

# Scripps's Murrelet Egg Size model

Amelia J. DuVall & Marcela Todd

4/11/2021

This is v.2021-06-04

## Introduction

This document details steps taken to model Scripps's Murrelet (*Synthliboramphus scrippsi*) egg size at Santa Barbara Island within Channel Islands National Park from 2009-2017.

## Load and format data

```
egg <- read.csv(here("data", "SCMU_egg_data.csv"))
covars <- read.csv(here("data", "covariates", "covars.csv"))

## join covariate data with egg data by year
SCMUdf <- left_join(egg, covars, by = "Year") %>%
  filter(TrueOrder == TRUE) %>% # egg order known only
  select(Year, Observer, Plot, Size, EggOrder, ANCHL, BEUTI, NPGO, ONI, PDO, SST) %>%
  as_tibble()
```

## Null Intercept-Only Model with 2 random effects

This model includes observer and plot as random effects, but does not include any covariates.

```
## run model
nm <- lmer(Size ~ 1 + (1 | Observer) + (1 | Plot), data = SCMUdf, REML = TRUE)
```

```
## look at model output and estimates
summary(nm)
```

```
## Fixed Effects:
## coef.est  coef.se
## 1884.29    12.20
##
## Random Effects:
## Groups   Name      Std.Dev.
## Observer (Intercept) 17.22
## Plot      (Intercept) 24.49
## Residual              111.96
## ---
## number of obs: 753, groups: Observer, 27; Plot, 8
## AIC = 9263.1, DIC = 9268.5
## deviance = 9261.8
```

```
coef(nm) # these are the coefficients
```

```
## $Observer
##      (Intercept)
## AAY      1899.553
## AJB      1880.127
## AJD      1895.666
## AML      1886.089
## CAC      1876.699
## CEH      1880.914
## CEK      1880.307
## CLE      1879.914
## DLW      1874.348
## EWW      1891.898
## GRK      1882.978
## JAH      1902.680
## KMR      1885.299
## KWB      1880.009
## LAH      1883.315
## MEJ      1878.435
## MGB      1886.816
## NAG      1869.396
## PTL      1876.981
## RER      1893.489
## REW      1881.330
## SAA      1887.456
## SFC      1885.064
## SJK      1893.394
## SKT      1862.709
## SLA      1884.647
## SMC      1896.380
##
## $Plot
##      (Intercept)
## APNC      1905.622
## BH        1898.588
## BT        1850.797
## CC        1903.414
## DO        1885.298
## ESC       1882.827
## LC        1873.535
## WC        1874.258
##
## attr(,"class")
## [1] "coef.mer"
```

```
rane(nm) # these are the random effects
```

```
## $Observer
##      (Intercept)
## AAY  15.2610062
## AJB  -4.1654786
## AJD  11.3739567
## AML   1.7970244
```

```

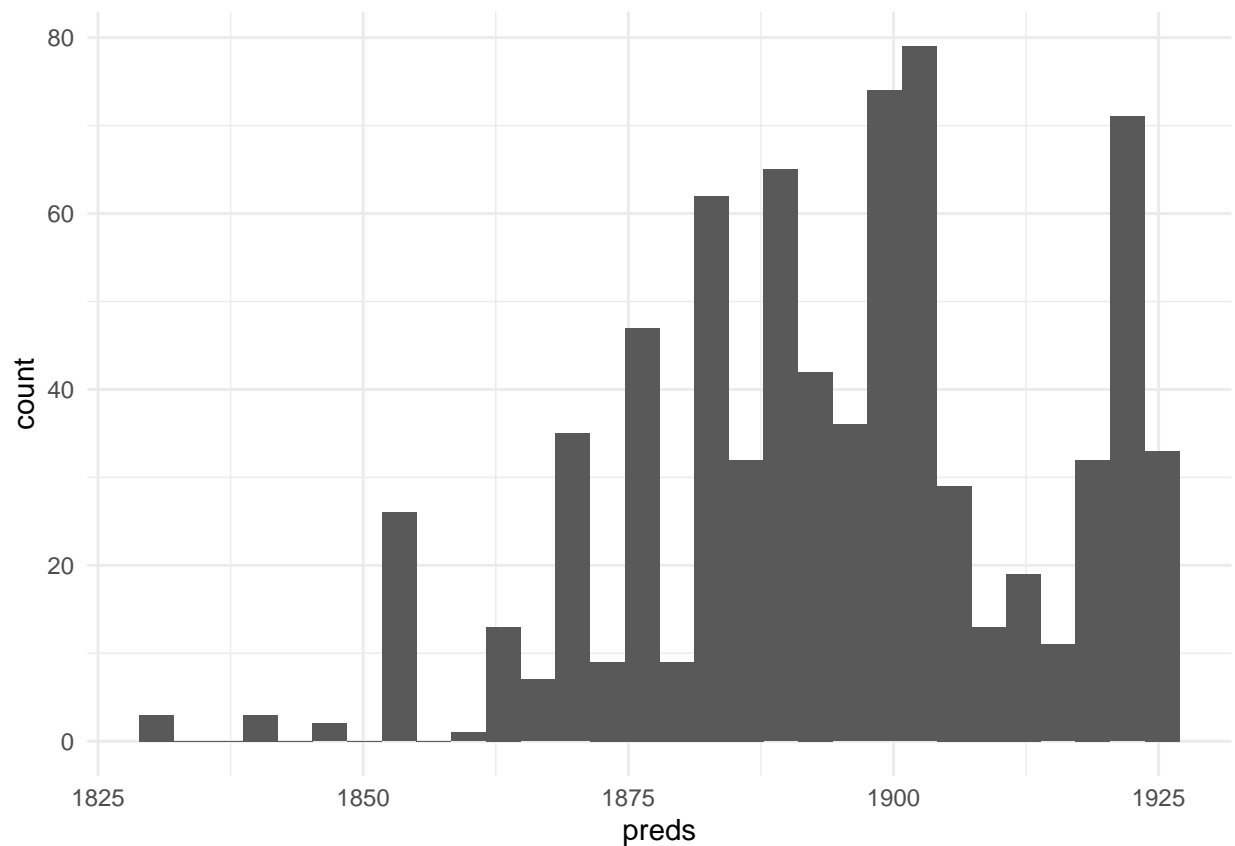
## CAC -7.5934214
## CEH -3.3784652
## CEK -3.9853109
## CLE -4.3779272
## DLW -9.9445690
## EWW 7.6052536
## GRK -1.3144290
## JAH 18.3876524
## KMR 1.0067101
## KWB -4.2835217
## LAH -0.9770916
## MEJ -5.8572070
## MGB 2.5241208
## NAG -14.8959509
## PTL -7.3117215
## RER 9.1963408
## REW -2.9625711
## SAA 3.1632622
## SFC 0.7713125
## SJK 9.1015277
## SKT -21.5831481
## SLA 0.3551011
## SMC 12.0875447
##
## $Plot
##      (Intercept)
## APNC 21.329246
## BH 14.295406
## BT -33.494909
## CC 19.121674
## DO 1.005254
## ESC -1.464948
## LC -10.757089
## WC -10.034635
##
## with conditional variances for "Observer" "Plot"
## you can store the model results to objects
obs.ranef <- ranef(nm)$Observer
plot.ranef <- ranef(nm)$Plot
## the mean of these values should be close to 0
mean(obs.ranef[[1]])

## [1] 3.494283e-13
mean(plot.ranef[[1]])

## [1] -7.280149e-12
## quick model diagnostics
## extract predicted values and plot
preds <- predict(nm)
ggplot() +
  geom_histogram(mapping = aes(preds)) +
  theme_minimal()

```

```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```



```
# we want these to look normally distributed
```

```
## extract residuals and plot
```

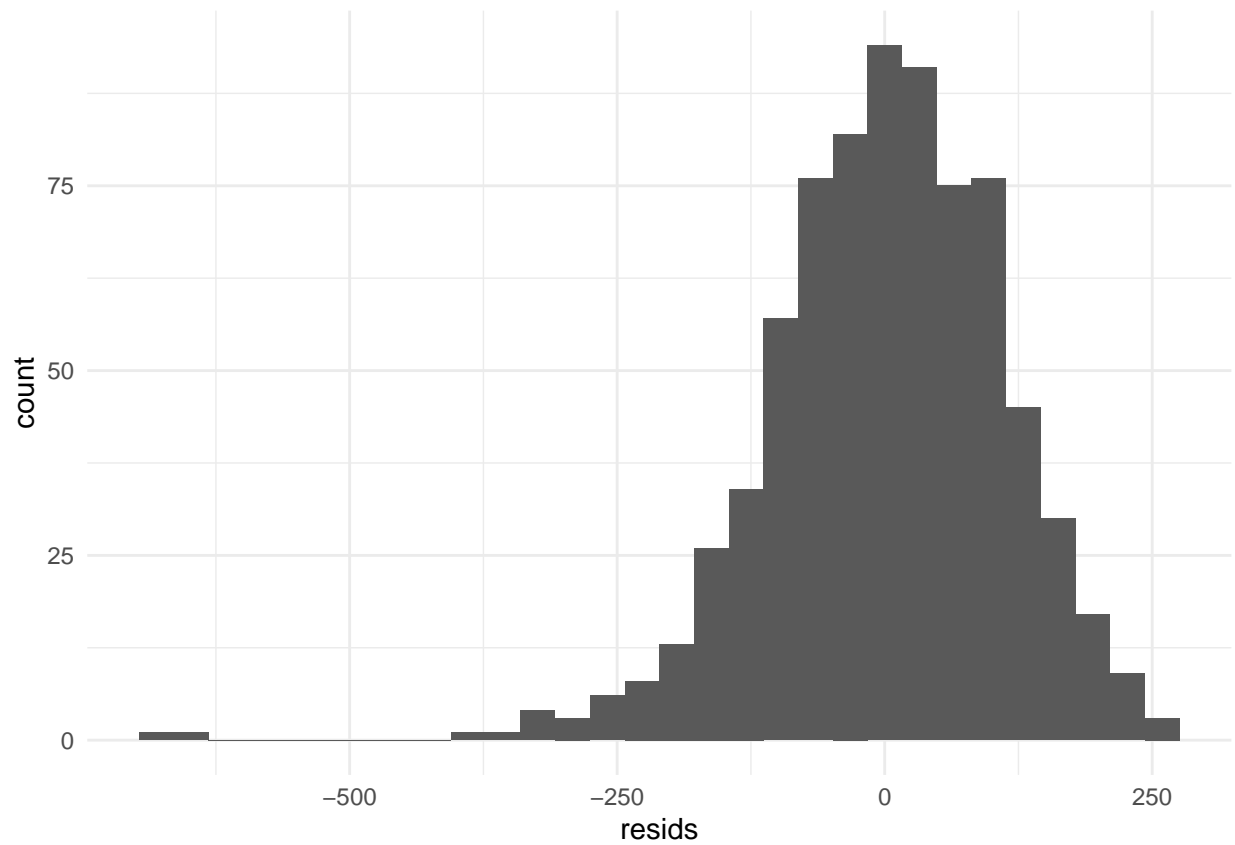
```
resids <- residuals(nm)
```

```
ggplot() +
```

```
  geom_histogram(mapping = aes(resids)) +
```

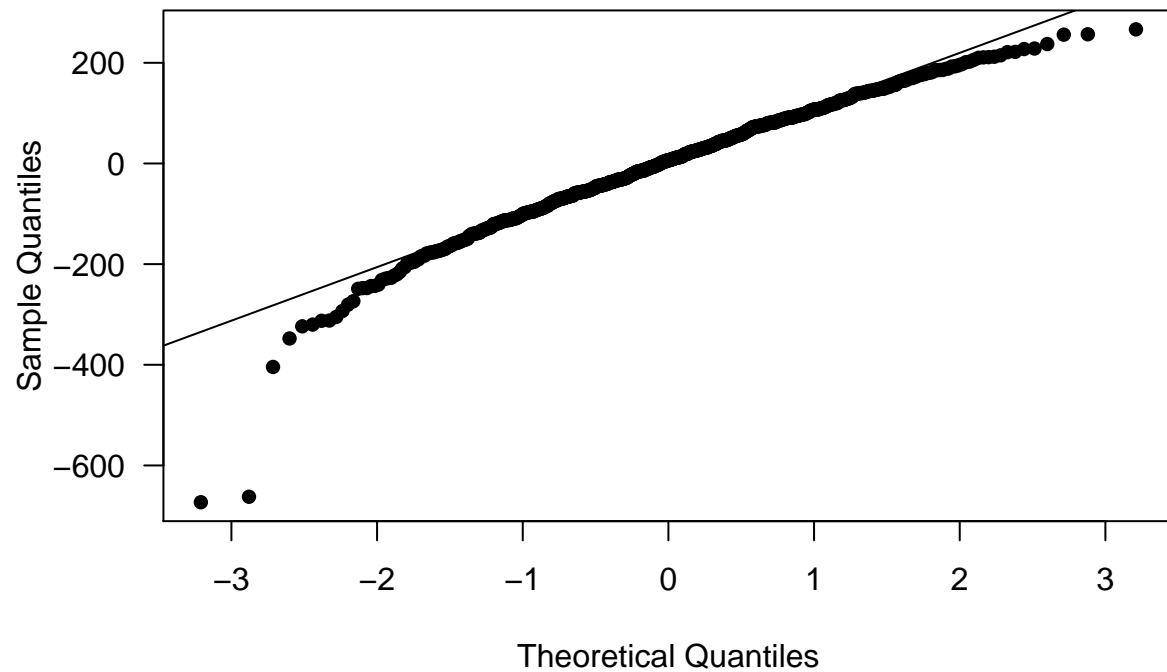
```
  theme_minimal()
```

```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```

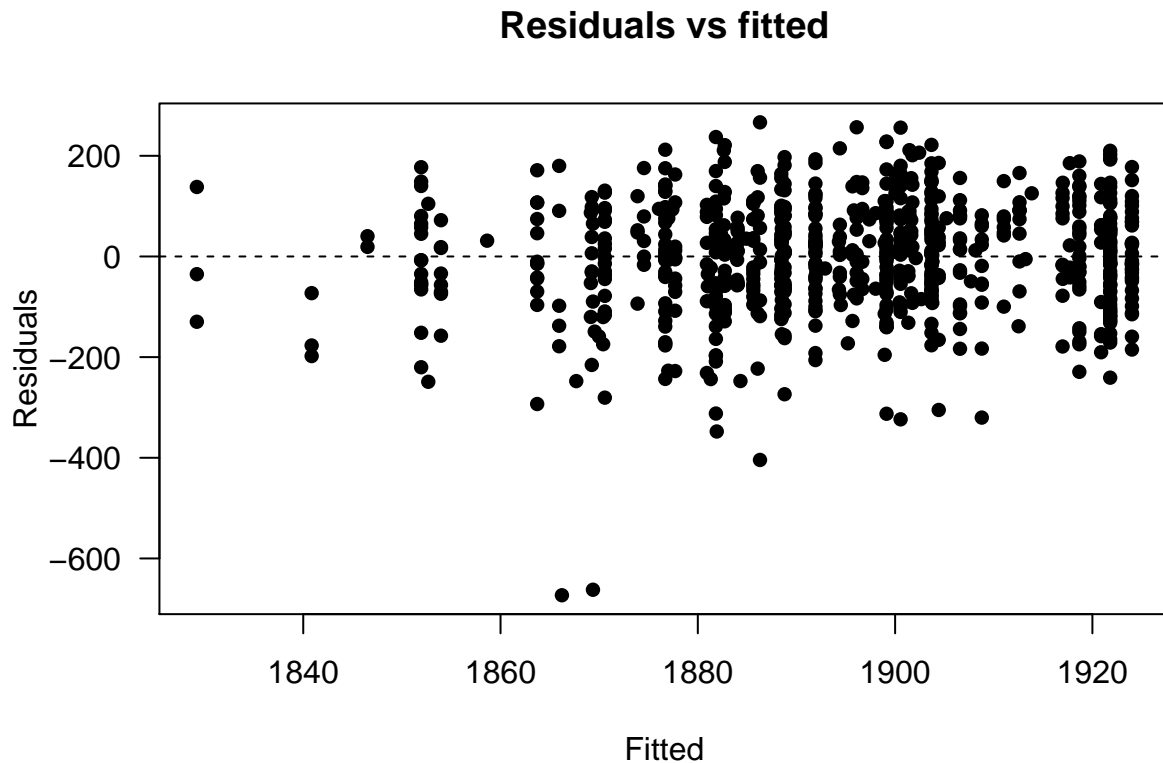


```
# we want these to look normally distributed  
  
# qq resids  
qqnorm(resids, main = "QQ plot (residuals)", las = 1, pch = 16)  
qqline(resids)
```

QQ plot (residuals)



```
## plot residuals versus fitted values
yh <- fitted(nm)
plot(yh, resid, las = 1, pch = 16,
     xlab = "Fitted", ylab = "Residuals",
     main = "Residuals vs fitted")
abline(h=0, lty = "dashed")
```



## Remove Correlated Predictors & Find Global Model

```
## create data frame specifying predictors to include
predictors <- as.data.frame(matrix(c(FALSE, TRUE), 2, 7)) # 7 potential predictors (includes EggOrder)

## add column names
cov_names <- colnames(predictors) <- colnames(SCMUdf[,5:11])

## create set of all possible combinations
full_set <- expand.grid(predictors) # 128 combinations

## select models with correlated predictors (see SCMU_egg_covariates.Rmd)
ii <- which(full_set$ANCHL + full_set$NPGO == 2 |
            full_set$ANCHL + full_set$ONI == 2 |
            full_set$ANCHL + full_set$PDO == 2 |
            full_set$BEUTI + full_set$ONI == 2 |
            full_set$BEUTI + full_set$PDO == 2 |
            full_set$NPGO + full_set$PDO == 2 |
            full_set$NPGO + full_set$SST == 2 |
            full_set$ONI + full_set$PDO == 2) # 98 models

## create reduced set of models and convert to a matrix for easier indexing
use_set <- as.matrix(full_set[-ii,])

## number of models in set
```

```

(n_mods <- nrow(use_set)) # 30 models out of potential 128

## [1] 30
## find max number of predictors in a model
rowSums(use_set) # only one model with 4 predictors (72)

## 1 2 3 4 5 6 7 8 9 10 13 14 17 18 25 26 33 34 65 66 67 68 69 70 71 72
## 0 1 1 2 1 2 2 3 1 2 2 3 1 2 2 3 1 2 1 2 2 3 2 3 3 4
## 81 82 97 98
## 2 3 2 3

## which predictors are included in this model?
cov_names[use_set[26,]] # "EggOrder" "ANCHL" "BEUTI" "SST"

## [1] "EggOrder" "ANCHL" "BEUTI" "SST"

```

## Likelihood Ratio Tests

We used LRTs using the global model to test the support for inclusion of random effects (Plot, Observer). There are NAs in the observer data from 2015. These NAs need to be removed prior to completing LRT tests. See <https://cran.r-project.org/web/packages/RLRsim/RLRsim.pdf> for info.

```

SCMUdf2 <- SCMUdf[-c(which(is.na(SCMUdf$Observer==TRUE))),]

## global model
bm_both <- lmer(Size ~ EggOrder + ANCHL + BEUTI + SST + (1 | Observer) + (1 | Plot), data = SCMUdf2, REML = TRUE)

## run model with plot RE only
bm_plot <- lmer(Size ~ EggOrder + ANCHL + BEUTI + SST + (1 | Plot), data = SCMUdf2, REML = FALSE)

## run model with obs RE only
bm_obs <- lmer(Size ~ EggOrder + ANCHL + BEUTI + SST + (1 | Observer), data = SCMUdf2, REML = FALSE)

## Exact RLRT test
# m is the reduced model containing only the RE to be tested (the random effect set to zero under the null hypothesis)

# observer set to zero under the null hypothesis
exactRLRT(m = bm_obs, mA = bm_both, m0 = bm_plot, seed = 16)

## Using restricted likelihood evaluated at ML estimators.
## Refit with method="REML" for exact results.

##
## simulated finite sample distribution of RLRT.
##
## (p-value based on 10000 simulated values)
##
## data:
## RLRT = 1.2984, p-value = 0.0946

# plot set to zero under the null hypothesis
exactRLRT(m = bm_plot, mA = bm_both, m0 = bm_obs, seed = 16)

## Using restricted likelihood evaluated at ML estimators.
## Refit with method="REML" for exact results.

```



```
##
## simulated finite sample distribution of RLRT.
##
## (p-value based on 10000 simulated values)
##
## data:
## RLRT = 3.8766, p-value = 0.0138
```

## Model Diagnostics

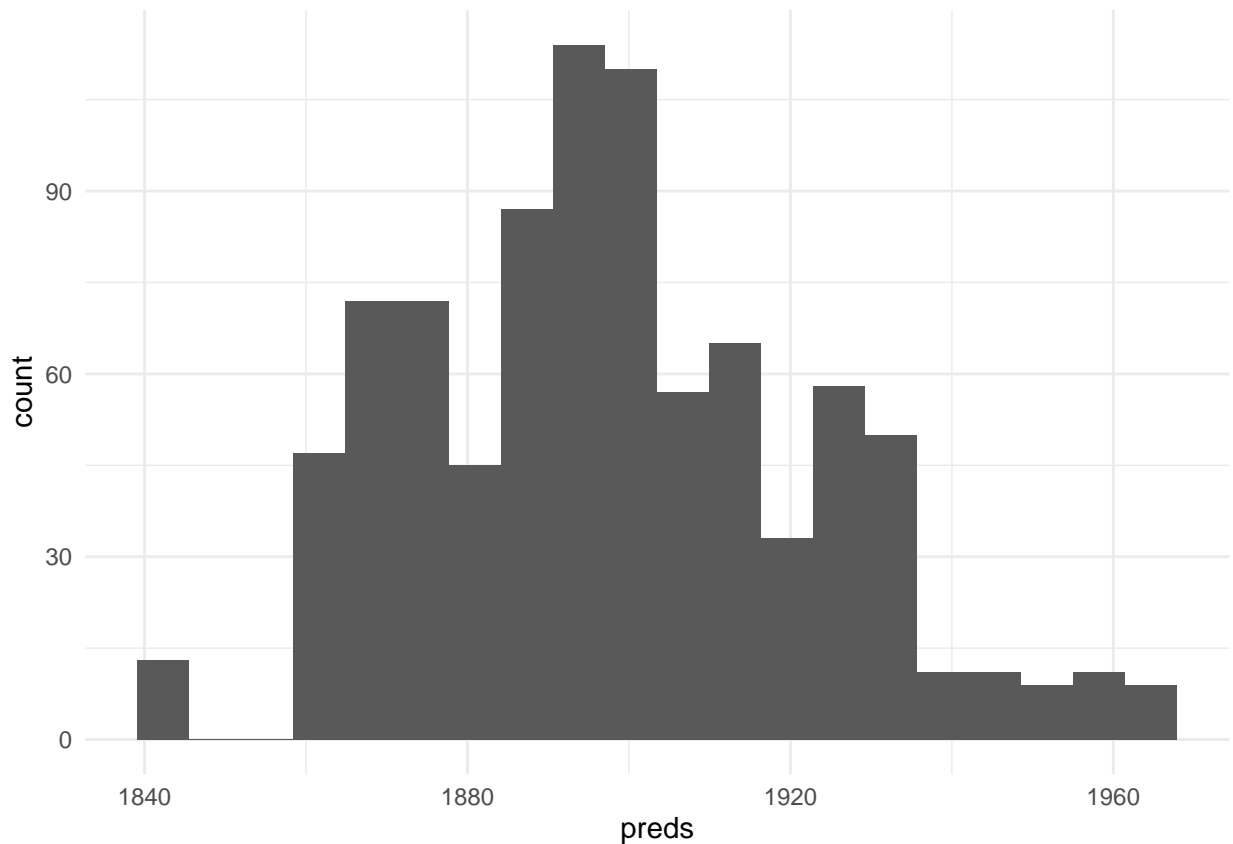
These diagnostics are done for the global model.

```
## run global model
global_mod <- lmer(Size ~ EggOrder + ANCHL + BEUTI + SST + (1 | Plot), data = SCMUdf, REML = TRUE)
```

## Residuals/Fitted Plots

### Histogram of Predicted Values

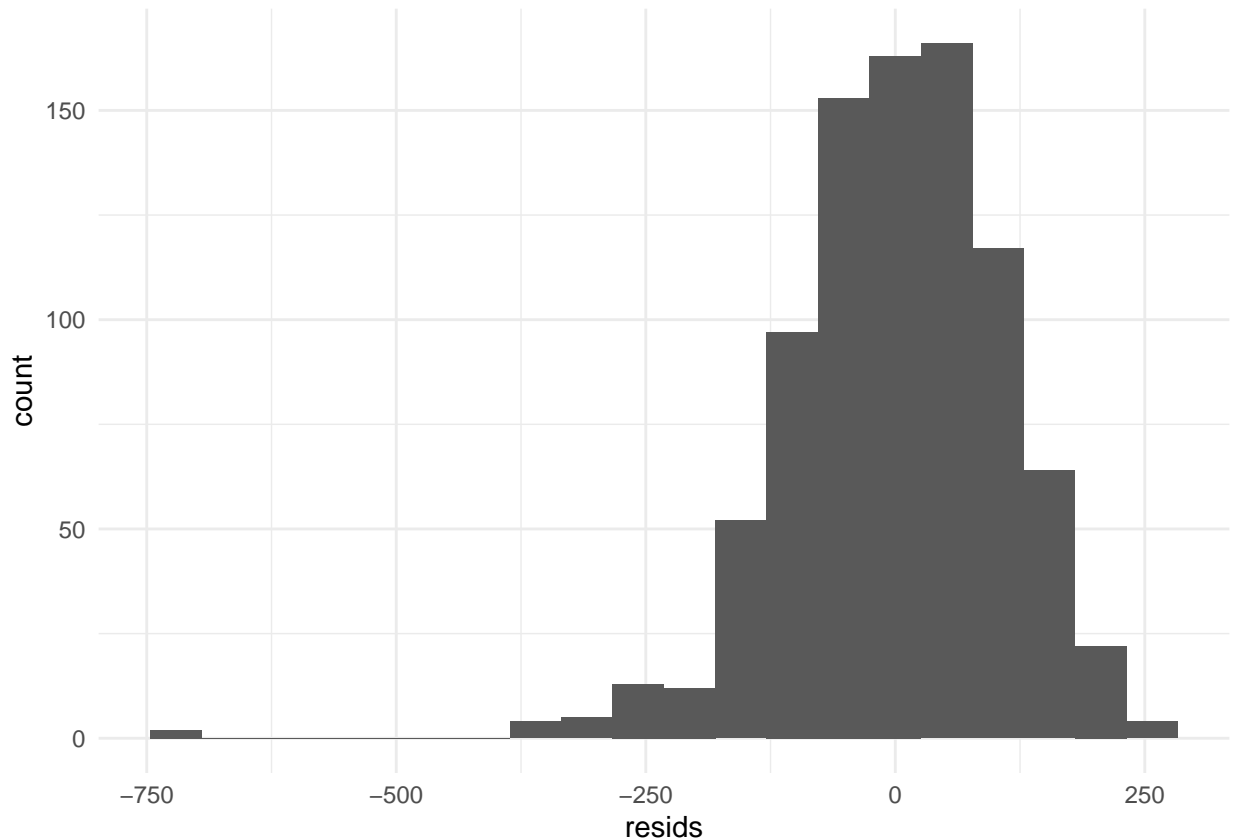
```
## extract predicted values and plot
preds <- predict(global_mod)
ggplot() +
  geom_histogram(mapping = aes(preds), bins = 20) + # set bins
  theme_minimal()
```



Since we assumed our data are normal, we want to see an approximately normal distribution of predicted values.

## Histogram of Residuals

```
## extract residuals and plot
resids <- residuals(global_mod)
ggplot() +
  geom_histogram(mapping = aes(resids), bins = 20) +
  theme_minimal()
```



Since we assumed our data are normal, we want to see an approximately normal distribution of residuals (differences between observed and predicted values of data).

## Model Coefficients

```
## extract coeffs and random effects
coef(global_mod) # this include fixed and random effects
```

```
## $Plot
##      (Intercept) EggOrderEgg2    ANCHL    BEUTI    SST
## APNC    1895.298    32.93263  4.806984 -11.3738  7.697737
## BH      1899.198    32.93263  4.806984 -11.3738  7.697737
## BT      1854.966    32.93263  4.806984 -11.3738  7.697737
## CC      1902.741    32.93263  4.806984 -11.3738  7.697737
## DO      1883.361    32.93263  4.806984 -11.3738  7.697737
## ESC     1883.376    32.93263  4.806984 -11.3738  7.697737
## LC      1876.946    32.93263  4.806984 -11.3738  7.697737
## WC      1874.641    32.93263  4.806984 -11.3738  7.697737
##
```

```
## attr("class")
## [1] "coef.mer"

ranef_pl <- ranef(global_mod)$Plot # plot random effect only

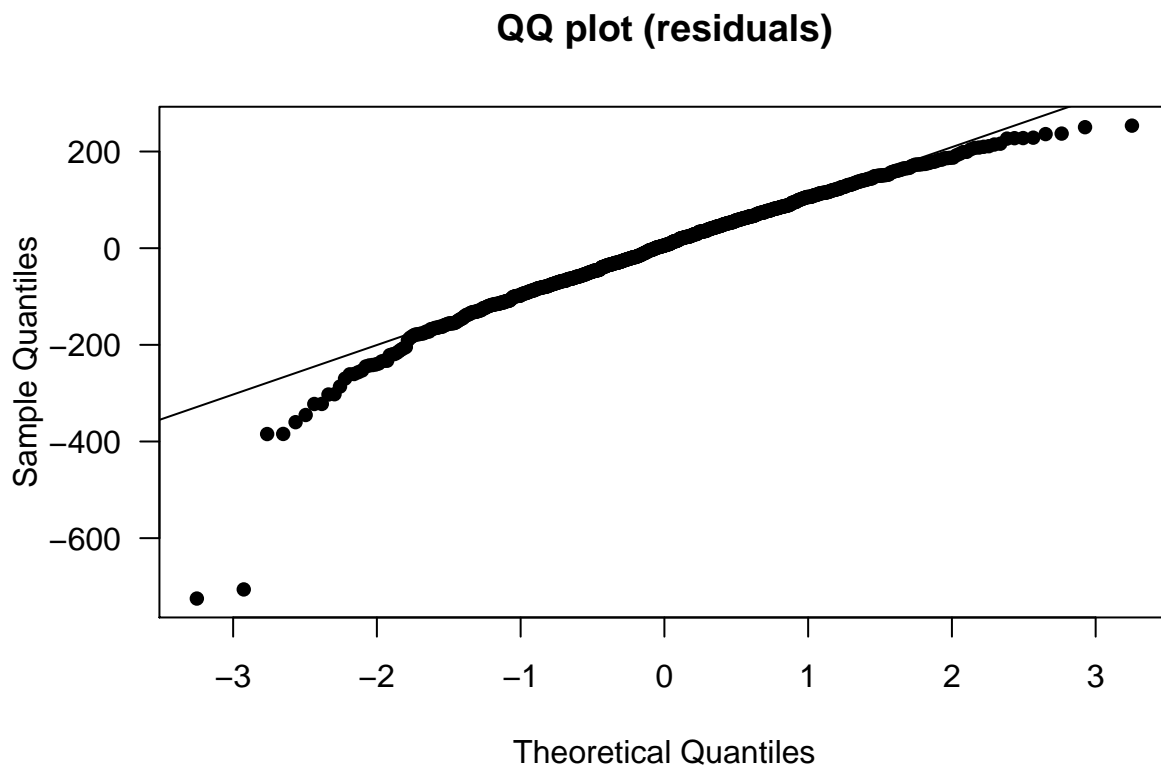
## look at data going into random effects
table(SCMUdf$Plot)

##
## APNC  BH  BT  CC  DO  ESC  LC  WC
## 115   31  16  275 192   1  240  4
```

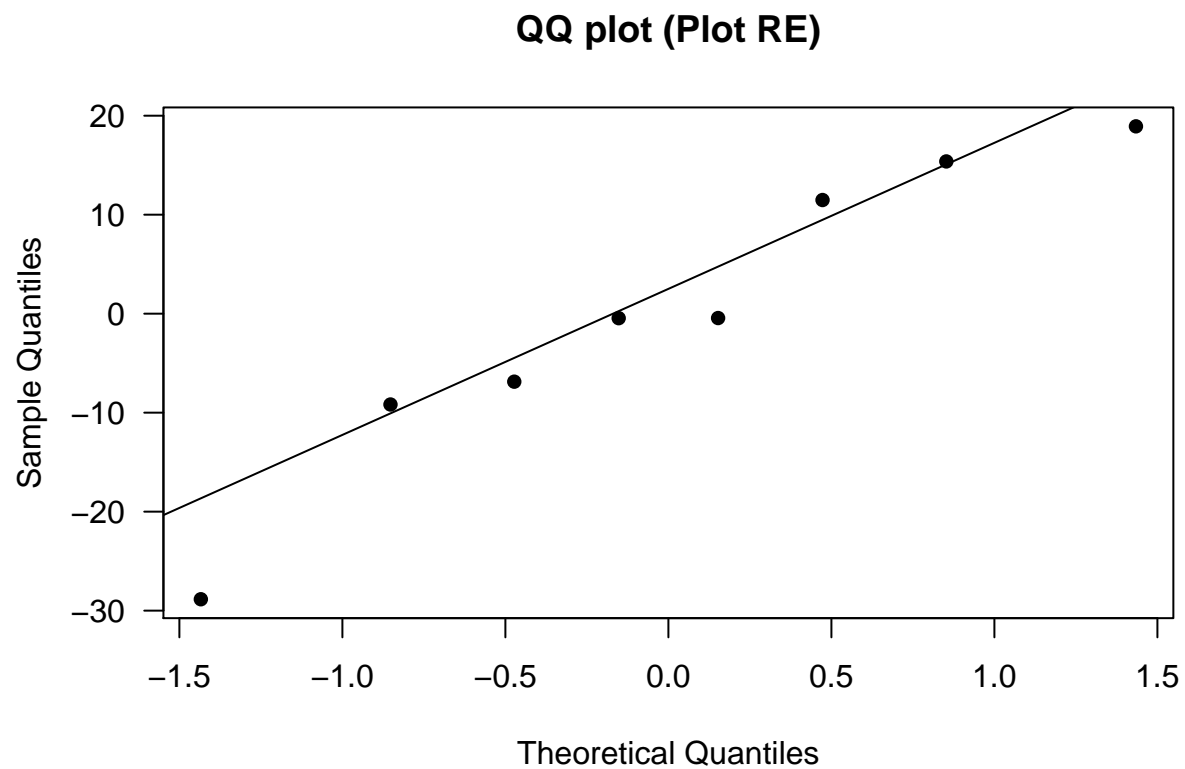
We can extract our model coefficients (for fixed and random effects) and look at them.

### Q-Q Plots

```
# qq resid
qqnorm(resids, main = "QQ plot (residuals)", las = 1, pch = 16)
qqline(resids)
```



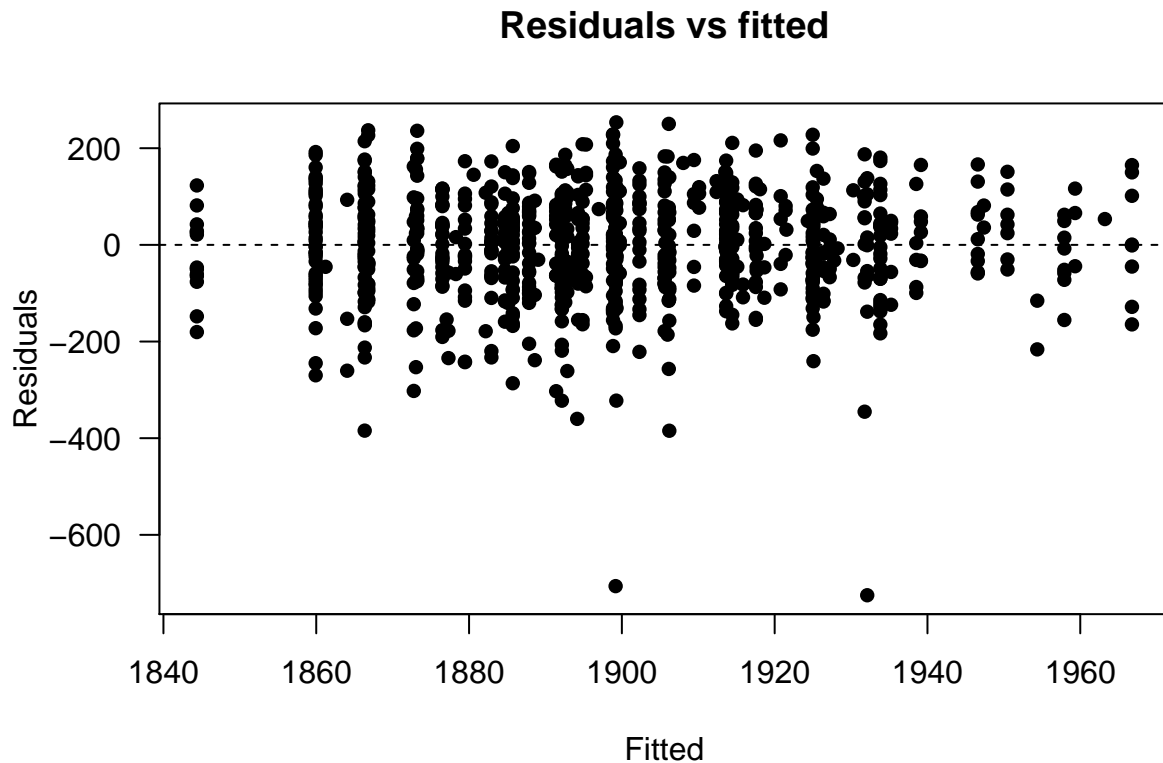
```
# qq Plot RE
qqnorm(unlist(ranef_pl), main = "QQ plot (Plot RE)", las = 1, pch = 16)
qqline(unlist(ranef_pl))
```



We want our points to fall approximately on the diagonal lines.

#### Fitted v Residuals

```
## plot residuals versus fitted values
yh <- fitted(global_mod)
plot(yh, resids, las = 1, pch = 16,
     xlab = "Fitted", ylab = "Residuals",
     main = "Residuals vs fitted")
abline(h=0, lty = "dashed")
```



We assume our errors are normally distributed with constant variance. We want this plot to look like a scatterplot of points, without any evidence of trends.

### Levene's test

We can formally test the assumption of homogenous variance via the Levene's Test, which compares the absolute values of the residuals among groups.

```
## split residuals into 2 groups
```

```
g1 <- resid[yh <= median(yh)]
```

```
g2 <- resid[yh > median(yh)]
```

```
## Levene's test
```

```
var.test(g1, g2)
```

```
##
```

```
## F test to compare two variances
```

```
##
```

```
## data: g1 and g2
```

```
## F = 0.90516, num df = 442, denom df = 430, p-value = 0.2983
```

```
## alternative hypothesis: true ratio of variances is not equal to 1
```

```
## 95 percent confidence interval:
```

```
## 0.7499399 1.0922349
```

```
## sample estimates:
```

```
## ratio of variances
```

```
## 0.9051588
```

There is no justification to reject the null hypothesis that the residuals are equal. F is close to 1 and it is

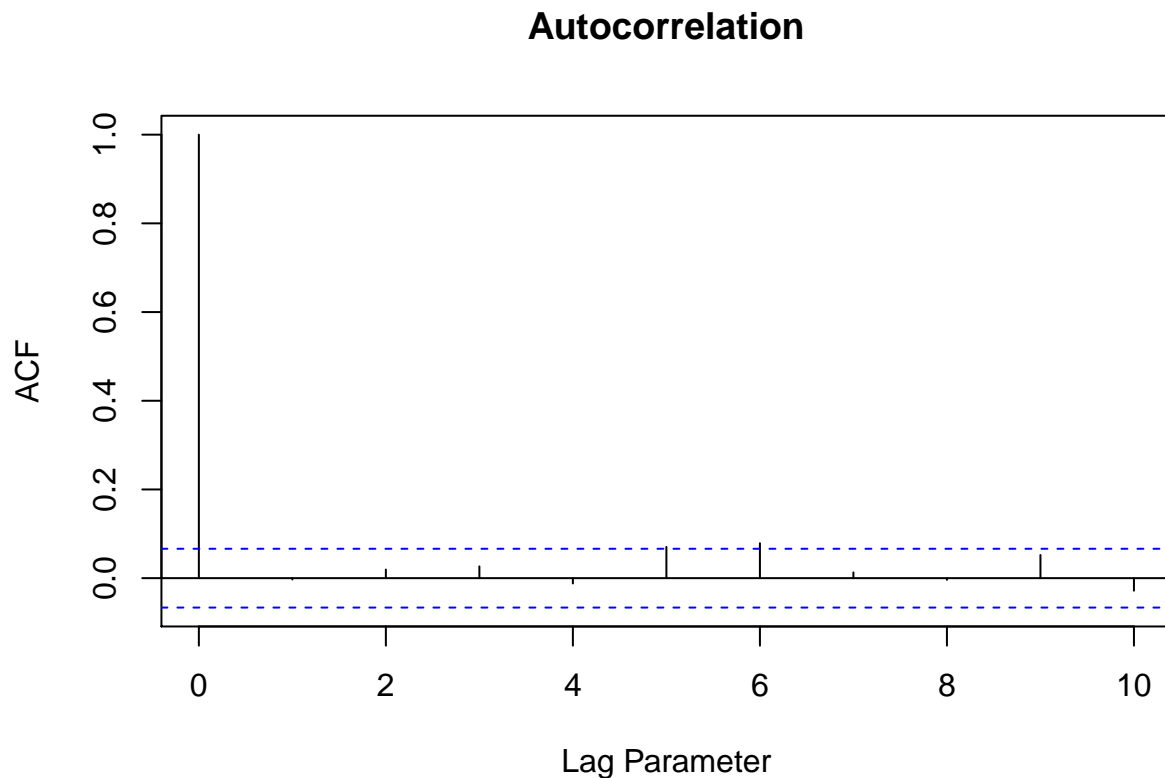
within the 95% confidence interval.

## Autocorrelation

We also assume our errors are independent (e.g., not correlated). An ACF plot can be used to look for autocorrelation.

```
# calculate the ACF for lags between 1 and 10
autocorrelation <- acf(resids, lag.max= 10, plot = FALSE)

# Plot figure
plot(autocorrelation,
     main="Autocorrelation",
     xlab="Lag Parameter",
     ylab="ACF")
```



The first value with 0 lag will always be autocorrelated because it's stacked on itself. But after that, we want to see the values within the blue dotted lines. There does not appear to be autocorrelation in the residuals.

## Identifying Outliers

[https://qerm514.github.io/website/labs/week\\_03/diagnostics\\_and\\_errors.html#unusual\\_observations](https://qerm514.github.io/website/labs/week_03/diagnostics_and_errors.html#unusual_observations)  
[https://qerm514.github.io/website/homework/week\\_03/hw\\_03\\_diagnostics\\_key.pdf](https://qerm514.github.io/website/homework/week_03/hw_03_diagnostics_key.pdf) Calculate the studentized residuals to look for outliers

```
## get studentized residuals
(stud_e <- rstudent(global_mod))
```

##	1	2	3	4	5	6
##	1.334692028	-1.432303962	-0.417831919	0.076619990	-1.126837630	0.216916981
##	7	8	9	10	11	12
##	-0.826880478	-1.450616843	-0.203144114	-0.467319488	1.489091460	0.805841181
##	13	14	15	16	17	18
##	0.227967785	-1.138748660	-0.957882066	0.845018269	-1.216715706	-0.822294182
##	19	20	21	22	23	24
##	-0.267352269	1.390594022	-1.216715706	-0.583806748	-1.077365634	1.381562004
##	25	26	27	28	29	30
##	0.133713679	0.214145892	-1.673382506	-0.708532092	0.712224053	1.372633482
##	31	32	33	34	35	36
##	0.056400801	-1.525830123	0.056400801	-1.076384817	-0.186666559	0.531278615
##	37	38	39	40	41	42
##	0.048685340	-1.461142191	0.245649304	0.461868921	-0.742033988	0.874635633
##	43	44	45	46	47	48
##	-0.900261227	0.970947865	-1.622487352	0.475627812	-0.267352269	-0.019692242
##	49	50	51	52	53	54
##	0.260957027	-0.563804529	-0.598130938	-0.259450616	0.086953468	0.506459533
##	55	56	57	58	59	60
##	-0.482167262	1.393179553	-1.182784114	0.498141330	-2.136341951	-1.468502916
##	61	62	63	64	65	66
##	0.974369907	1.288339556	0.152710509	-0.997215541	-1.138748660	-2.957215340
##	67	68	69	70	71	72
##	-0.247204090	-2.431092485	0.870721913	1.140919160	0.902205474	-0.216310733
##	73	74	75	76	77	78
##	-0.435312431	-0.308078585	0.790189055	-1.493543440	-2.773955087	0.904905192
##	79	80	81	82	83	84
##	-2.008493985	-0.468816730	0.351797798	-1.428092365	-0.759021397	0.725122357
##	85	86	87	88	89	90
##	-0.821010018	-1.896404891	1.461956800	0.973425978	0.434759960	-0.275249650
##	91	92	93	94	95	96
##	-0.620142977	0.382019338	1.108469710	0.084835095	0.757298346	-0.208697740
##	97	98	99	100	101	102
##	0.379606443	0.127803063	0.957647605	0.436294735	0.393623959	0.196942913
##	103	104	105	106	107	108
##	-1.057142678	-1.950051458	-0.245369619	-2.206043836	-0.722974893	-1.371681203
##	109	110	111	112	113	114
##	0.325043321	-0.164160591	-0.775055325	0.216410317	-0.038489038	0.524860316
##	115	116	117	118	119	120
##	-0.450357972	0.129414760	1.589527955	0.973662110	-1.200511770	-1.231340008
##	121	122	123	124	125	126
##	1.471268881	-0.360534027	-1.920754837	0.874032701	-0.992297001	1.052309305
##	127	128	129	130	131	132
##	-0.792496355	-0.233827956	-0.961959926	0.714295624	-0.356344443	-0.191620972
##	133	134	135	136	137	138
##	1.588709789	-0.578417428	0.759537822	1.524609141	0.612482243	-0.677440977
##	139	140	141	142	143	144
##	-0.081153118	0.553672027	2.088498840	1.008845307	1.434094862	-1.585426134
##	145	146	147	148	149	150
##	0.220123333	0.543951564	0.186424001	0.483670760	0.068859292	0.712811644
##	151	152	153	154	155	156
##	0.866426016	-0.022065661	-1.250882909	1.097201240	-0.448696911	1.377438964
##	157	158	159	160	161	162
##	-0.191956057	-0.584394548	-2.219988421	0.388703524	-0.584394548	0.639995429

##	163	164	165	166	167	168
##	-1.429888543	-0.617355406	0.202494199	0.766049993	-1.287583193	0.784033132
##	169	170	171	172	173	174
##	2.097926225	-2.228252612	1.924884388	0.179418896	-2.783974589	-0.307287428
##	175	176	177	178	179	180
##	1.332289773	1.492884429	0.748692478	-0.867415899	0.018688978	-0.209494506
##	181	182	183	184	185	186
##	1.919784087	-2.322523709	1.283363429	0.577983977	0.309588486	-1.060247012
##	187	188	189	190	191	192
##	0.477076081	0.771646431	0.480120579	1.042083079	-0.318155687	1.129659592
##	193	194	195	196	197	198
##	0.528938013	0.487467725	0.319585433	-0.842365750	-0.555558992	0.561951510
##	199	200	201	202	203	204
##	1.764146945	1.054168325	0.375417742	-0.059894672	-1.492542275	-0.185182744
##	205	206	207	208	209	210
##	1.970780078	0.025533881	1.008612129	1.168977287	-0.763946396	-0.223150262
##	211	212	213	214	215	216
##	-0.032383691	-2.248839586	0.368804746	1.473175112	0.998332220	0.270726910
##	217	218	219	220	221	222
##	1.320450433	-1.007768380	0.310401500	-1.299725605	-0.618838111	-0.906103777
##	223	224	225	226	227	228
##	1.622311938	-1.349318843	-2.629283562	0.699065538	0.379005478	-0.168999794
##	229	230	231	232	233	234
##	-0.219144068	1.269938803	1.878282514	0.980690589	-0.032383691	1.262799170
##	235	236	237	238	239	240
##	0.731049982	-2.478824898	0.521448276	0.432731485	0.704826204	0.310042679
##	241	242	243	244	245	246
##	-3.531928835	-1.653605688	-0.732534664	0.565541383	1.228494252	-0.683391873
##	247	248	249	250	251	252
##	0.188898068	0.071435567	0.071435567	1.600992158	1.708487560	-0.844312670
##	253	254	255	256	257	258
##	-1.583085378	-0.576486323	1.292603577	0.147215416	-0.908309271	-0.674119864
##	259	260	261	262	263	264
##	-1.539426252	-1.209221474	0.463038464	-0.427327667	-0.409499920	-0.141681823
##	265	266	267	268	269	270
##	0.524761239	-0.542135482	0.039750999	-0.525152710	-0.860733616	0.883203391
##	271	272	273	274	275	276
##	0.081139411	0.426668462	-0.973633484	-0.621307742	0.243157818	-0.905850273
##	277	278	279	280	281	282
##	0.328575685	0.936374330	-0.172909860	-0.313436030	-0.120304446	0.416748968
##	283	284	285	286	287	288
##	0.131563507	-0.142600294	-0.365001715	1.203179772	-0.284082902	-0.102167523
##	289	290	291	292	293	294
##	-0.176324254	0.285503306	2.166220788	-0.497547716	0.550558552	0.863179727
##	295	296	297	298	299	300
##	0.222359952	0.684095734	-0.669172823	0.665097660	-0.746912331	-1.030868927
##	301	302	303	304	305	306
##	-0.353537059	1.508550861	0.785540750	0.677680812	1.709687632	0.606925846
##	307	308	309	310	311	312
##	-1.108031312	1.125220112	-0.072385519	-0.740125254	0.313247326	0.179798732
##	313	314	315	316	317	318
##	-1.035271355	2.174832285	0.427251864	-0.388939916	-0.807445714	0.319277659
##	319	320	321	322	323	324
##	1.640882760	1.824439024	1.640882760	0.576017238	1.034645844	1.020429611



##	325	326	327	328	329	330
##	0.599904258	1.313601941	1.056157025	-0.333817851	-0.332900678	0.259317585
##	331	332	333	334	335	336
##	0.552119371	-0.857431613	-0.115897672	-0.878618297	-0.452555595	-0.091814872
##	337	338	339	340	341	342
##	0.589186177	-0.135024094	0.468325345	-0.022878337	0.881326939	-1.088938400
##	343	344	345	346	347	348
##	2.079446348	0.459628052	0.210035235	0.319277659	0.819480670	-0.623604980
##	349	350	351	352	353	354
##	-0.689593457	-0.461992703	-1.080442099	-0.110565683	-0.490343260	0.059661674
##	355	356	357	358	359	360
##	0.037636999	-0.352366111	-1.436415778	-1.034452258	0.267560435	-0.251294926
##	361	362	363	364	365	366
##	0.012087687	-1.752631038	-0.100562438	0.065167725	0.131459790	-2.144567779
##	367	368	369	370	371	372
##	-0.579338464	0.822658886	-0.561245098	-0.759414158	0.783210849	0.737264134
##	373	374	375	376	377	378
##	-0.596095624	0.045280105	-0.630714814	0.047029479	-0.160409441	-0.503608986
##	379	380	381	382	383	384
##	0.920398795	0.354061758	-0.172444299	1.920587709	0.414445712	0.416217239
##	385	386	387	388	389	390
##	0.310178454	-1.337472815	1.149652173	-0.094094416	0.682050584	0.778700519
##	391	392	393	394	395	396
##	-2.037402438	0.417928820	-0.651062247	-0.165157216	1.069483293	1.054022679
##	397	398	399	400	401	402
##	1.070311541	1.048869140	0.762755743	-0.327125560	1.589885223	-2.023032326
##	403	404	405	406	407	408
##	0.777070846	1.111753703	-1.010513104	1.458379679	0.812758115	0.764688320
##	409	410	411	412	413	414
##	-0.233809707	-0.796833756	-0.539340901	0.370718729	-0.128184132	0.495230698
##	415	416	417	418	419	420
##	-1.226647557	-0.316481314	0.209302551	0.264043920	-1.515356358	0.019742813
##	421	422	423	424	425	426
##	0.919533281	-1.624344748	0.412648633	0.810953458	0.191173140	-0.776403658
##	427	428	429	430	431	432
##	0.545601052	-0.100562438	0.503899407	0.053918055	1.221081077	-0.280743716
##	433	434	435	436	437	438
##	0.389216250	-0.424306566	0.322594290	-0.853302666	0.349644439	0.268371319
##	439	440	441	442	443	444
##	0.138891446	-0.722096326	1.105936102	-1.880365718	0.120598877	-0.147005096
##	445	446	447	448	449	450
##	-0.294112394	1.246460135	-0.232380362	-1.163175978	0.211015784	-0.129844332
##	451	452	453	454	455	456
##	-1.444540992	-0.328928391	0.195580589	-0.924757336	-0.298529413	-0.911894674
##	457	458	459	460	461	462
##	-0.861458391	-0.477888209	-0.915723238	0.025209823	-0.312127085	-0.570574317
##	463	464	465	466	467	468
##	0.798247124	0.631270332	0.191237612	-0.926567081	-0.526171988	-0.591614371
##	469	470	471	472	473	474
##	0.270000280	-0.395183136	-0.521418900	1.303560865	0.984032761	1.361759335
##	475	476	477	478	479	480
##	0.727945943	-1.102917364	-0.350464984	1.126377991	0.976711722	-1.261391596
##	481	482	483	484	485	486
##	0.828699224	0.122539040	-0.438502640	-0.815444928	1.325261184	-0.652042464

##	487	488	489	490	491	492
##	-0.054548086	0.250724984	0.034215726	1.180722307	0.398311516	0.663434271
##	493	494	495	496	497	498
##	1.367920422	0.262190807	1.601837131	0.804535794	-0.325357252	-0.279419171
##	499	500	501	502	503	504
##	0.644120014	0.241334918	0.477272903	-0.115879602	0.599100694	-0.152482955
##	505	506	507	508	509	510
##	0.712992352	-0.432096857	-0.500440837	-0.801587203	-0.279419171	1.301677709
##	511	512	513	514	515	516
##	0.392379329	0.029284735	0.113443300	0.618334574	-1.032720500	1.285897893
##	517	518	519	520	521	522
##	-0.737004730	0.008529960	-0.184106347	-1.428840326	0.950470928	0.489982802
##	523	524	525	526	527	528
##	-0.168750613	0.565563999	-0.866098875	0.235194397	0.543508727	1.384917371
##	529	530	531	532	533	534
##	-1.022323722	0.611880071	0.675725414	-3.539073821	0.530900776	0.606484091
##	535	536	537	538	539	540
##	0.045769914	0.194089974	-6.483703648	-0.087662229	-0.694788801	-1.585320450
##	541	542	543	544	545	546
##	-0.709704500	0.603173024	-0.801571288	-0.260162370	-0.725128940	-1.535642411
##	547	548	549	550	551	552
##	0.650374956	0.793532189	0.328340053	-0.239683398	1.112543369	-0.625394850
##	553	554	555	556	557	558
##	-0.677953758	0.659491776	-0.512252679	-0.194499503	0.656160014	-1.388804235
##	559	560	561	562	563	564
##	-1.096712603	0.326595353	-1.610838280	-0.252714049	-0.350352169	0.401425456
##	565	566	567	568	569	570
##	-1.637888713	1.077826474	-0.537094251	-0.351723040	0.098406948	0.163603635
##	571	572	573	574	575	576
##	-1.066134438	0.014844998	0.675994499	-0.743824056	-0.154525338	-0.681106680
##	577	578	579	580	581	582
##	-0.034741215	-0.659600727	0.454428203	-0.336220336	-1.425115602	1.239797926
##	583	584	585	586	587	588
##	0.270099722	-0.731152024	-0.020049004	1.717304965	1.229523555	2.090600841
##	589	590	591	592	593	594
##	-1.028680164	0.223822379	-0.228488049	1.092563061	1.162919645	-0.706150530
##	595	596	597	598	599	600
##	0.759265940	-0.193691499	0.473149512	-0.422253224	-0.641558018	-0.733302359
##	601	602	603	604	605	606
##	0.618067001	0.746637650	0.710153890	-0.427298732	0.129627897	-0.648691989
##	607	608	609	610	611	612
##	0.204925479	0.809877274	0.211536974	0.328982837	1.002712545	0.444592174
##	613	614	615	616	617	618
##	-0.878808746	-0.137915845	-0.370540503	0.077824024	1.829253691	-0.825236825
##	619	620	621	622	623	624
##	-0.905714862	-1.205511609	0.952529441	-1.003720043	0.151603205	-0.657948955
##	625	626	627	628	629	630
##	0.670076307	0.679932497	0.223052762	1.794093943	0.317646172	-0.037561735
##	631	632	633	634	635	636
##	0.603632662	0.075601032	0.744606568	-0.753781827	1.376174650	1.018472737
##	637	638	639	640	641	642
##	-0.627598919	0.285069019	1.681989123	1.164767768	-0.496945402	1.264056613
##	643	644	645	646	647	648
##	-0.645871064	1.190862364	0.948209881	1.598028663	-0.289341532	1.943238083

##	649	650	651	652	653	654
##	-0.628599301	-1.080872128	1.661721948	-0.616969776	-0.171484945	-0.450649303
##	655	656	657	658	659	660
##	-1.685028860	1.050100730	-1.331792914	-1.496377981	0.580046380	0.546044375
##	661	662	663	664	665	666
##	-0.169016874	0.356653889	-1.266696515	-0.741331322	-0.043479587	0.688910145
##	667	668	669	670	671	672
##	0.368305435	0.190450336	0.342111202	-1.518064091	0.375706649	0.175882771
##	673	674	675	676	677	678
##	-0.258464938	0.407369207	-0.042625697	0.596608218	1.162208276	1.562332633
##	679	680	681	682	683	684
##	0.613087131	-1.061229615	0.705764688	-0.261851827	1.087248374	-0.575825242
##	685	686	687	688	689	690
##	-0.761225209	0.317741808	-0.645042683	0.004873608	-0.430732612	-0.549760568
##	691	692	693	694	695	696
##	-1.185791315	-1.119520844	1.048421199	-0.143749041	-1.051777697	-0.932492769
##	697	698	699	700	701	702
##	-3.320518439	1.392883927	-0.037754587	1.202943521	-2.178443845	0.692587177
##	703	704	705	706	707	708
##	-1.374866270	-0.563712616	-0.532787375	-0.204833693	-0.581718391	0.354982088
##	709	710	711	712	713	714
##	0.973608783	-1.653135423	0.038822209	0.025005701	-2.211480498	-0.420387147
##	715	716	717	718	719	720
##	-0.202998063	1.105977053	0.422080351	-0.496383556	-0.567930030	-0.805269491
##	721	722	723	724	725	726
##	0.572637822	-1.211386898	-0.275157155	0.672118818	0.291510377	-0.085337378
##	727	728	729	730	731	732
##	0.524818845	1.202236851	0.827854913	1.006412640	-0.715091473	0.506798497
##	733	734	735	736	737	738
##	1.681488706	0.013077719	-1.708287059	1.722620390	-0.625449432	0.457209997
##	739	740	741	742	743	744
##	1.213358500	-3.173489960	-0.067386333	-2.968176046	2.334709316	0.998735725
##	745	746	747	748	749	750
##	-0.226577683	0.099573803	0.303680786	0.871487192	0.791472429	-1.191860476
##	751	752	753	754	755	756
##	-0.218013354	-0.418396308	-0.902263924	0.358006859	-0.320681238	1.448666666
##	757	758	759	760	761	762
##	0.657205847	0.913131024	0.156680027	-2.402716419	-1.006579834	-0.543621651
##	763	764	765	766	767	768
##	-0.428534785	0.563532474	-0.457906664	-0.696053247	0.018458497	0.472316891
##	769	770	771	772	773	774
##	2.302618349	0.711623679	-1.049792006	1.405722546	0.719037420	0.628666445
##	775	776	777	778	779	780
##	-1.064783169	1.020647110	-0.539815463	1.570582173	0.871235849	1.060353044
##	781	782	783	784	785	786
##	0.491630659	-2.360920974	0.067567271	-0.018620710	-0.280920080	0.412712878
##	787	788	789	790	791	792
##	-0.209777394	-0.004403171	1.619241133	-0.298997587	-0.516884736	-1.143123762
##	793	794	795	796	797	798
##	0.312197068	0.458310284	0.213865826	-0.776958440	0.801415821	0.268957771
##	799	800	801	802	803	804
##	0.423995816	0.757956837	0.969278916	-1.001084437	-0.757859889	0.942571409
##	805	806	807	808	809	810
##	-0.420848873	0.542797779	-0.544159727	-0.306812869	-0.302136580	-0.172672305

```
##           811           812           813           814           815           816
## -0.616484276 0.242339785 1.990859498 0.494657073 -0.361841915 0.577207509
##           817           818           819           820           821           822
## -0.518749435 0.443198444 -0.063901024 0.928432367 0.624161309 -0.457352831
##           823           824           825           826           827           828
## 1.205283640 0.108774299 -0.307946541 1.524957889 0.103339030 -0.848204405
##           829           830           831           832           833           834
## 1.532303051 0.587828398 -2.004063992 -1.070193659 -6.671648537 -1.429125982
##           835           836           837           838           839           840
## -0.469176808 1.055296759 0.033576640 -0.277926679 -0.006865249 -0.802801123
##           841           842           843           844           845           846
## -0.499400841 0.963297348 -0.474700782 -0.069076969 -0.286323129 0.140656156
##           847           848           849           850           851           852
## 1.269751669 -1.272346739 0.572785243 0.454987895 -0.536771984 0.222953353
##           853           854           855           856           857           858
## 1.160220188 -0.597871149 0.136907466 -0.665052470 1.393024587 0.390066905
##           859           860           861           862           863           864
## 0.574223459 -0.914802854 0.608953652 1.076139169 1.522288597 0.936751371
##           865           866           867           868           869           870
## -0.408318552 1.383929139 -1.182638805 0.330590954 0.496854396 0.005407740
##           871           872           873           874
## -0.413636938 0.751023077 -0.010734196 -1.517560932
```

```
## get sample size
n <- nrow(SCMUdf)

## Bonferroni correction: alpha/n
alpha <- 0.05/n

## critical t value
degf <- n - length(coef(global_mod))-1 # should be more due to REs?
t_crit <- qt(1 - alpha/2, degf)

## compare t_stud to t_crit
sum(stud_e > t_crit, na.rm = TRUE)
```

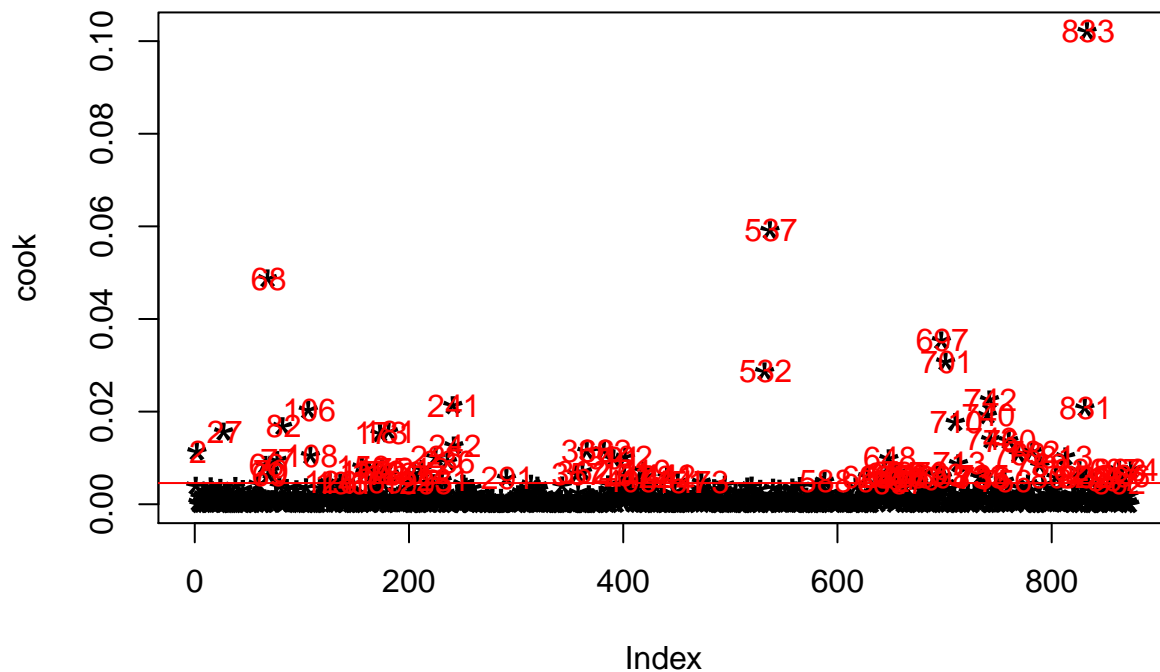
```
## [1] 0
```

## Cook's Distance

```
## Cook's D
cook <- cooks.distance(global_mod)

# Plot the Cook's Distance using the traditional 4/n criterion
sample_size <- nrow(SCMUdf)
plot(cook, pch="*", cex=2, main="Influential Obs by Cooks distance") # plot cook's distance
abline(h = 4/sample_size, col="red") # add cutoff line
text(x=1:length(cook)+1, y=cook, labels=ifelse(cook>4/sample_size, names(cook),""), col="red") # add l
```

### Influential Obs by Cooks distance



## Fit Candidate Models

```
## create empty matrix for storing results
mod_res <- matrix(NA, n_mods, 1)
colnames(mod_res) <- c("AIC")

## fit models and store AIC & BIC
for(i in 1:n_mods) {
  if(i == 1) {
    fmla <- "Size ~ 1 + (1 | Plot)"
  } else {
    fmla <- paste("Size ~ (1 | Plot) +", paste(cov_names[use_set[i,]], collapse = " + "))
  }
  mod_fit <- lmer(as.formula(fmla), data = SCMUdf, REML = TRUE)
  mod_res[i,"AIC"] <- AIC(mod_fit)
}

## create empty matrix for storing results
delta_res <- matrix(NA, n_mods, 1)
colnames(delta_res) <- c("deltaAIC")

## convert IC to deltaIC
delta_res[, "deltaAIC"] <- mod_res[, "AIC"] - min(mod_res[, "AIC"])
(delta_res <- round(delta_res, 2)) # round results
```

```

##      deltaAIC
## [1,]    46.71
## [2,]    30.00
## [3,]    33.15
## [4,]    16.13
## [5,]    35.29
## [6,]    18.40
## [7,]    27.49
## [8,]    10.44
## [9,]    24.40
## [10,]     7.37
## [11,]    17.14
## [12,]     0.00
## [13,]    31.96
## [14,]    14.62
## [15,]    18.42
## [16,]     1.09
## [17,]    26.12
## [18,]     9.04
## [19,]    36.41
## [20,]    19.58
## [21,]    28.84
## [22,]    11.83
## [23,]    25.65
## [24,]     8.64
## [25,]    21.66
## [26,]     4.61
## [27,]    26.89
## [28,]     9.60
## [29,]    22.92
## [30,]     5.84

## "best" models from our set
cov_names[use_set[12,]] # Egg order, BEUTI, NPGO

## [1] "EggOrder" "BEUTI"      "NPGO"
cov_names[use_set[16,]] # Egg order, NPGO, ONI

## [1] "EggOrder" "NPGO"        "ONI"
cov_names[use_set[26,]] # Egg order, ANCHL, BEUTI, SST (>2 AIC)

## [1] "EggOrder" "ANCHL"      "BEUTI"      "SST"
cov_names[use_set[30,]] # Egg order, PDO, SST (>2 AIC)

## [1] "EggOrder" "PDO"        "SST"
cov_names[use_set[10,]] # Egg order, NPGO (>2 AIC)

## [1] "EggOrder" "NPGO"
cov_names[use_set[24,]] # Egg order, BEUTI, SST (>2 AIC)

## [1] "EggOrder" "BEUTI"      "SST"

## run top models
topmod1 <- lmer(Size ~ EggOrder + BEUTI + NPGO + (1 | Plot), data = SCMUdf, REML = TRUE)

```

```

topmod2 <- lmer(Size ~ EggOrder + NPGO + ONI + (1 | Plot), data = SCMUdf, REML = TRUE)
topmod3 <- lmer(Size ~ EggOrder + ANCHL + BEUTI + SST + (1 | Plot), data = SCMUdf, REML = TRUE)
topmod4 <- lmer(Size ~ EggOrder + PDO + SST + (1 | Plot), data = SCMUdf, REML = TRUE)
topmod5 <- lmer(Size ~ EggOrder + NPGO + (1 | Plot), data = SCMUdf, REML = TRUE)
topmod6 <- lmer(Size ~ EggOrder + BEUTI + SST + (1 | Plot), data = SCMUdf, REML = TRUE)

## Model selection table
AIC.tab <- matrix(NA, nrow = 6, ncol = 3) # 6 rows for 6 top models
AIC.tab[1,1] <- AIC(topmod1) # AIC for topmod1 in first row, first column
AIC.tab[2,1] <- AIC(topmod2) # AIC for topmod2 in second row, first column
AIC.tab[3,1] <- AIC(topmod3) # AIC for topmod3 in second row, first column
AIC.tab[4,1] <- AIC(topmod4) # AIC for topmod4 in second row, first column
AIC.tab[5,1] <- AIC(topmod5) # AIC for topmod5 in second row, first column
AIC.tab[6,1] <- AIC(topmod6) # AIC for topmod6 in second row, first column
AIC.tab[,2] <- AIC.tab[,1] - min(AIC.tab[,1]) # calculate delta AIC
AIC.tab[,3] <- exp(-0.5*AIC.tab[,2])/(sum(exp(-0.5*AIC.tab[,2]))) # calculate model weights
colnames(AIC.tab) <- c("AIC", "deltaAIC", "model_weights")
print(AIC.tab)

##           AIC deltaAIC model_weights
## [1,] 10672.18 0.000000    0.564433704
## [2,] 10673.27 1.090108    0.327264573
## [3,] 10676.79 4.610461    0.056294240
## [4,] 10678.02 5.844698    0.030370563
## [5,] 10679.55 7.374504    0.014133824
## [6,] 10680.82 8.641014    0.007503096

```

## Top Models

Here we look at the top competitive models.

### Top Model 1

```

topmod1 <- lmer(Size ~ EggOrder + BEUTI + NPGO + (1 | Plot), data = SCMUdf, REML = TRUE)
summary(topmod1)

## Linear mixed model fit by REML ['lmerMod']
## Formula: Size ~ EggOrder + BEUTI + NPGO + (1 | Plot)
## Data: SCMUdf
##
## REML criterion at convergence: 10660.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -6.6372 -0.6084  0.0419  0.6738  2.3199
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Plot     (Intercept)         239.4    15.47
## Residual                    11850.7   108.86
## Number of obs: 874, groups: Plot, 8
##
## Fixed effects:

```

```
##               Estimate Std. Error t value
## (Intercept)  1887.427      8.104 232.901
## EggOrderEgg2   32.931      9.148   3.600
## BEUTI         -10.404      4.954  -2.100
## NPGO          -15.062      3.711  -4.059
##
## Correlation of Fixed Effects:
##               (Intr) EggOE2 BEUTI
## EggOrdrEgg2 -0.236
## BEUTI       0.078 -0.002
## NPGO       -0.065  0.000 -0.230
```

## Top Model 2

```
topmod2 <- lmer(Size ~ EggOrder + NPGO + ONI + (1 | Plot), data = SCMUdf, REML = TRUE)
summary(topmod2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: Size ~ EggOrder + NPGO + ONI + (1 | Plot)
## Data: SCMUdf
##
## REML criterion at convergence: 10661.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -6.6268 -0.6169  0.0493  0.6724  2.3808
##
## Random effects:
## Groups Name Variance Std.Dev.
## Plot (Intercept) 257.1 16.03
## Residual 11863.3 108.92
## Number of obs: 874, groups: Plot, 8
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)  1887.453      8.301 227.380
## EggOrderEgg2   33.196      9.154   3.626
## NPGO          -13.532      4.052  -3.340
## ONI           9.174      5.103   1.798
##
## Correlation of Fixed Effects:
##               (Intr) EggOE2 NPGO
## EggOrdrEgg2 -0.232
## NPGO       -0.079  0.009
## ONI       -0.077  0.019  0.452
```

## Prediction

```
topmod1 <- lmer(Size ~ EggOrder + BEUTI + NPGO + (1 | Plot), data = SCMUdf, REML = TRUE)
topmod2 <- lmer(Size ~ EggOrder + NPGO + ONI + (1 | Plot), data = SCMUdf, REML = TRUE)

# AIC tab for 2 top models
AIC.tab2 <- matrix(NA, nrow = 2, ncol = 3)
```



```

AIC.tab2[1,1] <- AIC(topmod1)
AIC.tab2[2,1] <- AIC(topmod2)
AIC.tab2[,2] <- AIC.tab2[,1] - min(AIC.tab2[,1])
AIC.tab2[,3] <- exp(-0.5*AIC.tab2[,2])/(sum(exp(-0.5*AIC.tab2[,2])))
print(AIC.tab2)

```

```

##           [,1]      [,2]      [,3]
## [1,] 10672.18 0.000000 0.6329873
## [2,] 10673.27 1.090108 0.3670127

```

*#we want predictions with all predictors but one held constant, and then we'll do this one-at-a-time for each predictor  
# this will allow us to produce nice plots looking at the marginal effect of each predictor*

*#first, set up a dataset with everything at its mean value (except EggOrder)*

```

set.seed(1)
SCMU.null <- SCMUdf[c(1:200),]
SCMU.null$EggOrder <- c(rep("Egg1",100),rep("Egg2",100))
SCMU.null$BEUTI <- mean(SCMUdf$BEUTI)
SCMU.null$NPGO <- mean(SCMUdf$NPGO)
SCMU.null$ONI <- mean(SCMUdf$ONI)
SCMU.null$ANCHL <- mean(SCMUdf$ANCHL)
SCMU.null$PDO <- mean(SCMUdf$PDO)
SCMU.null$SST <- mean(SCMUdf$SST)

```

*#I'm pretty sure you need some values of plot and observer but it doesn't matter which ones because we'll sample them later*

```

SCMU.null$Plot <- sample(SCMUdf$Plot,200,replace = TRUE)
SCMU.null$Observer <- sample(SCMUdf$Observer,200,replace = TRUE)

```

## BEUTI

*#then vary just one predictor at a time for prediction. For example, create the dataset SCMU.BEUTI that varies BEUTI*

```

SCMU.BEUTI <- SCMU.null
SCMU.BEUTI$BEUTI <- rep(seq(from = min(SCMUdf$BEUTI),to = max(SCMUdf$BEUTI),length.out = 100),2)

```

*#PREDICT FOR SCMU.BEUTI*

*#Pull together the random effects (do we want the models with)*

```

# obs.sd.1 <- as.data.frame(VarCorr(bm1))$sdcor[1]
# plot.sd.1 <- as.data.frame(VarCorr(bm1))$sdcor[2]
# resid.sd.1 <- as.data.frame(VarCorr(bm1))$sdcor[3]
#
# obs.sd.2 <- as.data.frame(VarCorr(bm2))$sdcor[1]
# plot.sd.2 <- as.data.frame(VarCorr(bm2))$sdcor[2]
# resid.sd.2 <- as.data.frame(VarCorr(bm2))$sdcor[3]
#
# obs.sd.3 <- as.data.frame(VarCorr(bm3))$sdcor[1]
# plot.sd.3 <- as.data.frame(VarCorr(bm3))$sdcor[2]
# resid.sd.3 <- as.data.frame(VarCorr(bm3))$sdcor[3]

```

```

plot.sd.1 <- as.data.frame(VarCorr(topmod1))$sdcor[1]
resid.sd.1 <- as.data.frame(VarCorr(topmod1))$sdcor[2]

```

```

plot.sd.2 <- as.data.frame(VarCorr(topmod2))$sdcor[1]
resid.sd.2 <- as.data.frame(VarCorr(topmod2))$sdcor[2]

```

```

sims <- 10000

# pv <- matrix(nrow = sims, ncol = nrow(SCMU.BEUTI))
# for(i in 1:sims){
#   #choose a model
#   model <- which(rmultinom(n = 1, size = 1, prob = c(AIC.tab[,3]))==1)
#   if(model == 1){
#     #we simulate conditioning on no specific random effects levels
#     y <- unlist(simulate(bm1))
#     bmod <- refit(bm1,y)
#     pv[i,] <- predict(bmod, re.form = ~0, newdata = SCMU.BEUTI) + rnorm(1,0,sd=obs.sd.1) + rnorm(1,0,
#   }
#   if(model == 2){
#     #we simulate conditioning on no specific random effects levels
#     y <- unlist(simulate(bm2))
#     bmod <- refit(bm2,y)
#     pv[i,] <- predict(bmod, re.form = ~0, newdata = SCMU.BEUTI) + rnorm(1,0,sd=obs.sd.2) + rnorm(1,0,
#   }
#   if(model == 3){
#     #we simulate conditioning on no specific random effects levels
#     y <- unlist(simulate(bm3))
#     bmod <- refit(bm3,y)
#     pv[i,] <- predict(bmod, re.form = ~0, newdata = SCMU.BEUTI) + rnorm(1,0,sd=obs.sd.3) + rnorm(1,0,
#   }
# }

## Marcela tried updating
pv.BEUTI <- matrix(nrow = sims, ncol = nrow(SCMU.BEUTI))
for(i in 1:sims){
  #choose a model
  model <- which(rmultinom(n = 1, size = 1, prob = c(AIC.tab2[,3]))==1)
  if(model == 1){
    #we simulate conditioning on no specific random effects levels
    y <- unlist(simulate(topmod1))
    bmod <- refit(topmod1,y)
    pv.BEUTI[i,] <- predict(bmod, re.form = ~0, newdata = SCMU.BEUTI) + rnorm(1,0,sd=plot.sd.1) + rnorm
  }
  if(model == 2){
    #we simulate conditioning on no specific random effects levels
    y <- unlist(simulate(topmod2))
    bmod <- refit(topmod2,y)
    pv.BEUTI[i,] <- predict(bmod, re.form = ~0, newdata = SCMU.BEUTI) + rnorm(1,0,sd=plot.sd.2) + rnorm
  }
}

```

```

## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular

```

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]





[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

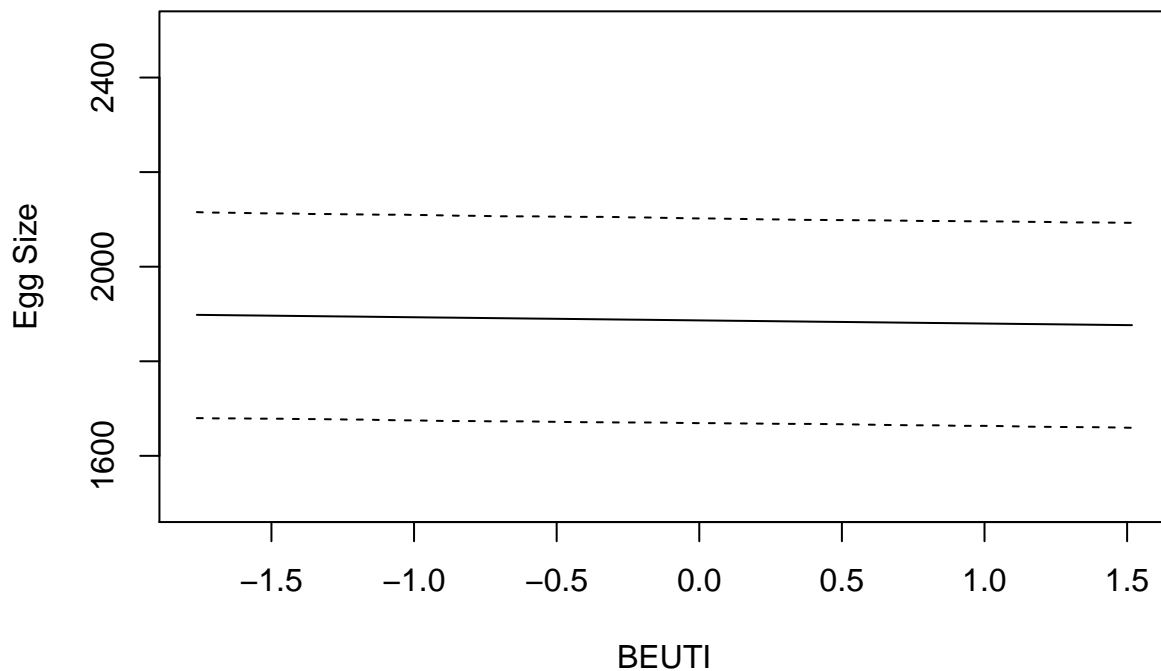


[illegible]

[illegible]

[illegible]

```
##SJC added - you can do plots like this of the predictions and 95% CIs against the individual predictors
plot(SCMU.BEUTI$BEUTI[1:100], y = apply(pv.BEUTI, 2, mean)[1:100], xlab = "BEUTI", ylab = "Egg Size", type = "n")
lines(SCMU.BEUTI$BEUTI[1:100], y = apply(pv.BEUTI, 2, function(x) quantile(x, probs = 0.025))[1:100], lty = 2)
lines(SCMU.BEUTI$BEUTI[1:100], y = apply(pv.BEUTI, 2, function(x) quantile(x, probs = 0.975))[1:100], lty = 2)
```



## NPGO

```
SCMU.NPGO <- SCMU.null
SCMU.NPGO$NPGO <- rep(seq(from = min(SCMUdf$NPGO), to = max(SCMUdf$NPGO), length.out = 100), 2)

plot.sd.1 <- as.data.frame(VarCorr(topmod1))$sdcor[1]
resid.sd.1 <- as.data.frame(VarCorr(topmod1))$sdcor[2]

plot.sd.2 <- as.data.frame(VarCorr(topmod2))$sdcor[1]
resid.sd.2 <- as.data.frame(VarCorr(topmod2))$sdcor[2]

sims <- 10000

pv.NPGO <- matrix(nrow = sims, ncol = nrow(SCMU.NPGO))
for(i in 1:sims){
  #choose a model
  model <- which(rmultinom(n = 1, size = 1, prob = c(AIC.tab2[, 3])) == 1)
  if(model == 1){
    #we simulate conditioning on no specific random effects levels
    y <- unlist(simulate(topmod1))
  }
}
```

```
## boundary (singular) fit: see ?isSingular
```

[illegible]

[illegible]

[illegible]



[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]



[illegible]

[illegible]

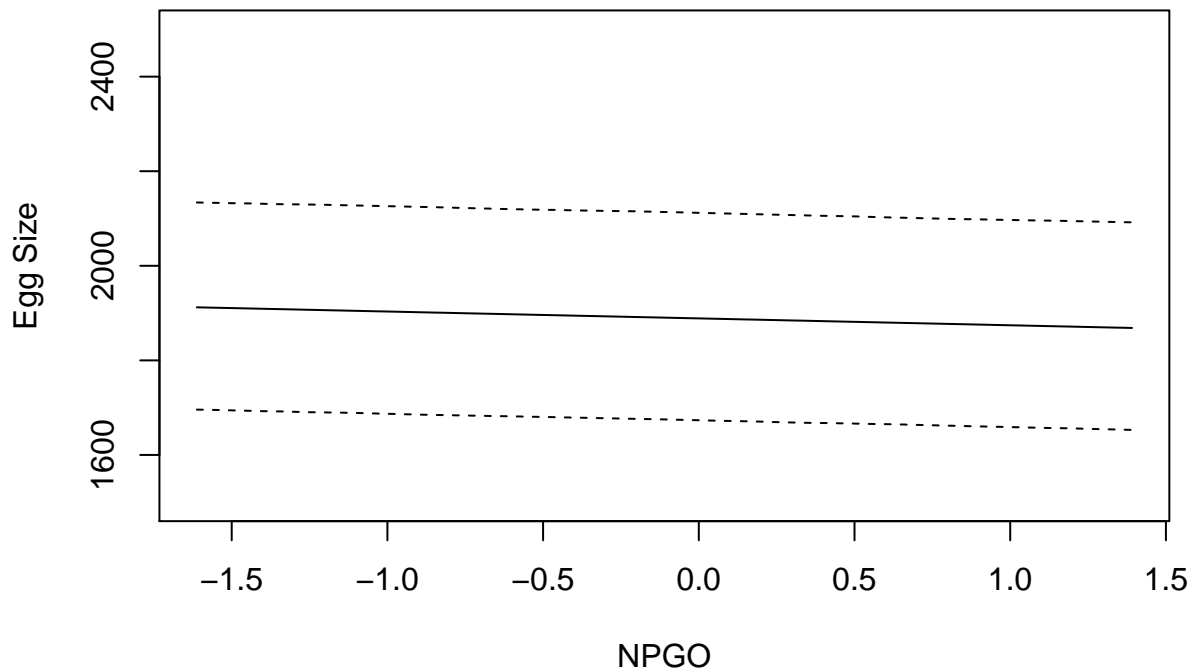
[illegible]

[illegible]

[illegible]

[illegible]

```
plot(SCMU.NPGO$NPGO[1:100], y = apply(pv.NPGO, 2, mean)[1:100], xlab = "NPGO", ylab = "Egg Size", type = "l",
lines(SCMU.NPGO$NPGO[1:100], y = apply(pv.NPGO, 2, function(x) quantile(x, probs = 0.025))[1:100], lty = 2)
lines(SCMU.NPGO$NPGO[1:100], y = apply(pv.NPGO, 2, function(x) quantile(x, probs = 0.975))[1:100], lty = 2)
```



## ONI

```
SCMU.ONI <- SCMU.null
SCMU.ONI$ONI <- rep(seq(from = min(SCMUdf$ONI),to = max(SCMUdf$ONI),length.out = 100),2)

plot.sd.1 <- as.data.frame(VarCorr(topmod1))$sdcor[1]
resid.sd.1 <- as.data.frame(VarCorr(topmod1))$sdcor[2]

plot.sd.2 <- as.data.frame(VarCorr(topmod2))$sdcor[1]
resid.sd.2 <- as.data.frame(VarCorr(topmod2))$sdcor[2]

sims <- 10000

pv.ONI <- matrix(nrow = sims, ncol = nrow(SCMU.ONI))
for(i in 1:sims){
  #choose a model
  model <- which(rmultinom(n = 1, size = 1,prob = c(AIC.tab2[,3]))==1)
  if(model == 1){
    #we simulate conditioning on no specific random effects levels
    y <- unlist(simulate(topmod1))
    bmod <- refit(topmod1,y)
    pv.ONI[i,] <- predict(bmod, re.form = ~0, newdata = SCMU.ONI) + rnorm(1,0,sd=plot.sd.1) + rnorm(1,0
  }
  if(model == 2){
    #we simulate conditioning on no specific random effects levels
```



```
y <- unlist(simulate(topmod2))
bmod <- refit(topmod2,y)
pv.ONI[i,] <- predict(bmod, re.form = ~0, newdata = SCMU.ONI) + rnorm(1,0,sd=plot.sd.2) + rnorm(1,0)
}
```

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]



[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

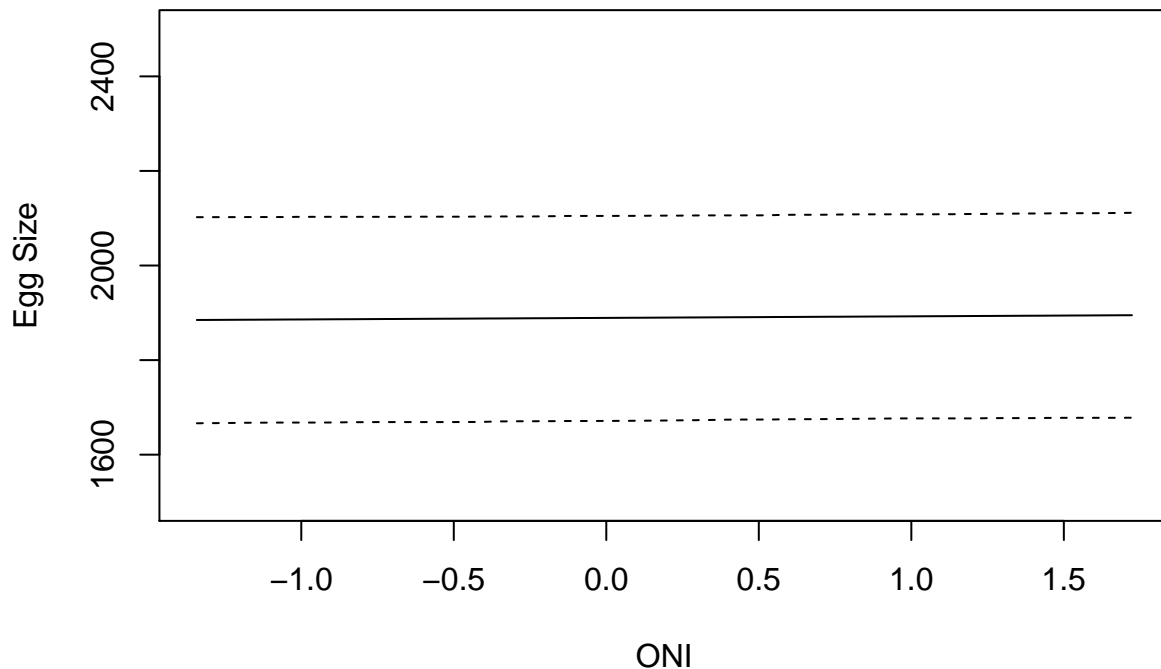
[illegible]



[illegible]

```
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
## boundary (singular) fit: see ?isSingular
```

```
plot(SCMU.ONI$ONI[1:100],y = apply(pv.ONI,2,mean)[1:100],xlab = "ONI",ylab = "Egg Size",type = "l",ylim = c(1600,2400))
lines(SCMU.ONI$ONI[1:100],y = apply(pv.ONI,2,function(x)quantile(x,probs= 0.025))[1:100],lty=2)
lines(SCMU.ONI$ONI[1:100],y = apply(pv.ONI,2,function(x)quantile(x,probs= 0.975))[1:100],lty=2)
```



## SST

```
# SCMU.SST <- SCMU.null
# SCMU.SST$SST <- rep(seq(from = min(SCMUdf$SST),to = max(SCMUdf$SST),length.out = 100),2)
#
# plot.sd.1 <- as.data.frame(VarCorr(topmod1))$sdcor[1]
# resid.sd.1 <- as.data.frame(VarCorr(topmod1))$sdcor[2]
#
```

```

# plot.sd.2 <- as.data.frame(VarCorr(topmod2))$sdcor[1]
# resid.sd.2 <- as.data.frame(VarCorr(topmod2))$sdcor[2]
#
# sims <- 10000
#
# pv.SST <- matrix(nrow = sims, ncol = nrow(SCMU.SST))
# for(i in 1:sims){
#   #choose a model
#   model <- which(rmultinom(n = 1, size = 1,prob = c(AIC.tab2[,3]))==1)
#   if(model == 1){
#     #we simulate conditioning on no specific random effects levels
#     y <- unlist(simulate(topmod1))
#     bmod <- refit(topmod1,y)
#     pv.SST[i,] <- predict(bmod, re.form = ~0, newdata = SCMU.SST) + rnorm(1,0,sd=plot.sd.1) + rnorm(1,0,sd=plot.sd.2)
#   }
#   if(model == 2){
#     #we simulate conditioning on no specific random effects levels
#     y <- unlist(simulate(topmod2))
#     bmod <- refit(topmod2,y)
#     pv.SST[i,] <- predict(bmod, re.form = ~0, newdata = SCMU.SST) + rnorm(1,0,sd=plot.sd.2) + rnorm(1,0,sd=plot.sd.1)
#   }
# }
#
# plot(SCMU.SST$SST[1:100],y = apply(pv.SST,2,mean)[1:100],xlab = "SST",ylab = "Egg Size",type = "l",ylt = 2)
# lines(SCMU.SST$SST[1:100],y = apply(pv.SST,2,function(x)quantile(x,probs= 0.025))[1:100],lty=2)
# lines(SCMU.SST$SST[1:100],y = apply(pv.SST,2,function(x)quantile(x,probs= 0.975))[1:100],lty=2)

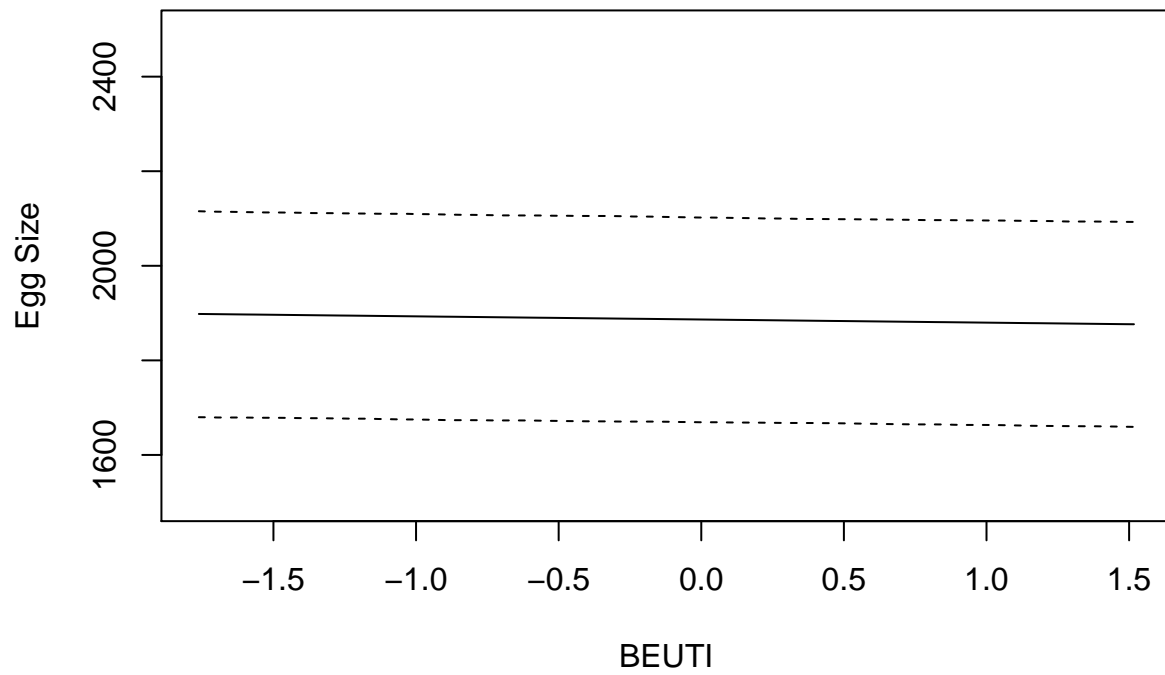
```

## Plots

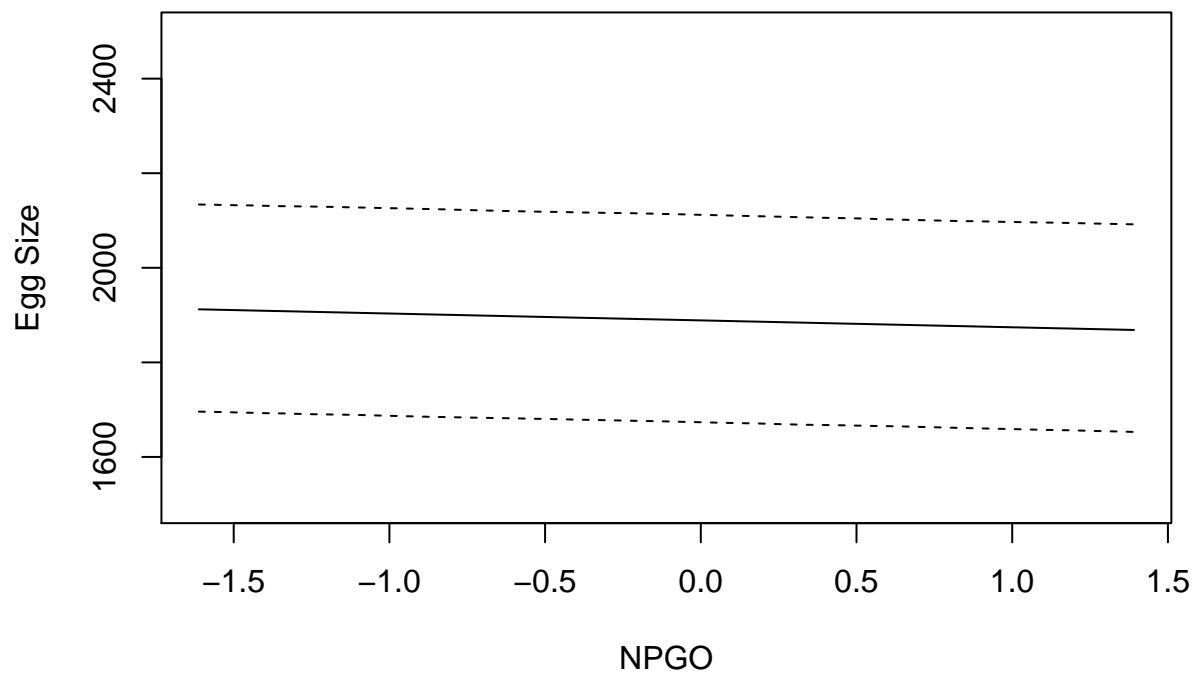
```

plot(SCMU.BEUTI$BEUTI[1:100],y = apply(pv.BEUTI,2,mean)[1:100],xlab = "BEUTI",ylab = "Egg Size",type = "l",ylt = 2)
lines(SCMU.BEUTI$BEUTI[1:100],y = apply(pv.BEUTI,2,function(x)quantile(x,probs= 0.025))[1:100],lty=2)
lines(SCMU.BEUTI$BEUTI[1:100],y = apply(pv.BEUTI,2,function(x)quantile(x,probs= 0.975))[1:100],lty=2)

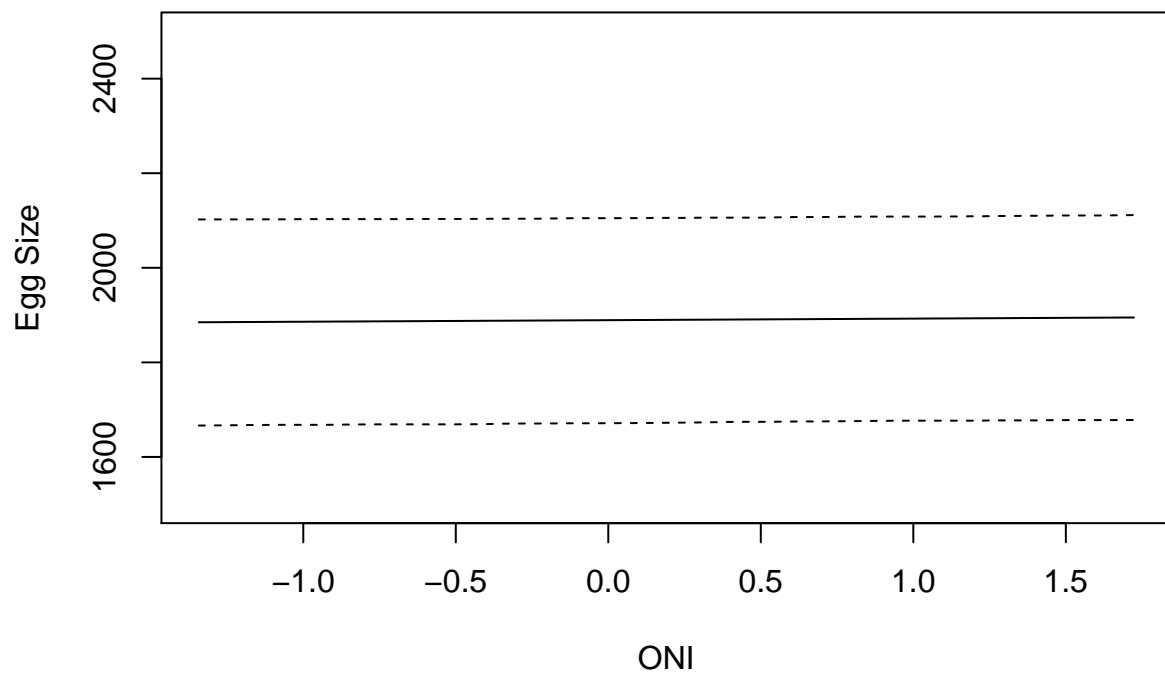
```



```
plot(SCMU.NPGO$NPGO[1:100],y = apply(pv.NPGO,2,mean)[1:100],xlab = "NPGO",ylab = "Egg Size",type = "l",
lines(SCMU.NPGO$NPGO[1:100],y = apply(pv.NPGO,2,function(x)quantile(x,probs= 0.025))[1:100],lty=2)
lines(SCMU.NPGO$NPGO[1:100],y = apply(pv.NPGO,2,function(x)quantile(x,probs= 0.975))[1:100],lty=2)
```



```
plot(SCMU.ONI$ONI[1:100],y = apply(pv.ONI,2,mean)[1:100],xlab = "ONI",ylab = "Egg Size",type = "l",ylim
lines(SCMU.ONI$ONI[1:100],y = apply(pv.ONI,2,function(x)quantile(x,probs= 0.025))[1:100],lty=2)
lines(SCMU.ONI$ONI[1:100],y = apply(pv.ONI,2,function(x)quantile(x,probs= 0.975))[1:100],lty=2)
```



```
# plot(SCMU.SST$SST[1:100],y = apply(pv.SST,2,mean)[1:100],xlab = "SST",ylab = "Egg Size",type = "l",yl
# lines(SCMU.SST$SST[1:100],y = apply(pv.SST,2,function(x)quantile(x,probs= 0.025))[1:100],lty=2)x
# lines(SCMU.SST$SST[1:100],y = apply(pv.SST,2,function(x)quantile(x,probs= 0.975))[1:100],lty=2)
```