DLMs and GAMs for Lake Washington data

```
library(MARSS)
library(mgcv)
library(dplyr)
library(forecast)
library(ggplot2)
library(lubridate)
library(viridis)
library(paletteer)
library(ggpubr)

col<-paletteer_d("nationalparkcolors::Everglades")
```

Data

```
dat <- as.data.frame(MARSS::lakeWAplanktonRaw)
dat$date <- make_date(dat$Year, dat$Month, day = 1)
```

The major change here is related to sewage in the lake – adding wastewater plants in the 1960s reduced phosphorous (TP) and in turn, blue green algae.

```
p1 <- ggplot(dat, aes(date, TP)) +
  geom_point() + ylab("Total phosphorous") + xlab("") + theme_bw()
p2 <- ggplot(dat, aes(date, log(Bluegreens+1))) +
  geom_point() + ylab("Ln Blue-green algae") + xlab("") + theme_bw()
#gridExtra::grid.arrange(p1,p2,nrow=2)
```

We can use the MARSS package to fit a DLM. We'll filter the data to only use counts before 1974, and log transform densities. We also z-score the covariate. This is a good example of imperfect data – there's a couple of missing observations in the covariate, which we can't have in a DLM or GAM – so let's just fill them in with a spline.

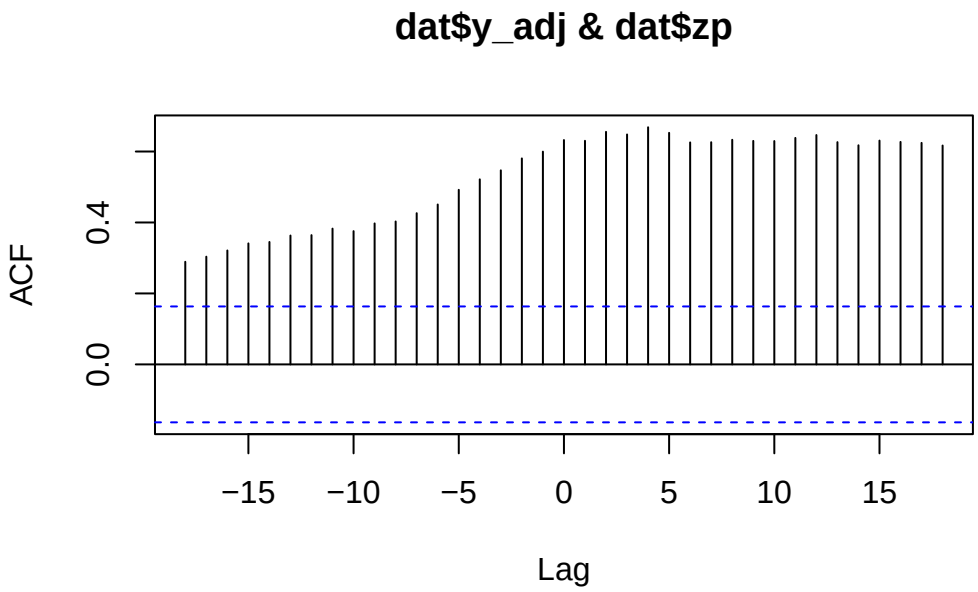
```
dat <- dplyr::filter(dat, Year < 1974) %>%
  dplyr::mutate(y = log(Bluegreens), zp = as.numeric(scale(TP)))

interpolated <- spline(dat$zp, xout = 1:nrow(dat))$y
dat$zp[which(is.na(dat$zp))] <- interpolated[which(is.na(dat$zp))]
```

The response data exhibit a strong seasonal cycle – and it's a good idea to de-season that to focus on the phosphorous effect.

```
# Fill in a few missing values
dat$y_interp <- dat$y
interpolated <- spline(dat$y, xout = 1:nrow(dat))$y
missing <- which(is.na(dat$y_interp))
dat$y_interp[missing] <- interpolated[missing]

dat <- dplyr::group_by(dat, Month) %>%
  dplyr::mutate(month_mean = mean(y,na.rm=T)) %>%
  dplyr::ungroup() %>%
  dplyr::mutate(y_adj = y_interp - month_mean)
```

Last, we should look at the lags between driver and response relationships. The CCF here indicates a 2-4 month lag, where TP and algae are more strongly associated with one another.

```
# We can also try to do a CCF analysis between phosphorous and algae

ccf(dat$y_adj, dat$zp)
```



We'll use a lag of 4 months.

```
lag_n <- 5
dat$lagged_zp <- c(rep(NA, lag_n), dat$zp[1:(nrow(dat)-lag_n)])
dat <- dat[-c(1:lag_n),]
```

##DLMs

Define the model – this block is basically copied from the MARSS book (salmon survival case study)

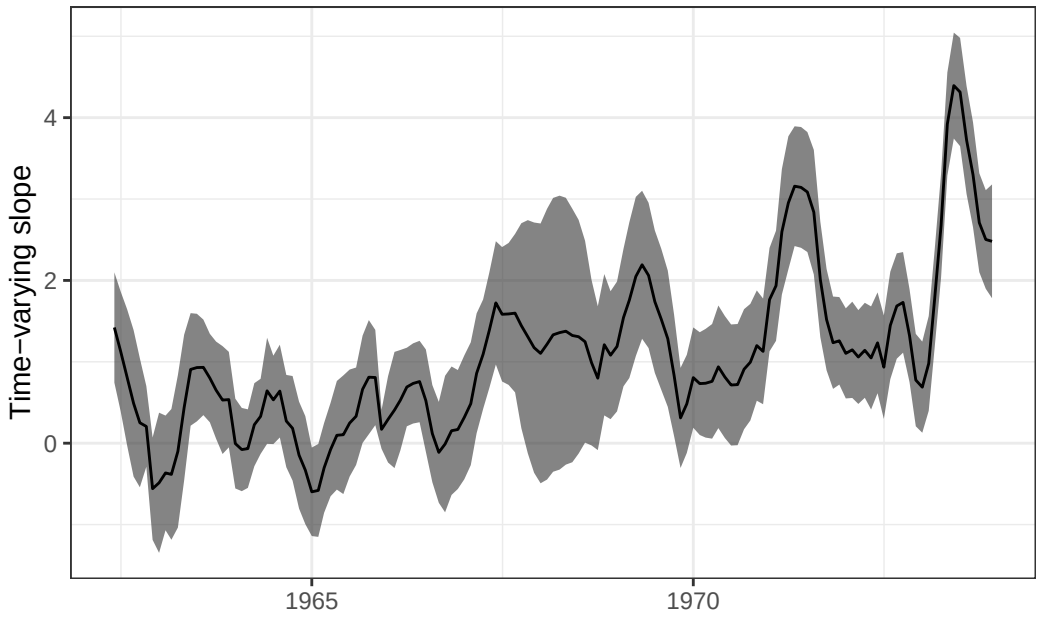
```
m <- 2
TT <- nrow(dat)
B <- diag(m) ## 2x2; Identity
U <- matrix(0, nrow = m, ncol = 1) ## 2x1; both elements = 0
Q <- matrix(list(0), m, m) ## 2x2; all 0 for now
diag(Q)[1] <- 0.0000001
diag(Q)[2] <- c("q.beta")
#diag(Q) <- c("q.alpha", "q.beta") ## 2x2; diag = (q1,q2)
Z <- array(NA, c(1, m, TT)) ## NxMxT; empty for now
Z[1, 1, ] <- rep(1, TT) ## Nx1; 1's for intercept
Z[1, 2, ] <- dat$lagged_zp ## Nx1; predictor variable
A <- matrix(0) ## 1x1; scalar = 0
```

```
R <- matrix("r") ## 1x1; scalar = r
## only need starting values for regr parameters
inits_list <- list(x0 = matrix(c(0, 0), nrow = m))
## list of model matrices & vectors
mod_list <- list(B = B, U = U, Q = Q, Z = Z, A = A, R = R)
# convert response to matrix
dat_mat <- matrix(dat$y_adj, nrow = 1)
# fit the model -- crank up the maxit to ensure convergence
dlm_1 <- MARSS(dat_mat, inits = inits_list, model = mod_list,
control = list(maxit=4000), method="TMB")
```

```
MARSS fit is
Estimation method: TMB
Estimation converged in 18 iterations.
Log-likelihood: -155.082
AIC: 318.1641   AICc: 318.4626

         Estimate
R.r         0.226
Q.q.beta    0.235
x0.X1       0.498
x0.X2       1.422
Initial states (x0) defined at t=0

Standard errors have not been calculated.
Use MARSSparamCIs to compute CIs and bias estimates.
```

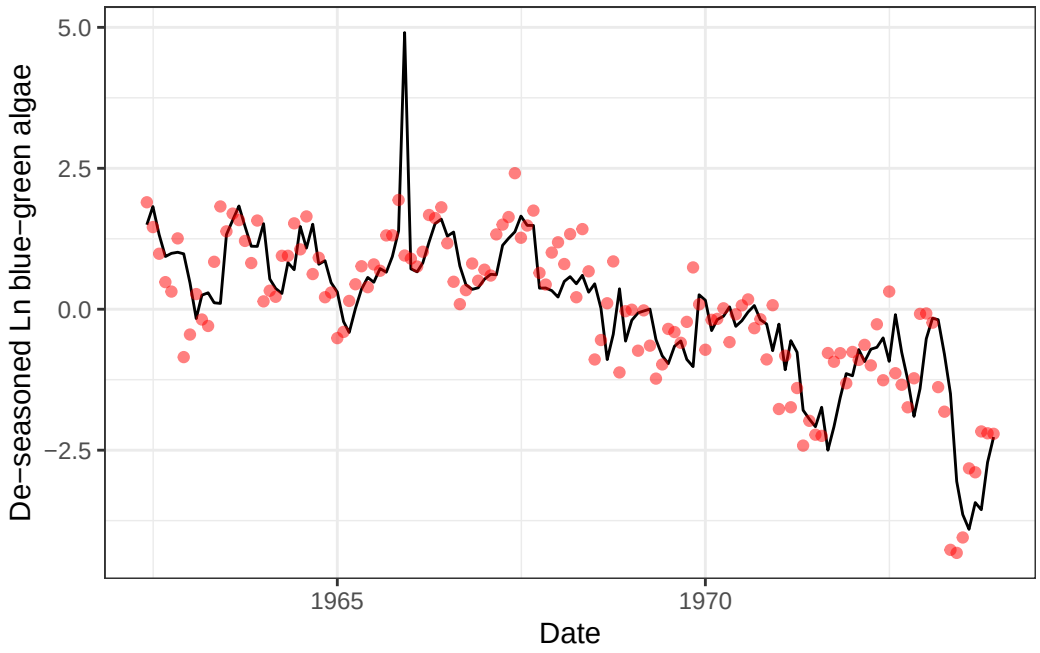
Let's put the state estimates back into the original dataframe and do some plotting. The slope is generally positive, which is what we expect – and exhibits clear variation through time

```
dat$int_est <- dlm_1$states[1,]
dat$int_se <- dlm_1$states.se[1,]

dat$slope_est <- dlm_1$states[2,]
dat$slope_se <- dlm_1$states.se[2,]
ggplot(dat, aes(date, slope_est)) +
geom_ribbon(aes(ymin=slope_est-2*slope_se, ymax = slope_est+2*slope_se), alpha=0.6) +
geom_line() + ylab("Time-varying slope") + xlab("") + theme_bw()
```



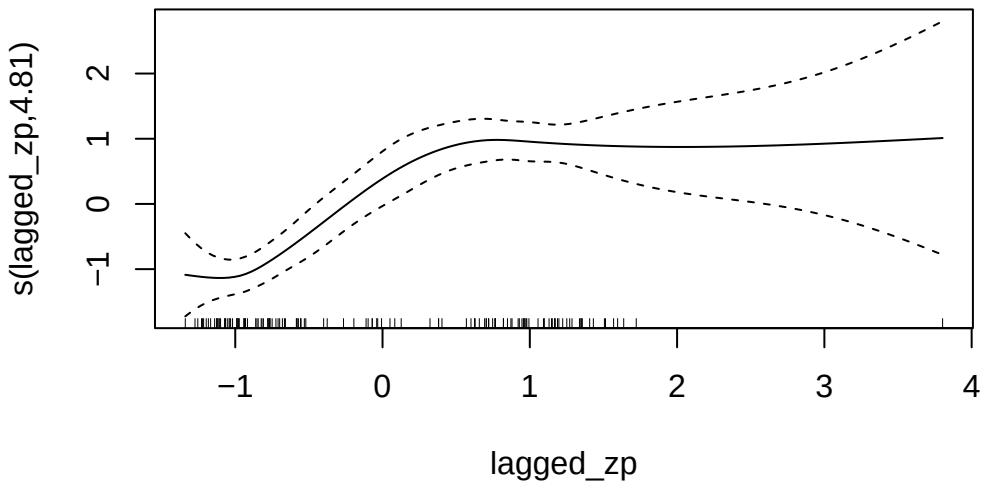
We can also plot the fitted values from our model, and some diagnostics

```
pred <- fitted(dlm_1)
dat$pred <- pred$.fitted
ggplot(dat, aes(date, pred)) +
geom_line() +
ylab("De-seasoned Ln blue-green algae") +
xlab("Date") +
theme_bw() +
geom_point(aes(date,y_adj), col="red",alpha=0.5)
```



GAMs

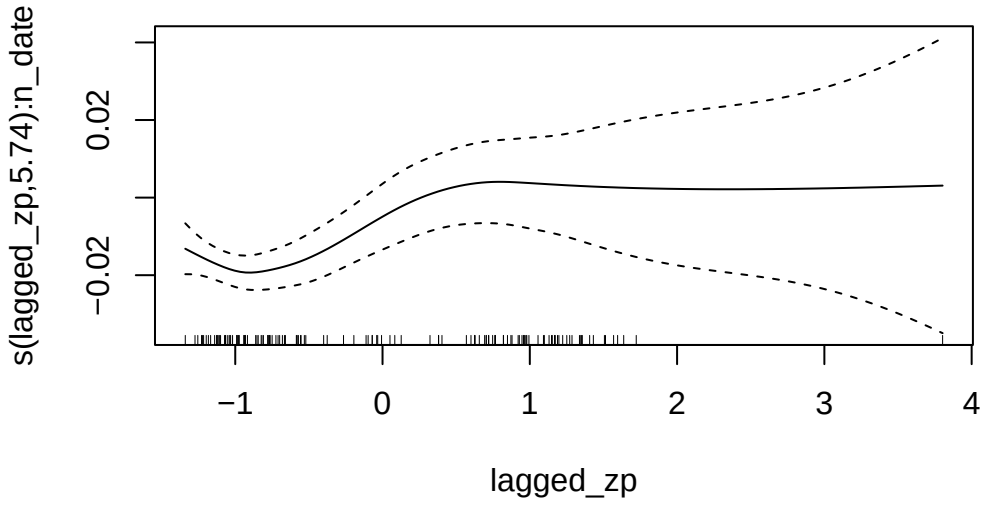
```
# The 'sp' parameter also controls the penalty on smoothing (below)
dat$n_date <- as.numeric(as.factor(dat$date))

gam_cr1 <- gam(y_adj ~ s(lagged_zp, bs = "cr"), data = dat)
gam_cr2 <- gam(y_adj ~ s(lagged_zp, by = n_date, bs = "cr"), data = dat)
gam_cr3 <- gam(y_adj ~ s(n_date, by = lagged_zp, bs = "cr"), data = dat)

plot_cr1 <- plot(gam_cr1, seWithMean = TRUE, n = nrow(dat))
```



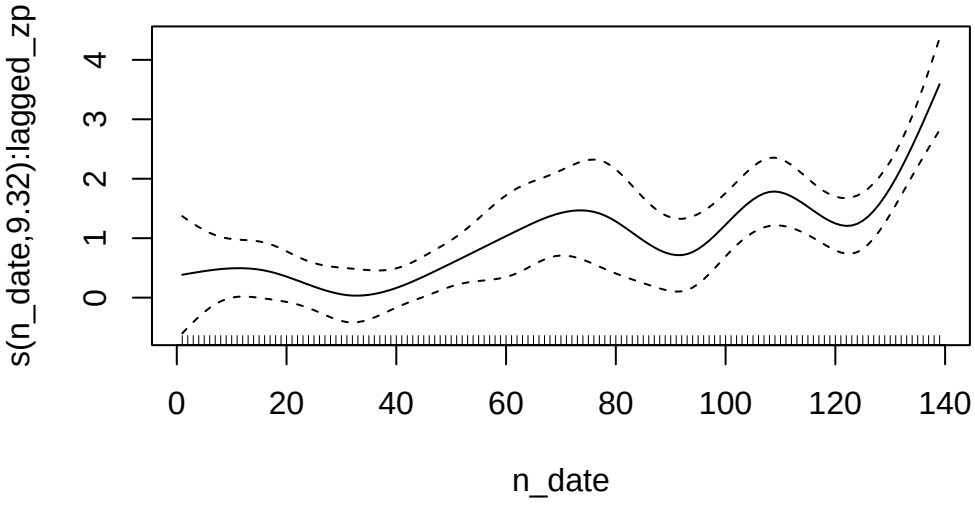

```
df_cr1 <- data.frame(x = plot_cr1[[1]]$x,
est = plot_cr1[[1]]$fit,
se = plot_cr1[[1]]$se)

p1 <- ggplot(df_cr1, aes(x, est)) +
geom_ribbon(aes(ymin = est - 2*se, ymax = est + 2*se), alpha = 0.4, col = NA, fill=viridis(1
theme_bw() +
geom_line(col = viridis(1)) +
xlab("Phosphorous") +
ylab("Effect")
ggsave(p1, filename = "Figure_S1_nonlinear_smooth.png", height = 5, width=7)
# make second plot showing fits from all 3 models
pred_1 <- dat
pred_1$pred <- predict(gam_cr1, se.fit=TRUE)$fit
pred_1$se <- predict(gam_cr1, se.fit=TRUE)$se.fit
pred_1$smooth <- "s(phos)"
pred_2 <- dat
pred_2$pred <- predict(gam_cr2, se.fit=TRUE)$fit
pred_2$se <- predict(gam_cr2, se.fit=TRUE)$se.fit
pred_2$smooth <- "s(phos,by=date)"
pred_3 <- dat
pred_3$pred <- predict(gam_cr3, se.fit=TRUE)$fit
pred_3$se <- predict(gam_cr3, se.fit=TRUE)$se.fit
```

```
pred_3$smooth <- "s(date,by=phos)"

d_all <- rbind(pred_1, pred_2, pred_3)
p2 <- ggplot(d_all, aes(date, y_adj, col = smooth)) +
  geom_point(col="black") +
  theme_bw() +
  geom_line(aes(date, pred), size=2,alpha=0.5) +
  xlab("") + ylab("Detrended cyanobacteria") +
  scale_color_viridis_d(option="magma",begin=0.2, end=0.8)
ggsave(p2, filename = "Figure_S2_nonlinear_v_nonstationary.png", height = 5, width=7)
```

```
# extract the smooth estimates with SEs to compare to DLM
plot_cr2 <- plot(gam_cr2, seWithMean = TRUE, n = nrow(dat))
```




```
plot_cr3 <- plot(gam_cr3, seWithMean = TRUE, n = nrow(dat))
```

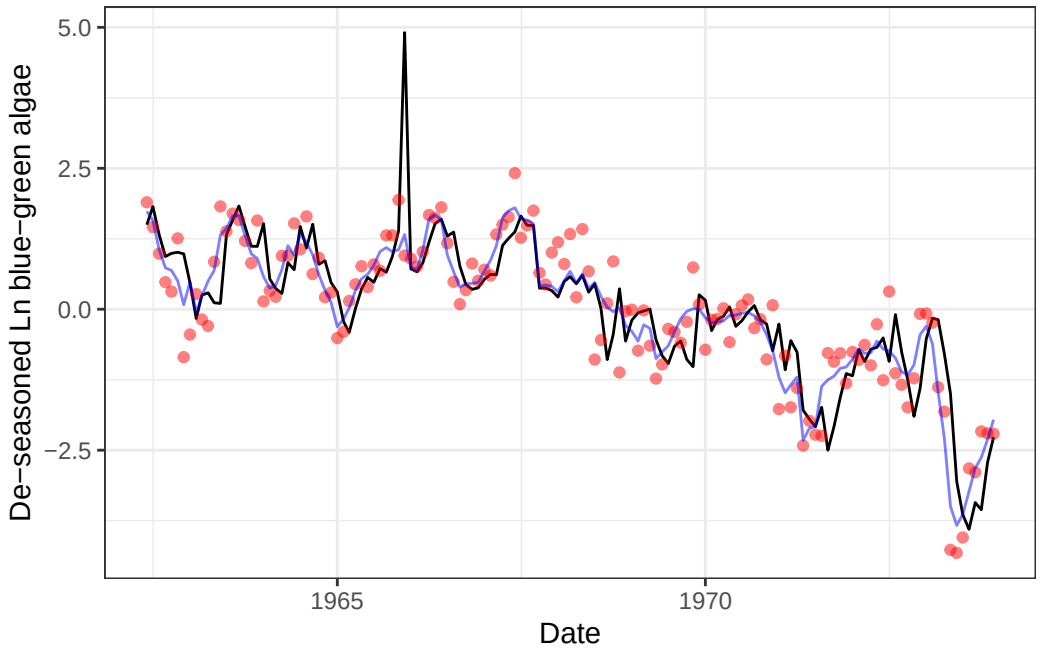



```
df_cr2 <- data.frame(lagged_zp = dat$lagged_zp,
est = plot_cr2[[1]]$fit,
se = plot_cr2[[1]]$se)

p3 <- ggplot(df_cr2, aes(lagged_zp, est)) +
geom_ribbon(aes(ymin = est - 2*se, ymax = est + 2*se), alpha = 0.4, col = NA, fill=viridis(1
theme_bw() +
geom_line(col = viridis(1)) +
xlab("Phosphorous") +
ylab("Date effect")

df_cr3 <- data.frame(date = dat$date,
est = plot_cr3[[1]]$fit,
se = plot_cr3[[1]]$se)

p4 <- ggplot(df_cr3, aes(date, est)) +
geom_ribbon(aes(ymin = est - 2*se, ymax = est + 2*se), alpha = 0.4, col = NA, fill=viridis(1
theme_bw() +
geom_line(col = viridis(1)) +
xlab("Date") +
ylab("Phosphorous effect")
#
# combo <- gridExtra::grid.arrange(p1,p2,p3,p4,ncol=1)
```

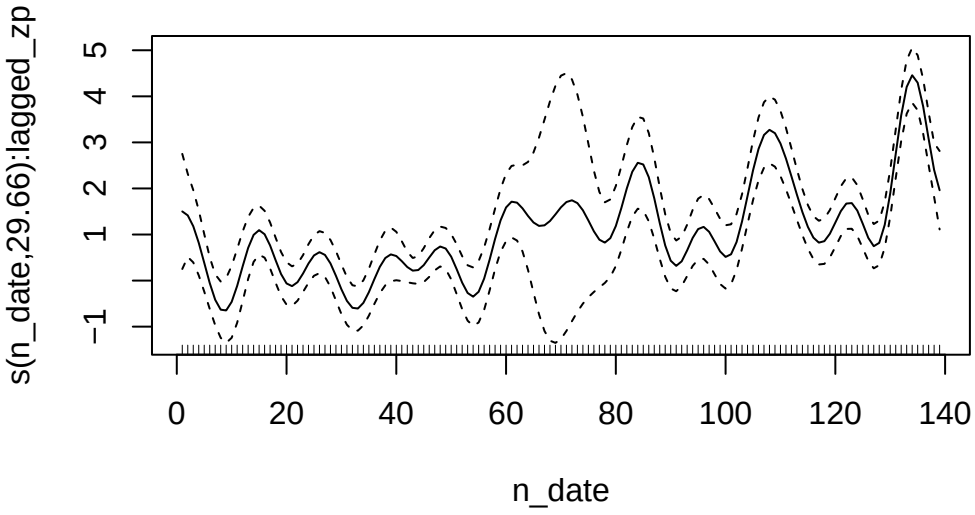
```r
# ggsave(combo, filename = "Fig_1.png", height=7, width=7)\

library(patchwork)

# Combine plots with labels using patchwork
combo <- (p1 + p2 + p3 + p4) +
  plot_layout(ncol = 1) +
  plot_annotation(tag_levels = "a") &
  theme(plot.tag.position = c(0.1, 0.95))
ggsave(combo, filename = "Fig_1.png", height=7, width=7)
```

Here is some more analysis on choices of setting up a GAM:

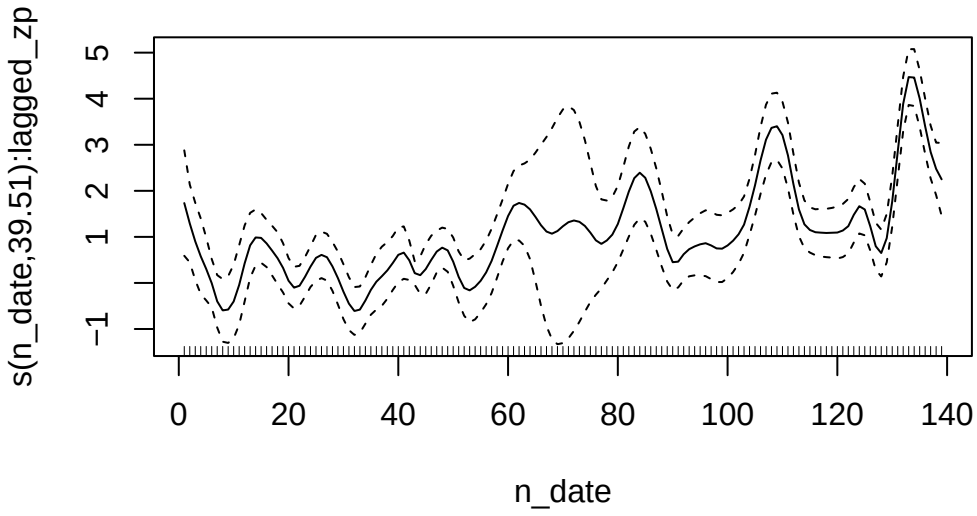
```r
# Maybe some discussion in the paper about why s(n_date,lagged_zp) and not
# the other way around?

# The 'sp' parameter also controls the penalty on smoothing (below)
dat$n_date <- as.numeric(as.factor(dat$date))
gam_cr <- gam(y_adj ~ s(n_date, by = lagged_zp, bs = "cr",k=nrow(dat)),
              data = dat)
gam_tp <- gam(y_adj ~ s(n_date, by = lagged_zp,k=nrow(dat)),
              data = dat) # k is ignored
gam_gp <- gam_cr <- gam(y_adj ~ s(n_date, by = lagged_zp, bs = "gp",k=nrow(dat)),
                        data = dat)

dat$pred_gam <- predict(gam_tp)

ggplot(dat, aes(date, pred)) +
  geom_line() + ylab("De-seasoned Ln blue-green algae") +
  xlab("Date") + theme_bw() +
  geom_point(aes(date,y_adj), col="red",alpha=0.5) +
  geom_line(aes(date,pred_gam), col="blue",alpha=0.5)
```



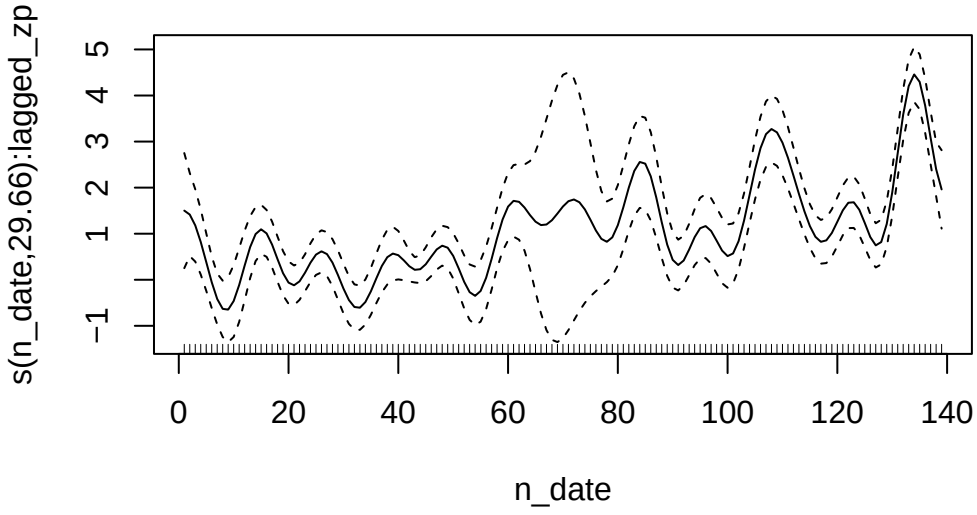

```
# extract the smooth estimates with SEs to compare to DLM
plot_cr <- plot(gam_cr, seWithMean = TRUE, n = nrow(dat))
```



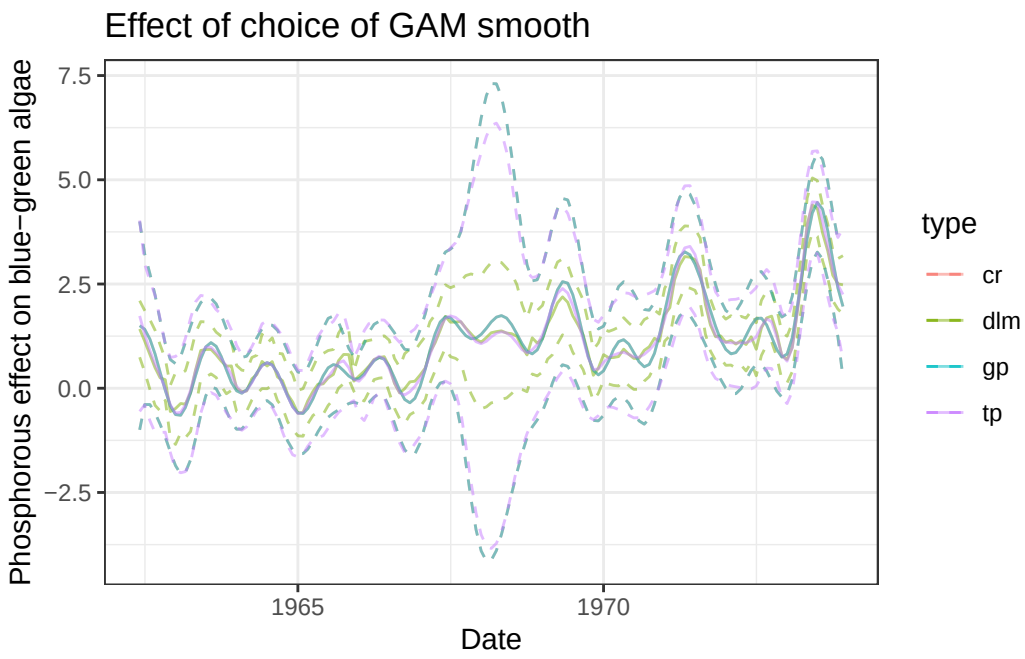
```r
plot_tp <- plot(gam_tp, seWithMean = TRUE, n = nrow(dat))
```



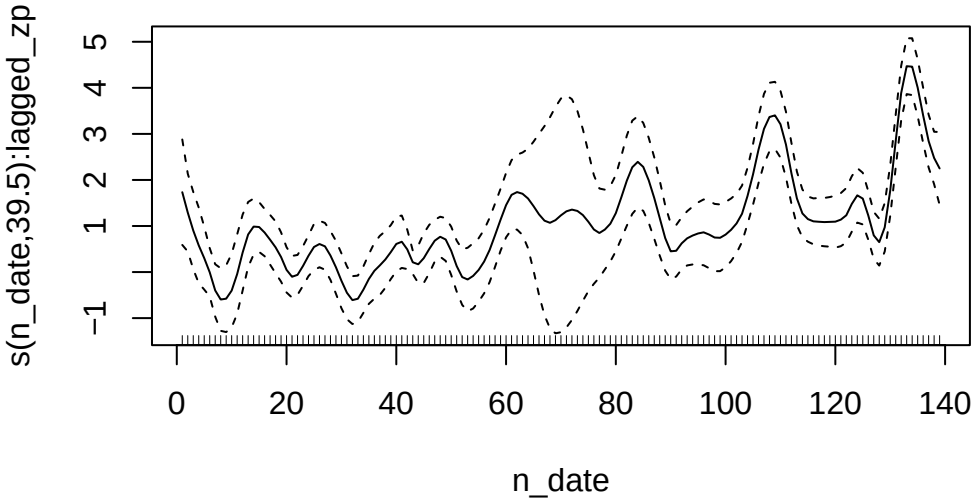

```r
plot_gp <- plot(gam_gp, seWithMean = TRUE, n = nrow(dat))
```



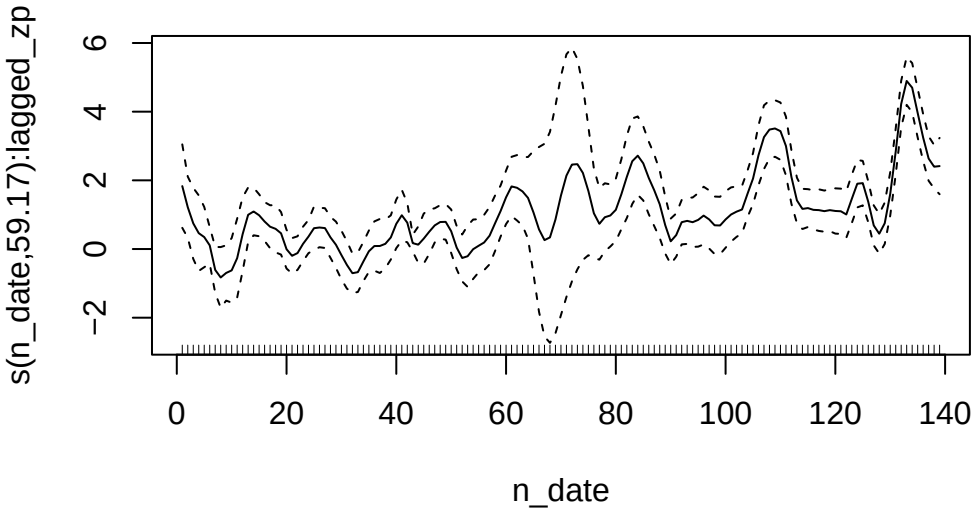
```r
df_cr <- data.frame(date = dat$date,
                    est = plot_cr[[1]]$fit,
                    se = plot_cr[[1]]$se, type="cr")
df_tp <- data.frame(date = dat$date,
                    est = plot_tp[[1]]$fit,
                    se = plot_tp[[1]]$se, type="tp")
df_gp <- data.frame(date = dat$date,
                    est = plot_gp[[1]]$fit,
                    se = plot_gp[[1]]$se, type="gp")
df_dlm <- data.frame(date = dat$date,
                     est = dat$slope_est,
                     se = dat$slope_se, type="dlm")
df_smooth <- rbind(df_cr, df_tp, df_gp, df_dlm)

#df_smooth <- rbind(df_cr,  df_gp)
df_smooth_type<-df_smooth
ggplot(df_smooth, aes(date, est, col=type, fill=type)) +
  geom_line(aes(date,est-2*se), alpha=0.5, linetype=2) +
  geom_line(aes(date,est+2*se), alpha=0.5, linetype=2) +
  geom_line(aes(date,est), alpha=0.5) +
  theme_bw() +
  xlab("Date") +
  ylab("Phosphorous effect on blue-green algae") +
  ggtitle("Effect of choice of GAM smooth")
```



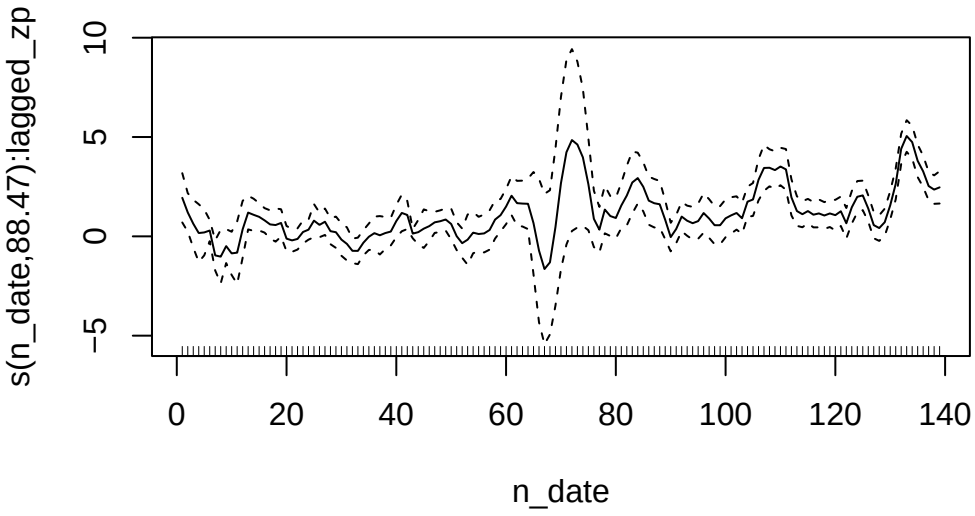

```
gam_cr30 <- gam(y_adj ~ s(n_date, by = lagged_zp, bs = "cr",
                          k=nrow(dat)), data = dat)
gam_cr60 <- gam(y_adj ~ s(n_date, by = lagged_zp, bs = "cr",
                          k=nrow(dat),sp=16), data = dat)
gam_cr90 <- gam(y_adj ~ s(n_date, by = lagged_zp, bs = "cr",
                          k=nrow(dat),sp=2.5), data = dat)
gam_cr120 <- gam(y_adj ~ s(n_date, by = lagged_zp, bs = "cr",
                           k=nrow(dat),sp=0.3), data = dat)

plot_cr30 <- plot(gam_cr30, seWithMean = TRUE, n = nrow(dat))
```



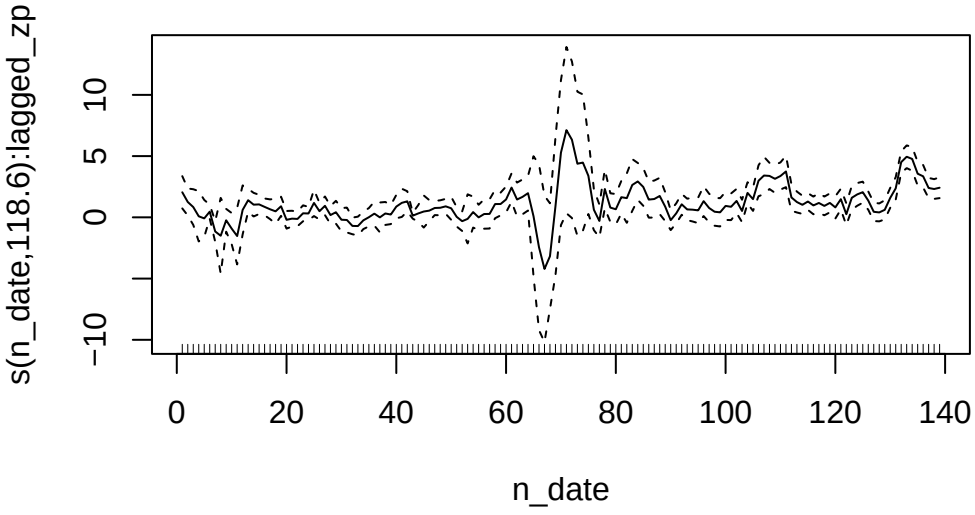

```
plot_cr60 <- plot(gam_cr60, seWithMean = TRUE, n = nrow(dat))
```



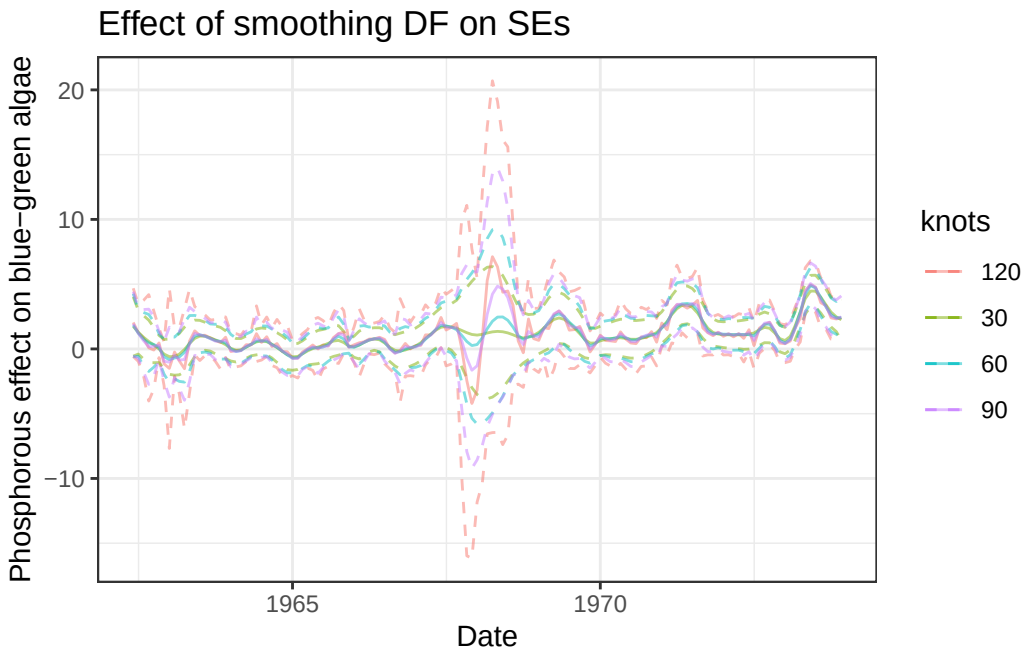
```r
plot_cr90 <- plot(gam_cr90, seWithMean = TRUE, n = nrow(dat))
```




```r
plot_cr120 <- plot(gam_cr120, seWithMean = TRUE, n = nrow(dat))
```



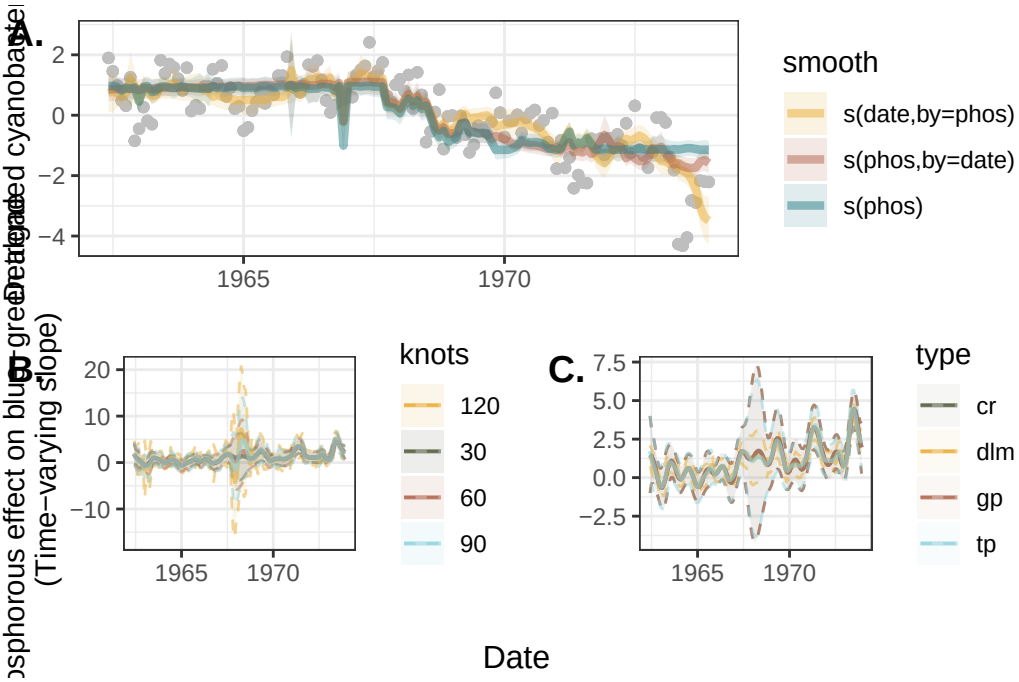
```
df_30 <- data.frame(date = dat$date,
                    est = plot_cr30[[1]]$fit,
                    se = plot_cr30[[1]]$se, knots="30")
df_60 <- data.frame(date = dat$date,
                    est = plot_cr60[[1]]$fit,
                    se = plot_cr60[[1]]$se, knots="60")
df_90 <- data.frame(date = dat$date,
                    est = plot_cr90[[1]]$fit,
                    se = plot_cr90[[1]]$se, knots="90")
df_120 <- data.frame(date = dat$date,
                     est = plot_cr120[[1]]$fit,
                     se = plot_cr120[[1]]$se, knots="120")
df_smooth <- rbind(df_30, df_60, df_90, df_120)
df_smooth_knots<-df_smooth
ggplot(df_smooth, aes(date, est, col=knots, fill=knots)) +
  geom_line(aes(date,est-2*se), alpha=0.5, linetype=2) +
  geom_line(aes(date,est+2*se), alpha=0.5, linetype=2) +
  geom_line(aes(date,est), alpha=0.5) +
  theme_bw() + xlab("Date") + ylab("Phosphorous effect on blue-green algae") +
  ggtitle("Effect of smoothing DF on SEs")
```



Coding Figure 2 all together

```
panel.a <- ggplot(d_all, aes(date, y_adj, col = smooth)) +
  geom_point(col="grey") +
  theme_bw() +
  xlab("Year")+
    geom_ribbon(aes(ymin = pred-2*se, ymax = pred+2*se, y = NULL, fill=smooth),
              alpha = 0.15, colour = NA)+
  scale_fill_manual(values=c(col[4],col[3],col[2]))+
  scale_colour_manual(values=c(col[4],col[3],col[2]))+
  geom_line(aes(date, pred), size=1.5,alpha=0.5) +
  xlab("") + ylab("Detrended cyanobacteria")
 # scale_color_viridis_d(option="magma",begin=0.2, end=0.8)

panel.b <-ggplot(df_smooth_knots, aes(date, est, col=knots, fill=knots)) +
  geom_line(aes(date,est-2*se), alpha=0.5, linetype=2) +
  geom_line(aes(date,est+2*se), alpha=0.5, linetype=2) +
     geom_ribbon(aes(ymin = est-2*se, ymax = est+2*se, y = NULL, fill=knots),
              alpha = 0.1, colour = NA)+
  geom_line(aes(date,est), alpha=0.6, lwd=0.75) +
  ylim(c(-17,21))+
  scale_colour_manual(values=c(col[4],col[5],col[3],col[1]))+
  scale_fill_manual(values=c(col[4],col[5],col[3],col[1]))+
  #ggtitle("Effect of smoothing DF on SEs")+
  theme_bw() + xlab("") + ylab("Phosphorous effect on blue-green algae \n (Time-varying slop

panel.c<-ggplot(df_smooth_type, aes(date, est, col=type)) +
       geom_ribbon(aes(ymin = est-2*se, ymax = est+2*se, y = NULL, fill=type),
              alpha = 0.05, colour = NA)+
  geom_line(aes(date,est-2*se), alpha=0.5, linetype=2) +
  geom_line(aes(date,est+2*se), alpha=0.5, linetype=2) +
  geom_line(aes(date,est), alpha=0.6, lwd=0.75) +
  scale_colour_manual(values=c(col[5],col[4],col[3],col[1]))+
  scale_fill_manual(values=c(col[5],col[4],col[3],col[1]))+
  #ggtitle("Effect of choice of GAM smooth")+
  #ylim(c(-17,21))+
  theme_bw() + xlab("") + ylab("")

bottom_panel <-ggarrange(panel.b, panel.c,widths=c(1.05,1), nrow=1,labels=c("B.", "C."))
bottom_panel<-annotate_figure(bottom_panel, bottom = text_grob("Date"))

top_panel<-ggarrange(panel.a,labels=c("A."),nrow=1)

figure2<-ggarrange(top_panel,bottom_panel, nrow=2)
```

```
figure2
```




```
ggsave(figure2, filename = "Figure_S2_GAMtypes.png",bg="white", height = 8, width=8.5)
```

‘‘‘