

Do pingers reduce interactions between bottlenose dolphins and nets around the Balearic Islands

José María Brotons¹, Zaida Munilla¹, Antonio María Grau¹, Luke Rendell^{2,*}

¹Office of Fisheries Management, Government of the Balearic Islands, Foners 10, Palma de Mallorca 07006, Balearic Islands, Spain.

²Sea Mammal Research Unit, School of Biology, University of St. Andrews, Fife KY16 8LB, UK

*Corresponding author. Email: ler4@st-andrews.ac.uk

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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 brand into the model (term labelled PINGER_COMBO) as well as treatment shows one brand 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 treatment only:

```

> 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 brand 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
```

PPUE:

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 PPUE is in Euros/50 m net:

```
> summary(gmod0)

Call:
glm(formula = PPUE ~ 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(PPUE ~ 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: PPUE

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(PPUE ~ factor(PINGER_TREATMENT_CODE) + (1|VESSEL), family = Gamma(link="log"))
> summary(gmod3lmer)
Generalized linear mixed model fit using Laplace
Formula: PPUE ~ factor(PINGER_TREATMENT_CODE) + (1 | VESSEL)
Data: ppue.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 PPUE is known to vary seasonally, we introduced MONTH as a factor:

```
> gmod4lmer <- lmer(PPUE ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE) + (1|VESSEL), family =
Gamma(link="log"))
> summary(gmod4lmer)
Generalized linear mixed model fit using Laplace
Formula: PPUE ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE) + (1 | VESSEL)
Data: ppue.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: ppue.data.new
Models:
gmod3lmer: PPUE ~ factor(PINGER_TREATMENT_CODE) + (1 | VESSEL)
gmod4lmer: PPUE ~ 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 = PPUE ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE),
random = ~1 | VESSEL, family = Gamma(link = "log"))
> summary(gmod2)
Linear mixed-effects model fit by maximum likelihood
Data: ppue.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: PPUE ~ 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 = PPUE ~ factor(MONTH) + factor(PINGER_COMBO),
  random = ~1 | VESSEL, family = Gamma(link = "log"))
```

```
> summary(gmod3)
Linear mixed-effects model fit by maximum likelihood
Data: ppue.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: PPUE ~ 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 brand; 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 brand 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:

```
> gmod1 <- lmer(PPUE ~ factor(MONTH) + (1|VESSEL), family = Gamma(link="log"), method='PQL')
```

```
> gmod12 <- lmer(PPUE ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE) + (1|VESSEL), family =
Gamma(link="log"), method='PQL')
```

```
> gmod13 <- lmer(PPUE ~ factor(MONTH) + factor(PINGER_COMBO) + (1|VESSEL), family = Gamma(link="log"),
method='PQL')
```

```
> anova(gmod1,gmod12)
Data: ppue.data.new
Models:
gmod1: PPUE ~ factor(MONTH) + (1 | VESSEL)
gmod12: PPUE ~ factor(MONTH) + factor(PINGER_TREATMENT_CODE) + (1 | VESSEL)
      Df    AIC    BIC logLik Chisq Chi Df Pr(>Chisq)
gmod1   7  551.29  586.43 -268.64
gmod12  9  554.60  599.79 -268.30  0.6831     2    0.7107
```

```
> anova(gmod1,gmod13)
Data: ppue.data.new
Models:
gmod1: PPUE ~ factor(MONTH) + (1 | VESSEL)
gmod13: PPUE ~ factor(MONTH) + factor(PINGER_COMBO) + (1 | VESSEL)
      Df    AIC    BIC logLik Chisq Chi Df Pr(>Chisq)
gmod1   7  551.29  586.43 -268.64
gmod13 13  552.47  617.73 -263.24 10.815     6    0.09426 .
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```