Improved Partial Effects Plots for GAMs Looking at the Plankton Community

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Contents

Introduction

This notebook reprises selected analyses using GAMs, and then develops nicer partial effects plots than the `mgcv` defaults.

In particular, I'm interested in generating marginal plots as follows.

1. Zoop density vs. Turbidity
2. Zoop diversity vs. Chl & Zoop diversity vs. Turb (combined 2-part figure)
3. Eurytemora density vs. Turbidity
4. Barnacle vs. Chl & Barnacle vs. Temp (combined 2-part figure)
5. Acartia vs. Temp & Acartia vs. Salinity (combined 2-part figure)

Building Multi-panel Graphics

In this notebook, I build up the combined plots for our mixed model GAMS piecewise. Originally, I was working with marginal graphics produced by the `ggemmeans()` function. I was producing separate graphics for each marginal mean (see below), and had to combine them. Since I was working with completed graphics (not data frames) I could not rely on `ggplot2`'s faceting capabilities.

The approach I use here is to pull marginal means for each marginal predictor, graph them in `ggplot`, then assemble multi-panel graphic using `grid.arrange()` (which generates a display) or `arrangeGrob()` (which does not).

Since the `ggemmeans()` function no longer works the same way (see below), this is no longer strictly necessary, but I retain this approach as a minimal rearrangement of existing code. A companion notebook will look at generating graphics using faceting, by building up suitably arranged data frames. That has the advantage of **not** adding extra axis titles and labels between the two plots.

General Instructions to Authors About Graphics

The instructions to authors suggests figure widths should line up with columns, and proposes figure widths should be:

39 mm ~ 1.54 inches 84 mm ~ 3.30 inches 129 mm ~ 5.04 inches 174 mm ~ 6.85 inches

With height not to exceed 235 mm (9.25 inches).

RMarkdown / `knitr` likes figure dimensions in inches. 174 mm is about 6.85 inches

Load Libraries

```
library(tidyverse)
#> -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
#> v dplyr     1.1.1     v readr     2.1.4
#> v forcats   1.0.0     v stringr   1.5.0
#> v ggplot2   3.4.1     v tibble    3.2.1
#> v lubridate 1.9.2     v tidyr     1.3.0
#> v purrr     1.0.1
#> -- Conflicts ------------------------------------------ tidyverse_conflicts() --
#> x dplyr::filter() masks stats::filter()
#> x dplyr::lag()    masks stats::lag()
#> i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become error
library(readxl)
library(mgcv)      # for GAM models
#> Loading required package: nlme
#>
#> Attaching package: 'nlme'
#>
#> The following object is masked from 'package:dplyr':
#>
#>     collapse
#>
#> This is mgcv 1.8-42. For overview type 'help("mgcv-package")'.
library(emmeans)
library(ggeffects)
library(gridExtra) # or could use related functions in `cowplot`
#>
#> Attaching package: 'gridExtra'
#>
#> The following object is masked from 'package:dplyr':
#>
#>     combine
```

Set Graphics Theme

This sets `ggplot()`graphics for no background, no grid lines, etc. in a clean format suitable for (some) publications.

```
theme_set(theme_classic())
```

Input Data

Folder References

```
data_folder <- "Original_Data"

dir.create(file.path(getwd(), 'figures'), showWarnings = FALSE)
```

Load Data

```
filename.in <- "penob.station.data EA 3.12.20.xlsx"
file_path <- file.path(data_folder, filename.in)
station_data <- read_excel(file_path,
                           sheet="Final", col_types = c("skip", "date",
                                                        "numeric", "text", "numeric",
                                                        "text", "skip", "skip",
                                                        "skip",
                                                        rep("numeric", 10),
                                                        "text",
                                                        rep("numeric", 47),
                                                        "text",
                                                        rep("numeric", 12))) %>%
  rename_with(~ gsub(" ", "_", .x)) %>%
  rename_with(~ gsub("\\.", "_", .x)) %>%
  rename_with(~ gsub("\\?", "", .x)) %>%
  rename_with(~ gsub("%", "pct", .x)) %>%
  rename_with(~ gsub("_Abundance", "", .x)) %>%
  filter(! is.na(date))
#> New names:
#> * `` -> `...61`
```

```
names(station_data)[10:12]
#> [1] "discharge_week_cftpersec" "discharg_day"
#> [3] "discharge_week_max"
names(station_data)[10:12] <- c('disch_wk', 'disch_day', 'disch_max')
```

Station names are arbitrary, and Erin previously expressed interest in renaming them from Stations 2, 4, 5 and 8 to Stations 1,2,3,and 4.

The `factor()` function by default sorts levels before assigning numeric codes, so a convenient way to replace the existing station codes with sequential numbers is to create a factor and extract the numeric indicator values with `as.numeric()`.

```
station_data <- station_data %>%
  mutate(station = factor(as.numeric(factor(station))))
head(station_data)
```

```
#> # A tibble: 6 x 76
#>   date                year month month_num season riv_km station station_num
#>   <dttm>             <dbl> <chr>     <dbl> <chr>   <dbl> <fct>         <dbl>
#> 1 2013-05-28 00:00:00  2013 May           5 Spring  22.6  1                1
#> 2 2013-05-28 00:00:00  2013 May           5 Spring  13.9  2                2
#> 3 2013-05-28 00:00:00  2013 May           5 Spring   8.12 3                3
#> 4 2013-05-28 00:00:00  2013 May           5 Spring   2.78 4                4
#> 5 2013-07-25 00:00:00  2013 July          7 Summer  22.6  1                1
#> 6 2013-07-25 00:00:00  2013 July          7 Summer  13.9  2                2
#> # i 68 more variables: depth <dbl>, disch_wk <dbl>, disch_day <dbl>,
#> #   disch_max <dbl>, tide_height <dbl>, Full_Moon <dbl>, Abs_Moon <dbl>,
#> #   Spring_or_Neap <chr>, ave_temp_c <dbl>, ave_sal_psu <dbl>,
#> #   ave_turb_ntu <dbl>, ave_do_mgperl <dbl>, ave_DO_Saturation <dbl>,
#> #   ave_chl_microgperl <dbl>, sur_temp <dbl>, sur_sal <dbl>, sur_turb <dbl>,
#> #   sur_do <dbl>, sur_chl <dbl>, bot_temp <dbl>, bot_sal <dbl>, bot_turb <dbl>,
#> #   bot_do <dbl>, bot_chl <dbl>, max_temp <dbl>, max_sal <dbl>, ...
```

Subsetting to Desired Data Columns

I base selection of predictor variables here on the ones used in the manuscript.

```
base_data <- station_data %>%
  rename(Date = date,
         Station = station,
         Year = year) %>%
  select(-c(month, month_num)) %>%
  mutate(Month = factor(as.numeric(format(Date, format = '%m')),
                                                levels = 1:12,
                                                labels = month.abb),
         DOY = as.numeric(format(Date,format = '%j')),
         season = factor(season, levels = c('Spring', 'Summer', 'Fall')),
         is_sp_up = season == 'Spring' & Station == 1,
         Yearf = factor(Year)) %>%
  rename(Season = season,
         Density = combined_density,
         Temp = ave_temp_c,
         Sal = ave_sal_psu,
         Turb = sur_turb,
         AvgTurb = ave_turb_ntu,
         DOsat = ave_DO_Saturation,
         Chl = ave_chl_microgperl,
         Fish = `___61`,
         RH = Herring
         ) %>%
  select(Date, Station, Year, Yearf, Month, Season, is_sp_up, DOY, riv_km,
         disch_wk, disch_day, disch_max,
         Temp, Sal, Turb, AvgTurb, DOsat, Chl,
         Fish, RH,
         Density, H, SEI,
         Acartia, Balanus, Eurytemora, Polychaete, Pseudocal, Temora) %>%
  arrange(Date, Station)
head(base_data)
#> # A tibble: 6 x 29
```

```
#>   Date                Station  Year Yearf Month Season is_sp_up   DOY riv_km
#>   <dttm>              <fct>   <dbl> <fct> <fct> <fct>  <lgl>    <dbl>  <dbl>
#> 1 2013-05-28 00:00:00 1        2013 2013  May   Spring TRUE       148  22.6
#> 2 2013-05-28 00:00:00 2        2013 2013  May   Spring FALSE      148  13.9
#> 3 2013-05-28 00:00:00 3        2013 2013  May   Spring FALSE      148   8.12
#> 4 2013-05-28 00:00:00 4        2013 2013  May   Spring FALSE      148   2.78
#> 5 2013-07-25 00:00:00 1        2013 2013  Jul   Summer FALSE      206  22.6
#> 6 2013-07-25 00:00:00 2        2013 2013  Jul   Summer FALSE      206  13.9
#> # i 20 more variables: disch_wk <dbl>, disch_day <dbl>, disch_max <dbl>,
#> #   Temp <dbl>, Sal <dbl>, Turb <dbl>, AvgTurb <dbl>, DOsat <dbl>, Chl <dbl>,
#> #   Fish <dbl>, RH <dbl>, Density <dbl>, H <dbl>, SEI <dbl>, Acartia <dbl>,
#> #   Balanus <dbl>, Eurytemora <dbl>, Polychaete <dbl>, Pseudocal <dbl>,
#> #   Temora <dbl>
```

```
rm(station_data)
```

Complete Cases

This drops only two samples, one for missing Zooplankton data, one for missing fish data. We needed this data set to run The `step()` function in other notebooks, but here it is just a step towards the next version, which is what we will actually use.

```
complete_data <- base_data %>%
  select(Season, Station, Yearf,
         is_sp_up, Temp, Sal, Turb, Chl, Fish, RH,
         Density, H,
         Acartia, Balanus, Eurytemora, Polychaete, Pseudocal, Temora) %>%
  filter(complete.cases(.))
```

Reduced Data

The low salinity spring samples are doing something rather different, and they complicate model fitting. Models are far better behaved if we exclude a few extreme samples. These are low salinity, low zooplankton samples. We have two complementary ways to specify which samples to omit, without just omitting "outliers". The first is to restrict modeling to "marine" samples over a certain salinity range, and the other is to omit spring upstream samples, which include most of the problematic samples. We eventually decided to go with the first approach.

```
drop_low <- complete_data %>%
  filter(Sal > 10)    # Pulls three samples, including one fall upstream sample
                      # a fourth low salinity sample lacks zooplankton data
#drop_sp_up <- complete_data %>%
#  filter(! is_sp_up)  # drops four samples
```

```
rm(complete_data)
```

Total Zooplankton Density

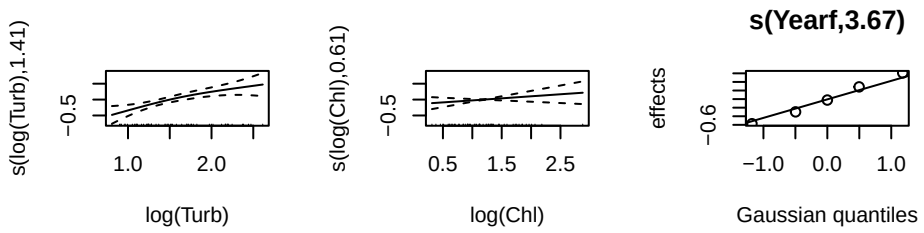
I fit a simplified model without `Station`. The full model has the same concurvity problems as before, leading the full model to fails to converge. While I could alter the convergence criteria to search for a solution, we

know the model that includes Station will have concurvity problems, so there is little point.

Reduced Complexity Model

```
density_gam<- gam(log(Density) ~
                          #s(Temp, bs="ts", k = 5) +
                          #s(Sal, bs="ts", k = 5) +
                          s(log(Turb), bs="ts", k = 5) +
                          s(log(Chl), bs="ts", k = 5) +
                          #s(log1p(Fish),bs="ts", k = 5) +
                          s(Yearf, bs = 're'),
                        data = drop_low, family = 'gaussian')
summary(density_gam)
#>
#> Family: gaussian
#> Link function: identity
#>
#> Formula:
#> log(Density) ~ s(log(Turb), bs = "ts", k = 5) + s(log(Chl), bs = "ts",
#>     k = 5) + s(Yearf, bs = "re")
#>
#> Parametric coefficients:
#>             Estimate Std. Error t value Pr(>|t|)
#> (Intercept)   8.1283     0.2307   35.23   <2e-16 ***
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> Approximate significance of smooth terms:
#>                 edf Ref.df     F  p-value
#> s(log(Turb)) 1.4120      4  6.18 0.000253 ***
#> s(log(Chl))  0.6072      4  0.83 0.122462
#> s(Yearf)     3.6720      4 10.52 1.63e-06 ***
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> R-sq.(adj) =  0.561   Deviance explained = 60.8%
#> GCV = 0.26018  Scale est. = 0.22853   n = 55
```

```
oldpar <- par(mfrow = c(2,3))
plot(density_gam)
par(oldpar)
```



Changes in `ggemmeans()` Function Require a New Approach

Graphics from `ggemmeans()` now Fail

```
ggp1 <- ggemmeans(density_gam, terms = 'Turb')
#> Can't compute estimated marginal means, 'emmeans::emmeans()' returned an error.
#>
#> Reason: undefined columns selected
#> You may try 'ggpredict()' or 'ggeffect()'.
ggp2 <- ggemmeans(density_gam, terms = 'Chl')
#> Can't compute estimated marginal means, 'emmeans::emmeans()' returned an error.
#>
#> Reason: undefined columns selected
#> You may try 'ggpredict()' or 'ggeffect()'.
```

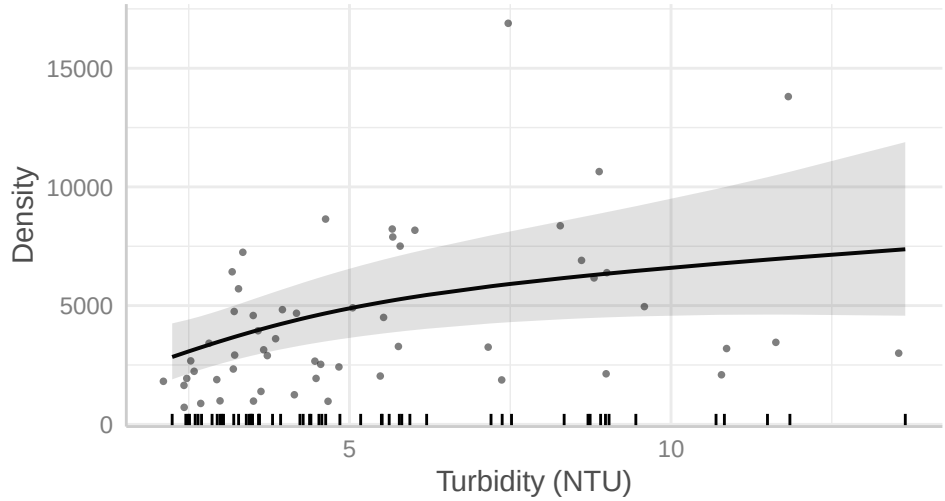
I'm not sure why that error is popping up. That used to work, as documented in the version of this notebook saved in November of 2022. Chances are, there has been a change in how either `ggemmeans()` or `emmeans()` itself handles names. The change does not affect simple testing code, so the effect probably relates to transformed predictor variables, possibly only in the context of GAMs.

`ggpredict()` does not do what we want

We'll first take the advice in the warning messagess and try using `ggpredict()`, but it does not work well. `ggpredict()` produces conditional means, not marginal means. The result is that regardless of the year chosen, the data do not line up all that well with the (multi-year) raw data. Perhaps the best apparent fit is for 2016.

```
ggp1 <- ggpredict(density_gam, terms = 'Turb',
                  condition = c(Yearf = 2016))
#> Model has log-transformed response. Back-transforming predictions to
#>   original response scale. Standard errors are still on the log-scale.
```

```
plot(ggp1, add.data  = TRUE,
     dot.alpha = 0.5, dot.size = 1) +
  geom_rug(aes(y = NULL)) +
  ggtitle('') +
  xlab(expression("Turbidity" ~ "(NTU)"))# +
```




```
 # scale_y_continuous( limits = c(0,9000), breaks = c(0, 2000, 4000, 6000, 8000))
```

At first blush that looks like it worked, but the data do not line up well with the (conditional) predictions and the error bars are too narrow. The arbitrary selection of 2016 as the reference year is *ad hoc*. It would be far better to use `emmeans` or `effects` to produce marginal means. Unfortunately, `effects' does no know how to handle GAM models, so we need to use`emmeans‘.

Generating a similar graphic “by hand”

I can “roll my own” by calling `emmeans` directly and building up graphics step by step. The following works if I am explicit about the `log()` term in the call. I believe that is a new wrinkle, and probably explains why the call to `ggemmeans()` no longer works. I used to be able to call emmeans only referring to “Turb”, not “log(Turb)”.

First, we calculate 25 points for predictions.

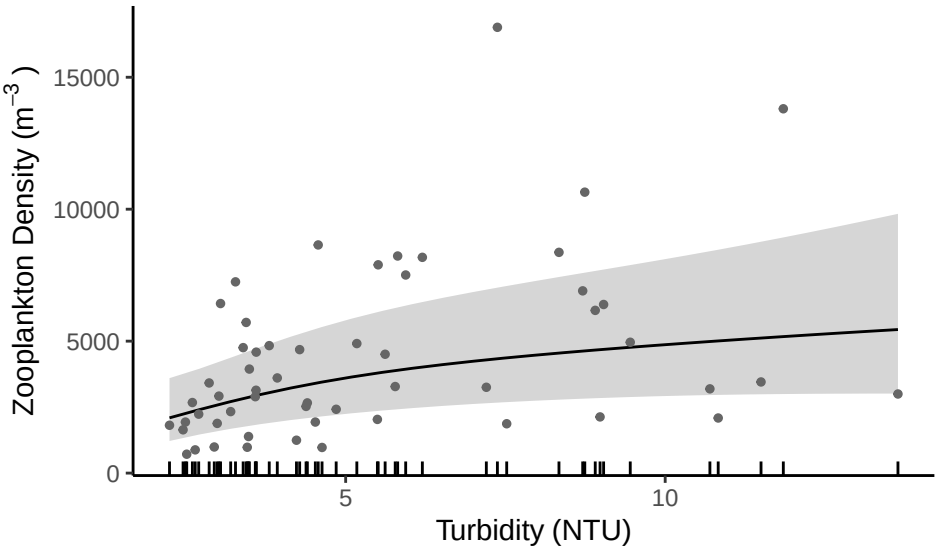
```
r <- range(drop_low$Turb)
stops = seq(r[1], r[2], length.out = 25)
```

Then we calculate the marginal means.

```
test_emms <- emmeans(density_gam, 'log(Turb)',
                         at = list(`log(Turb)` = log(stops), 'Yearf' = 2015, Chl = 3.86),
                         type = 'response')
test_emms <- as_tibble(test_emms) %>%
  mutate(Turb = exp(`log(Turb)`)) %>%
```

```
  relocate(Turb)
test_emms
#> # A tibble: 25 x 7
#>     Turb `log(Turb)` response    SE    df lower.CL upper.CL
#>    <dbl>       <dbl>    <dbl> <dbl> <dbl>    <dbl>    <dbl>
#>  1  2.24       0.808    2093.  564.  48.3    1218.    3598.
#>  2  2.72       1.00     2408.  596.  48.3    1465.    3959.
#>  3  3.19       1.16     2705.  645.  48.3    1675.    4367.
#>  4  3.67       1.30     2977.  701.  48.3    1854.    4780.
#>  5  4.14       1.42     3224.  757.  48.3    2011.    5170.
#>  6  4.62       1.53     3445.  811.  48.3    2146.    5529.
#>  7  5.09       1.63     3641.  860.  48.3    2265.    5852.
#>  8  5.57       1.72     3815.  904.  48.3    2370.    6142.
#>  9  6.04       1.80     3971.  944.  48.3    2462.    6402.
#> 10  6.52       1.87     4111.  980.  48.3    2545.    6639.
#> # i 15 more rows
```

```
ggplot(test_emms, aes(Turb, response)) +
  geom_ribbon(aes(ymin = lower.CL, ymax = upper.CL), alpha = 0.20) +
  geom_line() +
  #geom_point() +
  geom_point(data = drop_low, mapping = aes(x = Turb, y = Density),
             size = 1, color = "gray40") +
  geom_rug(data = drop_low, mapping = aes(x = Turb, y = NULL)) +
  xlab(expression("Turbidity" ~ "(NTU)")) +
  ylab(expression("Zooplankton Density (" * m ^-3 ~ ")" ))
```



Note that this graphic is simpler than the one produced by `ggpredict()` (and `ggeffects()` or `ggemmeans()`). In particular, it does not have the grid in back of the figure.

Functions to capture that logic

I create some helper functions to manage much of the repetitive coding.

Find Evenly Spaced Points

```
find_stops <- function(.dat, .predictor, .nstops = 25) {
  .predictor <- ensym(.predictor)
  r <- range(.dat[[.predictor]])
  stops = seq(r[1], r[2], length.out = .nstops)

  return(stops)
}
```

Conduct The Analysis

```
marginal_analysis <- function(.dat, .predictor, .model,
                              .nstops = 25, .logx = TRUE, .transy = TRUE) {
  .predictor <- ensym(.predictor)

  the_name <- as.character(.predictor)
  the_log_name <- paste0("log(", the_name, ")")

  # The following finds stops linear in the original predictor scale.
  # That is appropriate for the planned graphics, where both axes are
  # untransformed.
  stops <- find_stops(.dat, !!.predictor, .nstops)
  # browser()
  if (.logx) {
    stopslist <- list(log(stops))
    names(stopslist) <- the_log_name

    emms <- emmeans(.model, the_log_name,
                    at = stopslist,
                    type = 'response')
    emms <- as_tibble(emms)
    #browser()
    emms <- emms %>%
      mutate( !!the_name := exp(emms[[the_log_name]]))
  }
  else {
    #browser()
    stopslist <- list(stops)
    names(stopslist) <- the_name

    emms <- emmeans(.model, the_name,
                    at = stopslist,
                    type = 'response')
    emms <- as_tibble(emms)

  }
  #The default name of the output of emmeans() differs if the response
  #variable is transformed or untransformed. This makes it consistent.
  if (! .transy) {
    emms <-  emms %>%
```

```
      rename(response = emmean)
  }
  return(emms)
}
```

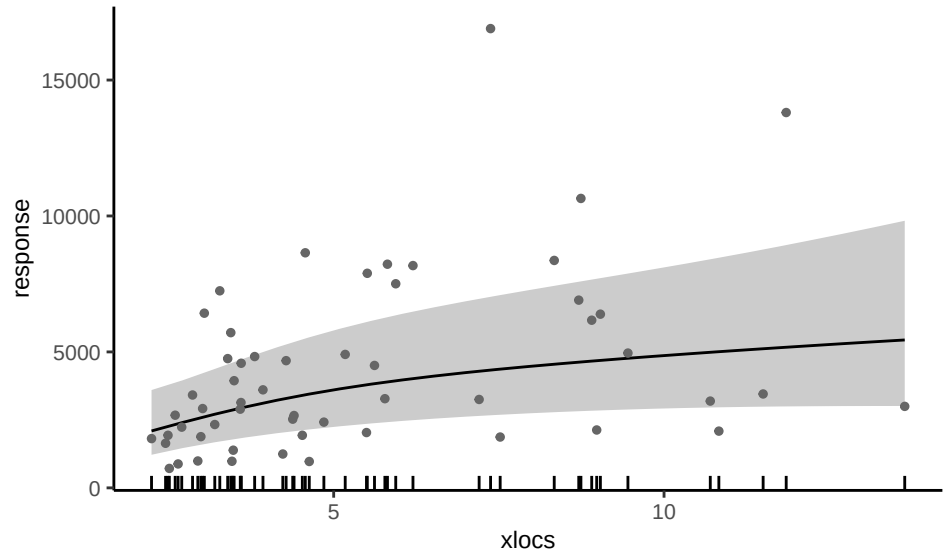
```
a <- marginal_analysis(drop_low, Turb,
                           .model = density_gam)
```

Construct a Plot

This function does not handle axis labels (to simplify the code). You still have to change them manually.

```
marginal_plot <- function(.emms, .data, .predictor, .response) {
  #browser()
  .predictor   <- ensym(.predictor)
  .response    <- ensym(.response)
  the_name     <- as.character(.predictor)
  the_log_name <- paste0("log(", the_name, ")")

  xlocs <- .emms[[the_name]]

  #"response" is the default name of the output column in `emmeans()`
  # lower.CL and # upper.CL are also default column names.

  ggplot(.emms, aes(xlocs, response)) +
    geom_ribbon(aes(ymin = lower.CL, ymax = upper.CL), fill = "grey80") +
    geom_line() +
    geom_point(data = .data, mapping = aes(x = !!.predictor, y = !!.response),
             size = 1, color = "gray40") +
    geom_rug(data = .data, mapping = aes(x = !!.predictor, y = NULL)) +
    theme(axis.title = element_text(size = 9),
          axis.text = element_text(size = 8))
}
```

```
marginal_plot(a, drop_low, Turb, Density)
```



Total Zooplankton Density, Revisited

Generate Data

```
p1.data <- marginal_analysis(drop_low, Turb, density_gam,
                                  .nstops = 25, .logx = TRUE)
p2.data <- marginal_analysis(drop_low, Chl, density_gam,
                                  .nstops = 25, .logx = TRUE)
```

Generate Graphics

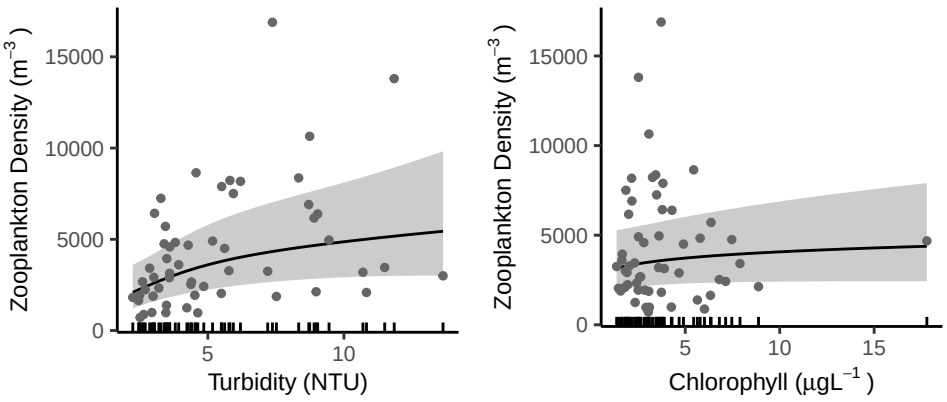
```
plt1 <- marginal_plot(p1.data, drop_low, Turb, Density) +
  xlab(expression("Turbidity" ~ "(NTU)")) +
  ylab(expression("Zooplankton Density (" * m ^-3 ~ ")" ))
```

```
plt2 <- marginal_plot(p2.data, drop_low, Chl, Density) +
  xlab(expression("Chlorophyll (" * mu * g * L ^-1 ~")")) +
  ylab(expression("Zooplankton Density (" * m ^-3 ~ ")" ))
```

Assemble the Multi-panel Plot

`grid.arrange()` automatically generates output, so is useful in interactive data analysis. (In this context, `arrangeGrob()' would be similar, but not produce immediate graphic output.)  If you save output to a variable, the result is a`gtable', not a simple plot. Some functions know what to do with that, others don't.

```
grphc <- grid.arrange(plt1, plt2, ncol = 2, nrow = 1)
```



Save the Plot

```
ggsave(file='figures/density.png', grphc,
width = 5.04, height = 2.2)
ggsave('figures/density.pdf', grphc, device = cairo_pdf,
width = 5.04, height = 2.2)
```

Supplementary Graphic

Here I save only `plt1` as a separate figure. This graphic is the same height as the others, but slightly wider than a half plot, to correspond to widths recommended in the instructions to authors.

```
ggsave('figures/density by turbidity.png', plt1,
         width = 3.30, height = 2.2)
ggsave('figures/density by turbidity.pdf', plt1, device = cairo_pdf,
       width = 3.30, height = 2.2)
```

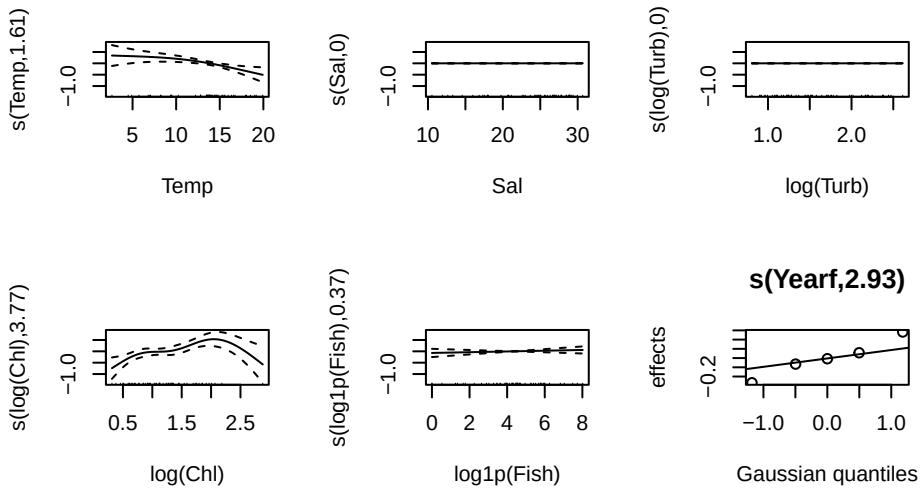
Shannon Diversity

Model on Reduced Data

```
shannon_gam_no_low <- gam(H ~
                      s(Temp, bs="ts", k = 5) +
                      s(Sal, bs="ts", k = 5) +
                      s(log(Turb), bs="ts", k = 5) +
                      s(log(Chl), bs="ts", k = 5) +
                      s(log1p(Fish),bs="ts", k = 5) +
                      s(Yearf, bs = 're'),
                    data = drop_low, family = 'gaussian')
summary(shannon_gam_no_low)
#>
#> Family: gaussian
#> Link function: identity
```

```
#>
#> Formula:
#> H ~ s(Temp, bs = "ts", k = 5) + s(Sal, bs = "ts", k = 5) + s(log(Turb),
#>     bs = "ts", k = 5) + s(log(Chl), bs = "ts", k = 5) + s(log1p(Fish),
#>     bs = "ts", k = 5) + s(Yearf, bs = "re")
#>
#> Parametric coefficients:
#>             Estimate Std. Error t value Pr(>|t|)
#> (Intercept)   1.3310     0.1142   11.66  3.1e-15 ***
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> Approximate significance of smooth terms:
#>                     edf Ref.df      F  p-value
#> s(Temp)        1.615e+00      4  4.222 0.002901 **
#> s(Sal)         2.259e-08      4  0.000 0.257386
#> s(log(Turb))   1.369e-08      4  0.000 0.608480
#> s(log(Chl))    3.767e+00      4 11.002 0.000252 ***
#> s(log1p(Fish)) 3.675e-01      4  0.167 0.197576
#> s(Yearf)       2.929e+00      4  2.802 0.008131 **
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> R-sq.(adj) =  0.417   Deviance explained = 51.1%
#> GCV =    0.2  Scale est. = 0.1648    n = 55
```

```
oldpar <- par(mfrow = c(2,3))
plot(shannon_gam_no_low)
```




```
par(oldpar)
```

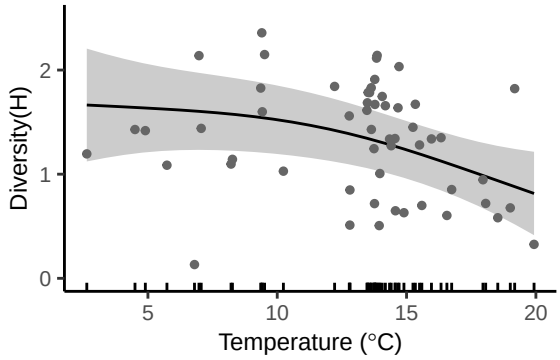
Generate Data

```
p1.data <- marginal_analysis(drop_low, Temp, shannon_gam_no_low,
                             .nstops = 25,
                             .logx = FALSE, .transy = FALSE)
```

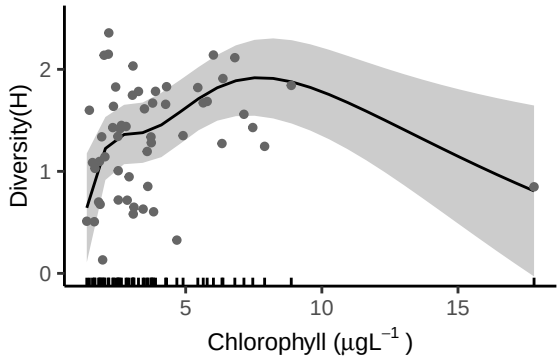
```
p2.data <- marginal_analysis(drop_low, Chl, shannon_gam_no_low,
                             .nstops = 25,
                             .logx = TRUE,  .transy = FALSE)
```

Generate Graphics

```
plt1 <- marginal_plot(p1.data, drop_low, Temp, H ) +
  xlab(expression("Temperature (" * degree * "C)")) +
  ylab("Diversity(H)")+
  scale_y_continuous(breaks = c(0:2)) +
  coord_cartesian(ylim = c(0, 2.5))
plt1
```

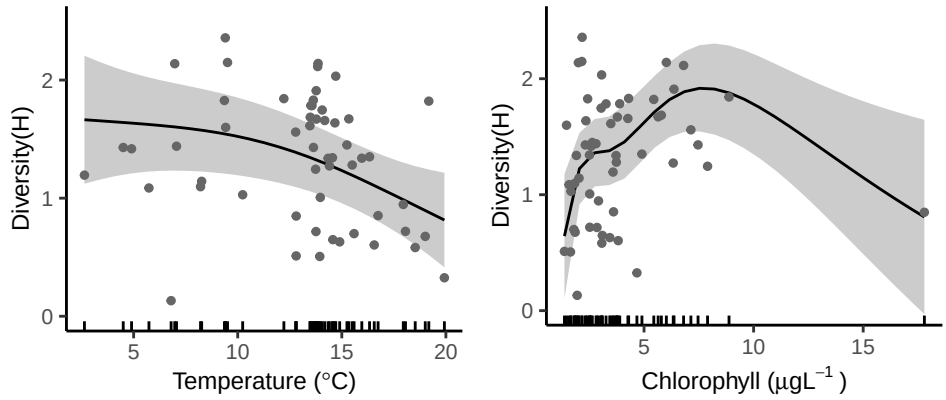



```
plt2 <- marginal_plot(p2.data, drop_low, Chl, H) +
  xlab(expression("Chlorophyll (" * mu * g * L ^-1 ~")")) +
  ylab("Diversity(H)")+
  scale_y_continuous(breaks = c(0:2)) +
  coord_cartesian(ylim = c(0, 2.5))
plt2
```



Assemble the Multi-panel Plot

```
grphc <- grid.arrange(plt1, plt2, # alternatives here from cowplot and other packages,
ncol = 2, nrow = 1)
```



Save the Plot

```
ggsave(file='figures/shannon.png', grphc,
         width = 5, height = 2.2)
ggsave('figures/shannon.pdf', grphc, device = cairo_pdf,
       width = 5, height = 2.2)
```

Single Species Models

Model Choice

Our model alternatives are similar to the choices we had for the Total Density model. The problem is, we can't use any of the continuous data distributions in GAMS with zero values (at least relying on the canonical link functions) because (log(0) = -Inf; 1/0 = Inf, 1 / 0*0 = Inf). The easiest solution is to add some finite small quantity to the density data, and predict that. Here we predict log(Density + 1) using Gaussian models.

Automating Analysis of Separate Species

I automate analysis of all species by using a "nested" Tibble. This is a convenient alternative to writing a "for" loop to run multiple identical analyses.

I create a "long" data source, based on our reduced data set (which omits low salinity samples).

```
spp_data <- drop_low %>%
  select(Yearf, Season, Station, Temp,
           Sal, Turb, Chl, Fish,
           Acartia, Balanus, Eurytemora) %>%
  pivot_longer(-c(Yearf:Fish), names_to = 'Species', values_to = 'Density')
```

Next, I create a function to run the analysis. This function takes a data frame or tibble as an argument. The tibble must have data columns with the correct names.

The initial GAM fits for some species had a lot of wiggles in them, to an extent that I thought did not make much scientific sense, so I decided to reduce the dimensionality of the GAM smoothers, by adding the parameter `k= 4`. Lower numbers constrain the GAM to fit smoother lines, which I think improve interpretability with noisy environmental data.

```
my_gam <- function(.dat) {

  gam(log1p(Density) ~
        s(Temp, bs="ts", k = 5) +
        s(Sal, bs="ts", k = 5) +
        s(log(Turb), bs="ts", k = 5) +
        s(log(Chl), bs="ts", k = 5) +
        s(log1p(Fish),bs="ts", k = 5) +
        s(Yearf, bs = 're'),
      data = .dat, family = "gaussian")
}
```

Next, I create the nested tibble, and conduct the analysis on each species....

```
spp_analysis <- spp_data %>%
  group_by(Species) %>%
  nest() %>%
  mutate(gam_mods = map(data, my_gam))
```

We are now ready to look at the model results. While we could do that programmatically using a "for" loop, it's awkward to look through a long list of output, so I step through each species of interest manually. This also gives me a bit more control over what graphics to produce for each species, since the best models differ.

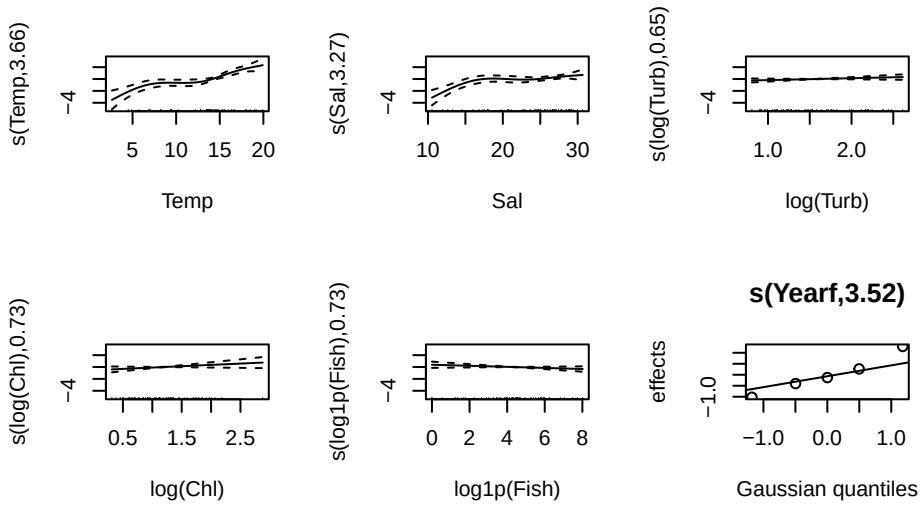
Acartia

```
spp = 'Acartia'
mod <- spp_analysis$gam_mods[spp_analysis$Species == spp][[1]]
dat <- spp_analysis$data[spp_analysis$Species == spp][[1]]
summary(mod)
#>
#> Family: gaussian
#> Link function: identity
#>
#> Formula:
#> log1p(Density) ~ s(Temp, bs = "ts", k = 5) + s(Sal, bs = "ts",
#>     k = 5) + s(log(Turb), bs = "ts", k = 5) + s(log(Chl), bs = "ts",
#>     k = 5) + s(log1p(Fish), bs = "ts", k = 5) + s(Yearf, bs = "re")
#>
#> Parametric coefficients:
#>             Estimate Std. Error t value Pr(>|t|)
#> (Intercept)    6.598      0.371   17.78   <2e-16 ***
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
```

```
#> Approximate significance of smooth terms:
#>                   edf Ref.df      F  p-value
#> s(Temp)        3.6631      4 31.950  < 2e-16 ***
#> s(Sal)         3.2713      4  7.570 0.000232 ***
#> s(log(Turb))   0.6538      4  0.637 0.076037 .
#> s(log(Chl))    0.7323      4  1.316 0.055331 .
#> s(log1p(Fish)) 0.7316      4  0.610 0.080622 .
#> s(Yearf)       3.5153      4 11.237 6.14e-07 ***
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> R-sq.(adj) =  0.763   Deviance explained = 81.8%
#> GCV = 0.93657  Scale est. = 0.70553   n = 55
```

Plot GAM

```
oldpar <- par(mfrow = c(2,3))
plot(mod)
```



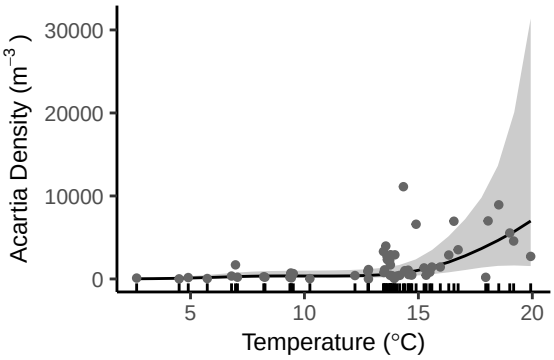

```
par(oldpar)
```

Combined Graphic

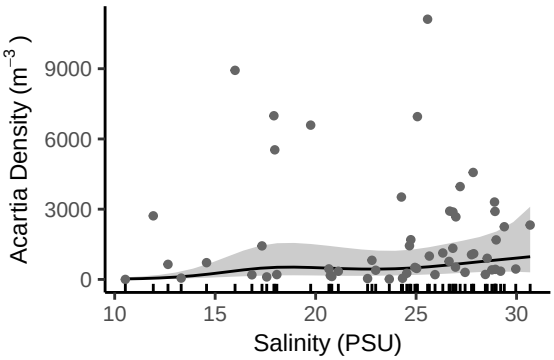
```
p1.data <- marginal_analysis(dat, Temp, mod,
                             .nstops = 25, .logx = FALSE)

p2.data <- marginal_analysis(dat, Sal, mod,
                             .nstops = 25, .logx = FALSE)
```

GenerateFData ####Generate Graphics

```
plt1 <- marginal_plot(p1.data, dat, Temp, Density) +
  xlab(expression("Temperature (" * degree * "C)")) +
  ylab(expression("Acartia Density (" * m ^-3 ~ ")" ))
plt1
```




```
plt2 <- marginal_plot(p2.data, dat, Sal, Density) +
  xlab(expression("Salinity" ~ "(PSU)")) +
  ylab(expression("Acartia Density (" * m ^-3 ~ ")" ))
plt2
```



Assemble The Multi-panel Plot

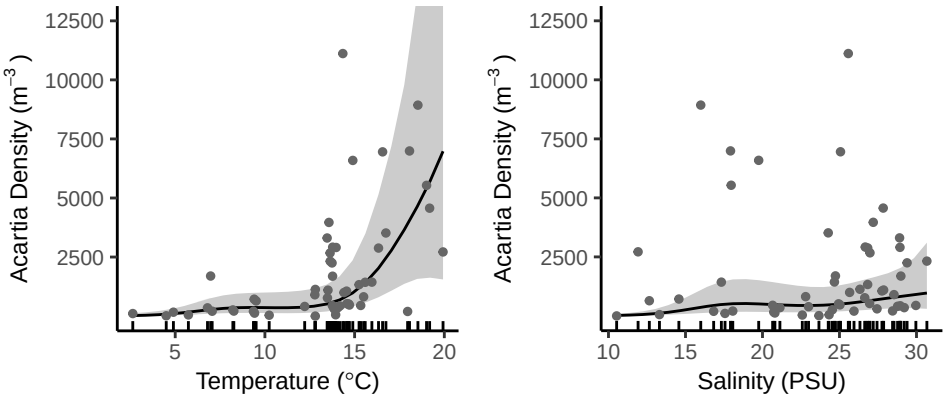
Adjust Vertical Axes so They Match Since we are generating separate graphics, `ggplot2` makes different choices about the axis breaks and limits. In particular, `ggplot2` makes decisions based on the extremes of the error bands, which we actually don't need to show. As a result, we need to be explicit about axis properties. A subtlety here: setting axis limits with `coord_cartesian()` does not remove data, thus "clipping" the error band to the visible range vertically. If we used `ylim()` instead, the error band gets truncated (horizontally) once either extreme extends outside of the visual plot area.

```
plt1 <- plt1 +
  scale_y_continuous(breaks = c(1:5*2500)) +
  coord_cartesian(ylim = c(0, 12500))
```

```
plt2 <- plt2 +
  scale_y_continuous(breaks = c(1:5*2500)) +
  coord_cartesian(ylim = c(0, 12500))
```

```
grphc <- grid.arrange(plt1, plt2, ncol = 2, nrow = 1) #generates graphic
```

Save Multi-Panel Graphic




```
ggsave(file='figures/Acartia.png', grphc,
         width = 5.04, height = 2.2)
ggsave('figures/Acartia.pdf', grphc, device = cairo_pdf,
       width = 5.04, height = 2.2)
```

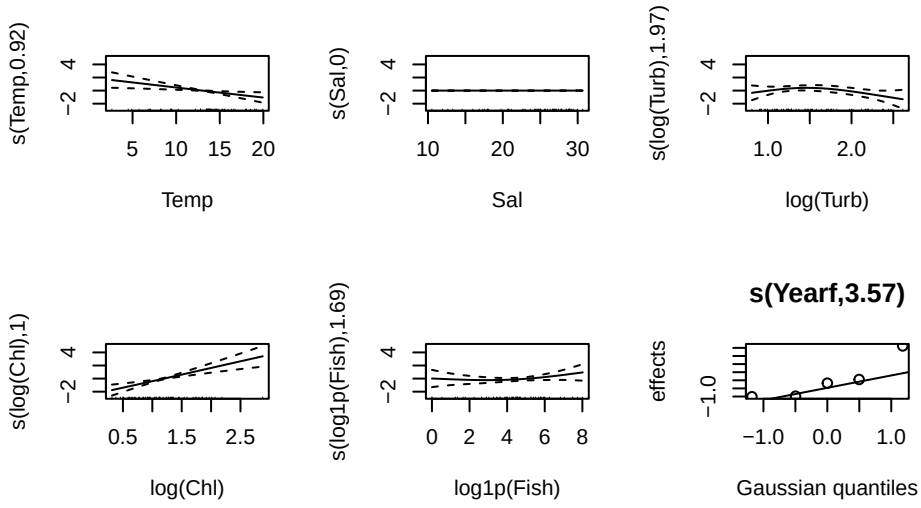
Balanus

```
spp = 'Balanus'
mod <- spp_analysis$gam_mods[spp_analysis$Species == spp][[1]]
dat <- spp_analysis$data[spp_analysis$Species == spp][[1]]
summary(mod)
#>
#> Family: gaussian
#> Link function: identity
#>
#> Formula:
#> log1p(Density) ~ s(Temp, bs = "ts", k = 5) + s(Sal, bs = "ts",
#>     k = 5) + s(log(Turb), bs = "ts", k = 5) + s(log(Chl), bs = "ts",
#>     k = 5) + s(log1p(Fish), bs = "ts", k = 5) + s(Yearf, bs = "re")
#>
#> Parametric coefficients:
#>             Estimate Std. Error t value Pr(>|t|)
#> (Intercept)   3.6930     0.6478   5.701 8.74e-07 ***
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#>
#> Approximate significance of smooth terms:
#>                       edf Ref.df      F  p-value
#> s(Temp)        9.192e-01      4  2.998  0.00414 **
#> s(Sal)         1.782e-10      4  0.000  0.52552
#> s(log(Turb))   1.967e+00      4  1.779  0.06016 .
#> s(log(Chl))    1.004e+00      4 14.125 2.07e-05 ***
#> s(log1p(Fish)) 1.686e+00      4  0.691  0.22444
#> s(Yearf)       3.568e+00      4  7.912 1.75e-05 ***
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> R-sq.(adj) =  0.581   Deviance explained = 65.2%
#> GCV = 2.7021  Scale est. = 2.2038    n = 55
```

Plot GAM

```
oldpar <- par(mfrow = c(2,3))
plot(mod)
```




```
par(oldpar)
```

Combined Graphic

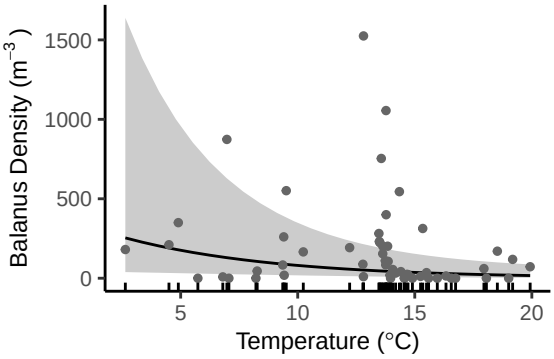
```
p1.data <- marginal_analysis(dat, Temp, mod,
                                    .nstops = 25,
                                    .logx = FALSE)

p2.data <- marginal_analysis(dat, Chl, mod,
```

```
                                .nstops = 25,
                                .logx = TRUE)
```

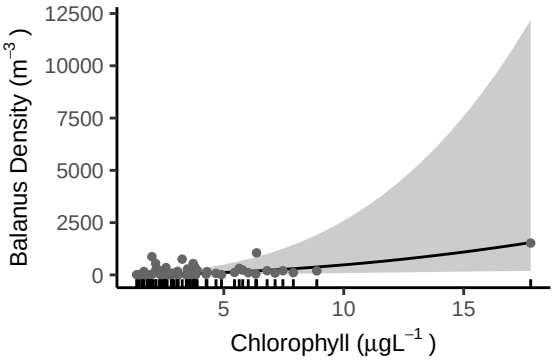
Generate Data

```
plt1 <- marginal_plot(p1.data, dat, Temp, Density) +
  xlab(expression("Temperature (" * degree * "C)")) +
  ylab(expression("Balanus Density (" * m ^-3 ~ ")" ))

plt1
```

Generate Graphics




```
plt2 <- marginal_plot(p2.data, dat, Chl, Density) +
  xlab(expression("Chlorophyll (" * mu * g * L ^-1 ~")")) +
  ylab(expression("Balanus Density (" * m ^-3 ~ ")" ))
plt2
```



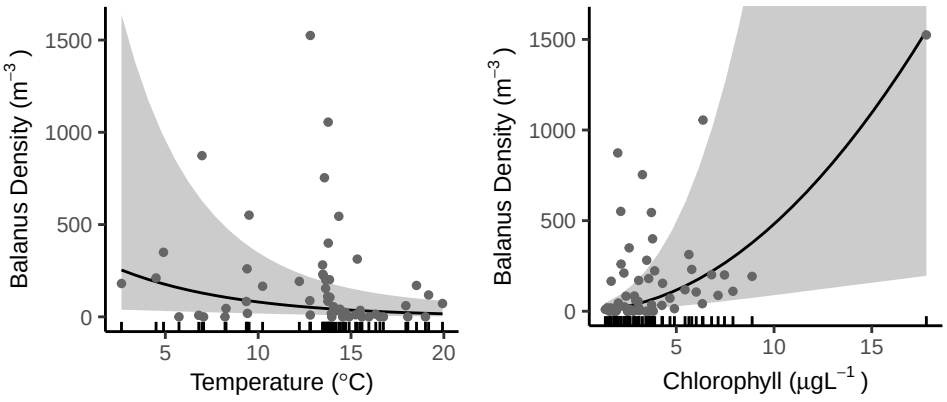
Assemble the Multi-panel Plot

```
plt1 <- plt1 +
  scale_y_continuous(breaks = c(0:3*500)) +
  coord_cartesian(ylim = c(0, 1600))

plt2 <- plt2 +
  scale_y_continuous(breaks = c(0:3*500)) +
  coord_cartesian(ylim = c(0, 1600))
```

Adjust Vertical Axis so They Match

```
grphc <- grid.arrange(plt1, plt2, ncol = 2, nrow = 1) #generates graphic
```

Save Multi-Panel Graphic




```
ggsave(file='figures/Balanus.png', grphc,
         width = 5.04, height = 2.2)
ggsave('figures/Balanus.pdf', grphc, device = cairo_pdf,
       width = 5.05, height = 2.2)
```

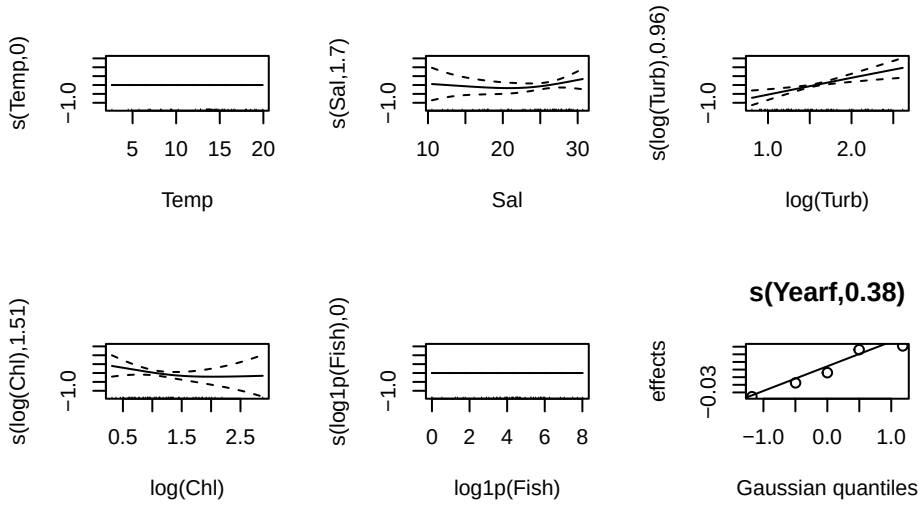
Eurytemora

```
spp =  "Eurytemora"
mod <- spp_analysis$gam_mods[spp_analysis$Species == spp][[1]]
dat <- spp_analysis$data[spp_analysis$Species == spp][[1]]
summary(mod)
#>
#> Family: gaussian
#> Link function: identity
#>
#> Formula:
#> log1p(Density) ~ s(Temp, bs = "ts", k = 5) + s(Sal, bs = "ts",
```

```
#>     k = 5) + s(log(Turb), bs = "ts", k = 5) + s(log(Chl), bs = "ts",
#>     k = 5) + s(log1p(Fish), bs = "ts", k = 5) + s(Yearf, bs = "re")
#>
#> Parametric coefficients:
#>             Estimate Std. Error t value Pr(>|t|)
#> (Intercept)   6.5275     0.1297   50.34   <2e-16 ***
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> Approximate significance of smooth terms:
#>                       edf Ref.df     F  p-value
#> s(Temp)        8.514e-10      4 0.000 0.522777
#> s(Sal)         1.698e+00      4 0.439 0.360992
#> s(log(Turb))   9.561e-01      4 3.326 0.000375 ***
#> s(log(Chl))    1.509e+00      4 0.541 0.241190
#> s(log1p(Fish)) 4.650e-10      4 0.000 0.340527
#> s(Yearf)       3.805e-01      4 0.101 0.368007
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> R-sq.(adj) =  0.241   Deviance explained = 30.5%
#> GCV = 0.91936  Scale est. = 0.8267    n = 55
```

Plot GAM

```
oldpar <- par(mfrow = c(2,3))
plot(mod)
```



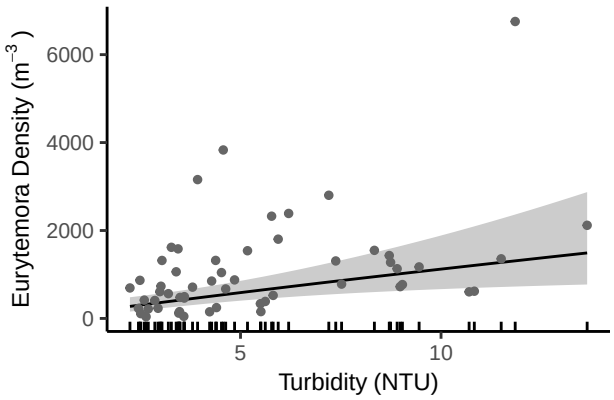

```
par(oldpar)
```

```
p1.data <- marginal_analysis(dat, Turb, mod,
                                  .nstops = 25, .logx = TRUE)
```

Generate Data

Generate Graphic

```
plt1 <- marginal_plot(p1.data, dat, Turb, Density) +
  xlab(expression("Turbidity" ~ "(NTU)")) +
  ylab(expression("Eurytemora Density (" * m ^-3 ~ ")" ))
plt1
```




```
ggsave(file='figures/Eurytemora.png',
         width = 3.3, height = 2.2)
ggsave('figures/Eurytemora.pdf', device = cairo_pdf,
       width = 3.3, height = 2.2)
```

```
ggsave(file='figures/Eurytemora_sq.png',
         width = 3.3, height = 3.3)
ggsave('figures/Eurytemora_sq.pdf', device = cairo_pdf,
       width = 3.3, height = 3.3)
```