Latitudinal and bathymetrical species richness patterns in the NW Pacific and adjacent Arctic Ocean

Hanieh Saeedi [1,2,3*], Mark J. Costello [4], Dan Warren [5], Angelika Brandt [1,2]
[1*] Senckenberg Research Institute and Museum, Senckenberganlage 25, 60325 Frankfurt am Main, Germany
[2*] Goethe-University of Frankfurt, FB 15, Institute for Ecology, Evolution and Diversity, Max-von-Laue-Str. 13, 60439 Frankfurt am Main, Germany
[3*] OBIS data manager, Deep-Sea Node, Frankfurt am Main, Germany
[4] Institute of Marine Science, University of Auckland, Auckland 1142, New Zealand
[5] Senckenberg Biodiversity and Climate Research Centre, Senckenberganlage 25, 60325 Frankfurt am Main, Germany

Table S1. Datasets used in this study. The first 145 datasets were extracted from GBIF and the remaining 204 from OBIS. Each is ranked by number of records per dataset.

Dataset title as provided in GBIF or OBIS	Number of Records
NMNH Extant Specimen Records	56000
Fish specimens of Kagoshima University Museum	34000
The molluscs collection (IM) of the Muséum national d'Histoire naturelle (MNHN - Paris)	15000
Zooplankton Eastern Arctic Ocean Polarstern, 1995-1998	12000
CAS Invertebrate Zoology (IZ)	11000
Archives of the Arctic Seas Zooplankton	10000
NOAA Deep Sea Corals Research and Technology Program	7000
Arctic Ocean Diversity	6000
Field Museum of Natural History (Zoology) Fish Collection	6000
Arctic benthic invertebrate collection of the Zoological Institute of the Russian Academy of Science	5000
Queensland Museum provider for OZCAM	5000
Continuous Plankton Recorder Dataset (SAHFOS)	4000
Mollusca collection of National Museum of Nature and Science	4000
Diveboard - Scuba diving citizen science observations	3000
Fish collection of National Museum of Nature and Science	3000
Fishbase	3000
Invertebrates Collection of the Swedish Museum of Natural History	2000
LACM Vertebrate Collection	2000
Ophiuroidea collections of the Zoological Institute Russian Academy of Sciences	2000
Vulnerable marine ecosystems in the South Pacific Ocean region	2000
Composition and distribution of the biomass of zooplankton in the central Arctic Basin 1975, 1976, 1977	1000
Crustacea Collection of Natural History Museum and Institute, Chiba	1000
Fish Collection of Hokkaido University	1000
SIO Marine Vertebrate Collection	1000
Structures and Nutrition Requirements of Macrozoobenthic Communities in the area of the Lomonossov Ridge, 1995-1998	1000
The fishes collection (IC) of the Muséum national d'Histoire naturelle (MNHN - Paris)	1000
UWFC Ichthyology Collection	1000
Museum of Comparative Zoology, Harvard University	863
Diversity of the Indo-Pacific (DIPnet)	859
Mollusca specimens of Toyama Science Museum	858
Biological observations from the Dana Expedition Reports	625
Occurrence records of southern African aquatic biodiversity	584

Museums Victoria provider for OZCAM	566
Natural History Museum (London) Collection Specimens	530
COMARGIS: Information System on Continental Margin Ecosystems	503
RBINS DaRWIN	481
Bernice P. Bishop Museum	475
The echinoderm collection (IE) of the Muséum national d'Histoire naturelle (MNHN - Paris)	469
IPOE_Benthos_Steffens	454
Marine invertabrate(ECHINODERMATA) specimen database of Osaka Museum of Natural History	424
Fish Collection of Natural History Museum and Institute, Chiba	385
Australian Institute of Marine Science (AIMS) - Surveys of Octocorals communities, benthic cover and environmental factors on coral reefs of Palau (2003 - 2005)	376
Vertebrate Zoology Division - Ichthyology, Yale Peabody Museum	343
KUBI Ichthyology Tissue Collection	322
The crustaceans collection (IU) of the Muséum national d'Histoire naturelle (MNHN - Paris)	318
Scleractinia specimens of Kuroshio Biological Research Foundation	294
Arctic Marine Fish Museum Specimens	245
Invertebrate Zoology Division, Yale Peabody Museum	224
Mollusca specimens of Wakayama Prefectural Museum of Natural History	223
Planktic foraminifera abundance of Hole 7-62A	212
Marine Invertebrata specimen database of Osaka Museum of Natutal History	206
Gorgonacea specimens of Kuroshio Biological Research Foundation	197
Zoological Museum Amsterdam, University of Amsterdam (NL) - Bryozoa	188
Australian Institute of Marine Science (AIMS) - Surveys of Octocoral communities, benthic cover and environmental factors on coral reefs of Hong Kong. (1999)	173
Crustacea specimens of Ryukyu University Museum (Fujukan)	157
Natural History Museum Rotterdam (NL) - Mollusca collection	150
Fish Collection of Coastal Branch of Natural History Museum and Institute, Chiba	140
KUBI Ichthyology Collection	134
Echinodermata specimens of Kuroshio Biological Research Foundation	124
Molluscus specimens of Toyohashi Museum of Natural History	107
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Kamptozoa collection of National Museum of Nature and Science	99
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Cascadia Research Blue Whale Photo IDs for US West Coast, 1972-2004	1
Cirripedia distribution data from: Deep-sea fauna of European seas - an annotated species check-list of benthic invertebrates living deeper than 2000 m in the seas bordering Europe	1
Deep-Sea Hydrothermal Vent Endemic Brachyuran Family Bythograeidae	1
Derawan Green Turtles Tracking (aggregated per 1-degree cell)	1

Echinoidea distribution data from: Deep-sea fauna of European seas - an annotated species check-list of benthic invertebrates living deeper than 2000 m in the seas bordering Europe	1
Ecsenius niue, new species of blenniid fish, and new distribution records for other species in the Opsifrontalis species group	1
iziko South African Museum - Marine Mammal Collection	1
iziko South African Museum - Mollusc Collection	1
Mysida and Lophogastrida distribution data from: Deep-sea fauna of European seas - an annotated species check-list of benthic invertebrates living deeper than 2000 m in the seas bordering Europe	1
Pycnogonida distribution data from: Deep-sea fauna of European seas - an annotated species check-list of benthic invertebrates living deeper than 2000 m in the seas bordering Europe	1
SAM Herpetology	1
SOMBASE BIOCONSTRUCTORS	1
The Azooxanthellate Scleractinia (Coelenterata: Anthozoa) of Australia	1
Tulane University Museum of Natural History	1
USGS Alaska Science Center Polar Bear Maternal Dens	1

Supplementary Figures

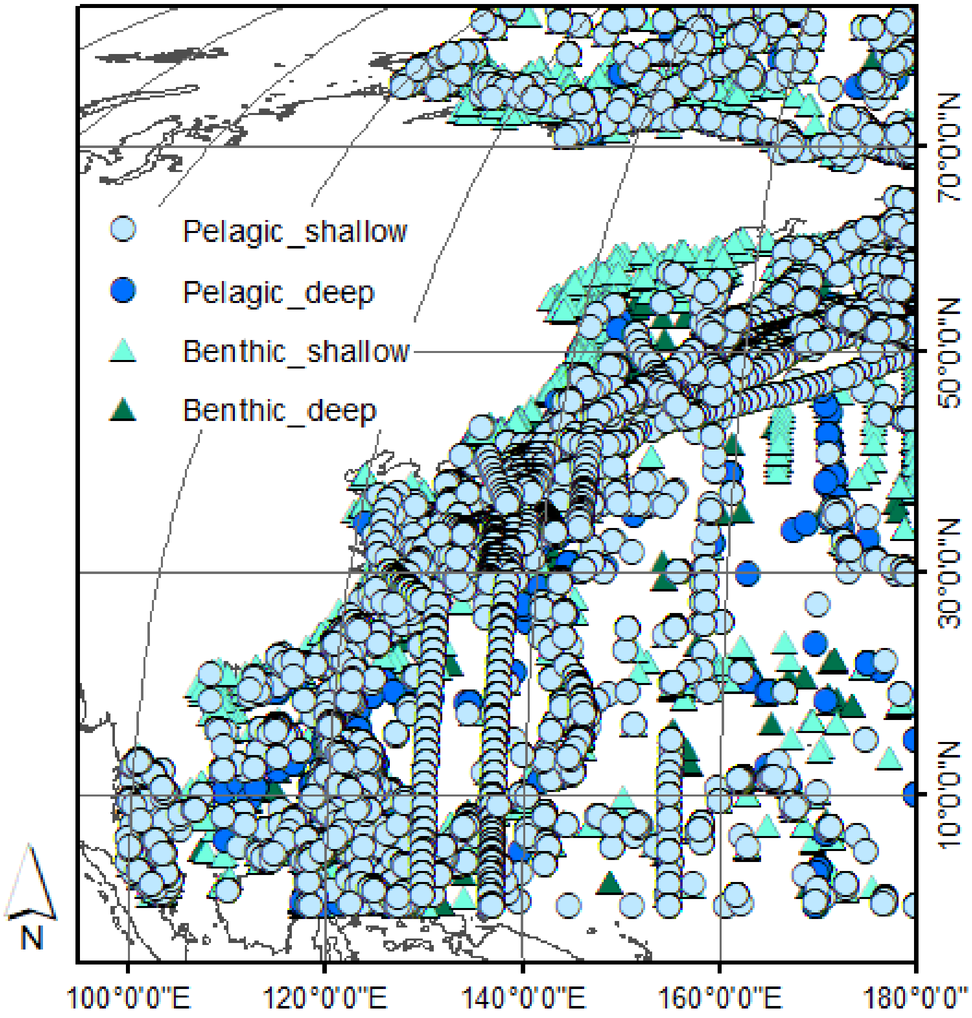


Fig. S1. Distribution map of pelagic and benthic shallow water (0-500m) and deep-sea (deeper than 500m) species in the NW Pacific and adjacent Arctic Ocean. In total 352,969 distribution records of four groups were mapped.

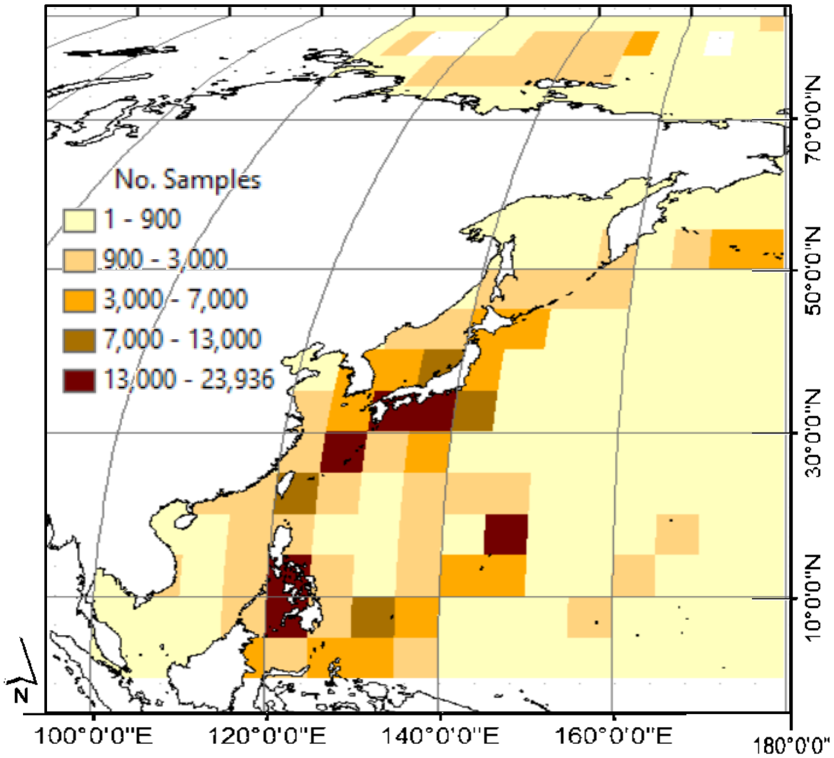


Fig. S2. Number of records in each 5˚N latitude-longitude cell of the NW Pacific and adjacent Arctic Ocean. The Japan, East China, Philippine Seas had the highest number of records; from 13,000 to around 24,000 records.

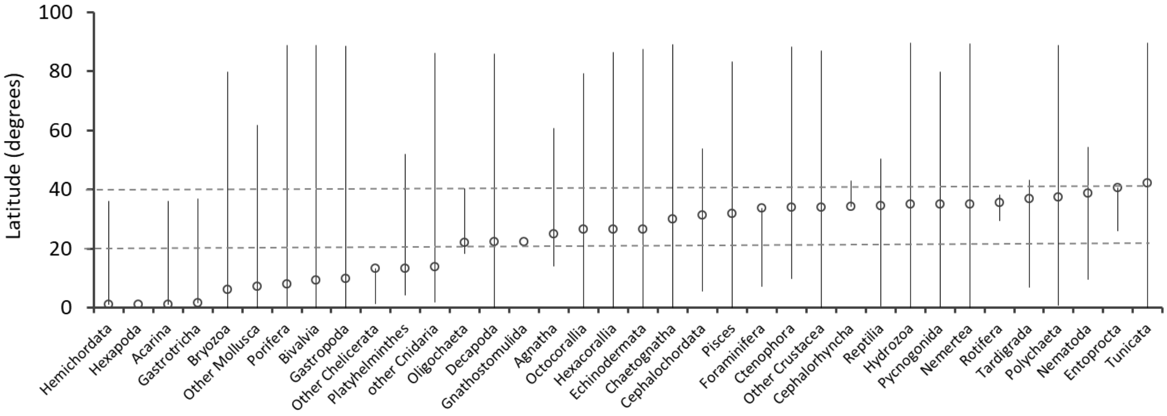
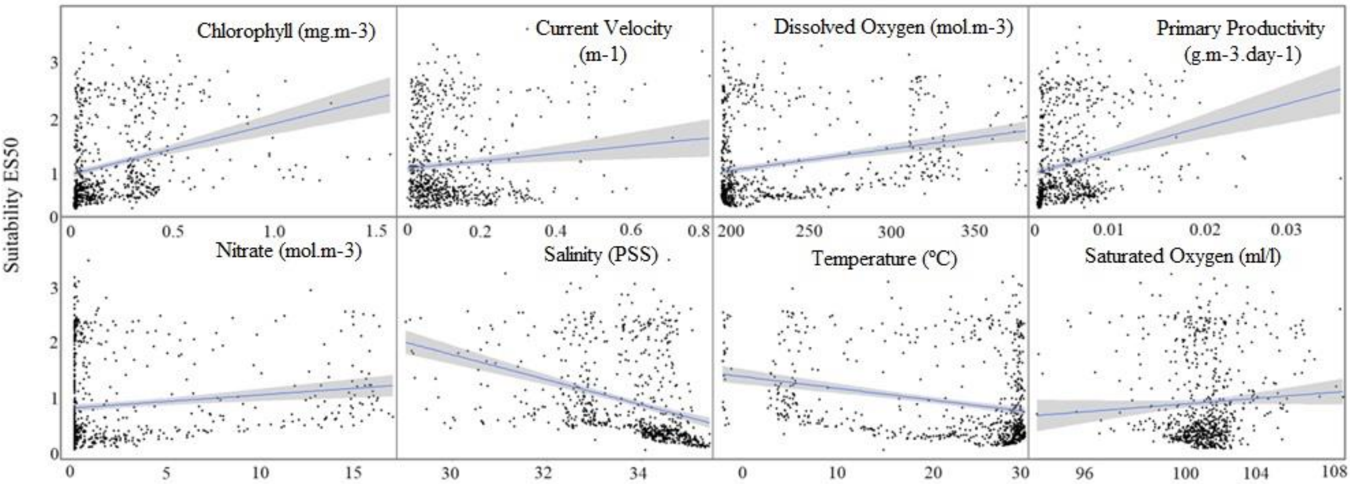


Fig. S3. Latitudinal ranges of higher taxa. The hollow circles show the mode of the distribution records, and indicator of sampling effort (not species richness), in each taxon.

Shallow water (5°)



Deep water (5°)

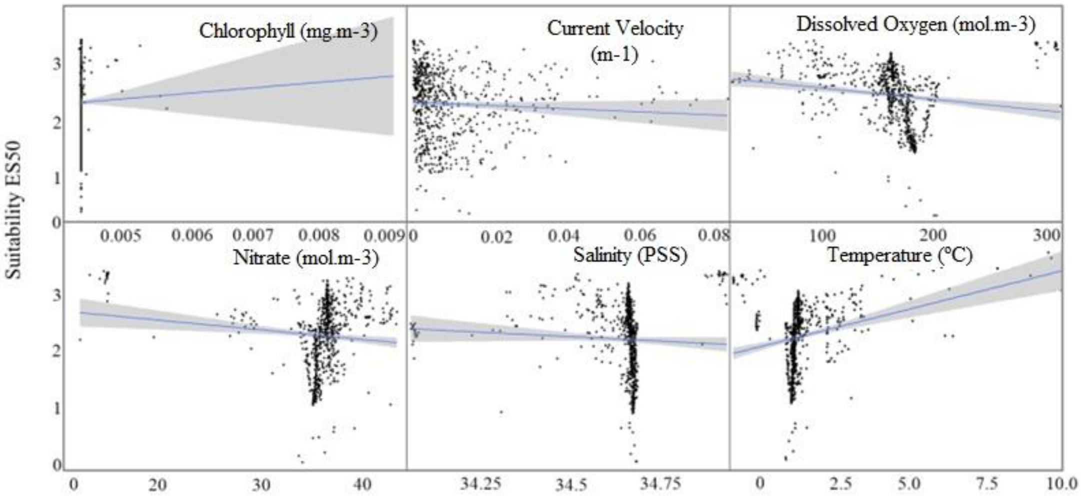


Fig. S4. Correlation matrix between suitability ES50 (suitable responses of ES50 to the environmental predictor variables) and environmental factors used in GAMs models for both shallow water (0-500 m) (top) and deep sea (>500 m) (bottom) species.

S1. Species Counts and Environment Based on Hexagons.

Species Counts and Environment

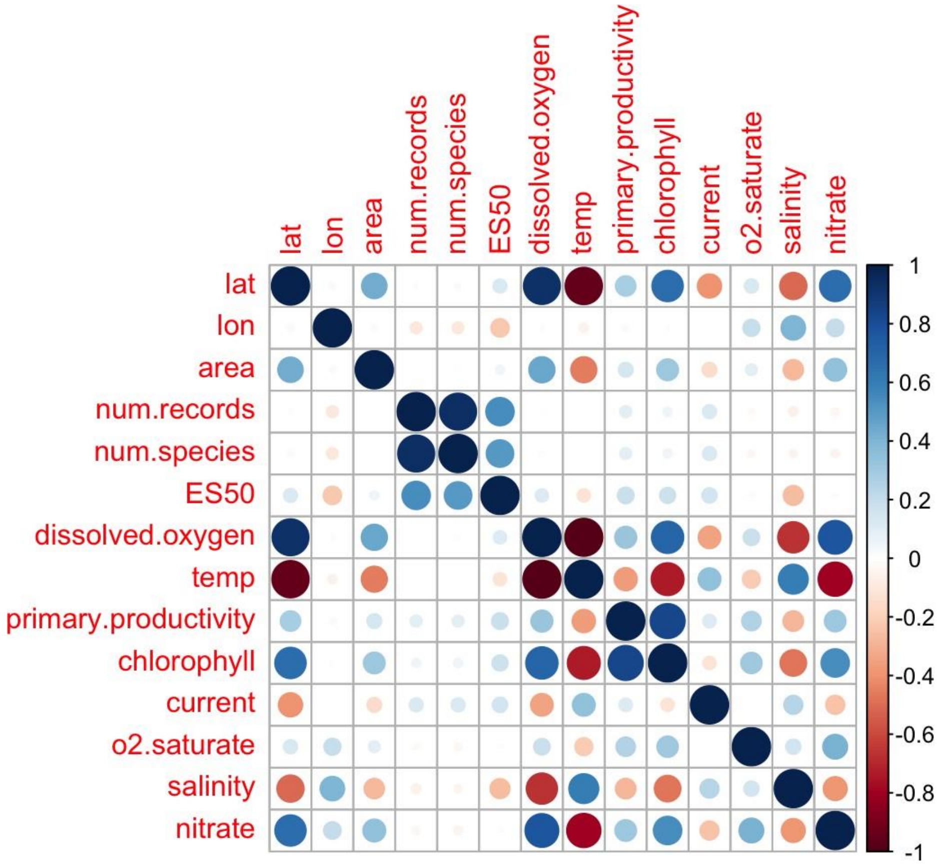
Setup

Shallow water

Data load-in and visualization

First we’re going to load in our data and then trim the data frame down to just the columns we need.

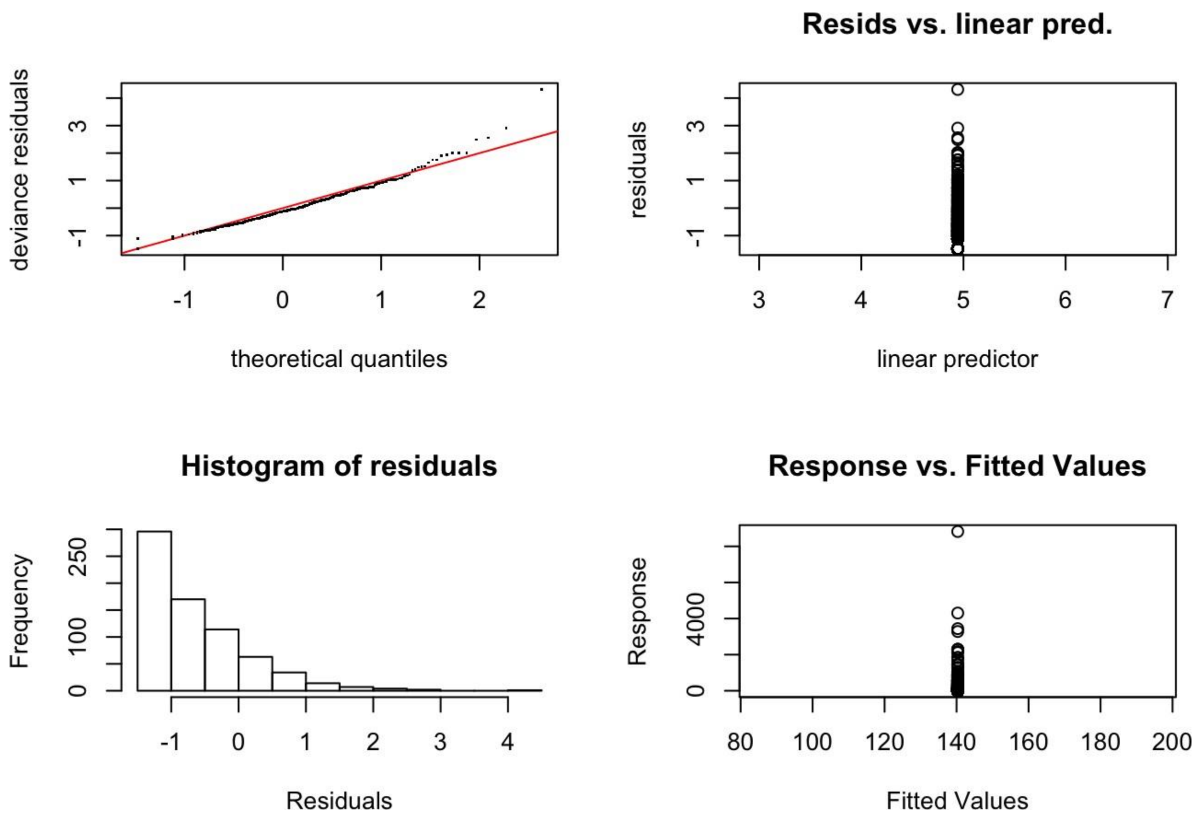
```
shallow <- read.csv("shallow.csv")
analysis.cols <- c("lat", "lon", "area", "num.records", "num.species", "ES50", "dissolved.oxygen", "temp", "primary.productivity", "chlorophyll", "current", "o2.saturate", "salinity", "nitrate")
shallow <- shallow[,analysis.cols]
shallow <- shallow[complete.cases(shallow),]
corrplot(cor(shallow))
```



GAMs for number of species, shallow water

We’re going to develop a number of GAMs here. The “intercept” GAM represents the fit of a model that assumes no relationship between the species counts and the environment and no spatial autocorrelation. The “latlon” model represents the fit of a model that fits spatial autocorrelation, but no environmental effects. The “env” model represents the combined effects of all environmental predictors, and the remainder of the models (“temp”, “oxygen”, etc.) estimate the effects of a single predictor at a time.

```
shallow.numsp.intercept <- gam(num.species ~ 1, data = shallow, family = "nb", meth
od = "REML", select = TRUE)
gam.check(shallow.numsp.intercept)
```

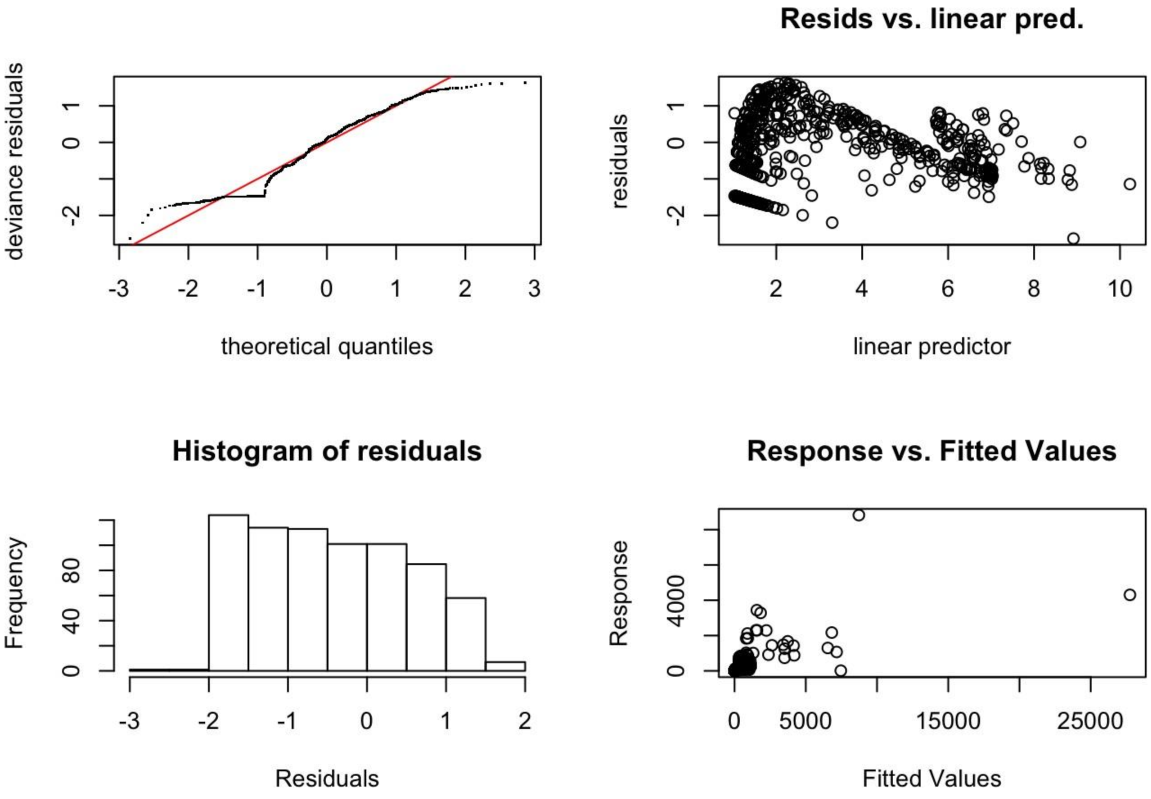


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 5 iterations.
## Gradient range [2.33879e-06,2.33879e-06]
## (score 3116.071 & scale 1).
## Hessian positive definite, eigenvalue range [382.9675,382.9675].
## Model rank =  1 / 1
```

```
summary(shallow.numsp.intercept)
```

```
##
## Family: Negative Binomial(0.161)
## Link function: log
##
## Formula:
## num.species ~ 1
##
## Parametric coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   4.94395    0.09386   52.67   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## R-sq.(adj) =      0   Deviance explained = 1.56e-09%
## -REML = 3116.1  Scale est. = 1         n = 705
```

```
shallow.numsp.numrec <- gam(num.species ~ s(num.records), data = shallow, family =
"nb", method = "REML", select = TRUE)
gam.check(shallow.numsp.numrec)
```

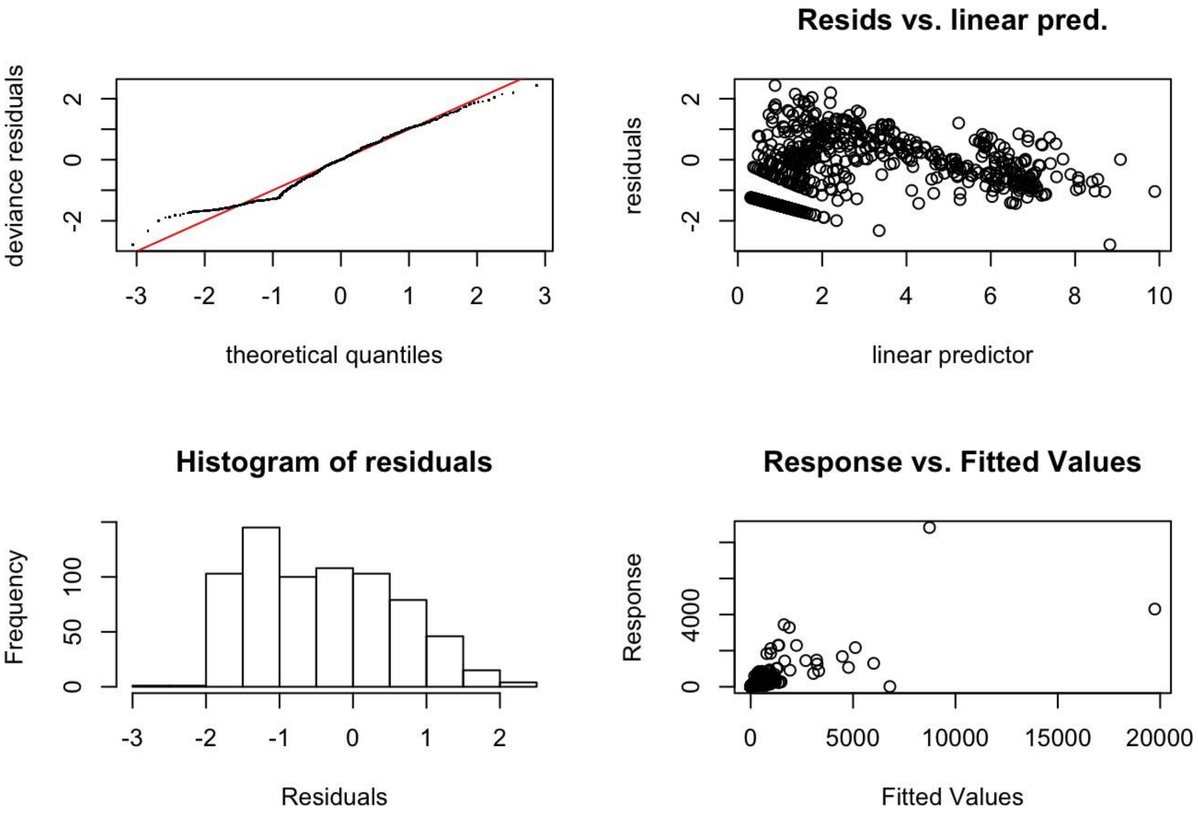


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 9  iterations.
## Gradient range [-3.306909e-05,0.0006015526]
## (score 2711.477 & scale 1).
## Hessian positive definite, eigenvalue range [0.4966568,212.487].
## Model rank =  10 / 10
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                    k'   edf k-index p-value
## s(num.records) 9.00 8.86    0.43  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.numsp.numrec)
```

```
##
## Family: Negative Binomial(0.641)
## Link function: log
##
## Formula:
## num.species ~ s(num.records)
##
## Parametric coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.75008    0.04959   55.46   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                  edf Ref.df Chi.sq  p-value
## s(num.records) 8.855      9   1964  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  -3.39   Deviance explained =   71%
## -REML = 2711.5  Scale est. = 1         n = 705
```

```
shallow.numsp.latlon <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.records), data =
shallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.numsp.latlon)
```

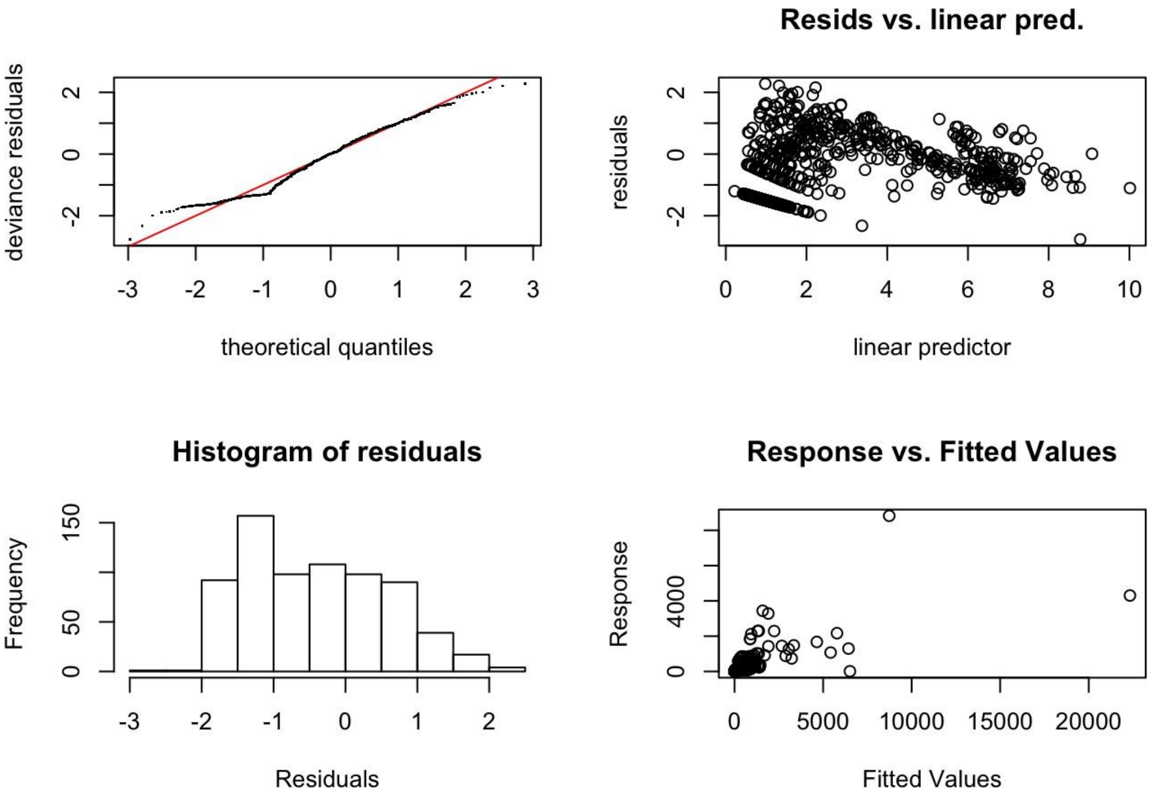


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 12 iterations.
## Gradient range [-9.356918e-05,0.001657861]
## (score 2690.814 & scale 1).
## Hessian positive definite, eigenvalue range [0.4975741,193.3047].
## Model rank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                   k'   edf k-index p-value
## s(lat,lon)     49.00 12.82    0.74  <2e-16 ***
## s(num.records)  9.00  8.84    0.48  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.numsp.latlon)
```

```
##
## Family: Negative Binomial(0.73)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") + s(num.records)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.6640     0.0474    56.2   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                   edf Ref.df   Chi.sq  p-value
## s(lat,lon)     12.824     49    66.67 1.85e-12 ***
## s(num.records)  8.844      9  1474.16  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  R-sq.(adj) =   -1.26   Deviance explained = 74.5%
## -REML = 2690.8  Scale est. = 1         n = 705
```

```
shallow.numsp.temp <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.records) +
s(temp), data = shallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.numsp.temp)
```

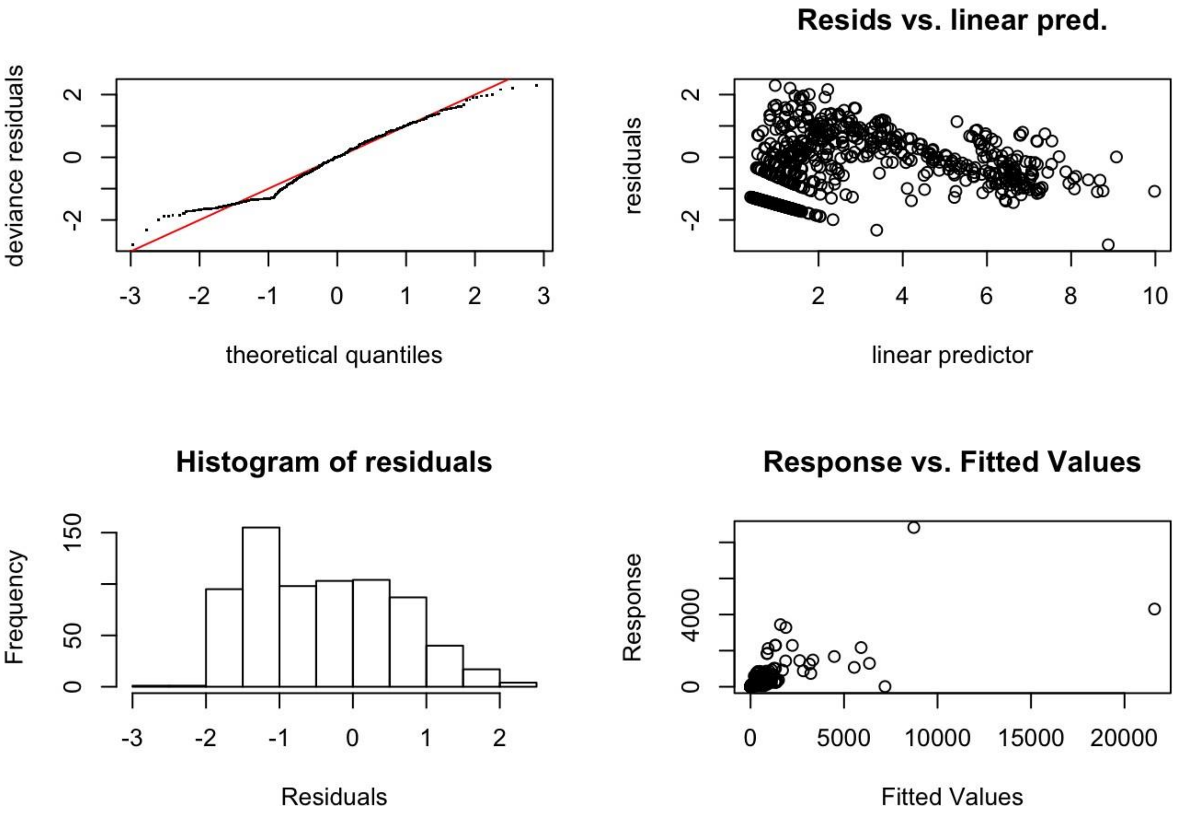


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 12 iterations.
## Gradient range [-9.719285e-05,0.0007917026]
## (score 2689.112 & scale 1).
## Hessian positive definite, eigenvalue range [9.717277e-05,195.1371].
## Model rank =  68 / 68
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                    k'  edf k-index p-value
## s(lat,lon)      49.00 7.53    0.74  <2e-16 ***
## s(num.records)   9.00 8.84    0.48  <2e-16 ***
## s(temp)          9.00 2.15    0.89    0.88
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.numsp.temp)
```

```
##
## Family: Negative Binomial(0.727)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s(temp)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.67036    0.04745   56.28   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                  edf Ref.df   Chi.sq  p-value
## s(lat,lon)     7.533     49   34.065 6.73e-08 ***
## s(num.records) 8.840      9 1555.054  < 2e-16 ***
## s(temp)        2.147      9    9.394 2.54e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  -1.82   Deviance explained = 74.2%
## -REML = 2689.1  Scale est. = 1         n = 705
```

```
shallow.numsp.oxygen <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.records)
 + s(dissolved.oxygen), data = shallow, family = "nb", method = "REML", select = T
RUE)
gam.check(shallow.numsp.oxygen)
```

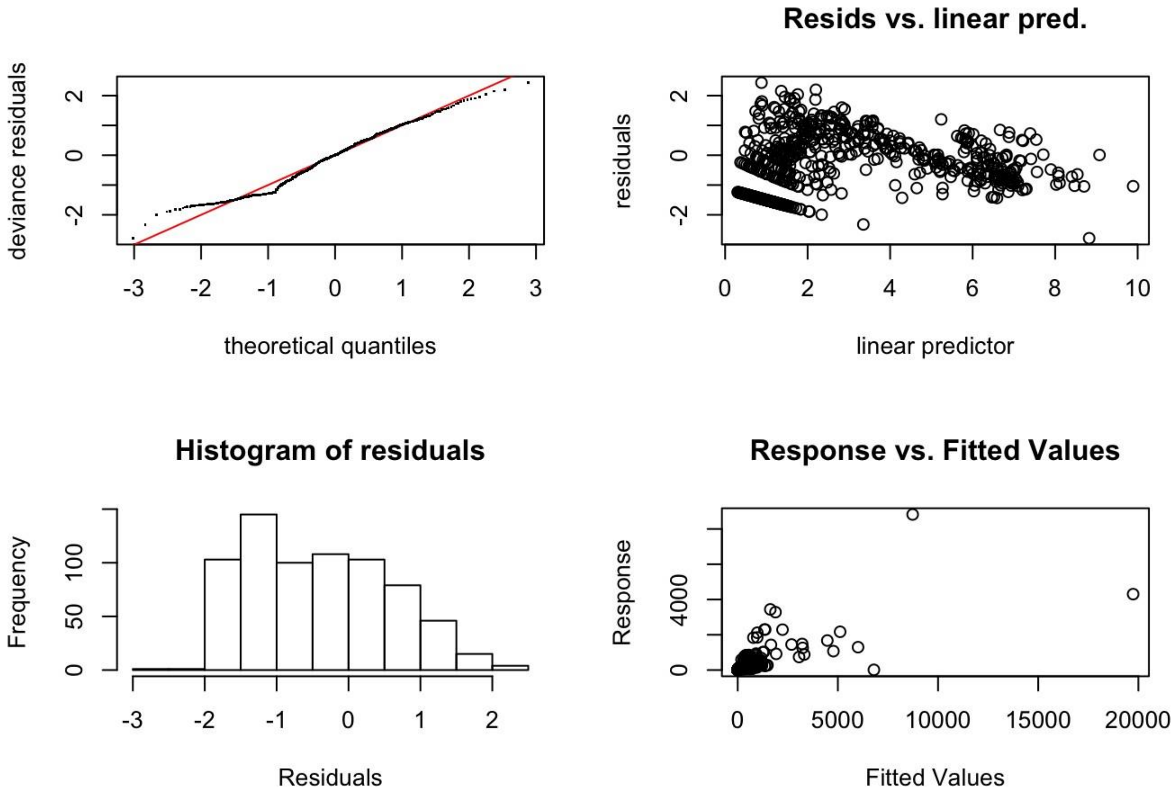


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 17 iterations.
## Gradient range [-0.0001833293,0.001605755]
## (score 2689.23 & scale 1).
## Hessian positive definite, eigenvalue range [0.0001832544,195.7092].
## Model rank =  68 / 68
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                         k'   edf k-index p-value
## s(lat,lon)           49.00  7.40    0.74   0.005 **
## s(num.records)        9.00  8.84    0.48  <2e-16 ***
## s(dissolved.oxygen)   9.00  1.98    0.84   0.495
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.numsp.oxygen)
```

```
##
## Family: Negative Binomial(0.725)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s(dissolved.oxygen)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.6720     0.0475   56.26   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                        edf Ref.df   Chi.sq  p-value
## s(lat,lon)           7.395     49   34.122 5.08e-08 ***
## s(num.records)       8.839      9 1554.175  < 2e-16 ***
## s(dissolved.oxygen) 1.977      9    9.037 2.38e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  -1.72   Deviance explained = 74.2%
## -REML = 2689.2Scale est. = 1         n = 705
```

```
shallow.numsp.prod <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.records) +
s(primary.productivity), data = shallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.numsp.prod)
```

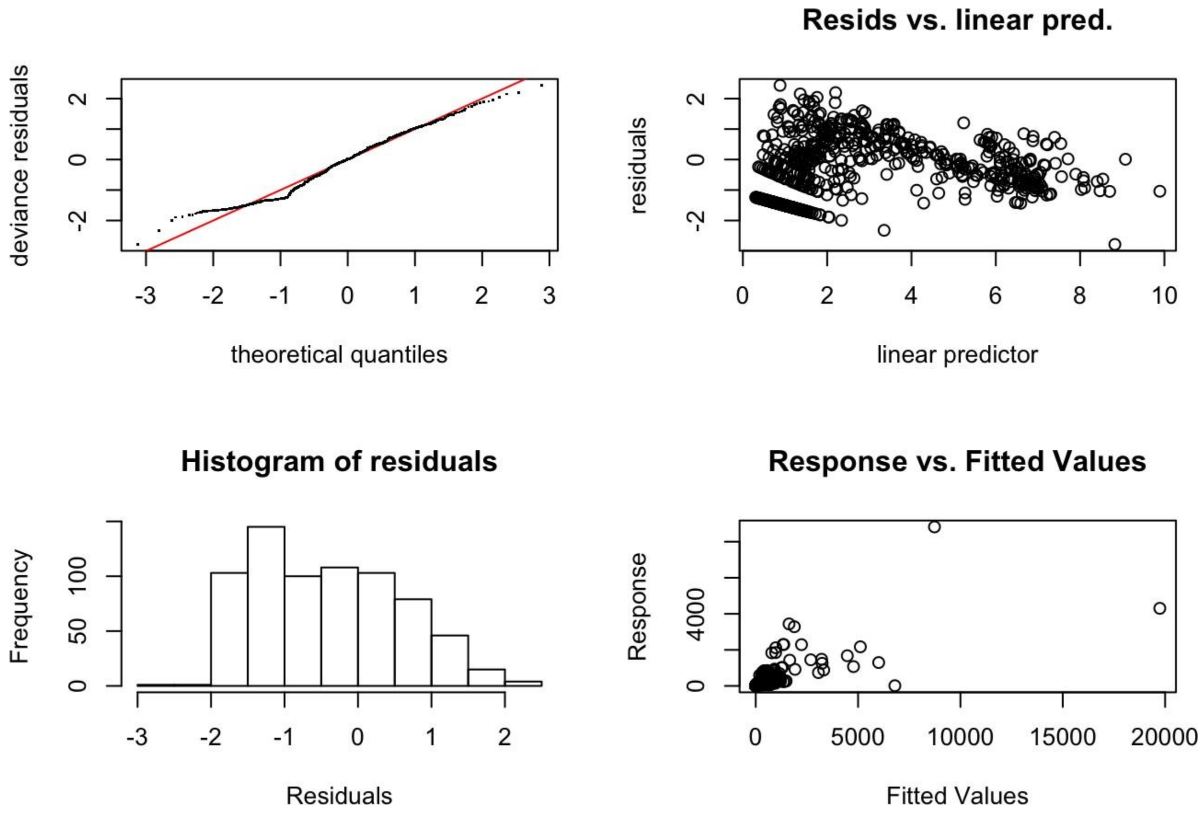


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 17 iterations.
## Gradient range [-0.0002133841,0.001419792]
## (score 2690.815 & scale 1).
## Hessian positive definite, eigenvalue range [0.0001387295,193.3042].
## Model rank =  68 / 68
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                               k'      edf k-index p-value
## s(lat,lon)              49.00000 12.82396    0.74  <2e-16 ***
## s(num.records)           9.00000  8.84415    0.48  <2e-16 ***
## s(primary.productivity)  9.00000  0.00125    0.83    0.31
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.numsp.prod)
```

```
##
## Family: Negative Binomial(0.73)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s(primary.productivity)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.6640     0.0474    56.2   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                               edf Ref.df   Chi.sq  p-value
## s(lat,lon)              12.823963     49   66.663 1.85e-12 ***
## s(num.records)           8.844153      9 1474.147  < 2e-16 ***
## s(primary.productivity)  0.001252      9    0.001    0.424
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  -1.26   Deviance explained = 74.5%
## -REML = 2690.8  Scale est. = 1         n = 705
```

```
shallow.numsp.chlorophyll <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.records)
+ s(chlorophyll), data = shallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.numsp.chlorophyll)
```

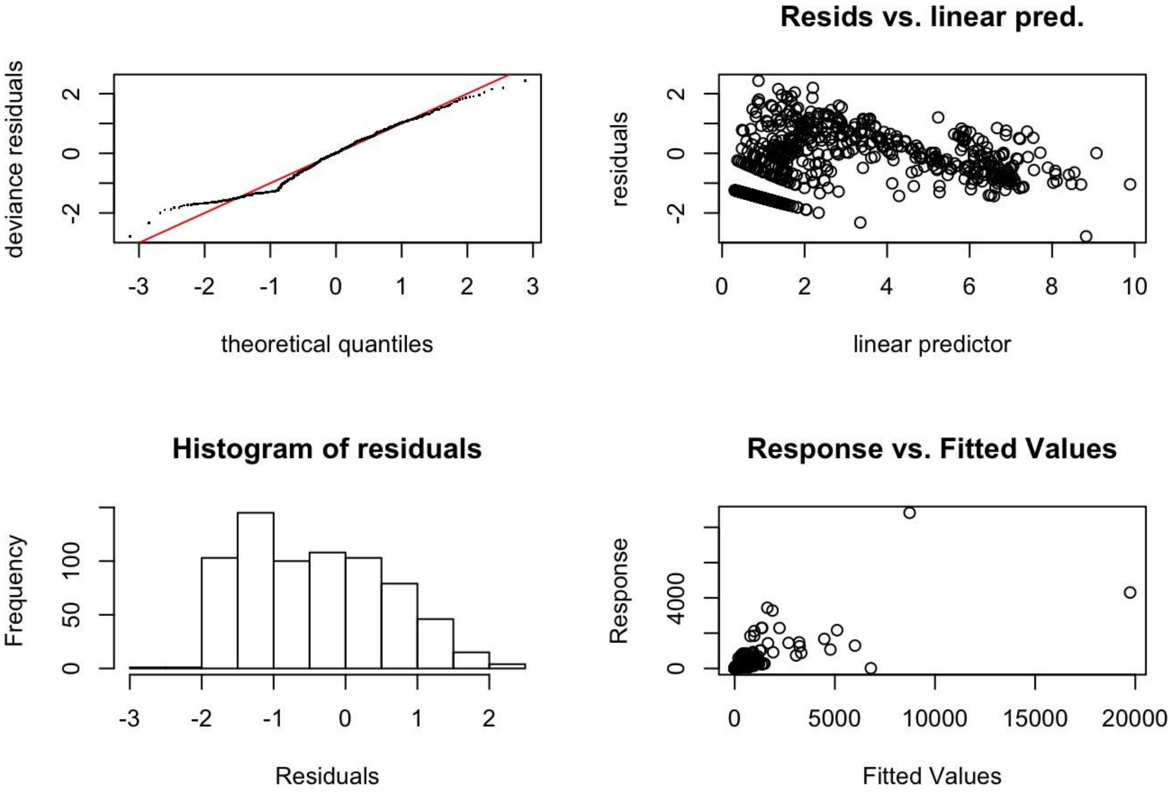


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 17 iterations.
## Gradient range [-0.0001761506,0.0009546675]
## (score 2690.814 & scale 1).
## Hessian positive definite, eigenvalue range [0.0001271656,193.3044].
## Model rank =  68 / 68
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                        k'      edf k-index p-value
## s(lat,lon)       49.00000 12.82359    0.74  <2e-16 ***
## s(num.records)    9.00000  8.84416    0.48  <2e-16 ***
##  s(chlorophyll)   9.00000  0.00143    0.79    0.05 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.numsp.chlorophyll)
```

```
##
## Family: Negative Binomial(0.73)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") +  s(num.records) +  s(chlorophyll)
##
## Parametric coefficients:
##                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)      2.6640     0.0474    56.2   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                       edf  Ref.df    Chi.sq   p-value
## s(lat,lon)       12.823594      49    66.641  1.86e-12 ***
## s(num.records)    8.844155       9  1474.164   < 2e-16 ***
## s(chlorophyll)    0.001435       9     0.001     0.375
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =   -1.26    Deviance explained = 74.5%
## -REML = 2690.8  Scale est. = 1            n = 705
```

```
shallow.numsp.current <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.records)
+  s(current), data = shallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.numsp.current)
```

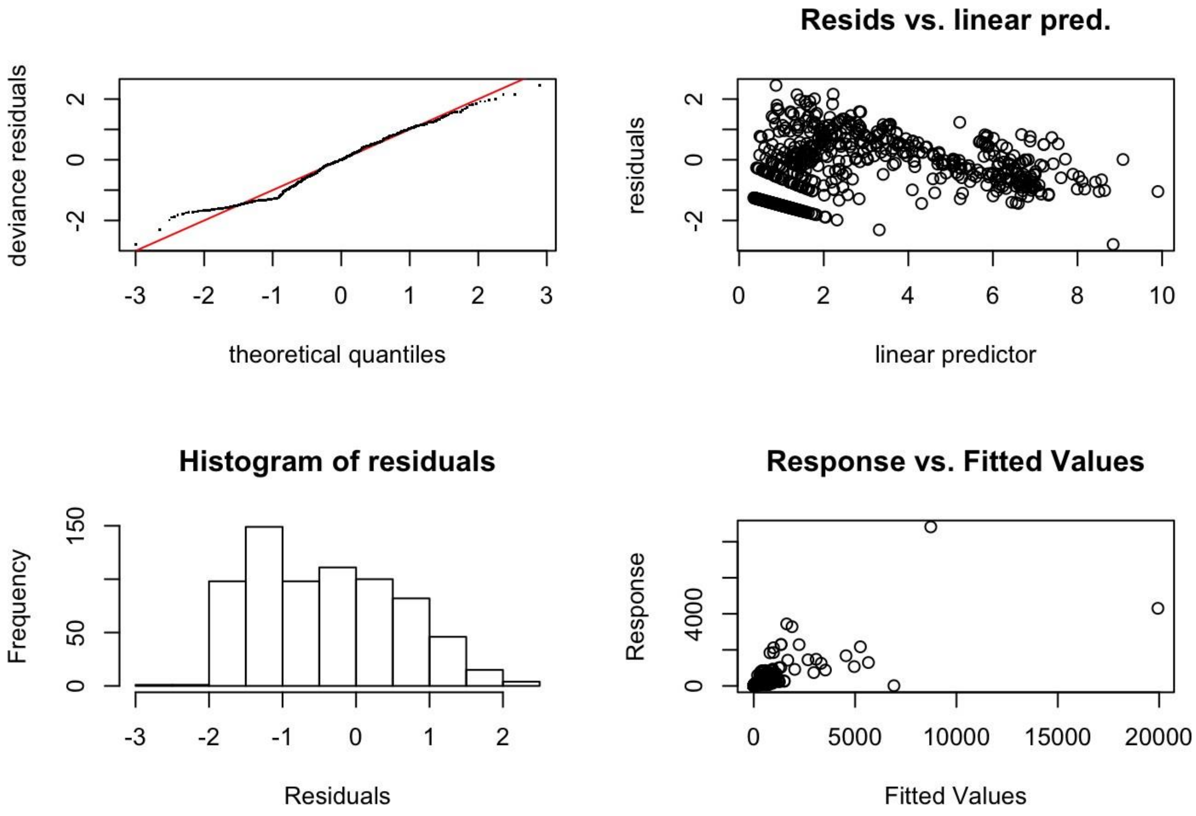


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 12 iterations.
## Gradient range [-0.0002338866,0.001733544]
## (score 2690.815 & scale 1).
## Hessian positive definite, eigenvalue range [0.0001043007,193.3042].
## Model rank =  68 / 68
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                      k'      edf k-index p-value
## s(lat,lon)     49.00000 12.82367    0.74  <2e-16 ***
## s(num.records)  9.00000  8.84415    0.48  <2e-16 ***
## s(current)      9.00000  0.00189    0.88    0.82
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.numsp.current)
```

```
##
## Family: Negative Binomial(0.73)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s(current)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.6640     0.0474    56.2   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                      edf Ref.df   Chi.sq  p-value
## s(lat,lon)     12.823667     49   66.655 1.86e-12 ***
## s(num.records)  8.844152      9 1474.107  < 2e-16 ***
## s(current)      0.001885      9    0.001    0.517
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  -1.26   Deviance explained = 74.5%
## -REML = 2690.8  Scale est. = 1         n = 705
```

```
shallow.numsp.o2.saturate <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.reco rds)
+  s(o2.saturate), data = shallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.numsp.o2.saturate)
```

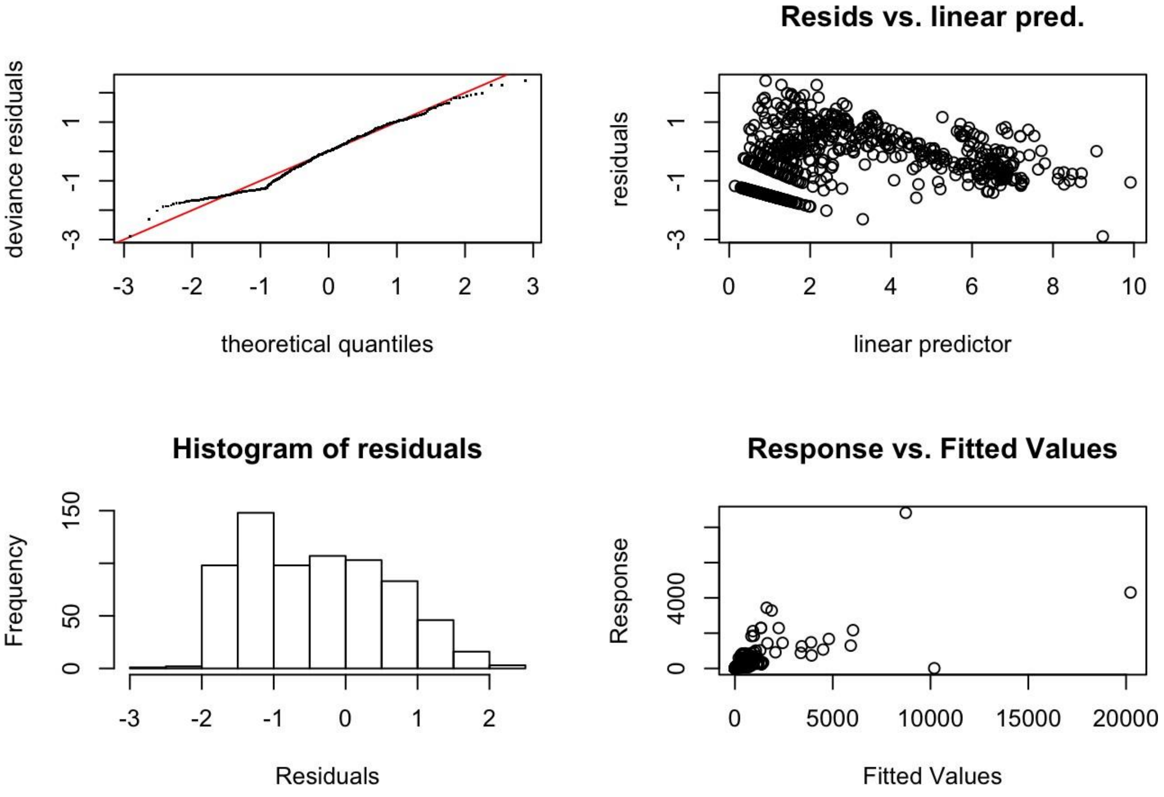


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 12 iterations.
## Gradient range [-0.0001888787,0.001738329]
## (score 2690.688 & scale 1).
## Hessian positive definite, eigenvalue range [0.0001887718,193.1974].
## Model rank =  68 / 68
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                     k'    edf k-index p-value
## s(lat,lon)      49.000 12.358    0.74  <2e-16 ***
## s(num.records)   9.000  8.844    0.48  <2e-16 ***
## s(o2.saturate)   9.000  0.617    0.86    0.65
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.numsp.o2.saturate)
```

```
##
## Family: Negative Binomial(0.73)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s(o2.saturate)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.66391    0.04739   56.21   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                    edf Ref.df   Chi.sq p-value
## s(lat,lon)     12.3585     49   63.474 3.3e-12 ***
## s(num.records)  8.8438      9 1480.231 < 2e-16 ***
## s(o2.saturate)  0.6173      9    1.012    0.15
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  -1.31   Deviance explained = 74.5%
## -REML = 2690.7  Scale est. = 1         n = 705
```

```
shallow.numsp.salinity <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.record
s) +  s(salinity), data = shallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.numsp.salinity)
```

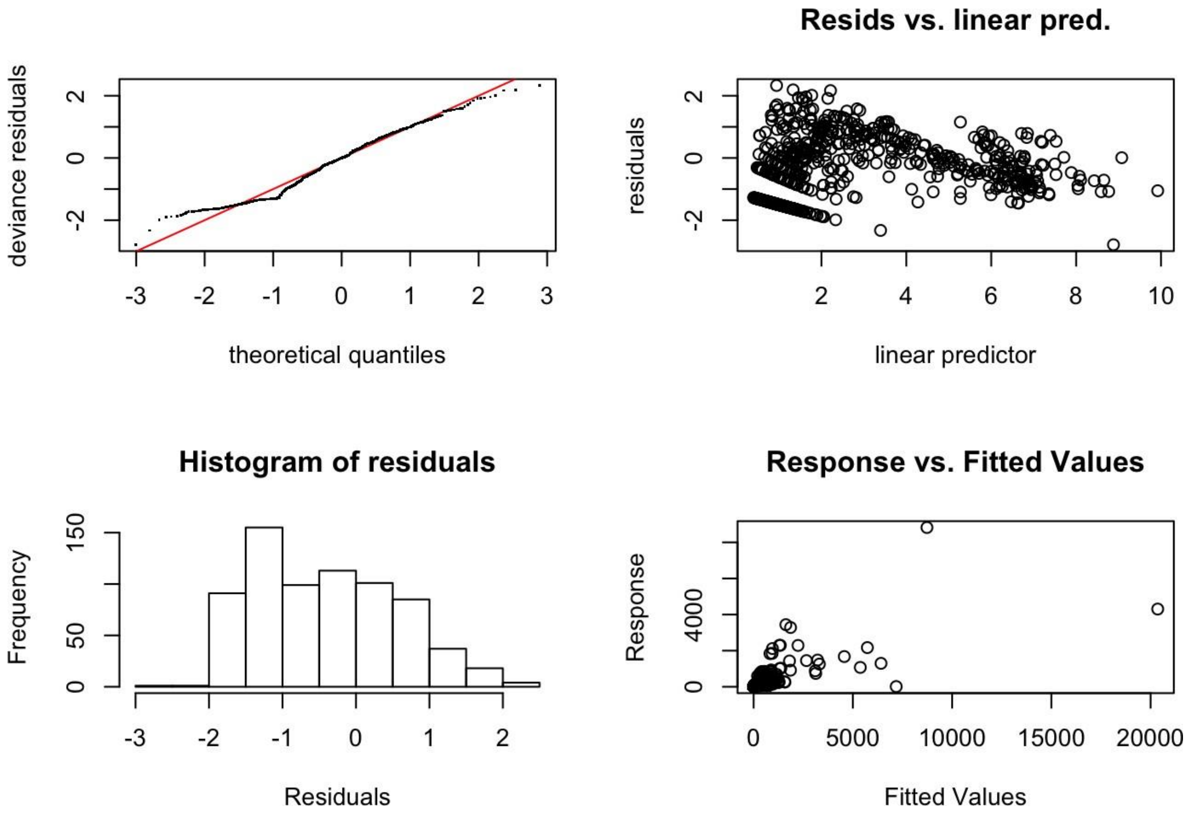


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 12 iterations.
## Gradient range [-0.0001653638,0.001587915]
## (score 2689.424 & scale 1).
## Hessian positive definite, eigenvalue range [0.002622196,193.1189].
## Model rank =  68 / 68
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                    k'   edf k-index p-value
## s(lat,lon)      49.00 10.73    0.75  <2e-16 ***
## s(num.records)   9.00  8.84    0.48  <2e-16 ***
## s(salinity)      9.00  1.72    0.82     0.1
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.numsp.salinity)
```

```
##
## Family: Negative Binomial(0.732)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s(salinity)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.66279    0.04735   56.23   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                   edf Ref.df   Chi.sq  p-value
## s(lat,lon)     10.728     49   28.168 0.000165 ***
## s(num.records)  8.843      9 1493.268  < 2e-16 ***
## s(salinity)     1.716      9    6.143 0.004691 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  -1.76   Deviance explained = 74.5%
## -REML = 2689.4  Scale est. = 1         n = 705
```

```
shallow.numsp.nitrate <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.records)
+  s(nitrate), data = shallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.numsp.nitrate)
```

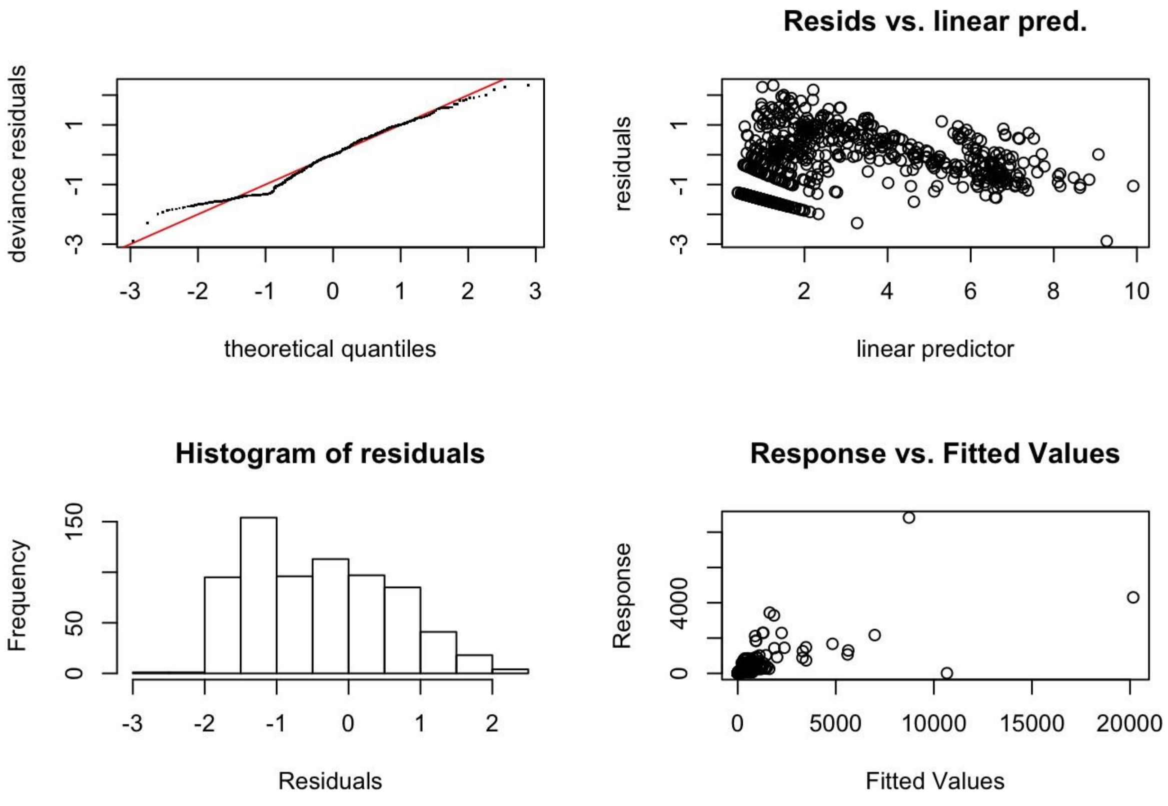


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 12 iterations.
## Gradient range [-0.0001123949,0.001608861]
## (score 2689.498 & scale 1).
## Hessian positive definite, eigenvalue range [0.0001123446,195.7503].
## Model rank =  68 / 68
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                   k'   edf k-index p-value
## s(lat,lon)     49.00  8.68    0.74  <2e-16 ***
## s(num.records)  9.00  8.84    0.48  <2e-16 ***
## s(nitrate)      9.00  1.44    0.81    0.08 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.numsp.nitrate)
```

```
##
## Family: Negative Binomial(0.725)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s(nitrate)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.67060    0.04751   56.21   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                  edf Ref.df    Chi.sq  p-value
## s(lat,lon)     8.683     49    42.889 3.87e-09 ***
## s(num.records) 8.844      9  1554.037  < 2e-16 ***
## s(nitrate)     1.442      9     6.317   0.0026 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  -1.48   Deviance explained = 74.2%
## -REML = 2689.5  Scale est. = 1         n = 705
```

```
shallow.numsp.env <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s
(temp) + s(dissolved.oxygen) + s(primary.productivity) + s(chlorophyll) + s(curren
t) + s(o2.saturate) + s(salinity) + s(nitrate), data = shallow, family = "nb", method =
"REML", select = TRUE)
gam.check(shallow.numsp.env)
```



```
##
## Method: REML   Optimizer: outer newton
## full convergence after 19 iterations.
## Gradient range [-0.0002419147,0.0007436145]
## (score 2687.494 & scale 1).
## eigenvalue range [-0.0001766961,195.6325].
## Model rank =  131 / 131
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                               k'      edf k-index p-value
## s(lat,lon)              4.90e+01 5.38e+00    0.74  <2e-16 ***
## s(num.records)          9.00e+00 8.84e+00    0.48  <2e-16 ***
## s(temp)                 9.00e+00 2.09e-03    0.89   0.850
## s(dissolved.oxygen)     9.00e+00 6.69e-01    0.84   0.395
## s(primary.productivity) 9.00e+00 1.59e-03    0.83   0.315
## s(chlorophyll)          9.00e+00 2.01e-03    0.80   0.050 *
## s(current)              9.00e+00 8.63e-04    0.88   0.790
## s(o2.saturate)          9.00e+00 8.60e-01    0.86   0.650
## s(salinity)             9.00e+00 8.51e-01    0.82   0.205
## s(nitrate)              9.00e+00 1.40e+00    0.80   0.065 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.numsp.env)
```

```
##
## Family: Negative Binomial(0.728)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s(temp) +
##       s(dissolved.oxygen) +  s(primary.productivity)  +  s(chlorophyll)  +
##       s(current) + s(o2.saturate) + s(salinity) +  s(nitrate)
##
## Parametric coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
##  (Intercept)    2.66998      0.04741     56.32    <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                                        edf  Ref.df    Chi.sq   p-value
## s(lat,lon)                   5.3823776      49    14.832  0.000545  ***
## s(num.records)               8.8397292       9  1609.506    < 2e-16  ***
## s(temp)                      0.0020898       9     0.001  0.143235
## s(dissolved.oxygen)          0.6685280       9     0.942  0.069083  .
## s(primary.productivity) 0.0015915       9     0.001  0.350595
## s(chlorophyll)               0.0020123       9     0.003  0.203619
## s(current)                   0.0008629       9     0.000  0.704874
## s(o2.saturate)               0.8599729       9     1.733  0.107133
## s(salinity)                  0.8513896       9     5.520  0.002008  **
## s(nitrate)                   1.4007490       9     5.087  0.007049  **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  R-sq.(adj) =   -1.85     Deviance explained = 74.3%
## -REML = 2687.5Scale  est.  =  1                n = 705
```

Model selection for number of species, shallow water

Here we use AIC to compare models for goodness of fit while penalizing for overparameterization. Models are ranked in order of AIC score, with lowest scoring model (model with the best compromise between fit and complexity) first in the list. The delta AIC represents how much the AIC score for each model differs from the top model, an can be used as an estimate of the relative support for each model. A delta AIC of 2 is considered to be potentially a significantly better fit, with higher delta AICs between models indicating increasingly larger differences in model fit while correcting for the number of parameters.

```
shallow.numsp.models <- list(shallow.numsp.intercept = shallow.numsp.intercept,
                              shallow.numsp.numrec = shallow.numsp.numrec,
                        shallow.numsp.latlon = shallow.numsp.latlon,
                        shallow.numsp.temp = shallow.numsp.temp,
                        shallow.numsp.oxygen = shallow.numsp.oxygen,
                        shallow.numsp.prod = shallow.numsp.prod,
                        shallow.numsp.chlorophyll = shallow.numsp.chlorophyll,
                        shallow.numsp.current = shallow.numsp.current,
                        shallow.numsp.o2.saturate = shallow.numsp.o2.saturate,
                        shallow.numsp.salinity = shallow.numsp.salinity,
                        shallow.numsp.nitrate = shallow.numsp.nitrate,
                        shallow.numsp.env = shallow.numsp.env)
shallow.numsp.aic.df <- data.frame(Model = names(shallow.numsp.models),
                              AIC = sapply(shallow.numsp.models, function(x) x$aic),
                             akaike.weights(sapply(shallow.numsp.models, function(x)
x$aic)))

shallow.numsp.aic.df <- shallow.numsp.aic.df[order(shallow.numsp.aic.df$AIC),]
shallow.numsp.aic.df$Cumulative.Weight <- cumsum(shallow.numsp.aic.df$weights)

kable(shallow.numsp.aic.df, row.names = FALSE)
```

Model	AIC	deltaAIC	rel.LL	weights	Cumulative.Weight
shallow.numsp.salinity	5318.205	0.0000000	1.0000000	0.2104098	0.2104098
shallow.numsp.env	5318.527	0.3222579	0.8511823	0.1790971	0.3895069
shallow.numsp.temp	5319.780	1.5747971	0.4550270	0.0957421	0.4852491
shallow.numsp.latlon	5320.046	1.8404896	0.3984215	0.0838318	0.5690808
shallow.numsp.prod	5320.047	1.8412992	0.3982602	0.0837979	0.6528787
shallow.numsp.chlorophyll	5320.047	1.8414643	0.3982274	0.0837909	0.7366696
shallow.numsp.current	5320.048	1.8427285	0.3979757	0.0837380	0.8204076
shallow.numsp.o2.saturate	5320.201	1.9957224	0.3686671	0.0775712	0.8979788
shallow.numsp.oxygen	5320.817	2.6119011	0.2709149	0.0570032	0.9549820
shallow.numsp.nitrate	5321.289	3.0839880	0.2139540	0.0450180	1.0000000
shallow.numsp.numrec	5374.309	56.1033173	0.0000000	0.0000000	1.0000000
shallow.numsp.intercept	6231.247	913.0422064	0.0000000	0.0000000	1.0000000

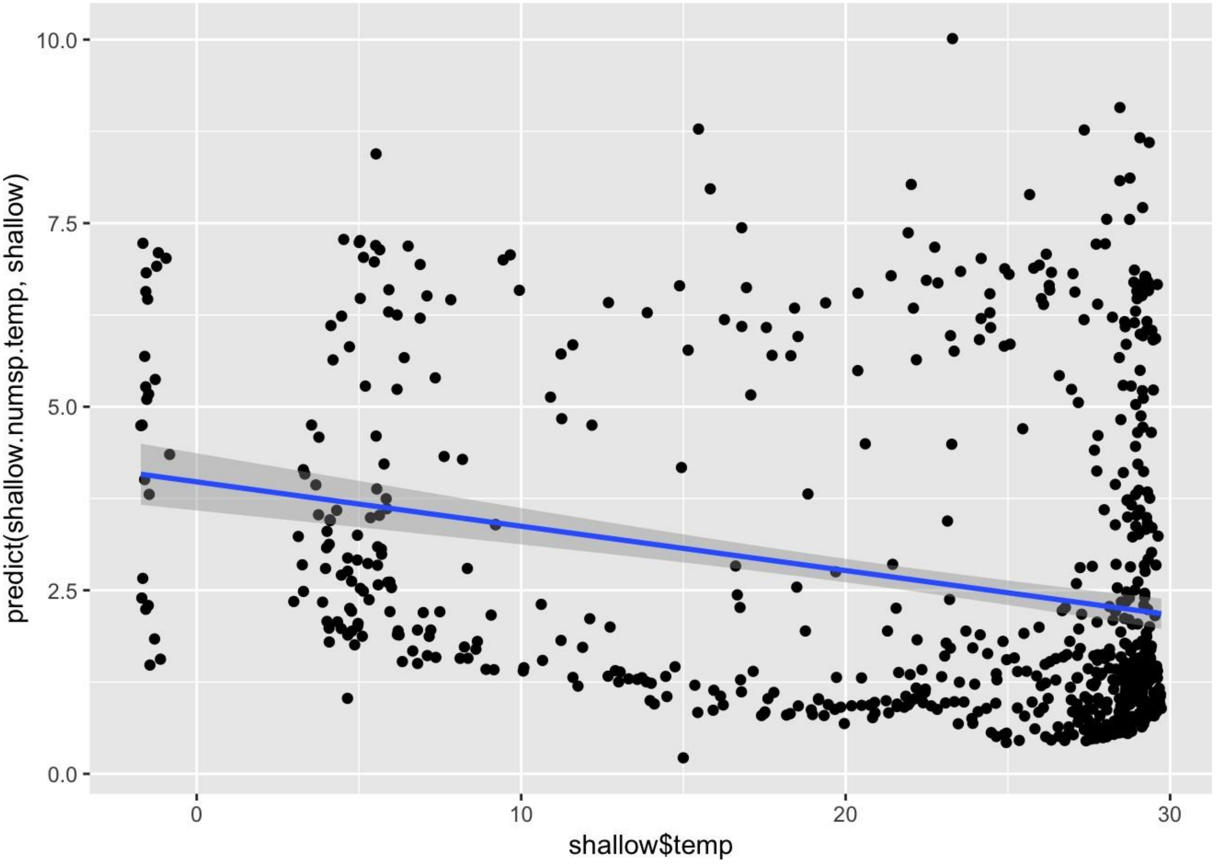
```
write.csv(shallow.numsp.aic.df, file = "shallow.numsp.aic.csv")
```

Here we see that the model containing salinity is the best fit, but many other models are almost as good. It is particularly noteworthy that the model containing only the effects of spatial autocorrelation (the “latlon” model) has a delta AIC of < 2 compared to the best-performing model. However, we know that latitude is highly correlated with several of the environmental predictors. That being the case, it is hard to determine which, if any, environmental predictors are affecting the number of species in shallow water. T

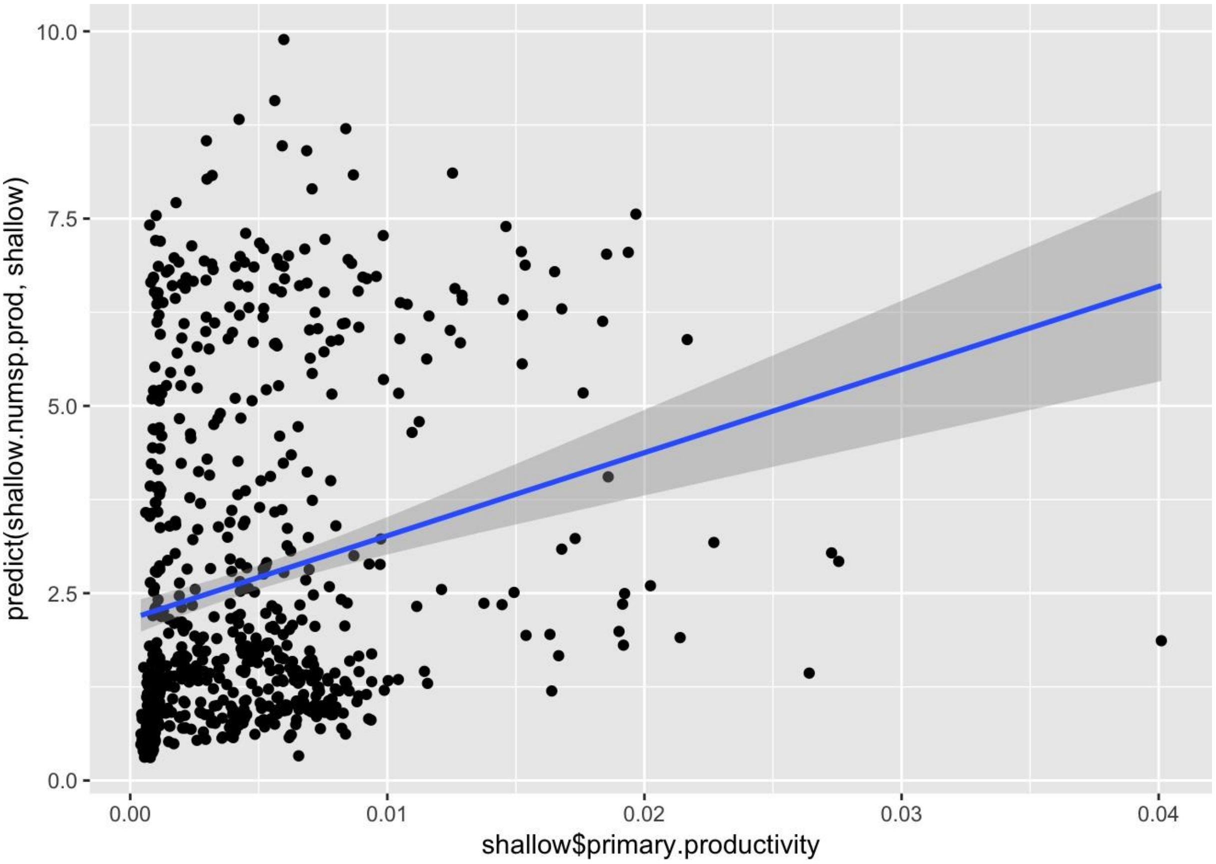
Plots for number of species, shallow water

Here we plot the effects of each environmental predictor from its respective single-variable model.

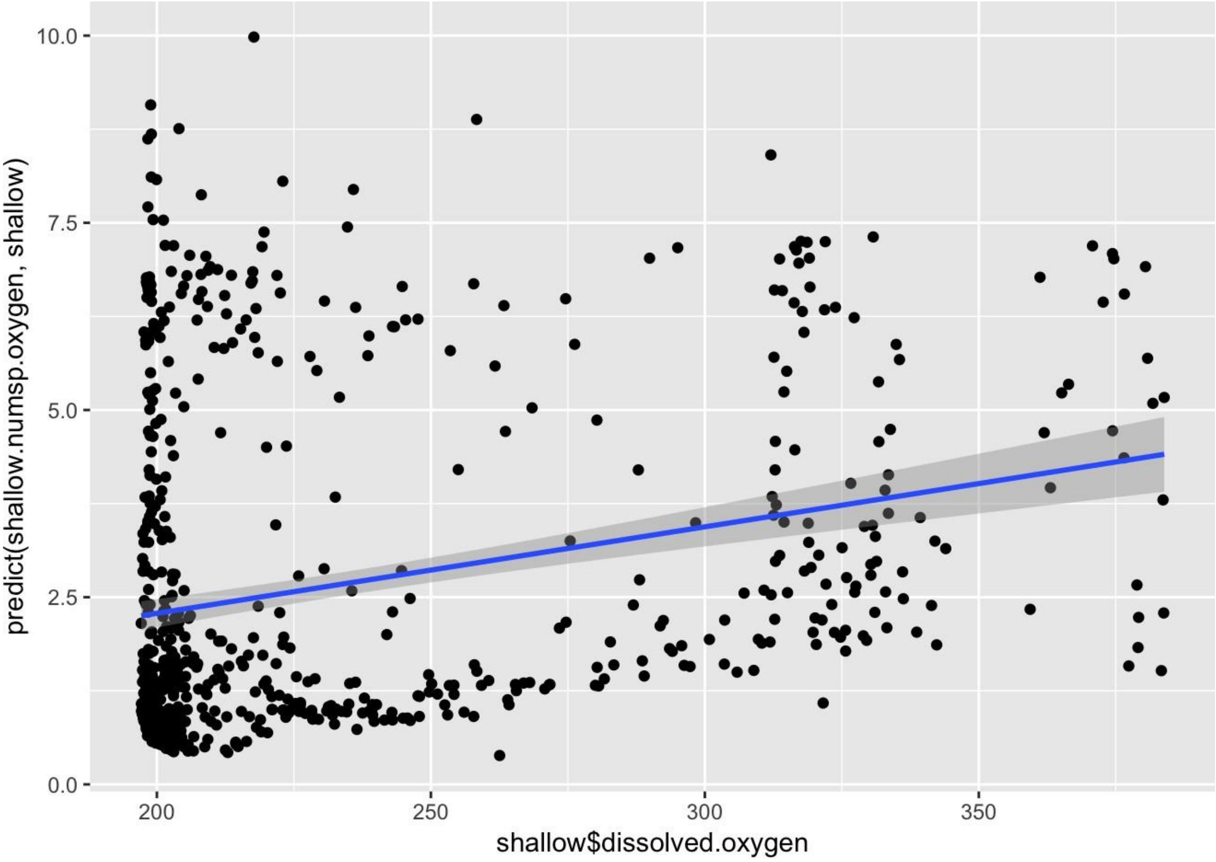
```
qplot(shallow$temp, predict(shallow.numsp.temp, shallow)) + geom_smooth(method = "g
am")
```



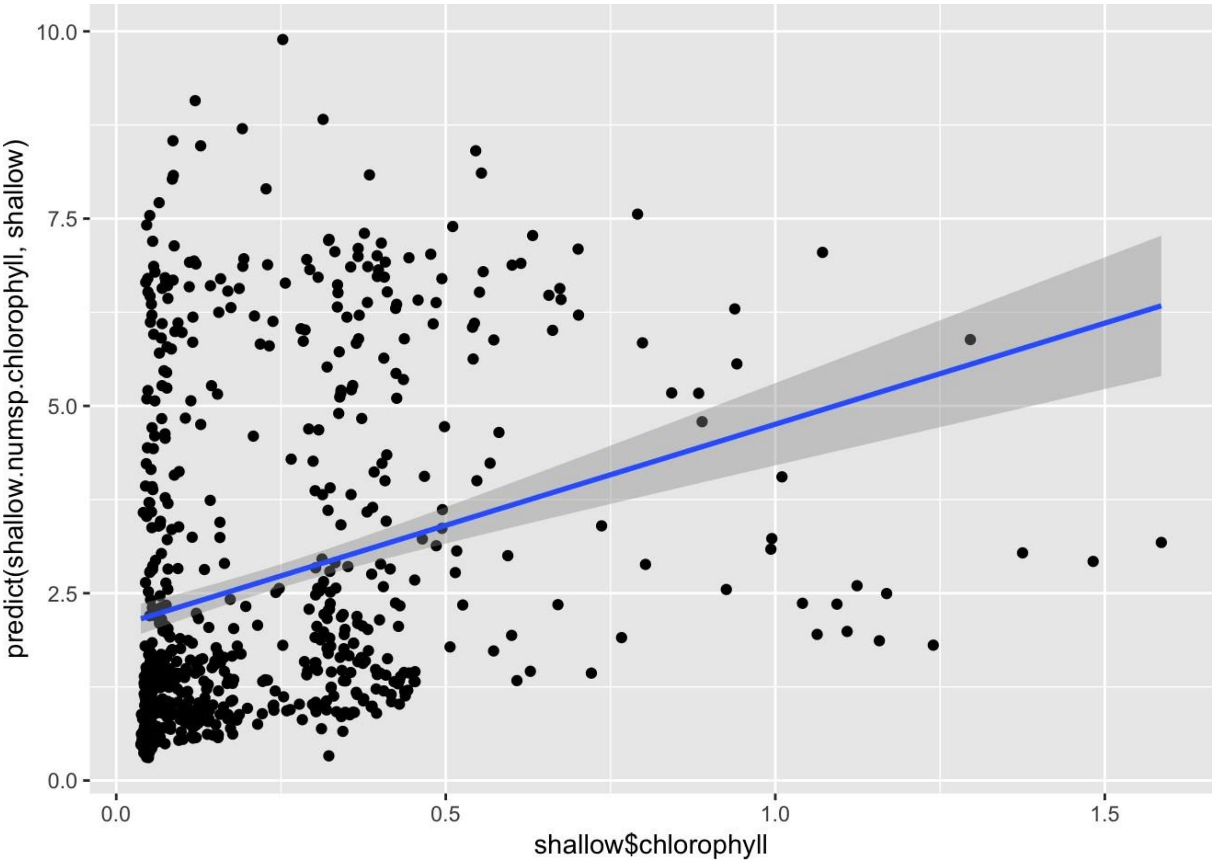
```
qplot(shallow$primary.productivity, predict(shallow.numsp.prod, shallow)) + geom_sm
ooth(method = "gam")
```



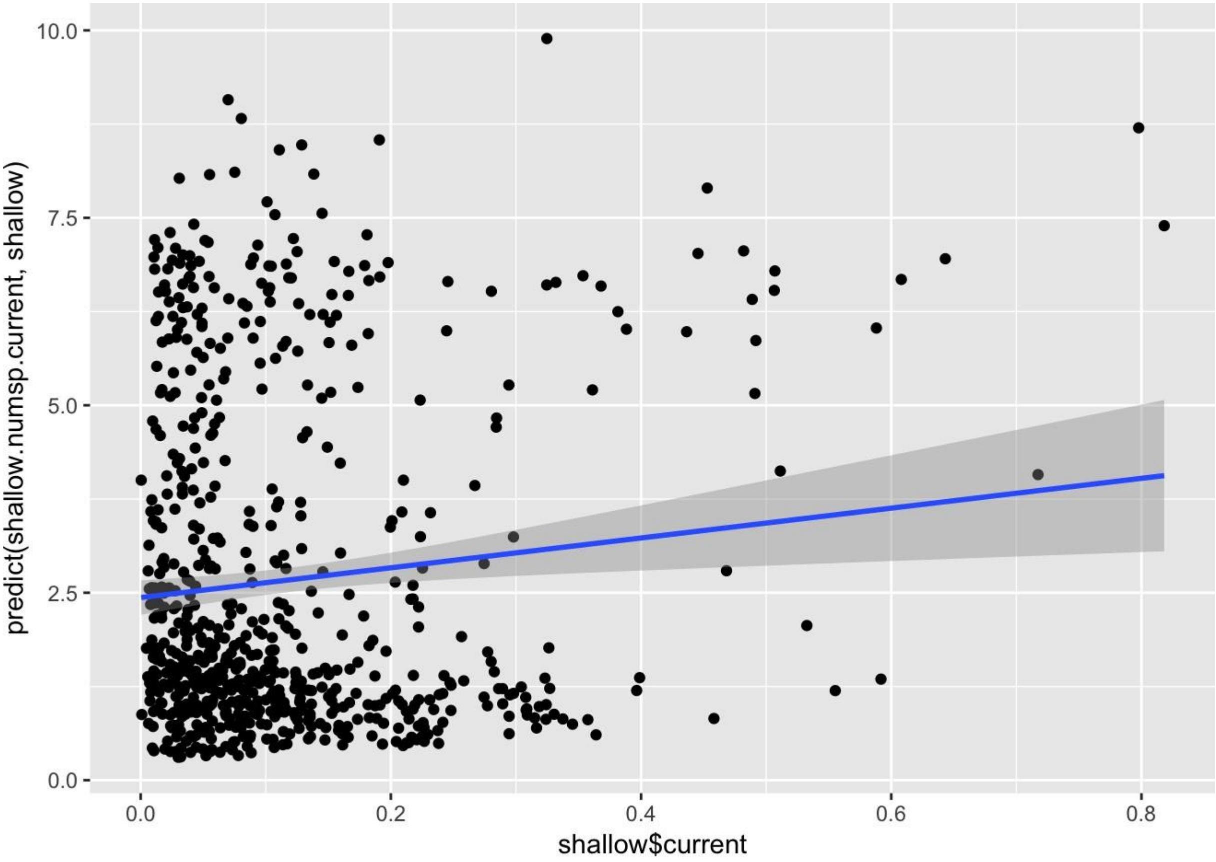
```
qplot(shallow$dissolved.oxygen, predict(shallow.numsp.oxygen, shallow)) + geom_smoo
th(method = "gam")
```



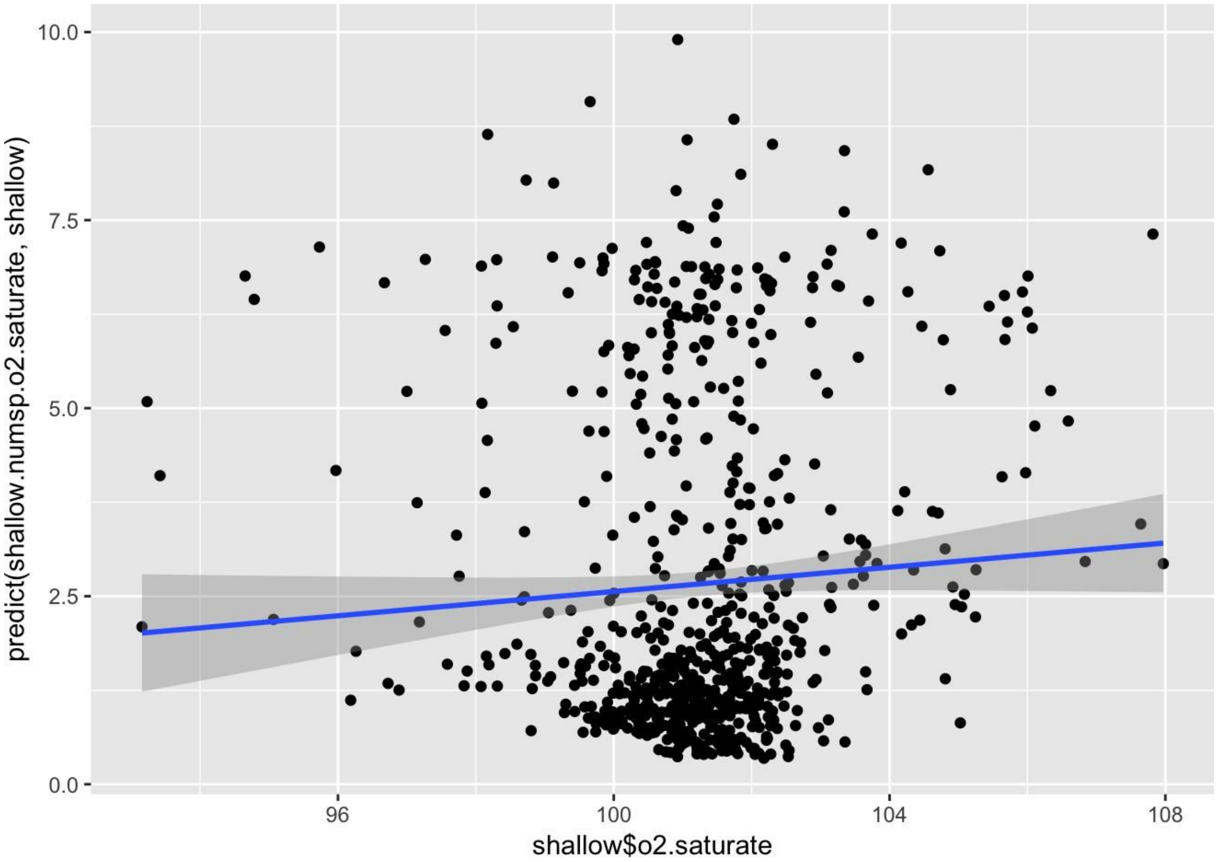
```
qplot(shallow$chlorophyll, predict(shallow.numsp.chlorophyll, shallow)) + geom_smoo
th(method = "gam")
```



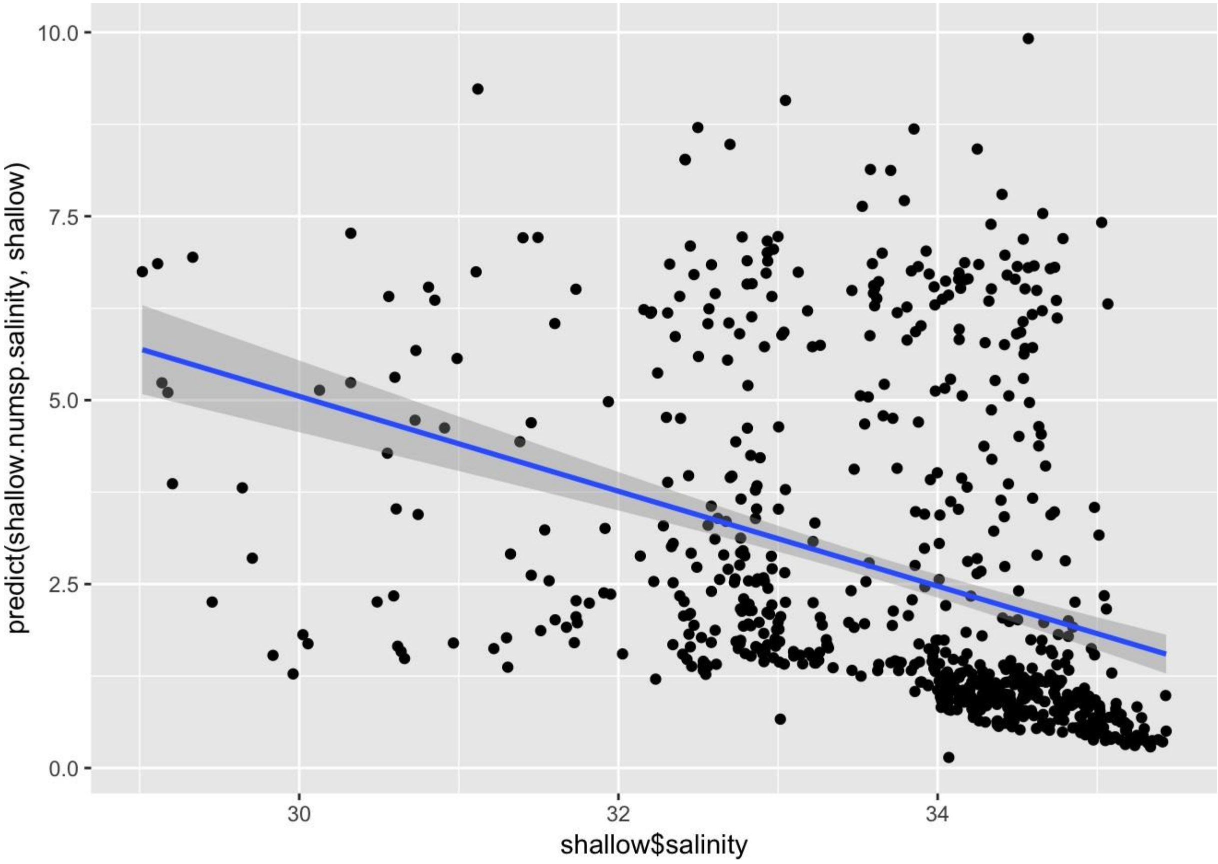
```
qplot(shallow$current,  predict(shallow.numsp.current,  shallow))   +   geom_smooth(metho
d =  "gam")
```



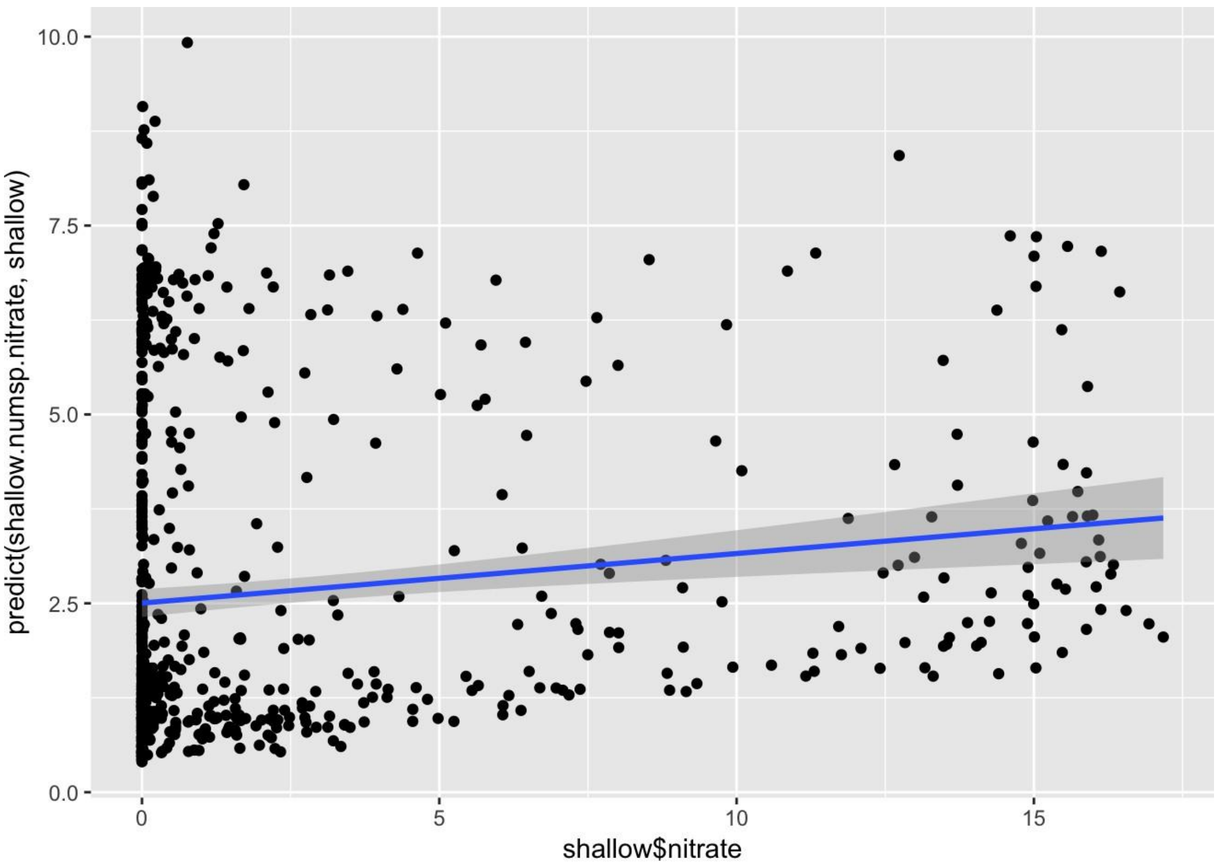
```
qplot(shallow$o2.saturate, predict(shallow.numsp.o2.saturate, shallow)) + geom_smoo
th(method = "gam")
```



```
qplot(shallow$salinity, predict(shallow.numsp.salinity, shallow)) + geom_smooth(met
hod = "gam")
```



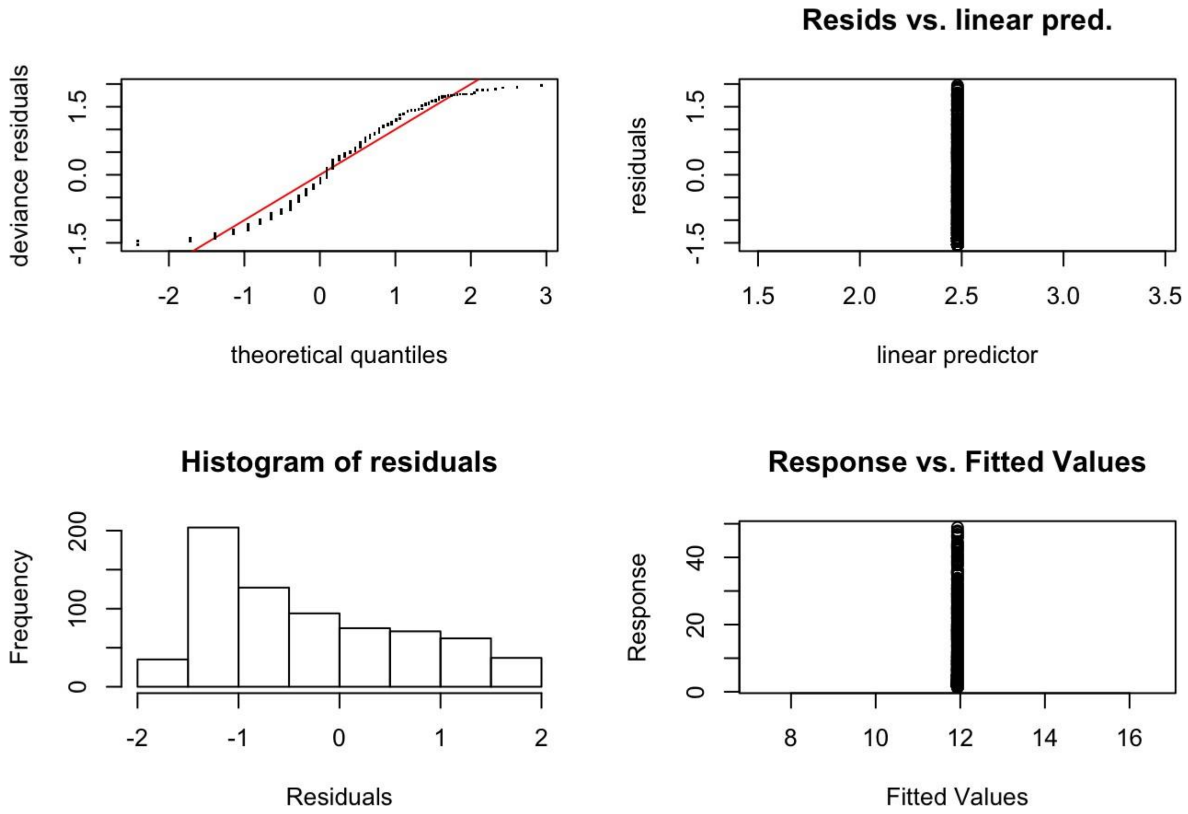
```
qplot(shallow$nitrate, predict(shallow.numsp.nitrate, shallow)) + geom_smooth(metho
d = "gam")
```



GAMs for ES50, shallow water

These models are identical to the above, except that the response variable is the species richness estimated from the rarefaction curves. These are meant to be estimates of species richness if all sites were sampled equally. Since these measurements are intended to take sampling effort into account, we exclude the “no.records” term for these models.

```
shallow.es50.intercept <- gam(ES50 ~ 1, data = shallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.es50.intercept)
```

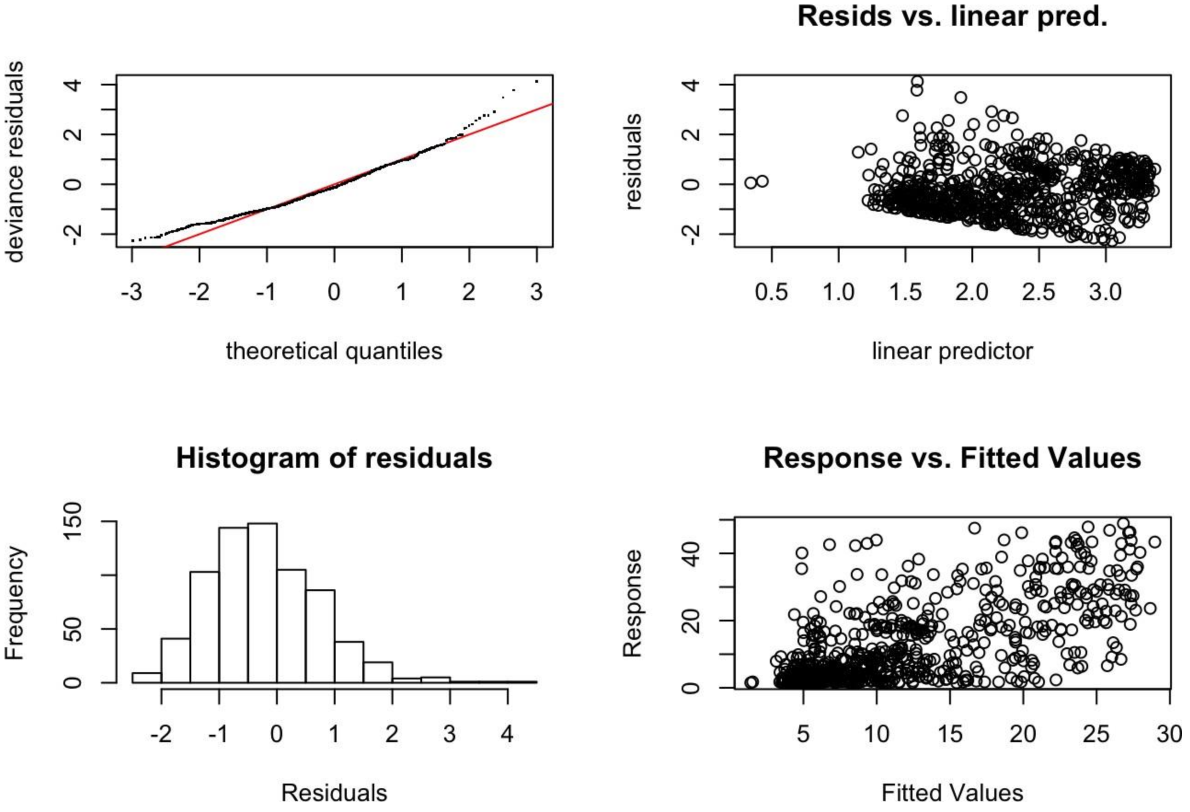


```
##
## Method: REML    Optimizer: outer newton
## full convergence after 3 iterations.
## Gradient range [5.595699e-09,5.595699e-09]
## (score 2476.994 & scale 1).
## Hessian positive definite, eigenvalue range [335.1861,335.1861].
## Model rank =  1 / 1
```

```
summary(shallow.es50.intercept)
```

```
##
## Family: Negative Binomial(1.231)
## Link function: log
##
## Formula:
## ES50 ~ 1
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.47939    0.03566   69.53   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## R-sq.(adj) =       0   Deviance explained = 3.56e-08%
## -REML =   2477  Scale est. = 1         n = 705
```

```
shallow.es50.latlon <- gam(ES50 ~ s(lat, lon, bs = "sos") , data = shallow, family
 = "nb", method = "REML", select = TRUE)
gam.check(shallow.es50.latlon)
```

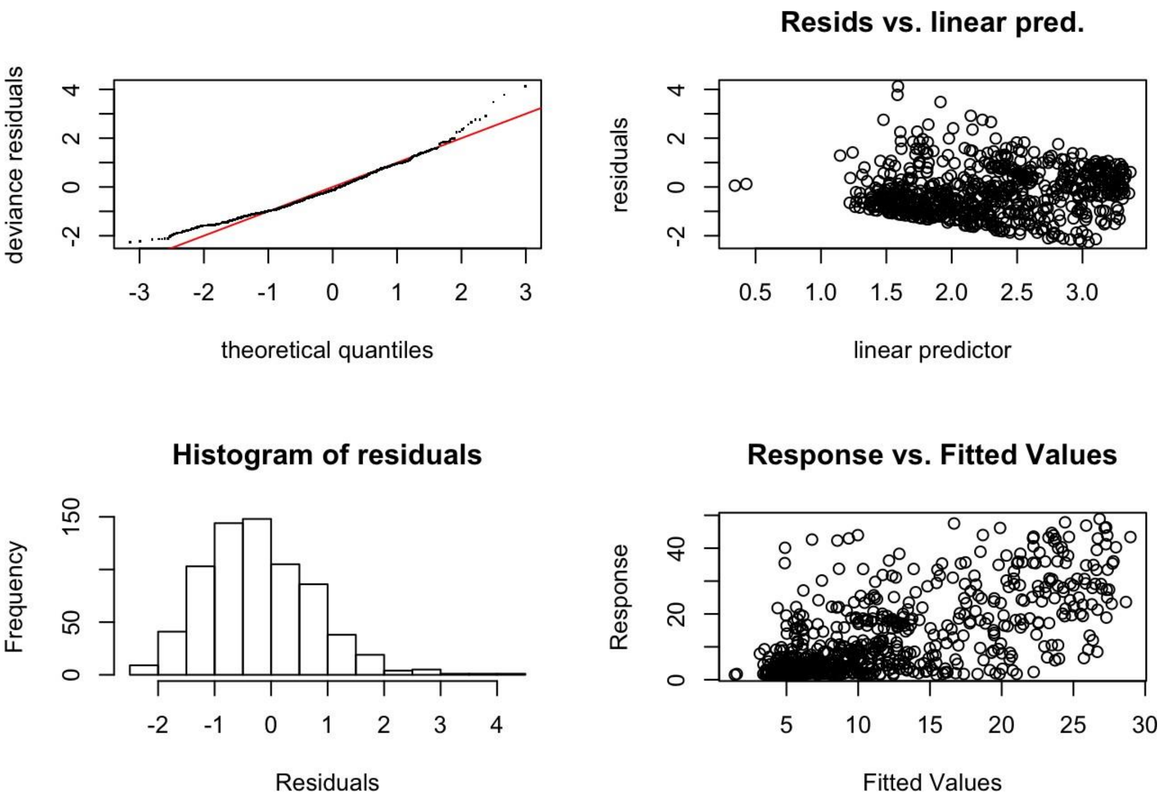


```
##
## Method: REML    Optimizer: outer newton
## full convergence after 3 iterations.
## Gradient range [-1.636573e-06,1.452781e-05]
## (score 2341.56 & scale 1).
## Hessian positive definite, eigenvalue range [9.722589,234.1502].
## Model rank =  50 / 50
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                 k'   edf k-index p-value
## s(lat,lon) 49.0 34.2     0.84  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.es50.latlon)
```

```
##
## Family: Negative Binomial(2.106)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs =  "sos")
##
## Parametric coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
##  (Intercept)    2.28253     0.02904    78.59    <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.'  0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                    edf Ref.df Chi.sq  p-value
## s(lat,lon)  34.23       49   436.6  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.'  0.1 ' ' 1
##
##  R-sq.(adj)  =    0.415     Deviance  explained  =    42%
## -REML = 2341.6   Scale   est.  =  1             n =  705
```

```
shallow.es50.temp  <-  gam(ES50  ~  s(lat, lon, bs  =  "sos")   + s(temp), data = shallow,
family  =  "nb",  method  =  "REML",  select  =  TRUE)
gam.check(shallow.es50.temp)
```

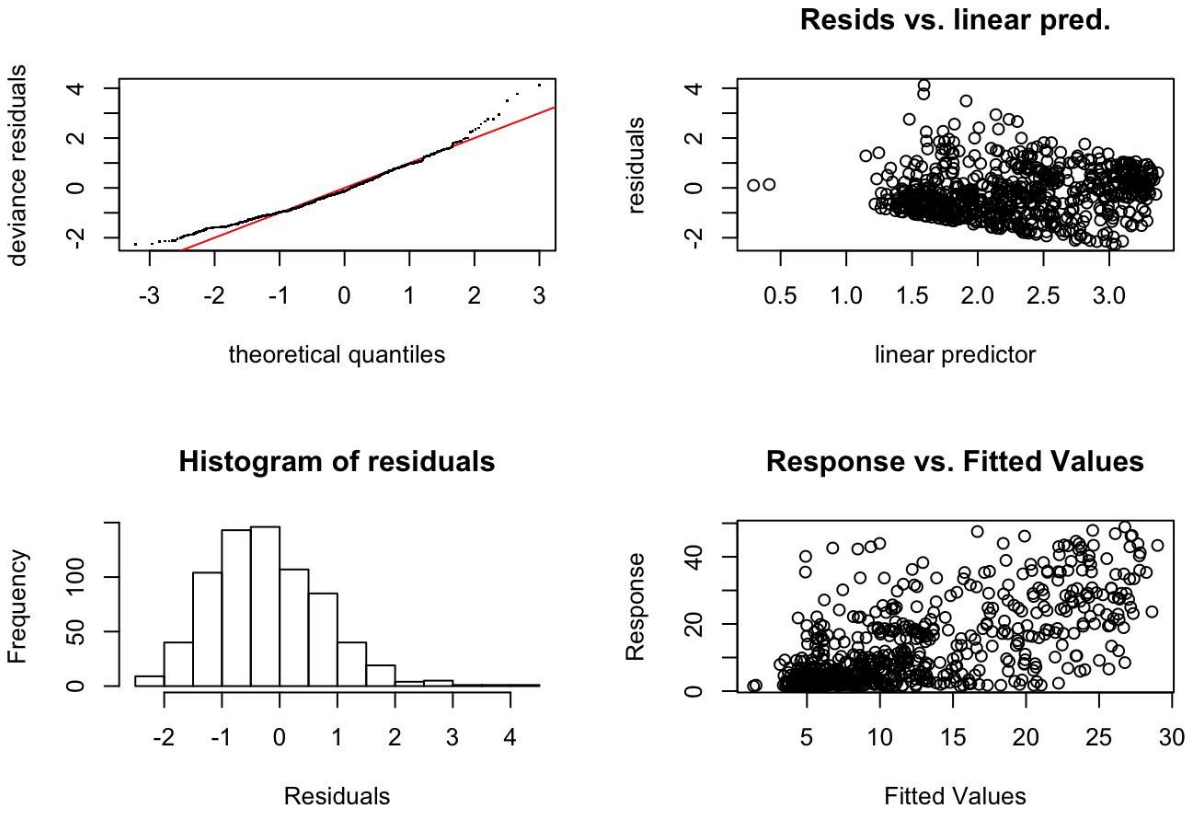


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 6 iterations.
## Gradient range [-0.0007373449,0.0003134109]
## (score 2341.561 & scale 1).
## Hessian positive definite, eigenvalue range [1.390536e-05,234.1496].
## Model rank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                   k'      edf k-index p-value
## s(lat,lon)  49.00000 34.23233    0.84  <2e-16 ***
## s(temp)      9.00000  0.00244    0.97    0.74
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.es50.temp)
```

```
##
## Family: Negative Binomial(2.106)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs = "sos") + s(temp)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.28253    0.02904   78.59   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                  edf Ref.df  Chi.sq p-value
## s(lat,lon) 34.232332     49 434.804  <2e-16 ***
## s(temp)     0.002443      9   0.001   0.511
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.415   Deviance explained =   42%
## -REML = 2341.6  Scale est. = 1         n = 705
```

```
shallow.es50.oxygen <- gam(ES50 ~ s(lat, lon, bs = "sos") + s(dissolved.oxygen),
data = shallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.es50.oxygen)
```

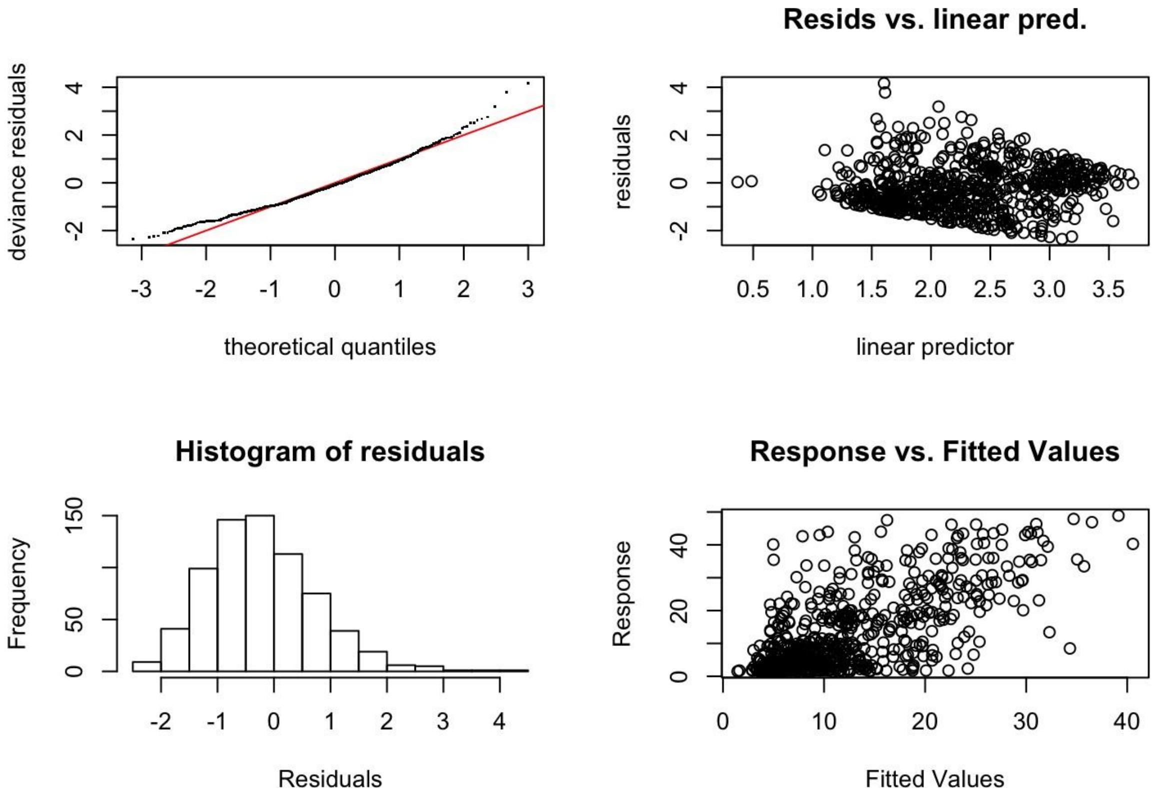


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 3 iterations.
## Gradient range [-0.0002385339,0.0001233648]
## (score 2341.47 & scale 1).
## Hessian positive definite, eigenvalue range [0.0002383868,233.6167].
## Model rank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                          k'    edf k-index p-value
## s(lat,lon)           49.000 33.884    0.84  <2e-16 ***
## s(dissolved.oxygen)   9.000  0.809    0.95     0.5
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.es50.oxygen)
```

```
##
## Family: Negative Binomial(2.109)
## Link function: log
##
## Formula:
## ES50  ~ s(lat, lon, bs = "sos") + s(dissolved.oxygen)
##
## Parametric coefficients:
##                 Estimate Std. Error z value  Pr(>|z|)
##  (Intercept)    2.28207     0.02903    78.62    <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                            edf  Ref.df   Chi.sq  p-value
## s(lat,lon)              33.884      49 416.405   <2e-16 ***
## s(dissolved.oxygen)      0.809       9   1.138   0.0899 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  R-sq.(adj) =   0.418    Deviance explained = 42.1%
## -REML = 2341.5  Scale est. = 1          n = 705
```

```
shallow.es50.prod <- gam(ES50 ~ s(lat, lon, bs = "sos") + s(primary.productivit
y), data = shallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.es50.prod)
```

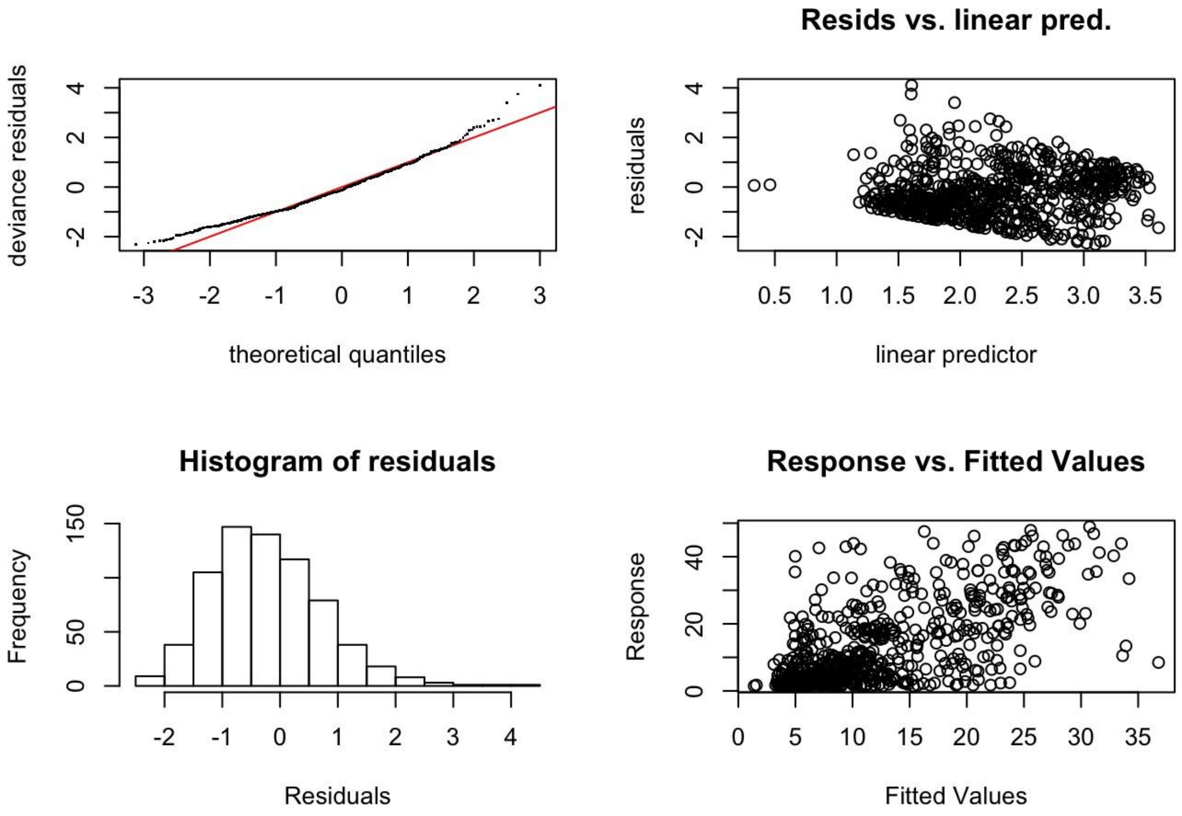


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 5 iterations.
## Gradient range [-1.662754e-06,3.139754e-06]
## (score 2331.933 & scale 1).
## Hessian positive definite, eigenvalue range [0.1293296,226.2702].
## Model rank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                              k'   edf k-index p-value
## s(lat,lon)                49.00 34.19    0.85  <2e-16 ***
## s(primary.productivity)  9.00  3.37    0.99    0.85
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.es50.prod)
```

```
##
## Family: Negative Binomial(2.209)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs = "sos") + s(primary.productivity)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.27083    0.02856   79.52   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                            edf Ref.df Chi.sq  p-value
## s(lat,lon)               34.19     49 422.70  < 2e-16 ***
## s(primary.productivity)  3.37      9  27.48 2.04e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.455   Deviance explained = 44.6%
## -REML = 2331.9  Scale est. = 1         n = 705
```

```
shallow.es50.chlorophyll <- gam(ES50 ~ s(lat, lon, bs = "sos") + s(chlorophyll),
data = shallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.es50.chlorophyll)
```

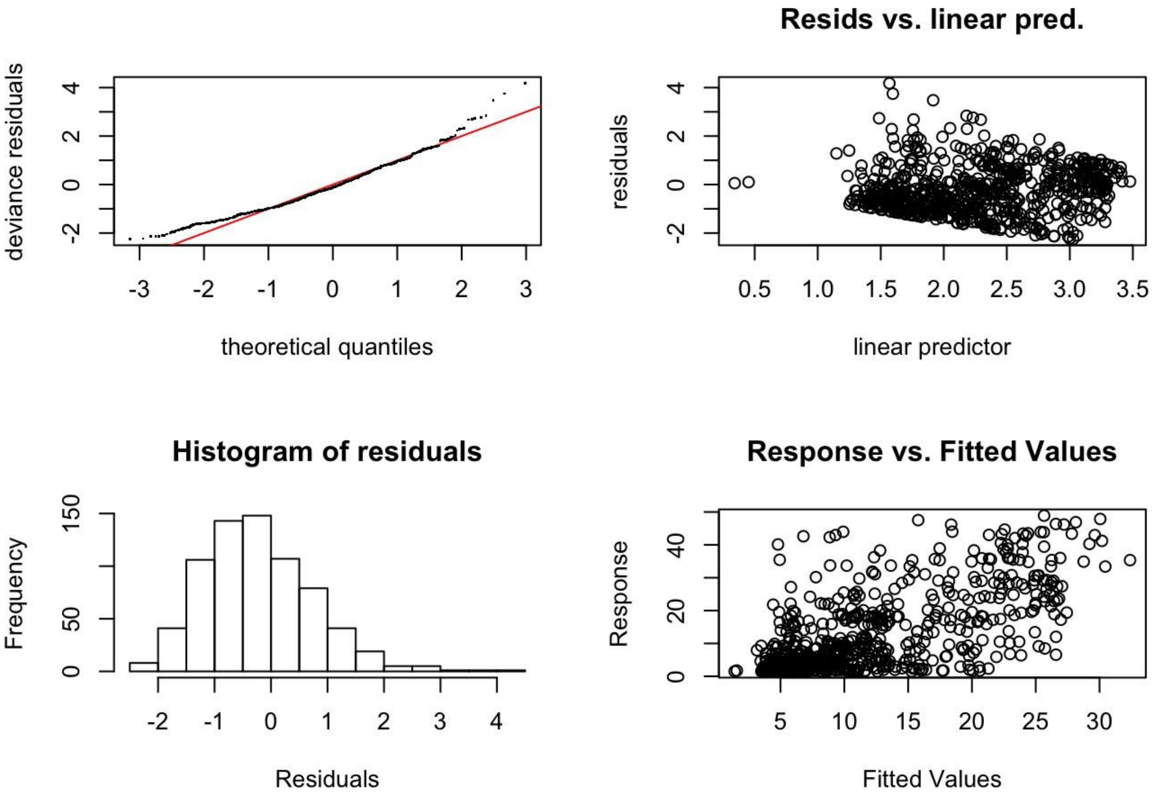


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 3 iterations.
## Gradient range [-1.322651e-05,9.523495e-05]
## (score 2339.164 & scale 1).
## Hessian positive definite, eigenvalue range [0.1412794,231.8289].
## Model rank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                  k'  edf k-index p-value
## s(lat,lon)     49.0 32.9    0.84  <2e-16 ***
## s(chlorophyll)  9.0  3.0    0.93    0.29
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.es50.chlorophyll)
```

```
##
## Family: Negative Binomial(2.132)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs = "sos") + s(chlorophyll)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.27910    0.02892   78.81   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                    edf Ref.df Chi.sq p-value
## s(lat,lon)      32.934     49 390.67  <2e-16 ***
## s(chlorophyll)   2.999      9  12.88   9e-04 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.418   Deviance explained = 42.8%
## -REML = 2339.2  Scale est. = 1         n = 705
```

```
shallow.es50.current <- gam(ES50 ~ s(lat, lon, bs = "sos") + s(current), data = s
hallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.es50.current)
```

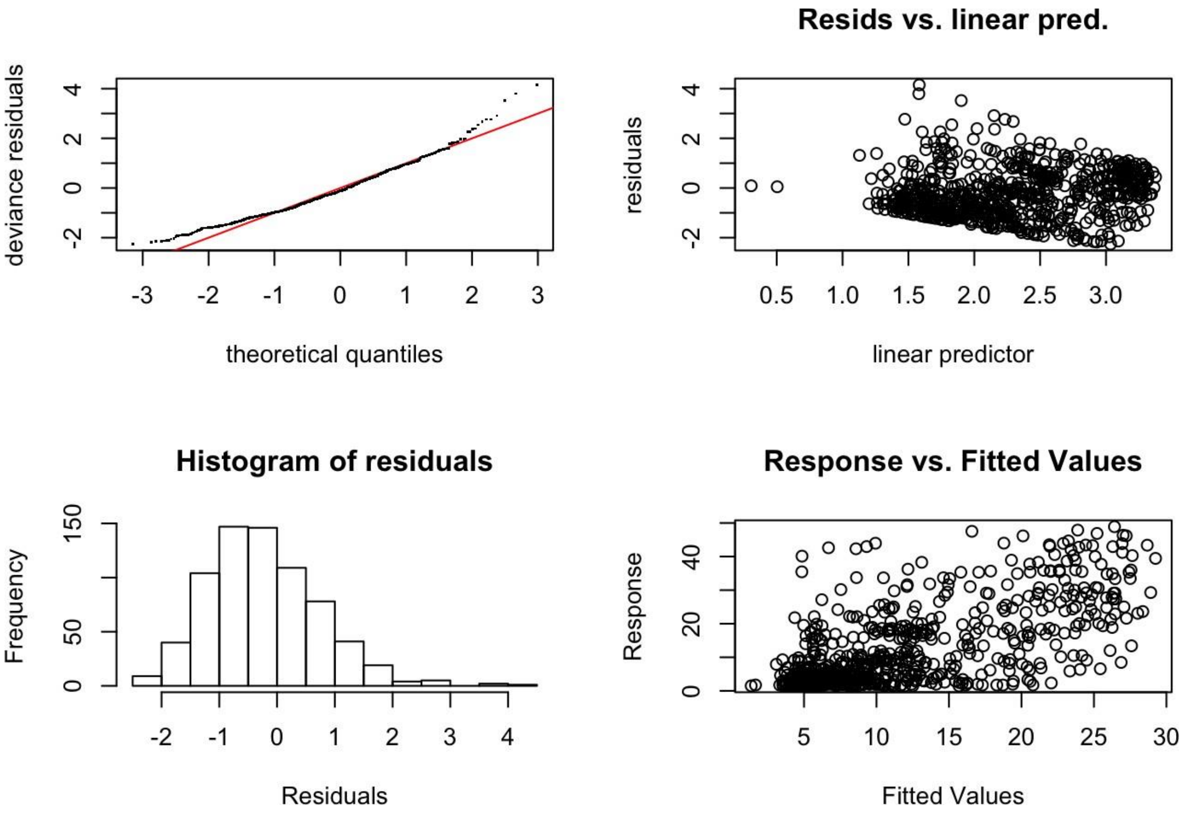


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 6 iterations.
## Gradient range [-0.0006727976,0.000479441]
## (score 2341.073 & scale 1).
## Hessian positive definite, eigenvalue range [0.0006722106,234.1461].
## Model rank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                  k'    edf k-index p-value
## s(lat,lon) 49.000 33.585    0.84  <2e-16 ***
## s(current)  9.000  0.664    0.89   0.045 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.es50.current)
```

```
##
## Family: Negative Binomial(2.105)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs = "sos") + s(current)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.28275    0.02904   78.59   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##               edf Ref.df  Chi.sq p-value
## s(lat,lon) 33.585     49 424.082  <2e-16 ***
## s(current)  0.664      9   1.992  0.0701 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =   0.42   Deviance explained = 41.9%
## -REML = 2341.1  Scale est. = 1         n = 705
```

```
shallow.es50.o2.saturate <- gam(ES50 ~ s(lat, lon, bs = "sos") + s(o2.saturate),
data = shallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.es50.o2.saturate)
```

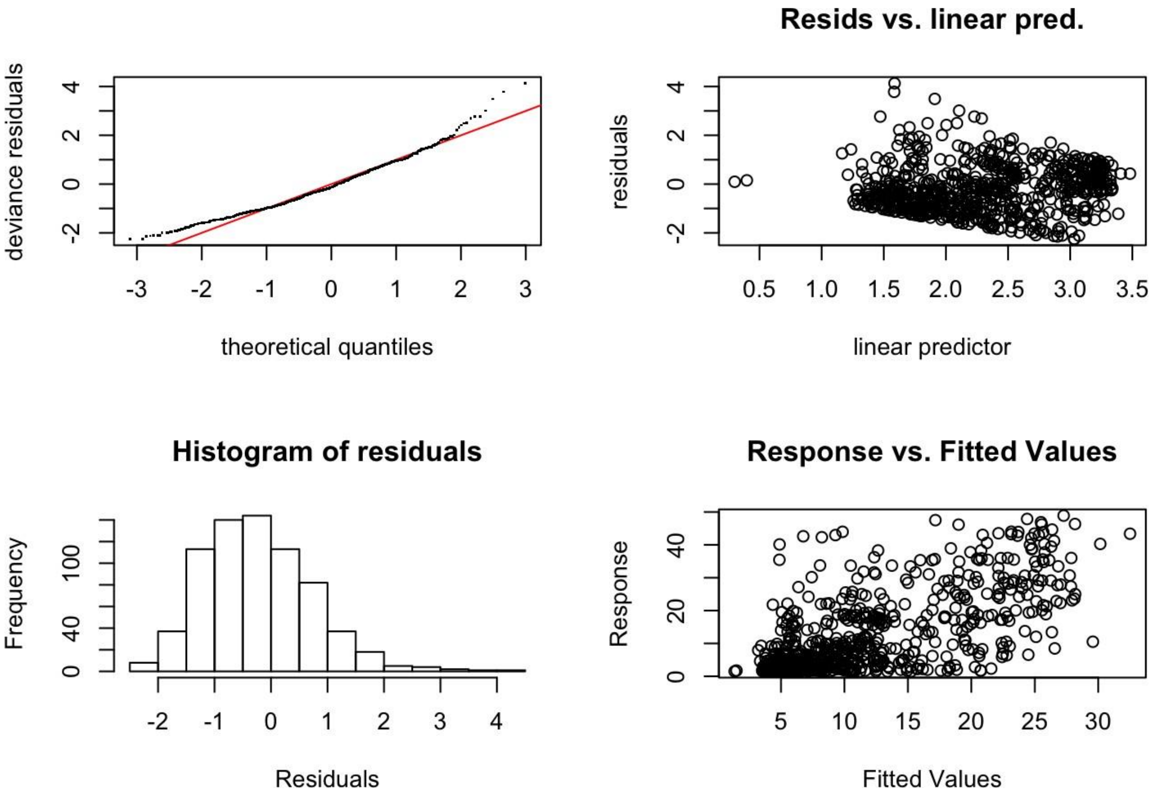


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 3 iterations.
## Gradient range [-0.0006824379,0.0001868394]
## (score 2341.236 & scale 1).
## Hessian positive definite, eigenvalue range [0.0002624635,233.1806].
## Model rank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                   k'   edf k-index p-value
## s(lat,lon)     49.00 34.06    0.84  <2e-16 ***
## s(o2.saturate)  9.00  1.17    0.85  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.es50.o2.saturate)
```

```
##
## Family: Negative Binomial(2.113)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs = "sos") + s(o2.saturate)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.28146    0.02901   78.65   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                  edf Ref.df  Chi.sq p-value
## s(lat,lon)     34.06     49 420.777  <2e-16 ***
## s(o2.saturate)  1.17      9   2.303  0.0988 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  R-sq.(adj) =  0.418   Deviance explained = 42.2%
## -REML = 2341.2  Scale est. = 1         n = 705
```

```
shallow.es50.salinity <- gam(ES50 ~ s(lat, lon, bs = "sos") + s(salinity), data =
shallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.es50.salinity)
```

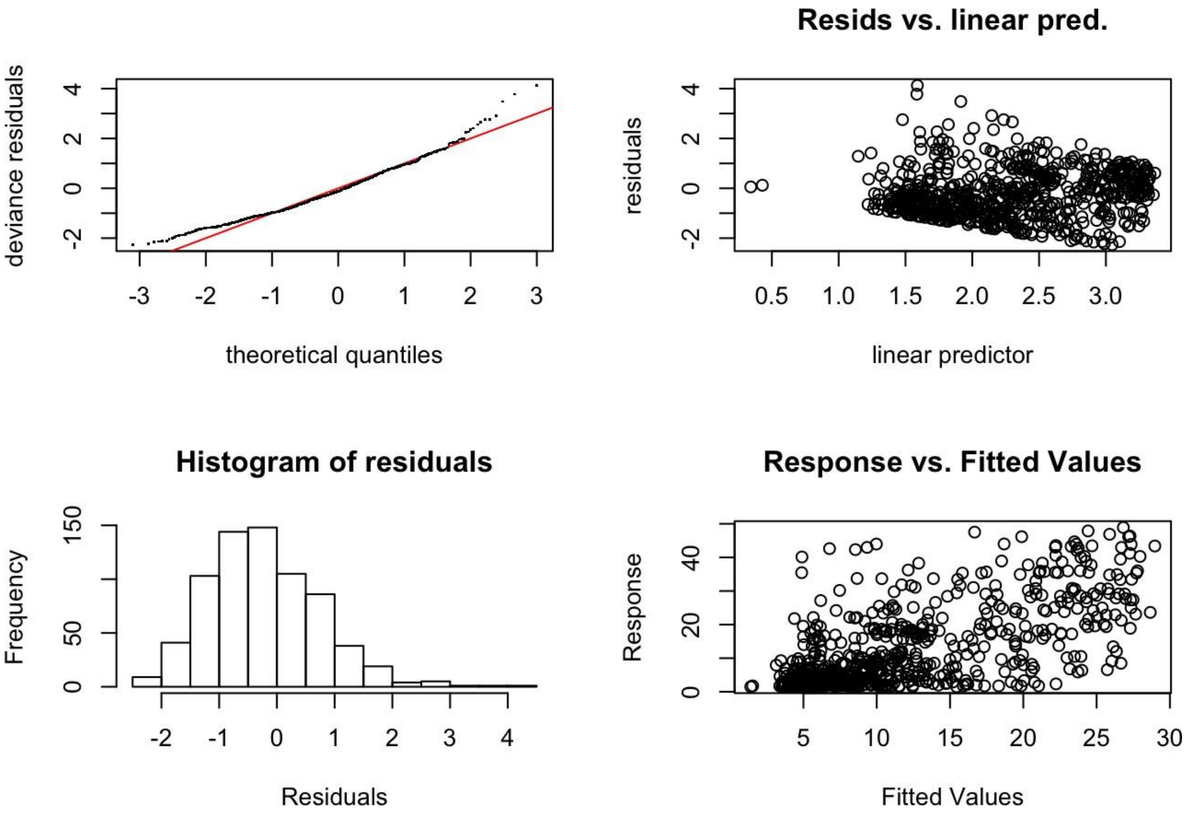


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 6 iterations.
## Gradient range [-0.001116754,0.0001808395]
## (score 2340.619 & scale 1).
## Hessian positive definite, eigenvalue range [0.0405921,233.8519].
## Model rank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                 k'   edf k-index p-value
## s(lat,lon)   49.00 33.18    0.84  <2e-16 ***
## s(salinity)   9.00  1.09    0.91   0.075 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.es50.salinity)
```

```
##
## Family: Negative Binomial(2.107)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs = "sos") + s(salinity)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.28242    0.02904    78.6   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                edf Ref.df  Chi.sq p-value
## s(lat,lon)  33.177     49 335.316  <2e-16 ***
## s(salinity)  1.092      9   4.042  0.0188 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.418   Deviance explained =   42%
## -REML = 2340.6  Scale est. = 1         n = 705
```

```
shallow.es50.nitrate <- gam(ES50 ~ s(lat, lon, bs = "sos") + s(nitrate), data = s
hallow, family = "nb", method = "REML", select = TRUE)
gam.check(shallow.es50.nitrate)
```

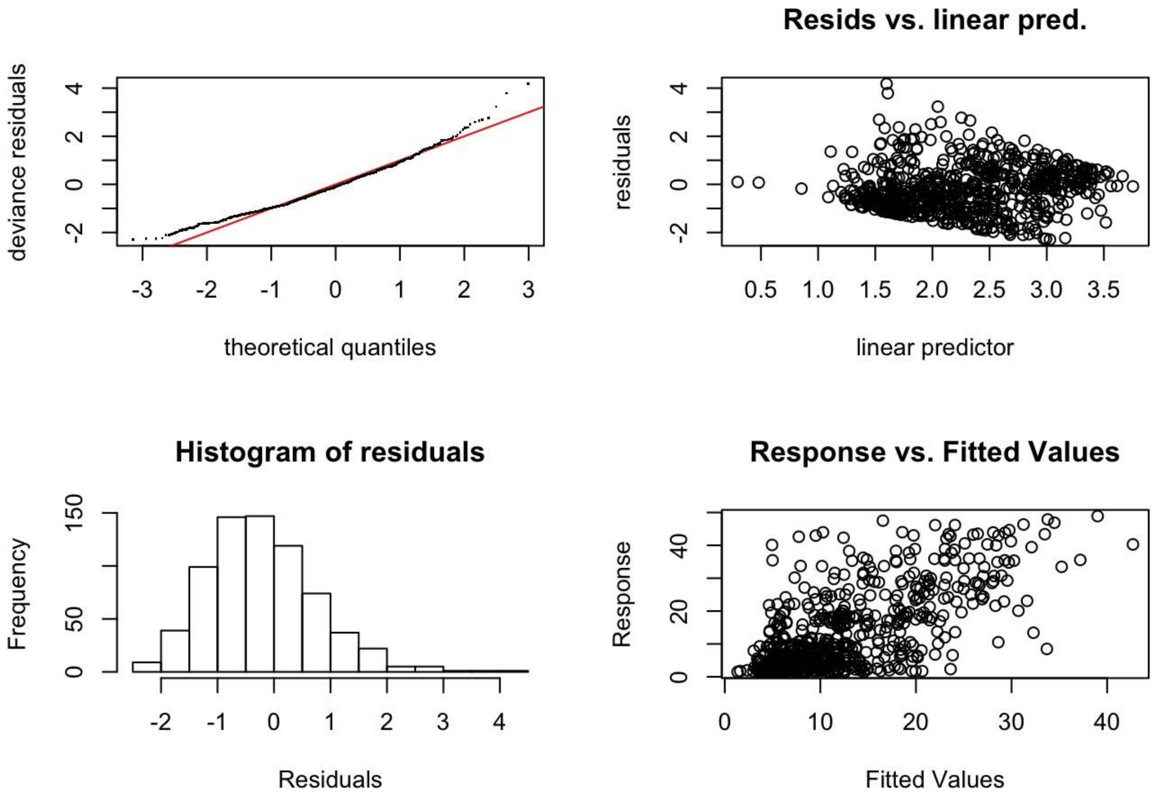


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 6 iterations.
## Gradient range [-0.0008761779,0.0005350955]
## (score 2341.561 & scale 1).
## Hessian positive definite, eigenvalue range [1.174703e-05,234.1503].
## Model rank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                 k'     edf k-index p-value
## s(lat,lon) 49.0000 34.2330    0.84  <2e-16 ***
## s(nitrate)  9.0000  0.0019    0.90    0.13
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.es50.nitrate)
```

```
##
## Family: Negative Binomial(2.106)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs =  "sos") +  s(nitrate)
##
## Parametric coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
##  (Intercept)    2.28253     0.02904    78.59    <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                          edf Ref.df Chi.sq  p-value
## s(lat,lon) 34.233015         49   436.6   <2e-16 ***
##  s(nitrate)  0.001901         9      0.0          1
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  R-sq.(adj)  =   0.415    Deviance  explained  =   42%
## -REML= 2341.6Scale  est.  =  1                   n = 705
```

```
shallow.es50.env <- gam(ES50 ~ s(lat, lon, bs = "sos") + s(temp) + s(dissolved.oxy
gen) + s(primary.productivity) + s(chlorophyll) + s(current) + s(o2.saturate) + s(s
alinity) + s(nitrate), data = shallow, family = "nb", method = "REML", select = TRU
E)
gam.check(shallow.es50.env)
```



```
##
## Method: REML   Optimizer: outer newton
## full convergence after 9 iterations.
## Gradient range [-0.001211478,6.695132e-05]
## (score 2331.218 & scale 1).
## Hessian positive definite, eigenvalue range [1.934616e-05,225.6091].
## Model rank =  122 / 122
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                               k'      edf k-index p-value
## s(lat,lon)              4.90e+01 3.30e+01    0.85  <2e-16 ***
## s(temp)                 9.00e+00 6.46e-04    0.99   0.850
## s(dissolved.oxygen)     9.00e+00 4.76e-01    0.95   0.515
## s(primary.productivity) 9.00e+00 3.37e+00    0.99   0.820
## s(chlorophyll)          9.00e+00 1.13e-03    0.93   0.300
## s(current)              9.00e+00 1.09e-03    0.90   0.075 .
## s(o2.saturate)          9.00e+00 4.17e-01    0.85   0.010 **
## s(salinity)             9.00e+00 8.96e-01    0.91   0.175
## s(nitrate)              9.00e+00 8.89e-02    0.91   0.100 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(shallow.es50.env)
```

```
##
## Family: Negative Binomial(2.212)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs = "sos") + s(temp) + s(dissolved.oxygen) +
##     s(primary.productivity) + s(chlorophyll) +  s(current)  +  s(o2.saturate)  +
##     s(salinity) + s(nitrate)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
##  (Intercept)  2.27029    0.02854   79.54   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                                edf Ref.df  Chi.sq  p-value
## s(lat,lon)               32.976231     49 340.790  < 2e-16  ***
## s(temp)                   0.000646      9   0.000   0.2707
## s(dissolved.oxygen)       0.476287      9   0.577   0.1161
## s(primary.productivity)   3.367451      9  26.460  2.2e-07  ***
## s(chlorophyll)            0.001128      9   0.001   0.3742
## s(current)                0.001091      9   0.001   0.4165
## s(o2.saturate)            0.417496      9   0.719   0.1609
## s(salinity)               0.896068      9   2.753   0.0356  *
## s(nitrate)                0.088862      9   0.089   0.2446
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =   0.456    Deviance explained = 44.7%
## -REML = 2331.2Scale  est. =  1          n =  705
```

Model selection for ES50, shallow water

```
shallow.es50.models <- list(shallow.es50.intercept = shallow.es50.intercept,
                            shallow.es50.latlon = shallow.es50.latlon,
                            shallow.es50.temp = shallow.es50.temp,
                            shallow.es50.oxygen = shallow.es50.oxygen,
                            shallow.es50.prod = shallow.es50.prod,
                            shallow.es50.chlorophyll = shallow.es50.chlorophyll,
                            shallow.es50.current = shallow.es50.current,
                            shallow.es50.o2.saturate = shallow.es50.o2.saturate,
                            shallow.es50.salinity = shallow.es50.salinity,
                            shallow.es50.nitrate = shallow.es50.nitrate,
                            shallow.es50.env = shallow.es50.env)
shallow.es50.aic.df <- data.frame(Model = names(shallow.es50.models),
                                   AIC = sapply(shallow.es50.models, function(x) x$aic),
                                  akaike.weights(sapply(shallow.es50.models,  function(x)
 x$aic)))

shallow.es50.aic.df <- shallow.es50.aic.df[order(shallow.es50.aic.df$AIC),]
shallow.es50.aic.df$Cumulative.Weight <- cumsum(shallow.es50.aic.df$weights)

kable(shallow.es50.aic.df, row.names = FALSE)
```

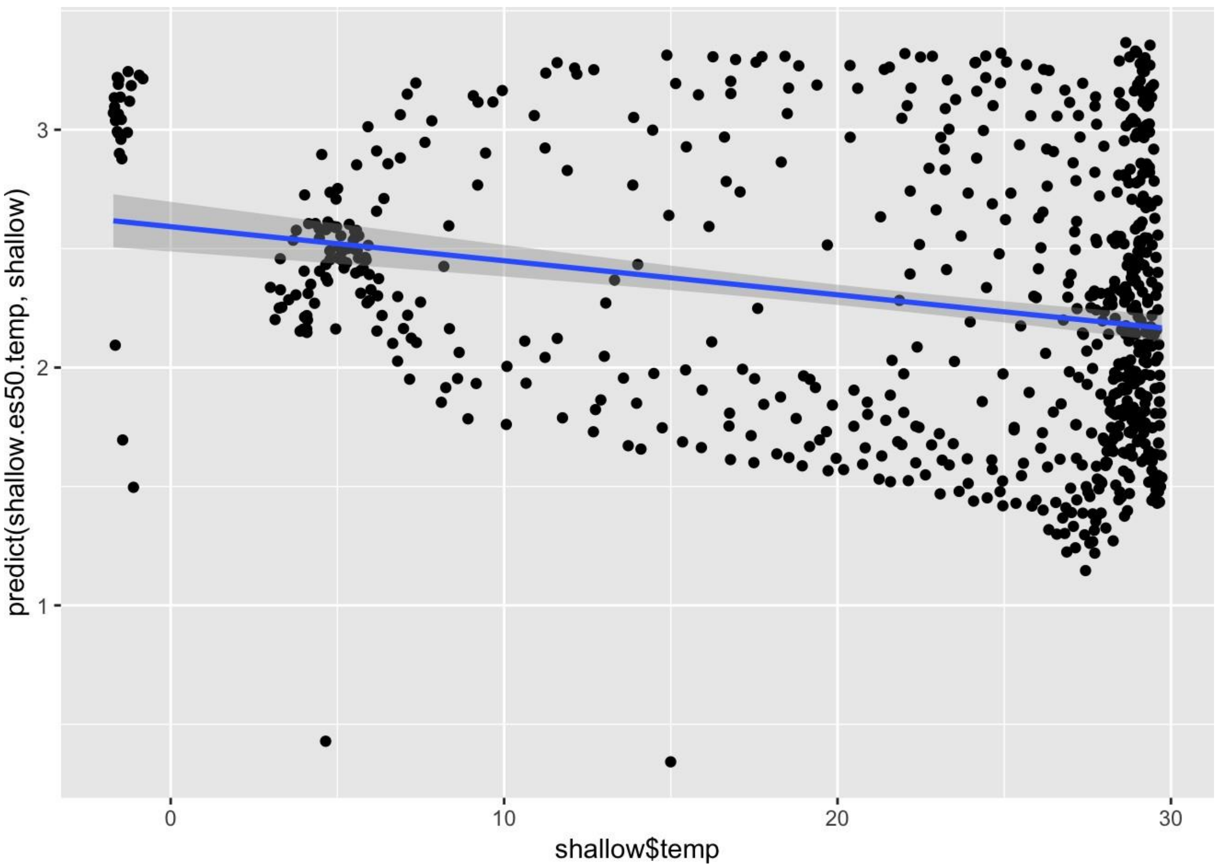
Model	AIC	deltaAIC	rel.LL	weights	Cumulative.Weight
shallow.es50.env	4598.298	0.0000000	1.0000000	0.5066030	0.5066030
shallow.es50.prod	4598.351	0.0529881	0.9738538	0.4933573	0.9999603
shallow.es50.chlorophyll	4617.762	19.4646455	0.0000593	0.0000301	0.9999904
shallow.es50.o2.saturate	4623.036	24.7379396	0.0000042	0.0000022	0.9999925
shallow.es50.oxygen	4623.785	25.4870104	0.0000029	0.0000015	0.9999940
shallow.es50.salinity	4624.051	25.7526841	0.0000026	0.0000013	0.9999953
shallow.es50.latlon	4624.161	25.8631607	0.0000024	0.0000012	0.9999965
shallow.es50.temp	4624.162	25.8644170	0.0000024	0.0000012	0.9999978
shallow.es50.nitrate	4624.164	25.8659651	0.0000024	0.0000012	0.9999990
shallow.es50.current	4624.537	26.2390899	0.0000020	0.0000010	1.0000000
shallow.es50.intercept	4951.158	352.8604444	0.0000000	0.0000000	1.0000000

```
write.csv(shallow.es50.aic.df, file = "shallow.es50.aic.csv")
```

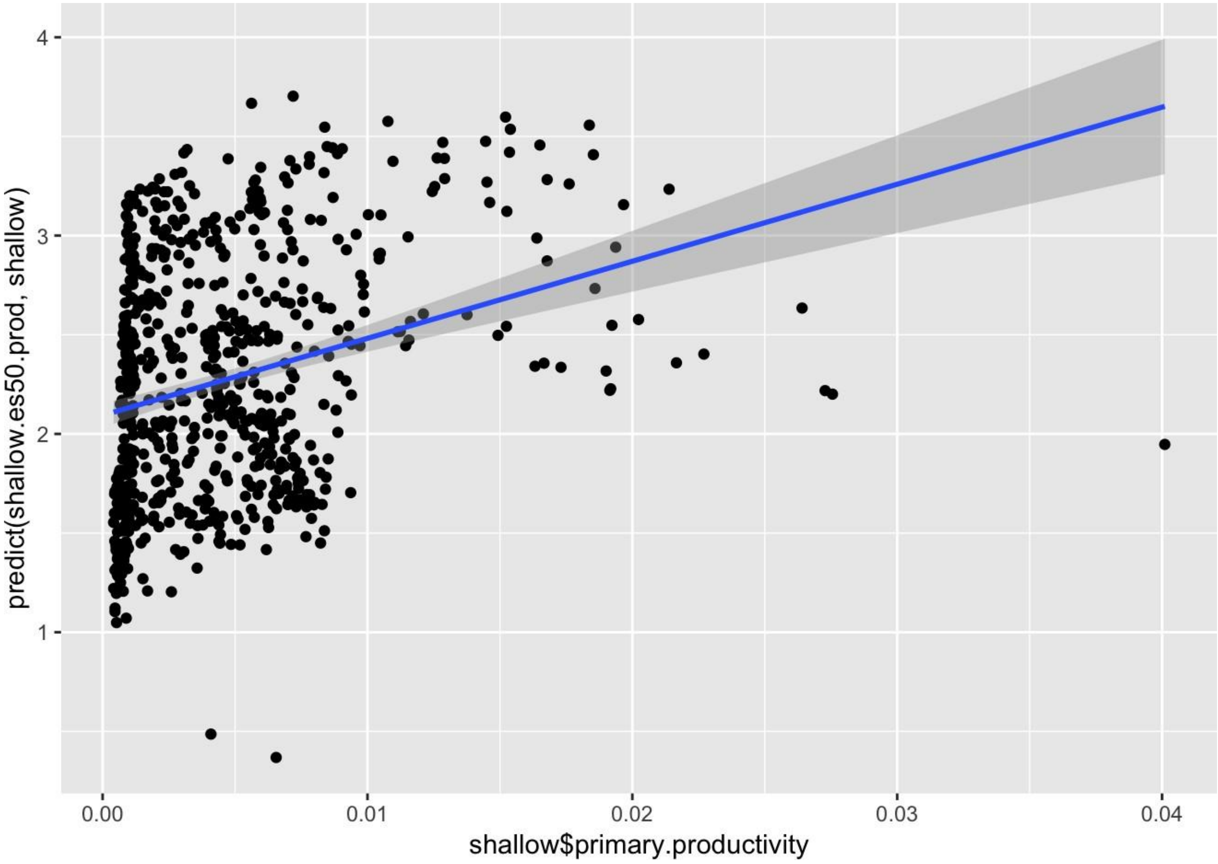
Here we find strong support for the effects of the environment on ES50 in shallow water. Given that primary productivity alone does almost as good a job as all environmental predictors at once, we believe that the predictive power here is mostly coming from primary productivity. The relatively poor performance of the spatial autocorrelation-only model (delta AIC of 29.6) suggests that there is significant predictive power in the environmental variables over and above what is expected due to spatial autocorrelation alone.

Plots for ES50, shallow water

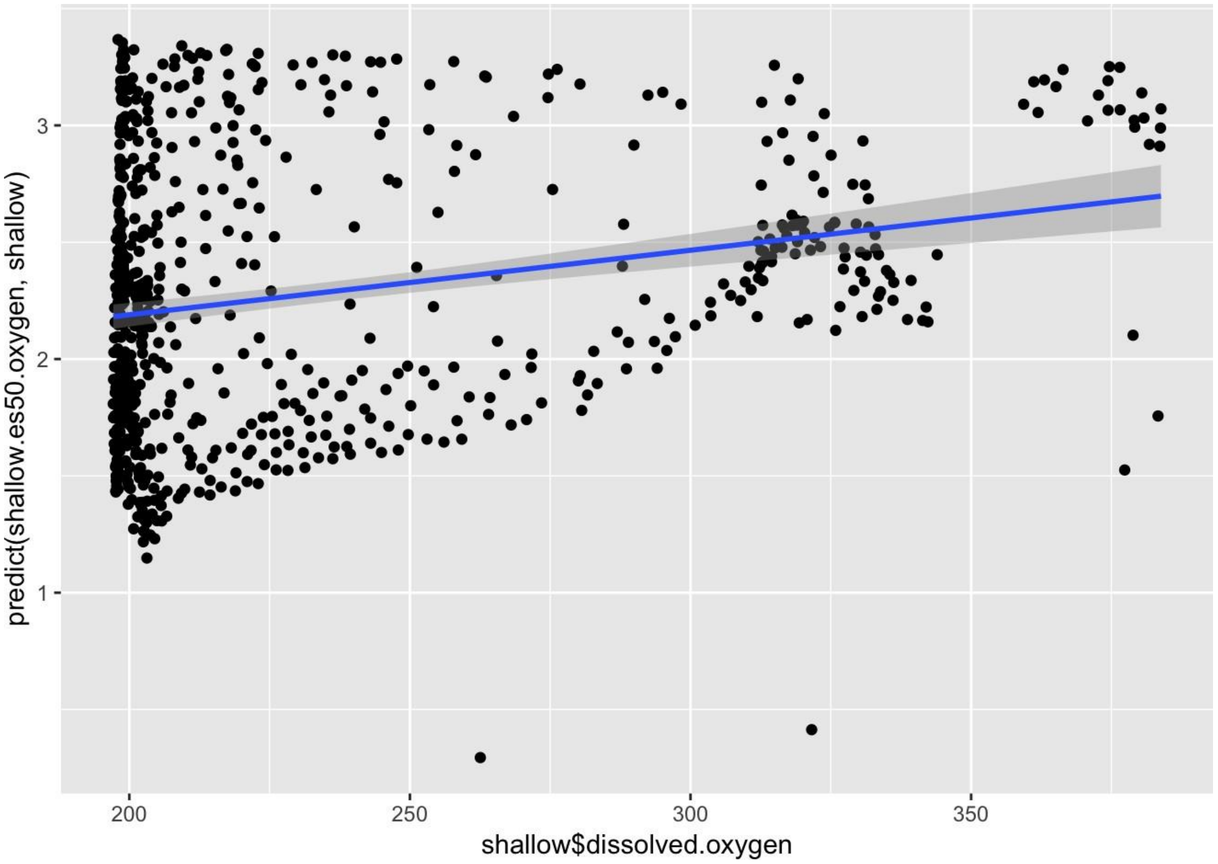
```
qplot(shallow$temp, predict(shallow.es50.temp, shallow)) + geom_smooth(method =  "ga
m")
```



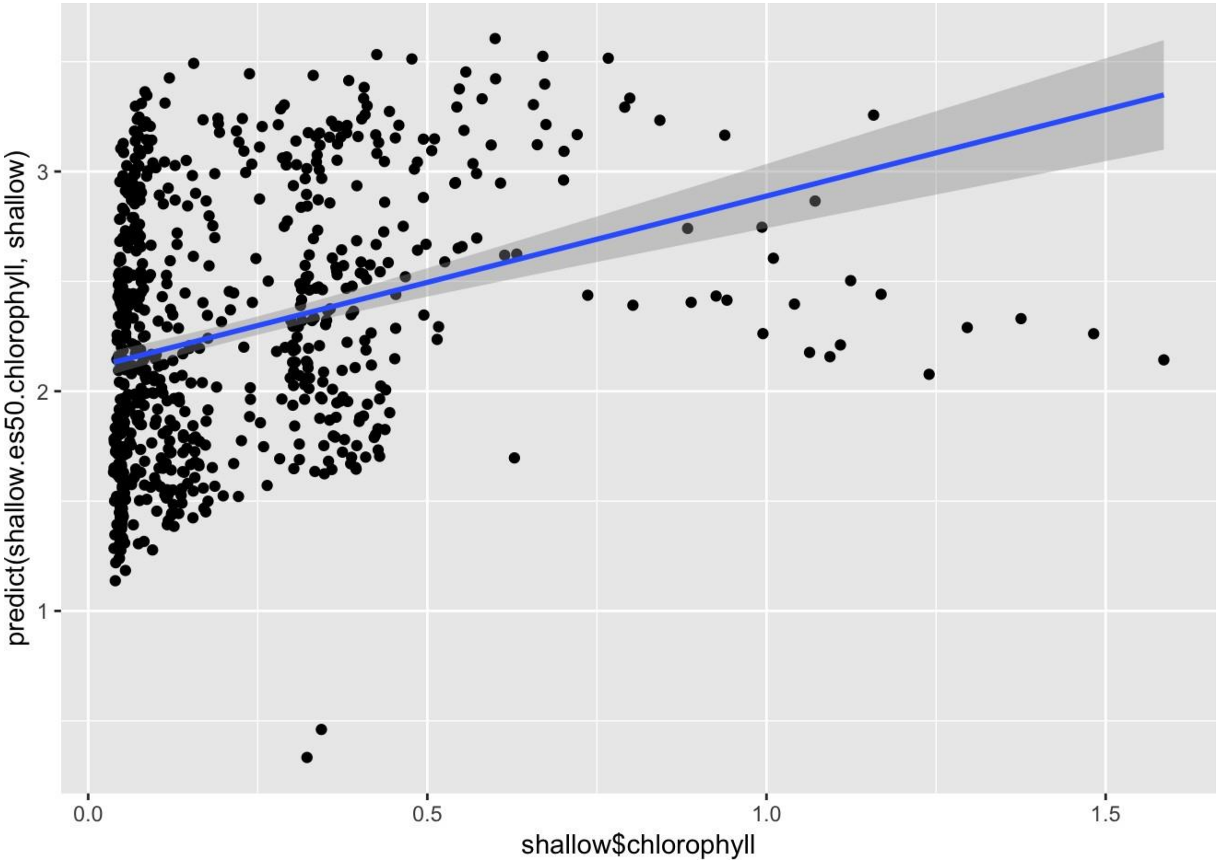
```
qplot(shallow$primary.productivity, predict(shallow.es50.prod, shallow)) + geom_smo
oth(method = "gam")
```



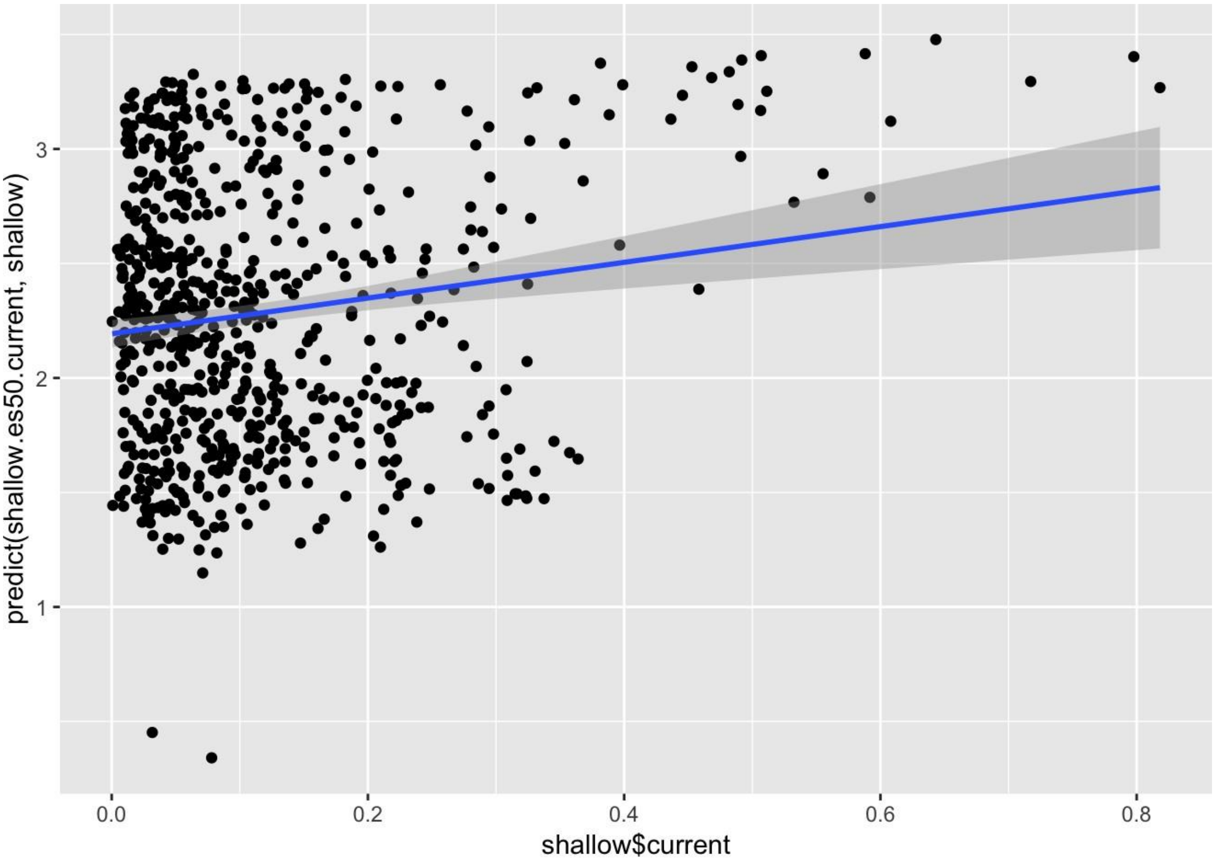
```
qplot(shallow$dissolved.oxygen, predict(shallow.es50.oxygen, shallow)) + geom_smoot
h(method = "gam")
```



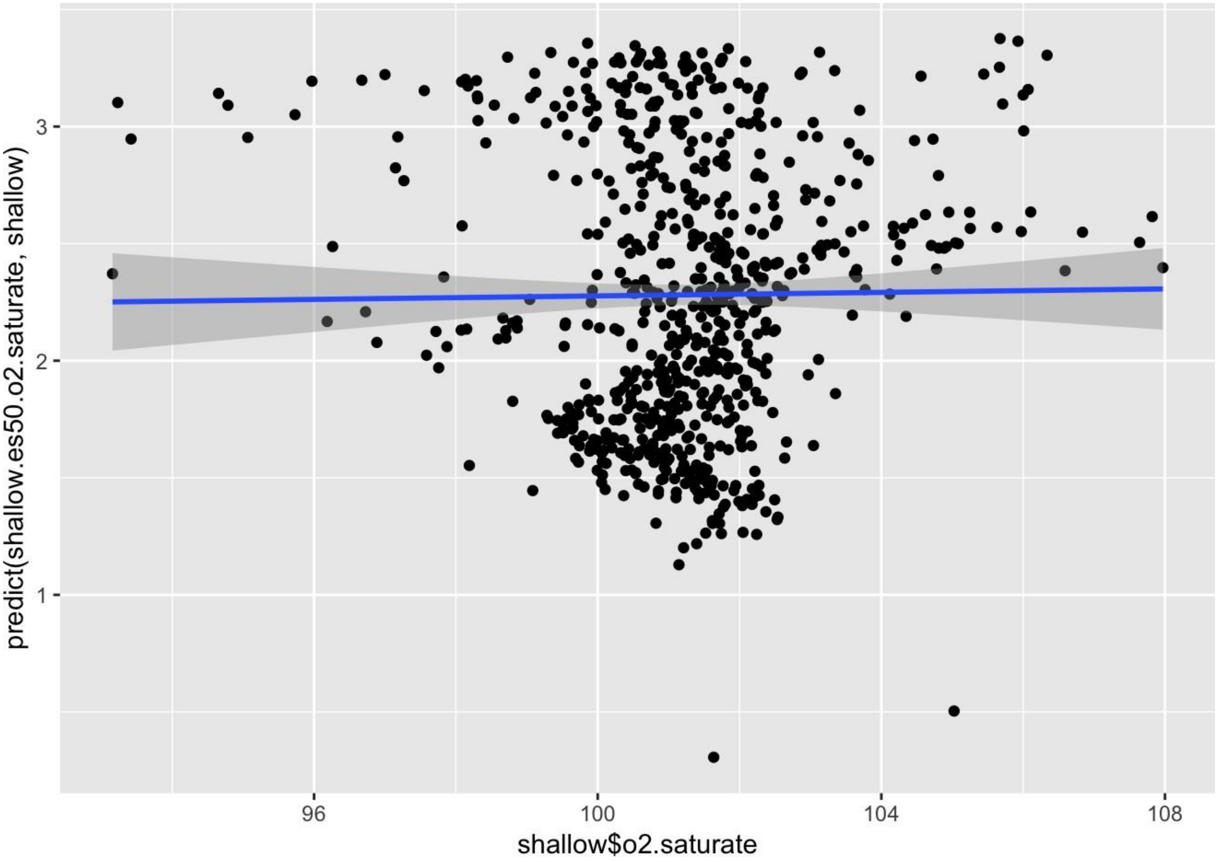
```
qplot(shallow$chlorophyll, predict(shallow.es50.chlorophyll, shallow)) + geom_smooth(method = "gam")
```



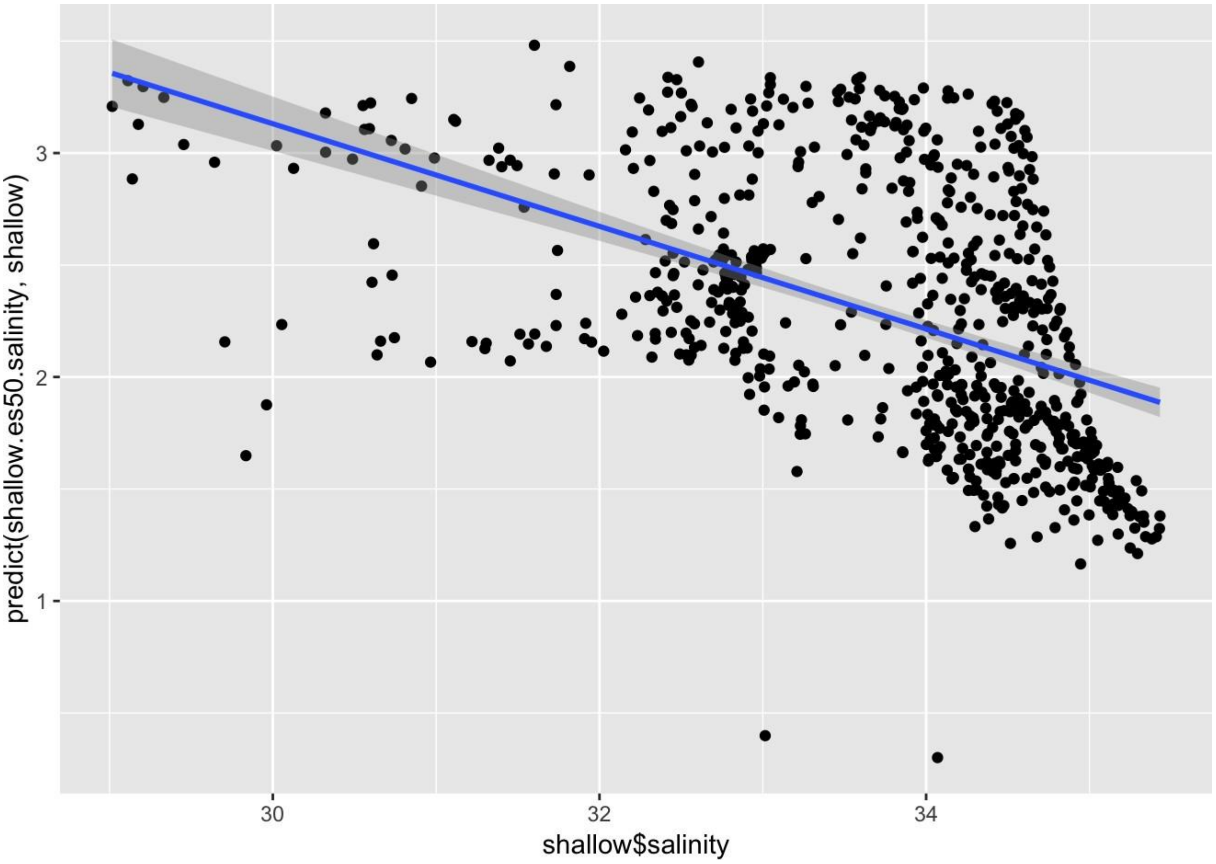
```
qplot(shallow$current, predict(shallow.es50.current, shallow)) + geom_smooth(method = "gam")
```



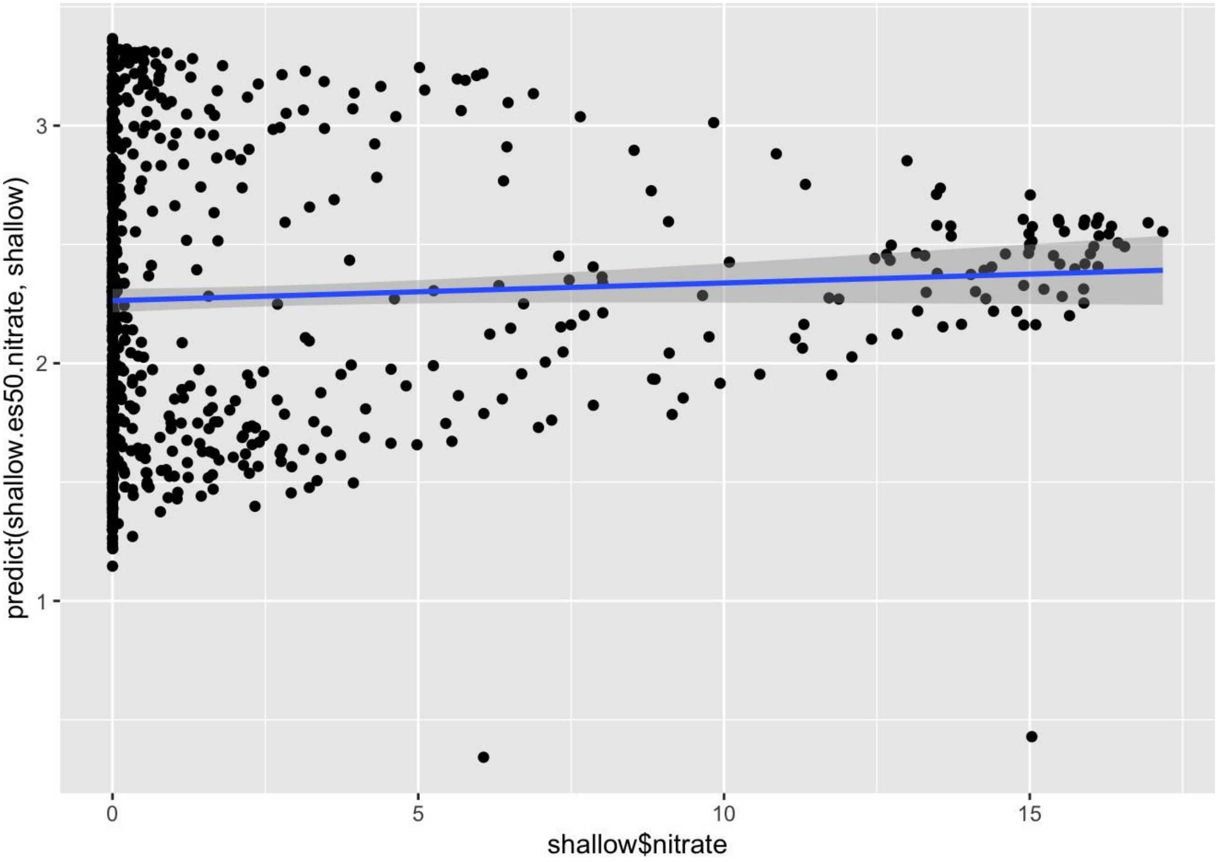
```
qplot(shallow$o2.saturate, predict(shallow.es50.o2.saturate, shallow)) + geom_smoot
h(method = "gam")
```



```
qplot(shallow$salinity,   predict(shallow.es50.salinity,   shallow))   +   geom_smooth(meth
od = "gam")
```



```
qplot(shallow$nitrate, predict(shallow.es50.nitrate, shallow)) + geom_smooth(method
= "gam")
```

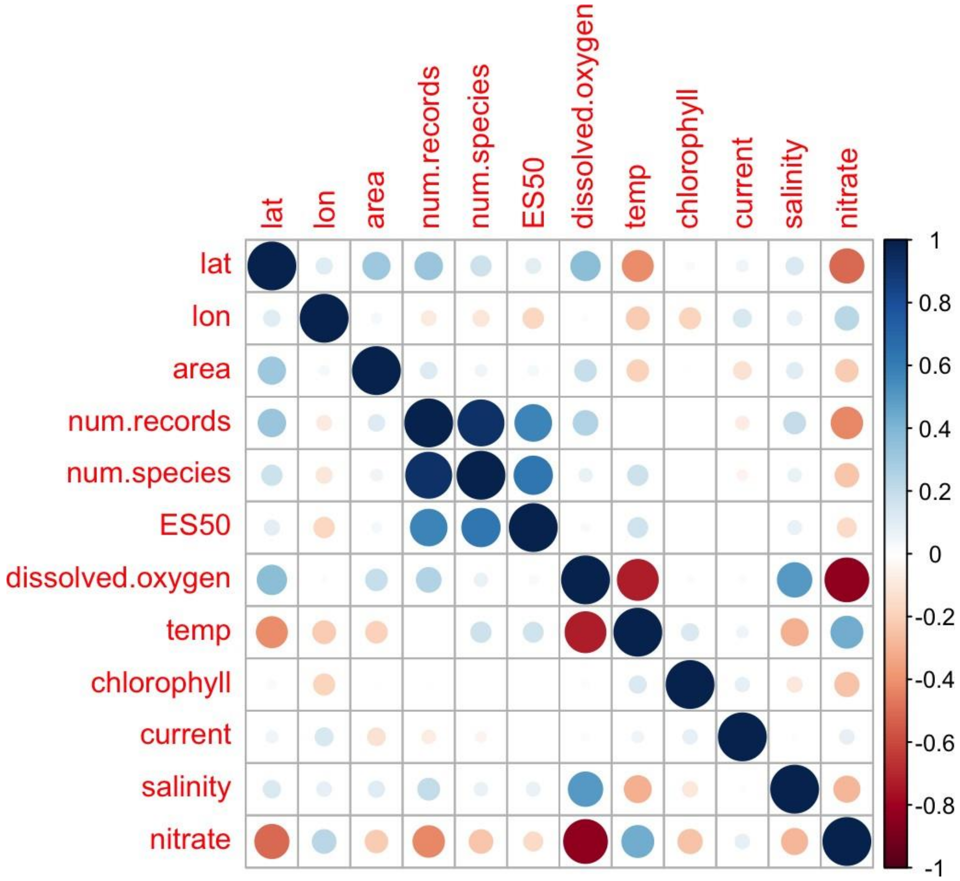


Deep water

Repeating the above analyses for deep-dwelling species.

Data load-in and visualization

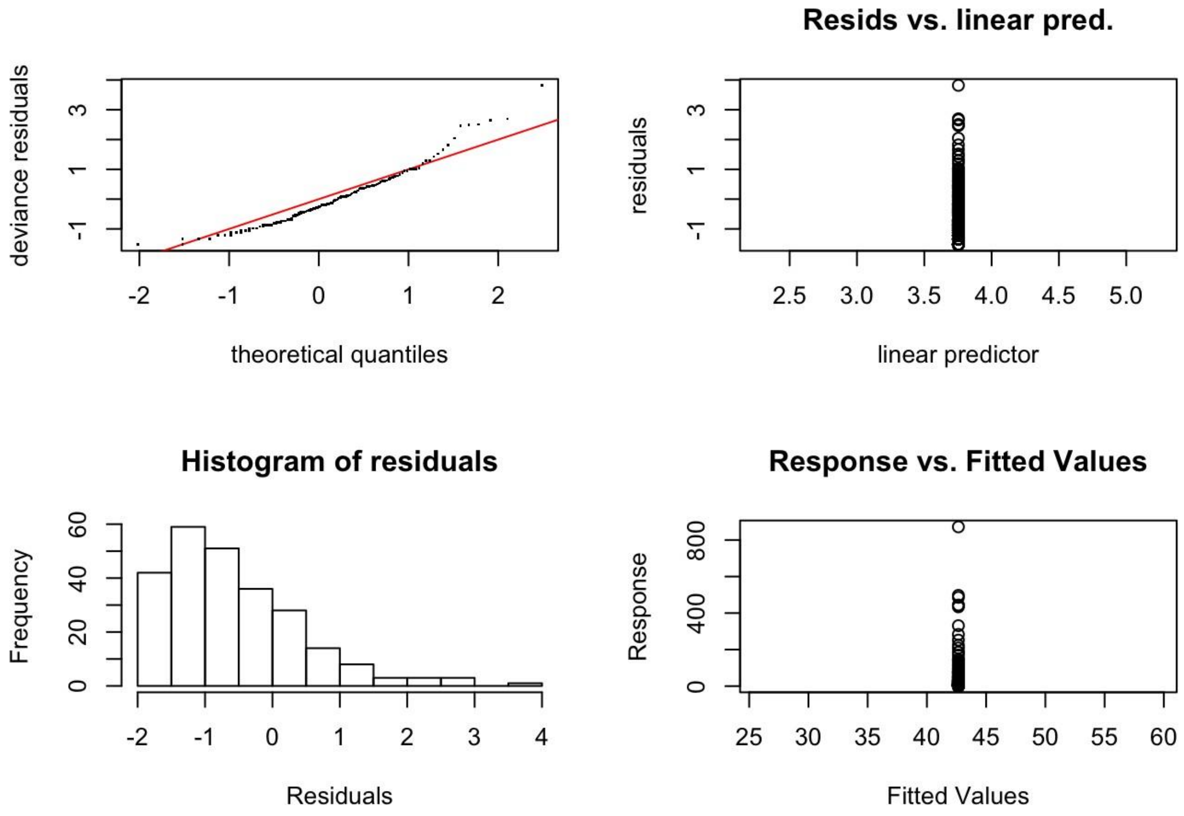
```
deep <- read.csv("deep.csv")
analysis.cols <- c("lat", "lon", "area", "num.records", "num.species", "ES50", "dissolved.oxygen", "temp", "chlorophyll", "current", "salinity", "nitrate")
deep <- deep[,analysis.cols]
deep <- deep[complete.cases(deep),]
corrplot(cor(deep))
```



GAMs for number of species, deep water

As above, we’re going to develop a number of GAMs including one for “intercept”, one for “latlon”, one for all environmental predictors (“env”), and then one for each individual predictor.

```
deep.numsp.intercept <- gam(num.species ~ 1, data = deep, family = "nb", method = "REML", select = TRUE)
gam.check(deep.numsp.intercept)
```

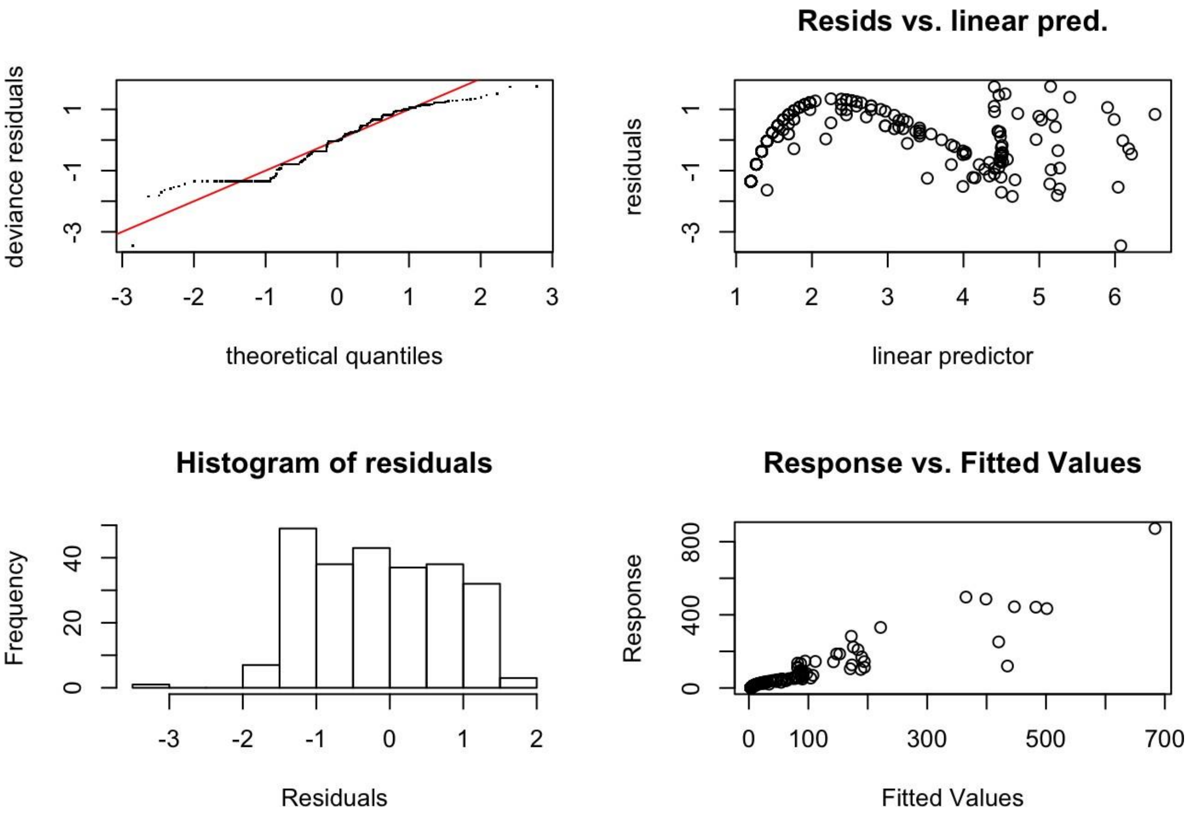


```
##
## Method: REML    Optimizer: outer newton
## full convergence after 4 iterations.
## Gradient range [1.064992e-07,1.064992e-07]
## (score 1115.547 & scale 1).
## Hessian positive definite, eigenvalue range [172.3917,172.3917].
## Model rank =  1 / 1
```

```
summary(deep.numsp.intercept)
```

```
##
## Family: Negative Binomial(0.446)
## Link function: log
##
## Formula:
## num.species ~ 1
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.75320    0.09555   39.28   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## R-sq.(adj) =  2.22e-16   Deviance explained = 1.42e-09%
## -REML = 1115.5  Scale est. = 1         n = 248
```

```
deep.numsp.numrec <- gam(num.species ~ s(num.records), data = deep, family = "nb",
 method = "REML", select = TRUE)
gam.check(deep.numsp.numrec)
```

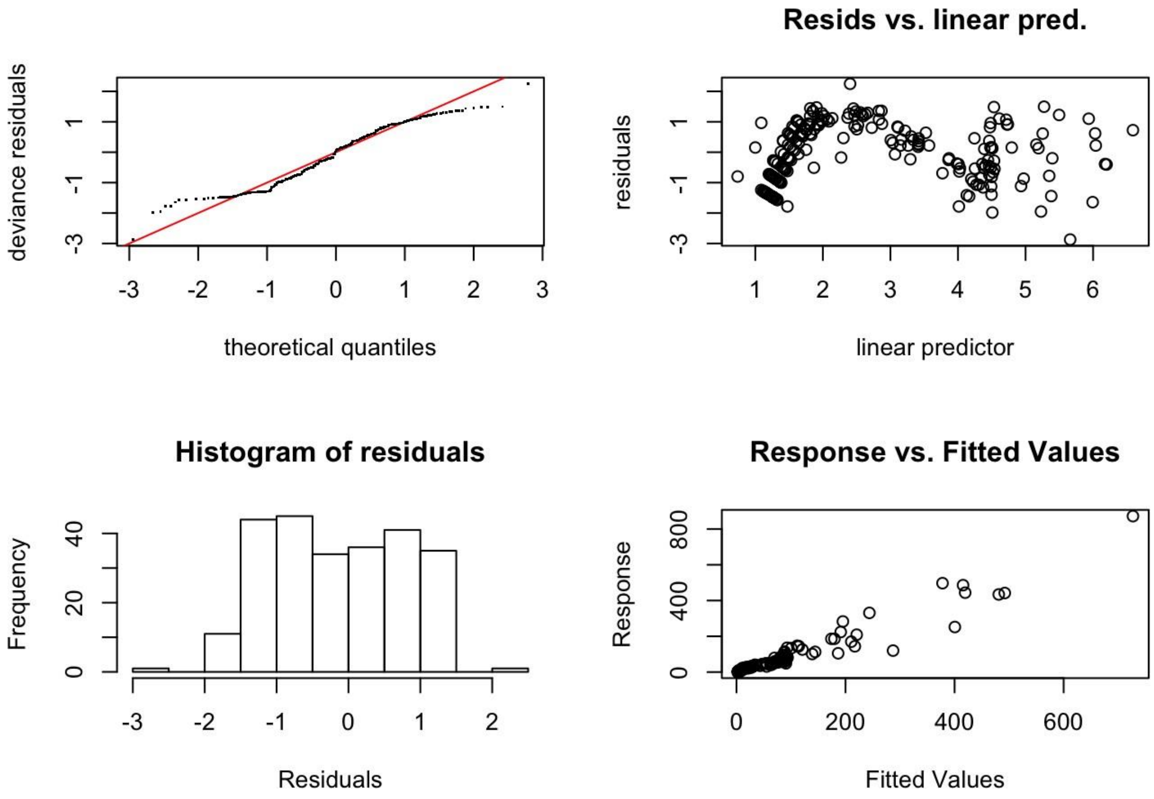


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 5 iterations.
## Gradient range [-7.448098e-08,3.599384e-07]
## (score 789.128 & scale 1).
## Hessian positive definite, eigenvalue range [0.4809454,38.37389].
## Model rank =  10 / 10
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                   k'  edf k-index p-value
## s(num.records) 9.00 8.69    0.27  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(deep.numsp.numrec)
```

```
##
## Family: Negative Binomial(11.031)
## Link function: log
##
## Formula:
## num.species ~ s(num.records)
##
## Parametric coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
##   (Intercept)    2.52278    0.03118    80.91    <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                          edf Ref.df Chi.sq  p-value
## s(num.records) 8.691          9     3245  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =   0.872    Deviance explained = 95.3%
## -REML = 789.13  Scale  est. = 1              n = 248
```

```
deep.numsp.latlon <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.records), da ta =
deep, family = "nb", method = "REML", select = TRUE) gam.check(deep.numsp.latlon)
```

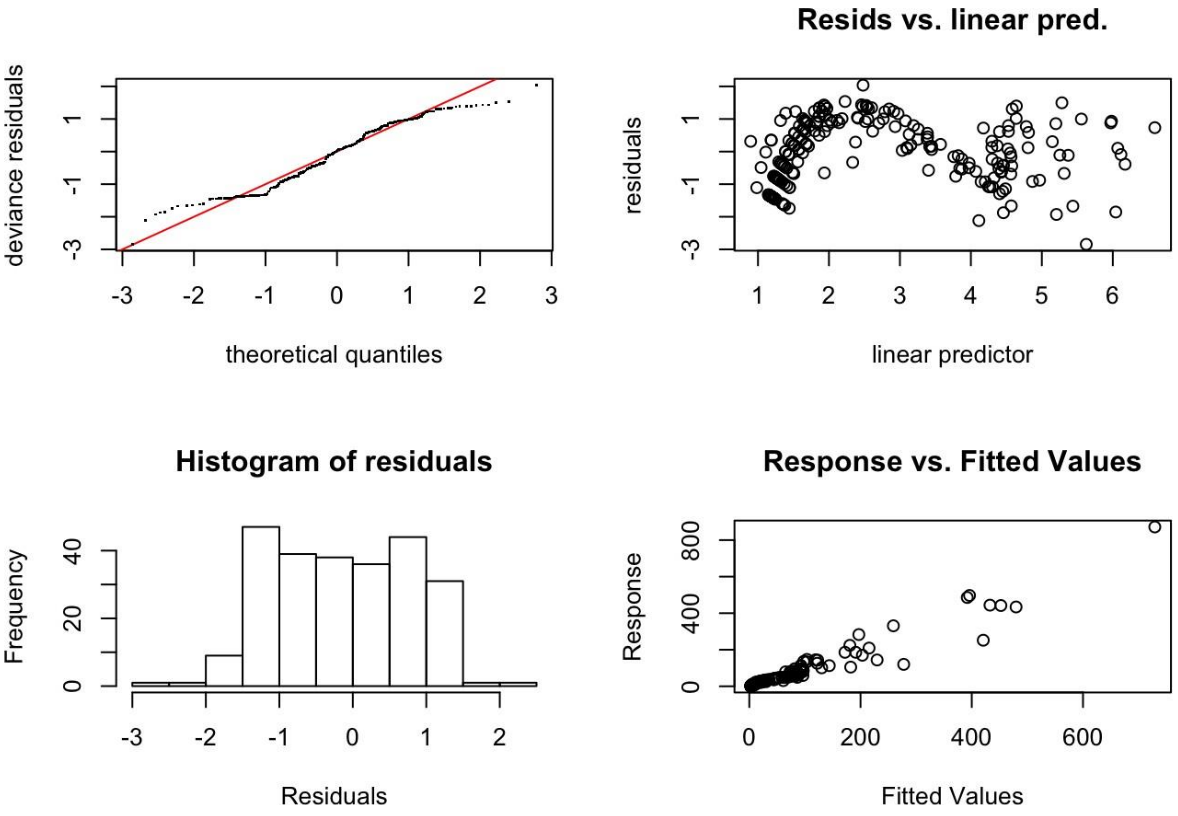


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 13 iterations.
## Gradient range [-2.084442e-06,1.813092e-05]
## (score 783.3275 & scale 1).
## Hessian positive definite, eigenvalue range [0.4865975,26.20744].
## Model rank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                     k'  edf k-index p-value
## s(lat,lon)       49.00 6.48    0.97    0.39
## s(num.records)    9.00 8.72    0.21  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(deep.numsp.latlon)
```

```
##
## Family: Negative Binomial(15.245)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") + s(num.records)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.5224     0.0294   85.81   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                  edf Ref.df  Chi.sq  p-value
## s(lat,lon)     6.482     49   28.61 4.42e-06 ***
## s(num.records) 8.721      9 3057.11  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.929   Deviance explained = 96.1%
## -REML = 783.33  Scale est. = 1         n = 248
```

```
deep.numsp.temp <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s(t
emp), data = deep, family = "nb", method = "REML", select = TRUE)
gam.check(deep.numsp.temp)
```

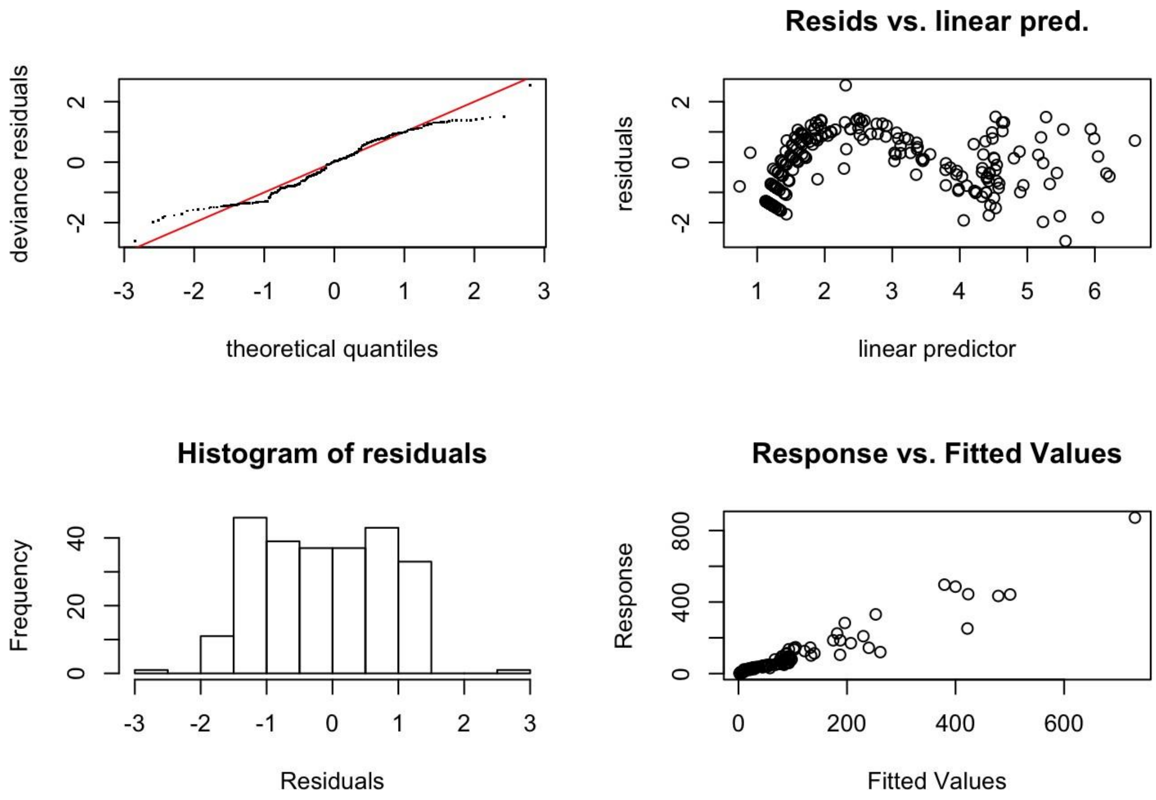


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 16 iterations.
## Gradient range [-0.0001830443,0.0002958337]
## (score 779.4414 & scale 1).
## Hessian positive definite, eigenvalue range [0.1047609,25.92906].
## Model rank =  68 / 68
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                    k'   edf k-index p-value
## s(lat,lon)      49.00  1.33    0.95    0.28
## s(num.records)   9.00  8.74    0.24  <2e-16 ***
## s(temp)          9.00  2.98    0.98    0.45
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(deep.numsp.temp)
```

```
##
## Family: Negative Binomial(16.141)
## Link function: log
##
## Formula:
## num.species ~ s(lat,  lon, bs = "sos") + s(num.records) + s(temp)
##
## Parametric coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
##   (Intercept)    2.52107     0.02916    86.47    <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                        edf Ref.df     Chi.sq   p-value
## s(lat,lon)          1.327       49      1.931      0.175
##  s(num.records)  8.739          9  3286.489   < 2e-16 ***
## s(temp)             2.977         9     24.634 1.36e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  R-sq.(adj)  =   0.932    Deviance explained = 96.2%
## -REML = 779.44 Scale  est. = 1               n = 248
```

```
deep.numsp.oxygen <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.records) +
s(dissolved.oxygen), data = deep, family = "nb", method = "REML", select = TRUE)
gam.check(deep.numsp.oxygen)
```

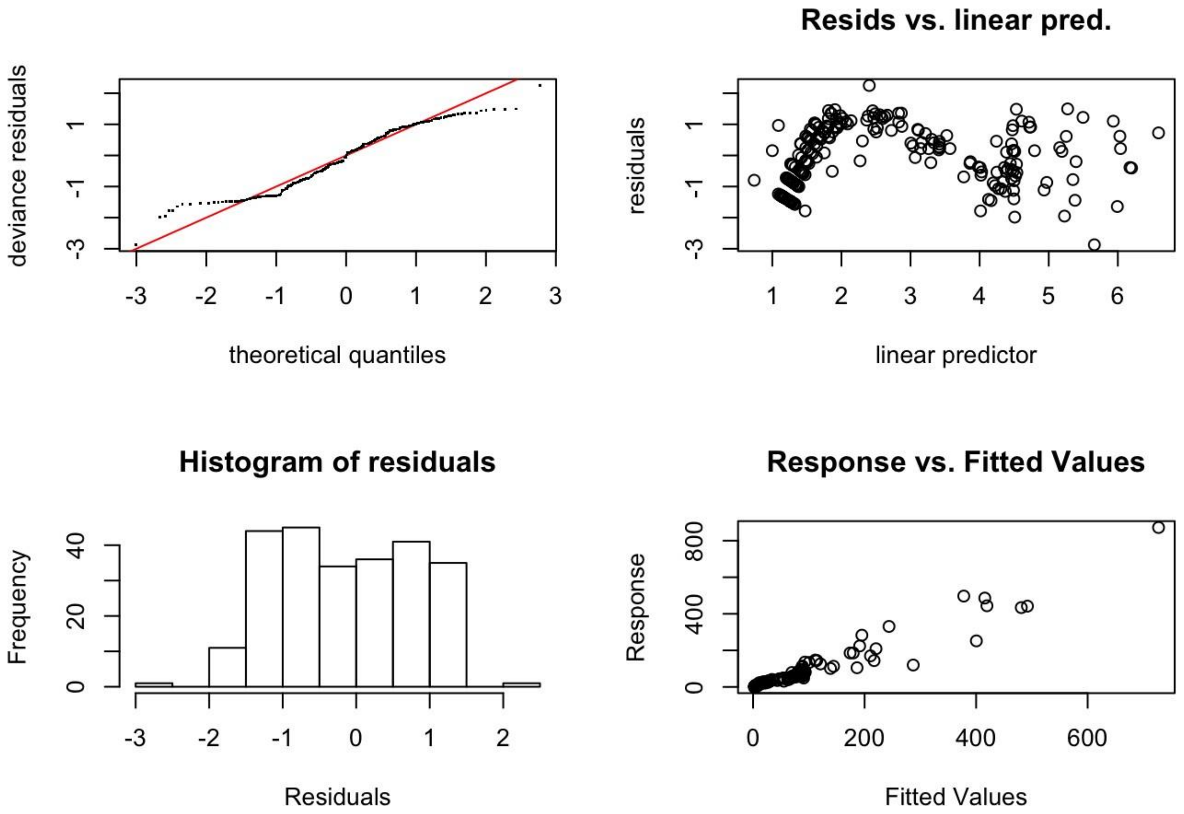


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 15 iterations.
## Gradient range [-4.828611e-06,3.365376e-06]
## (score 778.8793 & scale 1).
## Hessian positive definite, eigenvalue range [0.07966418,27.44467].
## Model rank =  68 / 68
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                         k'   edf k-index p-value
## s(lat,lon)          49.000 0.899    0.96    0.36
## s(num.records)       9.000 8.740    0.21  <2e-16 ***
## s(dissolved.oxygen)  9.000 1.799    0.97    0.49
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(deep.numsp.oxygen)
```

```
##
## Family: Negative Binomial(15.476)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s(dissolved.oxygen)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.5228     0.0293    86.1   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                        edf Ref.df   Chi.sq  p-value
## s(lat,lon)          0.8991     49    1.285    0.178
## s(num.records)      8.7404      9 3329.104  < 2e-16 ***
## s(dissolved.oxygen) 1.7995      9   23.743 2.24e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.929   Deviance explained = 96.1%
## -REML = 778.88  Scale est. = 1         n = 248
```

```
deep.numsp.chlorophyll <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.record
s) +  s(chlorophyll), data = deep, family = "nb", method = "REML", select = TRUE)
gam.check(deep.numsp.chlorophyll)
```

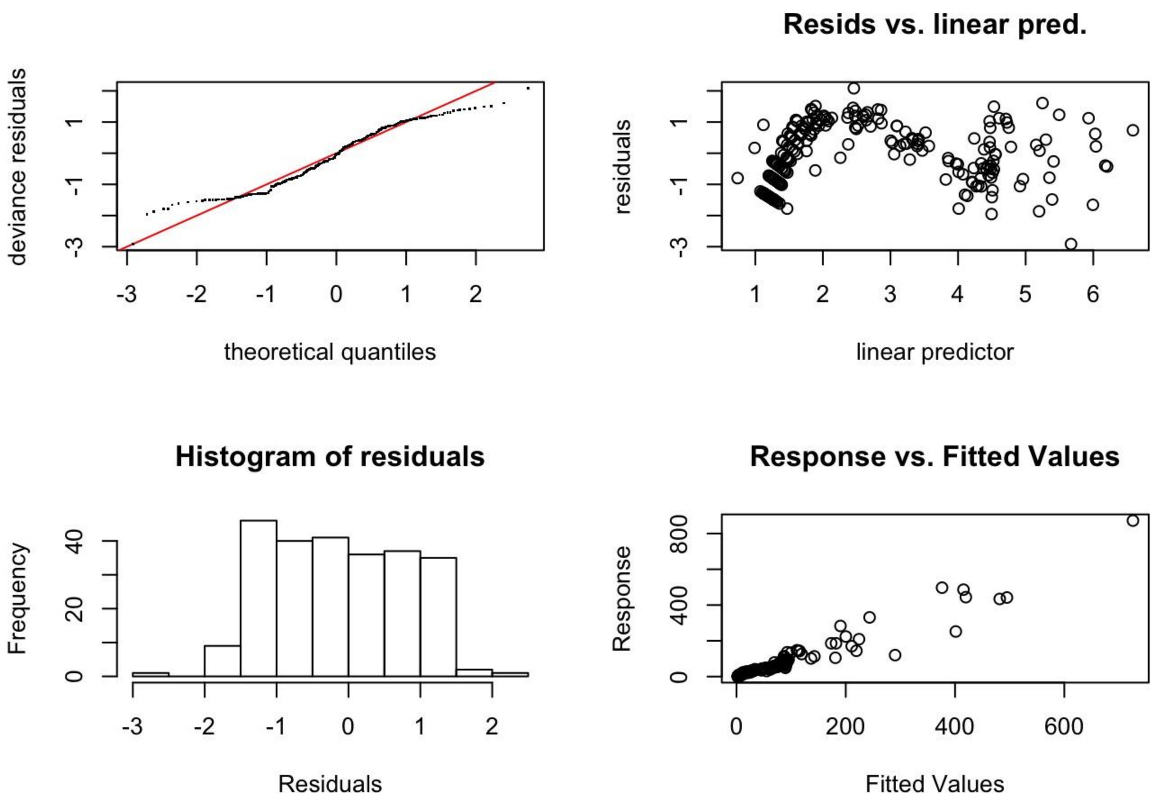


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 14 iterations.
## Gradient range [-1.60812e-05,3.281463e-06]
## (score 783.3275 & scale 1).
## Hessian positive definite, eigenvalue range [1.238047e-05,26.20742].
## Model rank =  68 / 68
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                         k'      edf k-index p-value
## s(lat,lon)        4.90e+01 6.48e+00    0.97    0.40
## s(num.records) 9.00e+00 8.72e+00    0.21  <2e-16 ***
## s(chlorophyll) 9.00e+00 9.72e-05    0.99    0.54
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(deep.numsp.chlorophyll)
```

```
##
## Family: Negative Binomial(15.245)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") +  s(num.records) +  s(chlorophyll)
##
## Parametric coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
##  (Intercept)     2.5224      0.0294    85.81   <2e-16 ***
## ---
## Signif. codes:   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                              edf  Ref.df   Chi.sq   p-value
## s(lat,lon)       6.482e+00       49      28.61 4.42e-06 ***
## s(num.records) 8.721e+00        9  3057.11  <  2e-16  ***
##  s(chlorophyll)  9.717e-05        9 0.00  0.535
## ---
## Signif. codes:   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  R-sq.(adj)  =   0.929    Deviance explained = 96.1%
## -REML = 783.33Scale  est. = 1                  n = 248
```

```
deep.numsp.current <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.records) +
s(current), data = deep, family = "nb", method = "REML", select = TRUE)
gam.check(deep.numsp.current)
```

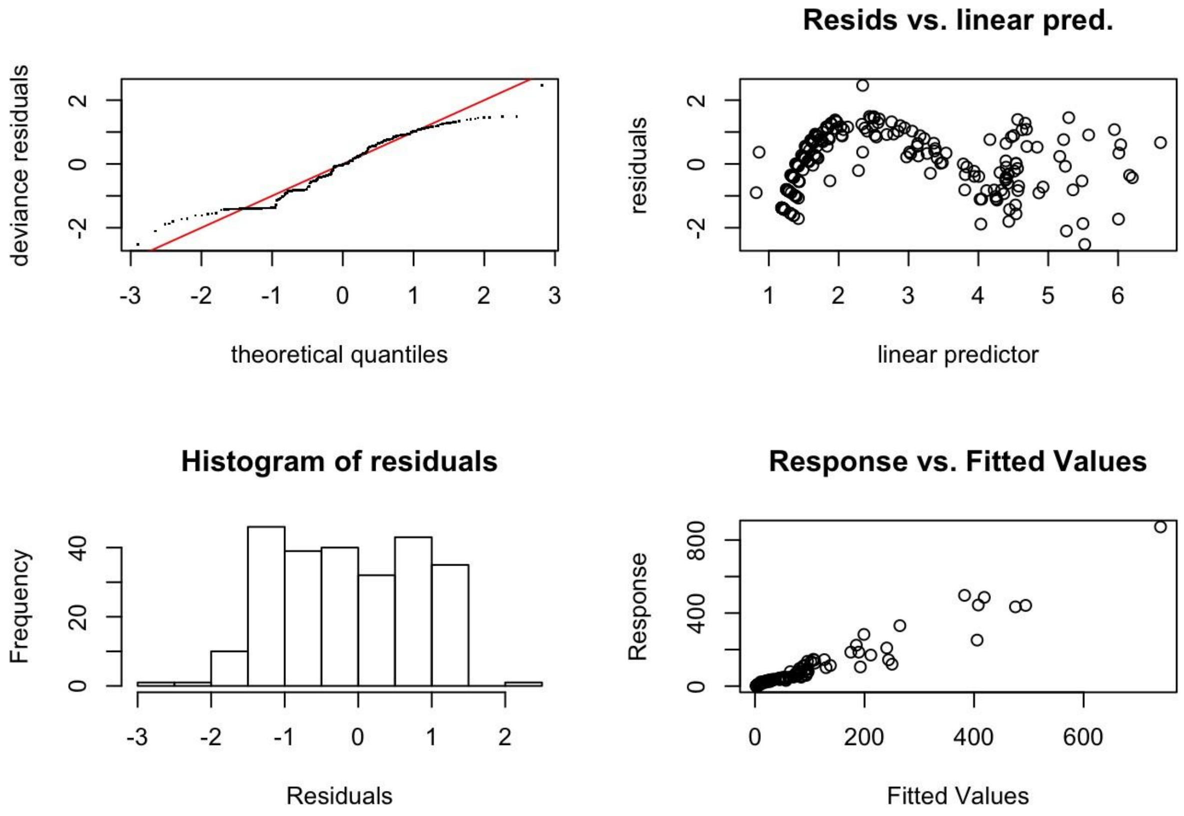


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 12 iterations.
## Gradient range [-7.866149e-05,0.0006824098]
## (score 783.122 & scale 1).
## Hessian positive definite, eigenvalue range [3.296297e-05,26.16876].
## Model rank =  68 / 68
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                      k'   edf k-index p-value
## s(lat,lon)       49.000 6.353    0.97    0.35
## s(num.records)    9.000 8.720    0.21  <2e-16 ***
## s(current)        9.000 0.708    0.98    0.54
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(deep.numsp.current)
```

```
##
## Family: Negative Binomial(15.378)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s(current)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.52214    0.02936   85.91   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                   edf Ref.df   Chi.sq  p-value
## s(lat,lon)     6.3530     49   28.396 3.48e-06 ***
## s(num.records) 8.7198      9 3072.017  < 2e-16 ***
## s(current)     0.7081      9    1.351    0.139
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.928   Deviance explained = 96.2%
## -REML = 783.12  Scale est. = 1         n = 248
```

```
deep.numsp.salinity <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.records) +
s(salinity), data = deep, family = "nb", method = "REML", select = TRUE)
gam.check(deep.numsp.salinity)
```

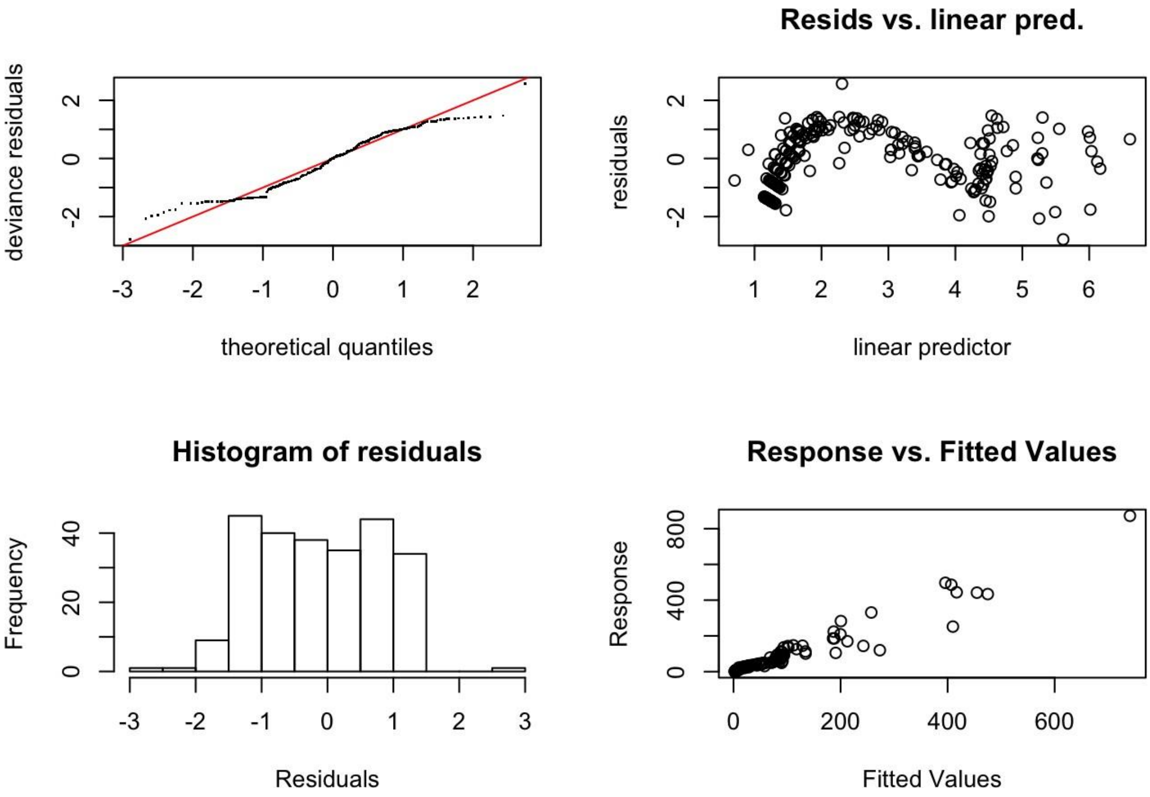


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 19 iterations.
## Gradient range [-4.890114e-05,6.436646e-05]
## (score 778.6788 & scale 1).
## Hessian positive definite, eigenvalue range [4.896408e-05,26.32655].
## Model rank =  68 / 68
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                      k'      edf k-index p-value
## s(lat,lon)     49.00000  0.00062    0.95    0.32
## s(num.records)  9.00000  8.74747    0.19  <2e-16 ***
## s(salinity)     9.00000  2.76874    0.92    0.20
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(deep.numsp.salinity)
```

```
##
## Family: Negative Binomial(16.098)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s(salinity)
##
## Parametric coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.52442    0.02907    86.83    <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                            edf  Ref.df    Chi.sq   p-value
## s(lat,lon)        0.0006202      49     0.001   0.391
## s(num.records) 8.7474679         9 3390.383   < 2e-16 ***
## s(salinity)      2.7687403        9     35.507 6.42e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =   0.936    Deviance explained = 96.2%
## -REML = 778.68  Scale est. = 1              n = 248
```

```
deep.numsp.nitrate <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.records) +
s(nitrate), data = deep, family = "nb", method = "REML", select = TRUE)
gam.check(deep.numsp.nitrate)
```

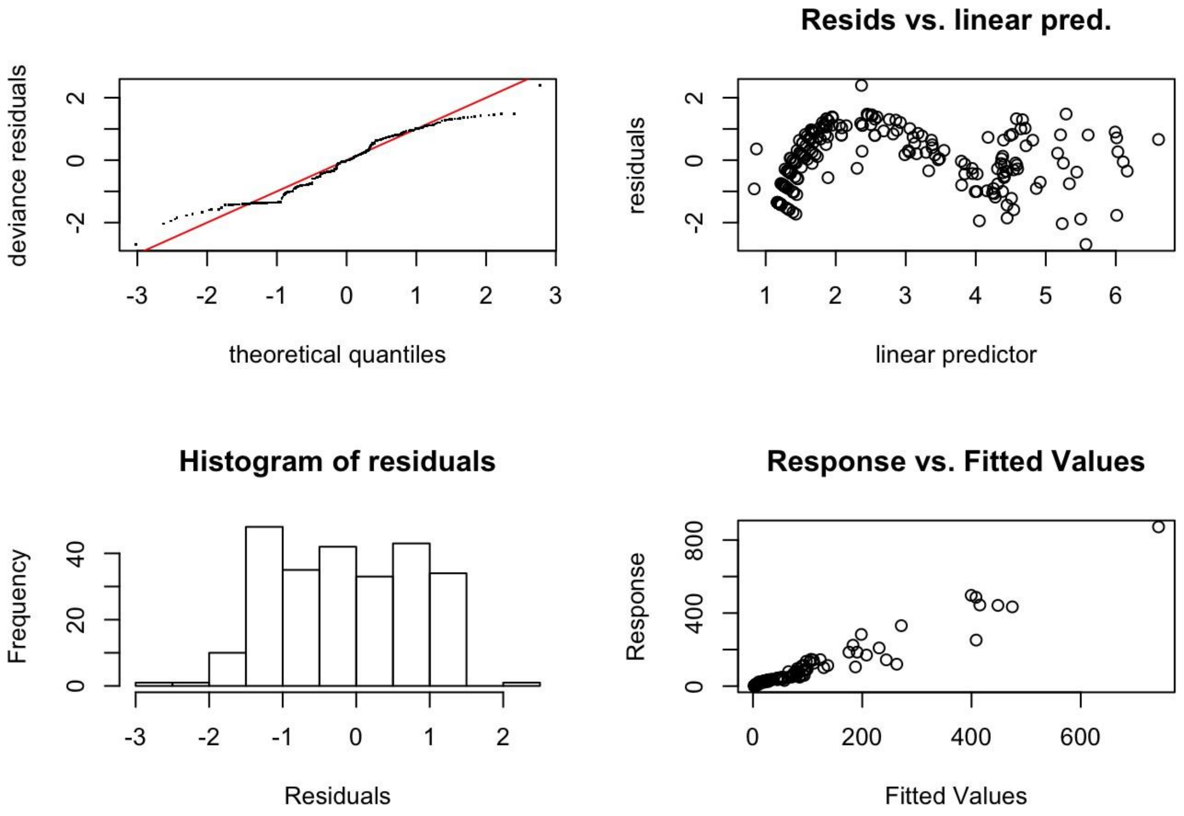


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 15 iterations.
## Gradient range [-0.000171565,7.103026e-05]
## (score 778.9375 & scale 1).
## Hessian positive definite, eigenvalue range [0.000171518,26.49127].
## Model rank =  68 / 68
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                     k'    edf k-index p-value
## s(lat,lon)      49.000  2.016    0.96    0.28
## s(num.records)   9.000  8.742    0.22  <2e-16 ***
## s(nitrate)       9.000  0.946    0.93    0.22
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(deep.numsp.nitrate)
```

```
##
## Family: Negative Binomial(15.952)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s(nitrate)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.52313    0.02915   86.56   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                   edf Ref.df   Chi.sq  p-value
## s(lat,lon)     2.0160     49    4.562   0.0495 *
## s(num.records) 8.7424      9 3467.571  < 2e-16 ***
## s(nitrate)     0.9461      9   17.430 1.87e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.935   Deviance explained = 96.2%
## -REML = 778.94  Scale est. = 1         n = 248
```

```
deep.numsp.env <- gam(num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s(te
mp) + s(dissolved.oxygen) + s(chlorophyll) + s(current) + s(salinity) + s(nitrat e),
data = deep, family = "nb", method = "REML", select = TRUE)
gam.check(deep.numsp.env)
```



```
## 
## Method: REML   Optimizer: outer newton
## full convergence after 13 iterations.
## Gradient range [-0.0003393487,0.0001655968]
## (score 778.3568 & scale 1).
## eigenvalue range [-3.960114e-05,26.01022].
## Model rank =  113 / 113 
## 
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
## 
##                          k'      edf k-index p-value    
## s(lat,lon)         4.90e+01 5.61e-01    0.96    0.33    
## s(num.records)     9.00e+00 8.74e+00    0.21  <2e-16 ***
## s(temp)            9.00e+00 1.29e+00    0.99    0.51    
## s(dissolved.oxygen) 9.00e+00 2.50e-04    0.99    0.55    
## s(chlorophyll)     9.00e+00 2.23e-04    1.00    0.63    
## s(current)         9.00e+00 1.33e-01    0.96    0.37    
## s(salinity)        9.00e+00 2.34e+00    0.93    0.18    
## s(nitrate)         9.00e+00 3.97e-04    0.94    0.30    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(deep.numsp.env)
```

```
##
## Family: Negative Binomial(16.363)
## Link function: log
##
## Formula:
## num.species ~ s(lat, lon, bs = "sos") + s(num.records) + s(temp) +
##       s(dissolved.oxygen) + s(chlorophyll) +  s(current)  +  s(salinity)  +
##       s(nitrate)
##
## Parametric coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
##   (Intercept)    2.52257      0.02904     86.86    <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                                      edf  Ref.df     Chi.sq   p-value
##  s(lat,lon)               0.5611688       49       0.730  0.206615
##  s(num.records)         8.7441673         9  3279.706    < 2e-16  ***
##  s(temp)                  1.2898582         9       3.262  0.048569  *
##   s(dissolved.oxygen) 0.0002496         9       0.000  0.479536
##  s(chlorophyll)          0.0002232         9       0.000  0.751210
##  s(current)               0.1331032         9       0.150  0.277828
##  s(salinity)              2.3436500         9      12.671  0.000285  ***
##  s(nitrate)               0.0003972         9       0.000  0.507870
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  R-sq.(adj)  =   0.938    Deviance explained = 96.3%
## -REML = 778.36Scale  est.  =  1                n =  248
```

Model selection for number of species, deep water

```
deep.numsp.models <- list(deep.numsp.intercept = deep.numsp.intercept,
                               deep.numsp.numrec = deep.numsp.numrec,
                             deep.numsp.latlon = deep.numsp.latlon,
                             deep.numsp.temp = deep.numsp.temp,
                             deep.numsp.oxygen = deep.numsp.oxygen,
                             deep.numsp.chlorophyll = deep.numsp.chlorophyll,
                             deep.numsp.current = deep.numsp.current,
                             deep.numsp.salinity = deep.numsp.salinity,
                             deep.numsp.nitrate = deep.numsp.nitrate,
                             deep.numsp.env = deep.numsp.env)
deep.numsp.aic.df <- data.frame(Model = names(deep.numsp.models),
                                   AIC = sapply(deep.numsp.models, function(x) x$aic),
                                  akaike.weights(sapply(deep.numsp.models, function(x) x
$aic)))

deep.numsp.aic.df <- deep.numsp.aic.df[order(deep.numsp.aic.df$AIC),]
deep.numsp.aic.df$Cumulative.Weight <- cumsum(deep.numsp.aic.df$weights)

kable(deep.numsp.aic.df, row.names = FALSE)
```

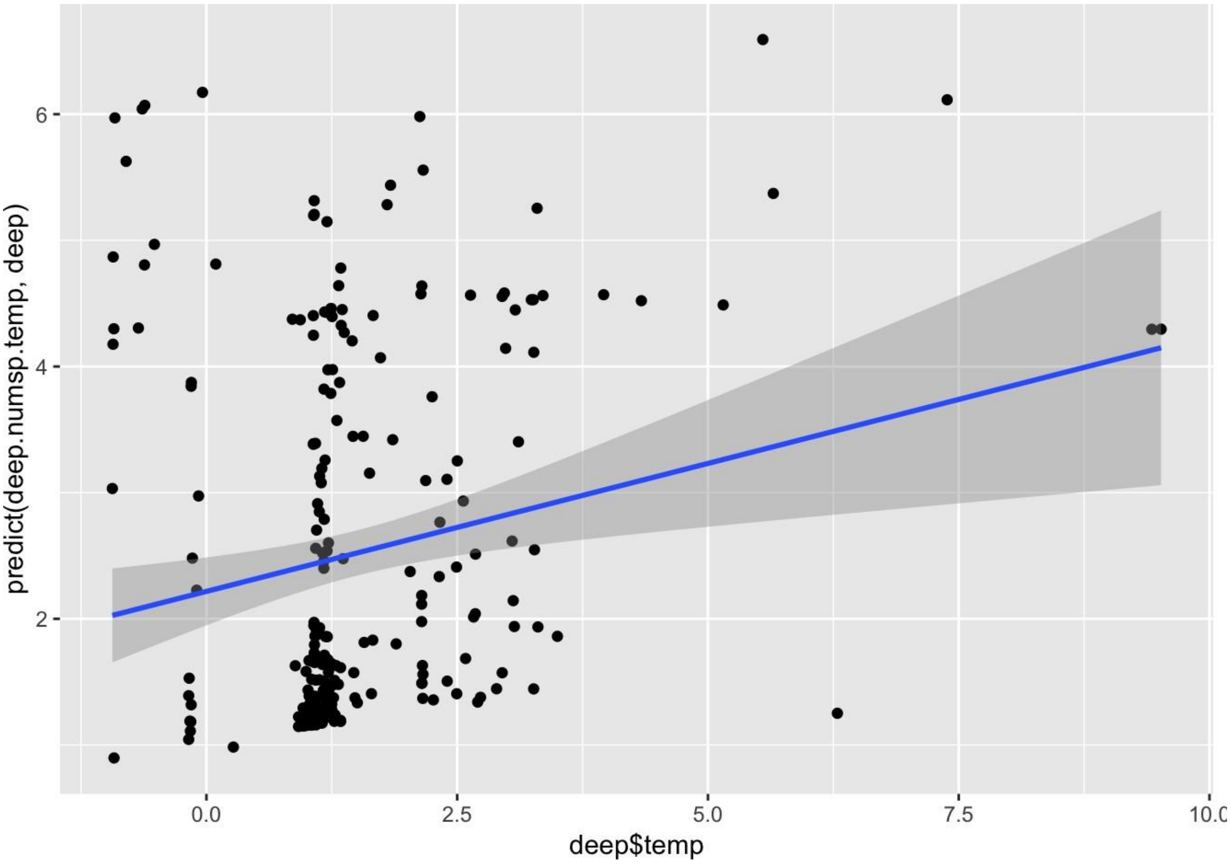
Model	AIC	deltaAIC	rel.LL	weights	Cumulative.Weight
deep.numsp.env	1503.752	0.0000000	1.0000000	0.3916404	0.3916404
deep.numsp.salinity	1504.519	0.7670844	0.6814433	0.2668807	0.6585211
deep.numsp.temp	1505.273	1.5213809	0.4673436	0.1830306	0.8415517
deep.numsp.oxygen	1507.051	3.2996823	0.1920804	0.0752264	0.9167781
deep.numsp.nitrate	1507.071	3.3192946	0.1902061	0.0744924	0.9912705
deep.numsp.current	1513.226	9.4747427	0.0087616	0.0034314	0.9947019
deep.numsp.latlon	1513.744	9.9923088	0.0067639	0.0026490	0.9973510
deep.numsp.chlorophyll	1513.744	9.9924113	0.0067636	0.0026489	0.9999998
deep.numsp.numrec	1533.111	29.3590199	0.0000004	0.0000002	1.0000000
deep.numsp.intercept	2230.235	726.4832924	0.0000000	0.0000000	1.0000000

```
write.csv(deep.numsp.aic.df, file = "deep.numsp.aic.csv")
```

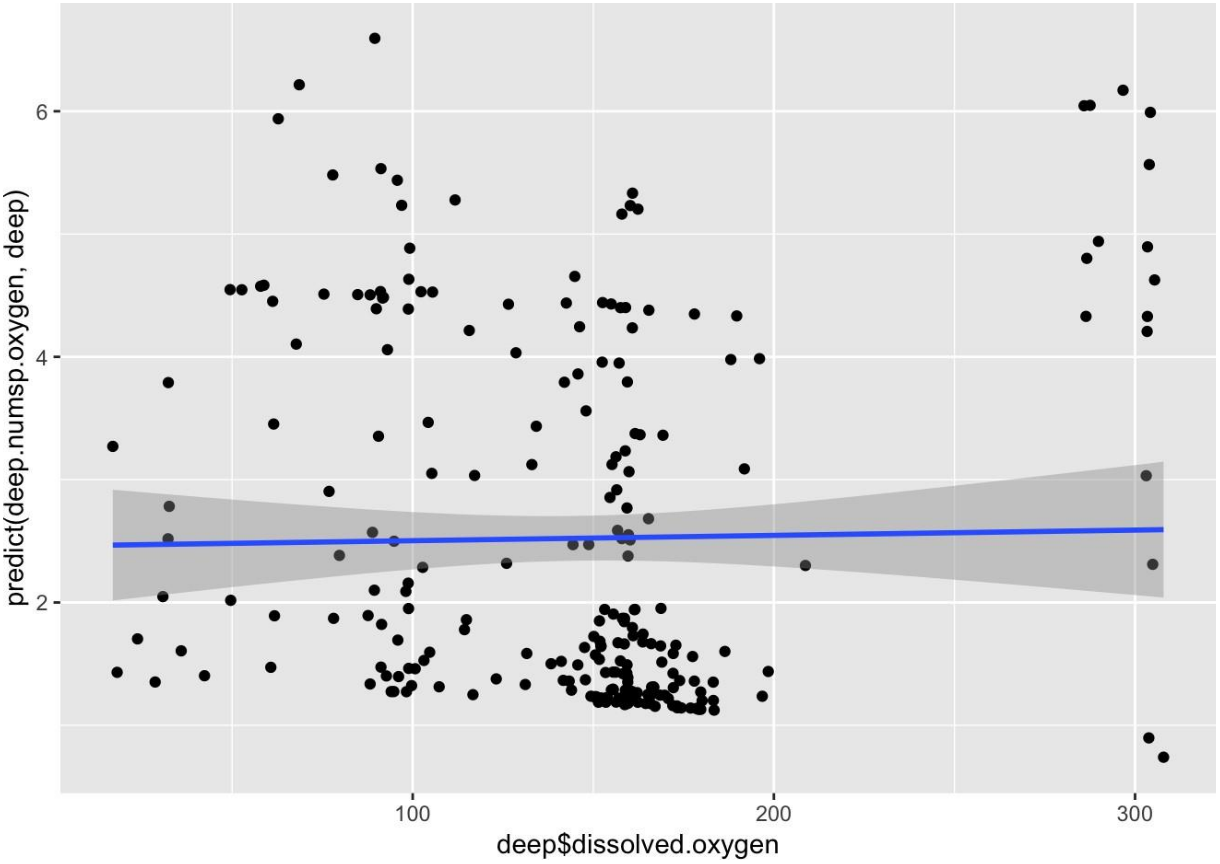
We find that the best model is the one that contains all environmental predictor variables. The second best model is one that contains only the effects of oxygen, but the delta AIC between that model and the best model is 7.18, indicating that the oxygen-only model is a relatively poor fit to the data. We find strong evidence that the “env” model outperforms the model using spatial autocorrelation alone (delta AIC = 10.18).

Plots for number of species, deep water

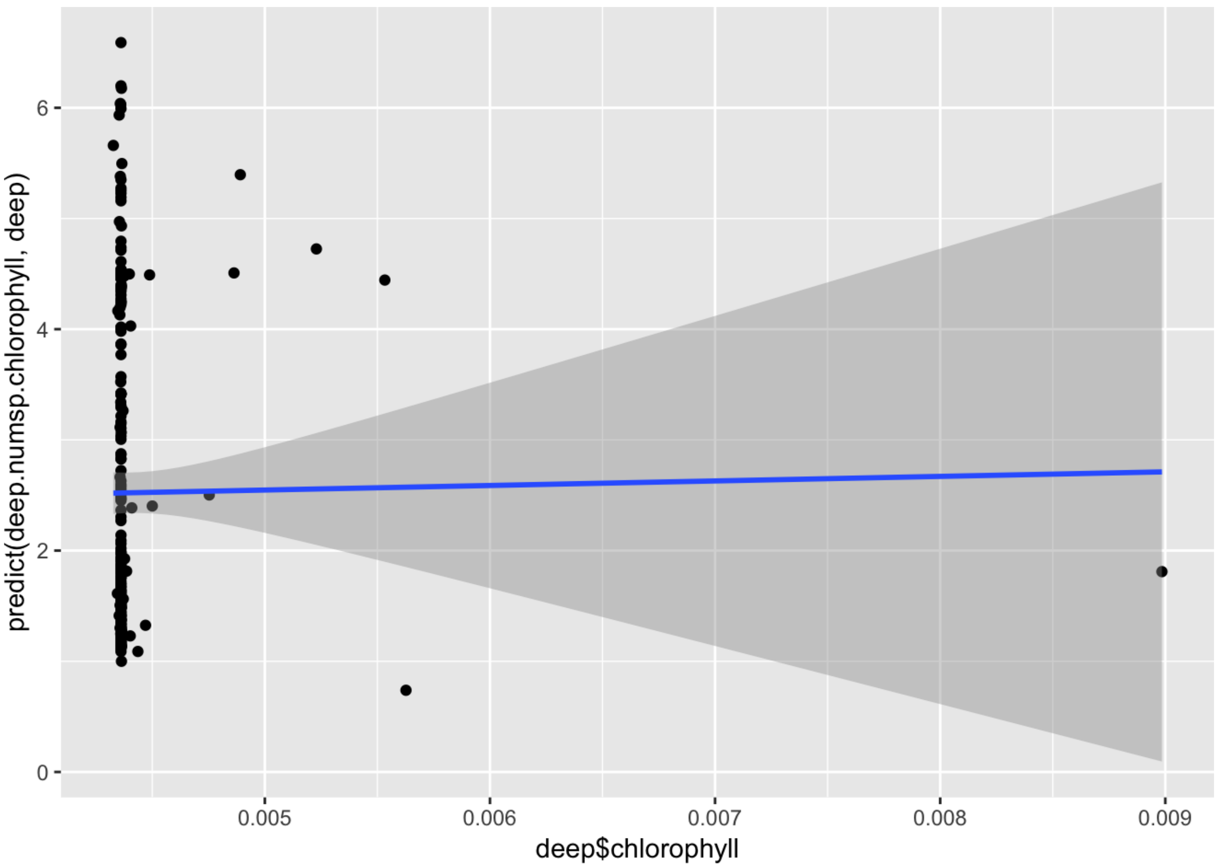
```
qplot(deep$temp, predict(deep.numsp.temp, deep)) + geom_smooth(method = "gam")
```



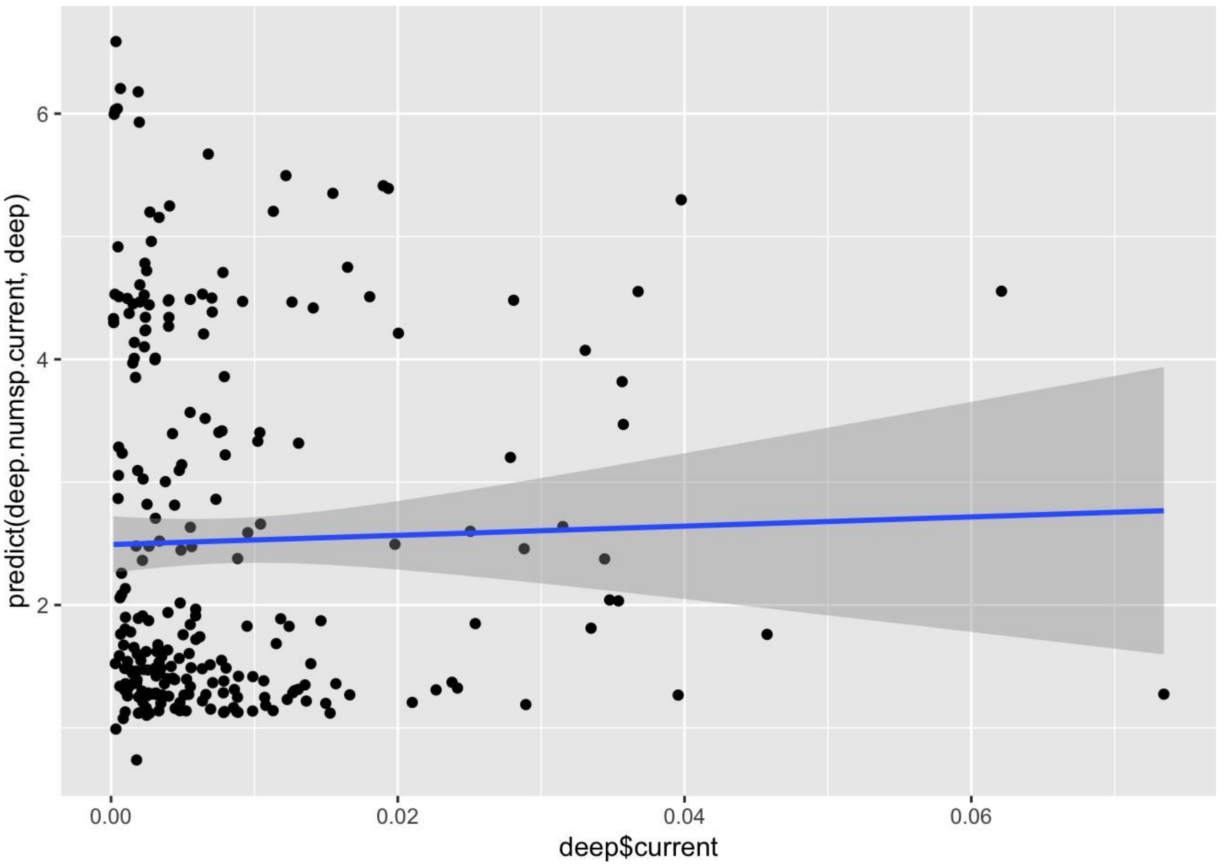
```
qplot(deep$dissolved.oxygen, predict(deep.numsp.oxygen, deep)) + geom_smooth(method
= "gam")
```



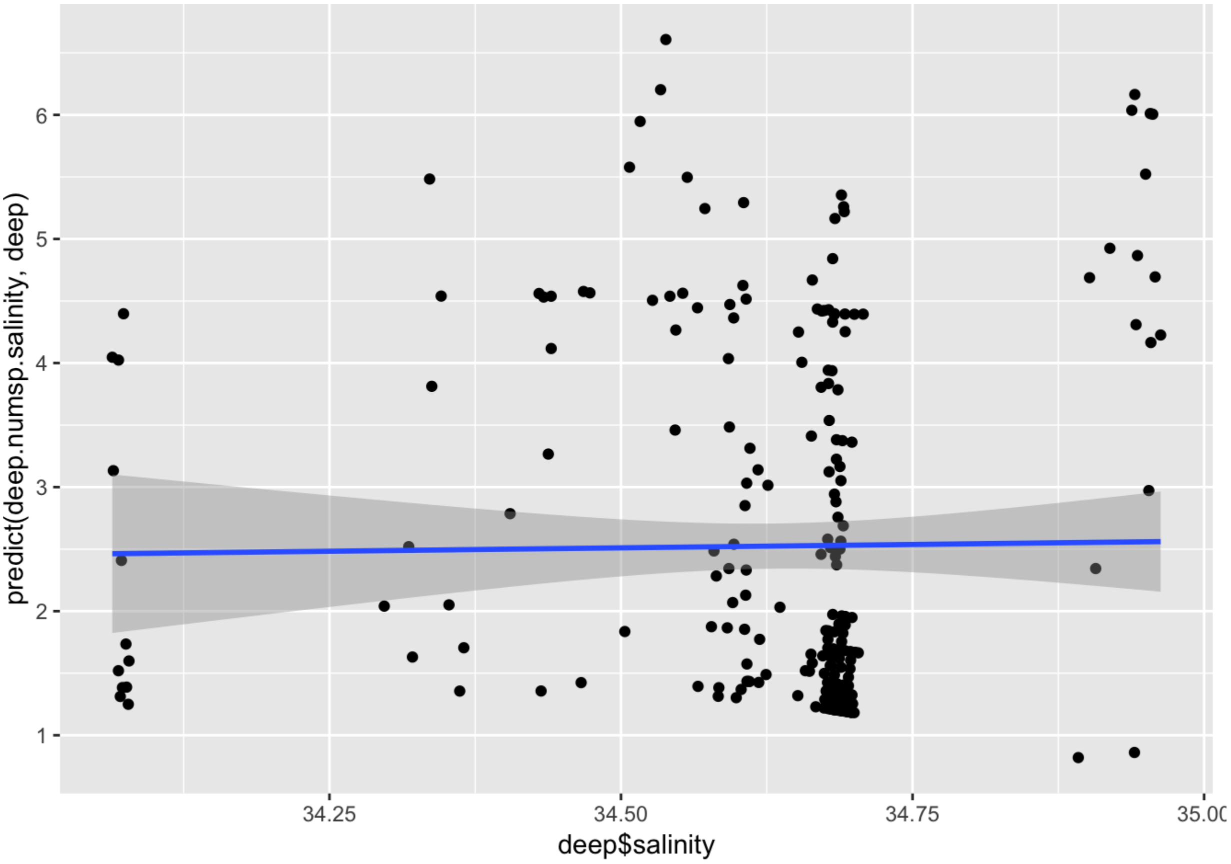
```
qplot(deep$chlorophyll, predict(deep.numsp.chlorophyll, deep)) + geom_smooth(method
= "gam")
```



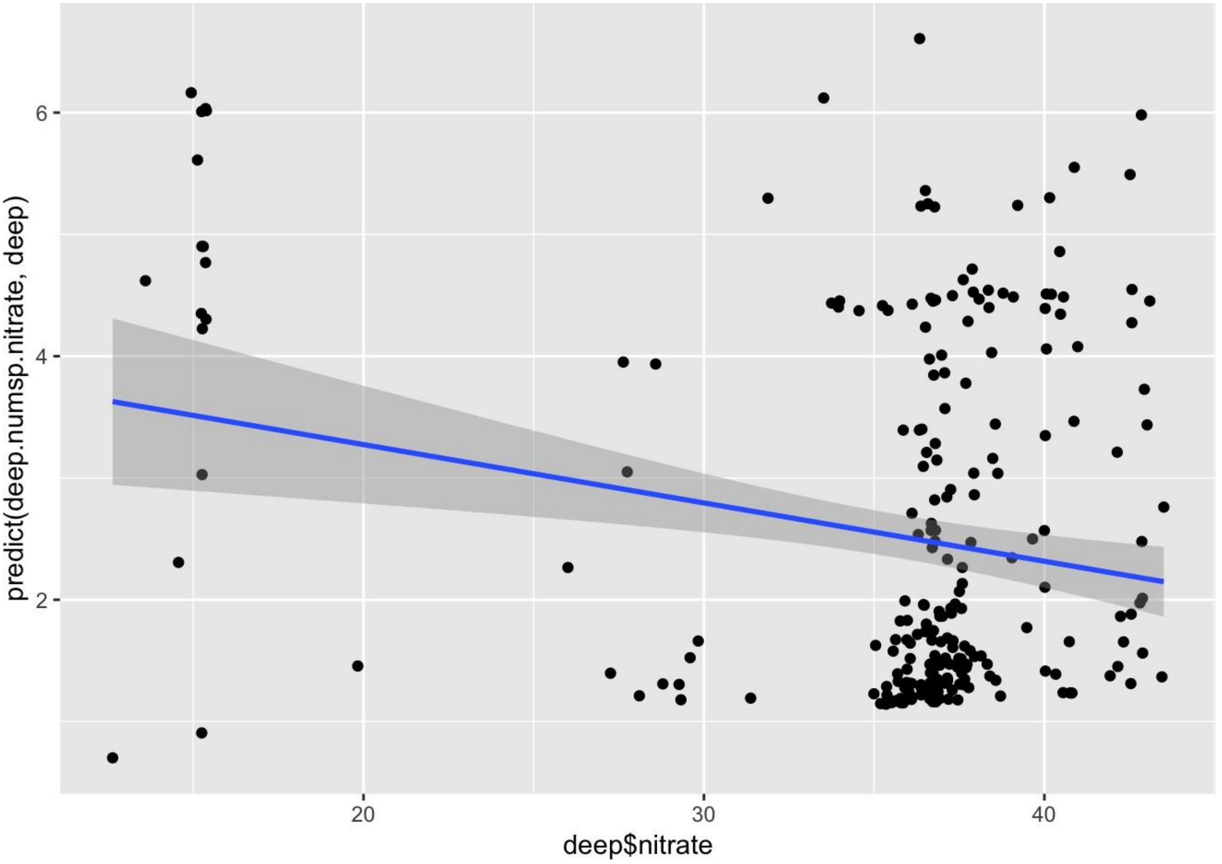
```
qplot(deep$current, predict(deep.numsp.current, deep)) + geom_smooth(method = "gam"
)
```



```
qplot(deep$salinity, predict(deep.numsp.salinity, deep)) + geom_smooth(method  =  "ga
m")
```



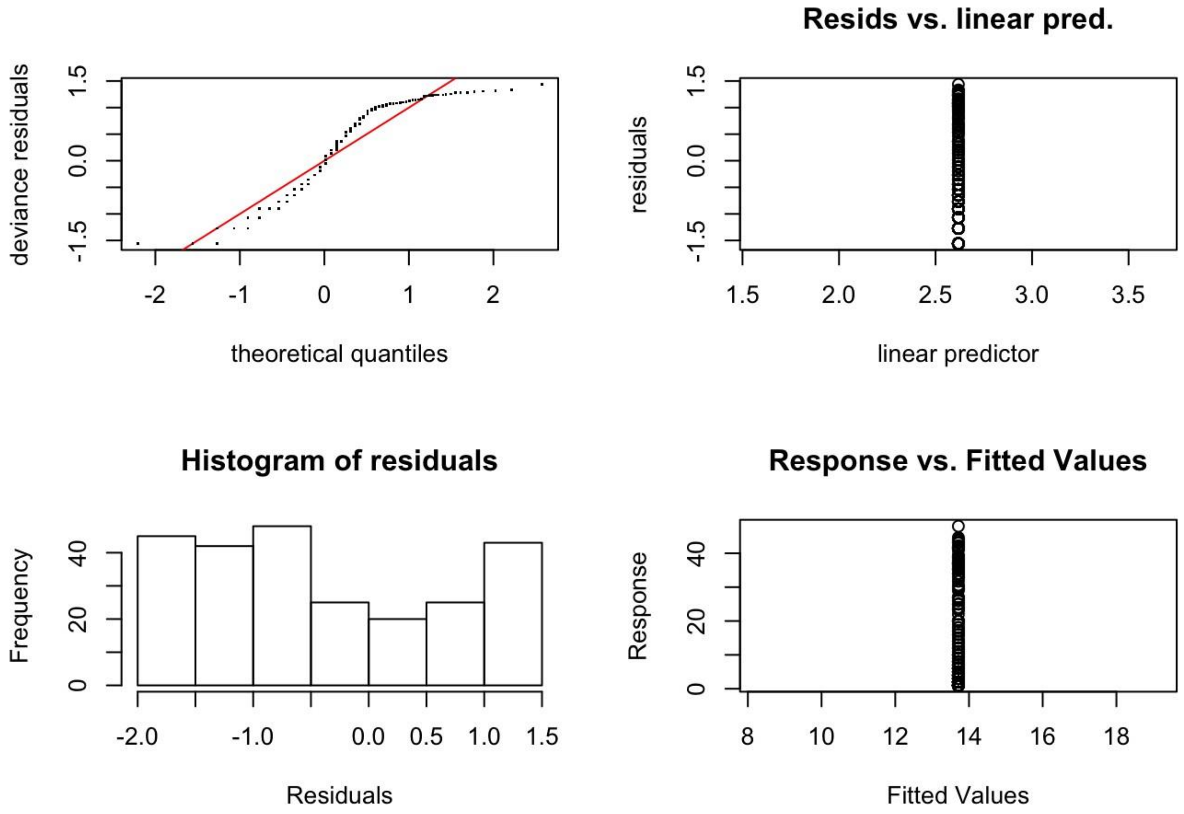
```
qplot(deep$nitrate, predict(deep.numsp.nitrate, deep)) + geom_smooth(method = "gam"
)
```



GAMs for ES50, deep water

We're now doing GAMs for the effects of the environment on the number of species estimated from rarefaction analyses. As above, we remove the "no.records" term because it is already included in the calculation of ES50.

```
deep.es50.intercept <- gam(ES50 ~ 1, data = deep, family = "nb", method = "REML", s
elect = TRUE)
gam.check(deep.es50.intercept)
```

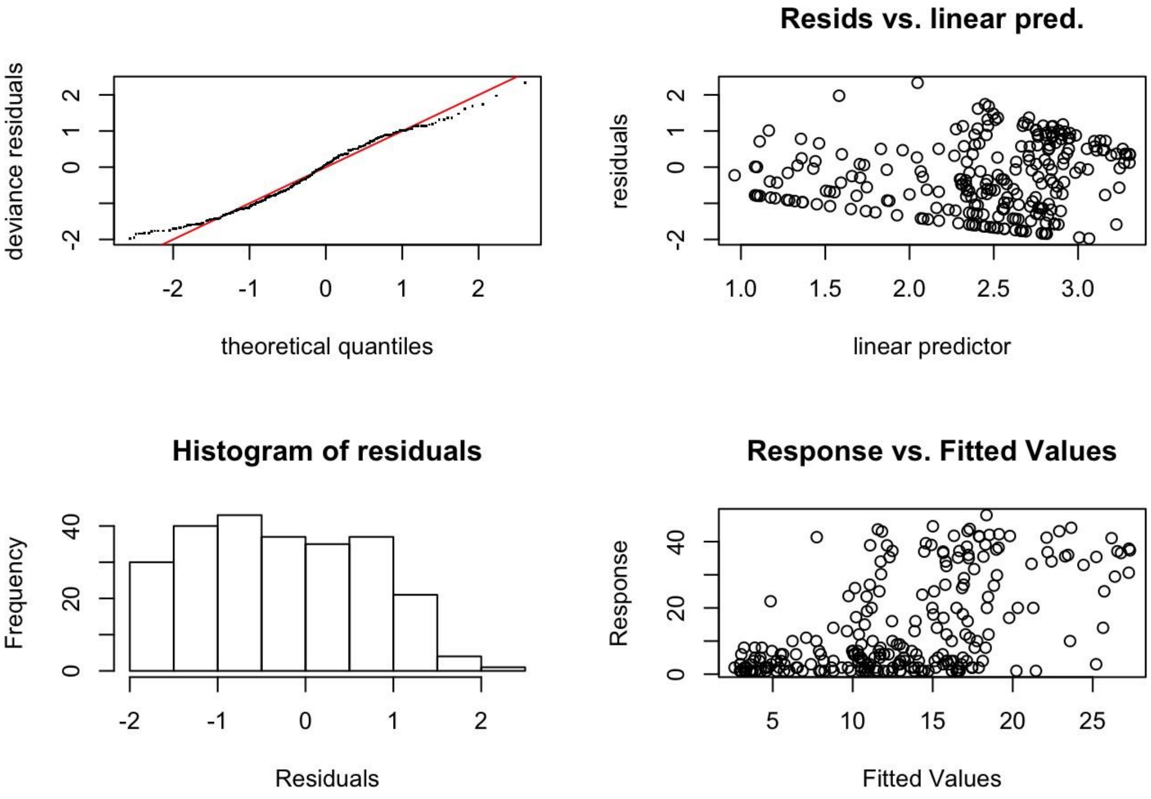


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 3 iterations.
## Gradient range [2.716585e-10,2.716585e-10]
## (score 906.5347 & scale 1).
## Hessian positive definite, eigenvalue range [130.3561,130.3561].
## Model rank =  1 / 1
```

```
summary(deep.es50.intercept)
```

```
##
## Family: Negative Binomial(0.863)
## Link function: log
##
##   Formula:
## ES50 ~ 1
##
## Parametric coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.61829     0.07046    37.16    <2e-16 ***
## ---
## Signif. codes:    0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## R-sq.(adj) =          0     Deviance explained = 1.93e-08%
## -REML = 906.53     Scale est. = 1              n = 248
```

```
deep.es50.latlon <- gam(ES50 ~ s(lat, lon, bs = "sos") , data = deep, family = "nb"
, method = "REML", select = TRUE)
gam.check(deep.es50.latlon)
```

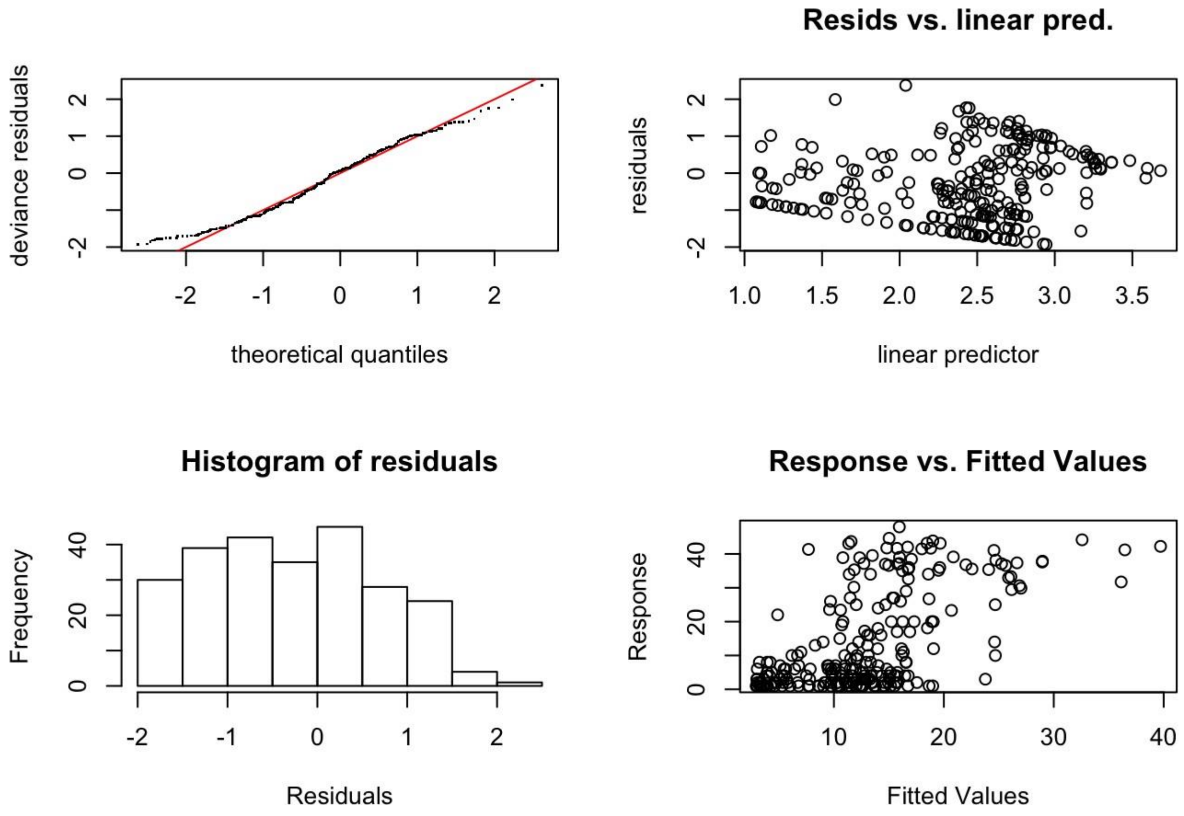


```
##
##Method:REML   Optimizer: outer newton
## full convergence after 4  iterations.
## Gradient range [-1.143111e-06,4.094961e-07]
## (score 889.619 & scale 1).
## Hessian positive definite, eigenvalue range [2.532821,104.0371].
## Model rank =  50 / 50
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                k' edf k-index p-value
## s(lat,lon)  49   17    0.86    0.13
```

```
summary(deep.es50.latlon)
```

```
##
## Family: Negative Binomial(1.121)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs = "sos")
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.43192    0.06339   38.36   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##              edf Ref.df Chi.sq  p-value
## s(lat,lon) 17.04     49  89.19 1.66e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.229   Deviance explained =   28%
## -REML = 889.62  Scale est. = 1         n = 248
```

```
deep.es50.temp <- gam(ES50 ~ s(lat, lon, bs = "sos")  + s(temp), data = deep, famil y
= "nb", method = "REML", select = TRUE)
gam.check(deep.es50.temp)
```

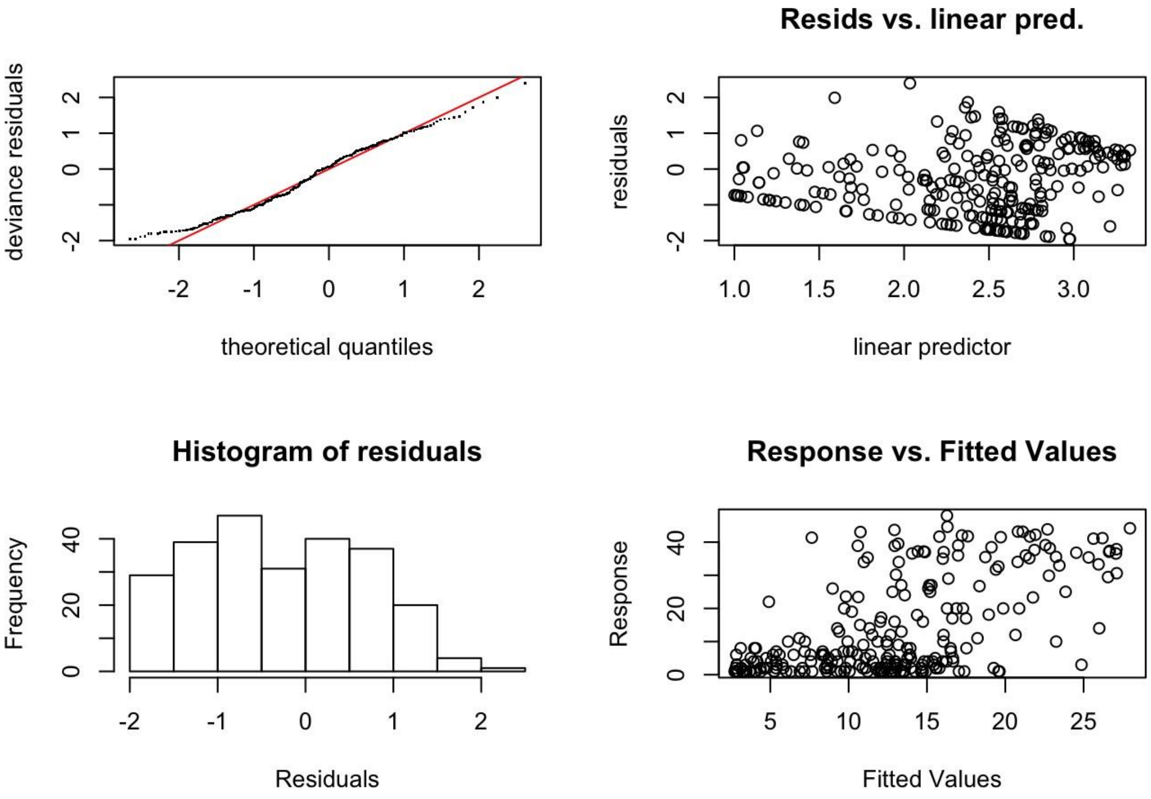


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 9 iterations.
## Gradient range [-0.0004680909,0.0003360787]
## (score 887.7525 & scale 1).
## Hessian positive definite, eigenvalue range [0.0004680402,102.684].
## Model rank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                k'    edf k-index p-value
## s(lat,lon) 49.000 16.799    0.89    0.34
## s(temp)     9.000  0.847    0.77    0.01 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(deep.es50.temp)
```

```
##
## Family: Negative Binomial(1.146)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs =  "sos") +  s(temp)
##
## Parametric coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)      2.4218        0.0628     38.56     <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                      edf   Ref.df  Chi.sq  p-value
## s(lat,lon)  16.7991         49 89.108 9.68e-16***
## s(temp)        0.8467         9   5.169   0.00824 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =   0.278    Deviance explained = 29.6%
## -REML = 887.75 Scale est. = 1               n = 248
```

```
deep.es50.oxygen <- gam(ES50 ~ s(lat, lon, bs = "sos")  +  s(dissolved.oxygen), dat a
= deep, family = "nb", method = "REML", select = TRUE) gam.check(deep.es50.oxygen)
```

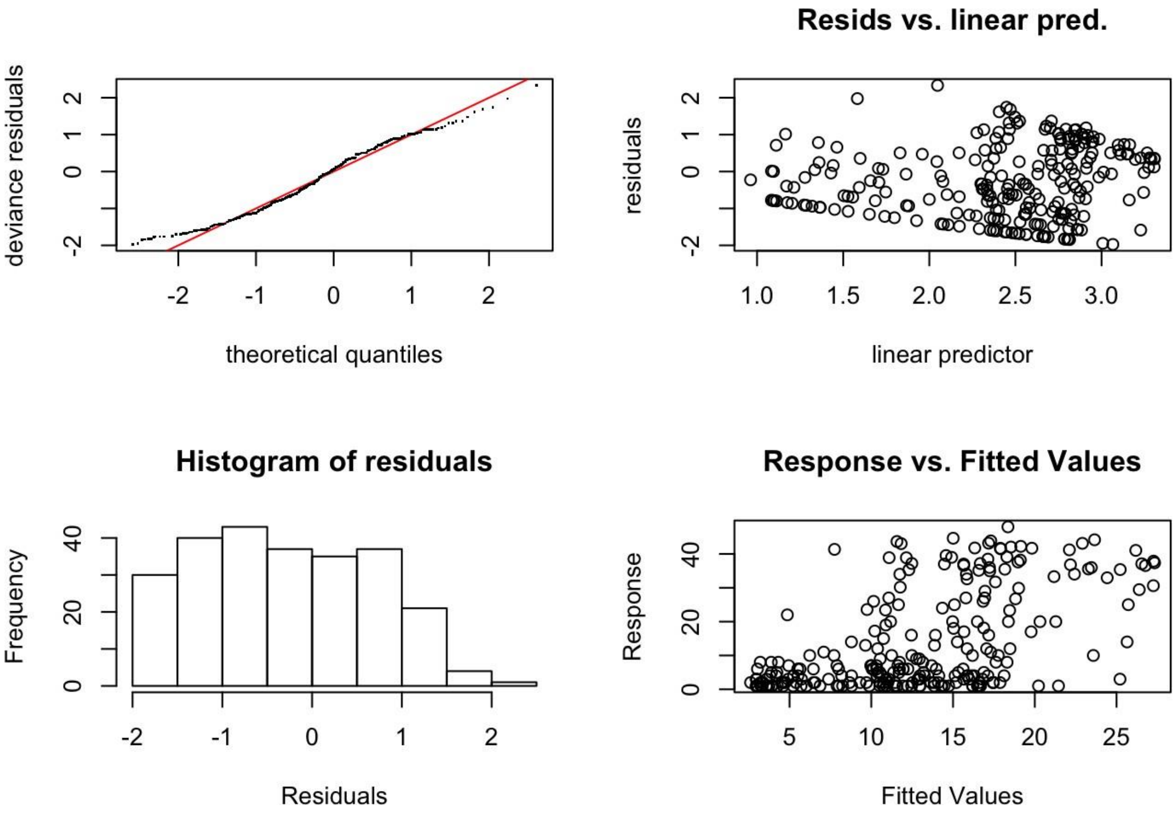


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 4 iterations.
## Gradient range [-0.0001959342,0.0001265859]
## (score 888.3044 & scale 1).
## Hessian positive definite, eigenvalue range [0.0001958078,100.738].
## Model rank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                        k'   edf k-index p-value
## s(lat,lon)          49.00 18.08    0.90    0.32
## s(dissolved.oxygen)  9.00  1.28    0.94    0.67
```

```
summary(deep.es50.oxygen)
```

```
##
## Family: Negative Binomial(1.159)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs = "sos") + s(dissolved.oxygen)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.41289    0.06254   38.58   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                        edf Ref.df Chi.sq  p-value
## s(lat,lon)          18.080     49 82.598 2.87e-14 ***
## s(dissolved.oxygen)  1.282      9  4.827   0.0105 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.276   Deviance explained = 30.9%
## -REML =  888.3  Scale est. = 1         n = 248
```

```
deep.es50.chlorophyll <- gam(ES50 ~ s(lat, lon, bs = "sos") + s(chlorophyll), data = deep, family = "nb", method = "REML", select = TRUE)
gam.check(deep.es50.chlorophyll)
```

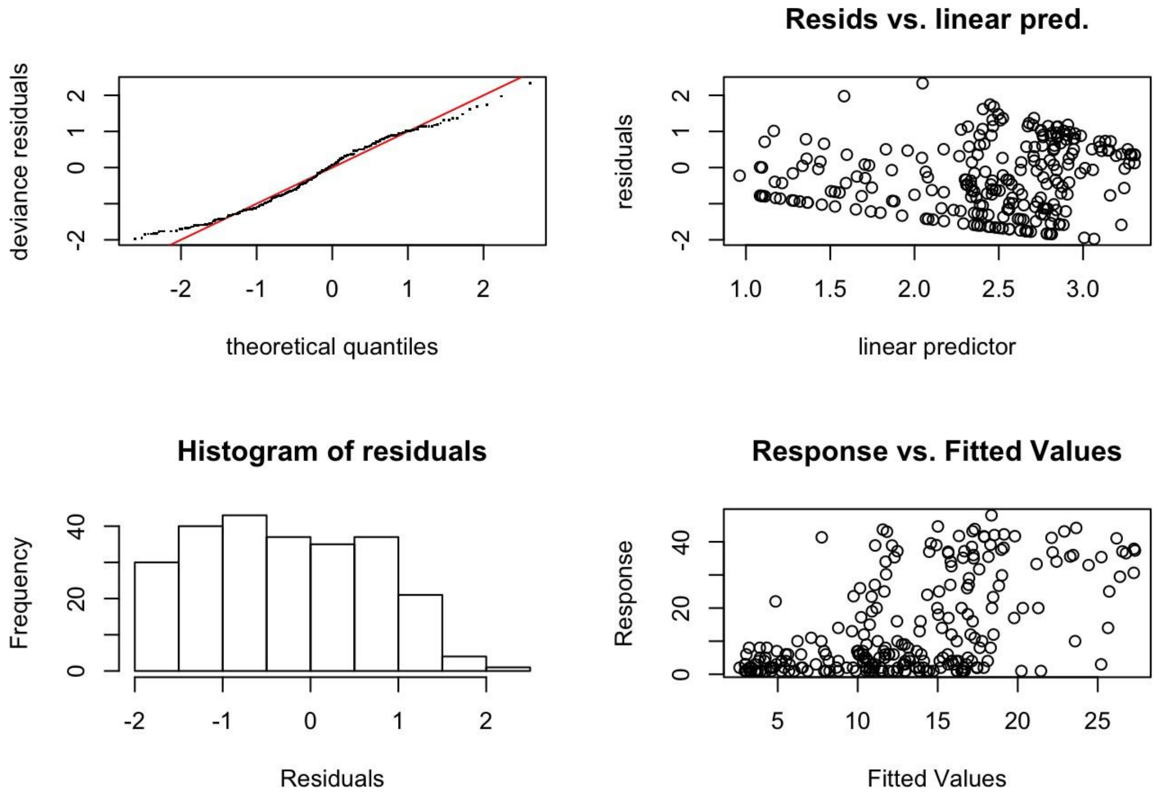


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 6 iterations.
## Gradient range [-0.0003322345,0.0002701815]
## (score 889.6193 & scale 1).
## Hessian positive definite, eigenvalue range [2.314382e-05,104.0372].
## Model rank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                      k'      edf k-index p-value
## s(lat,lon)      4.90e+01 1.70e+01    0.86    0.12
## s(chlorophyll) 9.00e+00 9.76e-04    0.94    0.71
```

```
summary(deep.es50.chlorophyll)
```

```
##
## Family: Negative Binomial(1.121)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs = "sos") + s(chlorophyll)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.43192    0.06339   38.36   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                       edf Ref.df Chi.sq  p-value
## s(lat,lon)      1.704e+01     49  89.18 1.66e-15 ***
## s(chlorophyll) 9.758e-04      9   0.00    0.824
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  R-sq.(adj) =   0.229   Deviance explained =   28%
## -REML= 889.62 Scale est. = 1          n = 248
```

```
deep.es50.current <- gam(ES50 ~ s(lat, lon, bs = "sos") + s(current), data = dee
p, family = "nb", method = "REML", select = TRUE)
gam.check(deep.es50.current)
```

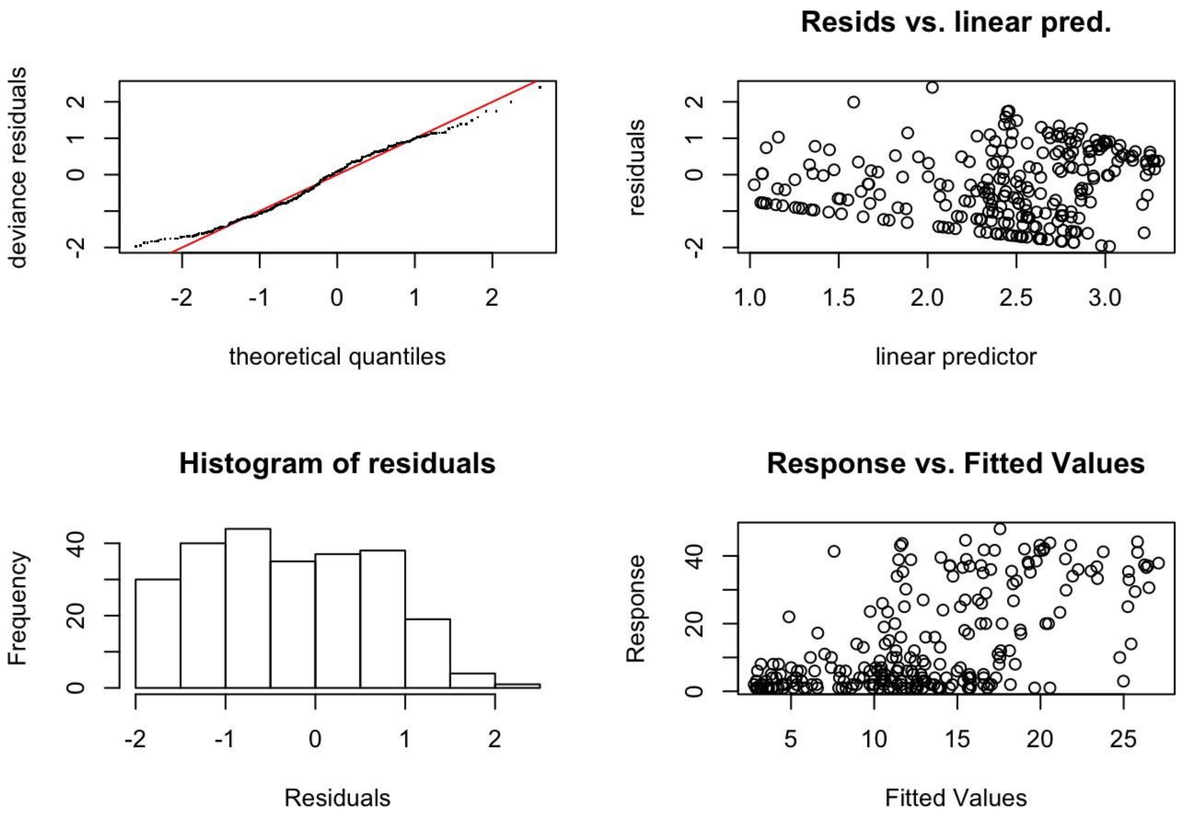


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 7 iterations.
## Gradient range [-0.0004904038,0.0002815296]
## (score 889.6195 & scale 1).
## Hessian positive definite, eigenvalue range [5.346121e-06,104.0371].
## Modelrank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                  k'      edf k-index p-value
## s(lat,lon) 49.00000 17.03618    0.86   0.145
##  s(current)  9.00000  0.00136    0.83   0.085 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(deep.es50.current)
```

```
##
## Family: Negative Binomial(1.121)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs = "sos") + s(current)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
##  (Intercept)  2.43192    0.06339   38.36   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                   edf Ref.df Chi.sq  p-value
## s(lat,lon) 17.036183     49  89.18 1.66e-15 ***
##  s(current)  0.001356      9   0.00     0.72
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  R-sq.(adj) =  0.229   Deviance explained =   28%
## -REML = 889.62  Scale est. = 1         n = 248
```

```
deep.es50.salinity <- gam(ES50 ~ s(lat, lon, bs = "sos") + s(salinity), data = de
ep, family = "nb", method = "REML", select = TRUE)
gam.check(deep.es50.salinity)
```

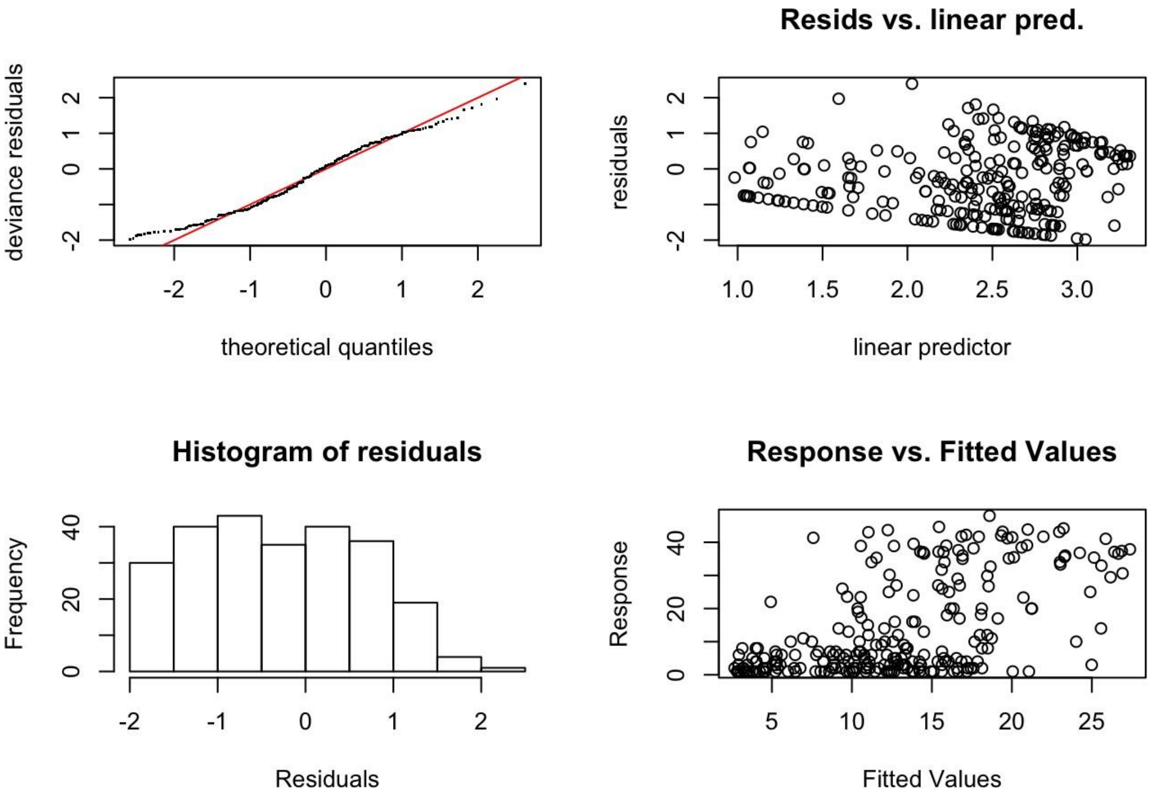


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 4 iterations.
## Gradient range [-0.0004229958,0.0001480549]
## (score 889.1231 & scale 1).
## Hessian positive definite, eigenvalue range [5.59459e-05,101.5801].
## Model rank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                 k'   edf k-index p-value
## s(lat,lon)   49.00 17.11    0.88    0.24
## s(salinity)   9.00  1.62    0.93    0.59
```

```
summary(deep.es50.salinity)
```

```
##
## Family: Negative Binomial(1.145)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs = "sos") + s(salinity)
##
## Parametric coefficients:
##                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)     2.41959    0.06284    38.5   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                  edf Ref.df Chi.sq  p-value
## s(lat,lon)     17.11     49 86.501 1.16e-15 ***
## s(salinity)     1.62      9  4.004   0.0373 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.261   Deviance explained = 29.9%
## -REML = 889.12  Scale est. = 1         n = 248
```

```
deep.es50.nitrate <- gam(ES50 ~ s(lat, lon, bs = "sos") + s(nitrate), data = dee
p, family = "nb", method = "REML", select = TRUE)
gam.check(deep.es50.nitrate)
```

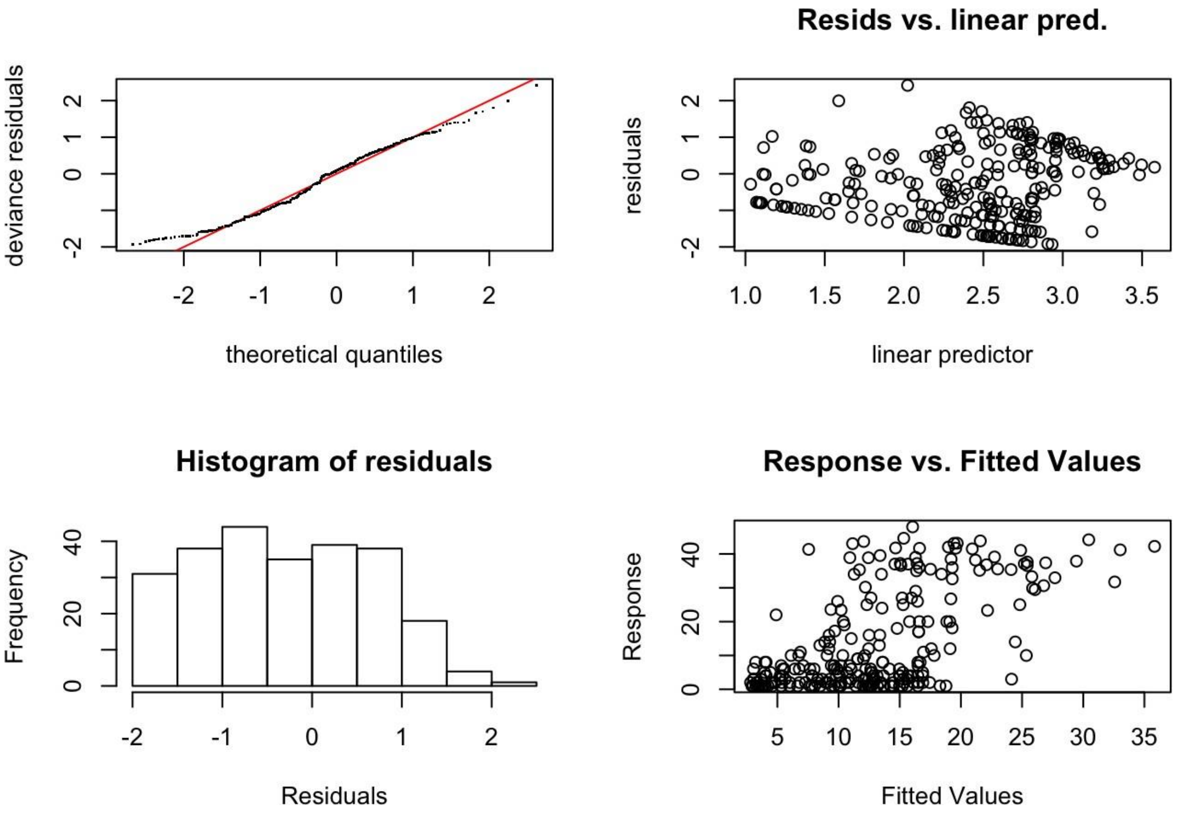


```
##
## Method: REML   Optimizer: outer newton
## full convergence after 4 iterations.
## Gradient range [-0.0001644731,7.83587e-05]
## (score 889.0222 & scale 1).
## Hessian positive definite, eigenvalue range [0.0001644127,102.0879].
## Model rank =  59 / 59
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                k'   edf k-index p-value
## s(lat,lon) 49.00 17.34    0.88    0.19
## s(nitrate)  9.00  1.15    0.85    0.10
```

```
summary(deep.es50.nitrate)
```

```
##
## Family: Negative Binomial(1.141)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs = "sos") + s(nitrate)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.42141    0.06295   38.46   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##               edf Ref.df Chi.sq  p-value
## s(lat,lon) 17.344     49 81.402 2.79e-14 ***
## s(nitrate)  1.149      9  2.899    0.041 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =   0.25   Deviance explained = 29.6%
## -REML = 889.02  Scale est. = 1         n = 248
```

```
deep.es50.env <- gam(ES50 ~ s(lat, lon, bs= "sos") + s(temp) + s(dissolved.oxyge
n) + s(chlorophyll) + s(current) + s(salinity) + s(nitrate), data = deep, family =
"nb", method = "REML", select = TRUE)
gam.check(deep.es50.env)
```



```
##
## Method: REML   Optimizer: outer newton
## full convergence after 13 iterations.
## Gradient range [-0.0002630044,0.0001745135]
## (score 886.9873 & scale 1).
## Hessian positive definite, eigenvalue range [3.801833e-06,101.7219].
## Model rank =  104 / 104
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                          k'      edf k-index p-value
## s(lat,lon)          4.90e+01 1.59e+01    0.90   0.315
## s(temp)             9.00e+00 8.60e-01    0.79   0.025 *
## s(dissolved.oxygen) 9.00e+00 4.99e-05    0.93   0.580
## s(chlorophyll)      9.00e+00 3.76e-05    0.95   0.635
## s(current)          9.00e+00 3.27e-05    0.85   0.100 .
## s(salinity)         9.00e+00 6.62e-01    0.93   0.565
## s(nitrate)          9.00e+00 8.86e-01    0.89   0.270
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(deep.es50.env)
```

```
##
## Family: Negative Binomial(1.159)
## Link function: log
##
## Formula:
## ES50 ~ s(lat, lon, bs = "sos") + s(temp) + s(dissolved.oxygen) +
##     s(chlorophyll) + s(current) + s(salinity) + s(nitrate)
##
## Parametric coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.41592    0.06252   38.64   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                           edf Ref.df Chi.sq  p-value
## s(lat,lon)          1.588e+01     49 74.255  1.6e-13 ***
## s(temp)             8.596e-01      9  5.854  0.00488 **
## s(dissolved.oxygen) 4.994e-05      9  0.000  0.43457
## s(chlorophyll)      3.756e-05      9  0.000  0.94571
## s(current)          3.274e-05      9  0.000  1.00000
## s(salinity)         6.615e-01      9  2.046  0.03428 *
## s(nitrate)          8.861e-01      9  1.547  0.10430
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.287   Deviance explained = 30.5%
## -REML = 886.99  Scale est. = 1         n = 248
```

Model selection for ES50, deep water

```
deep.es50.models <- list(deep.es50.intercept = deep.es50.intercept,
                         deep.es50.latlon = deep.es50.latlon,
                         deep.es50.temp = deep.es50.temp,
                         deep.es50.oxygen = deep.es50.oxygen,
                         deep.es50.chlorophyll = deep.es50.chlorophyll,
                         deep.es50.current = deep.es50.current,
                         deep.es50.salinity = deep.es50.salinity,
                         deep.es50.nitrate = deep.es50.nitrate,
                         deep.es50.env = deep.es50.env)
deep.es50.aic.df <- data.frame(Model = names(deep.es50.models),
                               AIC = sapply(deep.es50.models, function(x) x$aic),
                              akaike.weights(sapply(deep.es50.models, function(x) x$a
ic)))

deep.es50.aic.df <- deep.es50.aic.df[order(deep.es50.aic.df$AIC),]
deep.es50.aic.df$Cumulative.Weight <- cumsum(deep.es50.aic.df$weights)

kable(deep.es50.aic.df, row.names = FALSE)
```

Model	AIC	deltaAIC	rel.LL	weights	Cumulative.Weight
deep.es50.env	1751.424	0.0000000	1.0000000	0.3917528	0.3917528
deep.es50.oxygen	1752.042	0.6181978	0.7341082	0.2875889	0.6793417

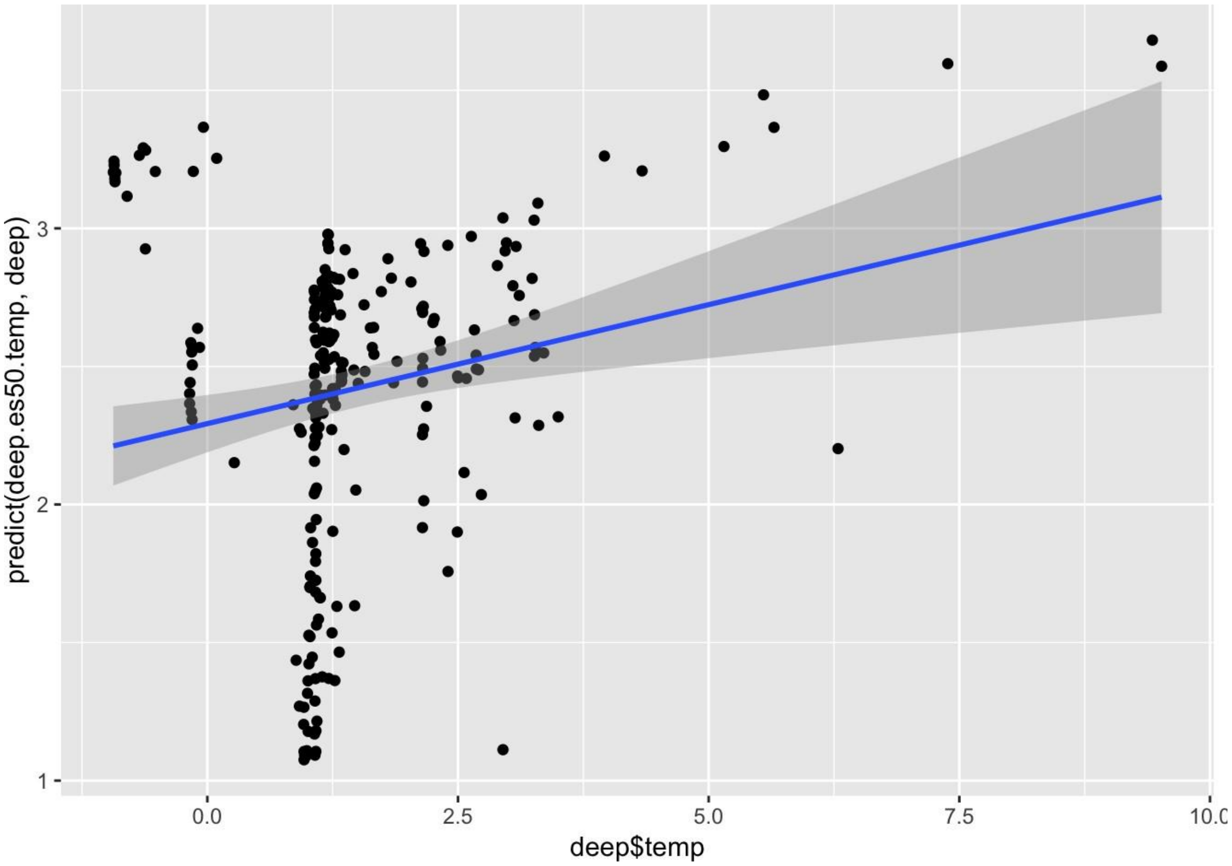
Model	AIC	deltaAIC	rel.LL	weights	Cumulative.Weight
deep.es50.temp	1753.522	2.0980682	0.3502759	0.1372216	0.8165632
deep.es50.salinity	1754.545	3.1215021	0.2099783	0.0822596	0.8988228
deep.es50.nitrate	1755.165	3.7416483	0.1539967	0.0603286	0.9591514
deep.es50.latlon	1758.141	6.7175613	0.0347776	0.0136242	0.9727757
deep.es50.chlorophyll	1758.143	6.7191041	0.0347508	0.0136137	0.9863894
deep.es50.current	1758.143	6.7195658	0.0347428	0.0136106	1.0000000
deep.es50.intercept	1811.602	60.1779873	0.0000000	0.0000000	1.0000000

```
write.csv(deep.es50.aic.df, file = "deep.es50.aic.csv")
```

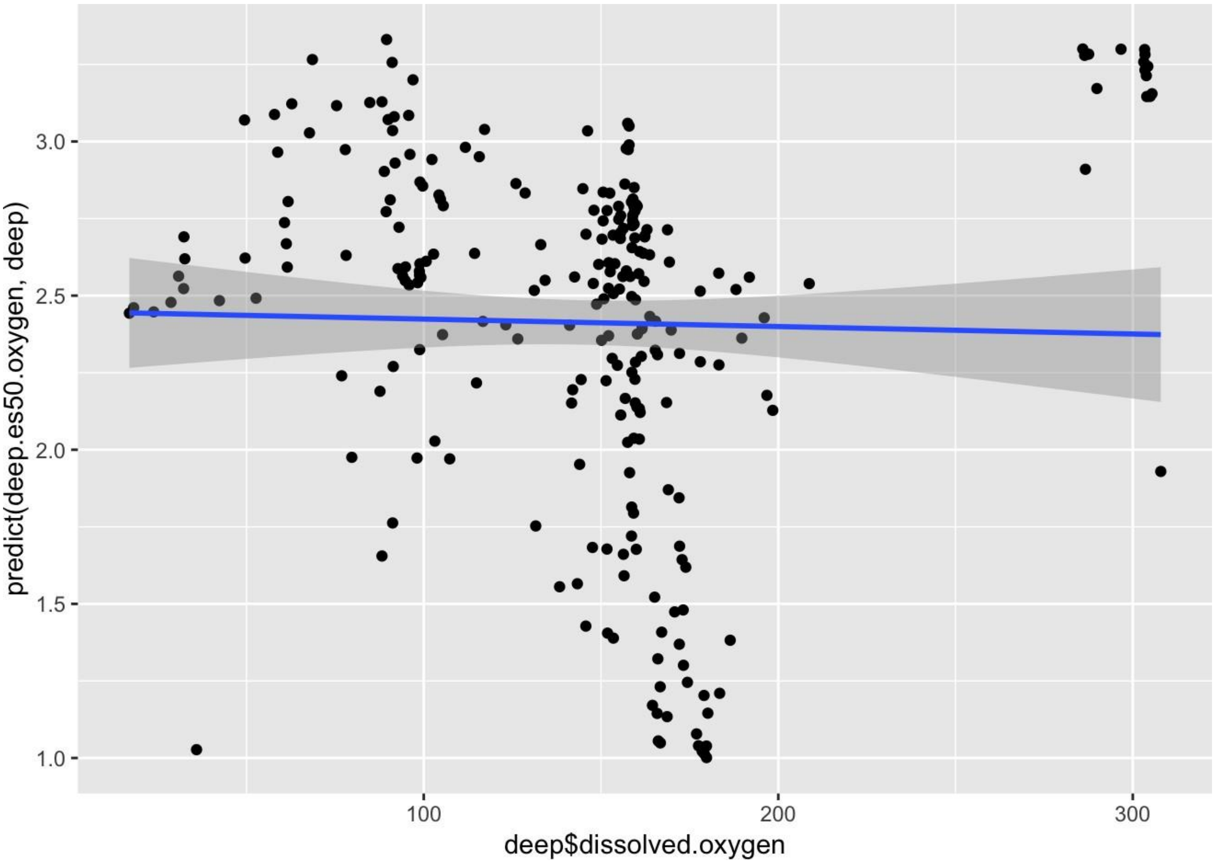
We find that model selection supports the importance of the environment in explaining the number of species in a community. These results are only moderately strong, however; the delta AIC between the “env” model and the one for spatial autocorrelation is only 3.65. We also note that there is no strong signal indicating which predictor variable is important in explaining ES50; both oxygen and salinity are within delta AIC of 2 compared to the full model.

Plots for ES50, deep water

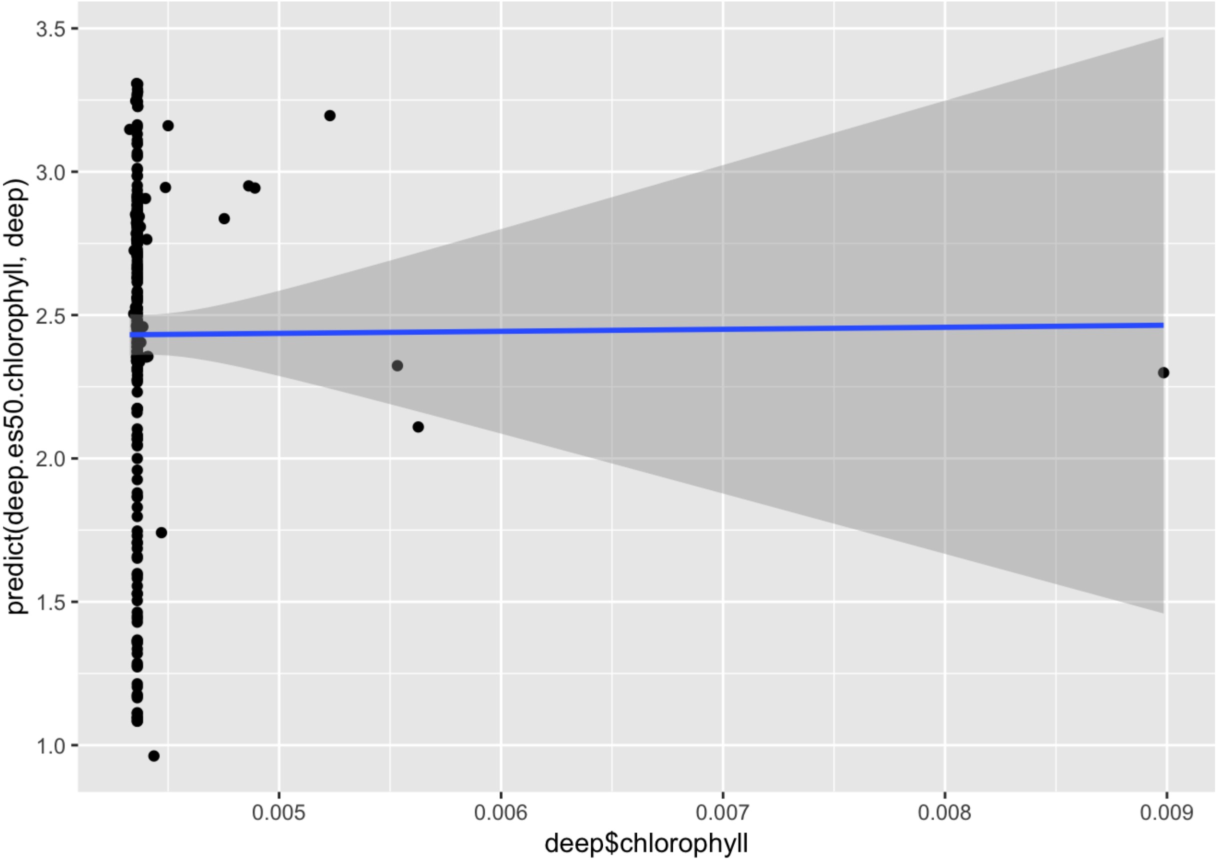
```
qplot(deep$temp, predict(deep.es50.temp, deep)) + geom_smooth(method = "gam")
```



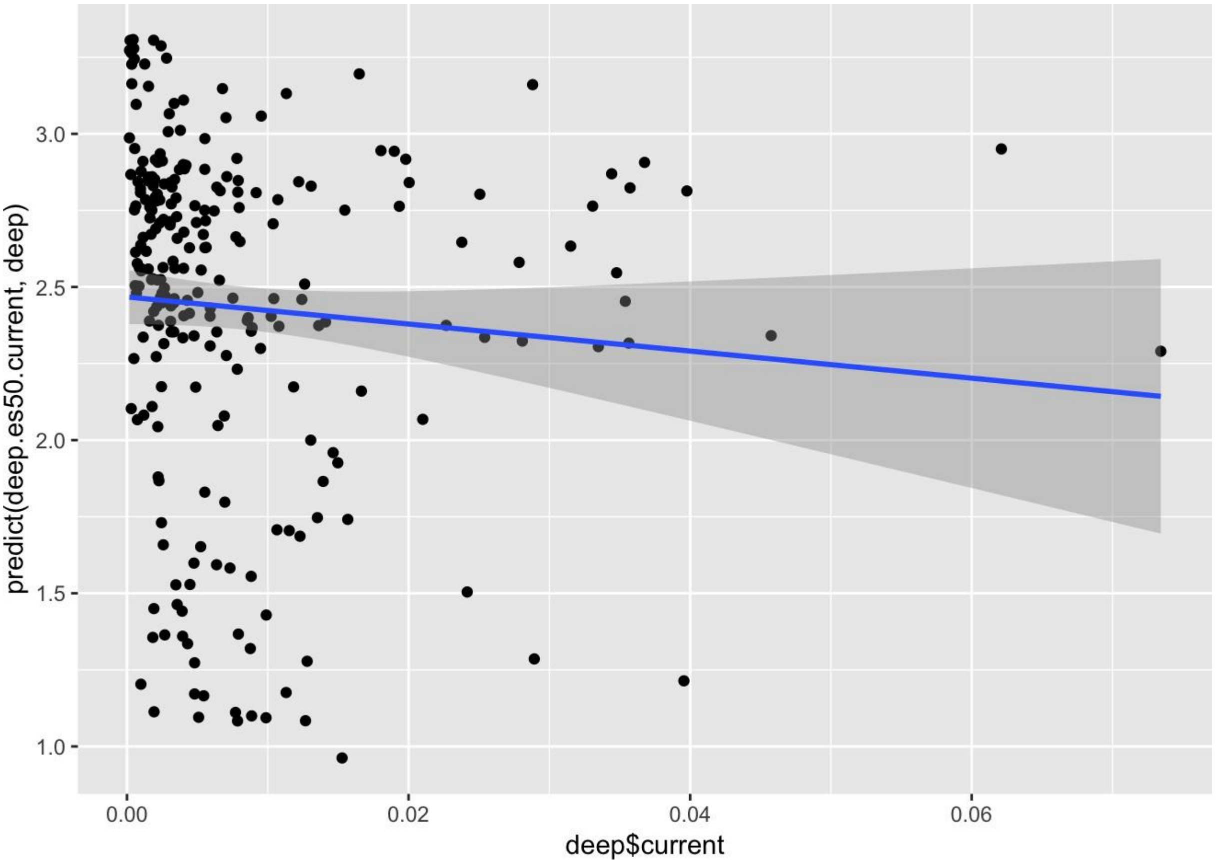
```
qplot(deep$dissolved.oxygen, predict(deep.es50.oxygen, deep)) + geom_smooth(method
= "gam")
```



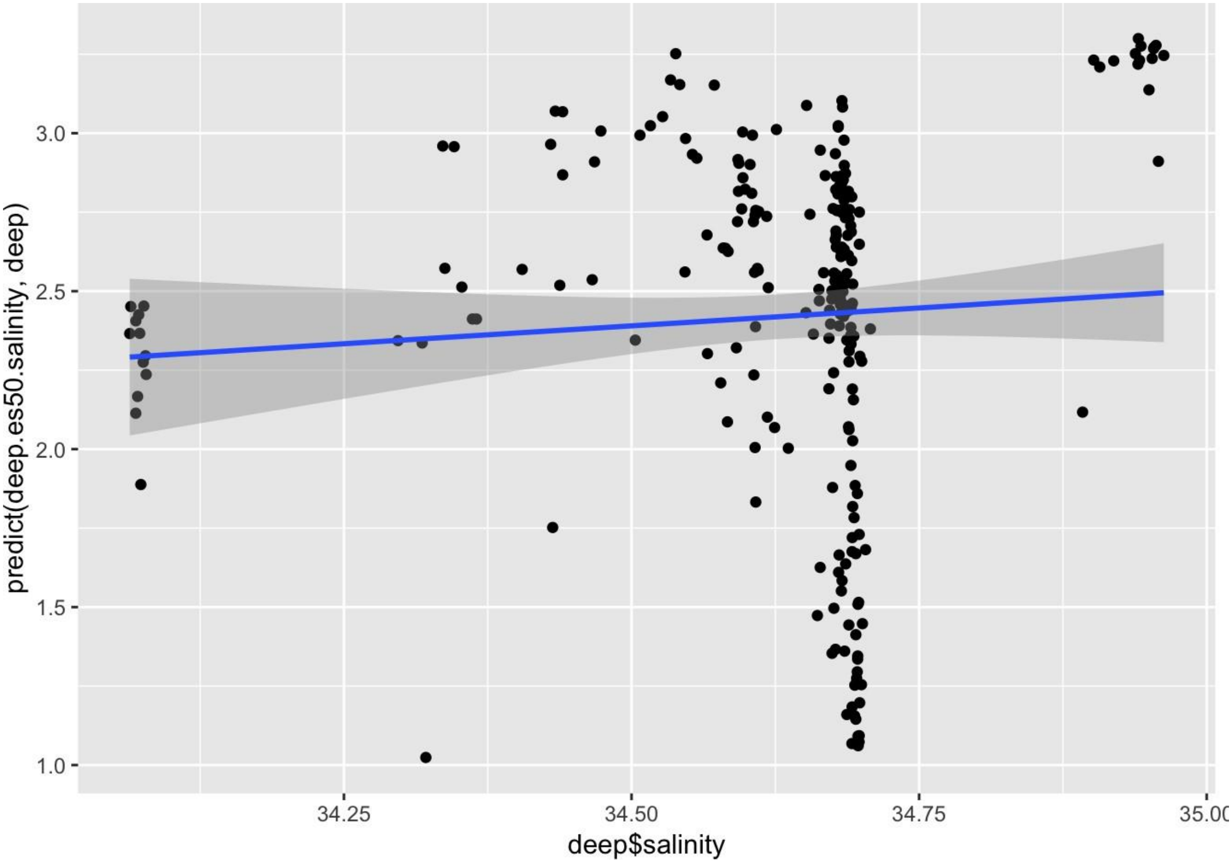
```
qplot(deep$chlorophyll, predict(deep.es50.chlorophyll, deep)) + geom_smooth(method
= "gam")
```



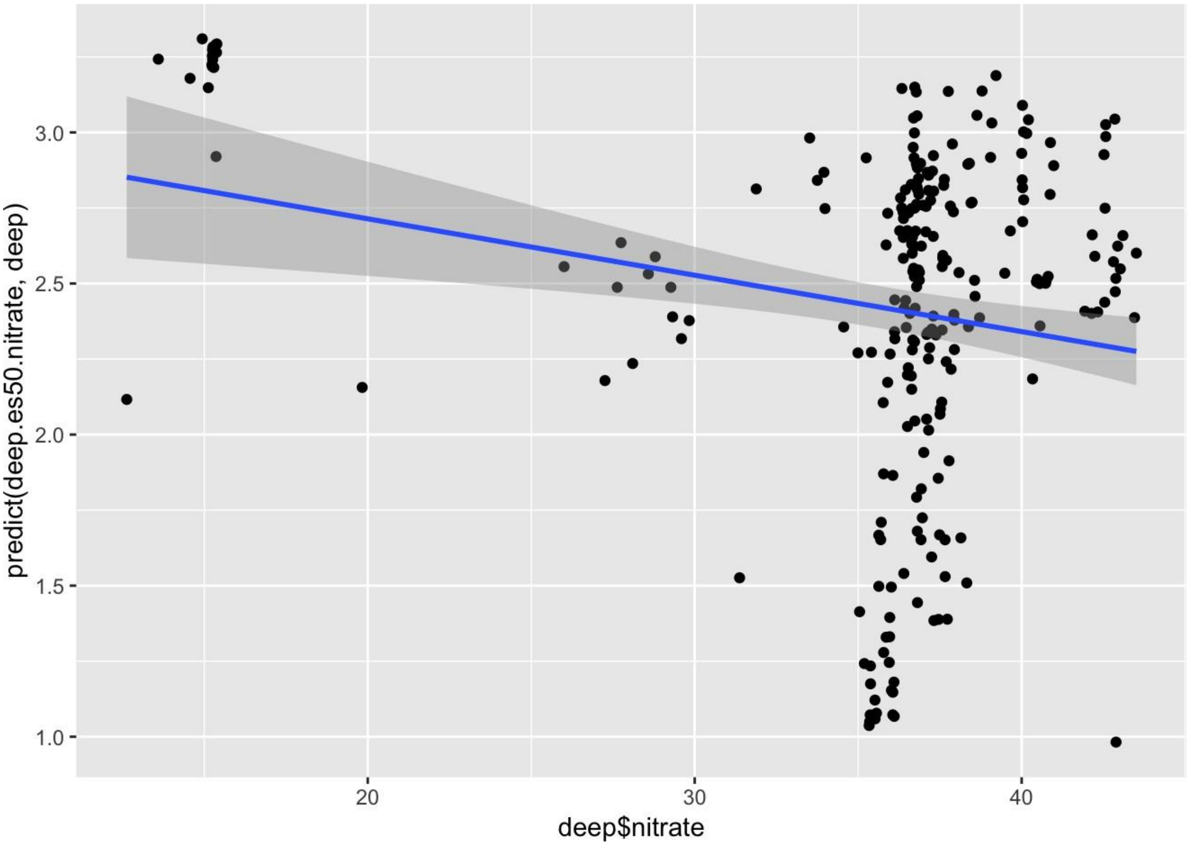
```
qplot(deep$current, predict(deep.es50.current, deep)) + geom_smooth(method = "gam")
```



```
qplot(deep$salinity, predict(deep.es50.salinity, deep)) +  geom_smooth(method  =  "gam")
```



```
qplot(deep$nitrate, predict(deep.es50.nitrate, deep)) + geom_smooth(method = "gam")
```


predict(deep.es50.nitrate, deep)
3.0
2.5
2.0
1.5
1.0
20
30
40
deep$nitrate

S2. Species Counts and Environment Based on 5° Latitudinal Bands.

Species Counts and Environment, 5 degree bands

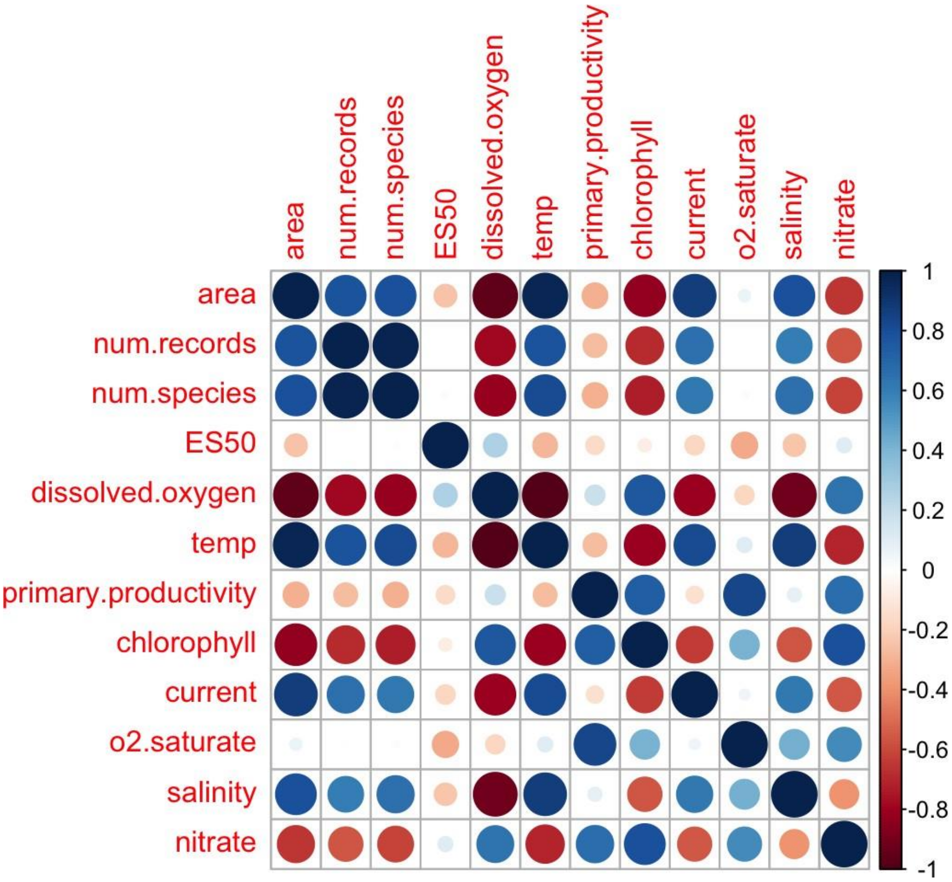
Setup

Shallow water

Data load-in and visualization

First we’re going to load in our data and then trim the data frame down to just the columns we need.

```
shallow <- read.csv("shallow.5.degree.csv")
analysis.cols <- c("area", "num.records", "num.species", "ES50", "dissolved.oxygen", "temp", "primary.productivity", "chlorophyll", "current", "o2.saturate", "salinity", "nitrate")
shallow <- shallow[,analysis.cols]
shallow <- shallow[complete.cases(shallow),]
corrplot(cor(shallow))
```



GLMs for number of species, shallow water

We’re going to develop a number of GLMs here. The “intercept” glm represents the fit of a model that assumes no relationship between the species counts and the environment and no spatial autocorrelation. The “numrec” model represents the fit of a model that only contains sampling bias. The remainder of the models (“temp”, “oxygen”, etc.) estimate the effects of a single predictor at a time, controlling for number of records.

```
shallow.numsp.intercept <- glm(num.species ~ 1, family = "poisson", data = shallow)
summary(shallow.numsp.intercept)
```

```
##
## Call:
## glm(formula = num.species ~ 1, family = "poisson", data = shallow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -119.171   -66.422    -9.743    36.253   137.422
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) 8.871672   0.002961    2996   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 77725  on 15  degrees of freedom
## Residual deviance: 77725  on 15  degrees of freedom
## AIC: 77885
##
## Number of Fisher Scoring iterations: 5
```

```
shallow.numsp.numrec <- glm(num.species ~ num.records, family = "poisson", data = s
hallow)
summary(shallow.numsp.numrec)
```

```
##
## Call:
## glm(formula = num.species ~ num.records, family = "poisson",
##     data = shallow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -76.324  -35.422    4.397   16.433   50.351
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) 7.985e+00  5.350e-03    1492   <2e-16 ***
## num.records 7.009e-05  2.770e-07     253   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 77725  on 15  degrees of freedom
## Residual deviance: 22879  on 14  degrees of freedom
## AIC: 23041
##
## Number of Fisher Scoring iterations: 5
```

```
shallow.numsp.temp <- glm(num.species ~ num.records + temp, family = "poisson", dat
a = shallow)
summary(shallow.numsp.temp)
```

```
##
## Call:
## glm(formula = num.species ~ num.records + temp, family = "poisson",
##     data = shallow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -61.993  -25.333   -0.182   14.483   41.945
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) 7.613e+00  7.513e-03 1013.22   <2e-16 ***
## num.records 4.501e-05  3.955e-07  113.82   <2e-16 ***
## temp        3.653e-02  4.051e-04   90.17   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 77725  on 15  degrees of freedom
## Residual deviance: 14661  on 13  degrees of freedom
## AIC: 14825
##
## Number of Fisher Scoring iterations: 5
```

```
shallow.numsp.oxygen <- glm(num.species ~ num.records + dissolved.oxygen, family
= "poisson", data = shallow)
summary(shallow.numsp.oxygen)
```

```
##
## Call:
## glm(formula = num.species ~ num.records + dissolved.oxygen, family = "poisson",
##     data = shallow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -55.481  -21.004    2.088   17.144   37.645
##
## Coefficients:
##                    Estimate Std. Error z value Pr(>|z|)
## (Intercept)       1.021e+01  2.223e-02  459.27   <2e-16 ***
## num.records       4.296e-05  3.932e-07  109.25   <2e-16 ***
## dissolved.oxygen -7.578e-03  7.637e-05  -99.22   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 77725  on 15  degrees of freedom
## Residual deviance: 12441  on 13  degrees of freedom
## AIC: 12605
##
## Number of Fisher Scoring iterations: 5
```

```
shallow.numsp.prod <- glm(num.species ~ num.records + primary.productivity, famil
y = "poisson", data = shallow)
summary(shallow.numsp.prod)
```

```
##
## Call:
## glm(formula = num.species ~ num.records + primary.productivity,
##     family = "poisson", data = shallow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -79.472  -40.316    7.588   18.270   50.049
##
## Coefficients:
##                        Estimate Std. Error z value Pr(>|z|)
## (Intercept)           8.142e+00  8.451e-03  963.39   <2e-16 ***
## num.records           6.768e-05  2.936e-07  230.54   <2e-16 ***
## primary.productivity -2.639e+01  1.138e+00  -23.18   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 77725  on 15  degrees of freedom
## Residual deviance: 22337  on 13  degrees of freedom
## AIC: 22501
##
## Number of Fisher Scoring iterations: 5
```

```
shallow.numsp.chlorophyll <- glm(num.species ~ num.records + chlorophyll, family
= "poisson", data = shallow)
summary(shallow.numsp.chlorophyll)
```

```
##
## Call:
## glm(formula = num.species ~  num.records  +  chlorophyll,  family  =  "poisson",
##       data =  shallow)
##
## Deviance Residuals:
##       Min         1Q    Median          3Q        Max
## -64.497   -29.226     -8.027      15.647     52.590
##
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)      8.662e+00    9.461e-03    915.52     <2e-16 ***
## num.records   5.093e-05    3.639e-07    139.95     <2e-16 ***
## chlorophyll -1.610e+00    1.991e-02    -80.86     <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 77725    on 15    degrees of freedom
## Residual deviance: 16006   on 13   degrees of freedom
## AIC: 16170
##
## Number of Fisher Scoring iterations: 5
```

```
shallow.numsp.current <- glm(num.species ~   num.records + current, family = "poisso
n", data = shallow)
summary(shallow.numsp.current)
```

```
##
## Call:
## glm(formula = num.species ~  num.records  +  current,  family  =  "poisson",
##       data =  shallow)
##
## Deviance Residuals:
##       Min         1Q    Median          3Q        Max
## -71.570   -28.902     -1.892      16.834     54.011
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
##  (Intercept)  7.802e+00    7.112e-03 1097.03     <2e-16 ***
##  num.records  6.242e-05    3.321e-07    187.94     <2e-16 ***
## current         2.769e+00    6.449e-02    42.94     <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 77725    on 15    degrees of freedom
## Residual deviance: 21151   on 13   degrees of freedom
## AIC: 21315
##
## Number of Fisher Scoring iterations: 5
```

```
shallow.numsp.o2.saturate <- glm(num.species ~ num.records + o2.saturate, family
= "poisson", data = shallow)
summary(shallow.numsp.o2.saturate)
```

```
##
## Call:
## glm(formula = num.species ~ num.records + o2.saturate, family = "poisson",
##     data = shallow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -76.524  -35.726    4.632   16.408   50.325
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)   8.225e+00  2.504e-01  32.847   <2e-16 ***
## num.records   7.008e-05  2.773e-07 252.696   <2e-16 ***
## o2.saturate -2.373e-03  2.474e-03  -0.959    0.337
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 77725  on 15  degrees of freedom
## Residual deviance: 22878  on 13  degrees of freedom
## AIC: 23042
##
## Number of Fisher Scoring iterations: 5
```

```
shallow.numsp.salinity <- glm(num.species ~ num.records + salinity, family = "poi
sson", data = shallow)
summary(shallow.numsp.salinity)
```

```
##
## Call:
## glm(formula = num.species ~ num.records + salinity, family = "poisson",
##     data = shallow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -54.003   -14.680     4.552    11.755    34.503
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.139e+00  1.063e-01  -29.52   <2e-16 ***
## num.records  6.123e-05  3.193e-07  191.77   <2e-16 ***
## salinity     3.356e-01  3.166e-03  106.01   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 77725.1  on 15  degrees of freedom
## Residual deviance:  9843.3  on 13  degrees of freedom
## AIC: 10008
##
## Number of Fisher Scoring iterations: 5
```

```
shallow.numsp.nitrate <-glm(num.species ~ num.records + nitrate, family = "poiss
on", data = shallow)
summary(shallow.numsp.nitrate)
```

```
##
## Call:
## glm(formula = num.species ~ num.records + nitrate, family = "poisson",
##     data = shallow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -79.989   -29.903     3.061    19.810    45.032
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)  8.312e+00  7.430e-03 1118.66   <2e-16 ***
## num.records  5.822e-05  3.415e-07  170.50   <2e-16 ***
## nitrate     -5.945e-02  1.016e-03  -58.55   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 77725  on 15  degrees of freedom
## Residual deviance: 19093  on 13  degrees of freedom
## AIC: 19257
##
## Number of Fisher Scoring iterations: 5
```

Model selection for number of species, shallow water

Here we use AIC to compare models for goodness of fit while penalizing for overparameterization. Models are ranked in order of AIC score, with lowest scoring model (model with the best compromise between fit and complexity) first in the list. The delta AIC represents how much the AIC score for each model differs from the top model, an can be used as an estimate of the relative support for each model. A delta AIC of 2 is considered to be potentially a significantly better fit, with higher delta AICs between models indicating increasingly larger differences in model fit while correcting for the number of parameters.

```
shallow.numsp.models <- list(shallow.numsp.intercept = shallow.numsp.intercept,
                             shallow.numsp.temp = shallow.numsp.temp,
                             shallow.numsp.oxygen = shallow.numsp.oxygen,
                             shallow.numsp.prod = shallow.numsp.prod,
                             shallow.numsp.chlorophyll = shallow.numsp.chlorophyll,
                             shallow.numsp.numrec = shallow.numsp.numrec,
                             shallow.numsp.current = shallow.numsp.current,
                             shallow.numsp.o2.saturate = shallow.numsp.o2.saturate,
                             shallow.numsp.salinity = shallow.numsp.salinity,
                             shallow.numsp.nitrate = shallow.numsp.nitrate)
shallow.numsp.aic.df <- data.frame(Model = names(shallow.numsp.models),
                                   AIC = sapply(shallow.numsp.models, function(x) AICc
(x)),
                                  akaike.weights(sapply(shallow.numsp.models, function(x)
AICc(x))))


shallow.numsp.aic.df <- shallow.numsp.aic.df[order(shallow.numsp.aic.df$AIC),]
shallow.numsp.aic.df$Cumulative.Weight   <-  cumsum(shallow.numsp.aic.df$weights)

kable(shallow.numsp.aic.df, row.names = FALSE)
```

Model	AIC	deltaAIC	rel.LL	weights	Cumulative.Weight
shallow.numsp.salinity	10009.54	0.000	1	1	1
shallow.numsp.oxygen	12606.98	2597.441	0	0	1
shallow.numsp.temp	14827.07	4817.526	0	0	1
shallow.numsp.chlorophyll	16172.16	6162.624	0	0	1
shallow.numsp.nitrate	19259.05	9249.507	0	0	1
shallow.numsp.current	21316.87	11307.335	0	0	1
shallow.numsp.prod	22502.95	12493.406	0	0	1
shallow.numsp.numrec	23042.10	13032.562	0	0	1
shallow.numsp.o2.saturate	23044.26	13034.719	0	0	1
shallow.numsp.intercept	77885.64	67876.100	0	0	1

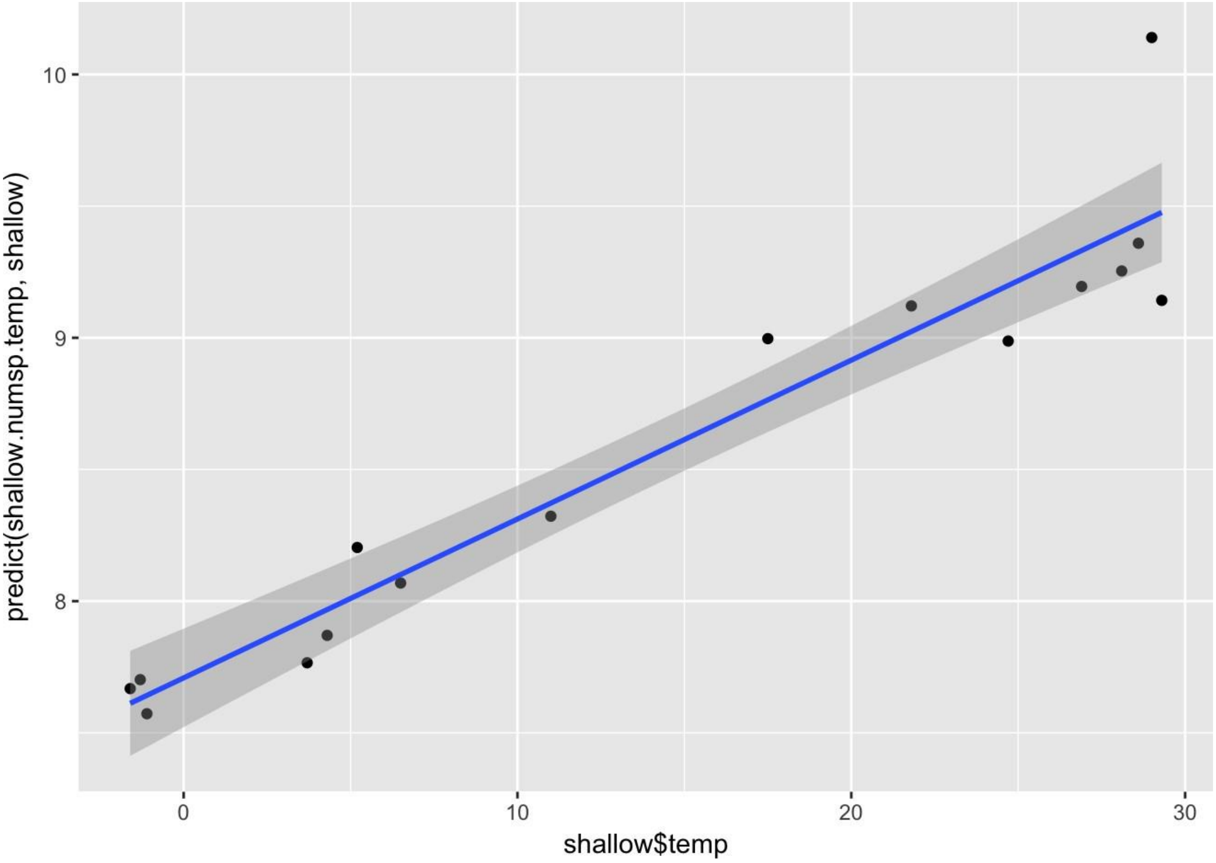
```
write.csv(shallow.numsp.aic.df, file = "shallow.5.degree.numsp.aic.csv")
```

Here we see that the model containing salinity is the best fit, but many other models are almost as good. It is particularly noteworthy that the model containing only the effects of sampling (the “numrec” model) has a delta AIC of < 2 compared to the best-performing model. This indicates that a model that contains only sampling effort is for all practical purposes as good as any model that contains an environmental predictor. As such, we cannot with confidence say that any environmental predictor is useful in explaining the number of species.

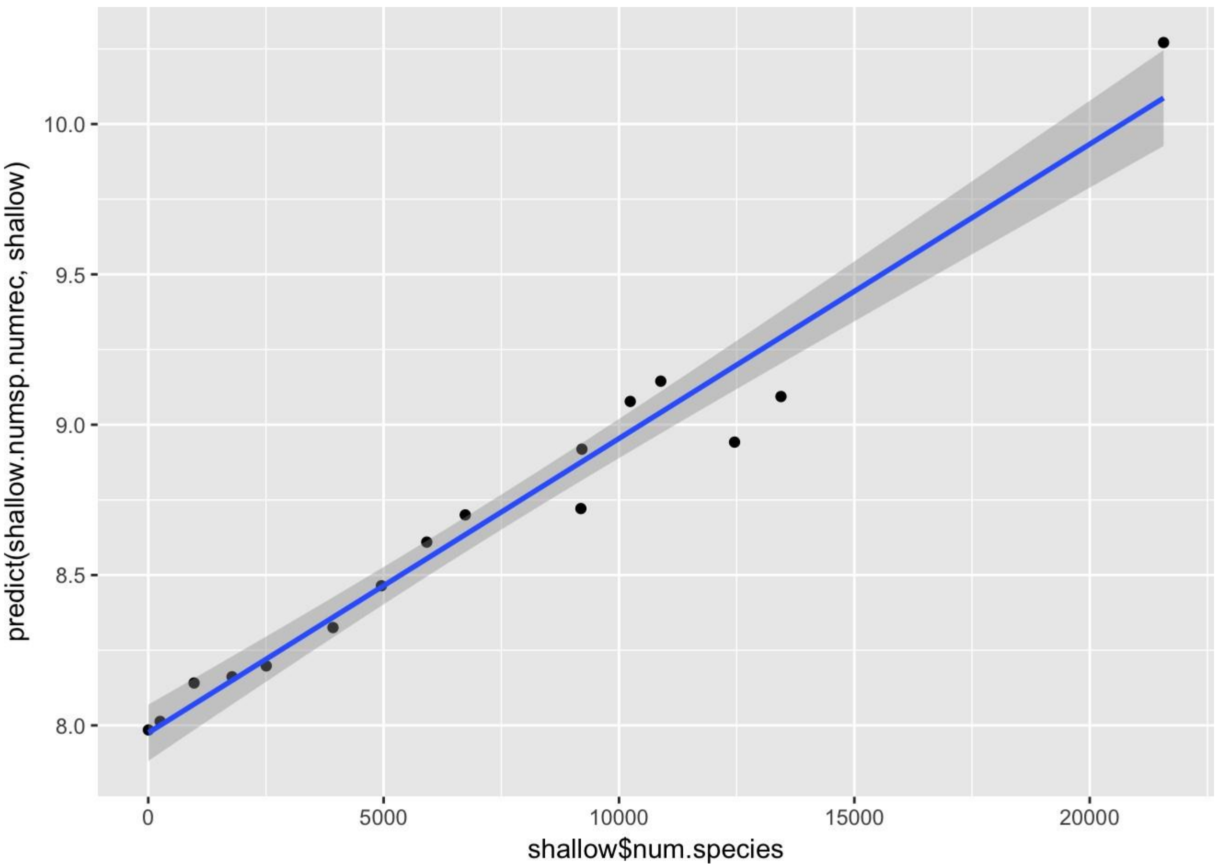
Plots for number of species, shallow water

Here we plot the effects of each environmental predictor from its respective single-variable model.

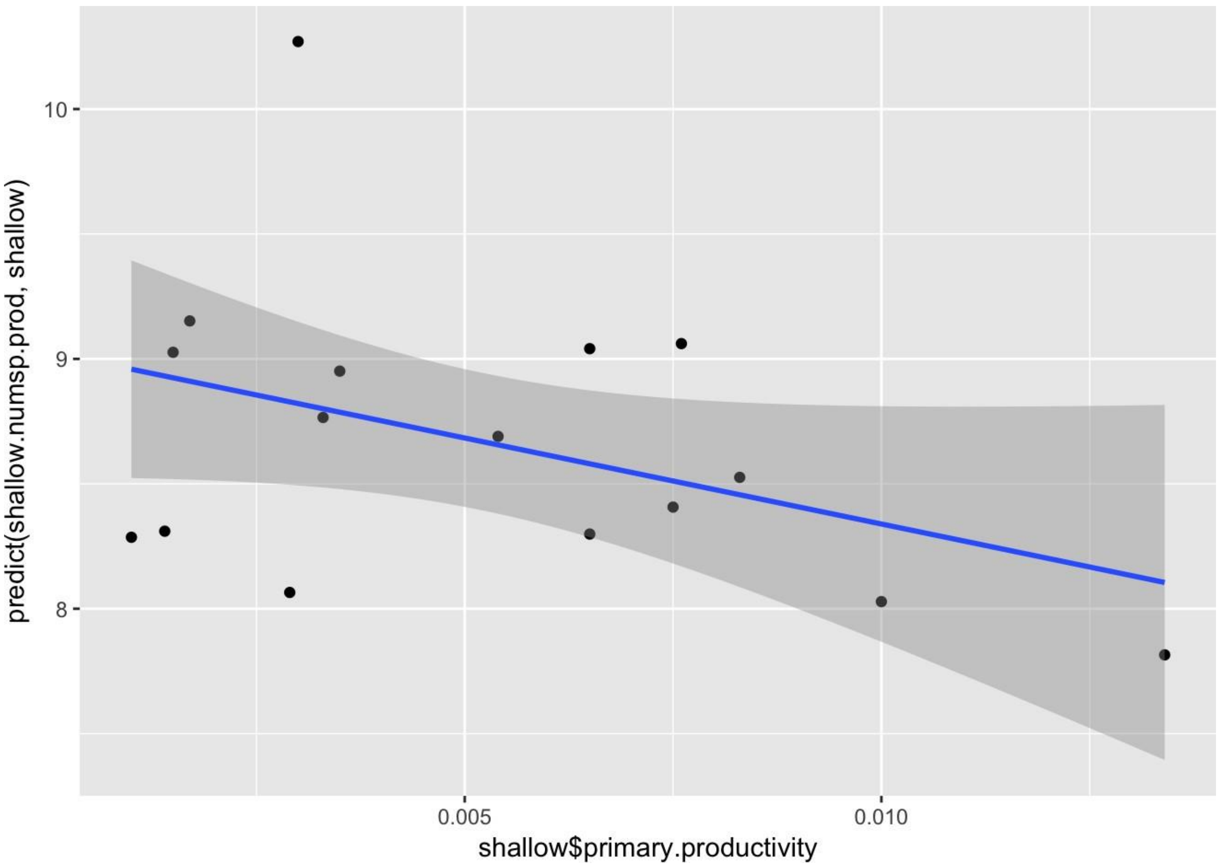
```
qplot(shallow$temp, predict(shallow.numsp.temp, shallow)) + geom_smooth(method = "g
lm")
```



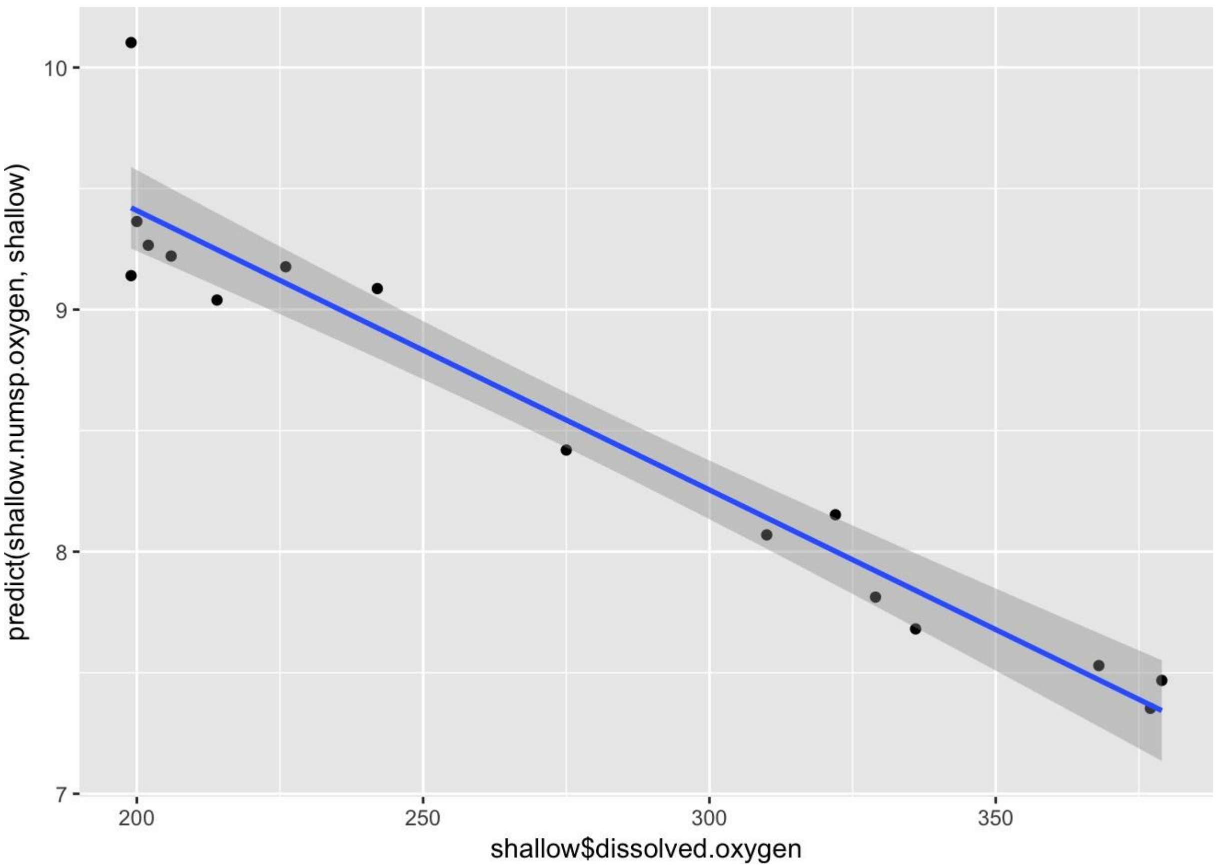
```
qplot(shallow$num.species, predict(shallow.numsp.numrec, shallow)) + geom_smooth(me
thod = "glm")
```



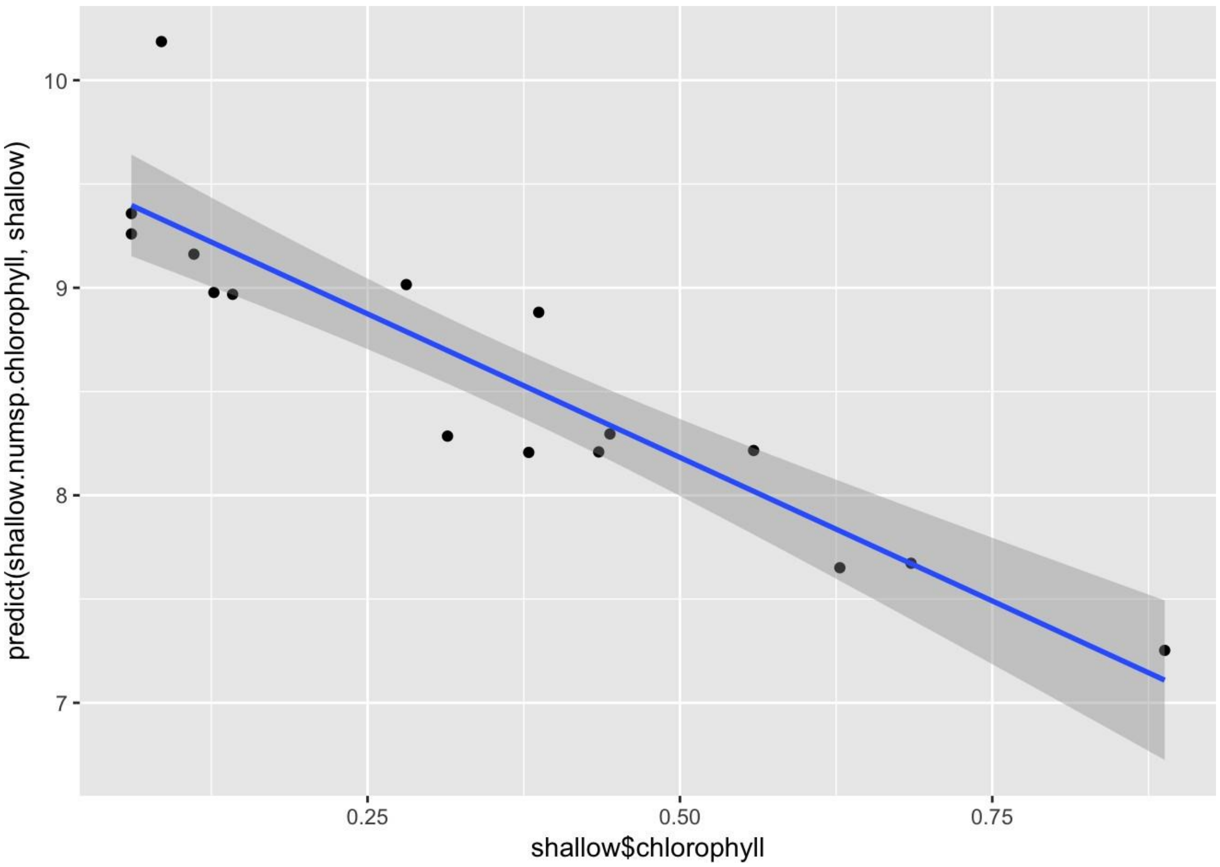
```
qplot(shallow$primary.productivity, predict(shallow.numsp.prod, shallow)) + geom_sm
ooth(method = "glm")
```



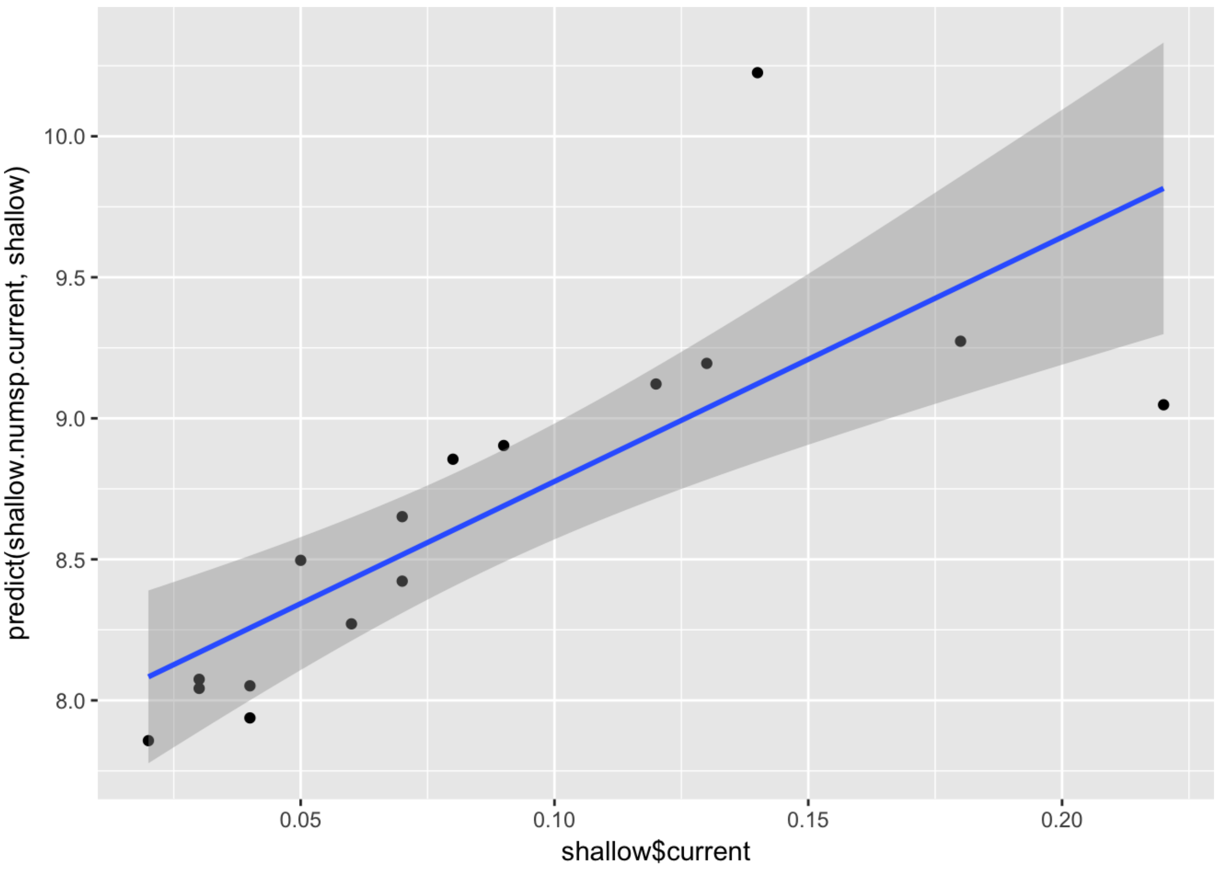
```
qplot(shallow$dissolved.oxygen, predict(shallow.numsp.oxygen, shallow)) + geom_smoo
th(method = "glm")
```



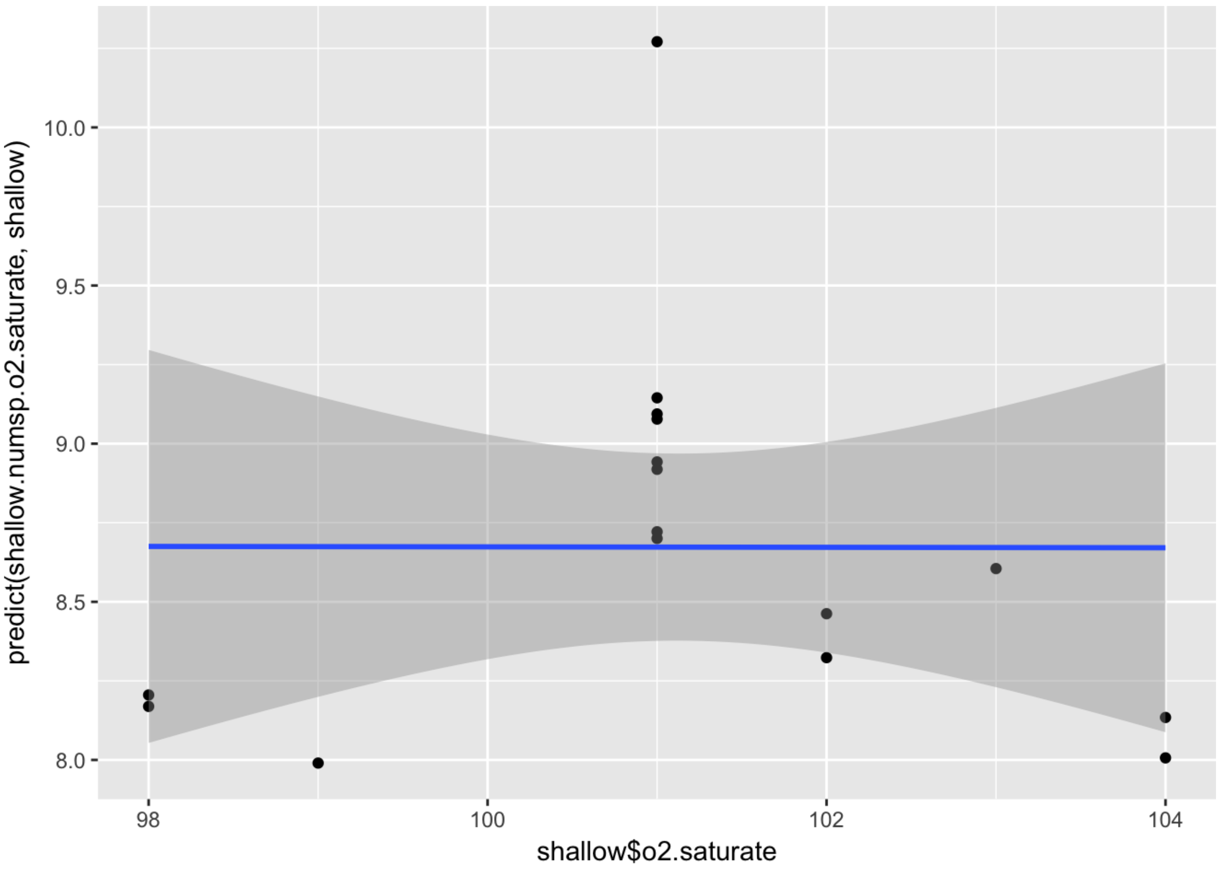
```
qplot(shallow$chlorophyll, predict(shallow.numsp.chlorophyll, shallow)) + geom_smoo
th(method = "glm")
```



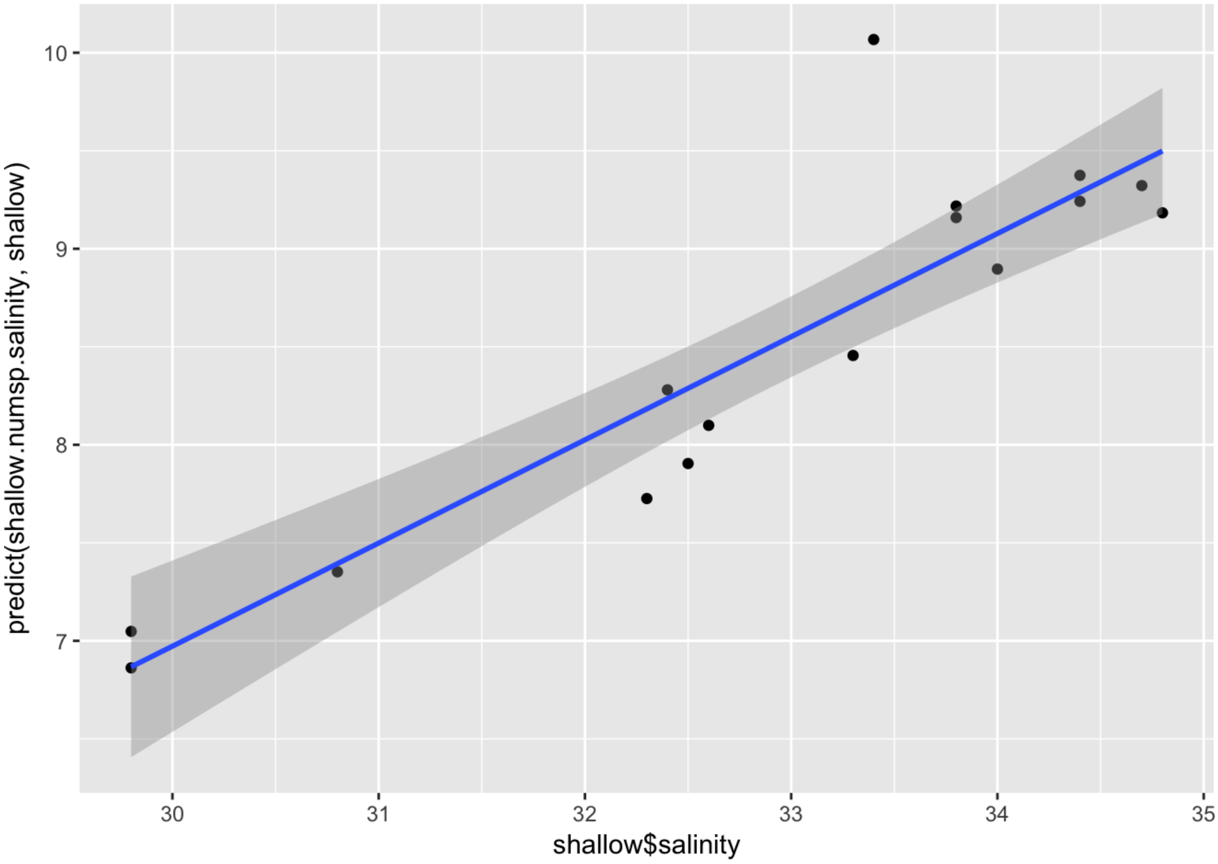
```
qplot(shallow$current, predict(shallow.numsp.current, shallow)) + geom_smooth(metho
d = "glm")
```



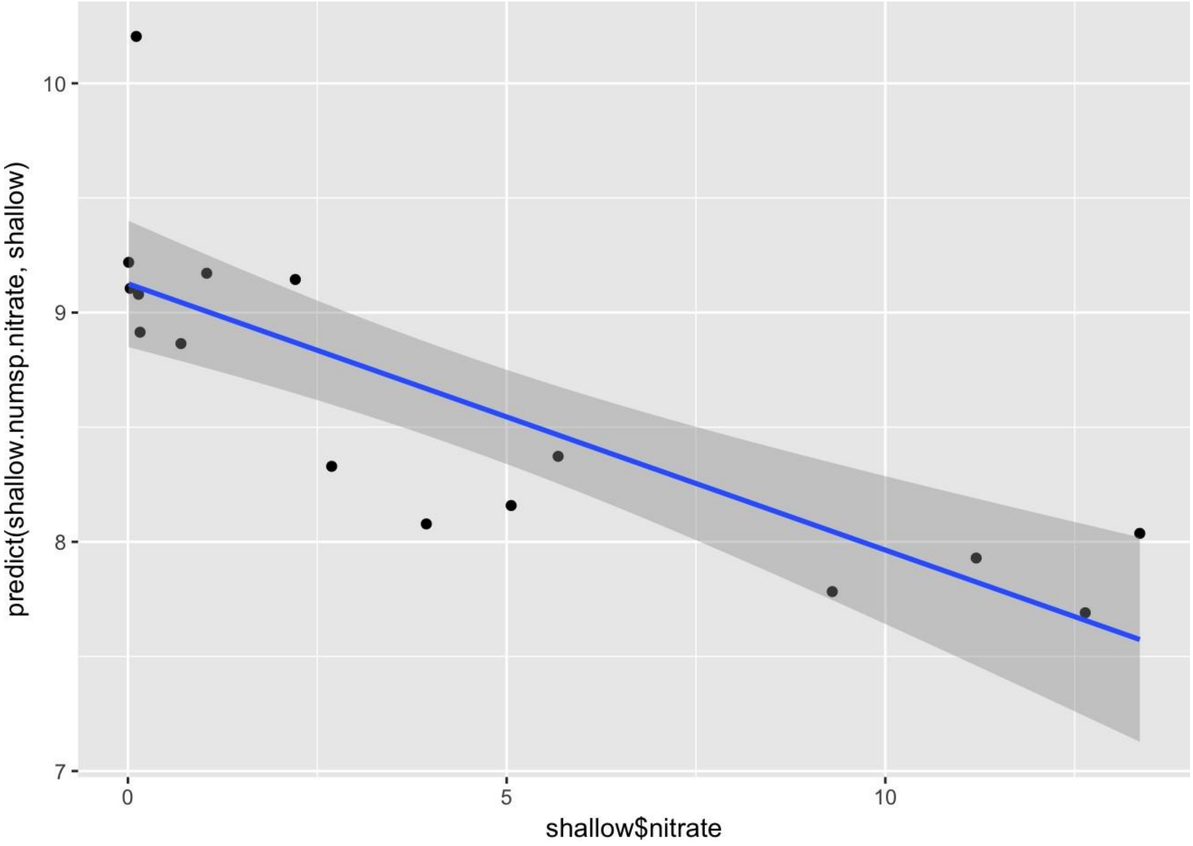
```
qplot(shallow$o2.saturate, predict(shallow.numsp.o2.saturate, shallow)) + geom_smoo
th(method = "glm")
```



```
qplot(shallow$salinity, predict(shallow.numsp.salinity, shallow)) + geom_smooth(met
hod = "glm")
```



```
qplot(shallow$nitrate, predict(shallow.numsp.nitrate, shallow)) + geom_smooth(metho
d = "glm")
```



GLMs for ES50, shallow water

These models are identical to the above, except that the response variable is the species richness estimated from the rarefaction curves. These are meant to be estimates of species richness if all sites were sampled equally. Since these measurements are intended to take sampling effort into account, we exclude the “num.records” term for these models.

```
shallow.es50.intercept <- glm(ES50 ~ 1, family = "poisson", data = shallow)
summary(shallow.es50.intercept)
```

```
##
## Call:
## glm(formula = ES50 ~ 1, family = "poisson", data = shallow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.6830  -0.5683  -0.1248   0.4342   3.1278
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.52072    0.07089   35.56   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 30.953  on 15  degrees of freedom
## Residual deviance: 30.953  on 15  degrees of freedom
## AIC: 101.37
##
## Number of Fisher Scoring iterations: 4
```

```
shallow.es50.temp <- glm(ES50 ~ temp, family = "poisson", data = shallow)
summary(shallow.es50.temp)
```

```
##
## Call:
## glm(formula = ES50 ~ temp, family = "poisson", data = shallow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -4.0864   -0.4847    0.0168    0.4444    2.5418
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.648781   0.106161  24.951   <2e-16 ***
## temp        -0.009224   0.005973  -1.544    0.122
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 30.953  on 15  degrees of freedom
## Residual deviance: 28.559  on 14  degrees of freedom
## AIC: 100.98
##
## Number of Fisher Scoring iterations: 4
```

```
shallow.es50.oxygen <- glm(ES50 ~ dissolved.oxygen, family = "poisson", data = shal
low)
summary(shallow.es50.oxygen)
```

```
##
## Call:
## glm(formula = ES50 ~ dissolved.oxygen, family = "poisson", data = shallow)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -4.1101   -0.4847   -0.0217    0.5021    2.5835
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)      2.113708   0.297882   7.096 1.29e-12 ***
## dissolved.oxygen 0.001467   0.001030   1.424    0.154
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 30.953  on 15  degrees of freedom
## Residual deviance: 28.934  on 14  degrees of freedom
## AIC: 101.36
##
## Number of Fisher Scoring iterations: 5
```

```
shallow.es50.prod <- glm(ES50 ~ primary.productivity, family = "poisson", data = sh
allow)
summary(shallow.es50.prod)
```

```
##
## Call:
## glm(formula = ES50 ~ primary.productivity, family = "poisson",
##     data = shallow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.7981  -0.6577   0.1055   0.4421   2.8239
##
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)            2.6137     0.1272  20.542   <2e-16 ***
## primary.productivity -18.1957    21.0964  -0.863    0.388
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 30.953  on 15  degrees of freedom
## Residual deviance: 30.197  on 14  degrees of freedom
## AIC: 102.62
##
## Number of Fisher Scoring iterations: 4
```

```
shallow.es50.chlorophyll <- glm(ES50 ~ chlorophyll, family = "poisson", data = shal
low)
summary(shallow.es50.chlorophyll)
```

```
##
## Call:
## glm(formula = ES50 ~ chlorophyll, family = "poisson", data = shallow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.5850  -0.6251  -0.0227   0.3515   3.1121
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.5634     0.1236  20.746   <2e-16 ***
## chlorophyll  -0.1234     0.2959  -0.417    0.677
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 30.953  on 15  degrees of freedom
## Residual deviance: 30.778  on 14  degrees of freedom
## AIC: 103.2
##
## Number of Fisher Scoring iterations: 4
```

```
shallow.es50.current <- glm(ES50 ~ current, family = "poisson", data = shallow)
summary(shallow.es50.current)
```

```
##
## Call:
## glm(formula = ES50 ~ current, family = "poisson", data = shallow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.9141  -0.4697   0.0144   0.5715   2.8536
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.6260     0.1285  20.436   <2e-16 ***
## current      -1.2585     1.3101  -0.961    0.337
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 30.953  on 15  degrees of freedom
## Residual deviance: 30.008  on 14  degrees of freedom
## AIC: 102.43
##
## Number of Fisher Scoring iterations: 4
```

```
shallow.es50.o2.saturate <- glm(ES50 ~ o2.saturate, family = "poisson", data = shal
low)
summary(shallow.es50.o2.saturate)
```

```
##
## Call:
## glm(formula = ES50 ~ o2.saturate, family = "poisson", data = shallow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -4.1129  -0.4209   0.1394   0.4739   2.2156
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  9.87123    4.18524   2.359   0.0183 *
## o2.saturate -0.07276    0.04147  -1.755   0.0793 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 30.953  on 15  degrees of freedom
## Residual deviance: 27.895  on 14  degrees of freedom
## AIC: 100.32
##
## Number of Fisher Scoring iterations: 4
```

```
shallow.es50.salinity <- glm(ES50 ~ salinity, family = "poisson", data = shallow)
summary(shallow.es50.salinity)
```

```
##
## Call:
## glm(formula = ES50 ~ salinity, family = "poisson", data = shallow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -4.1826  -0.3624   0.0295   0.5597   2.6606
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  4.34860    1.44031   3.019  0.00253 **
## salinity    -0.05563    0.04388  -1.268  0.20484
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 30.953  on 15  degrees of freedom
## Residual deviance: 29.379  on 14  degrees of freedom
## AIC: 101.8
##
## Number of Fisher Scoring iterations: 5
```

```
shallow.es50.nitrate <- glm(ES50 ~ nitrate, family = "poisson", data = shallow)
summary(shallow.es50.nitrate)
```

```
##
## Call:
## glm(formula = ES50 ~ nitrate, family = "poisson", data = shallow)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.6731  -0.4479  -0.1586   0.4444   3.1042
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) 2.484316   0.097391  25.509   <2e-16 ***
## nitrate     0.008352   0.015006   0.557    0.578
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 30.953  on 15  degrees of freedom
## Residual deviance: 30.646  on 14  degrees of freedom
## AIC: 103.07
##
## Number of Fisher Scoring iterations: 4
```

Model selection for ES50, shallow water

Here we use AIC to compare models for goodness of fit while penalizing for overparameterization. Models are ranked in order of AIC score, with lowest scoring model (model with the best compromise between fit and complexity) first in the list. The delta AIC represents how much the

AIC score for each model differs from the top model, an can be used as an estimate of the relative support for each model. A delta AIC of 2 is considered to be potentially a significantly better fit, with higher delta AICs between models indicating increasingly larger differences in model fit while correcting for the number of parameters.

```
shallow.es50.models <- list(shallow.es50.intercept = shallow.es50.intercept,
                            shallow.es50.temp = shallow.es50.temp,
                            shallow.es50.oxygen = shallow.es50.oxygen,
                            shallow.es50.prod = shallow.es50.prod,
                            shallow.es50.chlorophyll = shallow.es50.chlorophyll,
                            shallow.es50.current = shallow.es50.current,
                            shallow.es50.o2.saturate = shallow.es50.o2.saturate,
                            shallow.es50.salinity = shallow.es50.salinity,
                            shallow.es50.nitrate = shallow.es50.nitrate)
shallow.es50.aic.df <- data.frame(Model = names(shallow.es50.models),
                                   AIC = sapply(shallow.es50.models, function(x) AICc
(x)),
                                  akaike.weights(sapply(shallow.es50.models,  function(x)
 AICc(x))))

shallow.es50.aic.df <- shallow.es50.aic.df[order(shallow.es50.aic.df$AIC),]
shallow.es50.aic.df$Cumulative.Weight <- cumsum(shallow.es50.aic.df$weights)

kable(shallow.es50.aic.df, row.names = FALSE)
```

Model	AIC	deltaAIC	rel.LL	weights	Cumulative.Weight
shallow.es50.o2.saturate	101.2391	0.0000000	1.0000000	0.2104438	0.2104438
shallow.es50.intercept	101.6597	0.4206558	0.8103185	0.1705265	0.3809704
shallow.es50.temp	101.9027	0.6636585	0.7176098	0.1510166	0.5319869
shallow.es50.oxygen	102.2781	1.0390737	0.5947960	0.1251711	0.6571581
shallow.es50.salinity	102.7235	1.4843970	0.4760661	0.1001852	0.7573432
shallow.es50.current	103.3525	2.1133812	0.3476043	0.0731512	0.8304944
shallow.es50.prod	103.5417	2.3026027	0.3162250	0.0665476	0.8970420
shallow.es50.nitrate	103.9905	2.7513899	0.2526639	0.0531716	0.9502136
shallow.es50.chlorophyll	104.1220	2.8829527	0.2365782	0.0497864	1.0000000

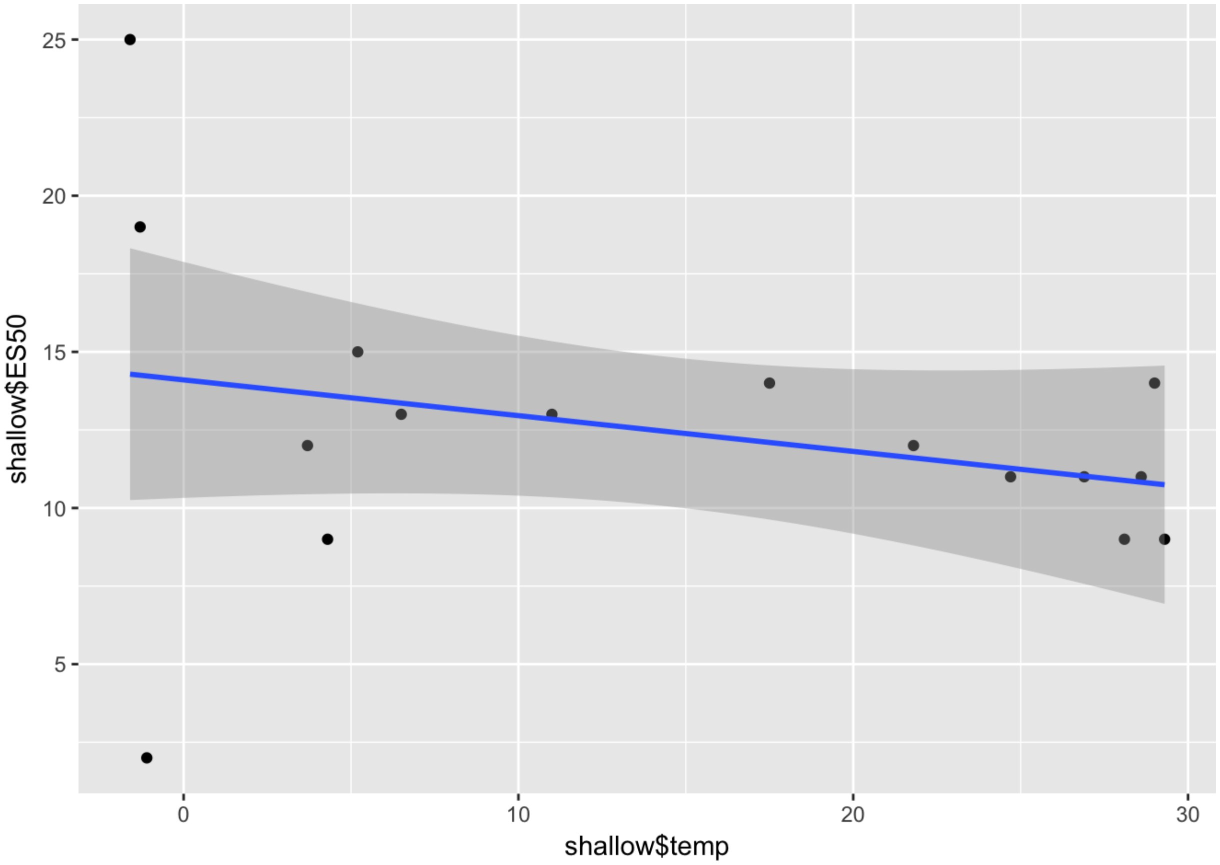
```
write.csv(shallow.es50.aic.df, file = "shallow.5.degree.es50.aic.csv")
```

Here we see that the model containing only the intercept is the best fit, indicating no support for any environmental variable as a useful predictor of ES50 in shallow water.

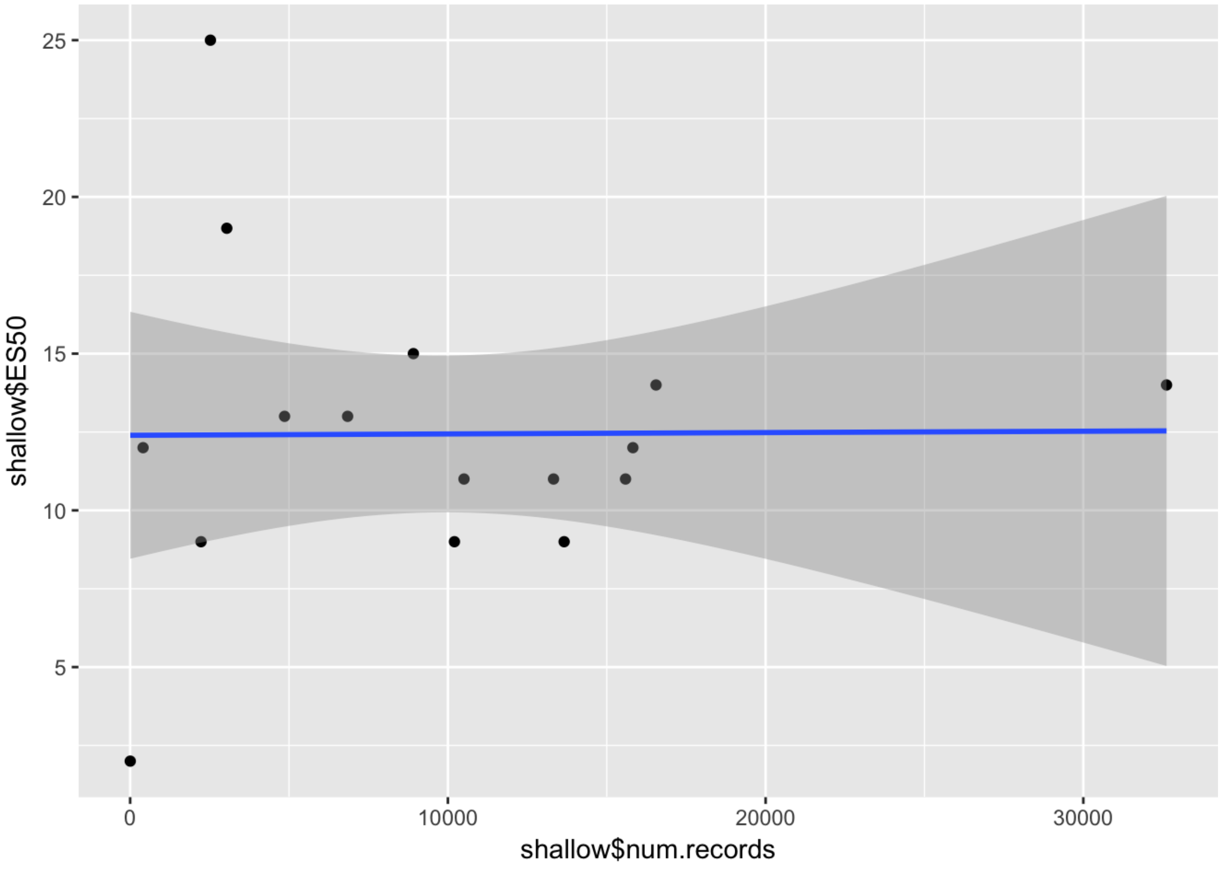
Plots for ES50, shallow water

Here we plot the effects of each environmental predictor from its respective single-variable model.

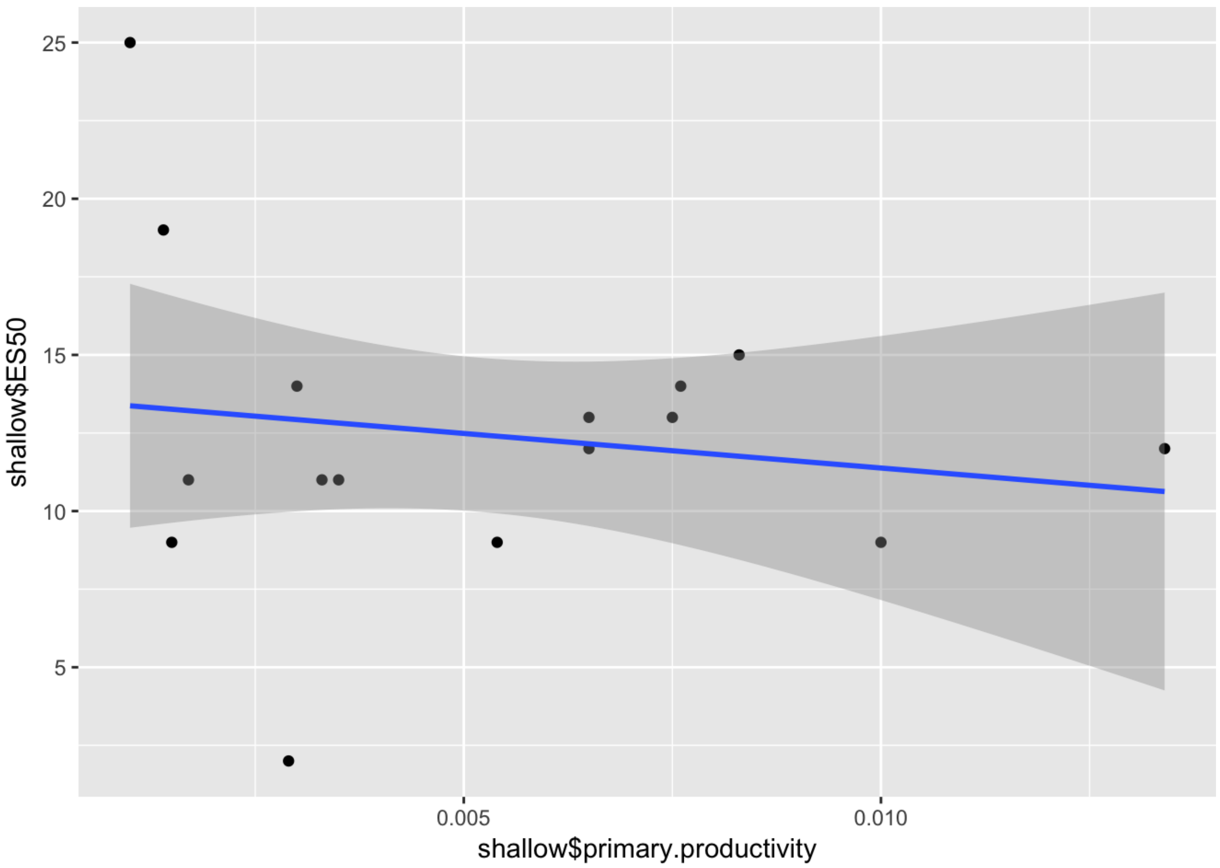
```
qplot(shallow$temp, shallow$ES50) + geom_smooth(method = "glm")
```



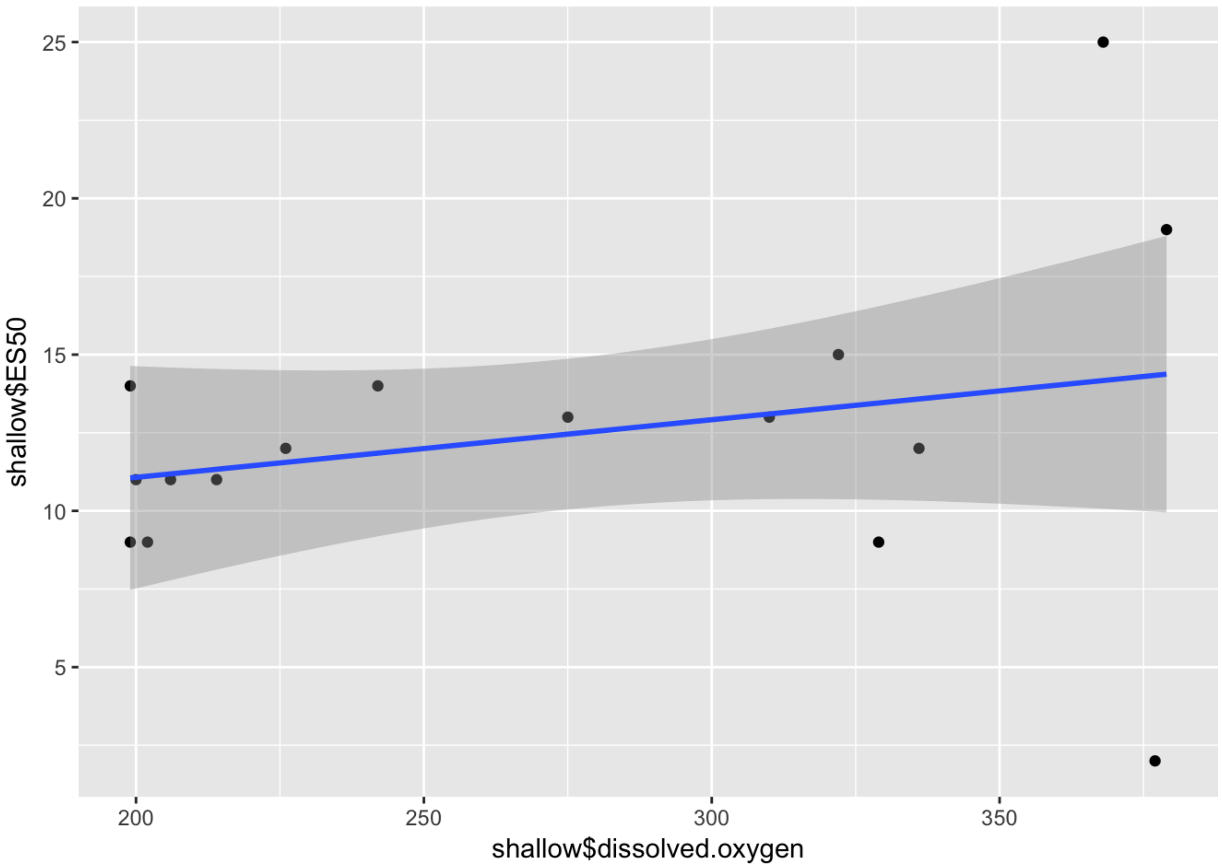
```
qplot(shallow$num.records, shallow$ES50) + geom_smooth(method = "glm")
```



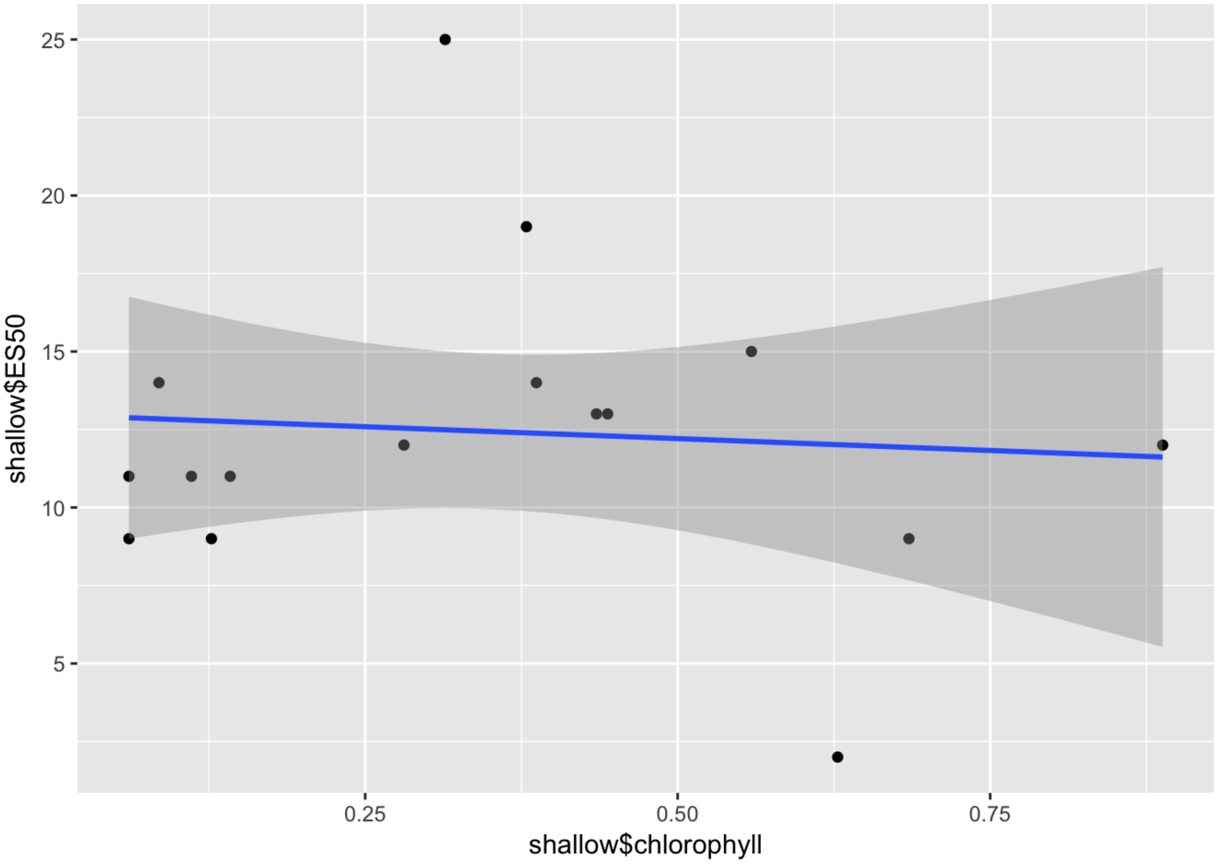
```
qplot(shallow$primary.productivity, shallow$ES50) + geom_smooth(method = "glm")
```



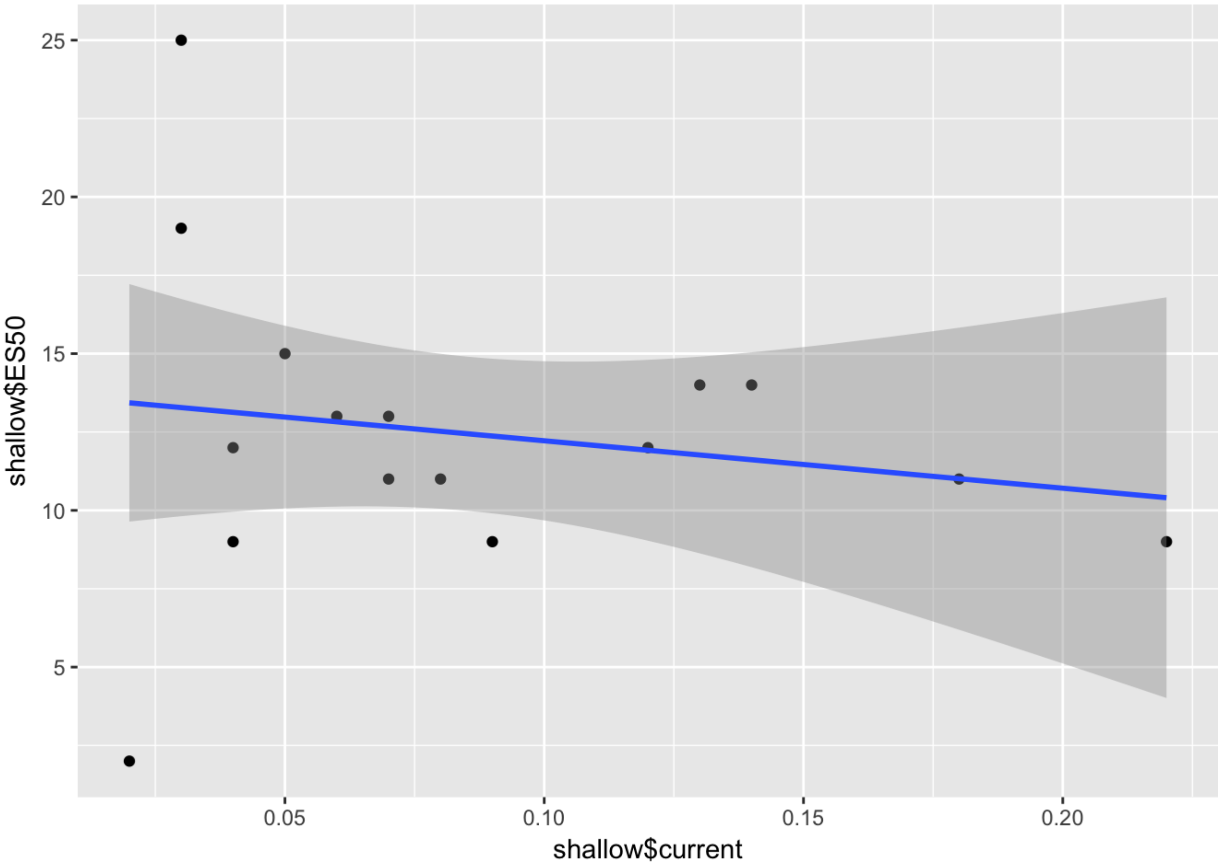
```
qplot(shallow$dissolved.oxygen, shallow$ES50) + geom_smooth(method = "glm")
```



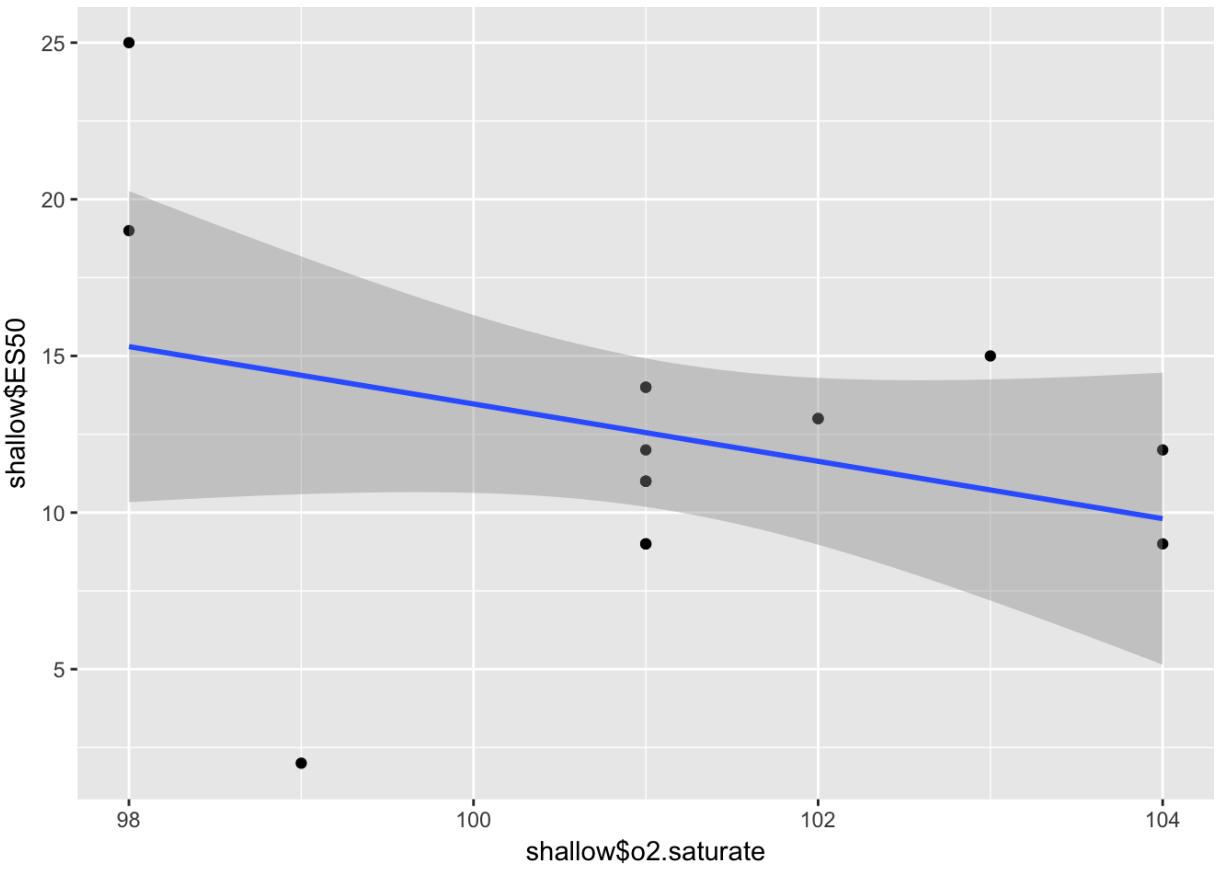
```
qplot(shallow$chlorophyll, shallow$ES50) + geom_smooth(method = "glm")
```



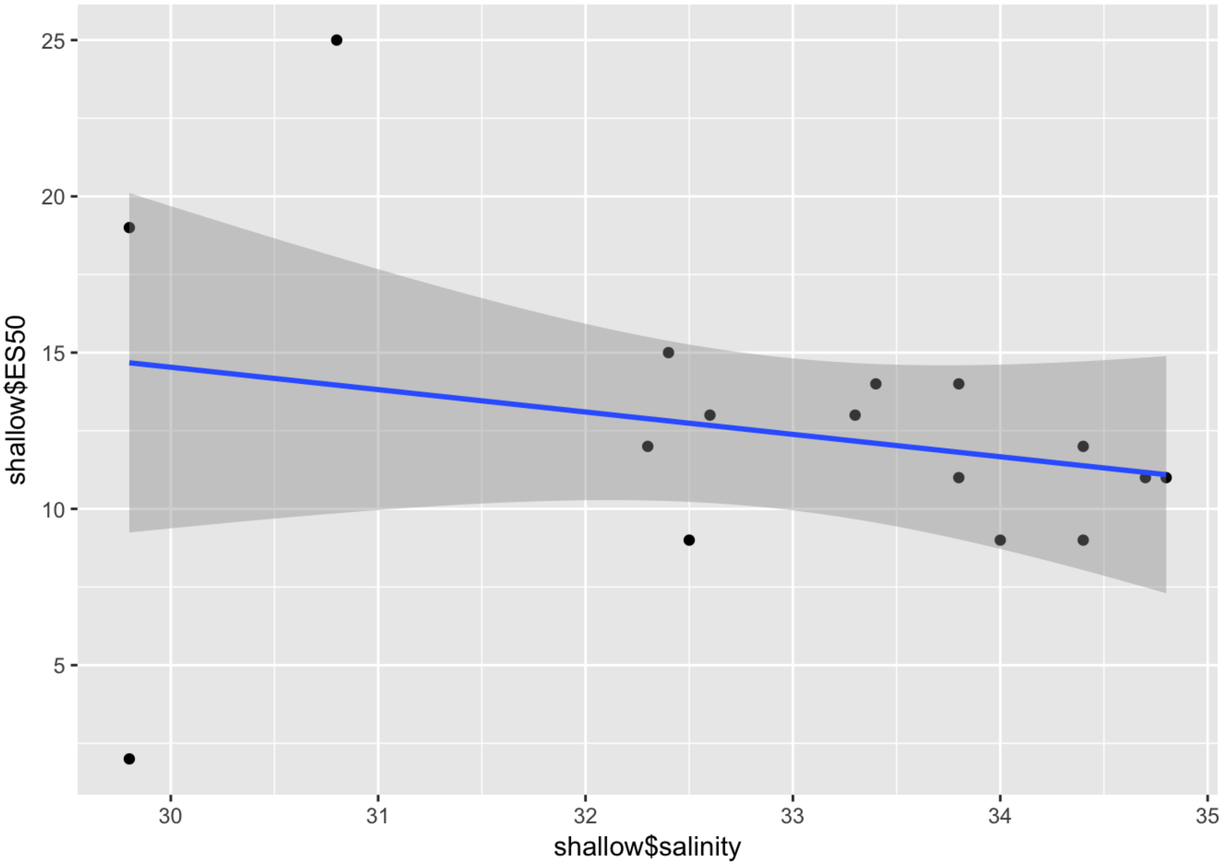
```
qplot(shallow$current, shallow$ES50) + geom_smooth(method = "glm")
```



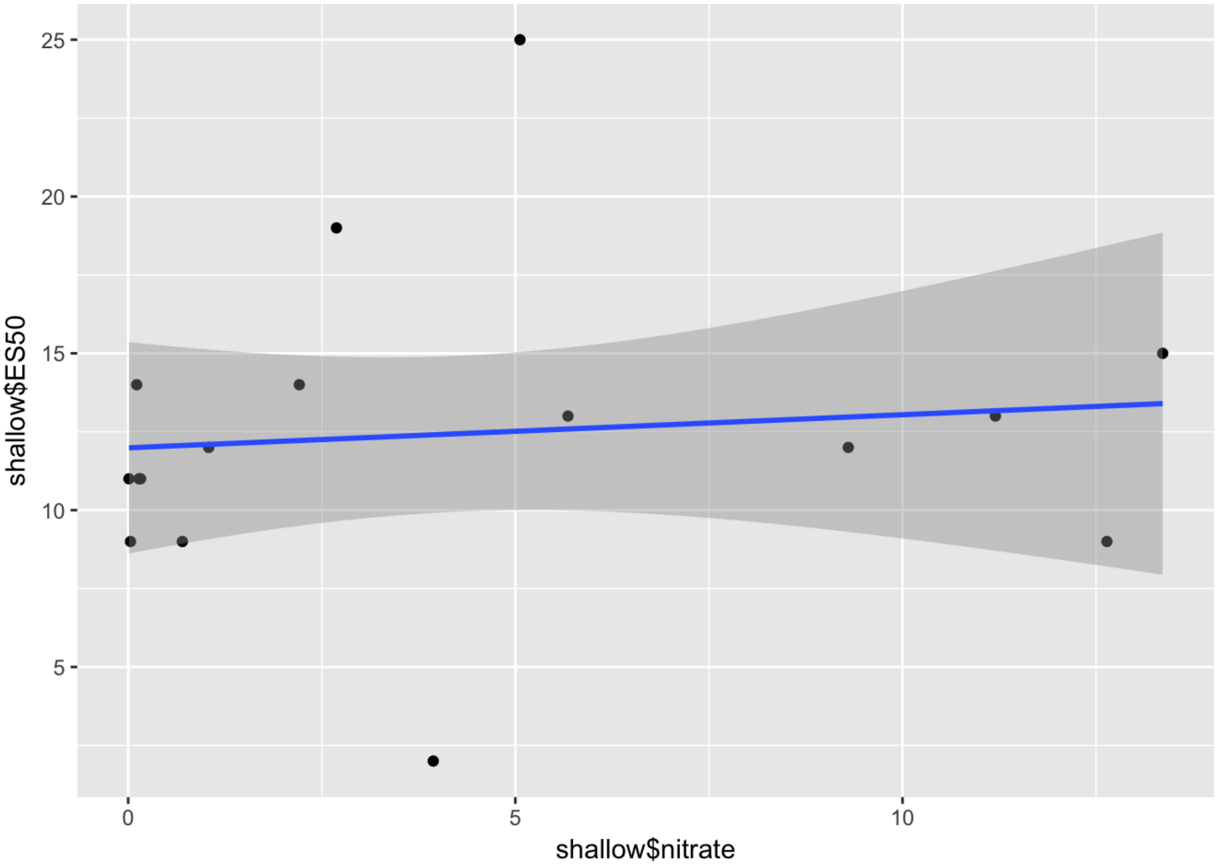
```
qplot(shallow$o2.saturate, shallow$ES50) + geom_smooth(method = "glm")
```



```
qplot(shallow$salinity, shallow$ES50) + geom_smooth(method = "glm")
```



```
qplot(shallow$nitrate, shallow$ES50) + geom_smooth(method = "glm")
```

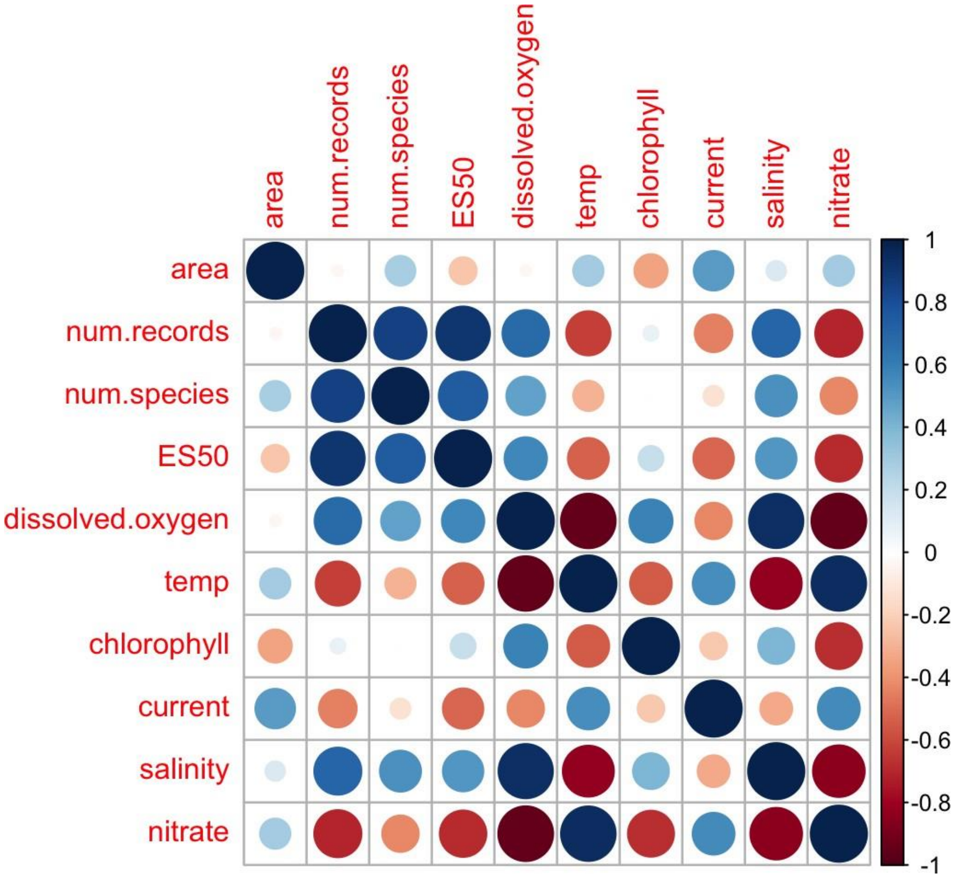


Deep water

Data load-in and visualization

First we're going to load in our data and then trim the data frame down to just the columns we need.

```
deep <- read.csv("deep.5.degree.csv")
analysis.cols <- c("area", "num.records", "num.species", "ES50", "dissolved.oxygen"
, "temp", "chlorophyll", "current", "salinity", "nitrate")
deep <- deep[,analysis.cols]
deep <- deep[complete.cases(deep),]
corrplot(cor(deep))
```



GLMs for number of species, deep water

We're going to develop a number of GLMs here. The "intercept" glm represents the fit of a model that assumes no relationship between the species counts and the environment and no spatial autocorrelation. The "latlon" model represents the fit of a model that fits spatial autocorrelation, but no environmental effects. The "env" model represents the combined effects of all environmental predictors, and the remainder of the models ("temp", "oxygen", etc.) estimate the effects of a single predictor at a time.

```
deep.numsp.intercept <- glm(num.species ~ 1, family = "poisson", data = deep)
summary(deep.numsp.intercept)
```

```
##
## Call:
## glm(formula = num.species ~ 1, family = "poisson", data = deep)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -34.368  -14.677   -8.063   11.747   43.628
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) 6.621139   0.009423   702.7   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 6924.5  on 14  degrees of freedom
## Residual deviance: 6924.5  on 14  degrees of freedom
## AIC: 7047.2
##
## Number of Fisher Scoring iterations: 5
```

```
deep.numsp.numrec <- glm(num.species ~ num.records, family = "poisson", data = dee
p)
summary(deep.numsp.numrec)
```

```
##
## Call:
## glm(formula = num.species ~ num.records, family = "poisson",
##     data = deep)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -24.113  -10.134   -4.026    6.374   26.968
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) 6.041e+00  1.443e-02  418.60   <2e-16 ***
## num.records 4.357e-04  6.318e-06   68.97   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 6924.5  on 14  degrees of freedom
## Residual deviance: 3013.2  on 13  degrees of freedom
## AIC: 3138
##
## Number of Fisher Scoring iterations: 5
```

```
deep.numsp.temp <- glm(num.species ~ num.records + temp, family = "poisson", data =
deep)
summary(deep.numsp.temp)
```

```
##
## Call:
## glm(formula = num.species ~ num.records + temp, family = "poisson",
##     data = deep)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -27.583   -8.959   -1.936    9.030   15.068
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) 5.386e+00  2.904e-02  185.44   <2e-16 ***
## num.records 6.214e-04  9.376e-06   66.28   <2e-16 ***
## temp        3.713e-01  1.367e-02   27.16   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 6924.5  on 14  degrees of freedom
## Residual deviance: 2303.3  on 12  degrees of freedom
## AIC: 2430
##
## Number of Fisher Scoring iterations: 5
```

```
deep.numsp.oxygen <- glm(num.species ~ num.records + dissolved.oxygen, family =
"poisson", data = deep)
summary(deep.numsp.oxygen)
```

```
##
## Call:
## glm(formula = num.species ~ num.records + dissolved.oxygen, family = "poisson",
##     data = deep)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -27.384   -9.683   -3.208   10.448   20.957
##
## Coefficients:
##                    Estimate Std. Error z value Pr(>|z|)
## (Intercept)       6.307e+00  2.787e-02  226.29   <2e-16 ***
## num.records       5.319e-04  1.096e-05   48.53   <2e-16 ***
## dissolved.oxygen -2.340e-03  2.154e-04  -10.87   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 6924.5  on 14  degrees of freedom
## Residual deviance: 2891.7  on 12  degrees of freedom
## AIC: 3018.4
##
## Number of Fisher Scoring iterations: 5
```

```
deep.numsp.chlorophyll <- glm(num.species ~ num.records + chlorophyll, family =
"poisson", data = deep)
summary(deep.numsp.chlorophyll)
```

```
##
## Call:
## glm(formula = num.species ~ num.records + chlorophyll, family = "poisson",
##     data = deep)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -24.058  -10.067   -3.955    6.157   27.056
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) 5.184e+00  8.279e-01   6.262 3.81e-10 ***
## num.records 4.362e-04  6.342e-06  68.776  < 2e-16 ***
## chlorophyll 1.939e+02  1.874e+02   1.035    0.301
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 6924.5  on 14  degrees of freedom
## Residual deviance: 3012.2  on 12  degrees of freedom
## AIC: 3138.9
##
## Number of Fisher Scoring iterations: 5
```

```
deep.numsp.current <- glm(num.species ~ num.records + current, family = "poisson",
data = deep)
summary(deep.numsp.current)
```

```
##
## Call:
## glm(formula = num.species ~ num.records + current, family = "poisson",
##     data = deep)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -20.1499  -11.5189    0.9779    6.6915   17.6137
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) 4.747e+00  4.264e-02  111.33   <2e-16 ***
## num.records 6.496e-04  9.417e-06   68.98   <2e-16 ***
## current     1.208e+02  3.541e+00   34.13   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 6924.5  on 14  degrees of freedom
## Residual deviance: 1915.3  on 12  degrees of freedom
## AIC: 2042
##
## Number of Fisher Scoring iterations: 4
```

```
deep.numsp.salinity <- glm(num.species ~  num.records +  salinity, family = "poisso
n", data = deep)
summary(deep.numsp.salinity)
```

```
##
## Call:
## glm(formula = num.species ~ num.records + salinity, family = "poisson",
##     data = deep)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -27.744   -9.292   -3.172    7.553   23.695
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.348e+01  3.423e+00   9.780  < 2e-16 ***
## num.records  5.147e-04  1.183e-05  43.513  < 2e-16 ***
## salinity    -7.938e-01  9.905e-02  -8.014 1.11e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 6924.5  on 14  degrees of freedom
## Residual deviance: 2949.8  on 12  degrees of freedom
## AIC: 3076.5
##
## Number of Fisher Scoring iterations: 5
```

```
deep.numsp.nitrate <- glm(num.species ~  num.records +  nitrate, family = "poisson"
, data = deep)
summary(deep.numsp.nitrate)
```

```
##
## Call:
## glm(formula = num.species ~ num.records + nitrate, family = "poisson",
##     data = deep)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -25.694   -9.033   -2.933   10.986   20.035
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) 4.348e+00  7.881e-02   55.16   <2e-16 ***
## num.records 6.670e-04  1.227e-05   54.37   <2e-16 ***
## nitrate     4.146e-02  1.871e-03   22.16   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 6924.5  on 14  degrees of freedom
## Residual deviance: 2473.9  on 12  degrees of freedom
## AIC: 2600.7
##
## Number of Fisher Scoring iterations: 5
```

Model selection for number of species, deep water

Here we use AIC to compare models for goodness of fit while penalizing for overparameterization. Models are ranked in order of AIC score, with lowest scoring model (model with the best compromise between fit and complexity) first in the list. The delta AIC represents how much the AIC score for each model differs from the top model, an can be used as an estimate of the relative support for each model. A delta AIC of 2 is considered to be potentially a significantly better fit, with higher delta AICs between models indicating increasingly larger differences in model fit while correcting for the number of parameters.

```
deep.numsp.models <- list(deep.numsp.intercept = deep.numsp.intercept,
                          deep.numsp.temp = deep.numsp.temp,
                          deep.numsp.numrec = deep.numsp.numrec,
                          deep.numsp.oxygen = deep.numsp.oxygen,
                          deep.numsp.chlorophyll = deep.numsp.chlorophyll,
                          deep.numsp.current = deep.numsp.current,
                          deep.numsp.salinity = deep.numsp.salinity,
                          deep.numsp.nitrate = deep.numsp.nitrate)
deep.numsp.aic.df <- data.frame(Model = names(deep.numsp.models),
                                AIC = sapply(deep.numsp.models, function(x) AICc(x)),
                               akaike.weights(sapply(deep.numsp.models, function(x) AI
Cc(x))))

deep.numsp.aic.df <- deep.numsp.aic.df[order(deep.numsp.aic.df$AIC),]
deep.numsp.aic.df$Cumulative.Weight <- cumsum(deep.numsp.aic.df$weights)

kable(deep.numsp.aic.df, row.names = FALSE)
```

Model	AIC	deltaAIC	rel.LL	weights	Cumulative.Weight
deep.numsp.current	2044.206	0.0000	1	1	1
deep.numsp.temp	2432.181	387.9754	0	0	1
deep.numsp.nitrate	2602.863	558.6573	0	0	1
deep.numsp.oxygen	3020.607	976.4008	0	0	1
deep.numsp.salinity	3078.730	1034.5245	0	0	1
deep.numsp.numrec	3138.989	1094.7832	0	0	1
deep.numsp.chlorophyll	3141.111	1096.9052	0	0	1
deep.numsp.intercept	7047.531	5003.3255	0	0	1

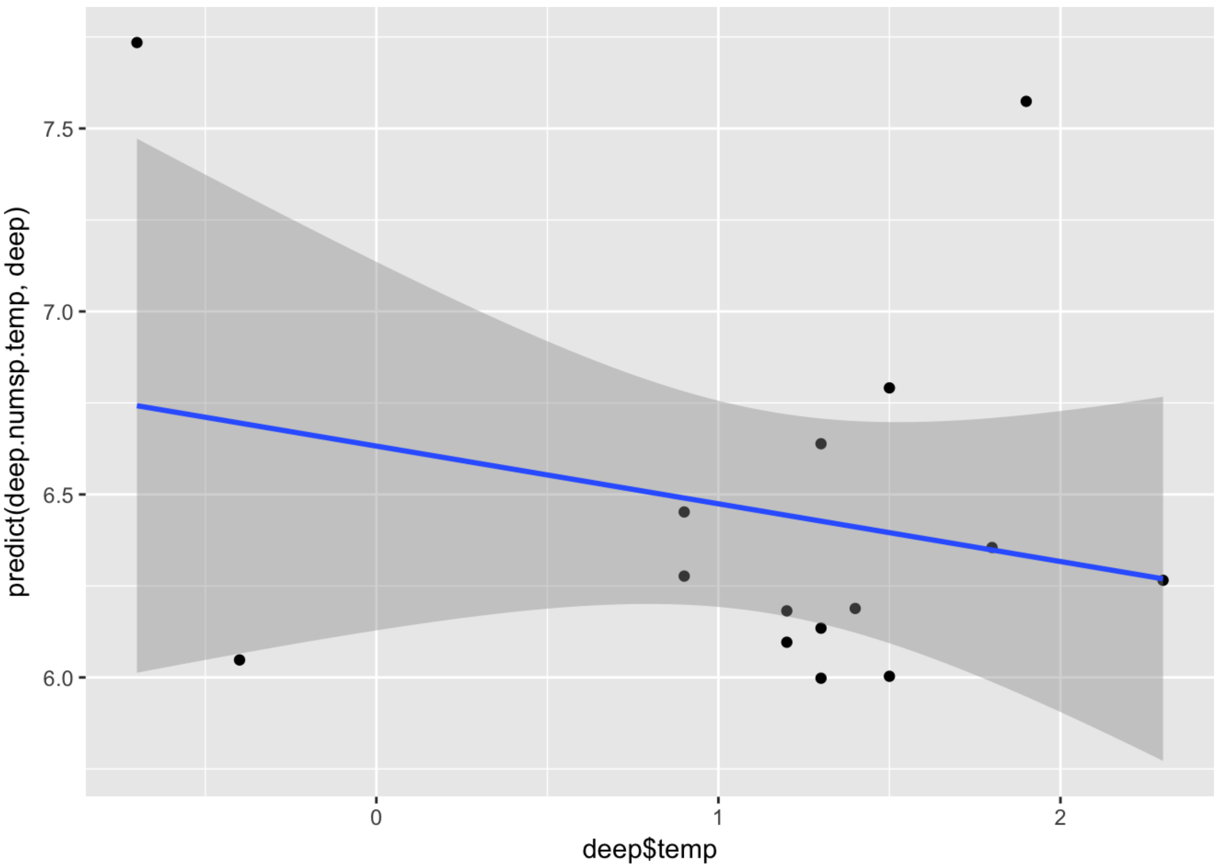
```
write.csv(deep.numsp.aic.df, file = "deep.5.degree.numsp.aic.csv")
```

Here we see that the models containing temperature and current have the best fit, with everything else having a delta AIC over 2. Notably the “numrec” model has a delta AIC over that threshold, indicating that temperature and current have some level of explanatory power for number of species.

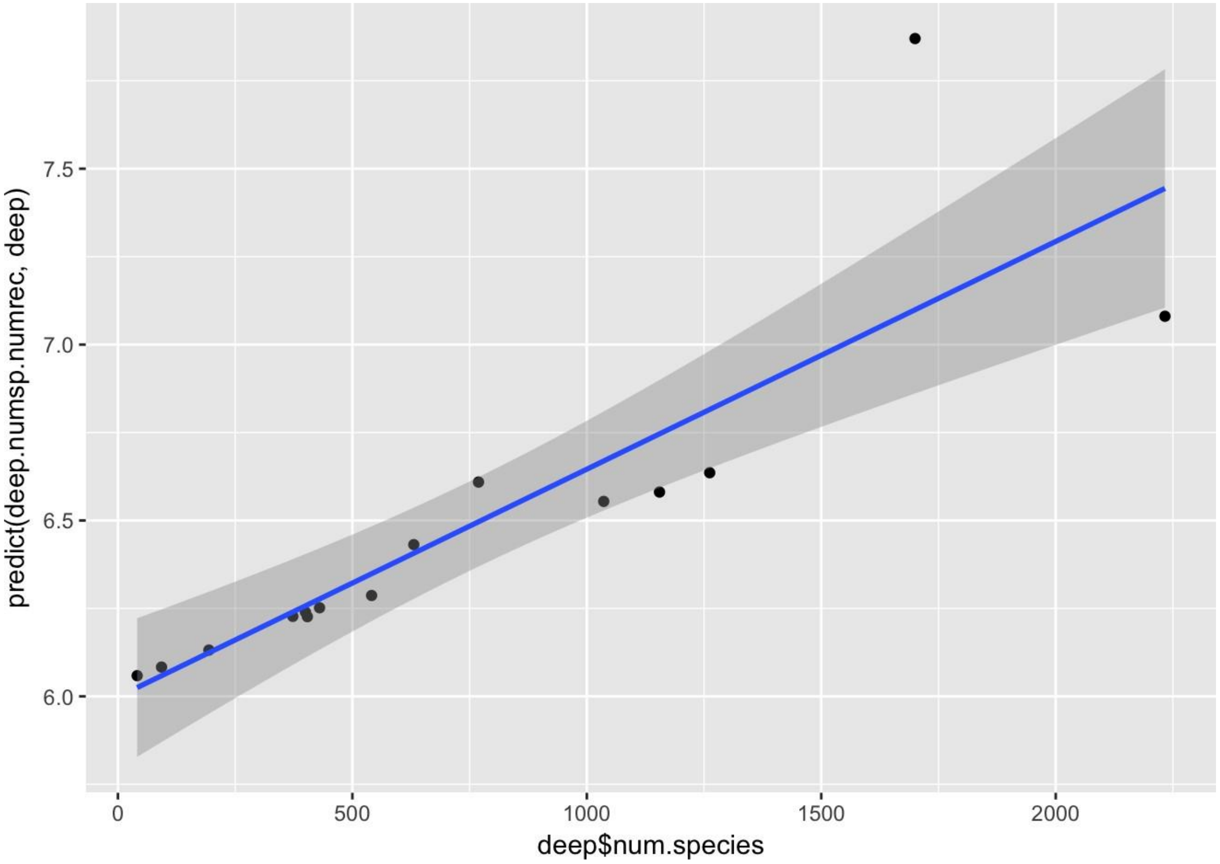
Plots for number of species, deep water

Here we plot the effects of each environmental predictor from its respective single-variable model.

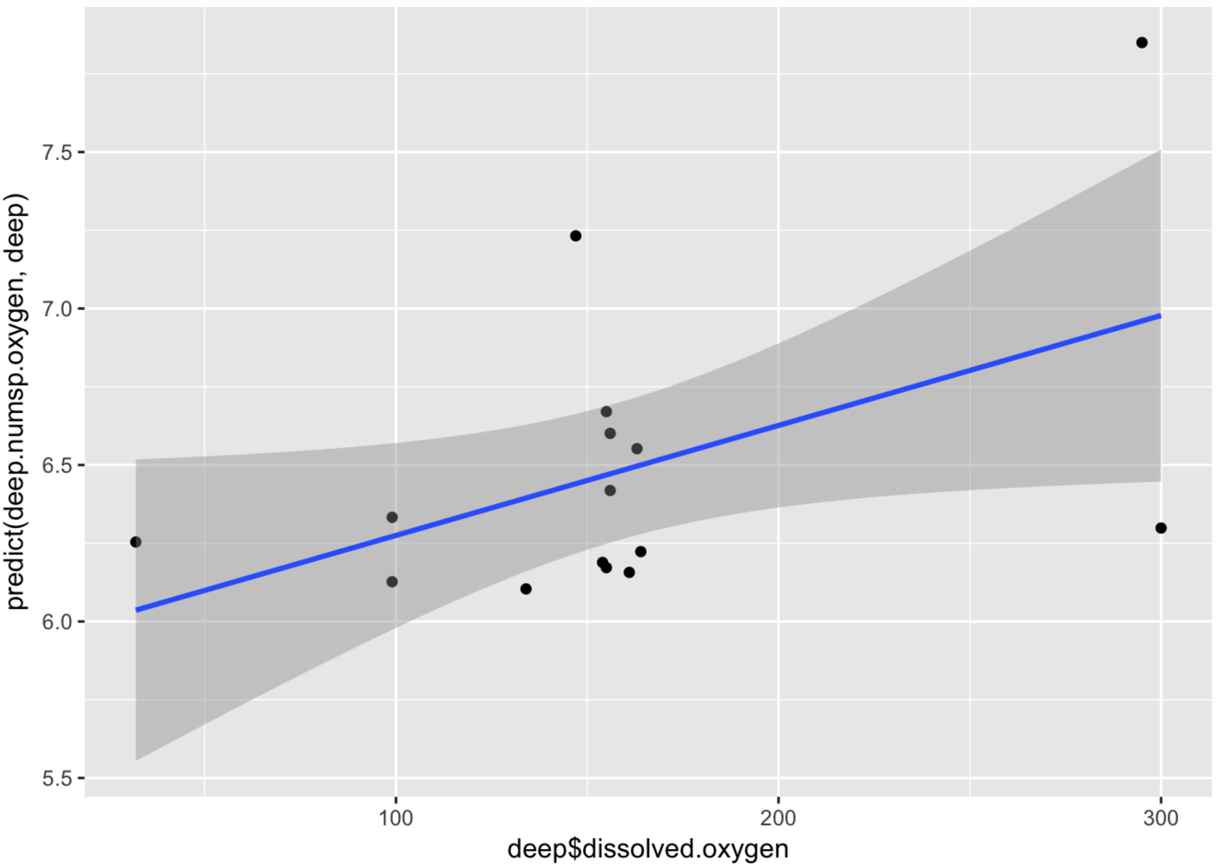
```
qplot(deep$temp, predict(deep.numsp.temp, deep)) + geom_smooth(method = "glm")
```



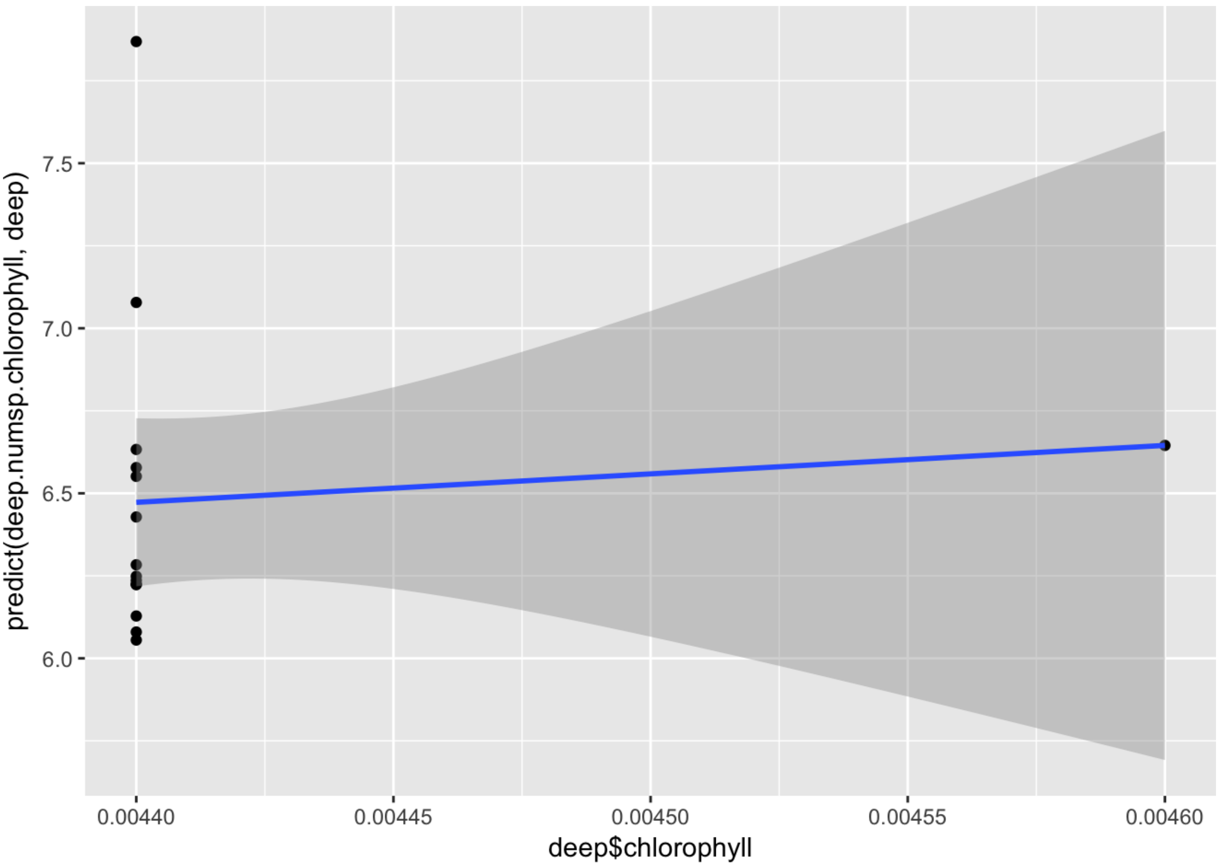
```
qplot(deep$num.species, predict(deep.numsp.numrec, deep)) + geom_smooth(method = "g
lm")
```



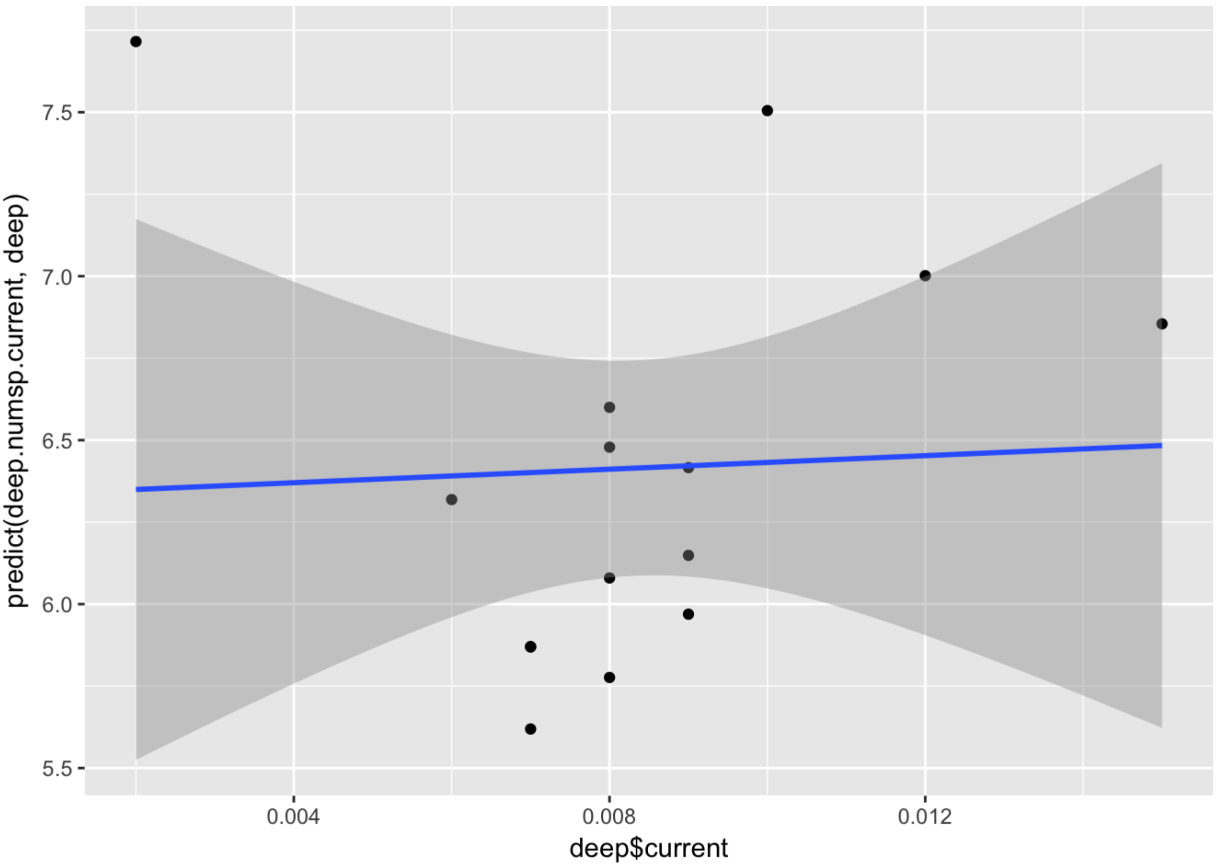
```
qplot(deep$dissolved.oxygen, predict(deep.numsp.oxygen, deep)) + geom_smooth(method
= "glm")
```



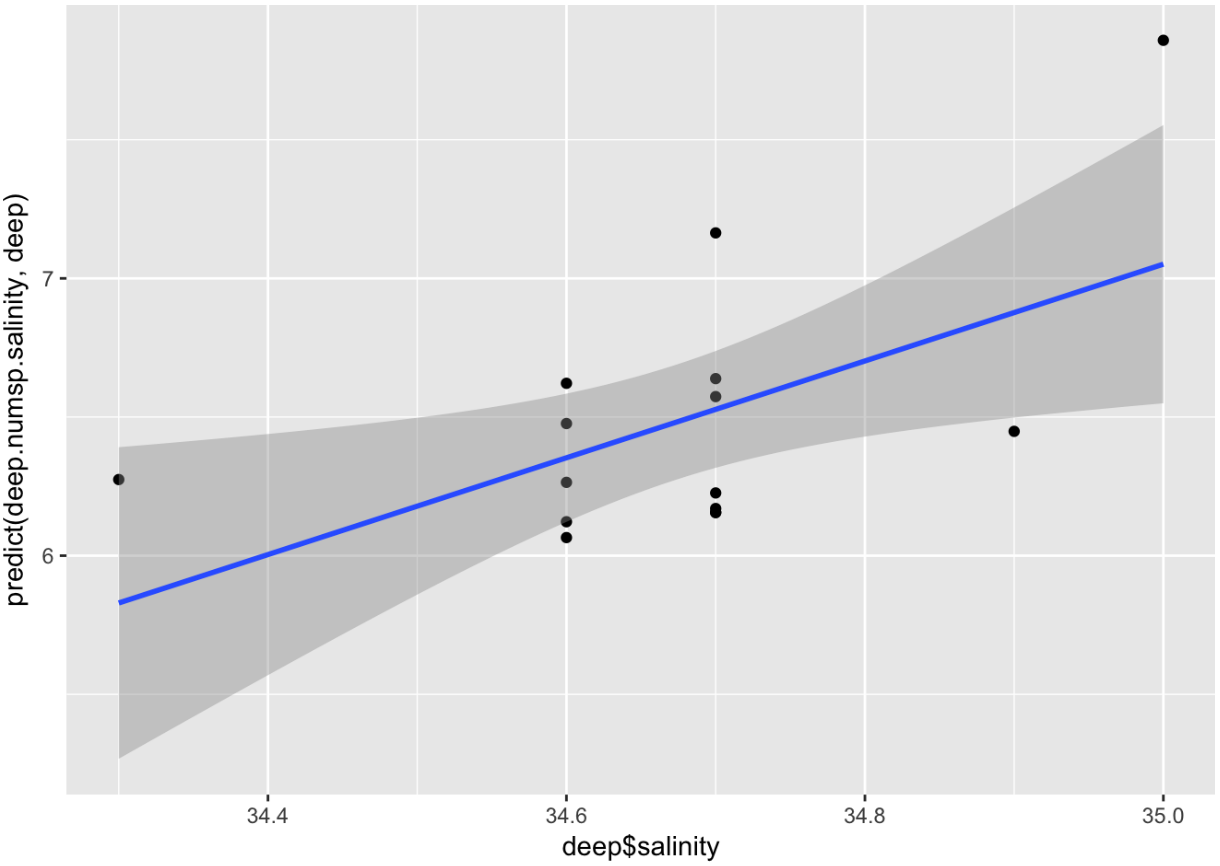
```
qplot(deep$chlorophyll, predict(deep.numsp.chlorophyll, deep)) +  geom_smooth(method
= "glm")
```



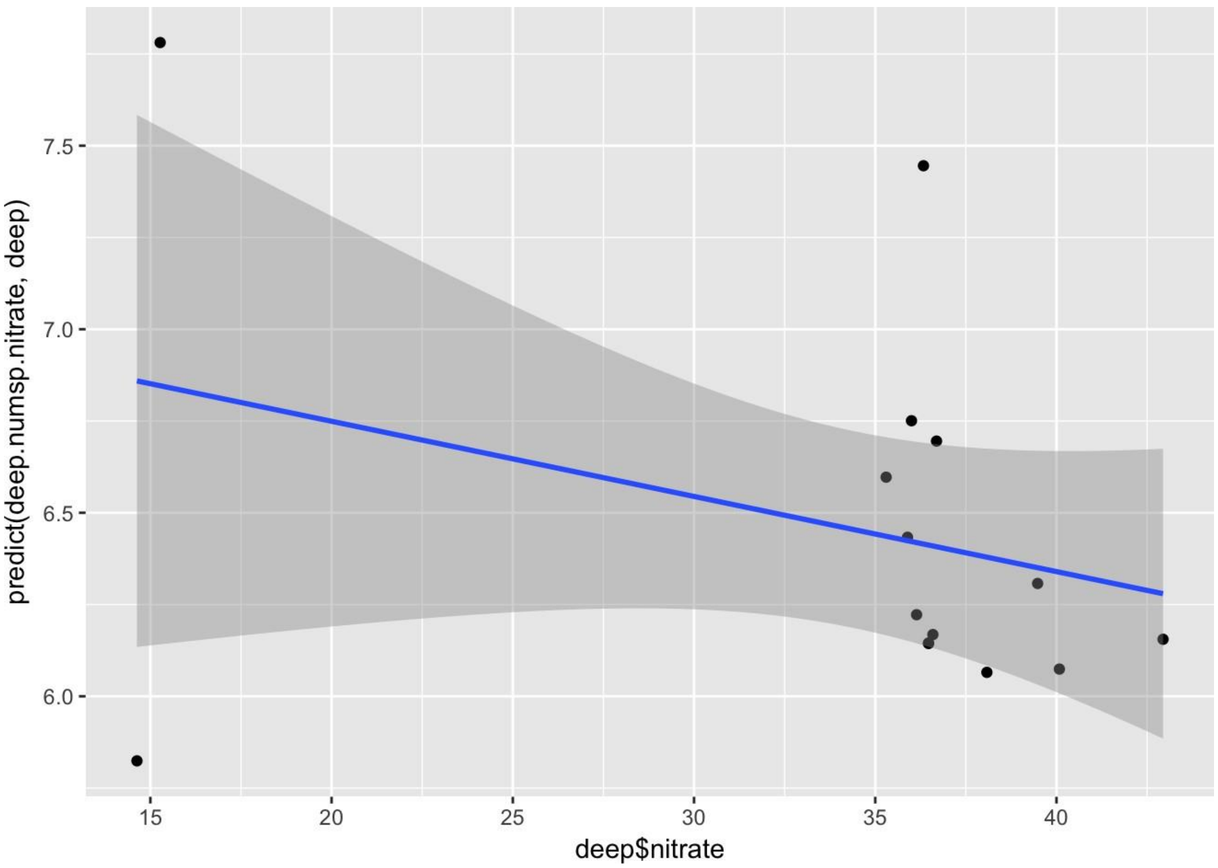
```
qplot(deep$current, predict(deep.numsp.current, deep)) + geom_smooth(method = "glm"
)
```



```
qplot(deep$salinity, predict(deep.numsp.salinity, deep)) + geom_smooth(method = "gl
m")
```



```
qplot(deep$nitrate, predict(deep.numsp.nitrate, deep)) + geom_smooth(method =  "glm"
)
```



GLMs for ES50, deep water

These models are identical to the above, except that the response variable is the species richness estimated from the rarefaction curves. These are meant to be estimates of species richness if all sites were sampled equally. Since these measurements are intended to take sampling effort into account, we exclude the “num.records” term for these models.

```
deep.es50.intercept <- glm(ES50 ~ 1, family = "poisson", data = deep)
summary(deep.es50.intercept)
```

```
##
## Call:
## glm(formula = ES50 ~ 1, family = "poisson", data = deep)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.8427  -1.0814  -0.3752   0.1541   3.9880
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.66723    0.06804    39.2   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 35.111  on 14  degrees of freedom
## Residual deviance: 35.111  on 14  degrees of freedom
## AIC: 103.75
##
## Number of Fisher Scoring iterations: 4
```

```
deep.es50.temp <- glm(ES50 ~ temp, family = "poisson", data = deep)
summary(deep.es50.temp)
```

```
##
## Call:
## glm(formula = ES50 ~ temp, family = "poisson", data = deep)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.7290  -0.8220  -0.2853   0.0377   3.1912
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.95448    0.10410  28.381  < 2e-16 ***
## temp        -0.26680    0.07986  -3.341 0.000835 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 35.111  on 14  degrees of freedom
## Residual deviance: 24.730  on 13  degrees of freedom
## AIC: 95.373
##
## Number of Fisher Scoring iterations: 4
```

```
deep.es50.oxygen <- glm(ES50 ~ dissolved.oxygen, family = "poisson", data = deep)
summary(deep.es50.oxygen)
```

```
##
## Call:
## glm(formula = ES50 ~ dissolved.oxygen, family = "poisson", data = deep)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.78608  -0.96314  -0.24994   0.05043   2.57468
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
##  (Intercept)     2.0903096  0.1815253  11.515  < 2e-16 ***
## dissolved.oxygen 0.0034819  0.0009681   3.597 0.000322 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 35.111  on 14  degrees of freedom
## Residual deviance: 22.866  on 13  degrees of freedom
## AIC: 93.509
##
## Number of Fisher Scoring iterations: 4
```

```
deep.es50.chlorophyll <- glm(ES50 ~ chlorophyll, family = "poisson", data = deep)
summary(deep.es50.chlorophyll)
```

```
##
## Call:
## glm(formula = ES50 ~ chlorophyll, family = "poisson", data = deep)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.7628  -0.9985  -0.2894  -0.0095   4.0896
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -3.962      5.307  -0.747    0.455
## chlorophyll 1501.463    1201.121   1.250    0.211
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 35.111  on 14  degrees of freedom
## Residual deviance: 33.671  on 13  degrees of freedom
## AIC: 104.31
##
## Number of Fisher Scoring iterations: 4
```

```
deep.es50.current <- glm(ES50 ~ current, family = "poisson", data = deep)
summary(deep.es50.current)
```

```
##
## Call:
## glm(formula = ES50  ~ current, family = "poisson", data = deep)
##
## Deviance Residuals:
##      Min        1Q    Median       3Q      Max
## -2.1418  -0.8155  -0.1136   0.5595   2.9705
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)     3.3315     0.2045  16.293  < 2e-16 ***
## current      -82.7742    24.9834  -3.313 0.000922 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 35.111  on 14  degrees of freedom
## Residual deviance: 24.136  on 13  degrees of freedom
## AIC: 94.779
##
## Number of Fisher Scoring iterations: 4
```

```
deep.es50.salinity <- glm(ES50 ~ salinity, family = "poisson", data = deep)
summary(deep.es50.salinity)
```

```
##
## Call:
## glm(formula = ES50 ~ salinity, family = "poisson", data = deep)
##
## Deviance Residuals:
##      Min        1Q    Median       3Q      Max
## -1.8960  -1.0256  -0.1811   0.2596   2.4965
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -49.9163    15.9064  -3.138 0.001700 **
## salinity      1.5158     0.4583   3.307 0.000942 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 35.111  on 14  degrees of freedom
## Residual deviance: 24.250  on 13  degrees of freedom
## AIC: 94.893
##
## Number of Fisher Scoring iterations: 4
```

```
deep.es50.nitrate <- glm(ES50 ~ nitrate, family = "poisson", data = deep)
summary(deep.es50.nitrate)
```

```
##
## Call:
## glm(formula = ES50 ~ nitrate, family = "poisson", data = deep)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.51928  -0.95869  -0.07878   0.16286   2.67794
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.675190   0.237422  15.480  < 2e-16 ***
## nitrate     -0.030235   0.007086  -4.267 1.98e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 35.111  on 14  degrees of freedom
## Residual deviance: 18.927  on 13  degrees of freedom
## AIC: 89.57
##
## Number of Fisher Scoring iterations: 4
```

Model selection for ES50, deep water

Here we use AIC to compare models for goodness of fit while penalizing for overparameterization. Models are ranked in order of AIC score, with lowest scoring model (model with the best compromise between fit and complexity) first in the list. The delta AIC represents how much the AIC score for each model differs from the top model, an can be used as an estimate of the relative support for each model. A delta AIC of 2 is considered to be potentially a significantly better fit, with higher delta AICs between models indicating increasingly larger differences in model fit while correcting for the number of parameters.

```
deep.es50.models <- list(deep.es50.intercept = deep.es50.intercept,
                         deep.es50.temp = deep.es50.temp,
                         deep.es50.oxygen = deep.es50.oxygen,
                         deep.es50.chlorophyll = deep.es50.chlorophyll,
                         deep.es50.current = deep.es50.current,
                         deep.es50.salinity = deep.es50.salinity,
                         deep.es50.nitrate = deep.es50.nitrate)
deep.es50.aic.df <- data.frame(Model = names(deep.es50.models),
                               AIC = sapply(deep.es50.models, function(x) AICc(x)),
                              akaike.weights(sapply(deep.es50.models, function(x)  AIC
c(x))))

deep.es50.aic.df <- deep.es50.aic.df[order(deep.es50.aic.df$AIC),]
deep.es50.aic.df$Cumulative.Weight <- cumsum(deep.es50.aic.df$weights)

kable(deep.es50.aic.df, row.names = FALSE)
```

Model	AIC	deltaAIC	rel.LL	weights	Cumulative.Weight
deep.es50.nitrate	90.57036	0.000000	1.0000000	0.7462194	0.7462194
deep.es50.oxygen	94.50935	3.938991	0.1395273	0.1041179	0.8503373

Model	AIC	deltaAIC	rel.LL	weights	Cumulative.Weight
deep.es50.current	95.77905	5.208689	0.0739516	0.0551841	0.9055214
deep.es50.salinity	95.89287	5.322507	0.0698606	0.0521313	0.9576527
deep.es50.temp	96.37322	5.802862	0.0549445	0.0410007	0.9986534
deep.es50.intercept	104.06178	13.491417	0.0011759	0.0008775	0.9995309
deep.es50.chlorophyll	105.31431	14.743947	0.0006286	0.0004691	1.0000000

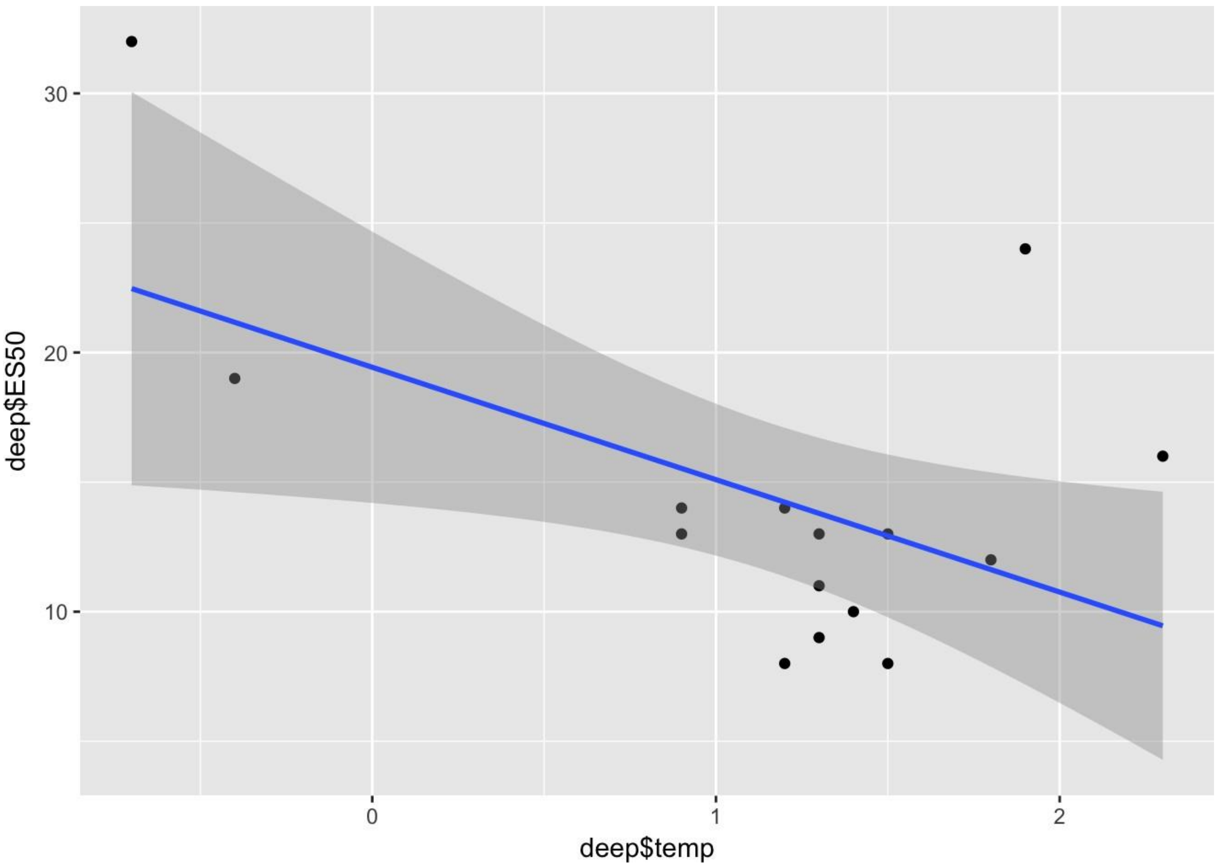
```
write.csv(deep.es50.aic.df, file = "deep.5.degree.es50.aic.csv")
```

We find that the model containing nitrate is the best fit, with other models having a delta AIC over 2. This indicates that nitrate is the best predictor for ES50 in the deep ocean.

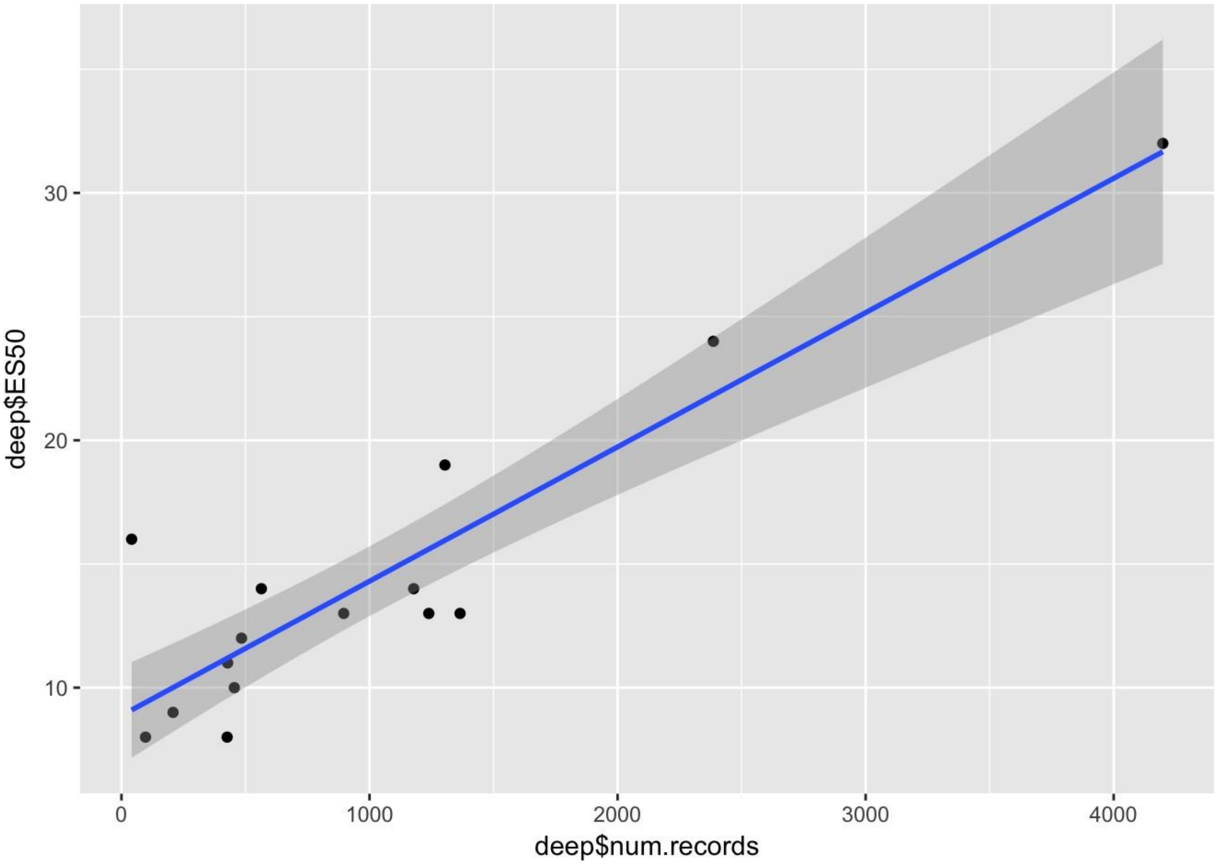
Plots for ES50, deep water

Here we plot the effects of each environmental predictor from its respective single-variable model.

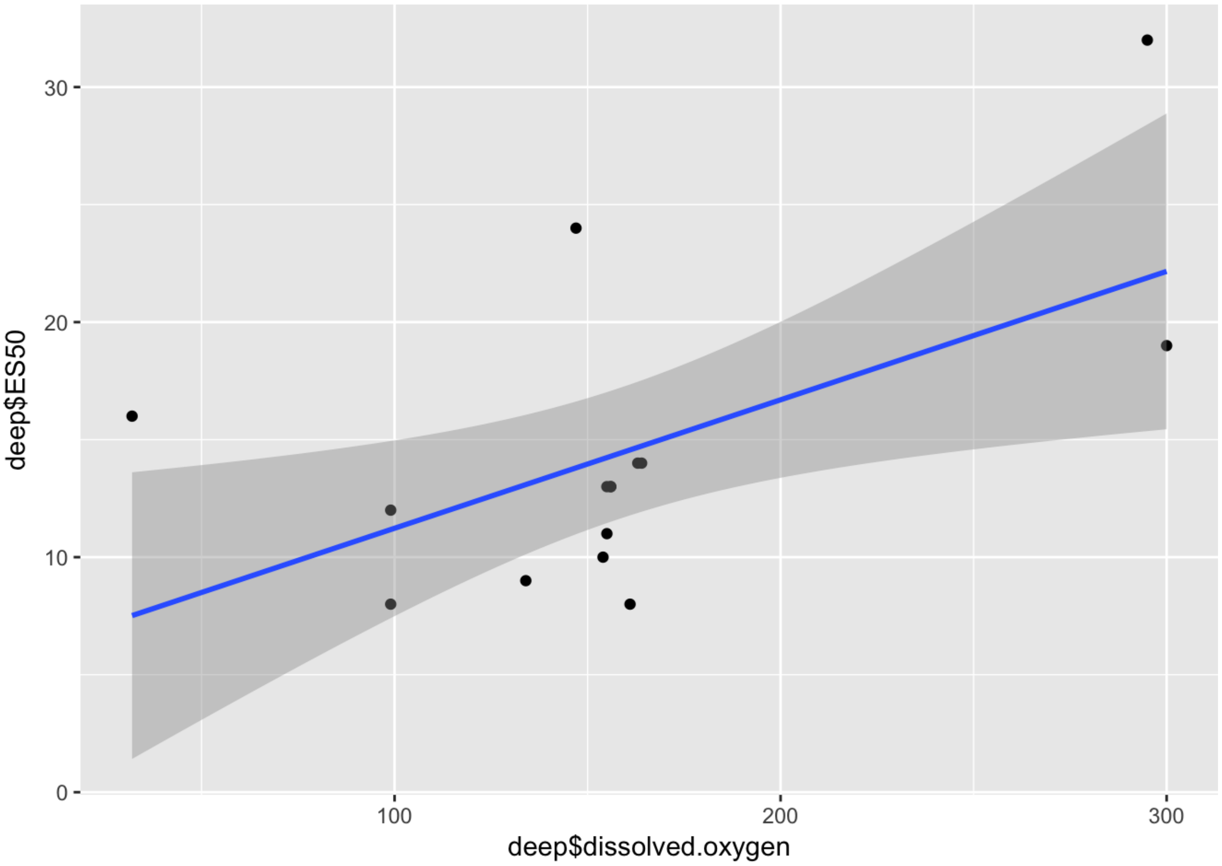
```
qplot(deep$temp, deep$ES50) + geom_smooth(method = "glm")
```



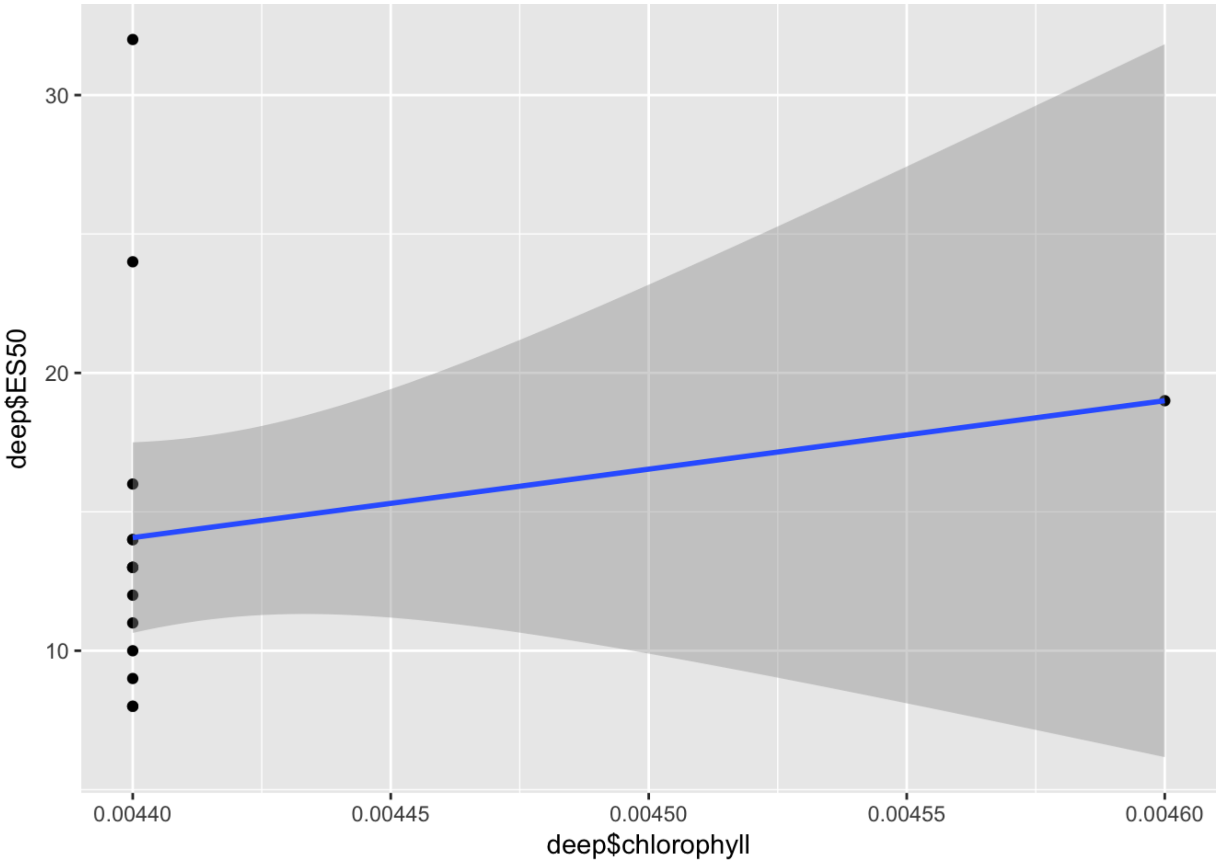
```
qplot(deep$num.records, deep$ES50) + geom_smooth(method = "glm")
```



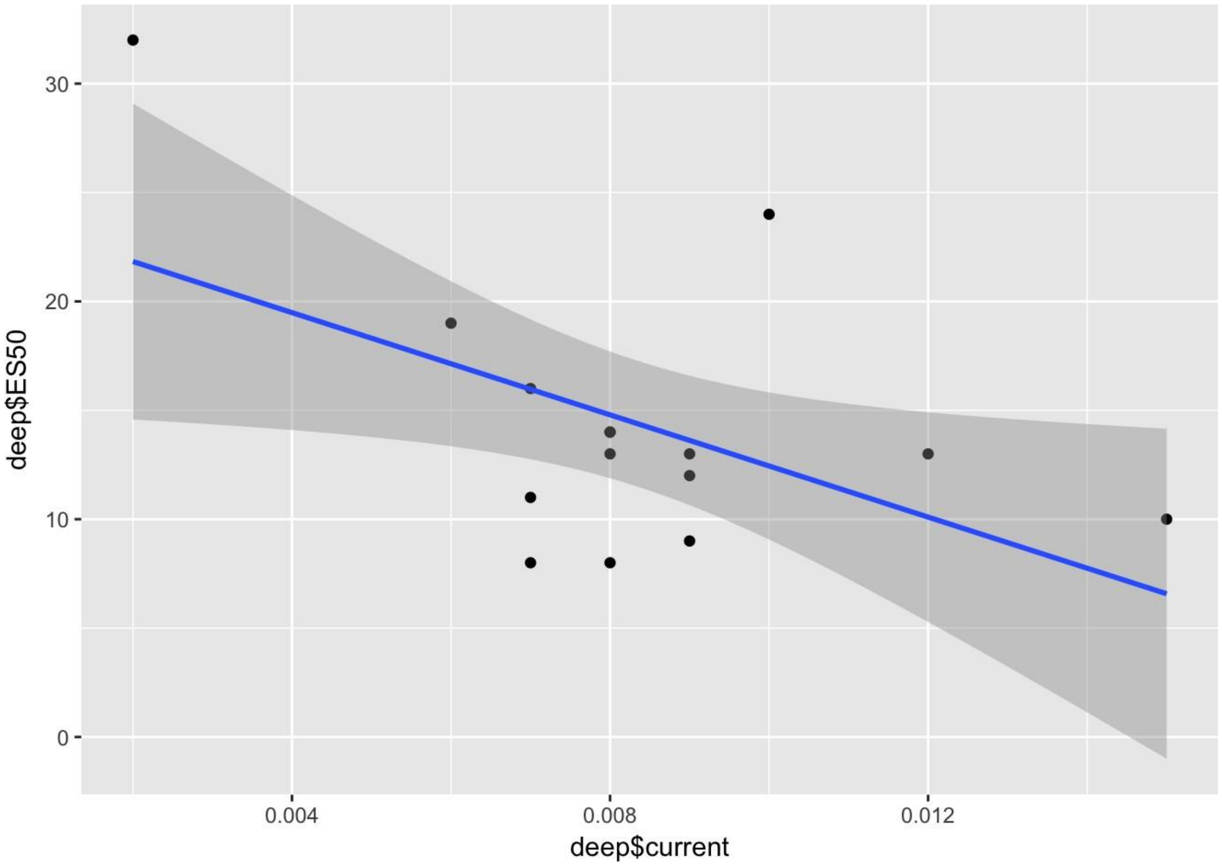
```
qplot(deep$dissolved.oxygen, deep$ES50) + geom_smooth(method = "glm")
```



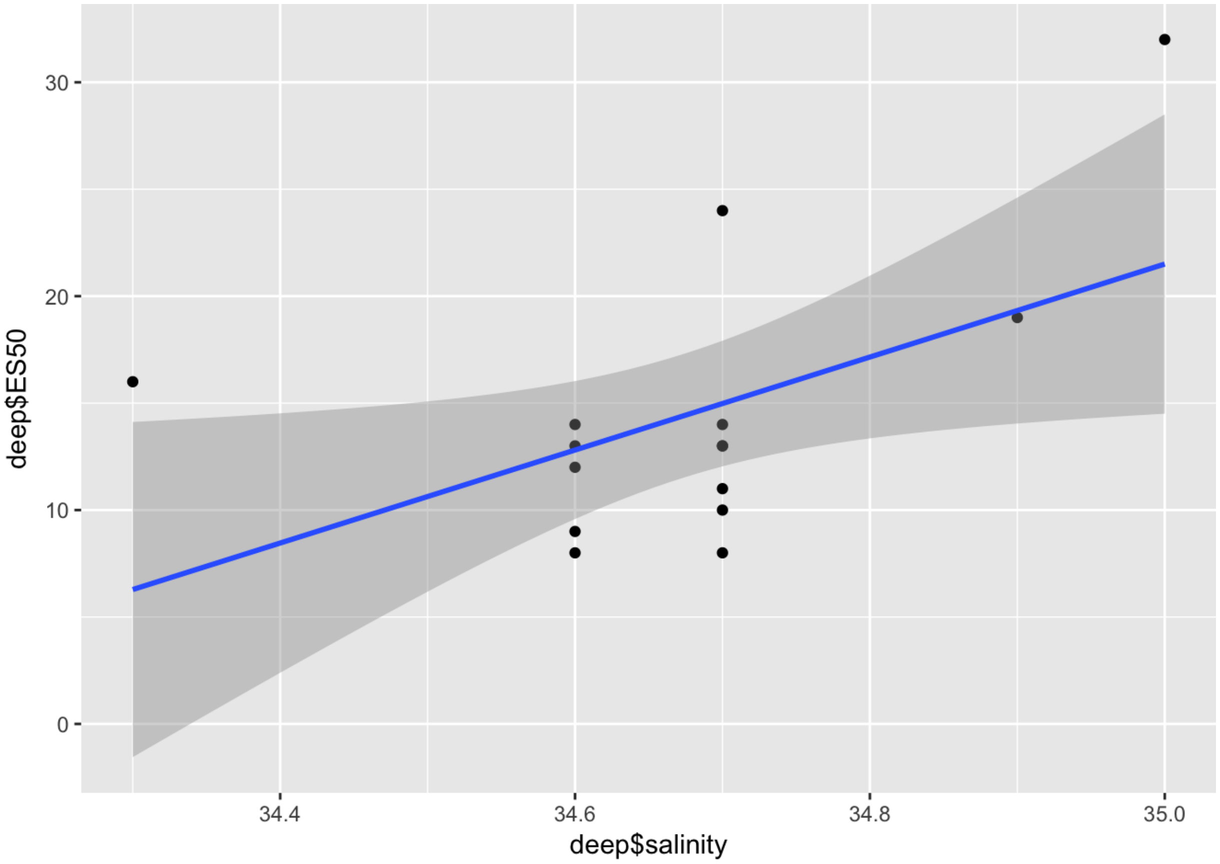
```
qplot(deep$chlorophyll, deep$ES50) + geom_smooth(method = "glm")
```



```
qplot(deep$current, deep$ES50) + geom_smooth(method = "glm")
```



```
qplot(deep$salinity, deep$ES50) + geom_smooth(method = "glm")
```



```
qplot(deep$nitrate, deep$ES50) + geom_smooth(method = "glm")
```