

Building article figures - simulation outputs

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19/11/2022 - Updated 04/06/2024 - 17/12/2024

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1 Library

```
library(dplyr)
library(ggplot2)
library(Hmisc)
library(corrplot)
library(gridExtra)
library(PerformanceAnalytics)
library(stats)
library(plyr)
library("ggpubr")
```

```
library("grid")
library(MASS)
```

2 Required data sets

```
WD <- ".."
PATH_OUTPUT <- file.path(WD, "Outputs_sim_smallarea")
PATH_FUNC <- file.path(WD, "Functions")
PATH_DATA <- file.path(WD, "Data")
PATH_FIG <- file.path(WD, "Figures_and_stats/Figures_sim_smallarea")
source(file.path(PATH_FUNC, "Prep_obs.R"))
source(file.path(PATH_FUNC, "stepAIC_gam.R"))
source(file.path(PATH_FUNC, "plot_gam_predictions.R"))

# raw_obs <- read.csv(file.path(
#   PATH_DATA,
#   "all_operations_on_fobs_observe_v9_fr_2005-2023.csv")
# )
# Ob7 <- prep_obs(Ob7 = raw_obs)
#
# Ob7 <- Ob7[Ob7$year>2013,]
# Ob7 <- Ob7[Ob7$year<2023,]
# Ob7_NLOG = Ob7 %>% filter(obj_conv=="NLOG")
# Ob7_NLOG$Zone <- as.factor(
#   ifelse(Ob7_NLOG$latitude<(-10) & Ob7_NLOG$longitude <= 50,"MOZ","WIO")
# )
world <- map_data("world")

NLOG_VE <- read.csv(file.path(PATH_OUTPUT, "NLOG_VE.csv"), header = TRUE)
VE <- NLOG_VE[,grepl('mean', names(NLOG_VE)) & !grepl('nlog', names(NLOG_VE))]
colnames(VE) <- gsub('MEAN', '', toupper(names(VE)))
names(VE)[which(names(VE) == 'CHLA')] <- 'Chla'

NLOG_VE$logNLOG <- log(NLOG_VE$nlogmean)
NLOG_VE$chlacr <- scale(NLOG_VE$chlamean)
NLOG_VE$slacr <- scale(NLOG_VE$slamean)
NLOG_VE$SSCIcr <- scale(NLOG_VE$SSCImean)
NLOG_VE$FSLEcr <- scale(NLOG_VE$FSLEmean)
NLOG_VE$MNcr <- scale(NLOG_VE$MNmean)

NLOG_VE_sup_zero_Moz <- NLOG_VE %>% dplyr::filter(Zone == 'MOZ', nlogmean > 0)
NLOG_VE_sup_zero_North <- NLOG_VE %>% dplyr::filter(Zone == 'WIO', nlogmean > 0)

LM4_North_chla <- lm(logNLOG ~ chlacr + slacr, data = NLOG_VE_sup_zero_North)
LM5_Moz_chla <- lm(logNLOG ~ slacr, data = NLOG_VE_sup_zero_Moz)

dfMN_epi<-read.csv(file.path(PATH_OUTPUT, "MN_epi_mean.csv"), header = T)
dfMN_u<-read.csv(file.path(PATH_OUTPUT, "MN_umeso_mean.csv"), header = T)
dfMN_mu<-read.csv(file.path(PATH_OUTPUT, "MN_mumeso_mean.csv"), header = T)
dfMN_ml<-read.csv(file.path(PATH_OUTPUT, "MN_mlmeso_mean.csv"), header = T)
dfMN_hml<-read.csv(file.path(PATH_OUTPUT, "MN_hmlmeso_mean.csv"), header = T)
```

```
# df_eff <- read.csv(file.path(PATH_OUTPUT, "df_eff.csv"), head = T)
# df_eff_new <- read.csv(file.path(PATH_OUTPUT, "df_eff_new_100.csv"), head = T)
```

3 Figure 1 : Study area (map)

```
fig1 <- ggplot(aes(x=c(35, 85), y=c(-25, 25)), data=NLOG_VE) +
  geom_point(data = NLOG_VE, mapping = aes(x = lon_grid, y = lat_grid,
                                            color = Zone),
            shape=1,size=.5) +
  geom_segment(aes(x=40,y=(-10),xend=50,yend=(-10)),linetype=2)+
  geom_segment(aes(x=50,y=(-10),xend=50,yend=(-15)),linetype=2)+
  geom_map(data = world, map = world, aes(x = long, y = lat, map_id = region),
          color = "black", fill = "lightgray", linewidth = 0.1) +
  xlim(min(35),max(85))+
  ylim(min(-25),max(20))+
  xlab("Longitude (deg)") +
  ylab("Latitude (deg)") +
  theme(panel.border = element_rect(fill = NA, colour = "black"))+
  theme(text = element_text(size = 10))+
  theme(axis.text.x = element_text(size = 10))+
  theme(axis.text.y = element_text(size = 10))+
  annotate(geom="label", x=55, y=-5, label="WIO",
          color="black", fontface="bold", size=3)+
  geom_segment(aes(x=54,y=(-15),xend=45,yend=(-13)),
          linetype=1, linewidth = .25)+
  annotate(geom="label", x=55, y=-15, label="MOZ",
          color="black", fontface="bold", size=3)
```

3.1 Save plot

```
ggsave(file=file.path(PATH_FIG, "Fig1_Study Area.png"), fig1,
       width = 10, height = 9, units = "cm")
ggsave(file=file.path(PATH_FIG, "Fig1.eps"), fig1,
       width = 10, height = 9, units = "cm")
```

4 Figure 4 : Scatter plots : NLOGs vs VE

4.1 SSCI

```
#SSCI
f4.ssci <- ggplot(NLOG_VE)+
  geom_point(aes(x = SSCImean, y = nlogmean, shape = Zone),size = 3)+
  scale_shape_manual(values = c(17, 1))+
  # scale_x_continuous(breaks=c(0,0.1,0.2,0.3,0.4,0.5,0.6,0.7))+
  xlab("Mean SSCI (m.s-1)") +
  ylab('Simulated NLOG abundance') +
  # scale_y_continuous(breaks=c(0,0.5,1,1.5,2,2.5))+
  theme(text = element_text(size = 17))+
  theme(axis.text.x = element_text(size = 18))+
  theme(axis.text.y = element_text(size = 18))+
  theme(legend.text = element_text(size=20))+
```

```

theme(legend.title = element_text(size=20))+
theme(legend.position = "none")+
theme(legend.key.size = unit(1, 'cm'))

```

4.2 SLA

```

#SLA
f4.sla <- ggplot(NLOG_VE)+
  geom_point(aes(x = slamean, y = nlogmean, shape = Zone),size = 3)+
  scale_shape_manual(values = c(17, 1))+
  # scale_x_continuous(breaks=c(-0.10,-0.05,0,0.05,0.10,0.15,0.20,0.25,0.30))+
  xlab("Mean SLA (m)")+
  ylab(" ")+
  # scale_y_continuous(breaks=c(0,0.5,1,1.5,2,2.5))+
  theme(text = element_text(size = 17))+
  theme(axis.text.x = element_text(size = 16))+
  theme(axis.text.y = element_text(size = 18))+
  theme(legend.text = element_text(size=20))+
  theme(legend.title = element_text(size=20))+
  theme(legend.position = "none")+
  theme(legend.key.size = unit(1, 'cm'))

```

4.3 FSLE

```

#FSLE
f4.fsle <- ggplot(NLOG_VE)+
  geom_point(aes(x = FSLEmean, y = nlogmean, shape = Zone),size = 3)+
  scale_shape_manual(values = c(17, 1))+
  # scale_x_continuous(breaks=c(-0.14,-0.12,-0.10,-0.08,-0.06,-0.04,-0.02,0))+
  xlab("Mean FSLE (days-1)")+
  ylab('Simulated NLOG abundance')+
  # scale_y_continuous(breaks=c(0,0.5,1,1.5,2,2.5))+
  theme(text = element_text(size = 17))+
  theme(axis.text.x = element_text(size = 18))+
  theme(axis.text.y = element_text(size = 18))+
  theme(legend.text = element_text(size=20))+
  theme(legend.title = element_text(size=20))+
  theme(legend.position = "none")+
  theme(legend.key.size = unit(1, 'cm'))

```

4.4 MN_Epi

```

#MN_Epi
f4.mn <- ggplot(NLOG_VE)+
  geom_point(aes(x = MNmean, y = nlogmean, shape = Zone),size = 3)+
  scale_shape_manual(values = c(17, 1))+
  # scale_x_continuous(breaks=seq(0.25,1.25,0.25))+
  xlab("Mean MN (g.m-2)")+
  ylab(" ")+
  # scale_y_continuous(breaks=c(0,0.5,1,1.5,2,2.5))+
  theme(text = element_text(size = 17))+
  theme(axis.text.x = element_text(size = 18))+

```

```

theme(axis.text.y = element_text(size = 18))+
theme(legend.text = element_text(size=20))+
theme(legend.title = element_text(size=20))+
theme(legend.position = "none")+
theme(legend.key.size = unit(1, 'cm'))

```

4.5 Chla

```

#Chla
f4.chla <- ggplot(NLOG_VE)+
  geom_point(aes(x = chlamean, y = nlogmean, shape = Zone),size = 3)+
  scale_shape_manual(values = c(17, 1))+
  # scale_x_continuous(breaks=seq(0,1,.1))+
  xlab("Mean Chl-a (mg.m-3)") +
  ylab('Simulated NLOG abundance') +
  # scale_y_continuous(breaks=seq(0,2.5,.5))+
  theme(text = element_text(size = 17))+
  theme(axis.text.x = element_text(size = 18))+
  theme(axis.text.y = element_text(size = 18))+
  theme(legend.text = element_text(size=20))+
  theme(legend.title = element_text(size=20))+
  theme(legend.position = "none")+
  theme(legend.key.size = unit(1, 'cm'))

```

4.6 Combine plots

```

fig4 <- ggarrange(f4.ssci,
                  f4.sla,
                  f4.fsle,
                  f4.mn,
                  f4.chla,
                  labels = c("(a)","(b)","(c)","(d)","(e)"),
                  font.label = list(size = 20),
                  label.x = 0.85,
                  label.y = 0.95,
                  ncol = 2, nrow = 3,
                  common.legend = TRUE, legend = "bottom")

```

4.7 Save plots

```

ggsave(file=file.path(PATH_FIG, "Fig4_Scatter plots.png"), fig4,
        width = 30, height = 25, units = "cm")
ggsave(file=file.path(PATH_FIG, "Fig4.eps"), fig4,
        width = 30, height = 25, units = "cm")

```

5 Figure : GAM WIO predictions

```

GAM_North <- mgcv::gam(
  logNLOG ~ s(chlamean, k = 6) + s(slamean, k = 6) + s(SSCImean, k=6) +
  s(FSLEmean, k = 6) + s(MNmean, k = 6),

```

```

data = NLOG_VE_sup_zero_North
)
GAM_North2 <- stepAIC.gam(GAM_North, verbose = T)

## ~~~ Iteration 1 ~~~
##
## Initial model: mgcv::gam( logNLOG ~ s(chlamean, k = 6) + s(slamean, k = 6) + s(SSCImean, k = 6) + s(MNmean, k = 6)
## AIC: 815951.4
##
## mgcv::gam( logNLOG ~ s(slamean, k = 6) + s(SSCImean, k = 6) + s(FSLEmean, k = 6) + s(MNmean, k = 6)
## AIC: 817709.7
##
## mgcv::gam( logNLOG ~ s(chlamean, k = 6) + s(SSCImean, k = 6) + s(FSLEmean, k = 6) + s(MNmean, k = 6)
## AIC: 817632.2
##
## mgcv::gam( logNLOG ~ s(chlamean, k = 6) + s(slamean, k = 6) + s(FSLEmean, k = 6) + s(MNmean, k = 6)
## AIC: 816777.2
##
## mgcv::gam( logNLOG ~ s(chlamean, k = 6) + s(slamean, k = 6) + s(SSCImean, k = 6) + s(MNmean, k = 6)
## AIC: 818789.9
##
## mgcv::gam( logNLOG ~ s(chlamean, k = 6) + s(slamean, k = 6) + s(SSCImean, k = 6) + s(FSLEmean, k = 6)
## AIC: 825224.8

# With error bars
p1 <- plot.gam.prediction(data = NLOG_VE_sup_zero_North,
  my_gam = GAM_North2,
  vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
  var_to_predict = "chlamean",
  xlabel = "Chl-a",
  ylabel = "NLOG sim",
  trans.back = exp)
p2 <- plot.gam.prediction(data = NLOG_VE_sup_zero_North,
  my_gam = GAM_North2,
  vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
  var_to_predict = "slamean",
  xlabel = "SLA",
  ylabel = "NLOG sim",
  trans.back = exp)
p3 <- plot.gam.prediction(data = NLOG_VE_sup_zero_North,
  my_gam = GAM_North2,
  vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
  var_to_predict = "MNmean",
  xlabel = "MN",
  ylabel = "NLOG sim",
  trans.back = exp)
p4 <- plot.gam.prediction(data = NLOG_VE_sup_zero_North,
  my_gam = GAM_North2,
  vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
  var_to_predict = "SSCImean",
  xlabel = "SSCI",
  ylabel = "NLOG sim",
  trans.back = exp)
p5 <- plot.gam.prediction(data = NLOG_VE_sup_zero_North,

```

```

my_gam = GAM_North2,
vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
var_to_predict = "FSLEmean",
xlabel = "FSLE",
ylabel = "NLOG sim",
trans.back = exp)
fig5 <- ggarrange(p1, p2, p3,
p4, p5,
labels = c("(a)", "(b)", "(c)", "(d)", "(e)'),
# font.label = list(size = 12),
label.x = 0,
label.y = 0.95,
ncol = 2, nrow = 3)
ggsave(file=file.path(PATH_FIG, "Fig_gam_predict_WI0.png"), fig5,
width = 12, height = 15, units = "cm")
ggsave(file=file.path(PATH_FIG, "Fig_gam_predict_WI0.eps"), fig5,
width = 12, height = 15, units = "cm")

```

```

# Without error bars
p1 <- plot.gam.prediction(data = NLOG_VE_sup_zero_North,
my_gam = GAM_North2,
vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
var_to_predict = "chlamean",
xlabel = "Chl-a",
ylabel = "NLOG sim",
lims.y = c(0, NA),
error.lines = F,
trans.back = exp)
p2 <- plot.gam.prediction(data = NLOG_VE_sup_zero_North,
my_gam = GAM_North2,
vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
var_to_predict = "slamean",
xlabel = "SLA",
ylabel = "NLOG sim",
lims.y = c(0, NA),
error.lines = F,
trans.back = exp)
p3 <- plot.gam.prediction(data = NLOG_VE_sup_zero_North,
my_gam = GAM_North2,
vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
var_to_predict = "MNmean",
xlabel = "MN",
ylabel = "NLOG sim",
lims.y = c(0, NA),
error.lines = F,
trans.back = exp)
p4 <- plot.gam.prediction(data = NLOG_VE_sup_zero_North,
my_gam = GAM_North2,
vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
var_to_predict = "SSCImean",
xlabel = "SSCI",
ylabel = "NLOG sim",
lims.y = c(0, NA),
error.lines = F,

```

```

        trans.back = exp)
p5 <- plot.gam.prediction(data = NLOG_VE_sup_zero_North,
        my_gam = GAM_North2,
        vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
        var_to_predict = "FSLEmean",
        xlabel = "FSLE",
        ylabel = "NLOG sim",
        lims.y = c(0, NA),
        error.lines = F,
        trans.back = exp)
fig5 <- ggarrange(p1, p2, p3,
        p4, p5,
        labels = c("(a)", "(b)", "(c)", "(d)", "(e)'),
        # font.label = list(size = 12),
        label.x = 0,
        label.y = 0.95,
        ncol = 2, nrow = 3)
ggsave(file=file.path(PATH_FIG, "Fig_gam_predict_WIO_no_errorline.png"), fig5,
        width = 15, height = 20, units = "cm")
ggsave(file=file.path(PATH_FIG, "Fig_gam_predict_WIO_no_errorline.eps"), fig5,
        width = 15, height = 20, units = "cm")

```

6 Figure : GAM Moz predictions

```

GAM_Moz <- mgcv::gam(
  logNLOG ~ s(chlamean, k = 6) + s(slamean, k = 6) + s(SSCImean, k = 6) +
    s(FSLEmean, k = 6) + s(MNmean, k = 6),
  data = NLOG_VE_sup_zero_Moz
)
GAM_Moz2 <- stepAIC.gam(GAM_Moz, verbose = T)

## ~~~ Iteration 1 ~~~
##
## Initial model: mgcv::gam( logNLOG ~ s(chlamean, k = 6) + s(slamean, k = 6) + s(SSCImean, k = 6) + s(
## AIC: 83335.05
##
## mgcv::gam( logNLOG ~ s(slamean, k = 6) + s(SSCImean, k = 6) + s(FSLEmean, k = 6) + s(MNmean, k = 6)
## AIC: 84166.63
##
## mgcv::gam( logNLOG ~ s(chlamean, k = 6) + s(SSCImean, k = 6) + s(FSLEmean, k = 6) + s(MNmean, k = 6)
## AIC: 83716.38
##
## mgcv::gam( logNLOG ~ s(chlamean, k = 6) + s(slamean, k = 6) + s(FSLEmean, k = 6) + s(MNmean, k = 6)
## AIC: 84298.61
##
## mgcv::gam( logNLOG ~ s(chlamean, k = 6) + s(slamean, k = 6) + s(SSCImean, k = 6) + s(MNmean, k = 6)
## AIC: 86639.04
##
## mgcv::gam( logNLOG ~ s(chlamean, k = 6) + s(slamean, k = 6) + s(SSCImean, k = 6) + s(FSLEmean, k = 6)
## AIC: 85048.46

# With error bars
p1 <- plot.gam.prediction(data = NLOG_VE_sup_zero_Moz,

```



```

my_gam = GAM_Moz2,
vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
var_to_predict = "chlamean",
xlabel = "Chl-a",
ylabel = "NLOG sim",
trans.back = exp)
p2 <- plot.gam.prediction(data = NLOG_VE_sup_zero_Moz,
my_gam = GAM_Moz2,
vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
var_to_predict = "slamean",
xlabel = "SLA",
ylabel = "NLOG sim",
trans.back = exp)
p3 <- plot.gam.prediction(data = NLOG_VE_sup_zero_Moz,
my_gam = GAM_Moz2,
vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
var_to_predict = "MNmean",
xlabel = "MN",
ylabel = "NLOG sim",
trans.back = exp)
p4 <- plot.gam.prediction(data = NLOG_VE_sup_zero_Moz,
my_gam = GAM_Moz2,
vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
var_to_predict = "SSCImean",
xlabel = "SSCI",
ylabel = "NLOG sim",
trans.back = exp)
p5 <- plot.gam.prediction(data = NLOG_VE_sup_zero_Moz,
my_gam = GAM_Moz2,
vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
var_to_predict = "FSLEmean",
xlabel = "FSLE",
ylabel = "NLOG sim",
trans.back = exp)
fig5 <- ggarrange(p1, p2, p3,
p4, p5,
labels = c("(a)", "(b)", "(c)", "(d)", "(e)"),
# font.label = list(size = 12),
label.x = 0,
label.y = 0.95,
ncol = 2, nrow = 3)
ggsave(file=file.path(PATH_FIG, "Fig_gam_predict_Moz.png"), fig5,
width = 12, height = 15, units = "cm")
ggsave(file=file.path(PATH_FIG, "Fig_gam_predict_Moz.eps"), fig5,
width = 12, height = 15, units = "cm")

# Without error bars
p1 <- plot.gam.prediction(data = NLOG_VE_sup_zero_Moz,
my_gam = GAM_Moz2,
vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
var_to_predict = "chlamean",
xlabel = "Chl-a",
ylabel = "NLOG sim",
lims.y = c(0, NA),

```

```

        error.lines = F,
        trans.back = exp)
p2 <- plot.gam.prediction(data = NLOG_VE_sup_zero_Moz,
        my_gam = GAM_Moz2,
        vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
        var_to_predict = "slamean",
        xlabel = "SLA",
        ylabel = "NLOG sim",
        lims.y = c(0, NA),
        error.lines = F,
        trans.back = exp)
p3 <- plot.gam.prediction(data = NLOG_VE_sup_zero_Moz,
        my_gam = GAM_Moz2,
        vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
        var_to_predict = "MNmean",
        xlabel = "MN",
        ylabel = "NLOG sim",
        lims.y = c(0, NA),
        error.lines = F,
        trans.back = exp)
p4 <- plot.gam.prediction(data = NLOG_VE_sup_zero_Moz,
        my_gam = GAM_Moz2,
        vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
        var_to_predict = "SSCImean",
        xlabel = "SSCI",
        ylabel = "NLOG sim",
        lims.y = c(0, NA),
        error.lines = F,
        trans.back = exp)
p5 <- plot.gam.prediction(data = NLOG_VE_sup_zero_Moz,
        my_gam = GAM_Moz2,
        vars = c("chlamean", "slamean", "MNmean", "SSCImean", "FSLEmean"),
        var_to_predict = "FSLEmean",
        xlabel = "FSLE",
        ylabel = "NLOG sim",
        lims.y = c(0, NA),
        error.lines = F,
        trans.back = exp)
fig5 <- ggarrange(p1, p2, p3,
        p4, p5,
        labels = c("(a)", "(b)", "(c)", "(d)", "(e)"),
        # font.label = list(size = 12),
        label.x = 0,
        label.y = 0.95,
        ncol = 2, nrow = 3)
ggsave(file=file.path(PATH_FIG, "Fig_gam_predict_Moz_no_errorline.png"), fig5,
        width = 15, height = 20, units = "cm")
ggsave(file=file.path(PATH_FIG, "Fig_gam_predict_Moz_no_errorline.eps"), fig5,
        width = 15, height = 20, units = "cm")

```

6.0.0.1 APPENDICES FIGURES

7 Appendix A1 : correlation matrix of Environmental variables (VE)

```
# change significance levels in chart.Correlation function:
chart.Correlation.modif <- function(R, histogram = TRUE,
                                   method = c("pearson", "kendall", "spearman"),
                                   ...)
{
  x = checkData(R, method = "matrix")
  if (missing(method))
    method = method[1]
  cormeth <- method
  panel.cor <- function(x, y, digits = 2, prefix = "",
                        use = "pairwise.complete.obs",
                        method = cormeth, cex.cor, ...) {

    usr <- par("usr")
    on.exit(par(usr))
    par(usr = c(0, 1, 0, 1))
    r <- cor(x, y, use = use, method = method)
    txt <- format(c(r, 0.123456789), digits = digits)[1]
    txt <- paste(prefix, txt, sep = " ")
    if (missing(cex.cor))
      cex <- 0.8/strwidth(txt)
    test <- cor.test(as.numeric(x), as.numeric(y), method = method)
    Signif <- symnum(test$p.value, corr = FALSE, na = FALSE,
                     cutpoints = c(0, 1/3*10**-2, 1), symbols = c("*", " "))
    text(0.5, 0.5, txt, cex = cex * (abs(r) + 0.3)/1.3)
    text(0.8, 0.8, Signif, cex = cex, col = 2)
  }
  f <- function(t) {
    dnorm(t, mean = mean(x), sd = sd.xts(x))
  }
  dotargs <- list(...)
  dotargs$method <- NULL
  rm(method)
  hist.panel = function(x, ... = NULL) {
    par(new = TRUE)
    hist(x, col = "light gray", probability = TRUE, axes = FALSE,
         main = "", breaks = "FD")
    lines(density(x, na.rm = TRUE), col = "red", lwd = 1)
    rug(x)
  }
  if (histogram)
    pairs(x, gap = 0, lower.panel = panel.smooth, upper.panel = panel.cor,
          diag.panel = hist.panel)
  else pairs(x, gap = 0, lower.panel = panel.smooth, upper.panel = panel.cor)
}
```

```
names(NLOG_VE)
```

```
## [1] "lat_grid" "lon_grid" "time"      "nlogmean" "nlogsd"   "chlamean"
## [7] "chlasd"   "sstmean"  "sstsd"    "slamean"  "slasd"    "FSLEmean"
## [13] "FSLEsd"   "SSCImean" "SSCIsd"   "MNmean"   "MNsd"     "Zone"
## [19] "year"     "month"    "Season"   "logNLOG"  "chlacr"   "slacr"
```

```
## [25] "SSCIcr" "FSLEcr" "MNcr"
my_data_ve <- NLOG_VE %>% dplyr::select(sstmean, SSCImean,
                                       slamean, FSLEmean, MNmean, chlamean)
colnames(my_data_ve) <- c("SST", "SSCI", "SLA", "FSLE", "MN", "Chl-a")
set.seed(12345678)
mydata_ve_spl <- my_data_ve[sample.int(dim(my_data_ve)[1], 10**4),]
png(filename = file.path(PATH_FIG, "Appendix_A1_corrMatrixEnv.png"),
     width = 20, height = 12, units = "cm", res = 300)
chart.Correlation.modif(mydata_ve_spl, histogram=TRUE, pch=20, method = "kendall")
dev.off()

## pdf
## 2
```

8 Appendix A2 : Predicted vs Observed Aim values

8.1 WIO

```
#North
pred.north <- predict(GAM_North2)
NLOG_VE_sup_zero_North$pred<-pred.north
A2.north <- ggplot(NLOG_VE_sup_zero_North, aes(x = logNLOG, y = pred))+
  geom_point()+
  xlim(min(NLOG_VE_sup_zero_North$logNLOG),max(NLOG_VE_sup_zero_North$logNLOG))+
  ylim(min(NLOG_VE_sup_zero_North$logNLOG),max(NLOG_VE_sup_zero_North$logNLOG))+
  geom_abline(slope = 1, intercept = 0)+
  xlab("Observed NLOG sim")+
  ylab("Predicted NLOG sim")+
  theme(text = element_text(size = 15))+
  theme(axis.text.x = element_text(size = 20))+
  theme(axis.text.y = element_text(size = 20))
```

8.2 Moz

```
LM_Moz <- lm(logNLOG ~ chlacr + slacr + SSICr + FSLEcr + MNcr,
             data = NLOG_VE_sup_zero_Moz)
LM_Moz2 <- stepAIC(LM_Moz)
```

```
## Start: AIC=22657.02
## logNLOG ~ chlacr + slacr + SSICr + FSLEcr + MNcr
##
##           Df Sum of Sq  RSS   AIC
## <none>                 61558 22657
## - slacr    1      378.3 61936 22793
## - chlacr   1      620.1 62178 22880
## - MNcr     1     2227.5 63785 23454
## - SSICr    1     3368.0 64926 23852
## - FSLEcr   1    10325.0 71883 26138
```

```
#Moz
pred.moz <- predict(LM_Moz2)
NLOG_VE_sup_zero_Moz$pred<-pred.moz
A2.moz <- ggplot(NLOG_VE_sup_zero_Moz, aes(x = logNLOG, y = pred))+
```

```

geom_point()+
xlim(min(NLOG_VE_sup_zero_Moz$logNLOG),max(NLOG_VE_sup_zero_Moz$logNLOG))+
ylim(min(NLOG_VE_sup_zero_Moz$logNLOG),max(NLOG_VE_sup_zero_Moz$logNLOG))+
geom_abline(slope = 1, intercept = 0)+
xlab("Observed NLOG sim")+
ylab("Predicted NLOG sim")+
theme(text = element_text(size = 15))+
theme(axis.text.x = element_text(size = 20))+
theme(axis.text.y = element_text(size = 20))

```

8.3 GAM Moz

```

#Moz
pred.moz <- predict(GAM_Moz2)
NLOG_VE_sup_zero_Moz$pred<-pred.moz
A2.moz.gam <- ggplot(NLOG_VE_sup_zero_Moz, aes(x = logNLOG, y = pred))+
  geom_point()+
  xlim(min(NLOG_VE_sup_zero_Moz$logNLOG),max(NLOG_VE_sup_zero_Moz$logNLOG))+
  ylim(min(NLOG_VE_sup_zero_Moz$logNLOG),max(NLOG_VE_sup_zero_Moz$logNLOG))+
  geom_abline(slope = 1, intercept = 0)+
  xlab("Observed NLOG sim")+
  ylab("Predicted NLOG sim")+
  theme(text = element_text(size = 15))+
  theme(axis.text.x = element_text(size = 20))+
  theme(axis.text.y = element_text(size = 20))

```

8.4 Combine plots

```

ApxA2 <- ggarrange(A2.north, A2.moz+
  ggpubr::rremove("ylab"),
  A2.moz.gam,
  labels = c("(a)", "(b)"),
  font.label = list(size = 20),
  label.x = 0.1,
  label.y = 0.95,
  ncol = 2, nrow = 2)

```

8.5 Save plots

```

ggsave(file=file.path(PATH_FIG, "Appendix_A2_pred vs obs.png"), ApxA2,
  width = 35, height = 20, units = "cm")
ggsave(file=file.path(PATH_FIG, "Appendix_A2_pred vs obs.eps"), ApxA2,
  width = 35, height = 20, units = "cm")

```