GAM of eDNA index vs oxygen

```r
dfsplit <- split(eDNAindxEnvData_cleanYr, eDNAindxEnvData_cleanYr$Species) # Split by
↪   species

for (i in 1:length(dfsplit)) { # For each species:
    species <- dfsplit[[i]]$Species[1] # Species name
    title <- paste(species, sep = " ", "eDNA Index vs Dissolved Oxygen") # Plot title,
↪   changed for eDNA
    print(title)

    # Plot the GAM + save it
    print(ggplot(dfsplit[[i]], aes(x = DO, y = eDNA_index)) + # plot this species
      geom_point(color = "orange2", alpha = 0.7) +
      geom_smooth(method = 'gam', se = F, color = "cornflowerblue") + # visualize GAM
      ggtitle(title) +
      theme_bw())
    ggsave(filename = paste(species, sep = "_", "eDNA_DO_GAM.png"), path =
↪   here("eDNA_Index_Hypoxia", "Plots", "GAM_Initial"), width = 2500, height = 2000,
↪   units = "px")

    # Make the GAM as an object and print some quality metrics
    ind_DO_GAM <- gam(eDNA_index ~ s(DO), bs = "cr", data = dfsplit[[i]])
    print(summary(ind_DO_GAM))

    print("GAM quality")
    print(paste("AIC: ", sep = "", AIC(ind_DO_GAM))) # quality metric
    print(summary(ind_DO_GAM)$sp.criterion)
    print(gam.check(ind_DO_GAM, k.rep = 1000)) # Bunch of graphs and also text output,
↪   which is used to check how the GAM is doing

      ## how to interpret
      # edf = effective degrees of freedom
      # GCV = generalized cross validation, an estimate of the mean square prediction
      ↪   error. comparing between models, lower GCV is better
      # Lower AIC is also better
      # Higher R^2 is better

    # system(paste(paste(paste("say", "Loop"), i), "Complete"))
}
```
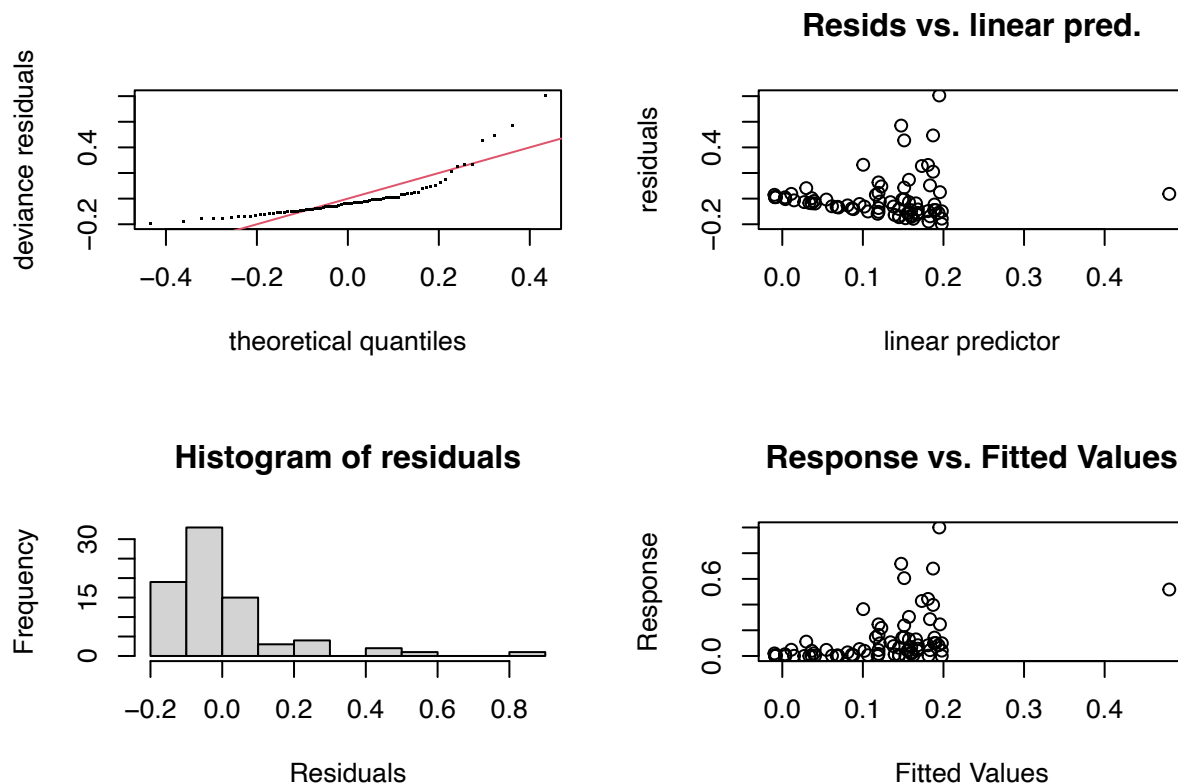
```
## [1] "Acartia longiremis eDNA Index vs Dissolved Oxygen"

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range
## (`stat_smooth()`).

## Warning: Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
```

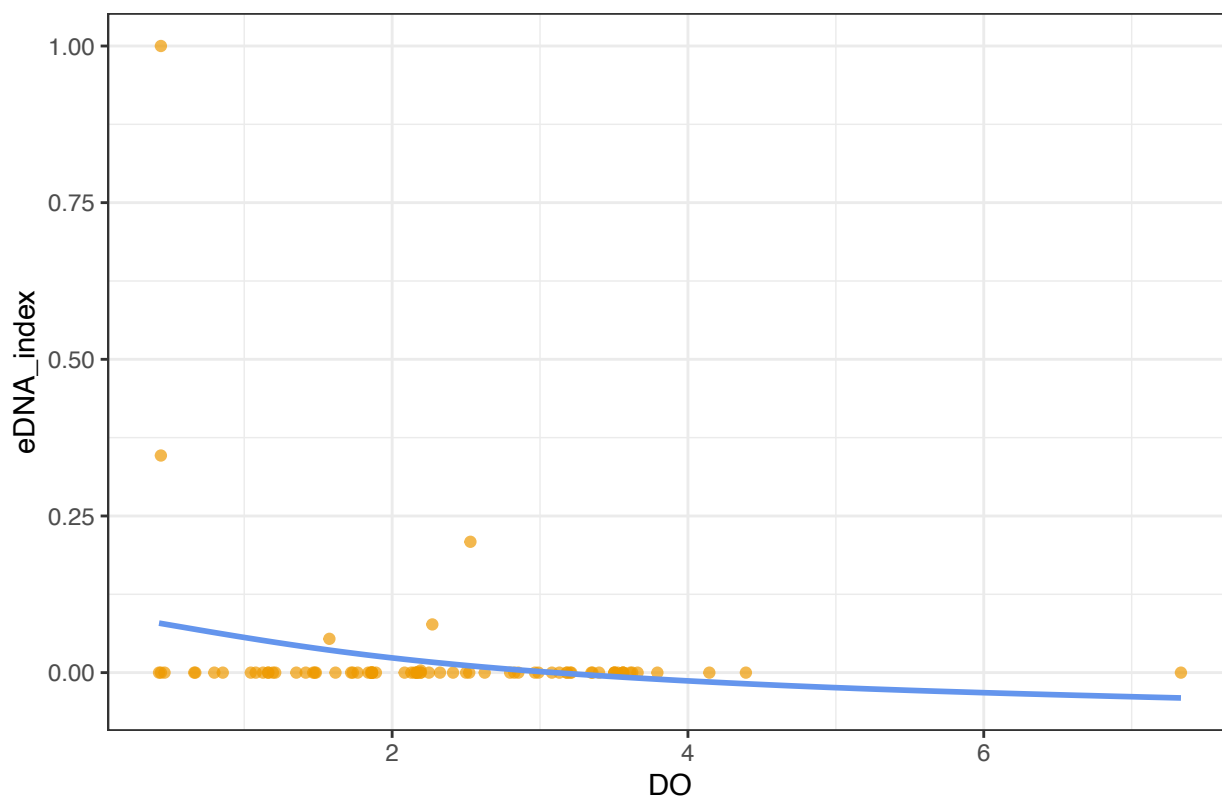# Acartia longiremis eDNA Index vs Dissolved Oxygen
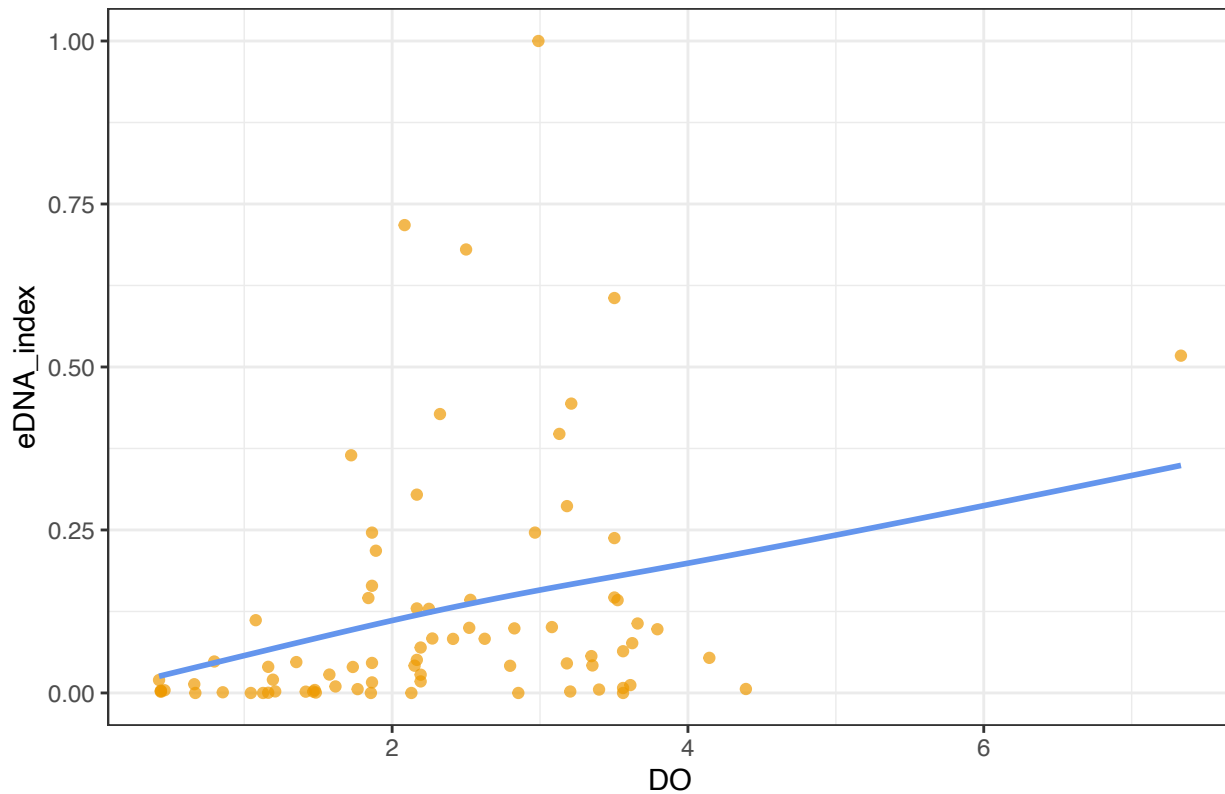

```
## 
## Family: gaussian 
## Link function: identity 
## 
## Formula:
## eDNA_index ~ s(DO)
## 
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.12233    0.01975   6.195 3.1e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Approximate significance of smooth terms:
##        edf Ref.df     F p-value
## s(DO) 3.918  4.742 3.529 0.00822 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## R-sq.(adj) =   0.16   Deviance explained = 20.3%
## GCV = 0.032463  Scale est. = 0.030416  n = 78
## [1] "GAM quality"
## [1] "AIC: -44.3267161286312"
##     GCV.Cp
## 0.03246284
```

Resids vs. linear pred.

Histogram of residuals
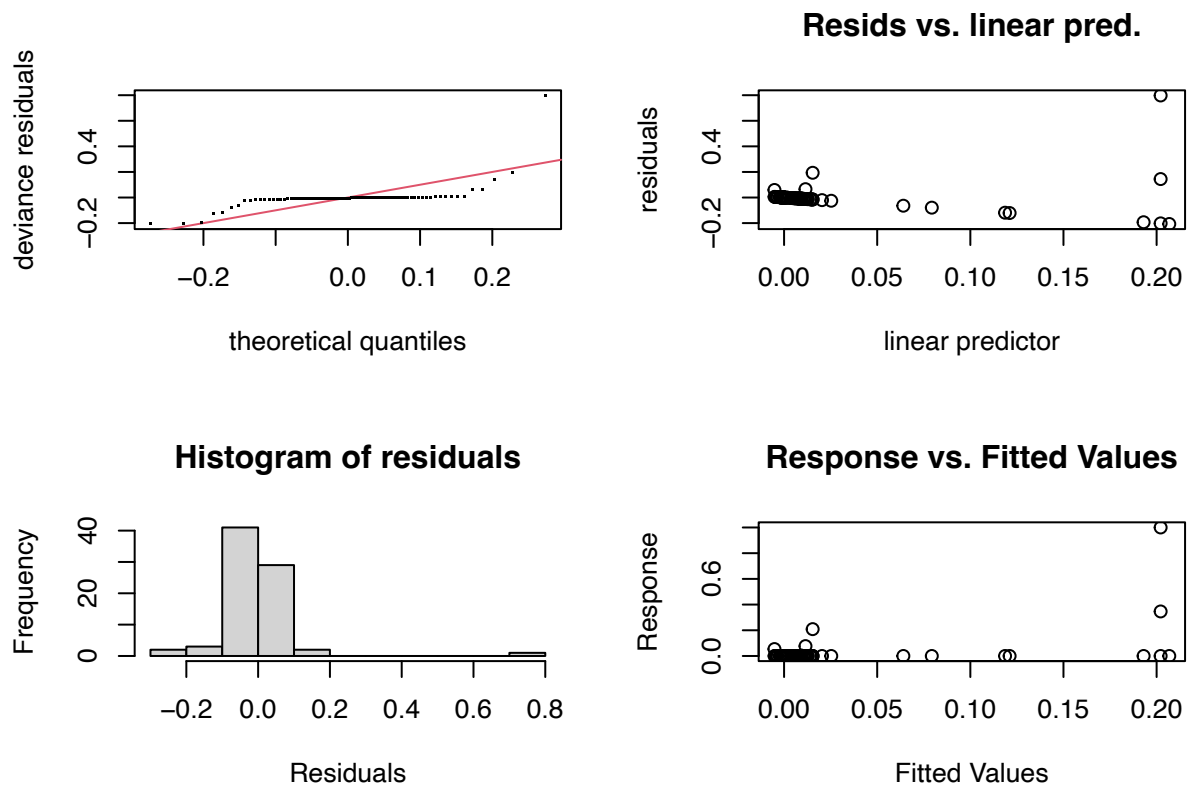
Response vs. Fitted Values


```
## 
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 4 iterations.
## The RMS GCV score gradient at convergence was 9.432252e-07 .
## The Hessian was positive definite.
## 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(DO) 9.00 3.92    1.13    0.89
## $mfrow
## [1] 2 2
## 
## [1] "Calanus pacificus eDNA Index vs Dissolved Oxygen"

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
```

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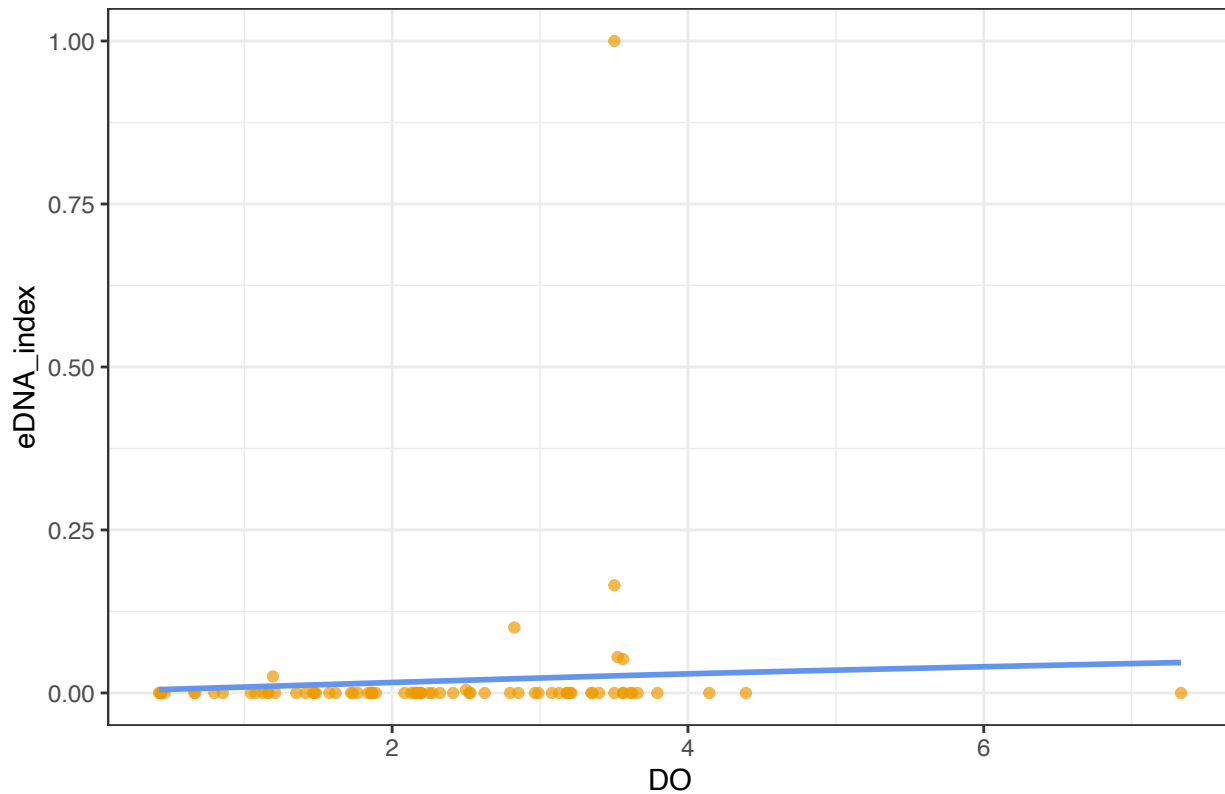## Calanus pacificus eDNA Index vs Dissolved Oxygen


```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## eDNA_index ~ s(DO)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.02166    0.01244   1.742   0.0858 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##         edf Ref.df     F p-value
## s(DO) 5.147  6.151 3.165 0.00818 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.182   Deviance explained = 23.7%
## GCV = 0.013095  Scale est. = 0.012063  n = 78
## [1] "GAM quality"
## [1] "AIC: -115.327310101293"
##     GCV.Cp
## 0.01309512
```

Resids vs. linear pred.

Histogram of residuals

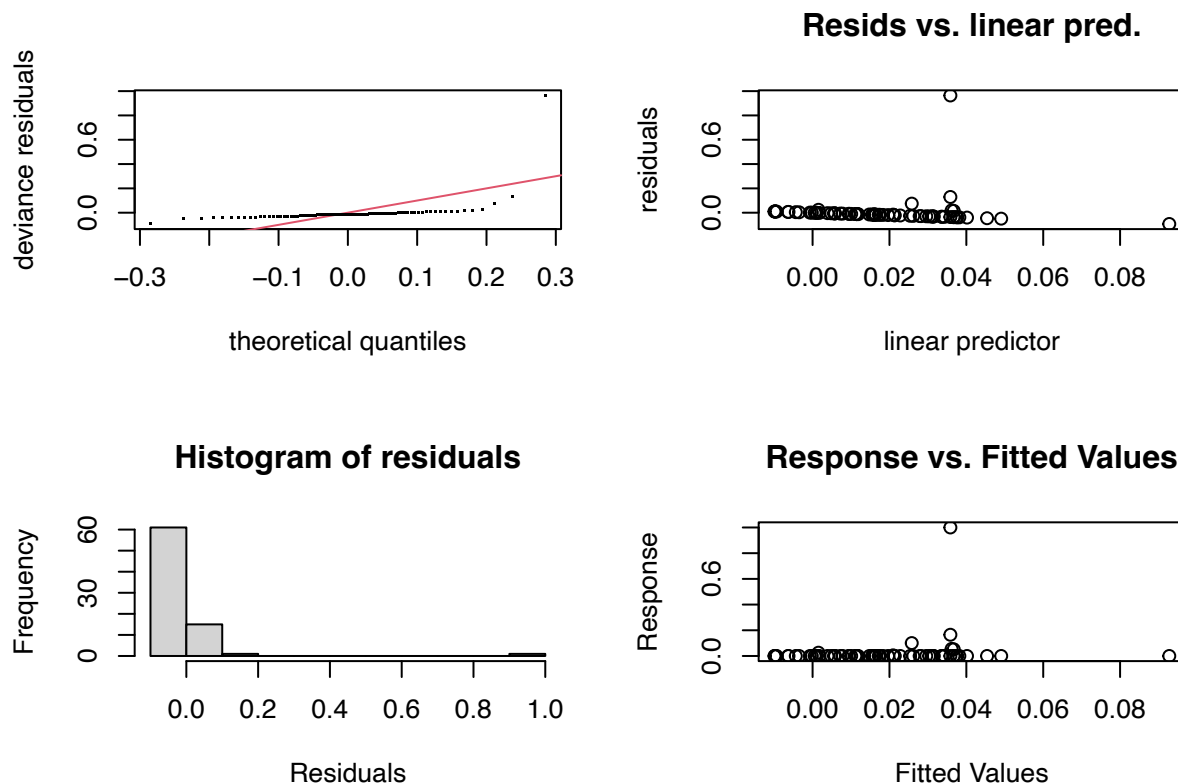**Response vs. Fitted Values**

```
## 
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 5 iterations.
## The RMS GCV score gradient at convergence was 1.620426e-07 .
## The Hessian was positive definite.
## 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(DO) 9.00 5.15    0.98    0.17
## $mfrow
## [1] 2 2
## 
## [1] "Centropages abdominalis eDNA Index vs Dissolved Oxygen"

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
```

Centropages abdominalis eDNA Index vs Dissolved Oxygen
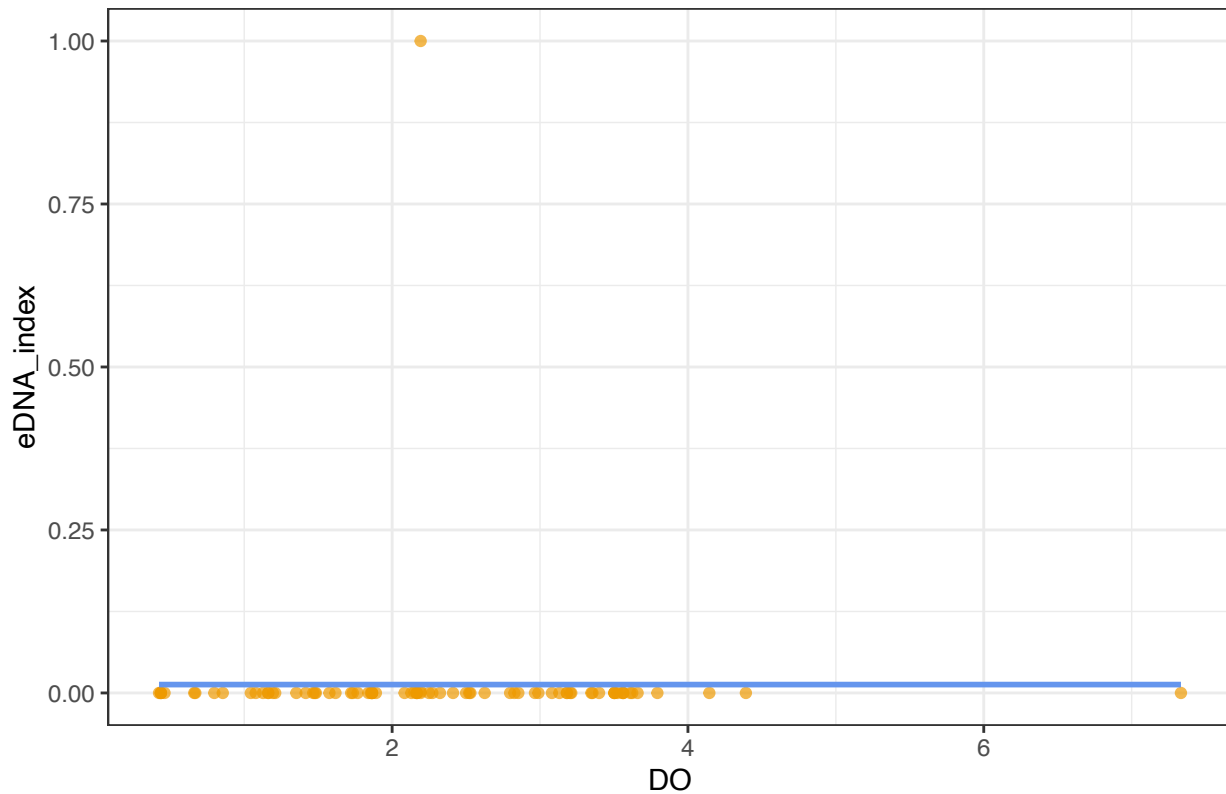


```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## eDNA_index ~ s(DO)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.01798    0.01296   1.388    0.169
##
## Approximate significance of smooth terms:
##       edf Ref.df      F p-value
## s(DO)   1      1 1.769   0.187
##
## R-sq.(adj) =  0.00989   Deviance explained = 2.27%
## GCV = 0.013441  Scale est. = 0.013096  n = 78
## [1] "GAM quality"
## [1] "AIC: -112.834263153192"
##     GCV.Cp
## 0.01344104
```

Resids vs. linear pred.

Histogram of residuals
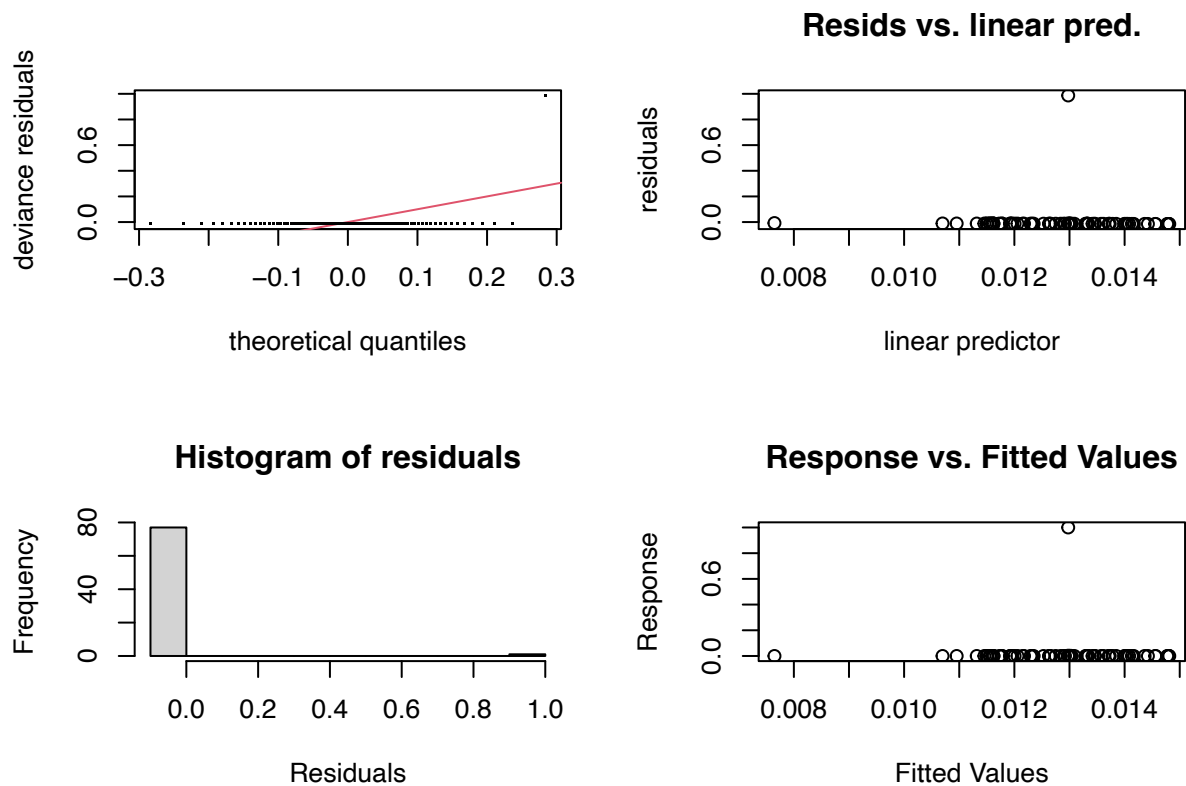
Response vs. Fitted Values


```
## 
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 8 iterations.
## The RMS GCV score gradient at convergence was 1.582062e-07 .
## The Hessian was positive definite.
## 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(DO)  9   1    0.89   0.047 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## $mfrow
## [1] 2 2
## 
## [1] "Clausocalanus parapergens eDNA Index vs Dissolved Oxygen"

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
```

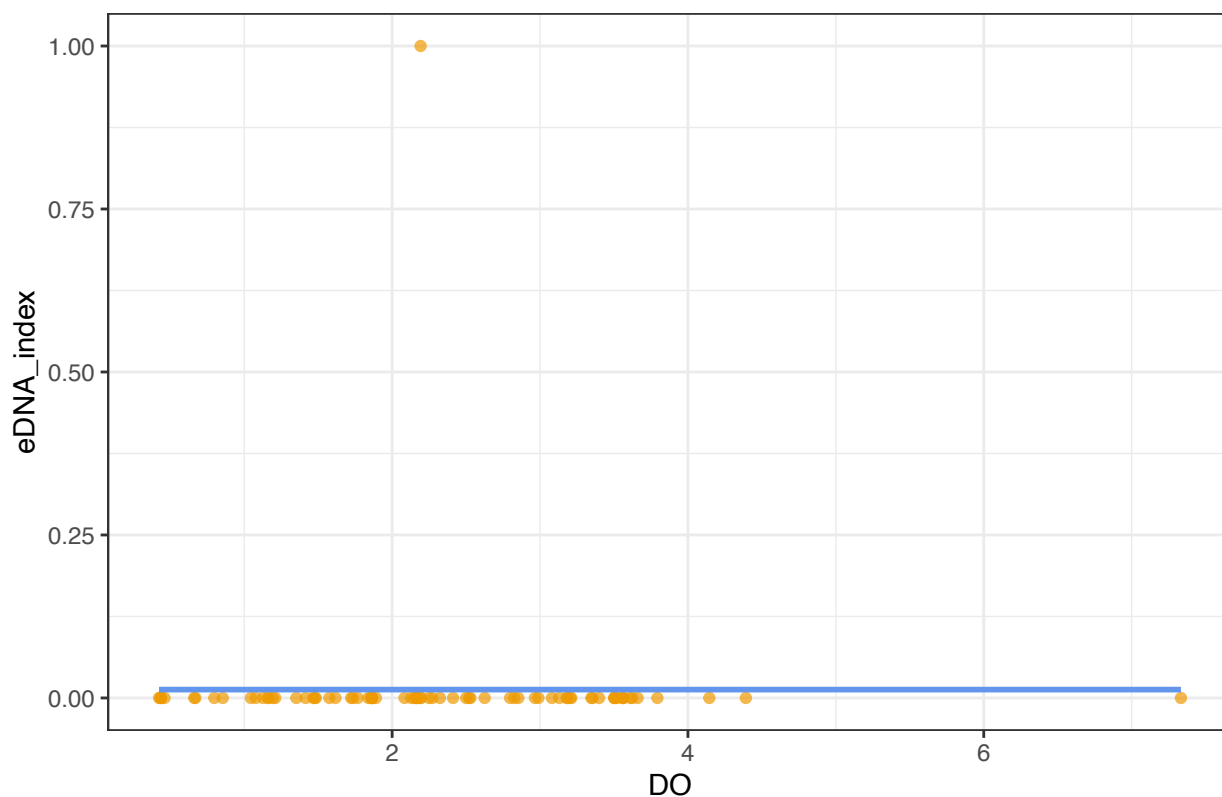## Clausocalanus parapergens eDNA Index vs Dissolved Oxygen


```
## 
## Family: gaussian
## Link function: identity
## 
## Formula:
## eDNA_index ~ s(DO)
## 
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.01286    0.01290   0.997    0.322
## 
## Approximate significance of smooth terms:
##       edf Ref.df      F p-value
## s(DO)   1      1 0.009   0.926
## 
## R-sq.(adj) =  -0.013   Deviance explained = 0.0114%
## GCV = 0.013328  Scale est. = 0.012987  n = 78
## [1] "GAM quality"
## [1] "AIC: -113.490730747714"
##    GCV.Cp
## 0.0133284
```

Resids vs. linear pred.

Histogram of residuals
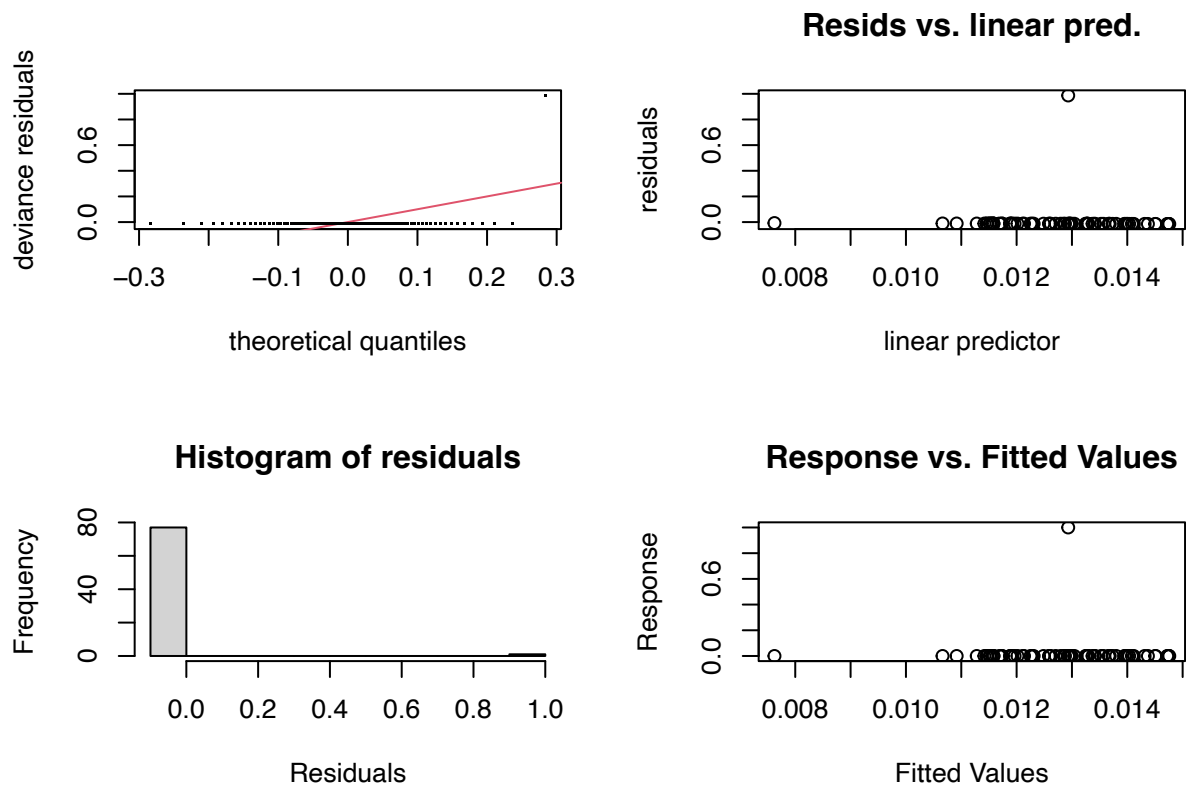
Response vs. Fitted Values

```
## 
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 9 iterations.
## The RMS GCV score gradient at convergence was 7.296207e-08 .
## The Hessian was positive definite.
## 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(DO)  9   1    1.03    0.55
## $mfrow
## [1] 2 2
## 
## [1] "Clausocalanus pergens eDNA Index vs Dissolved Oxygen"

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
```

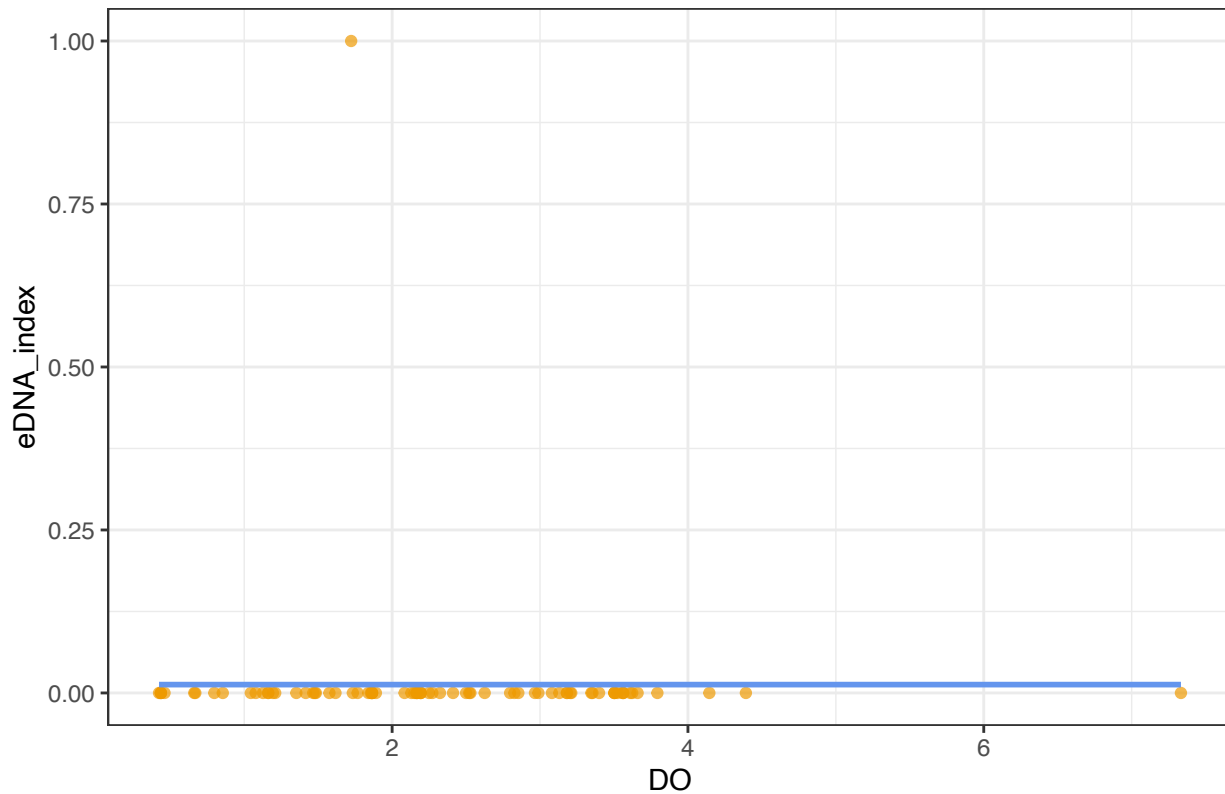## Clausocalanus pergens eDNA Index vs Dissolved Oxygen


```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## eDNA_index ~ s(DO)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.01282    0.01290   0.994    0.324
##
## Approximate significance of smooth terms:
##       edf Ref.df      F p-value
## s(DO)   1      1 0.009   0.926
##
## R-sq.(adj) =  -0.013   Deviance explained = 0.0113%
## GCV = 0.01333  Scale est. = 0.012988  n = 78
## [1] "GAM quality"
## [1] "AIC: -113.484174498507"
##     GCV.Cp
## 0.01332952
```

Resids vs. linear pred.

Histogram of residuals

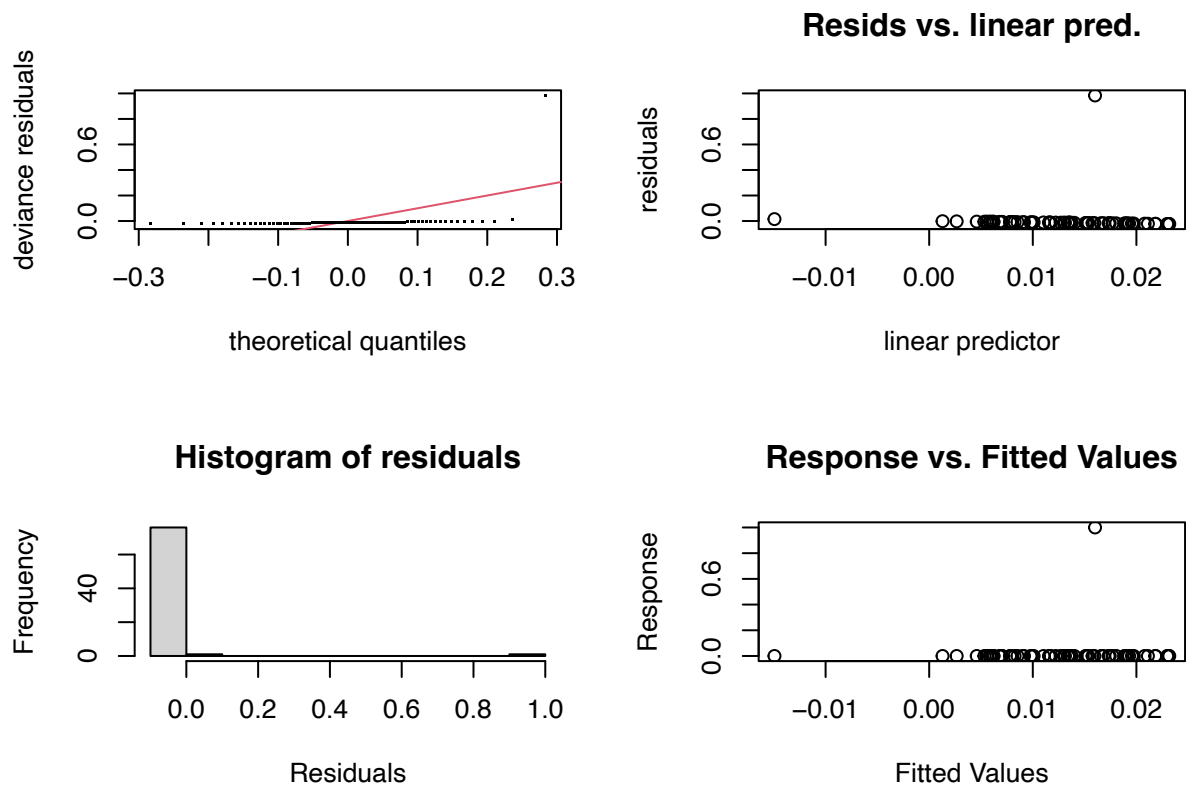## Response vs. Fitted Values


```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 9 iterations.
## The RMS GCV score gradient at convergence was 7.323085e-08 .
## The Hessian was positive definite.
## 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(DO)  9   1    1.03     0.5
## $mfrow
## [1] 2 2
##
## [1] "Diacyclops incolotaenia eDNA Index vs Dissolved Oxygen"

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
```

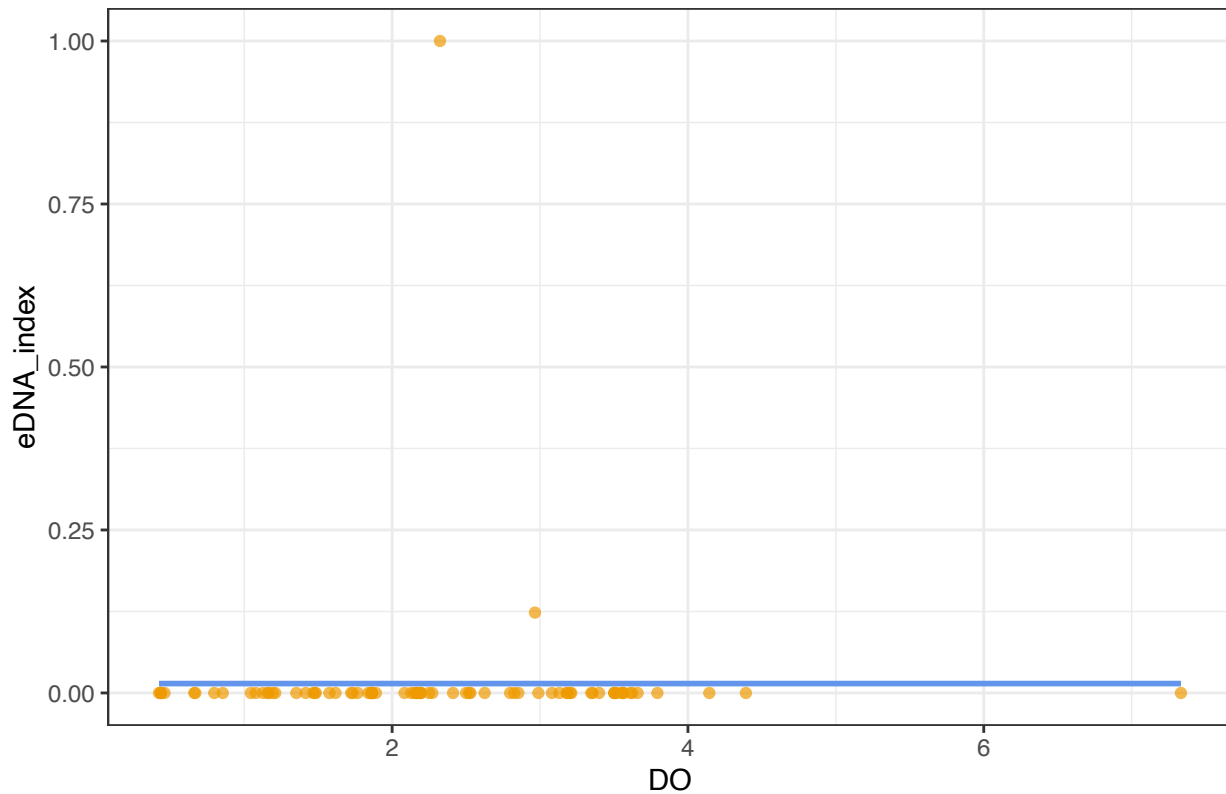# Diacyclops incolotaenia eDNA Index vs Dissolved Oxygen


```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## eDNA_index ~ s(DO)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.01282    0.01288   0.995    0.323
##
## Approximate significance of smooth terms:
##       edf Ref.df      F p-value
## s(DO)   1      1 0.246   0.621
##
## R-sq.(adj) =  -0.00988   Deviance explained = 0.323%
## GCV = 0.013288  Scale est. = 0.012947  n = 78
## [1] "GAM quality"
## [1] "AIC: -113.727748143016"
##     GCV.Cp
## 0.01328796
```

Resids vs. linear pred.

Histogram of residuals
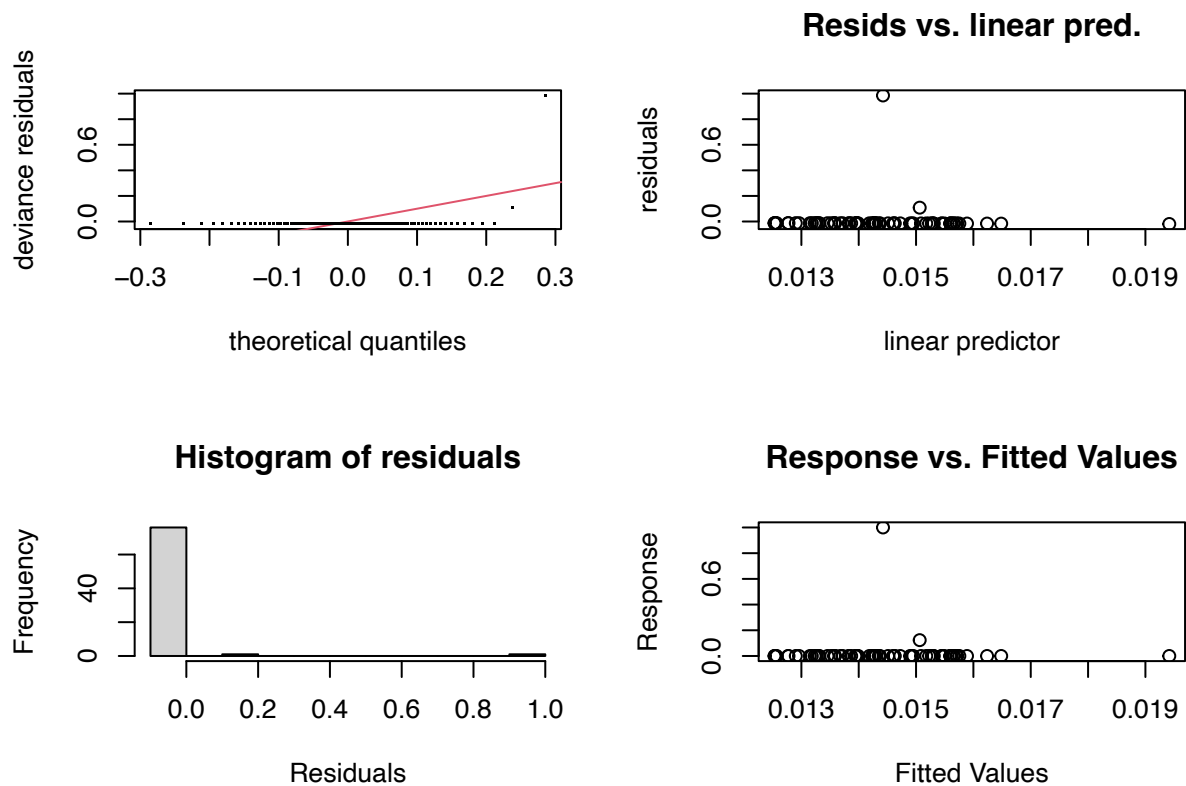
Response vs. Fitted Values

```
##
## Method: GCV    Optimizer: magic
## Smoothing parameter selection converged after 9 iterations.
## The RMS GCV score gradient at convergence was 8.729725e-08 .
## The Hessian was positive definite.
## 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(DO)  9   1    1.03    0.66
## $mfrow
## [1] 2 2
##
## [1] "Lucicutia flavicornis eDNA Index vs Dissolved Oxygen"

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
```

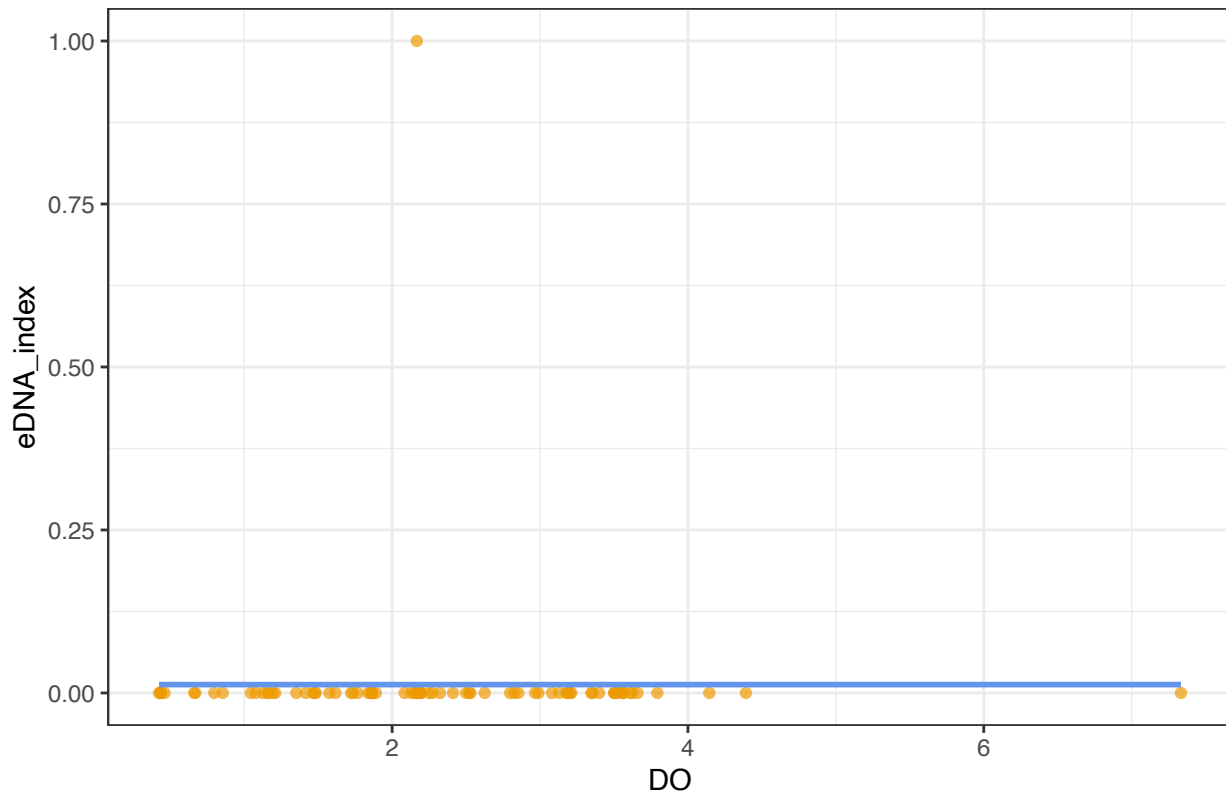## Lucicutia flavicornis eDNA Index vs Dissolved Oxygen


```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## eDNA_index ~ s(DO)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.01440    0.01298   1.109    0.271
##
## Approximate significance of smooth terms:
##       edf Ref.df      F p-value
## s(DO)   1      1 0.008   0.929
##
## R-sq.(adj) =  -0.0131   Deviance explained = 0.0104%
## GCV = 0.01349  Scale est. = 0.013144  n = 78
## [1] "GAM quality"
## [1] "AIC: -112.553063140206"
##     GCV.Cp
## 0.01348959
```

Resids vs. linear pred.

Histogram of residuals
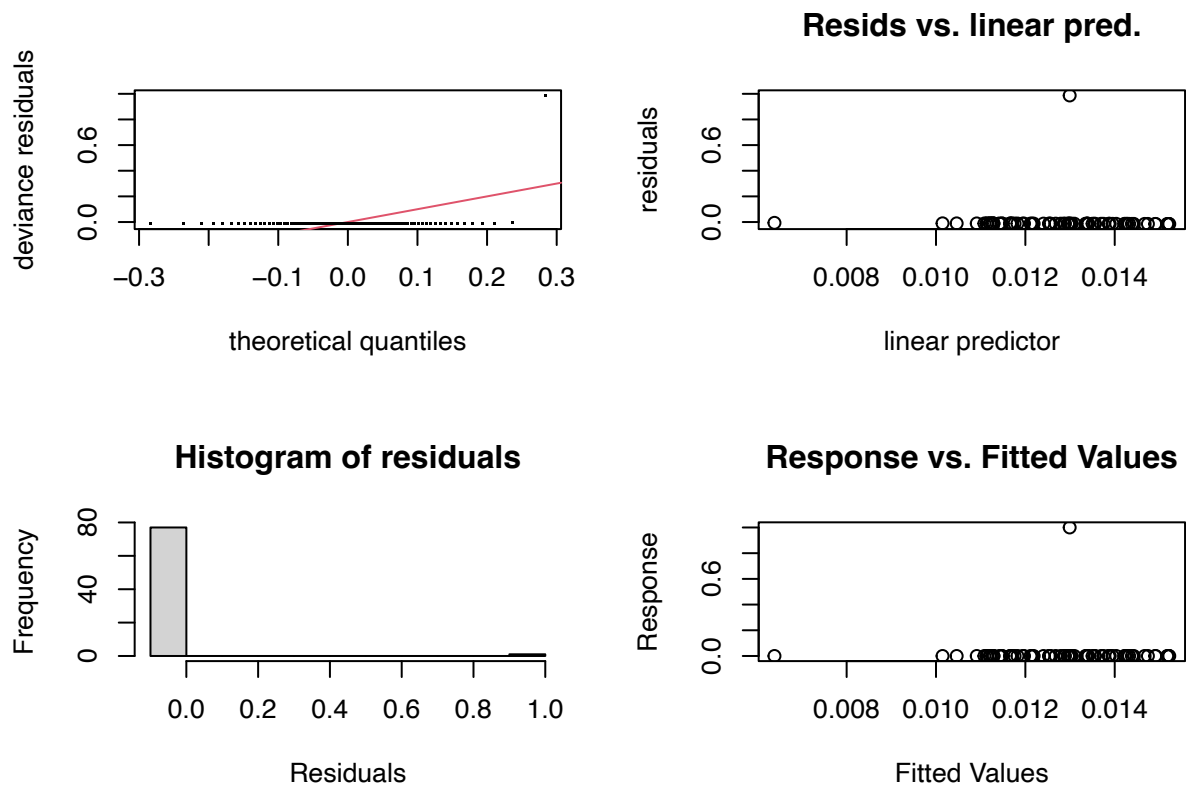
Response vs. Fitted Values

```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 9 iterations.
## The RMS GCV score gradient at convergence was 1.050211e-07 .
## The Hessian was positive definite.
## 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(DO)  9   1    1.03    0.58
## $mfrow
## [1] 2 2
##
## [1] "Metridia lucens eDNA Index vs Dissolved Oxygen"

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
```

Metridia lucens eDNA Index vs Dissolved Oxygen
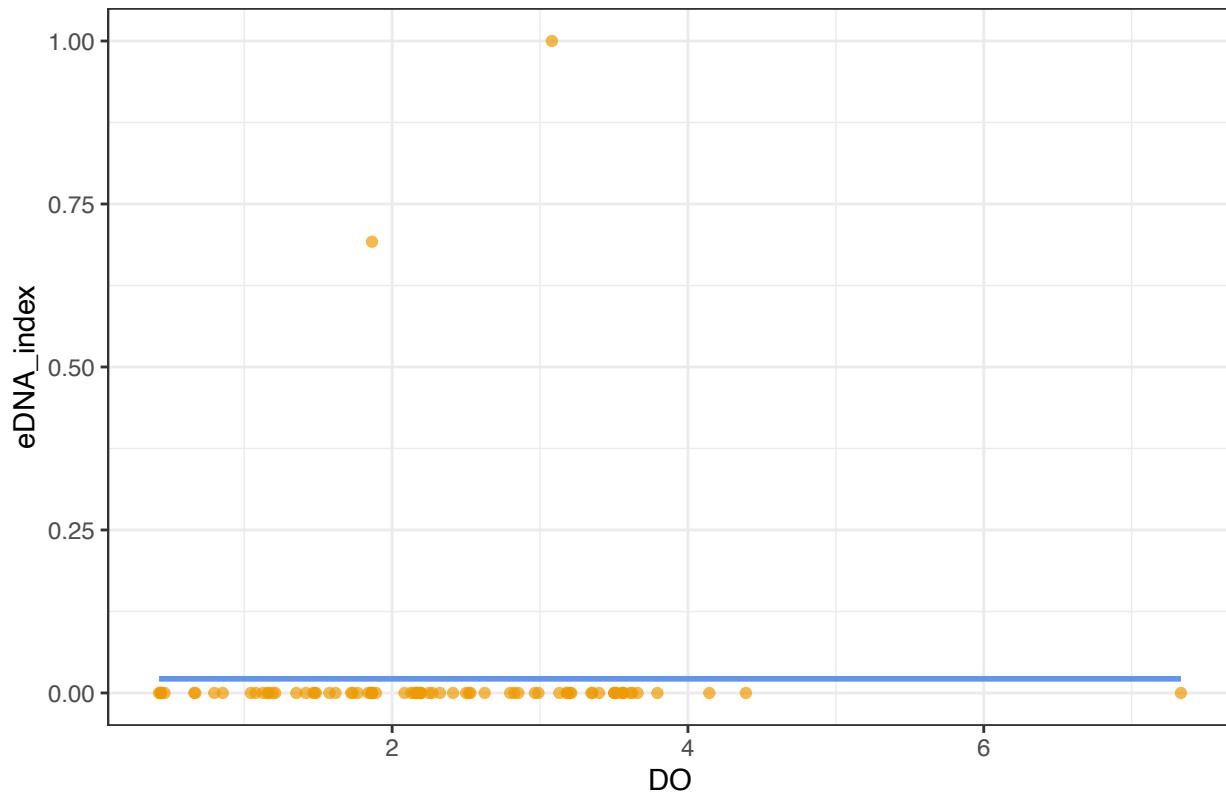


```
## 
## Family: gaussian
## Link function: identity
## 
## Formula:
## eDNA_index ~ s(DO)
## 
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.01282    0.01290   0.994    0.324
## 
## Approximate significance of smooth terms:
##       edf Ref.df      F p-value
## s(DO)   1      1 0.013   0.909
## 
## R-sq.(adj) =  -0.013   Deviance explained = 0.0174%
## GCV = 0.013329  Scale est. = 0.012987  n = 78
## [1] "GAM quality"
## [1] "AIC: -113.488891135054"
##     GCV.Cp
## 0.01332871
```

Resids vs. linear pred.

Histogram of residuals

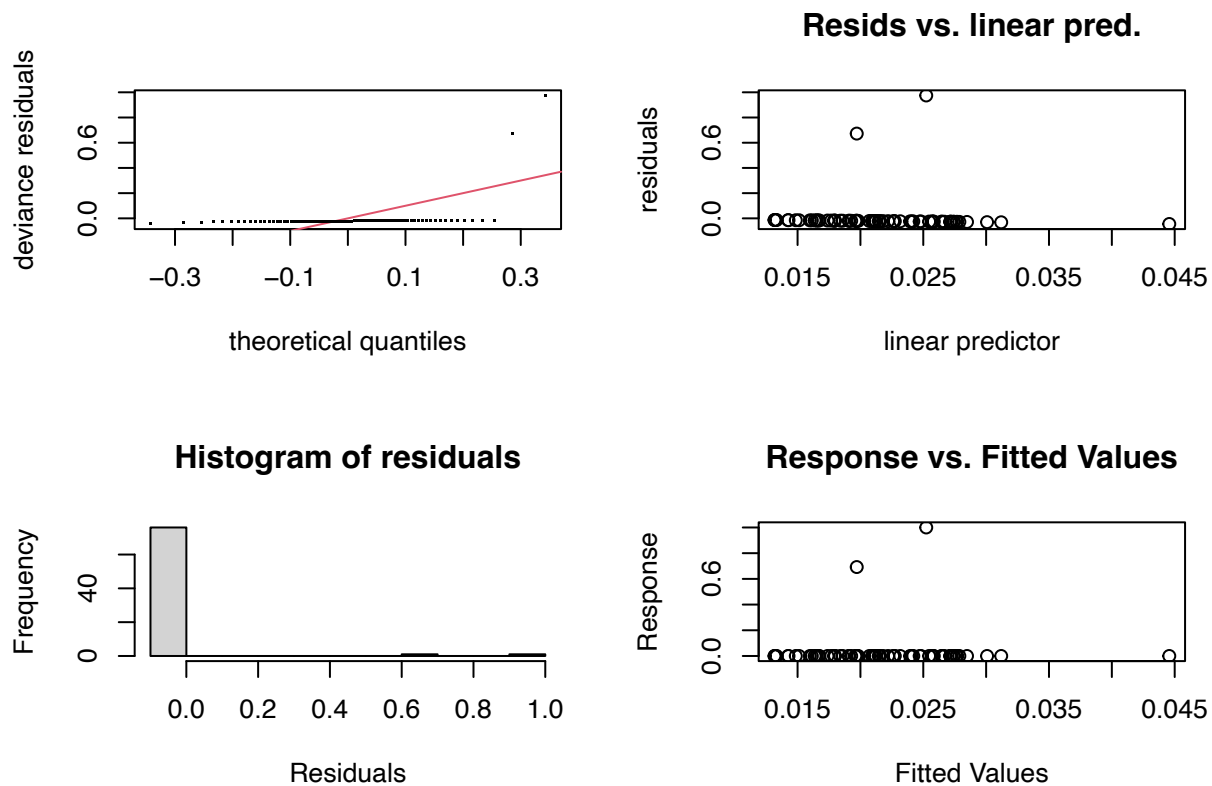**Response vs. Fitted Values**

```
## 
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 9 iterations.
## The RMS GCV score gradient at convergence was 7.384722e-08 .
## The Hessian was positive definite.
## 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(DO)  9   1    1.03    0.51
## $mfrow
## [1] 2 2
## 
## [1] "Metridia pacifica eDNA Index vs Dissolved Oxygen"

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
```

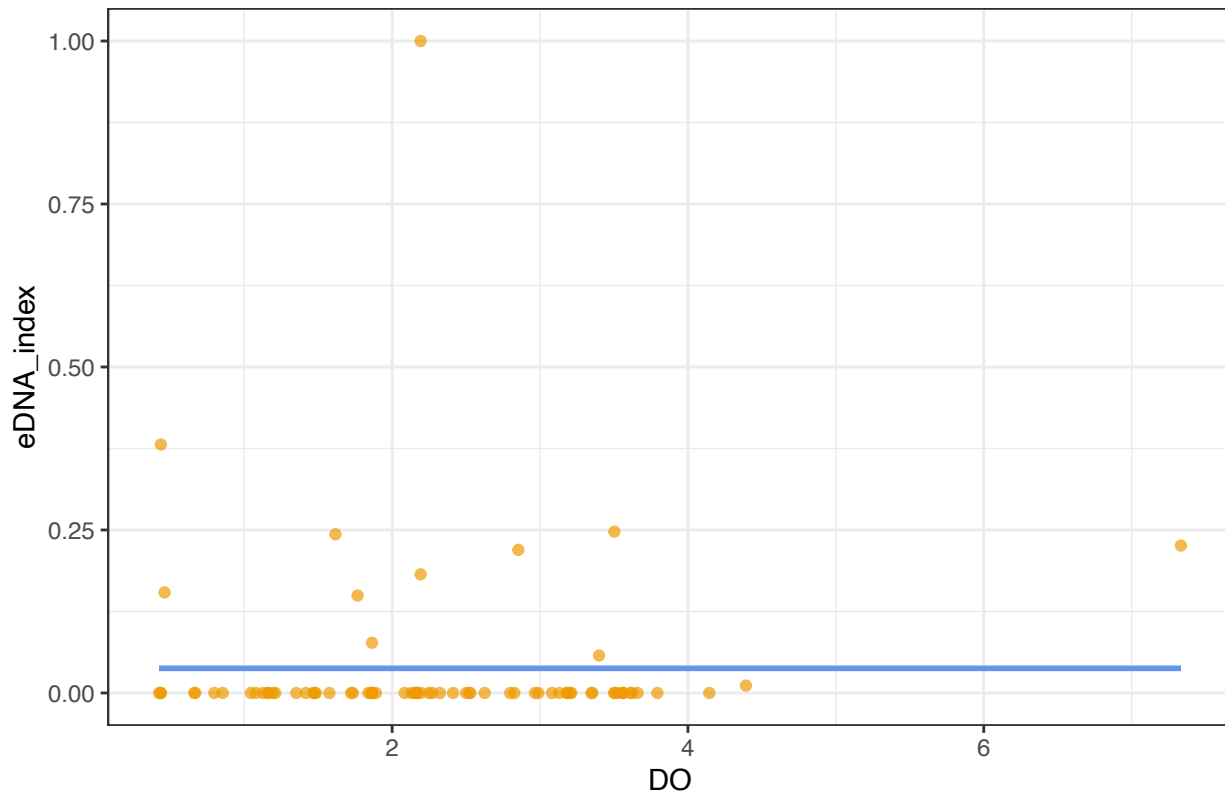# Metridia pacifica eDNA Index vs Dissolved Oxygen


```
## 
## Family: gaussian 
## Link function: identity 
## 
## Formula: 
## eDNA_index ~ s(DO) 
## 
## Parametric coefficients: 
##             Estimate Std. Error t value Pr(>|t|) 
## (Intercept)  0.02169    0.01559   1.392    0.168 
## 
## Approximate significance of smooth terms: 
##       edf Ref.df      F p-value 
## s(DO)   1      1 0.114   0.736 
## 
## R-sq.(adj) =  -0.0116   Deviance explained = 0.15% 
## GCV = 0.019448  Scale est. = 0.018949  n = 78 
## [1] "GAM quality" 
## [1] "AIC: -84.0181242154277" 
##     GCV.Cp 
## 0.01944813 
```

Resids vs. linear pred.

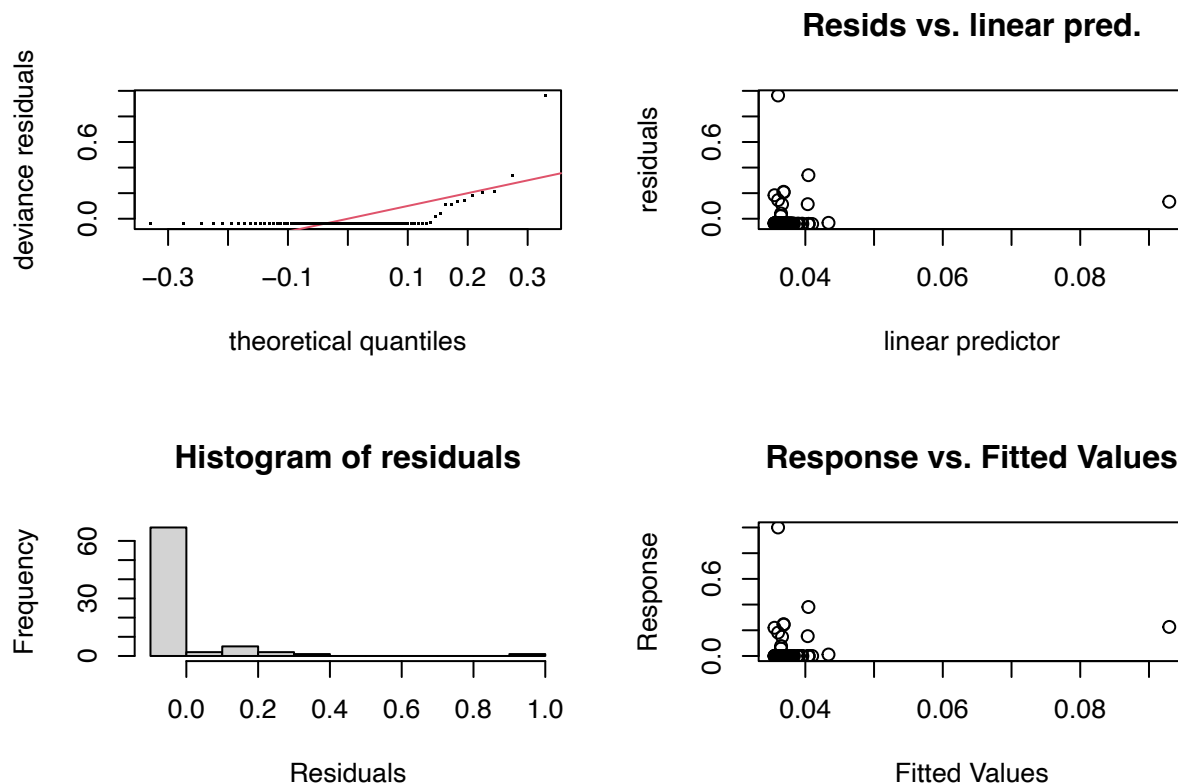**Histogram of residuals**

Response vs. Fitted Values


```
## 
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 9 iterations.
## The RMS GCV score gradient at convergence was 1.129112e-07 .
## The Hessian was positive definite.
## 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(DO)  9   1    1.04    0.67
## $mfrow
## [1] 2 2
## 
## [1] "Oithona similis eDNA Index vs Dissolved Oxygen"

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
```

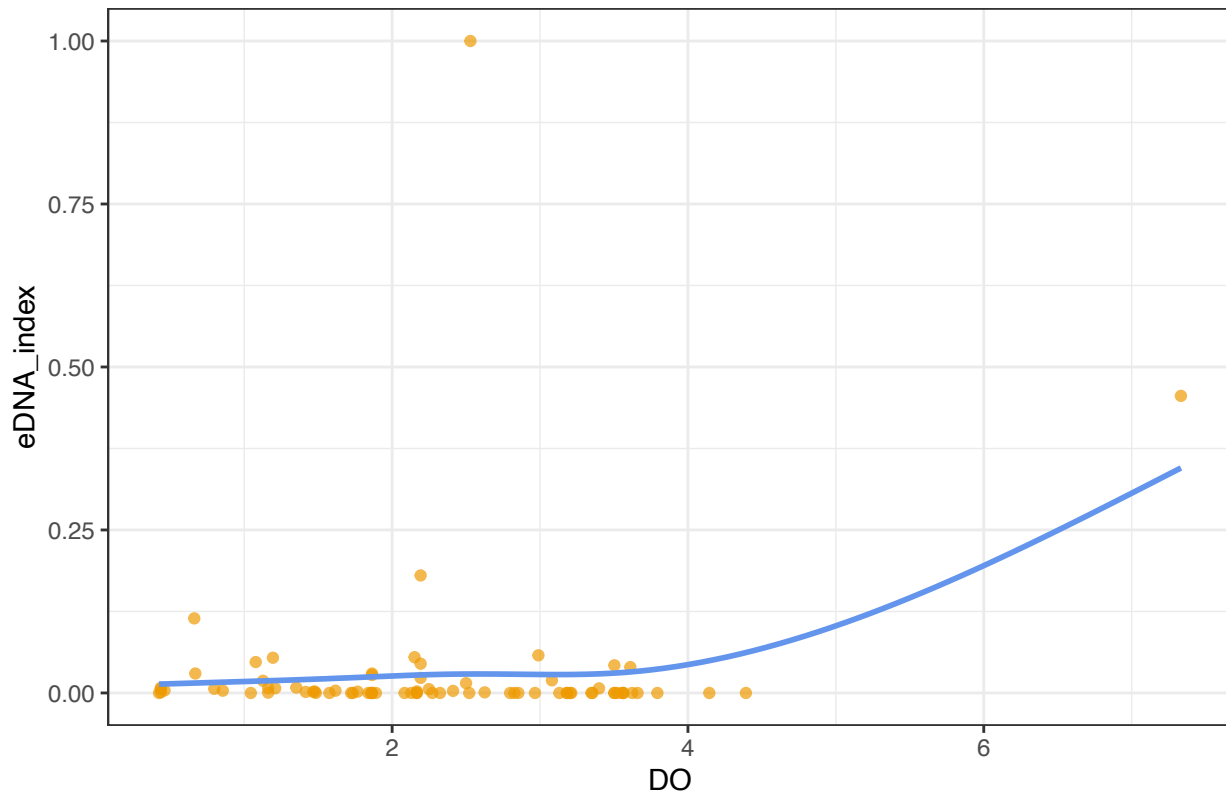# Oithona similis eDNA Index vs Dissolved Oxygen


```
## 
## Family: gaussian 
## Link function: identity 
## 
## Formula:
## eDNA_index ~ s(DO)
## 
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.03781    0.01499   2.523   0.0137 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Approximate significance of smooth terms:
##         edf Ref.df      F p-value
## s(DO) 1.407  1.711 0.267   0.789
## 
## R-sq.(adj) =  -0.00515   Deviance explained = 1.32%
## GCV = 0.018078  Scale est. = 0.01752   n = 78
## [1] "GAM quality"
## [1] "AIC: -89.7414115555766"
##     GCV.Cp
## 0.01807768
```

Resids vs. linear pred.

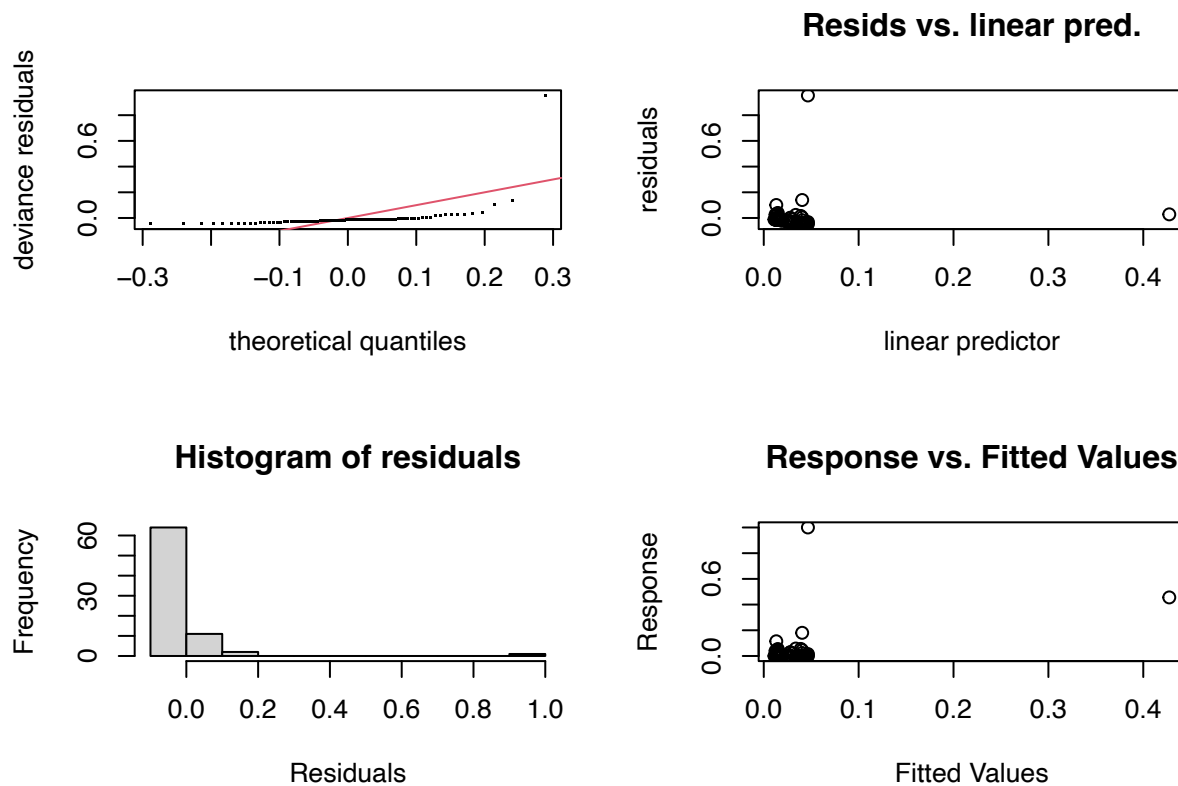**Histogram of residuals**

Response vs. Fitted Values

```
## 
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 5 iterations.
## The RMS GCV score gradient at convergence was 3.187024e-07 .
## The Hessian was positive definite.
## 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(DO) 9.00 1.41    0.93    0.15
## $mfrow
## [1] 2 2
## 
## [1] "Paracalanus sp. C AC-2013 eDNA Index vs Dissolved Oxygen"

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
```

Paracalanus sp. C AC−2013 eDNA Index vs Dissolved Oxygen
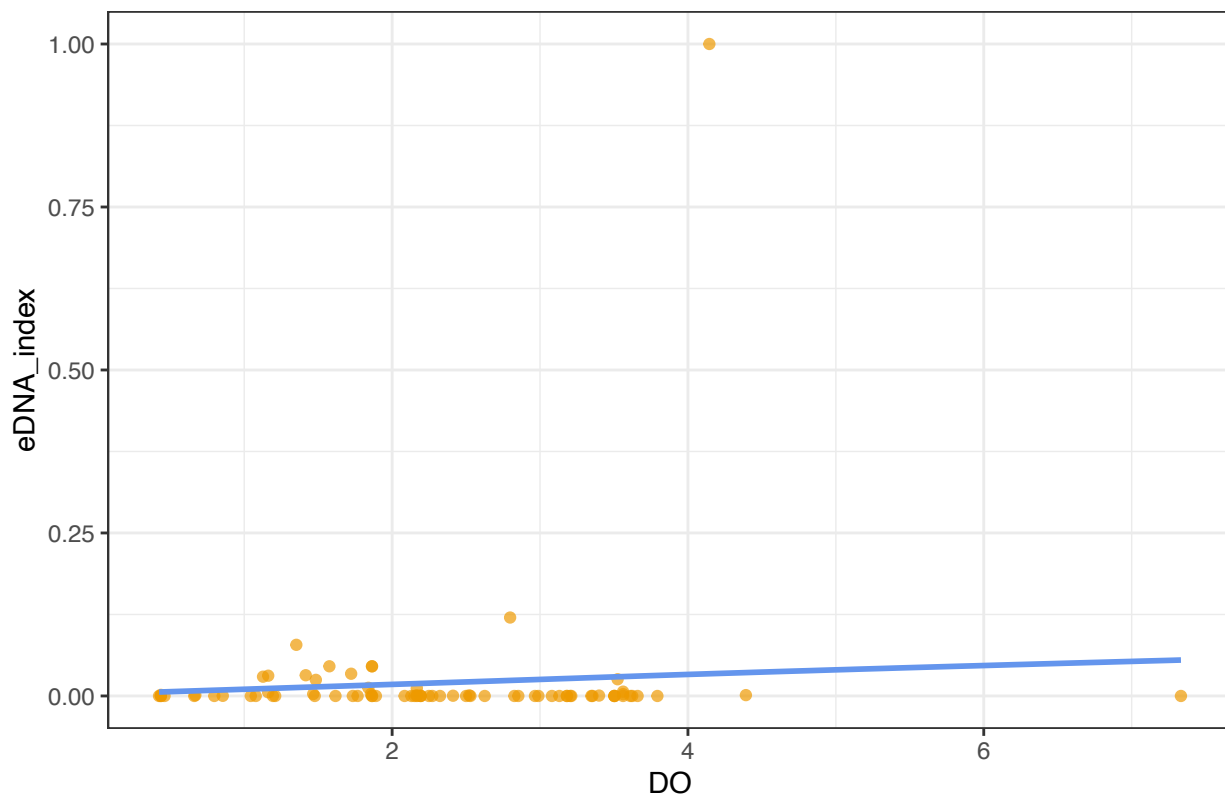


```
## 
## Family: gaussian 
## Link function: identity 
## 
## Formula:
## eDNA_index ~ s(DO)
## 
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.02998    0.01313   2.283   0.0253 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Approximate significance of smooth terms:
##         edf Ref.df     F p-value
## s(DO) 3.691  4.473 3.131  0.0156 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## R-sq.(adj) =   0.14   Deviance explained = 18.2%
## GCV = 0.014306  Scale est. = 0.013446  n = 78
## [1] "GAM quality"
## [1] "AIC: -108.210096766989"
##     GCV.Cp
## 0.01430627
```

Resids vs. linear pred.

Histogram of residuals
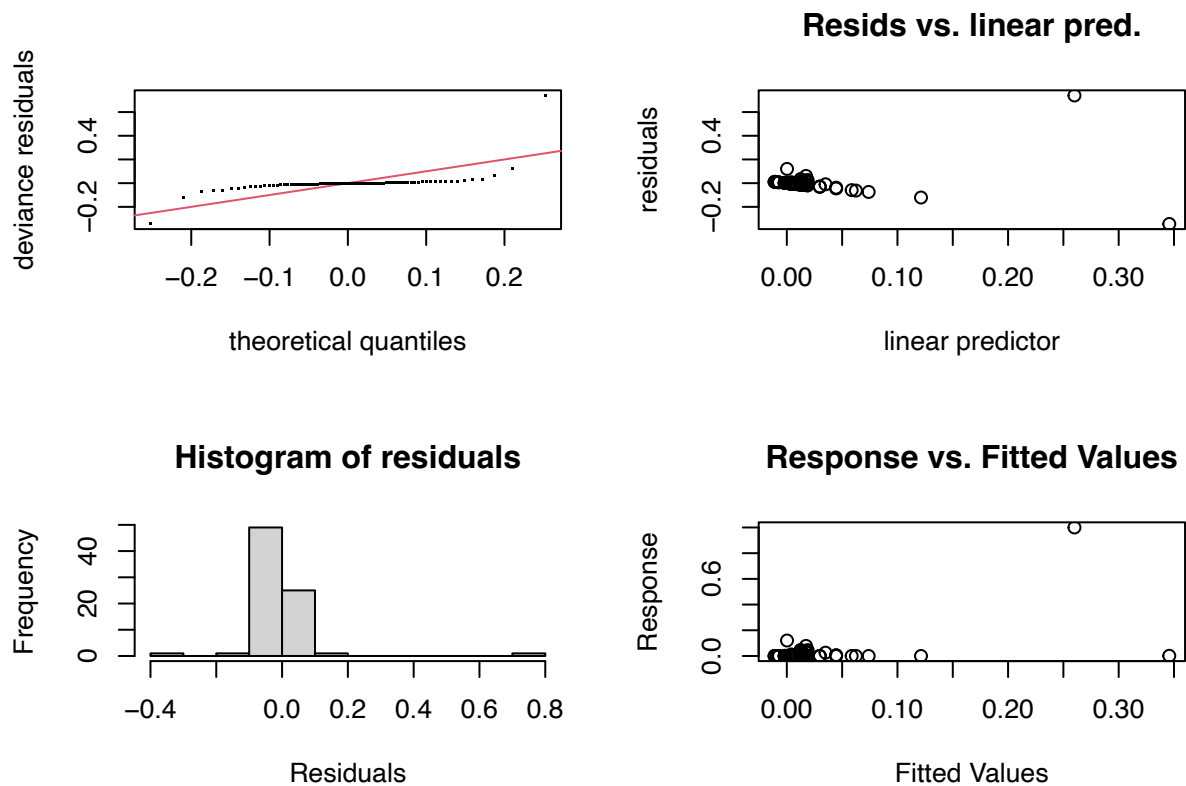
Response vs. Fitted Values

```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 4 iterations.
## The RMS GCV score gradient at convergence was 5.122255e-11 .
## The Hessian was positive definite.
## 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(DO) 9.00 3.69    1.08    0.98
## $mfrow
## [1] 2 2
##
## [1] "Pseudocalanus newmani eDNA Index vs Dissolved Oxygen"

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
```

Pseudocalanus newmani eDNA Index vs Dissolved Oxygen
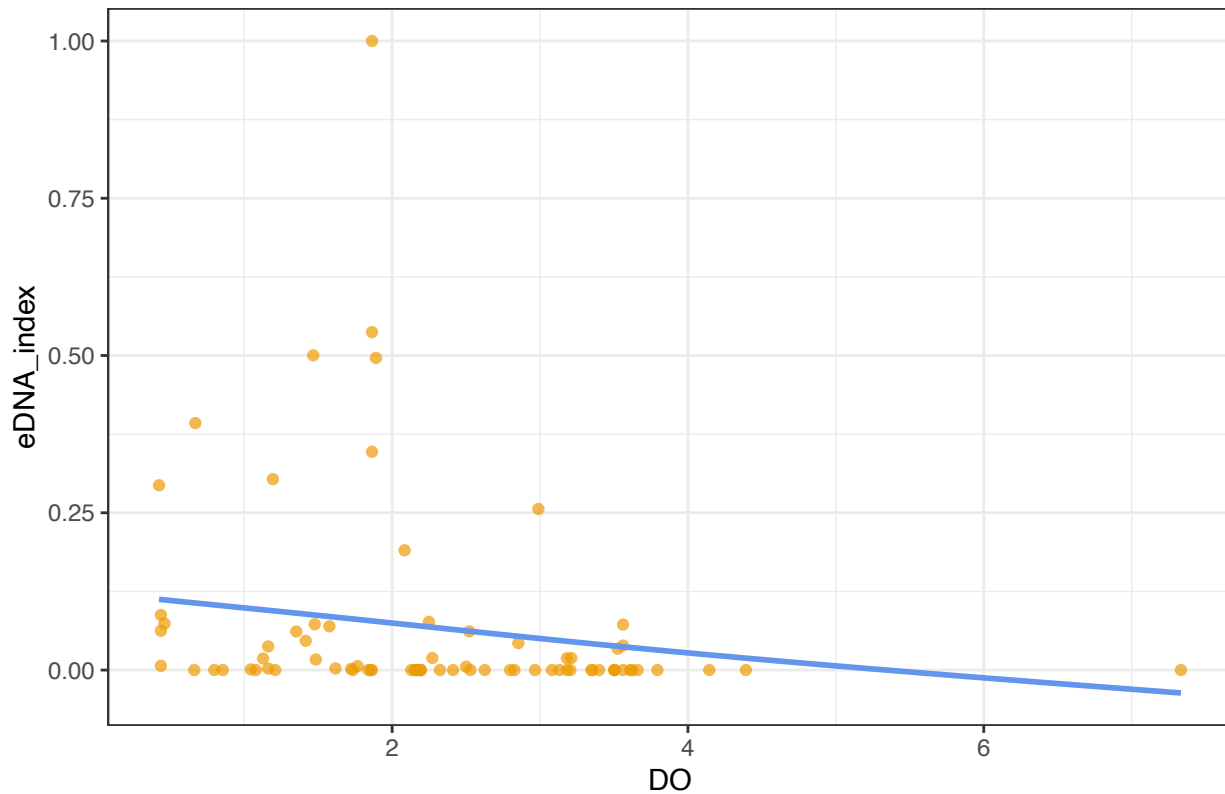


```
## 
## Family: gaussian 
## Link function: identity 
## 
## Formula:
## eDNA_index ~ s(DO)
## 
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.02007    0.01147    1.75   0.0845 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Approximate significance of smooth terms:
##         edf Ref.df      F p-value
## s(DO) 6.059  7.112 3.231 0.00492 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## R-sq.(adj) =  0.211   Deviance explained = 27.3%
## GCV = 0.011282  Scale est. = 0.010261  n = 78
## [1] "GAM quality"
## [1] "AIC: -127.120364551944"
##   GCV.Cp
## 0.011282
```

Resids vs. linear pred.

Histogram of residuals
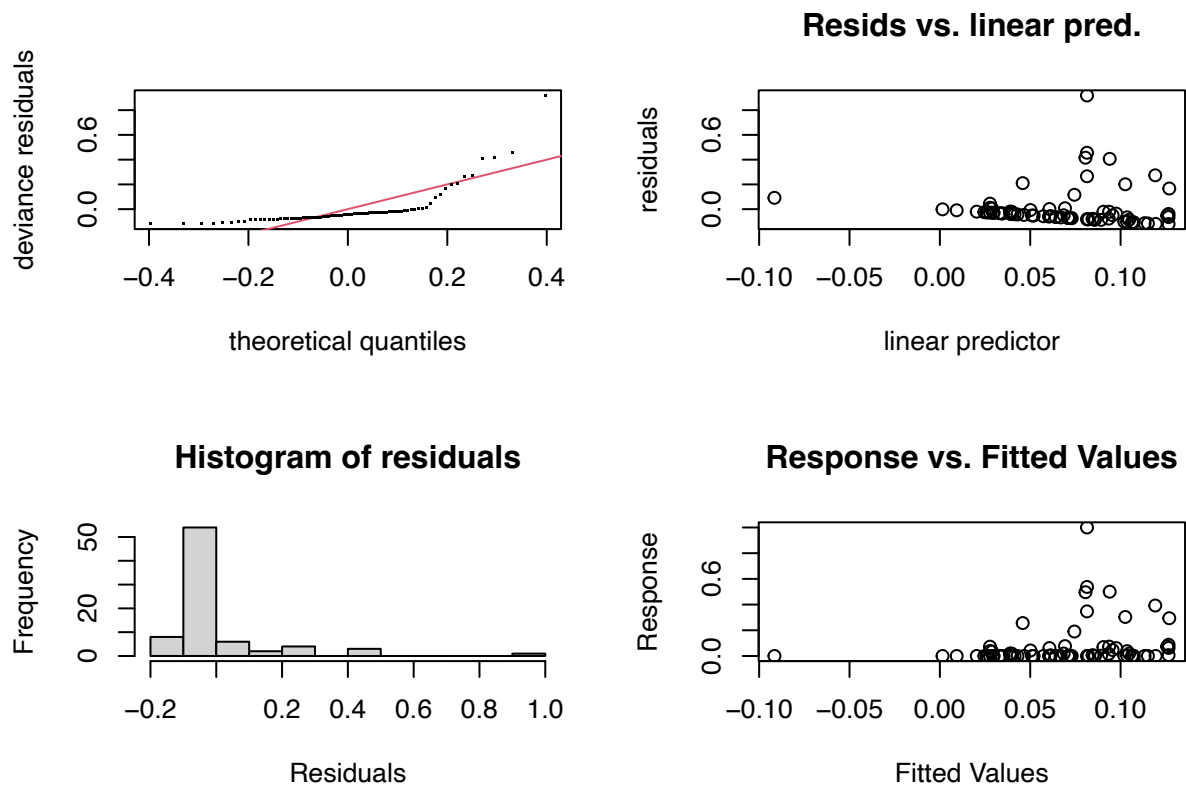
Response vs. Fitted Values

```
## 
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 6 iterations.
## The RMS GCV score gradient at convergence was 1.074935e-06 .
## The Hessian was positive definite.
## 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(DO) 9.00 6.06    1.46       1
## $mfrow
## [1] 2 2
## 
## [1] "Thermocyclops inversus eDNA Index vs Dissolved Oxygen"

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
```

Thermocyclops inversus eDNA Index vs Dissolved Oxygen
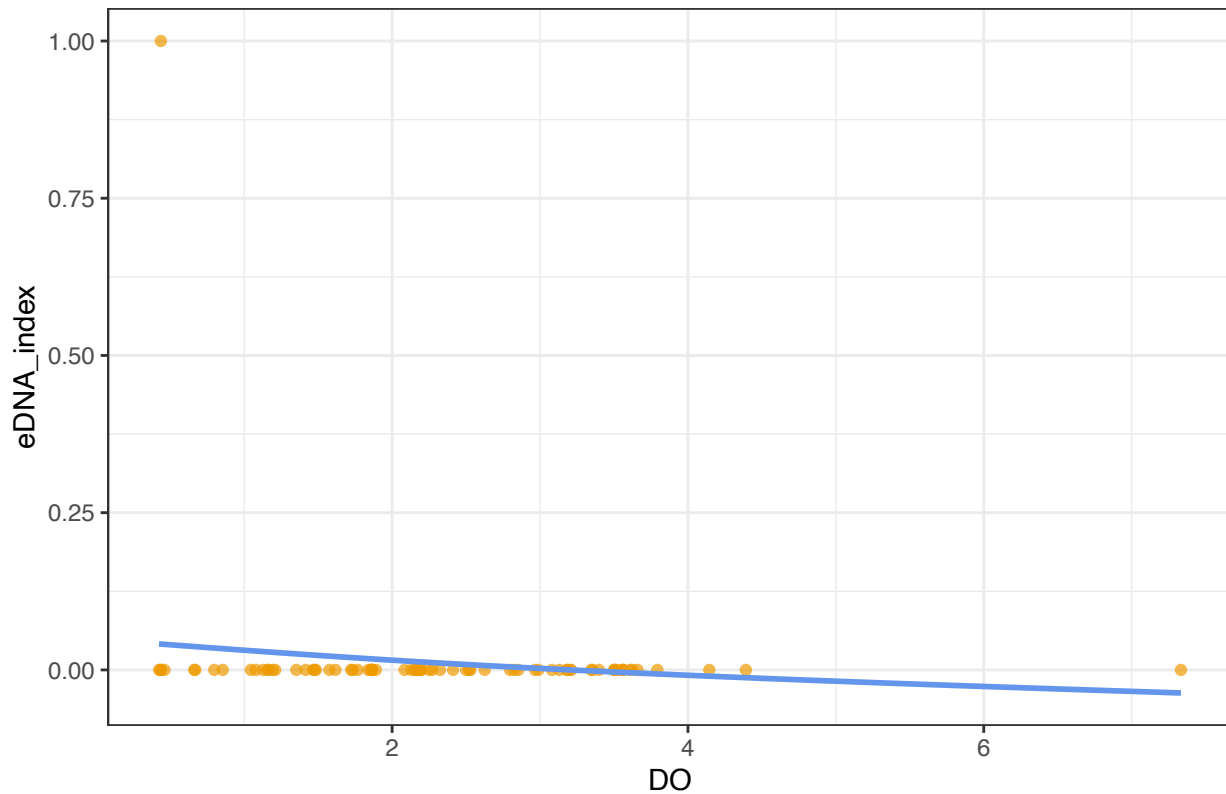


```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## eDNA_index ~ s(DO)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.06759    0.01806   3.742 0.000352 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##       edf Ref.df     F p-value
## s(DO)   1      1 4.118  0.0459 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.0389   Deviance explained = 5.14%
## GCV = 0.02612  Scale est. = 0.02545   n = 78
## [1] "GAM quality"
## [1] "AIC: -61.0125342830331"
##     GCV.Cp
## 0.02611981
```

Resids vs. linear pred.

Histogram of residuals

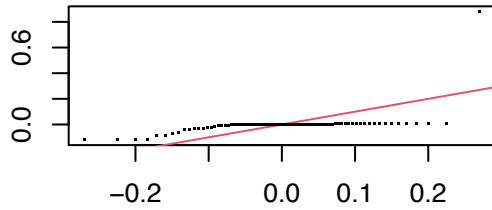**Response vs. Fitted Values**

```
##
## Method: GCV    Optimizer: magic
## Smoothing parameter selection converged after 10 iterations.
## The RMS GCV score gradient at convergence was 6.221389e-08 .
## The Hessian was positive definite.
## 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(DO)  9   1    0.53  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## $mfrow
## [1] 2 2
##
## [1] "Triconia minuta eDNA Index vs Dissolved Oxygen"

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).

## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'

## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
```

## Triconia minuta eDNA Index vs Dissolved Oxygen


```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## eDNA_index ~ s(DO)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.01282    0.01227   1.045    0.299
##
## Approximate significance of smooth terms:
##        edf Ref.df     F p-value
## s(DO) 3.516  4.264 1.961  0.0941 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.0841   Deviance explained = 12.6%
## GCV = 0.012464  Scale est. = 0.011743  n = 78
## [1] "GAM quality"
## [1] "AIC: -118.938625733174"
##     GCV.Cp
## 0.01246433
```
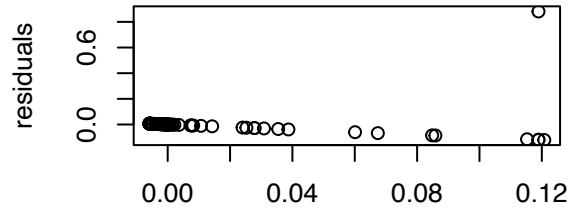
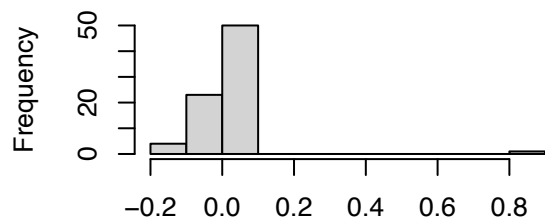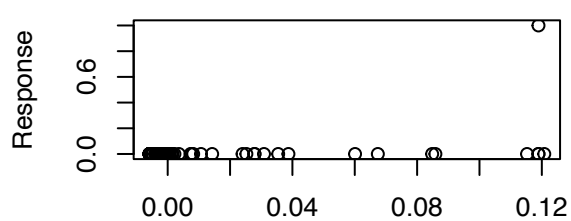**Resids vs. linear pred.**

Histogram of residuals

Response vs. Fitted Values

```
## 
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 4 iterations.
## The RMS GCV score gradient at convergence was 6.255304e-16 .
## The Hessian was positive definite.
## 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(DO) 9.00 3.52    1.18    0.99
## $mfrow
## [1] 2 2
```

```r
# I think I'm still having some issues w.r.t. the 2023 elimination issue

system("say G A M complete")

system("say Script complete")
```