500.98 -204.69 4.207      4     0.3787
```

Comparing these models to one with no pinger effects in:

```
> nullmod <- lmer(I ~ factor(MONTH) + (1 | VESSEL), family = binomial)
> summary(nullmod)
Generalized linear mixed model fit using Laplace
Formula: I ~ factor(MONTH) + (1 | VESSEL)
   Data: Pinger_month_edit
 Family: binomial(logit link)
 AIC   BIC logLik deviance
 435 470.3 -210.5      421
Random effects:
 Groups  Name        Variance Std.Dev.
 VESSEL (Intercept) 1.9000   1.3784
number of obs: 1148, groups: VESSEL, 60

Estimated scale (compare to  1 )  0.8092388

Fixed effects:
                Estimate Std. Error z value Pr(>|z|)
(Intercept)       -5.874      1.172  -5.012 5.39e-07 ***
factor(MONTH)8     2.638      1.205   2.190   0.0285 *
factor(MONTH)9     1.884      1.223   1.540   0.1235
factor(MONTH)10    2.811      1.205   2.332   0.0197 *
factor(MONTH)11    3.064      1.241   2.468   0.0136 *
factor(MONTH)12    5.118      1.279   4.001 6.31e-05 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:
            (Intr) f(MONTH)8 f(MONTH)9 f(MONTH)10 f(MONTH)11
fct(MONTH)8 -0.931
fct(MONTH)9 -0.940  0.900
fc(MONTH)10 -0.954  0.911     0.932
fc(MONTH)11 -0.929  0.889     0.897     0.915
fc(MONTH)12 -0.900  0.858     0.867     0.889      0.884
```

Only the model without make significantly improves fit:

```
> anova(nullmod,mod5)
Data: Pinger_month_edit
Models:
nullmod: I ~ factor(MONTH) + (1 | VESSEL)
mod5: I ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE) + (1 | VESSEL)
        Df     AIC     BIC  logLik  Chisq Chi Df Pr(>Chisq)
nullmod  7  435.02  470.34 -210.51
mod5     9  431.59  477.00 -206.79 7.4346      2     0.0243 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> anova(nullmod,mod6)
Data: Pinger_month_edit
Models:
nullmod: I ~ factor(MONTH) + (1 | VESSEL)
mod6: I ~ factor(MONTH) + factor(PINGER_COMBO) + (1 | VESSEL)
        Df     AIC     BIC  logLik  Chisq Chi Df Pr(>Chisq)
nullmod  7  435.02  470.34 -210.51
mod6    13  435.38  500.98 -204.69 11.642      6    0.07046 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

<u>CPUE:</u>

We used generalized linear models with a gamma distributed error function, after noticing a strong relationship between the mean and the variance of residuals in a Gaussian family GLM. First, a simple model with just the experimental conditions; response variable CPUE is in Euros/50m net:

```
> summary(gmod0)

Call:
glm(formula = CPUE ~ factor(PINGER_TREATMENT_CODE), family = Gamma(link = "log"))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.6461  -0.6021  -0.2198   0.2603   1.9235

Coefficients:
                              Estimate Std. Error t value Pr(>|t|)
(Intercept)                    1.07201    0.06021  17.803  < 2e-16 ***
factor(PINGER_TREATMENT_CODE)2  0.19889    0.07496   2.653  0.00808 **
factor(PINGER_TREATMENT_CODE)3  0.17719    0.06601   2.684  0.00738 **
```

```
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Gamma family taken to be 0.5221027)

    Null deviance: 579.82  on 1118  degrees of freedom
Residual deviance: 575.71  on 1116  degrees of freedom
AIC: 4715.4

Number of Fisher Scoring iterations: 5
```

As before, we fit a model with a fixed vessel effect:

```
gmod1 <- glm(CPUE ~ factor(VESSEL)+ factor(PINGER_TREATMENT_CODE),  family = Gamma(link = "log"))
```

and we find VESSEL is highly significant:

```
> anova(gmod1,test='F')
Analysis of Deviance Table

Model: Gamma, link: log

Response: CPUE

Terms added sequentially (first to last)


                              Df Deviance Resid. Df Resid. Dev      F Pr(>F)
NULL                                          1118     579.82
factor(VESSEL)                57   166.82      1061     413.00 8.0388 <2e-16 ***
factor(PINGER_TREATMENT_CODE)  1     0.33      1060     412.67 0.9063 0.3413
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

As before, because we are interested in the effect of treatment across vessels *in general*, then a mixed model would be better:

```
> gmod3lmer <- lmer(CPUE ~ factor(PINGER_TREATMENT_CODE) + (1|VESSEL), family = Gamma(link="log"))

> summary(gmod3lmer)
Generalized linear mixed model fit using Laplace
Formula: CPUE ~ factor(PINGER_TREATMENT_CODE) + (1 | VESSEL)
   Data: cpue.data.new
 Family: Gamma(log link)
   AIC   BIC logLik deviance
 533.6 553.7 -262.8    525.6
Random effects:
 Groups   Name        Variance Std.Dev.
 VESSEL  (Intercept) 0.038368 0.19588
 Residual             0.401486 0.63363
number of obs: 1119, groups: VESSEL, 58

Fixed effects:
                             Estimate Std. Error t value
(Intercept)                   1.08868    0.09633  11.301
factor(PINGER_TREATMENT_CODE)2  0.05346    0.12207   0.438
factor(PINGER_TREATMENT_CODE)3  0.11045    0.10490   1.053

Correlation of Fixed Effects:
                            (Intr) f(PINGER_TREATMENT_CODE)2
f(PINGER_TREATMENT_CODE)2 -0.789
f(PINGER_TREATMENT_CODE)3 -0.918  0.726
```

And we see that the AIC for this model (533.6) is greatly reduced compared to that for the first model (4715.4), and the likelihood is greatly increased:

```
> logLik(gmod0)
'log Lik.' -2353.699 (df=3)
> logLik(gmod3lmer)
'log Lik.' -262.7992 (df=4)
> 2*(-262.7992-(-2353.699))
[1] 4181.8
> pchisq(4181.8,1,lower=FALSE)
[1] 0
```

Next, because CPUE is known to vary seasonally, we introduced MONTH as a factor:

```
> gmod4lmer <- lmer(CPUE ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE) + (1|VESSEL), family =
Gamma(link="log"))
> summary(gmod4lmer)
Generalized linear mixed model fit using Laplace
Formula: CPUE ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE) + (1 | VESSEL)
   Data: cpue.data.new
 Family: Gamma(log link)
   AIC   BIC logLik deviance
 532.3 577.5 -257.2    514.3
Random effects:
 Groups   Name        Variance Std.Dev.
 VESSEL  (Intercept) 0.033657 0.18346
 Residual             0.396901 0.63000
number of obs: 1119, groups: VESSEL, 58

Fixed effects:
                                Estimate Std. Error t value
(Intercept)                      1.13720    0.10028  11.341
factor(MONTH)8                  -0.06132    0.06860  -0.894
factor(MONTH)9                  -0.01078    0.06713  -0.161
factor(MONTH)10                 -0.10660    0.06873  -1.551
factor(MONTH)11                 -0.28026    0.08035  -3.488
factor(MONTH)12                 -0.56386    0.13015  -4.332
factor(PINGER_TREATMENT_CODE)2  0.09232    0.11715   0.788
factor(PINGER_TREATMENT_CODE)3  0.15198    0.10108   1.504

Correlation of Fixed Effects:
                       (Intr) f(MONTH)8 f(MONTH)9 f(MONTH)10 f(MONTH)11 f(MONTH)12 f(PINGER_TREATMENT_CODE)2
fct(MONTH)8            -0.289
fct(MONTH)9            -0.345  0.531
fc(MONTH)10            -0.346  0.506     0.655
fc(MONTH)11            -0.274  0.457     0.556     0.562
fc(MONTH)12            -0.152  0.267     0.330     0.344      0.340
f(PINGER_TREATMENT_CODE)2 -0.702 -0.060    -0.052    -0.038     -0.052     -0.050
f(PINGER_TREATMENT_CODE)3 -0.808 -0.042    -0.079    -0.064     -0.098     -0.067      0.726
```

We see that this results in a marginally significantly better fit (AIC 532.3 vs 533.6):

```
> anova(gmod3lmer, gmod4lmer)
Data: cpue.data.new
Models:
gmod3lmer: CPUE ~ factor(PINGER_TREATMENT_CODE) + (1 | VESSEL)
gmod4lmer: CPUE ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE) + (1 | VESSEL)
          Df     AIC     BIC  logLik  Chisq Chi Df Pr(>Chisq)
gmod3lmer  4  533.60  553.68 -262.80
gmod4lmer  9  532.35  577.53 -257.17 11.248      5    0.04667 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Using glmmPQL to estimate p-values we get:

```
> gmod2<-glmmPQL(fixed = CPUE ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE),
    random = ~1 | VESSEL, family = Gamma(link = "log"))
> summary(gmod2)
Linear mixed-effects model fit by maximum likelihood
 Data: cpue.data.new
  AIC BIC logLik
   NA  NA     NA

Random effects:
 Formula: ~1 | VESSEL
        (Intercept)  Residual
StdDev:   0.3698607 0.6024558

Variance function:
 Structure: fixed weights
 Formula: ~invwt
Fixed effects: CPUE ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE)
                                    Value  Std.Error   DF   t-value p-value
(Intercept)                     1.2100510 0.15982885 1054  7.570917  0.0000
factor(MONTH)8                 -0.0996513 0.06858839 1054 -1.452889  0.1466
factor(MONTH)9                 -0.0655771 0.07156269 1054 -0.916359  0.3597
factor(MONTH)10                -0.1400352 0.07305222 1054 -1.916919  0.0555
factor(MONTH)11                -0.2738893 0.08515415 1054 -3.216394  0.0013
factor(MONTH)12                -0.6015509 0.13070233 1054 -4.602450  0.0000
factor(PINGER_TREATMENT_CODE)2 -0.0291238 0.19555400 1054 -0.148930  0.8816
factor(PINGER_TREATMENT_CODE)3  0.0899235 0.16739095 1054  0.537206  0.5912
```

```
Standardized Within-Group Residuals:
       Min         Q1        Med         Q3        Max
-1.6073439 -0.7029667 -0.2271670  0.4828192  4.1703116

Number of Observations: 1119
Number of Groups: 58
```

And when we introduce pinger brand into the analysis, results are unchanged:

```
> gmod3<-glmmPQL(fixed = CPUE ~ factor(MONTH) + factor(PINGER_COMBO),
    random = ~1 | VESSEL, family = Gamma(link = "log"))
> summary(gmod3)
Linear mixed-effects model fit by maximum likelihood
 Data: cpue.data.new
  AIC BIC logLik
   NA  NA     NA

Random effects:
 Formula: ~1 | VESSEL
        (Intercept)  Residual
StdDev:   0.3320931 0.6031873

Variance function:
 Structure: fixed weights
 Formula: ~invwt
Fixed effects: CPUE ~ factor(MONTH) + factor(PINGER_COMBO)
                           Value  Std.Error   DF   t-value p-value
(Intercept)             1.1950746 0.14737097 1054  8.109295  0.0000
factor(MONTH)8         -0.0871869 0.06867368 1054 -1.269583  0.2045
factor(MONTH)9         -0.0467440 0.07126024 1054 -0.655962  0.5120
factor(MONTH)10        -0.1293046 0.07279448 1054 -1.776297  0.0760
factor(MONTH)11        -0.2575059 0.08561832 1054 -3.007602  0.0027
factor(MONTH)12        -0.6044117 0.13078522 1054 -4.621406  0.0000
factor(PINGER_COMBO)21 -0.4038418 0.24238080   53 -1.666146  0.1016
factor(PINGER_COMBO)22 -0.0870602 0.22718936 1054 -0.383205  0.7016
factor(PINGER_COMBO)23  0.4724499 0.24728832   53  1.910523  0.0615
factor(PINGER_COMBO)31  0.0914042 0.17568949   53  0.520260  0.6050
factor(PINGER_COMBO)32  0.1725901 0.17317246   53  0.996637  0.3235
factor(PINGER_COMBO)33  0.0072308 0.17813492 1054  0.040592  0.9676


Standardized Within-Group Residuals:
       Min         Q1        Med         Q3        Max
-1.6053023 -0.7059294 -0.2381456  0.4823398  4.2799457

Number of Observations: 1119
Number of Groups: 58
```

So there are no significant effects for pinger treatment or make; omitting the MONTH term does not alter this conclusion. We confirm this by using the likelihoods from lmer models also fitted using PQL; we see that neither pinger treatment or make significantly improve the model fit or even reduce the AIC over a mixed model with month as a fixed factor and vessel as a random factor:

```
> gmodl <- lmer(CPUE ~ factor(MONTH) + (1|VESSEL), family = Gamma(link="log"), method='PQL')

> gmodl2 <- lmer(CPUE ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE) + (1|VESSEL), family =
Gamma(link="log"), method='PQL')

> gmodl3 <- lmer(CPUE ~ factor(MONTH) + factor(PINGER_COMBO) + (1|VESSEL), family = Gamma(link="log"),
method='PQL')

> anova(gmodl,gmodl2)
Data: cpue.data.new
Models:
gmodl: CPUE ~ factor(MONTH) + (1 | VESSEL)
gmodl2: CPUE ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE) + (1 | VESSEL)
       Df     AIC     BIC  logLik  Chisq Chi Df Pr(>Chisq)
gmodl   7  551.29  586.43 -268.64
gmodl2  9  554.60  599.79 -268.30 0.6831      2     0.7107

> anova(gmodl,gmodl3)
Data: cpue.data.new
Models:
gmodl: CPUE ~ factor(MONTH) + (1 | VESSEL)
gmodl3: CPUE ~ factor(MONTH) + factor(PINGER_COMBO) + (1 | VESSEL)
       Df     AIC     BIC  logLik  Chisq Chi Df Pr(>Chisq)
gmodl   7  551.29  586.43 -268.64
gmodl3 13  552.47  617.73 -263.24 10.815      6    0.09426 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```