

GAM of eDNA index vs oxygen

```
dfsplitted <- split(eDNAindxEnvData_cleanYr, eDNAindxEnvData_cleanYr$Species) # Split by
↳ species

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

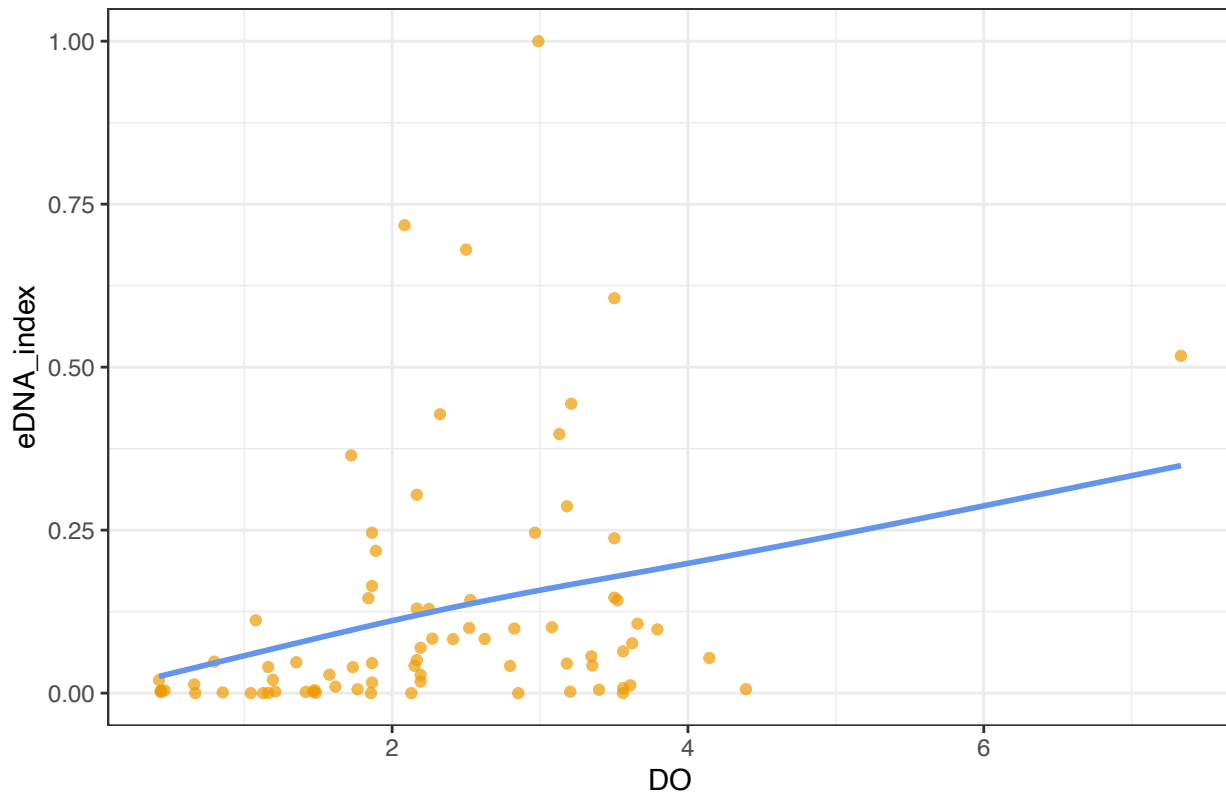
```
## [1] "Acartia longiremis"
## [1] "Acartia longiremis eDNA Index vs Dissolved Oxygen"

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

## Warning: Removed 1 row containing non-finite outside the scale range
```

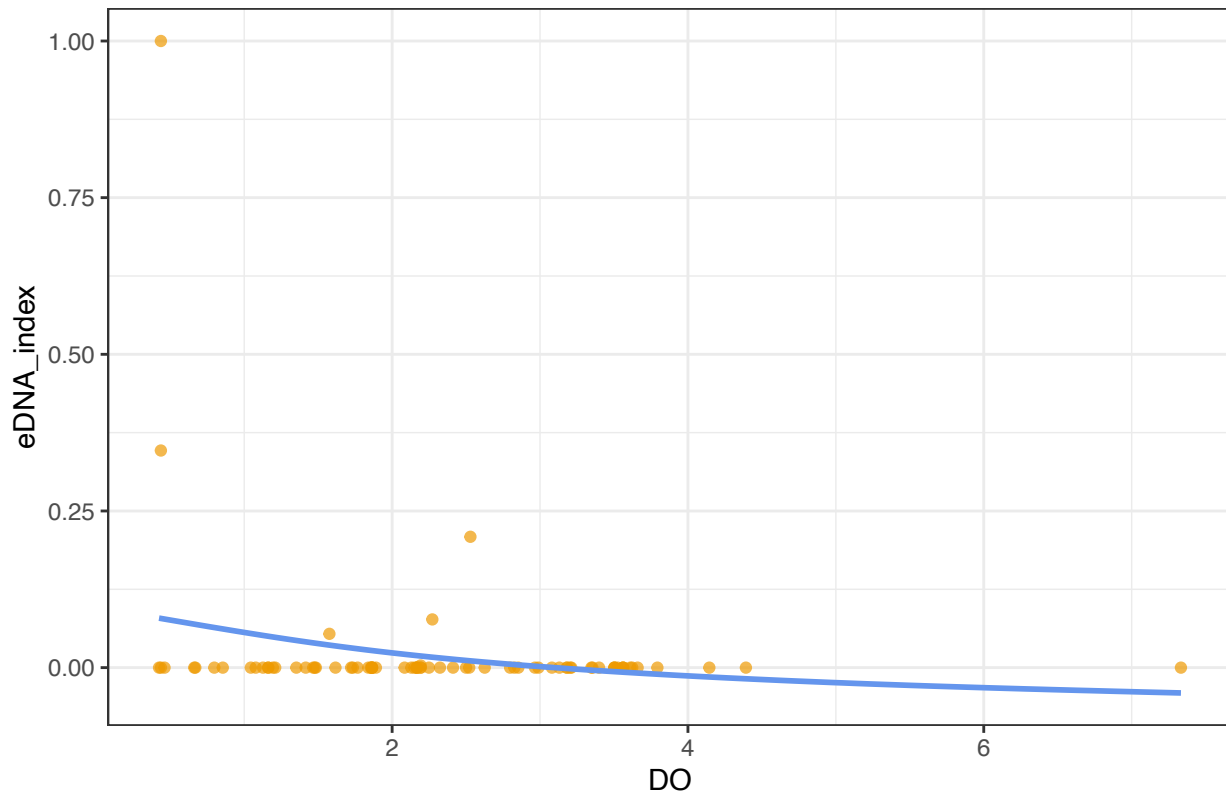
```
## (`stat_smooth()`).
## Warning: Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale range
## (`geom_point()`).
```

Acartia longiremis eDNA Index vs Dissolved Oxygen



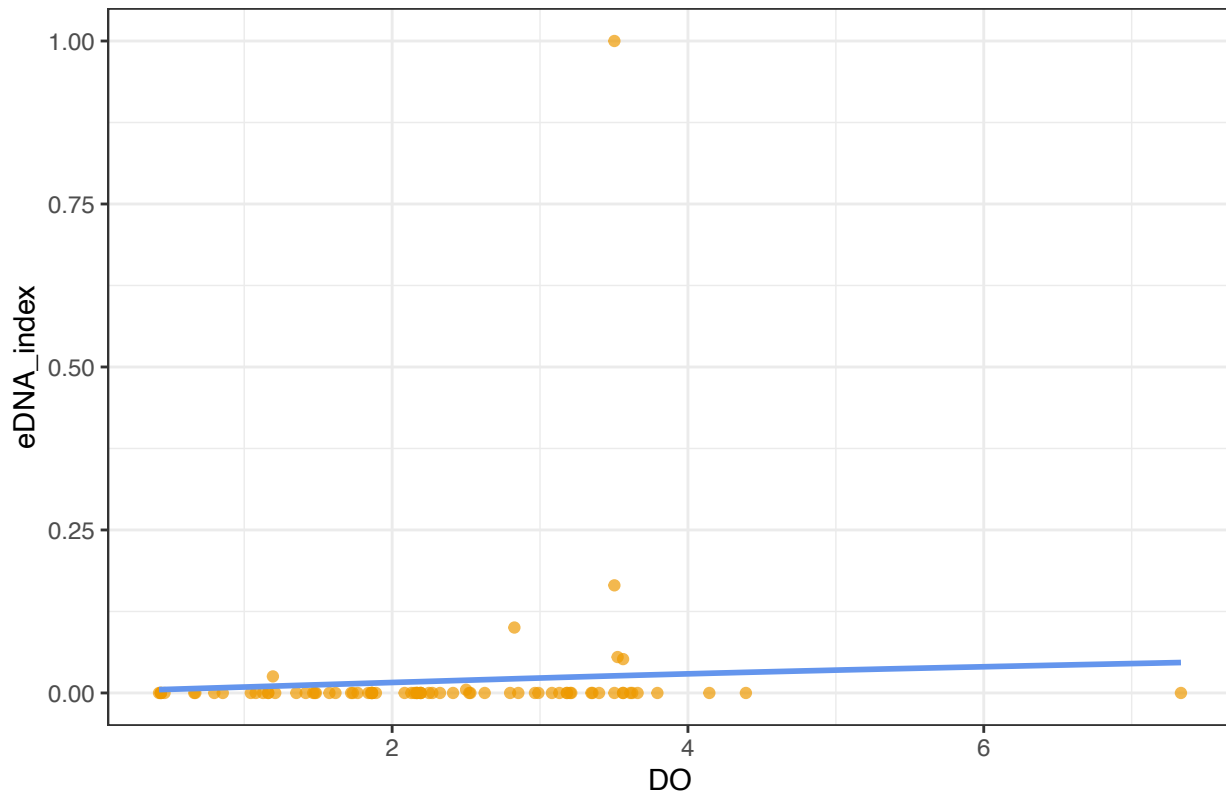
```
## [1] "Calanus pacificus"
## [1] "Calanus pacificus eDNA Index vs Dissolved Oxygen"
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the 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()`).
```

Calanus pacificus eDNA Index vs Dissolved Oxygen



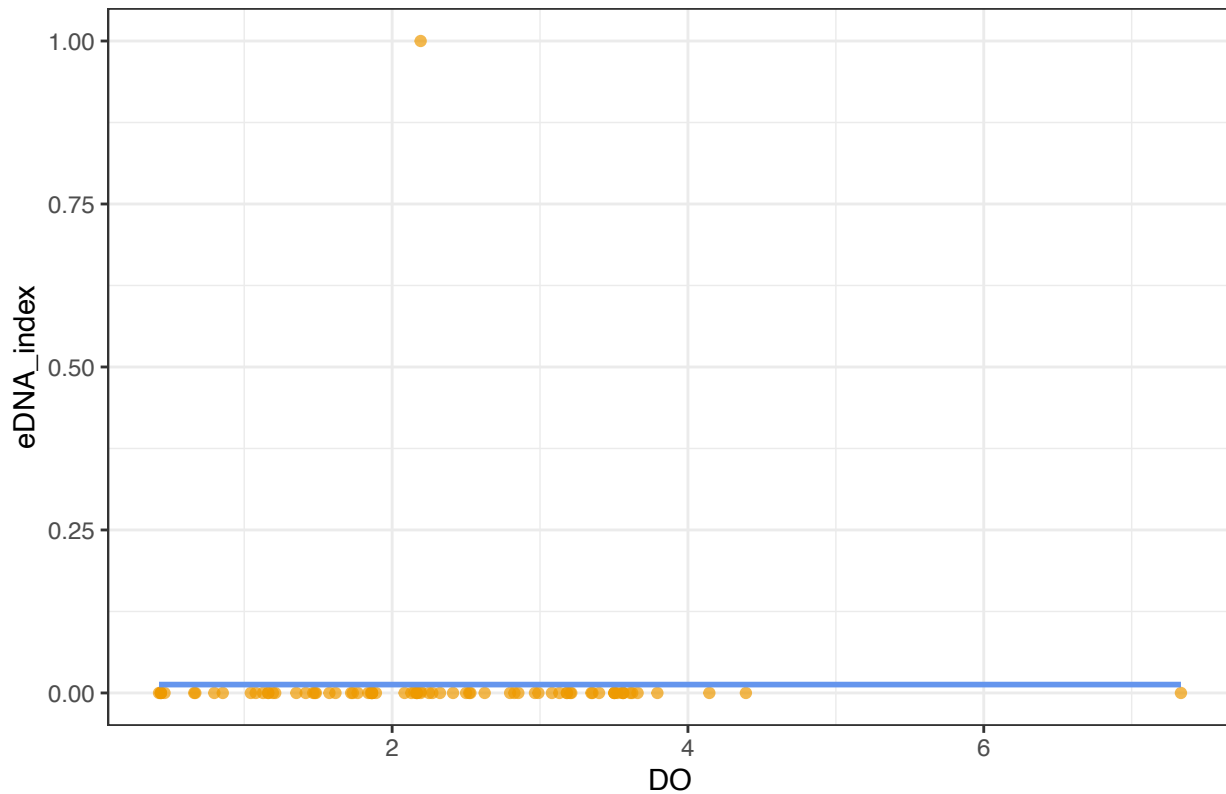
```
## [1] "Centropages abdominalis"
## [1] "Centropages abdominalis eDNA Index vs Dissolved Oxygen"
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values 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



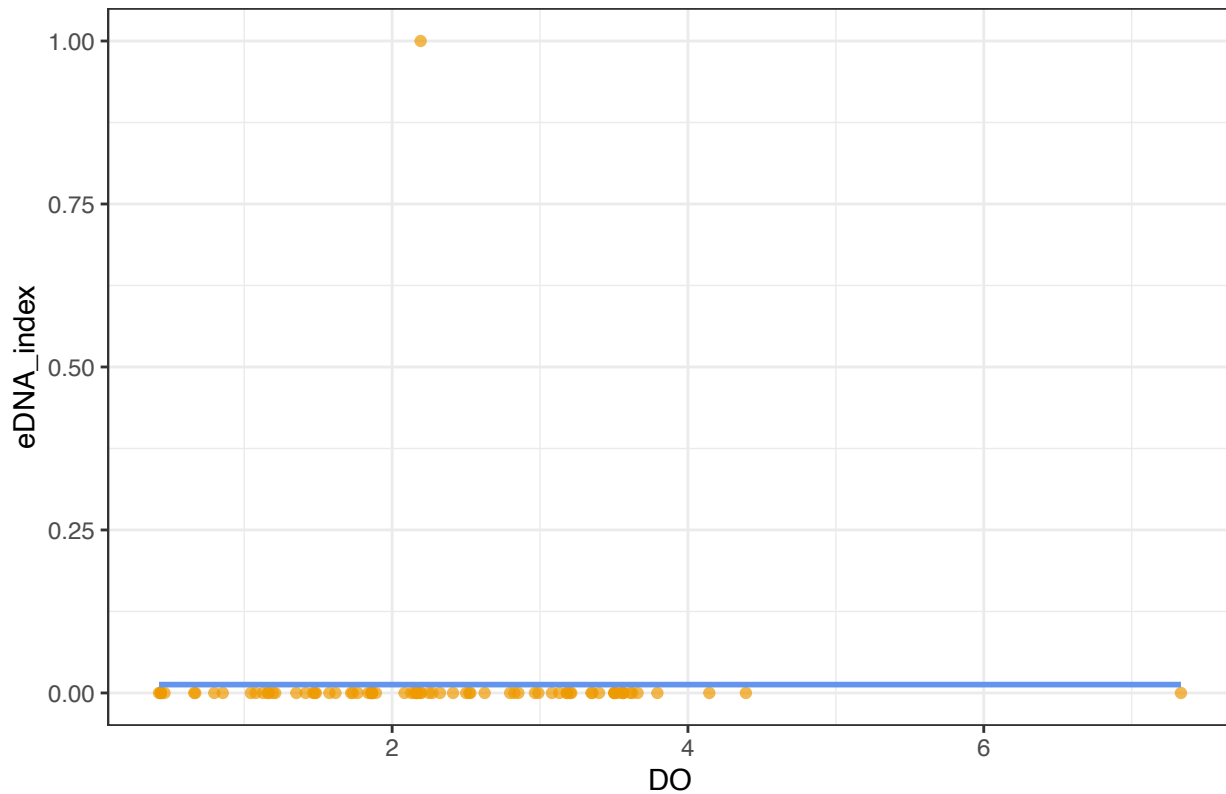
```
## [1] "Clausocalanus parapergens"
## [1] "Clausocalanus parapergens eDNA Index vs Dissolved Oxygen"
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values 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



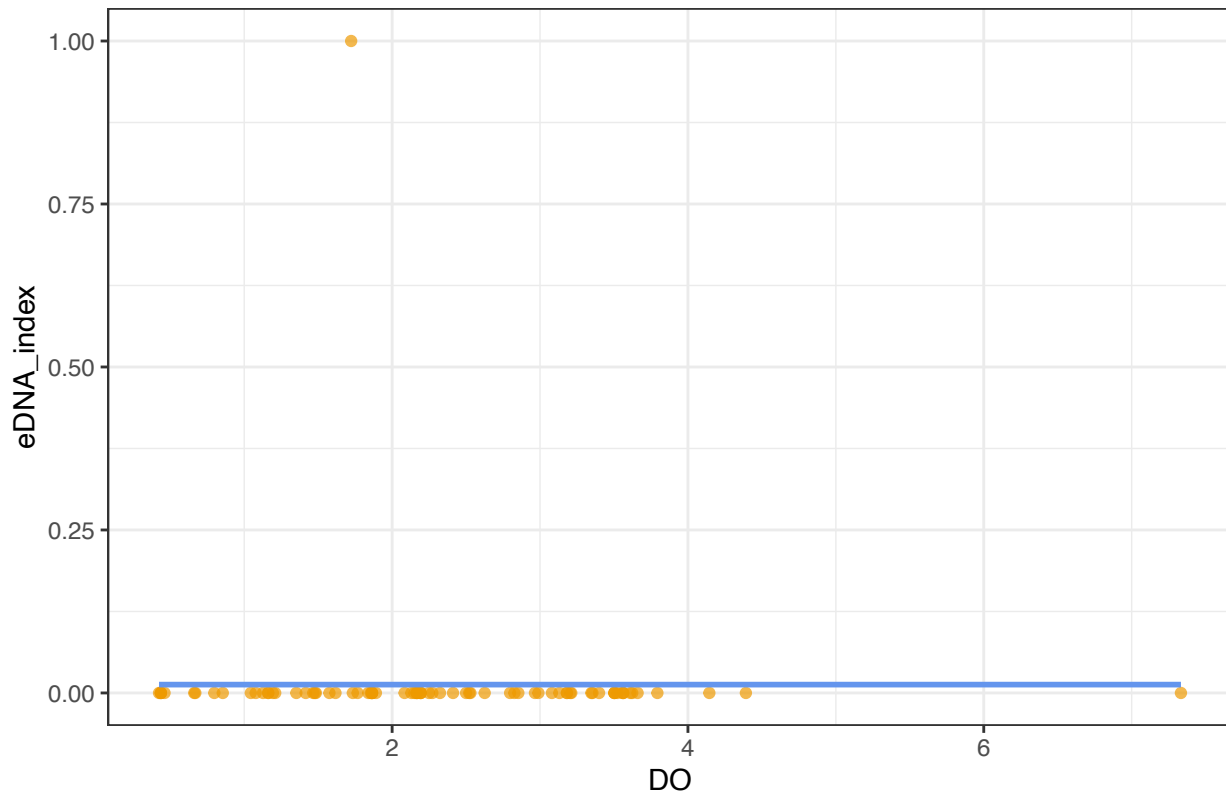
```
## [1] "Clausocalanus pergens"
## [1] "Clausocalanus pergens eDNA Index vs Dissolved Oxygen"
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside 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



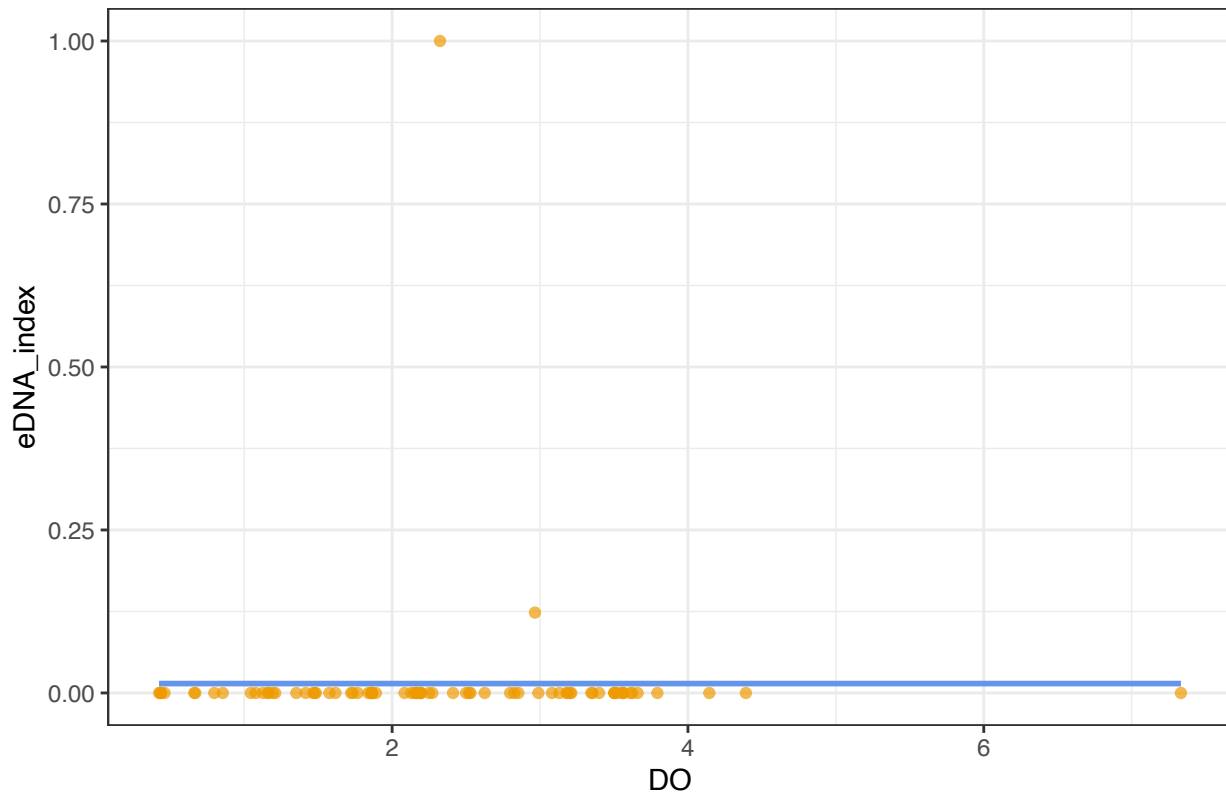
```
## [1] "Diacyclops incolotaenia"
## [1] "Diacyclops incolotaenia eDNA Index vs Dissolved Oxygen"
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values 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



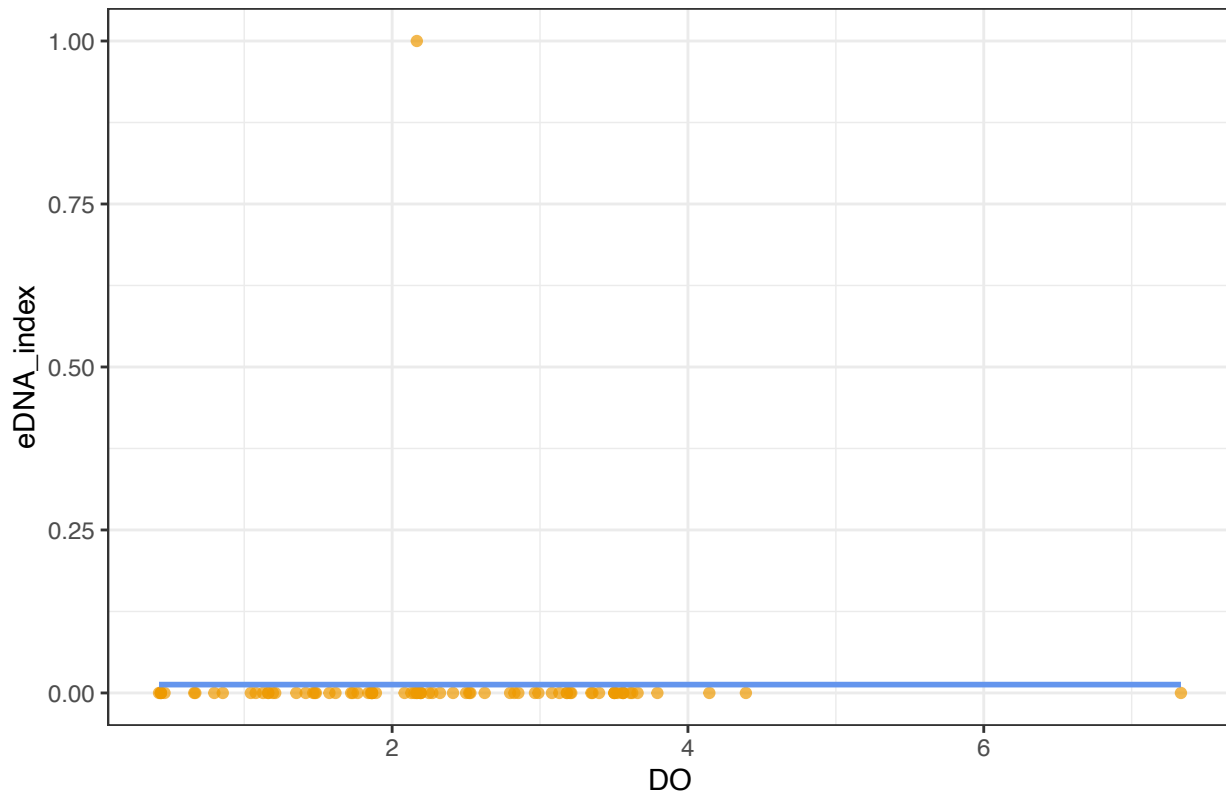
```
## [1] "Lucicutia flavicornis"
## [1] "Lucicutia flavicornis eDNA Index vs Dissolved Oxygen"
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside 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



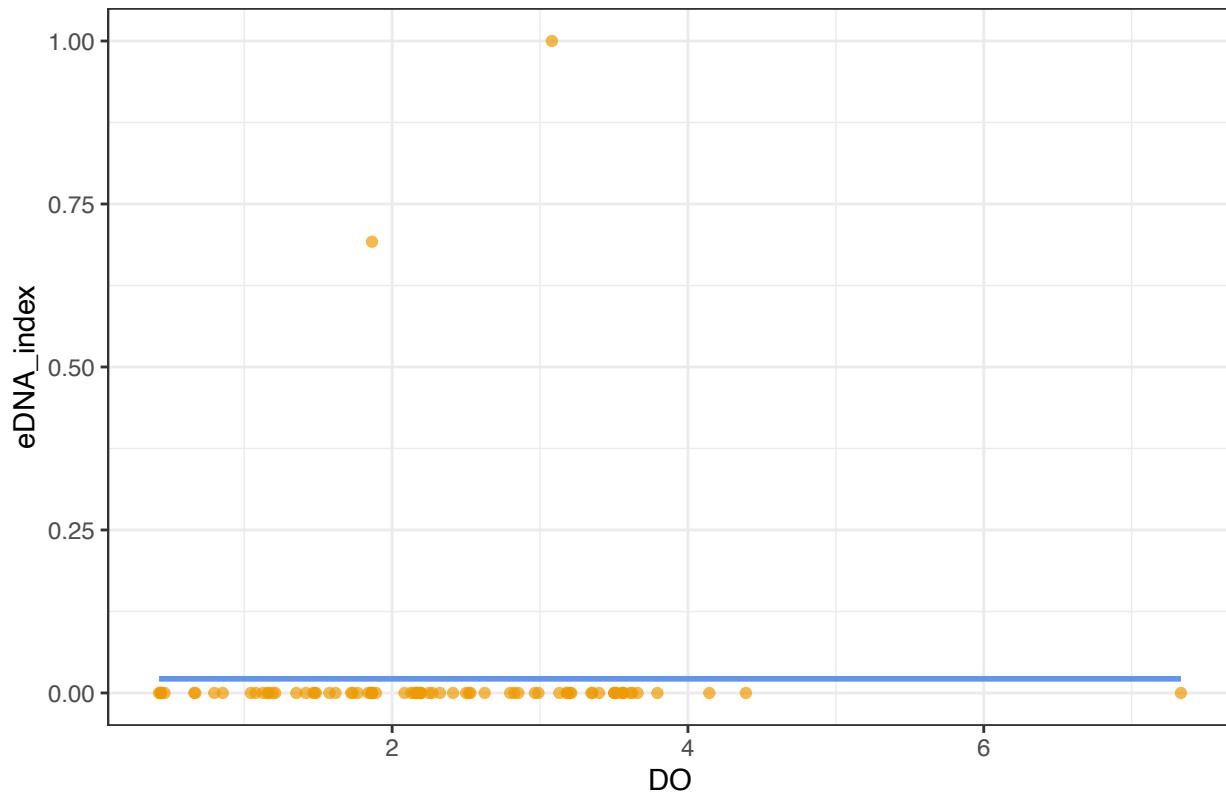
```
## [1] "Metridia lucens"
## [1] "Metridia lucens eDNA Index vs Dissolved Oxygen"
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale 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



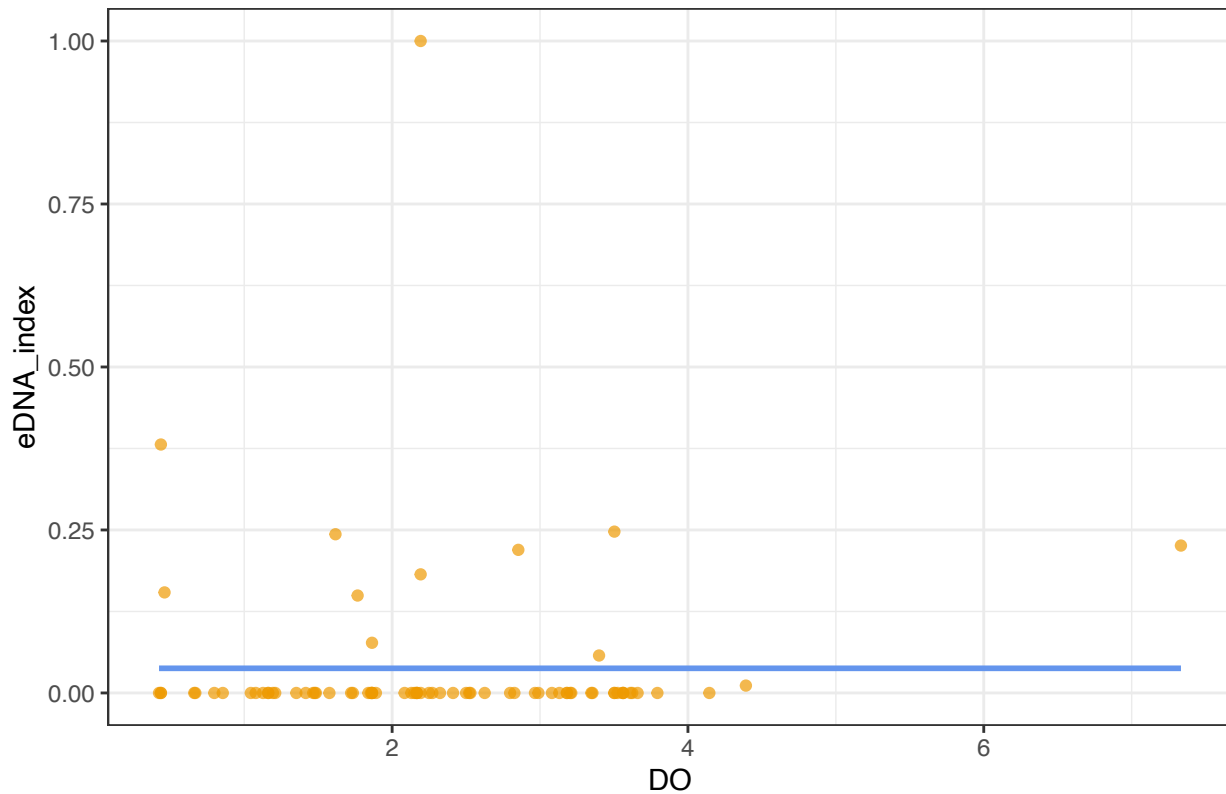
```
## [1] "Metridia pacifica"
## [1] "Metridia pacifica eDNA Index vs Dissolved Oxygen"
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the 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



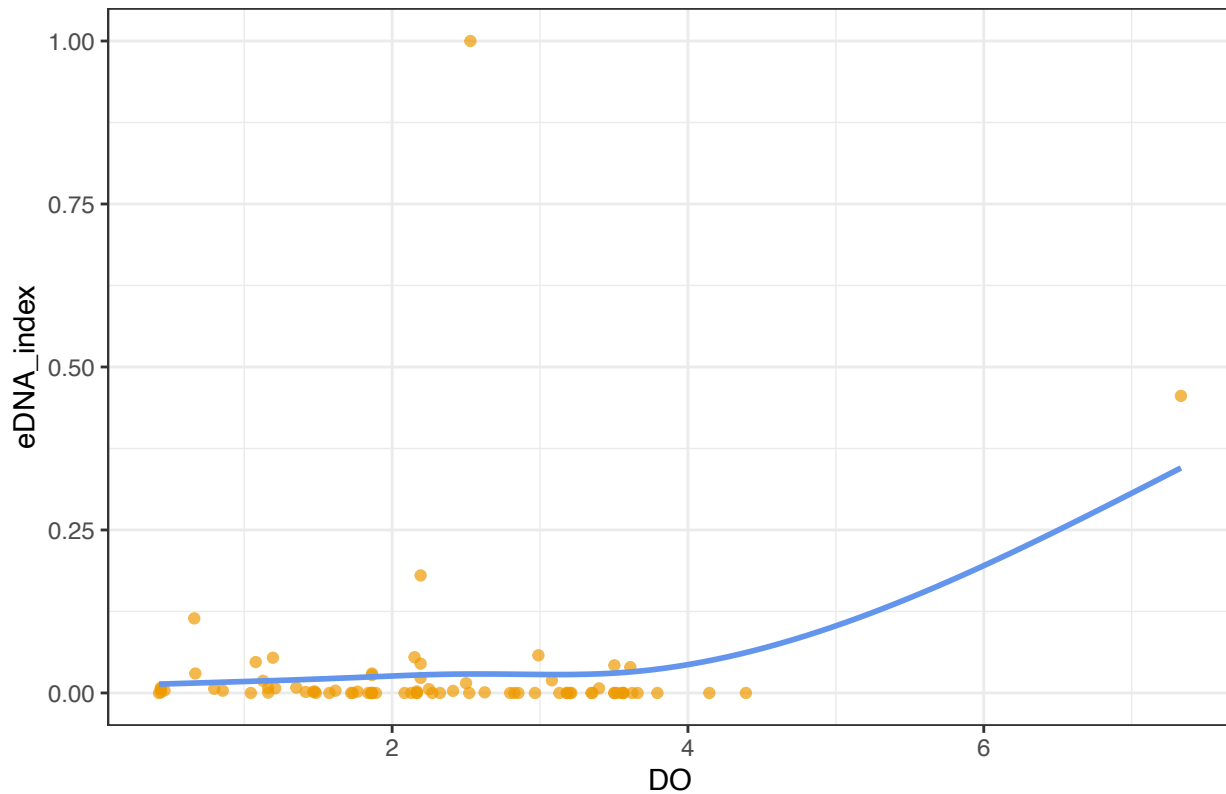
```
## [1] "Oithona similis"
## [1] "Oithona similis eDNA Index vs Dissolved Oxygen"
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside the scale 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



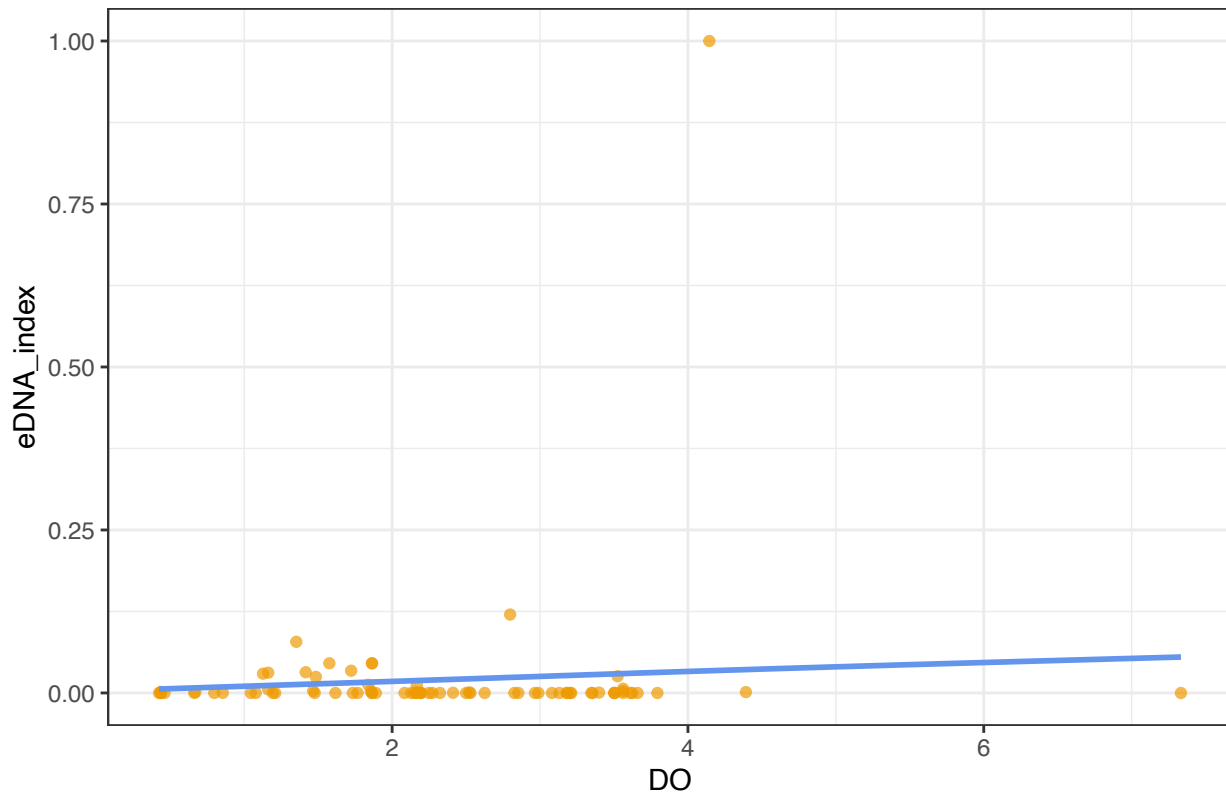
```
## [1] "Paracalanus sp. C AC-2013"
## [1] "Paracalanus sp. C AC-2013 eDNA Index vs Dissolved Oxygen"
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values 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



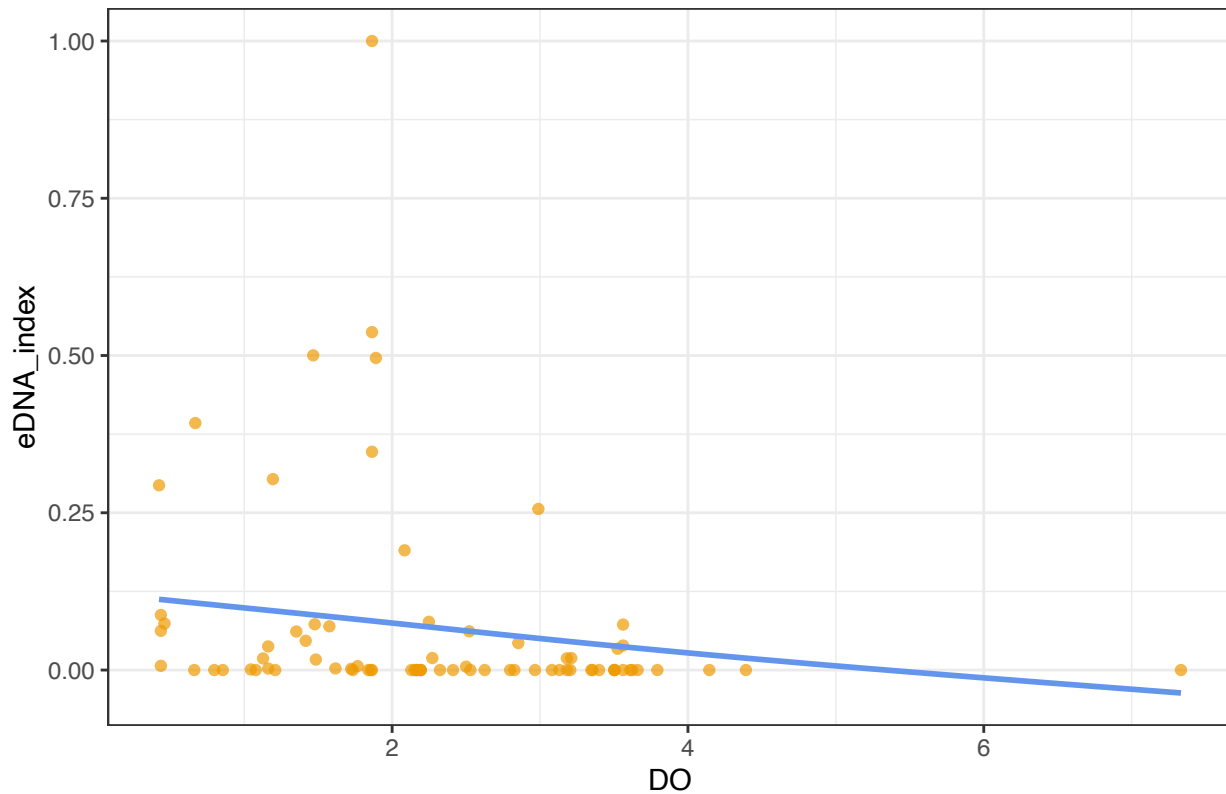
```
## [1] "Pseudocalanus newmani"
## [1] "Pseudocalanus newmani eDNA Index vs Dissolved Oxygen"
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside 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

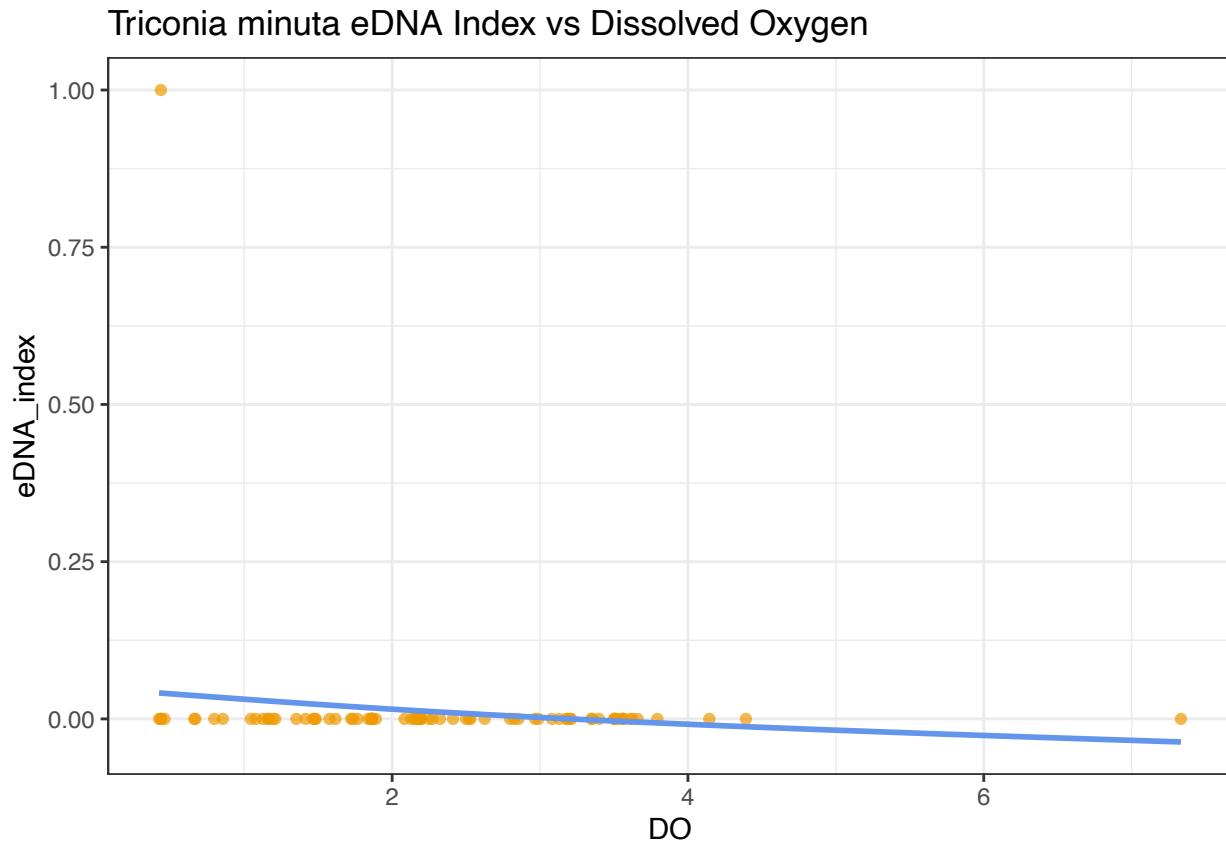


```
## [1] "Thermocyclops inversus"
## [1] "Thermocyclops inversus eDNA Index vs Dissolved Oxygen"
## `geom_smooth()` using formula = 'y ~ s(x, bs = "cs")'
## Warning: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
## Removed 1 row containing missing values or values outside 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



```
## [1] "Triconia minuta"
## [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()`).
```



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

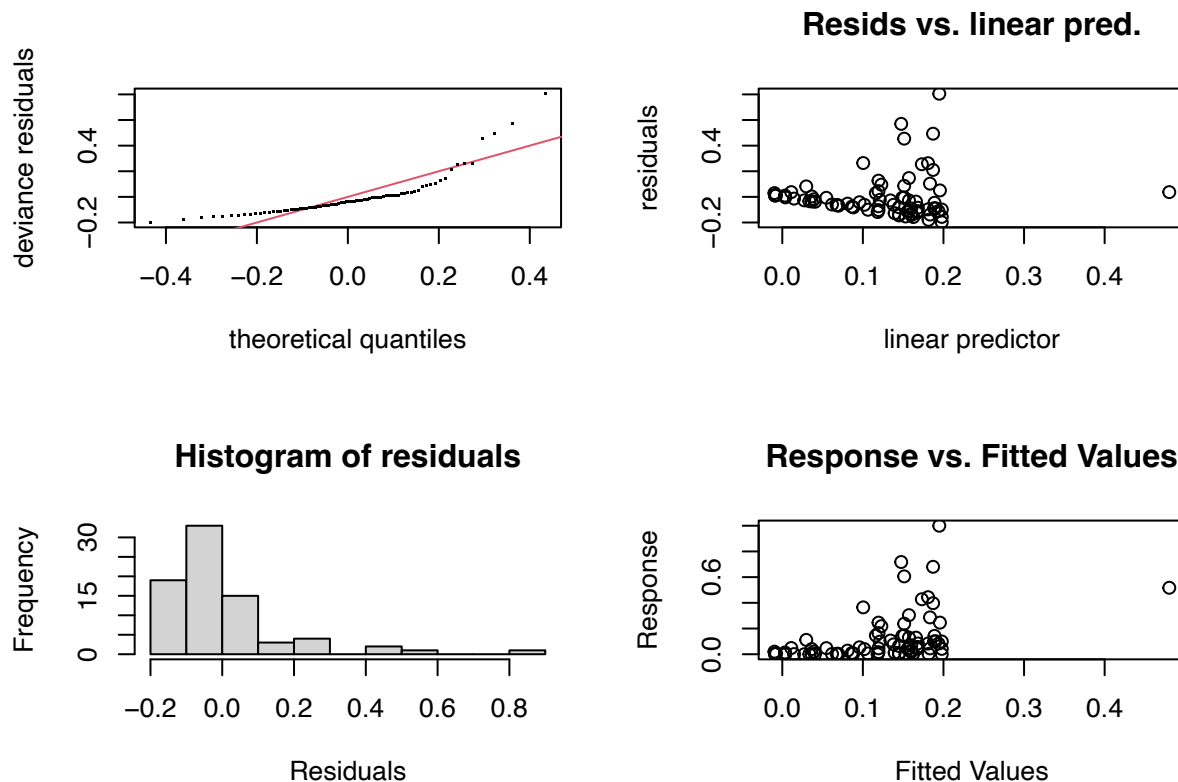
```
for (i in 1:length(dfsplit)) { # For each species:
  species <- dfsplit[[i]]$Species[1] # Species name for title and export png name
  title <- paste(species, sep = " ", "eDNA Index vs Dissolved Oxygen") # Plot title,
  ↪ changed for eDNA
  print(title)

  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
}
```

```
## [1] "Acartia longiremis eDNA Index vs Dissolved Oxygen"
##
## Family: gaussian
## Link function: identity
##
## Formula:
## eDNA_index ~ s(DO)
##
## Parametric coefficients:
```

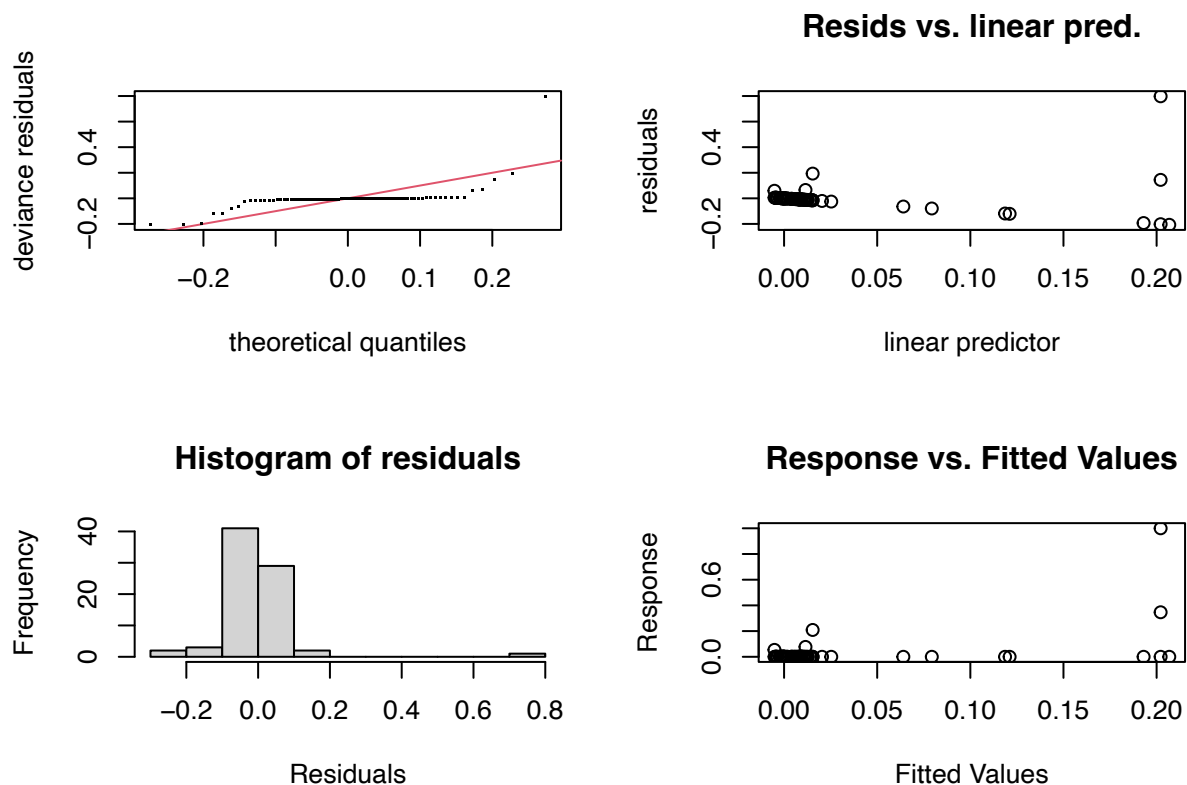
```
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.12233    0.01975   6.195  3.1e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##           edf Ref.df      F p-value
## s(D0)  3.918  4.742  3.529  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
```



```
##
## 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(D0)  9.00  3.92    1.13   0.87
```



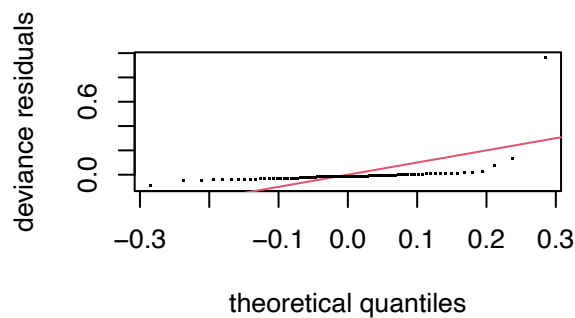
```
## $mfrow
## [1] 2 2
##
## [1] "Calanus pacificus eDNA Index vs Dissolved Oxygen"
##
## Family: gaussian
## Link function: identity
##
## Formula:
## eDNA_index ~ s(DO)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.02166   0.01244   1.742  0.0858 .
## ---
## 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
```



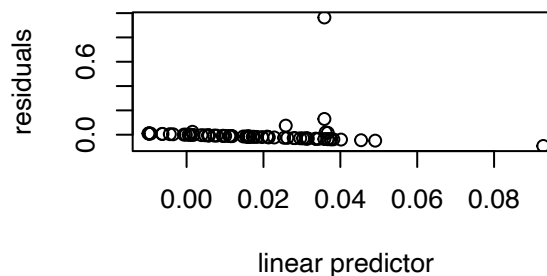
```

##
## 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(D0) 9.00 5.15    0.98    0.19
## $mfrow
## [1] 2 2
##
## [1] "Centropages abdominalis eDNA Index vs Dissolved Oxygen"
##
## Family: gaussian
## Link function: identity
##
## Formula:
## eDNA_index ~ s(D0)
##
## 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(D0)   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

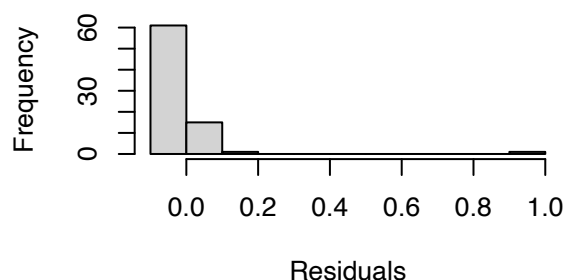
```



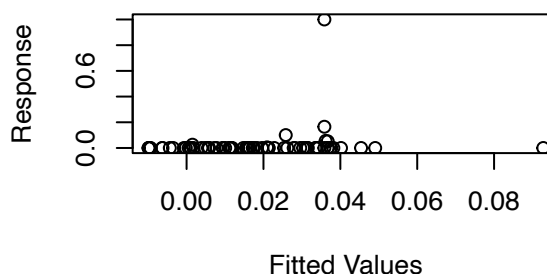
Resids vs. linear pred.



Histogram of residuals



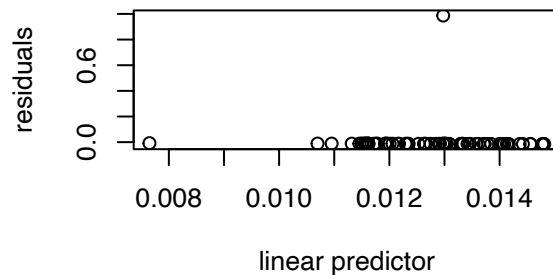
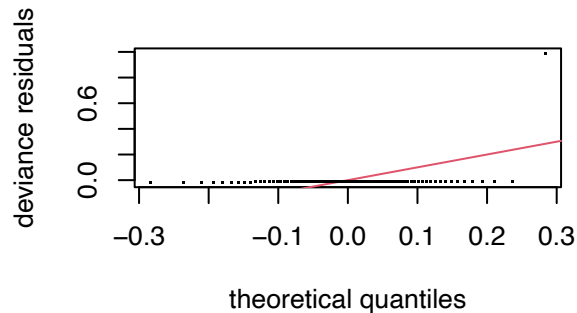
Response vs. Fitted Values



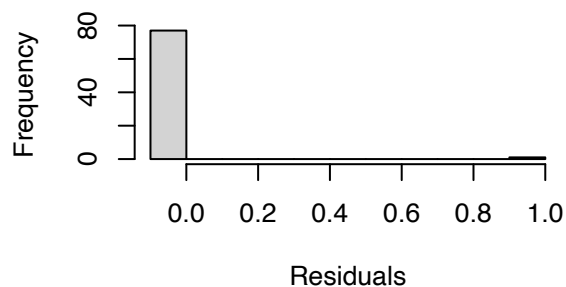
```
##
## Method: GCV Optimizer: magic
## Smoothing parameter selection converged after 8 iterations.
## The RMS GCV score gradient at convergence was 1.582062e-07 .
## The Hessian was positive definite.
## Model rank = 10 / 10
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##      k' edf k-index p-value
## s(D0) 9   1   0.89  0.046 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## $mfrow
## [1] 2 2
##
## [1] "Clausocalanus parapergens eDNA Index vs Dissolved Oxygen"
##
## Family: gaussian
## Link function: identity
##
## Formula:
## eDNA_index ~ s(D0)
##
## 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
```

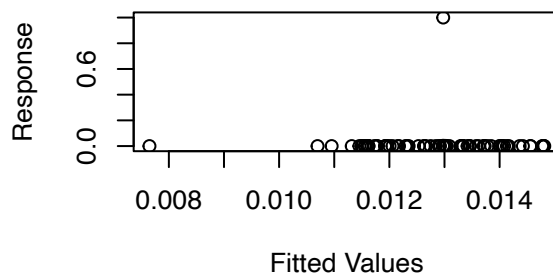
Resids vs. linear pred.



Histogram of residuals



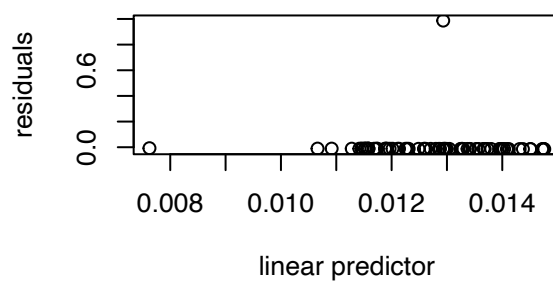
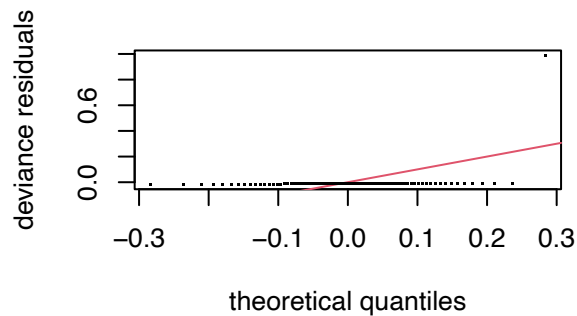
Response vs. Fitted Values



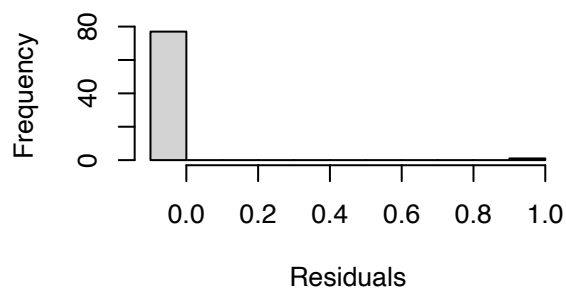
```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 9 iterations.
## The RMS GCV score gradient at convergence was 7.296207e-08 .
## The Hessian was positive definite.
## Model rank = 10 / 10
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## 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   0.53
## $mfrow
## [1] 2 2
##
## [1] "Clausocalanus pergens eDNA Index vs Dissolved Oxygen"
##
## Family: gaussian
## Link function: identity
```

```
##
## Formula:
## eDNA_index ~ s(D0)
##
## 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(D0)       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
```

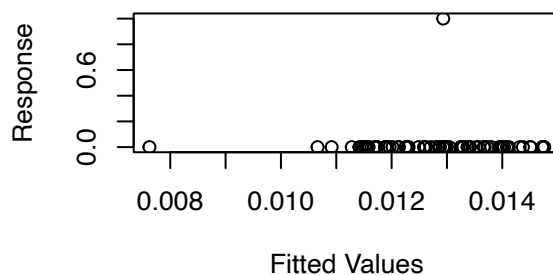
Resids vs. linear pred.



Histogram of residuals



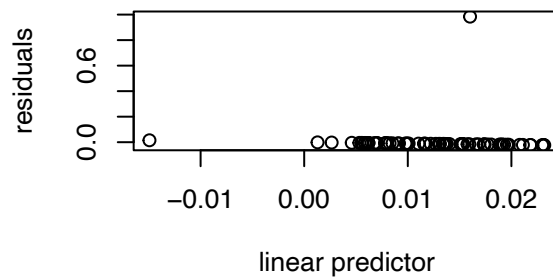
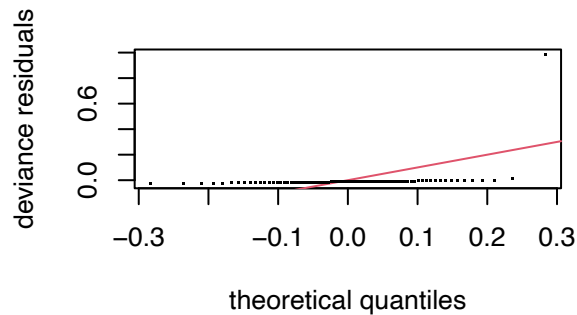
Response vs. Fitted Values



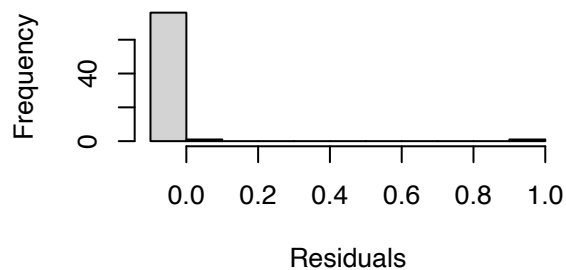
```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 9 iterations.
## The RMS GCV score gradient at convergence was 7.323085e-08 .
## The Hessian was positive definite.
## Model rank = 10 / 10
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## 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 0.52
## $mfrow
## [1] 2 2
##
## [1] "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
```

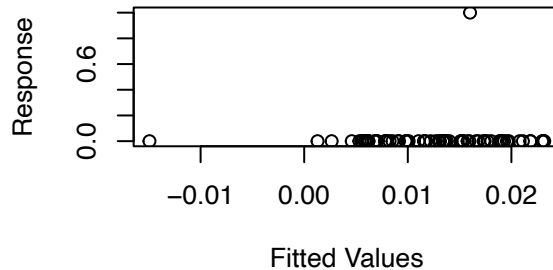
Resids vs. linear pred.



Histogram of residuals



Response vs. Fitted Values

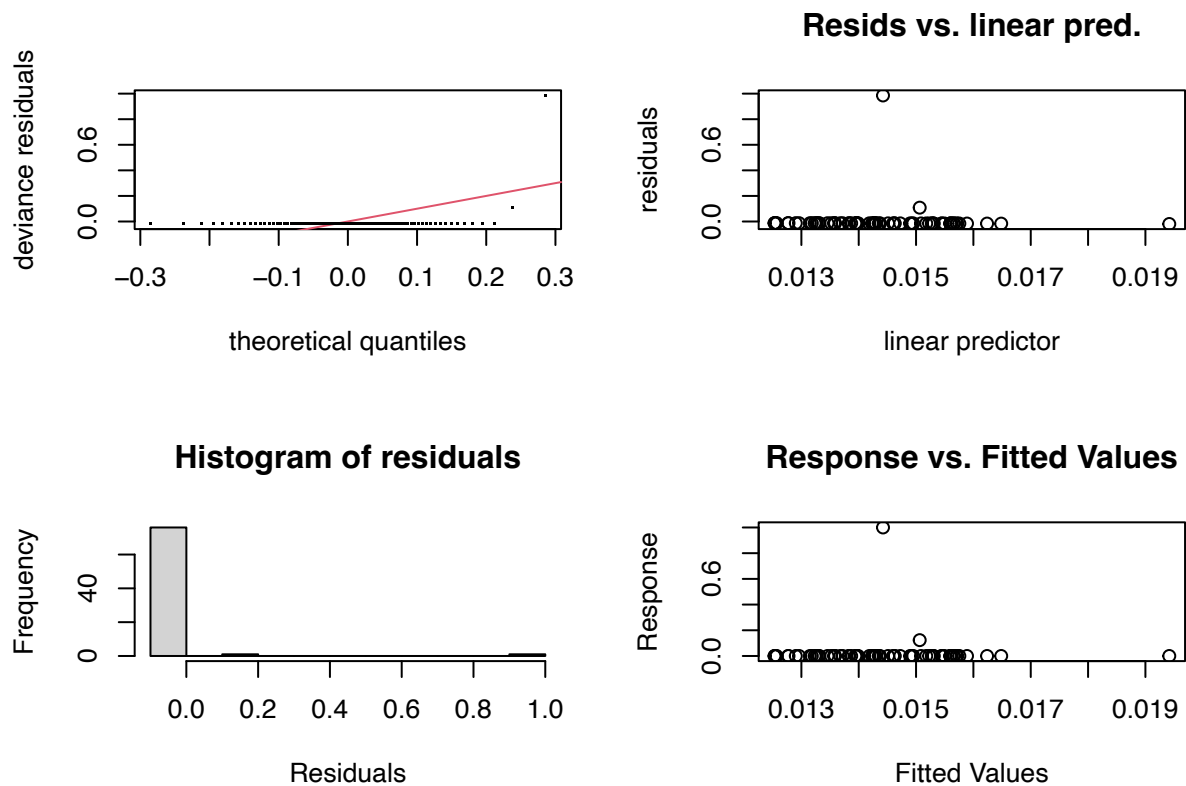


```
##
## Method: GCV  Optimizer: magic
## Smoothing parameter selection converged after 9 iterations.
```

```

## 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(D0) 9   1   1.03   0.69
## $mfrow
## [1] 2 2
##
## [1] "Lucicutia flavicornis eDNA Index vs Dissolved Oxygen"
##
## Family: gaussian
## Link function: identity
##
## Formula:
## eDNA_index ~ s(D0)
##
## 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(D0)   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

```

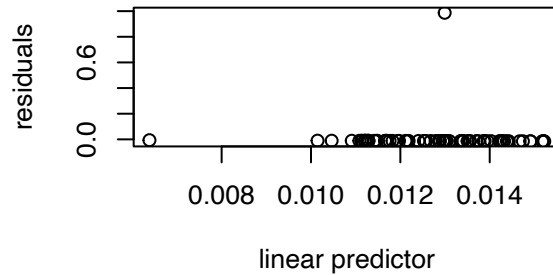
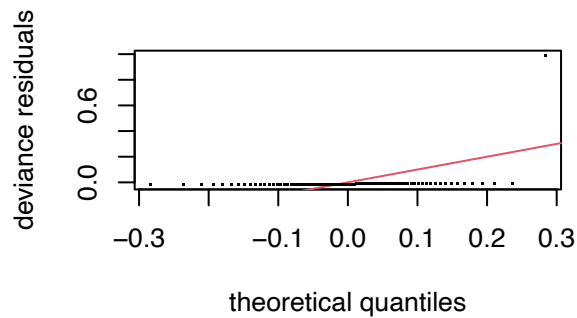


```
##
## Method: GCV Optimizer: magic
## Smoothing parameter selection converged after 9 iterations.
## The RMS GCV score gradient at convergence was 1.050211e-07 .
## The Hessian was positive definite.
## Model rank = 10 / 10
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##      k' edf k-index p-value
## s(D0) 9  1  1.03  0.61
## $mfrow
## [1] 2 2
##
## [1] "Metridia lucens eDNA Index vs Dissolved Oxygen"
##
## Family: gaussian
## Link function: identity
##
## Formula:
## eDNA_index ~ s(D0)
##
## 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
```

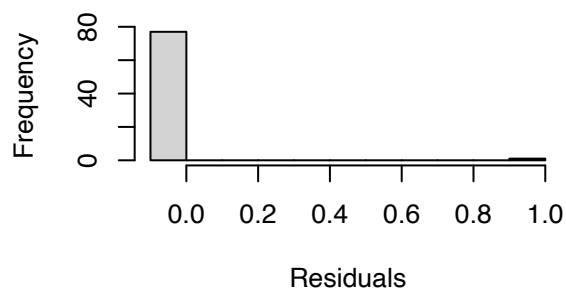


```
## s(D0) 1 1 0.013 0.909
##
## R-sq.(adj) = -0.013 Deviance explained = 0.0174%
## GCV = 0.013329 Scale est. = 0.012987 n = 78
## [1] "GAM quality"
## [1] "AIC: -113.488891135054"
## GCV.Cp
## 0.01332871
```

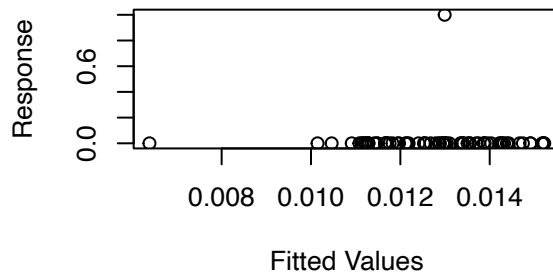
Resids vs. linear pred.



Histogram of residuals



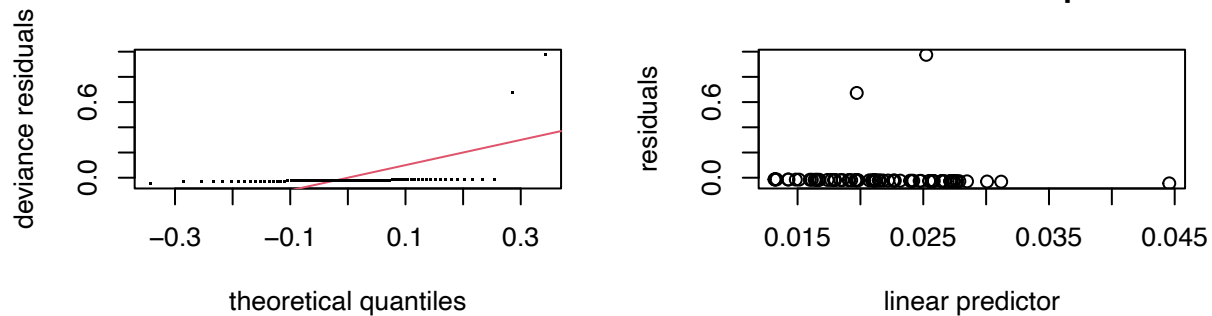
Response vs. Fitted Values



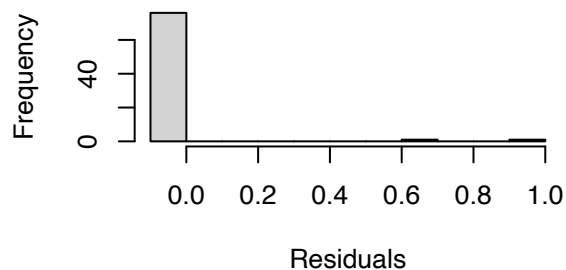
```
##
## Method: GCV Optimizer: magic
## Smoothing parameter selection converged after 9 iterations.
## The RMS GCV score gradient at convergence was 7.384722e-08 .
## The Hessian was positive definite.
## Model rank = 10 / 10
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##      k' edf k-index p-value
## s(D0) 9  1  1.03    0.53
## $mfrow
## [1] 2 2
##
## [1] "Metridia pacifica eDNA Index vs Dissolved Oxygen"
##
## Family: gaussian
## Link function: identity
##
## Formula:
```

```
## eDNA_index ~ s(D0)
##
## 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(D0)       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
```

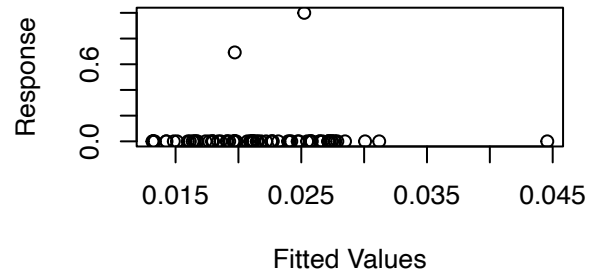
Resids vs. linear pred.



Histogram of residuals



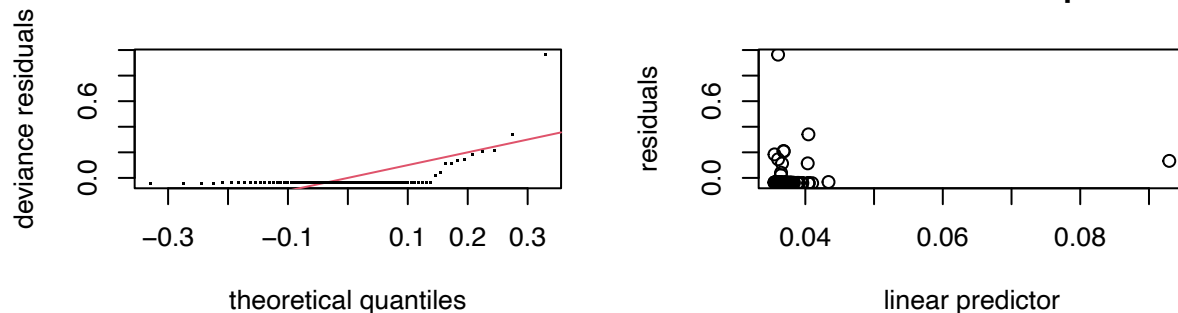
Response vs. Fitted Values



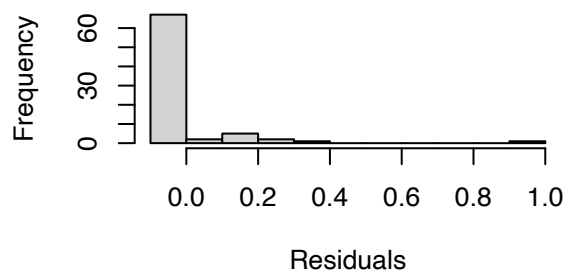
```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 9 iterations.
## The RMS GCV score gradient at convergence was 1.129112e-07 .
## The Hessian was positive definite.
## Model rank = 10 / 10
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##      k' edf k-index p-value
## s(D0) 9   1   1.04   0.63
## $mfrow
```

```
## [1] 2 2
##
## [1] "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
```

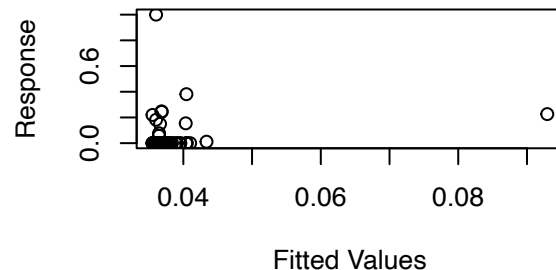
Resids vs. linear pred.



Histogram of residuals



Response vs. Fitted Values

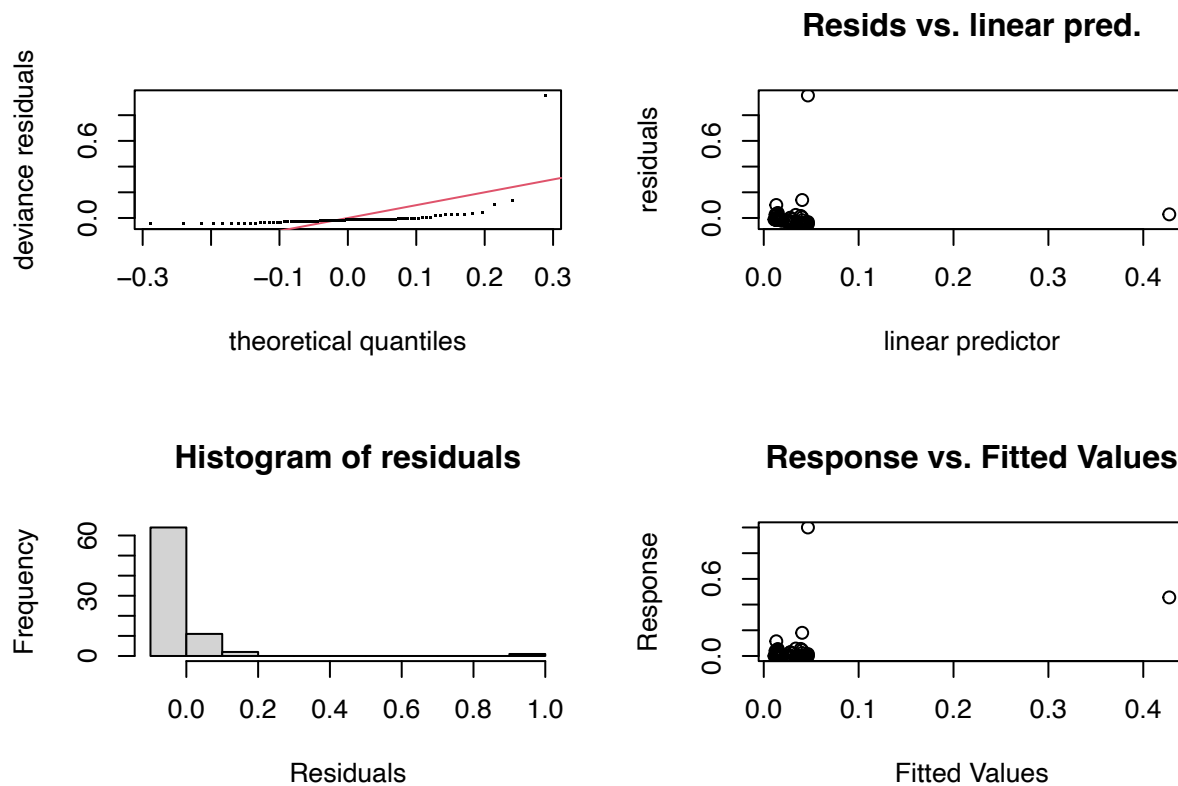


```
##
## Method: GCV  Optimizer: magic
## Smoothing parameter selection converged after 5 iterations.
```

```

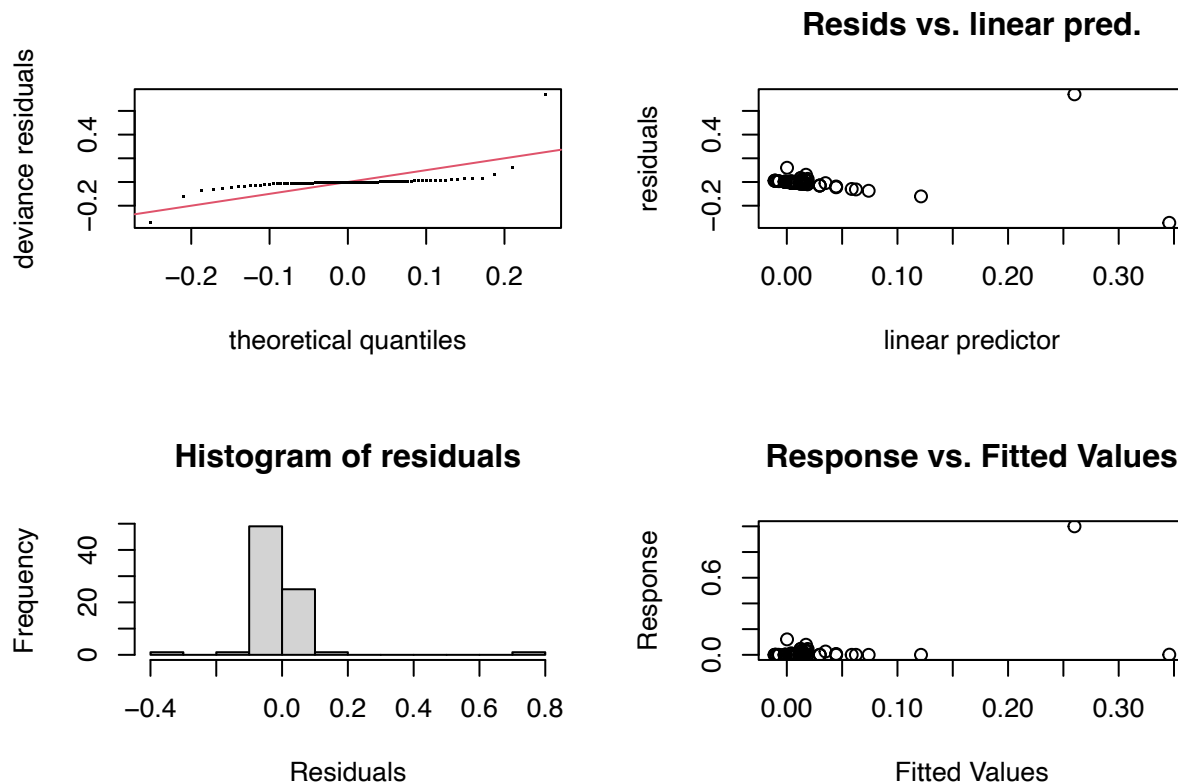
## The RMS GCV score gradient at convergence was 3.187024e-07 .
## The Hessian was positive definite.
## Model rank = 10 / 10
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##          k'   edf k-index p-value
## s(D0) 9.00 1.41    0.93    0.17
## $mfrow
## [1] 2 2
##
## [1] "Paracalanus sp. C AC-2013 eDNA Index vs Dissolved Oxygen"
##
## Family: gaussian
## Link function: identity
##
## Formula:
## eDNA_index ~ s(D0)
##
## 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(D0) 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

```



```
##
## 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(D0) 9.00 3.69   1.08   0.98
## $mfrow
## [1] 2 2
##
## [1] "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
##
```

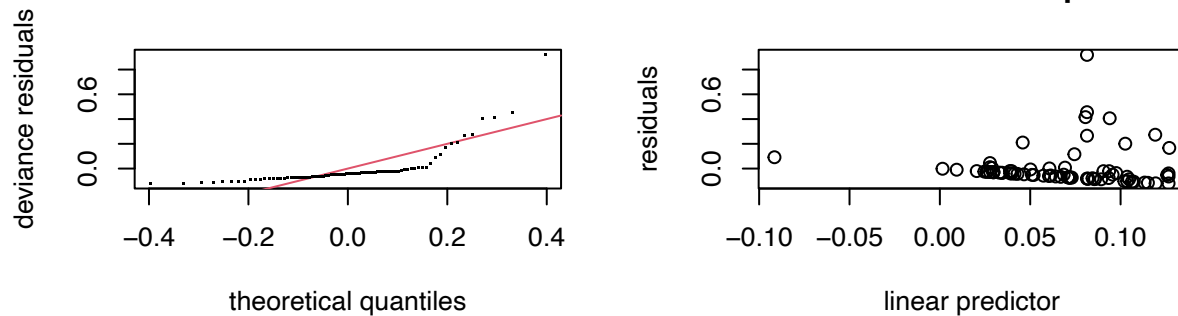
```
## Approximate significance of smooth terms:
##      edf Ref.df      F p-value
## s(DO) 6.059  7.112 3.231 0.00492 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.211   Deviance explained = 27.3%
## GCV = 0.011282   Scale est. = 0.010261   n = 78
## [1] "GAM quality"
## [1] "AIC: -127.120364551944"
##   GCV.Cp
## 0.011282
```



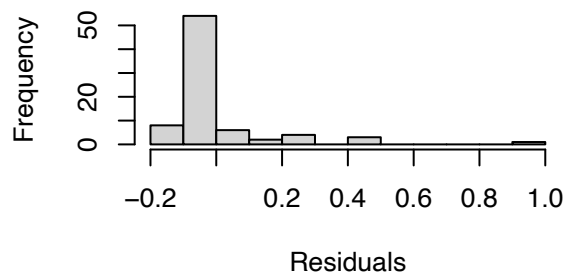
```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 6 iterations.
## The RMS GCV score gradient at convergence was 1.074935e-06 .
## The Hessian was positive definite.
## Model rank =  10 / 10
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## 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"
##
```

```
## Family: gaussian
## Link function: identity
##
## Formula:
## eDNA_index ~ s(D0)
##
## 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(D0)       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
```

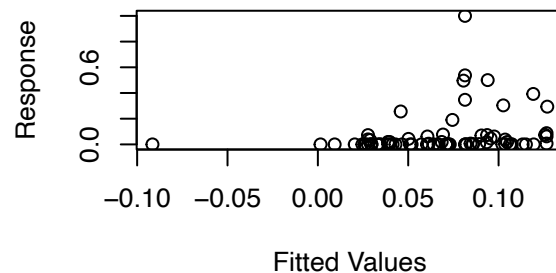
Resids vs. linear pred.



Histogram of residuals



Response vs. Fitted Values



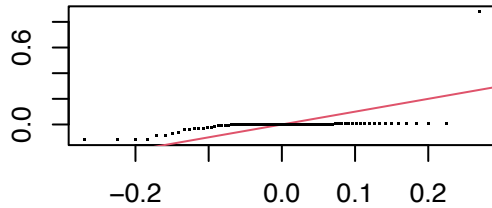
```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 10 iterations.
## The RMS GCV score gradient at convergence was 6.221389e-08 .
## The Hessian was positive definite.
```

```

## 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  0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## $mfrow
## [1] 2 2
##
## [1] "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

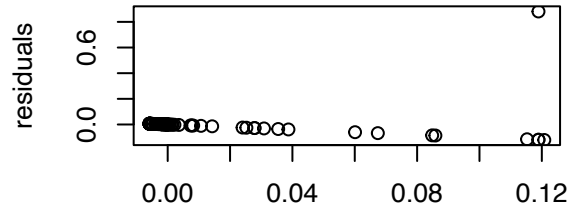
```


deviance residuals



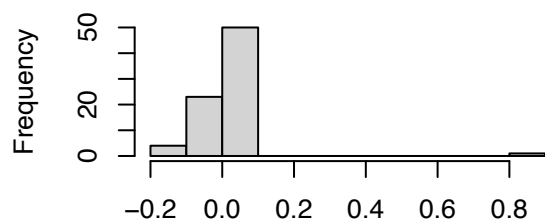
theoretical quantiles

Resids vs. linear pred.



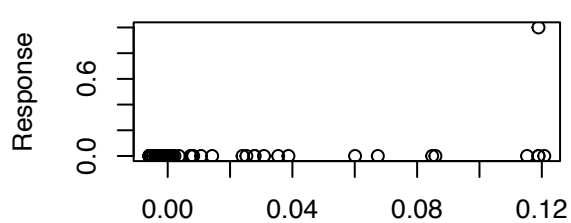
linear predictor

Histogram of residuals



Residuals

Response vs. Fitted Values



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(D0) 9.00 3.52   1.18   0.99
## $mfrow
## [1] 2 2
```

```
# 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("say Script complete")
```