



JRC TECHNICAL REPORT

Model based CFP indicators, F/F_{msy} and SSB

Mediterranean region case study

Giacomo Chato Osio, Ernesto Jardim, Coilin Minto, Finlay Scott and Ken Patterson

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Abstract

This work presents the application to Mediterranean stocks of a set of model-based indicators, being developed for monitoring the implementation of the Common Fisheries Policy (CFP). The work constitutes an application of the methodology, as such the results should not be used as representative of the CFP implementation in the Mediterranean. This document is mainly constituted of R code, showing how the indicators can be computed and presenting a set of diagnostics and stability tests. The models tested were a linear model, a linear mixed effects model with random intercept by stock, a GAMM with random intercept by stock and a GAMM with random intercept by Mediterranean GSA and species. The stability tests were designed to evaluate the estimates of recent (2003-2013) time series of trends in SSB and annual mean values of F/F_{msy} . The results were presented to the STECF's 2015 winter plenary (STECF-PLN-15-03).

Model based CFP indicators, F/F_{msy} and SSB

Mediterranean region case study

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1 Introduction

This work presents the application to Mediterranean stocks of a set of model-based indicators, being developed for monitoring the implementation of the Common Fisheries Policy (CFP). The work constitutes an application of the methodology, as such the results should not be used as representative of the CFP implementation in the Mediterranean. This document is mainly constituted of R code, showing how the indicators can be computed and presenting a set of diagnostics and stability tests. The models tested were a linear model, a linear mixed effects model with random intercept by stock, a GAMM with random intercept by stock and a GAMM with random intercept by Mediterranean GSA and species. The stability tests were designed to evaluate the estimates of recent (2003-2013) time series of trends in SSB and annual mean values of F/Fmsy. The results were presented to the STECF's 2015 winter plenary ([STECF-PLen-15-03](#)).

The models applied in this report were tested through a simulation study¹, where their statistical properties were evaluated.

2 Data preparation from STECF Stock Assessments results

This R Script was prepared to compile and prepare the database with stock assessment results from the STECF EWGs performing stock assessments for Mediterranean stocks from 2008 to 2014. All assessments have been organized in folders and the data (Catch, SSB, R, Landings, F) compiled by hand into a single csv file.

```
library(ggplot2)
library(lattice)
library(plyr)
library(dplyr)
library(gamm4)
library(reshape)
```

2.1 Load the data

```
stocks <- read.csv("Stocks_stecf_2014_12_02_2014.csv")

# bring in Fmsy estimates
stocks_msy <- read.csv("Stocks_stecf_2014_summary.csv")

stocks <- stocks[, 1:10]
stocks_msy <- subset(stocks_msy, select = c(GSA, Species, Stock, Fmsy))

stocks2 <- merge(stocks, stocks_msy, by = c("GSA", "Stock"), all.x = TRUE)
stocks2$Method <- NA
names(stocks2)[8] <- "Species"
stocks2 <- subset(stocks2, select = -Species.y)

# read assessment results from EWG 14-14
ewg14_14 <- read.csv("summary_assessments_ewg14_14.csv")

names(ewg14_14) <- c("Year", "value", "variable", "Meeting", "Stock", "Fmsy",
  "Comments", "GSA", "Method")

ewg <- cast(ewg14_14, Stock + Year + GSA + Comments + Fmsy + Meeting +
```

¹Coilin Minto. 2015. Testing model based indicators for monitoring the CFP performance. Ad-hoc contract report. pp 14

```

    Method ~ variable)
names(ewg) <- c("Stock", "Year", "GSA", "Comments", "Fmsy", "Meeting",
  "Method", "F", "Landings", "R", "SSB")
ewg$Species <- NA

# NEED TO UPDATE ASSESSMENTS FROM EWG 14_19, EWG 15_11 and 15_12, 15_19

temp2 <- rbind(stocks2, ewg)
temp2$key <- paste(temp2$Stock, temp2$GSA, temp2$Meeting, sep = "_")

```

2.2 Process the data

Emerging from the data preparation protocol, it is necessary to remove stock assessments that are obsolete or replaced by new area aggregations. Here we select stocks by the keys for species, area and meeting number.

```

obs <- c("ANE_17_STECF 13-19", "HKE_6_2011-11_STECF 11-14", "HKE_7_2013-11_STECF 13 -22",
  "HKE_9_2011-11_STECF 11-14", "MUT_6_STECF 13-19", "MUT_7_2012-11_STECF 12-19",
  "MUT_9_2013-04_STECF 13-05", "NEP_9_2011-11_STECF 11-14", "PIL_17_STECF 13-19",
  "WHB_6_2012-11_STECF 12-19", "WHB_9_2012-11_STECF 12-19")

temp3 <- temp2[!temp2$key %in% obs, ]

```

Discard assessment data from stock assessments that are not fully analytical e.g. VIT, SURBA etc and that have only 2-3 time points of estimates

```

discarded <- c("10_MTS", "15-16_ANK", "17_MTS", "18_MTS", "18_NEP", "25_MUT",
  "25_SPC", "9_MTS", "9_MUR", "9_POD")
discarded2 <- c("VIT", "VIT.", "VIT. ", "VIT. F is Fbar 1-3.", "VIT. F is Fbar 1-7.",
  "VIT. F is Fbar 3-7.", "SURBA")

temp3 <- temp3[!temp3$key %in% discarded, ]
temp3 <- temp3[!temp3$Comments %in% discarded2, ]

```

2.3 Compute $\frac{F}{F_{msy}}$

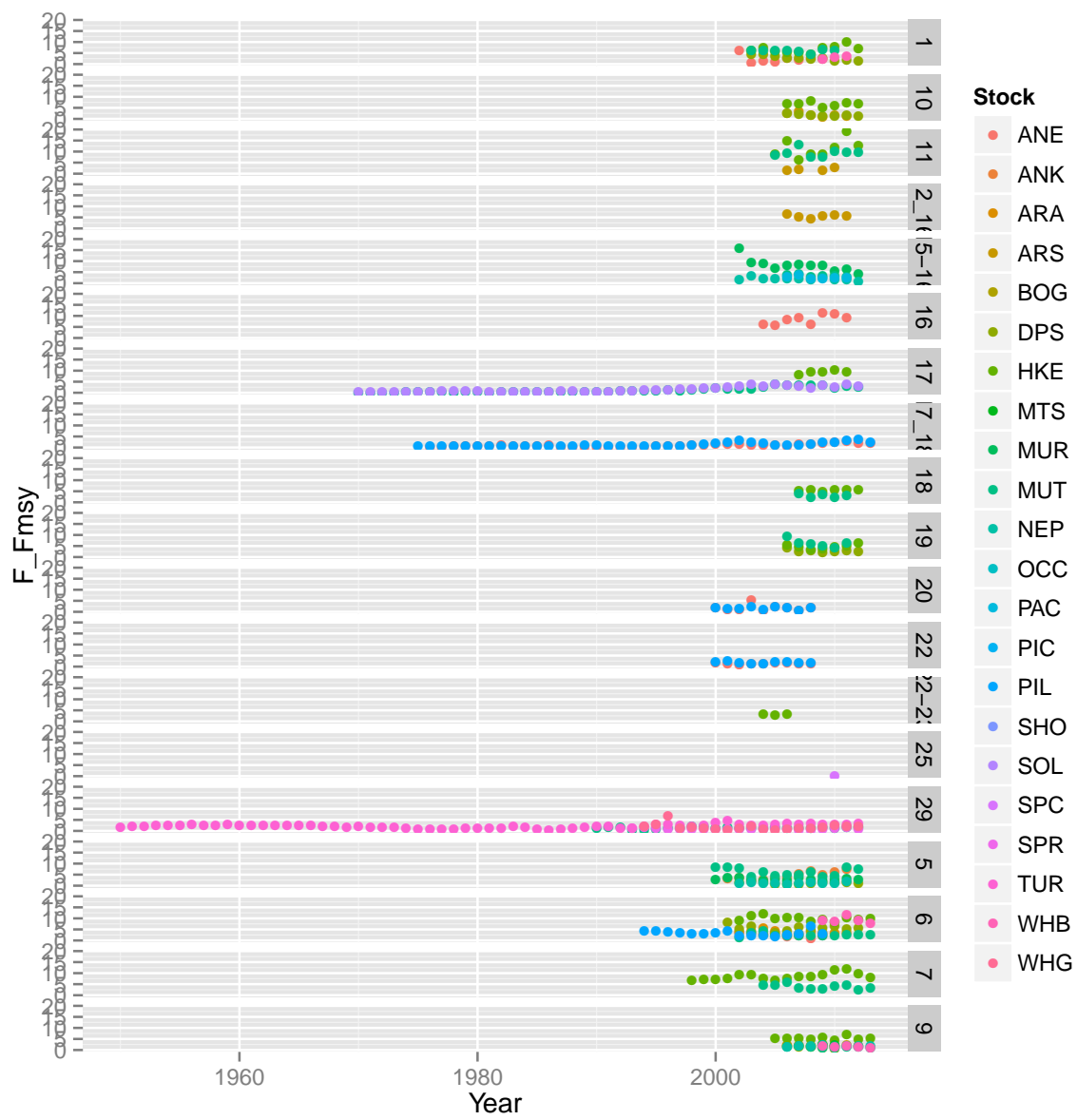
```

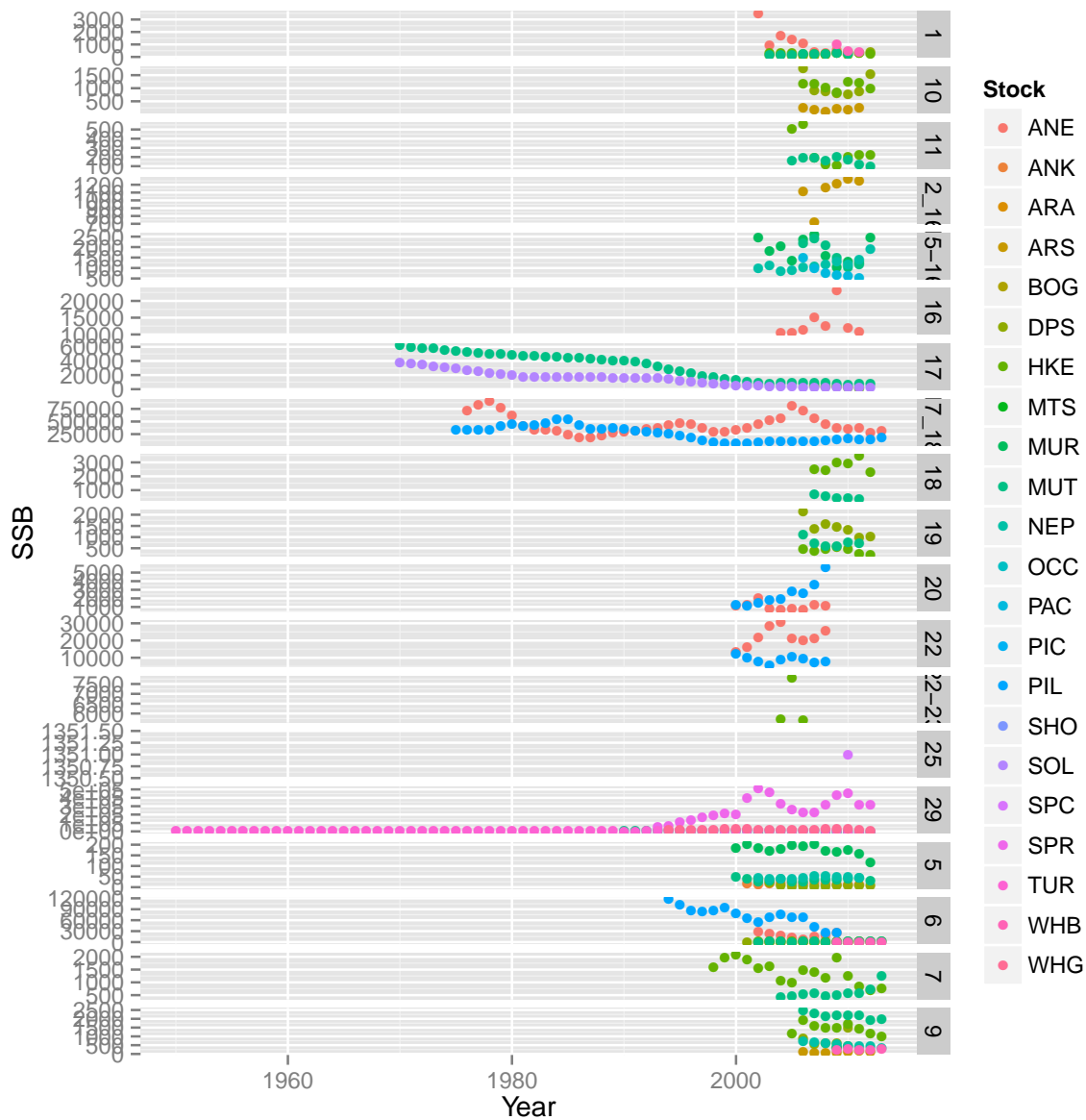
temp3$F_Fmsy <- temp3$F/temp3$Fmsy

species_groups_codes <- read.csv("species_groups_codes.csv", sep = ";")

temp3 <- merge(temp3, species_groups_codes, by.x = "Stock", by.y = "code",
  all.x = TRUE)
temp3$GSA <- as.character(temp3$GSA)
temp3$GSA <- ifelse(temp3$GSA == "dic-16", "12_16", temp3$GSA)
temp3$GSA <- as.factor(temp3$GSA)

```





Create a subset file with the variables of interest only and drop the Black Sea assessments (area 29).

```
groups <- subset(temp3, select = c("Year", "F_Fmsy", "GSA", "GROUP", "Stock",
  "key", "SSB"))
groups <- na.omit(groups)
groups <- droplevels(groups)
names(groups)[5] <- "species"

# remove Black Sea Area (29)
groups <- groups[!(groups$GSA == "29"), ]

groups$Stock2 <- paste(groups$GSA, groups$species, sep = "_")

# insert dummy variable for population scale prediction.
groups$dum1 <- rep(1, length(groups$Year))
```


3 Model Based indicator $\frac{F}{F_{msy}}$

Time series of $\frac{F}{F_{msy}}$ were built for each stock. A set of models were selected based on the simulation study and discussions therein.

- linear model
- linear mixed effects model with random intercept by stock
- GAMM with random intercept by stock
- GAMM with random intercept by GSA and species

To evaluate the models' fits, the usual diagnostics on residuals were used, together with the AIC and BIC. Furthermore, a test on the stability of the indicators with regards to changes in length of the time series, was carried out by fitting the models to 3 different periods, starting in 1950, 1980 and 2000, and all ending in 2013. The different indicators, computed for the period 2003 to 2013, were plotted and compared:

- 1950 - present => group 1
- 1980 - present => group 2
- 2000 - present => group 3

```
group1 <- groups[groups$Year > 1950, ]
group2 <- groups[groups$Year > 1980, ]
group3 <- groups[groups$Year > 2000, ]
```

3.1 Fit

```
# -----

# linear model
m1.1 <- glm(F_Fmsy ~ factor(Year), data = group1, family = Gamma("log"))
m1.2 <- glm(F_Fmsy ~ factor(Year), data = group2, family = Gamma("log"))
m1.3 <- glm(F_Fmsy ~ factor(Year), data = group3, family = Gamma("log"))

# -----

# linear mixed effects model with random intercept by stock
m2.1 <- gamm4(F_Fmsy ~ factor(Year), random = ~(1 | Stock2), data = group1,
  family = Gamma("log"))
m2.2 <- gamm4(F_Fmsy ~ factor(Year), random = ~(1 | Stock2), data = group2,
  family = Gamma("log"))
m2.3 <- gamm4(F_Fmsy ~ factor(Year), random = ~(1 | Stock2), data = group3,
  family = Gamma("log"))

# -----

# GAMM with random intercept by stock
m3.1 <- gamm4(F_Fmsy ~ s(Year), random = ~(1 | Stock2), data = group1,
  family = Gamma("log"))
m3.2 <- gamm4(F_Fmsy ~ s(Year), random = ~(1 | Stock2), data = group2,
  family = Gamma("log"))
```

```

m3.3 <- gamm4(F_Fmsy ~ s(Year), random = ~(1 | Stock2), data = group3,
  family = Gamma("log"))

# -----

# GAMM with random intercept by GSA and species
m4.1 <- gamm4(F_Fmsy ~ s(Year), random = ~(1 | GSA) + (1 | species), data = group1,
  family = Gamma("log"))
m4.2 <- gamm4(F_Fmsy ~ s(Year), random = ~(1 | GSA) + (1 | species), data = group2,
  family = Gamma("log"))
m4.3 <- gamm4(F_Fmsy ~ s(Year), random = ~(1 | GSA) + (1 | species), data = group3,
  family = Gamma("log"))

# -----

# all together !
mods <- list(m1.1, m2.1, m3.1, m4.1, m1.2, m2.2, m3.2, m4.2, m1.3, m2.3,
  m3.3, m4.3)
names(mods) <- c("m1.1", "m2.1", "m3.1", "m4.1", "m1.2", "m2.2", "m3.2",
  "m4.2", "m1.3", "m2.3", "m3.3", "m4.3")

```

3.2 Compare

```

gamms <- grep("m1.", names(mods))
yrs <- 2003:2013

```

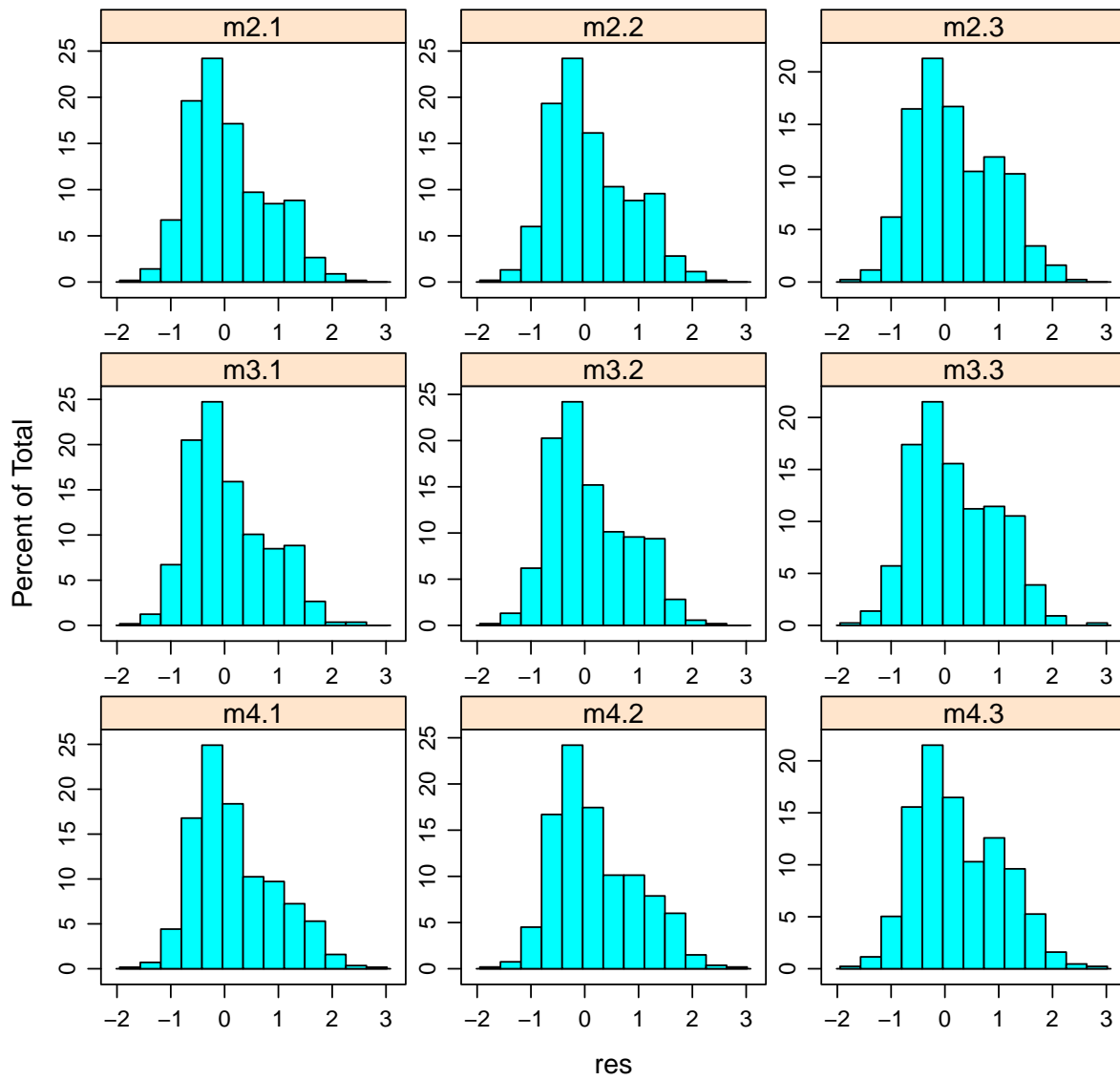
3.2.1 Residuals

```

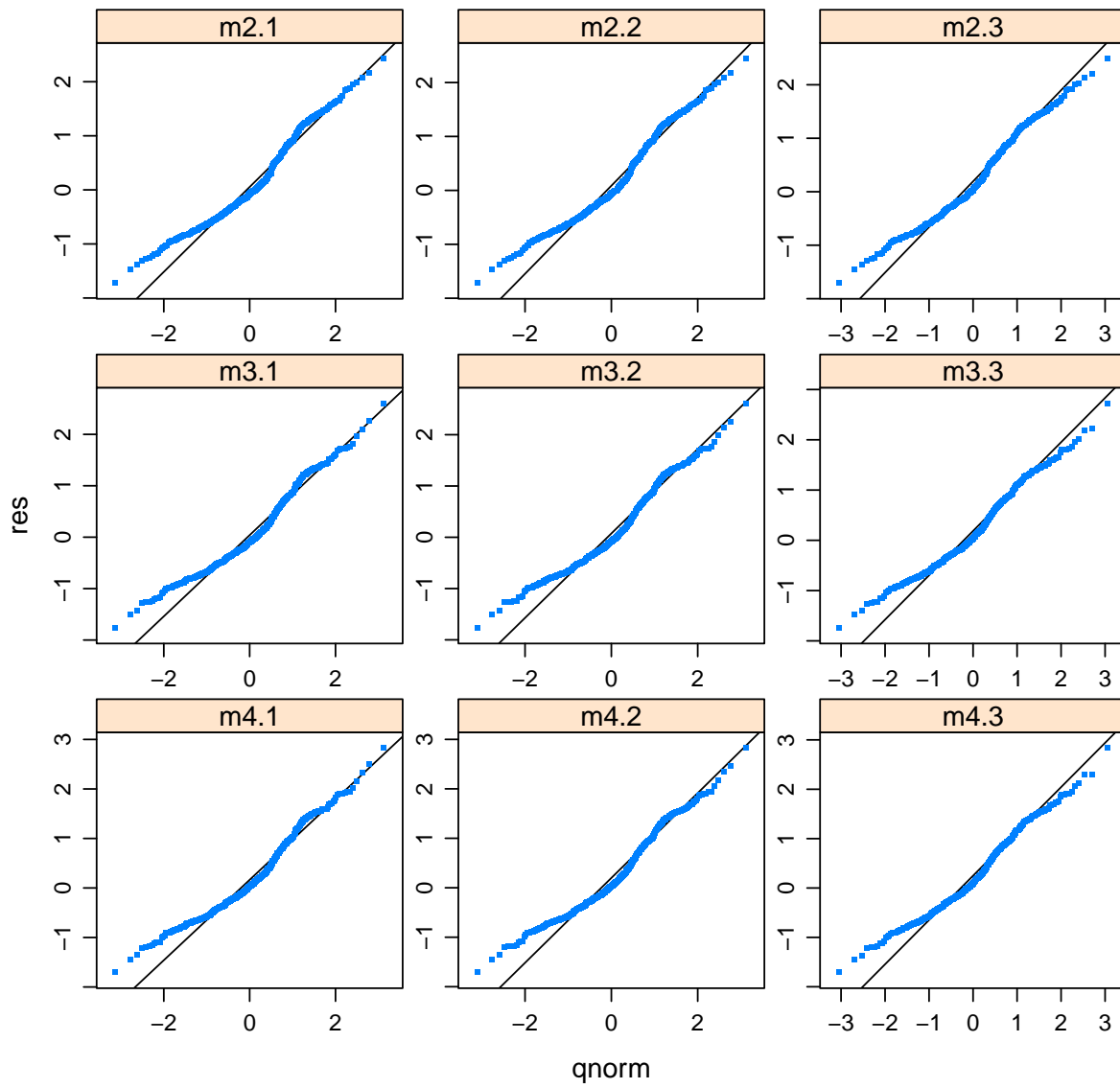
res <- lapply(mods[-gamms], function(x) data.frame(res = residuals(x$gam),
  pred = predict(x$gam)))
mod <- rep(names(mods)[-gamms], unlist(lapply(res, nrow)))
res <- do.call("rbind", res)
res$mod <- mod

```

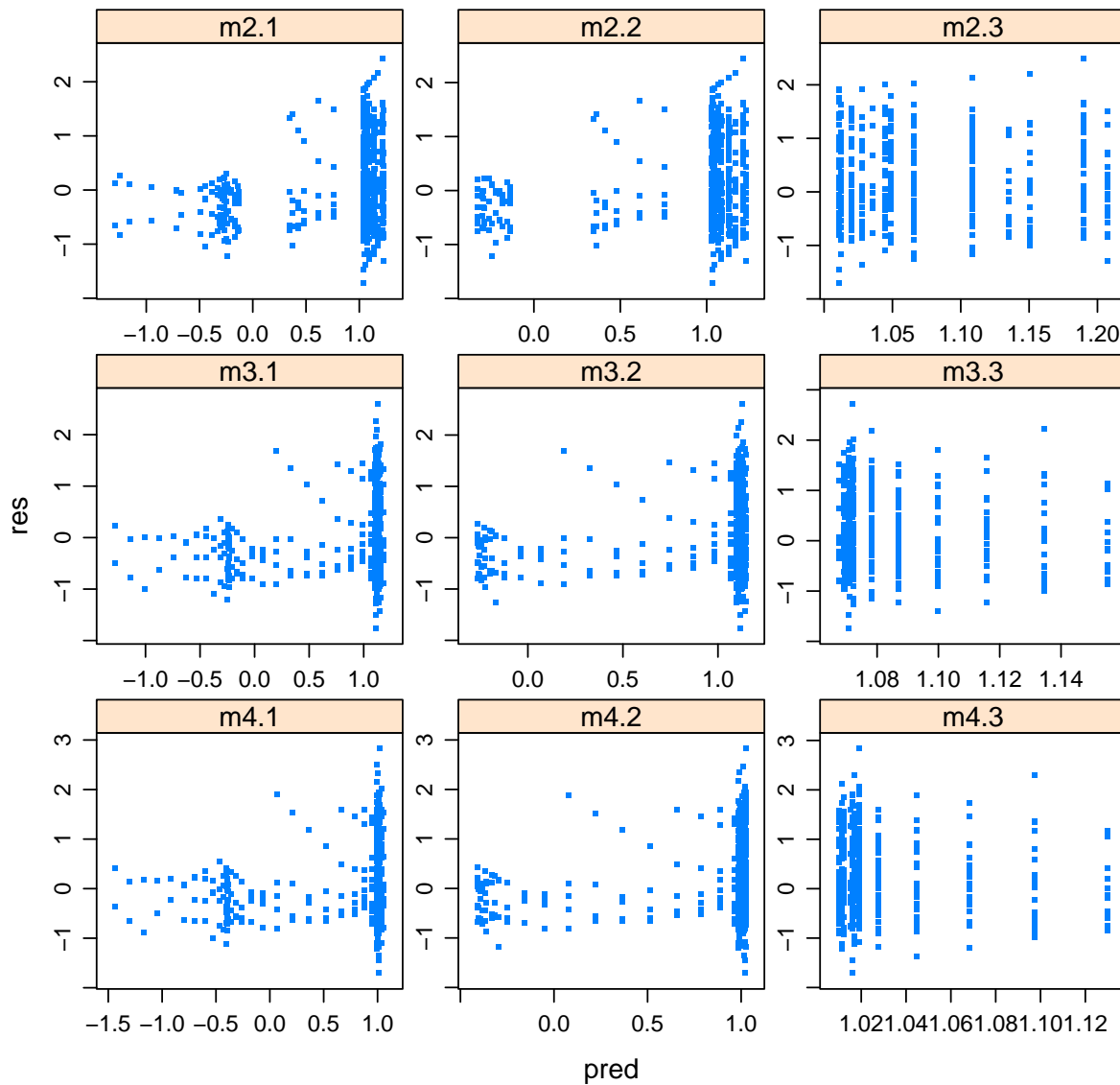
GAM term residuals distribution by model



GAM term residuals quantile plot by model

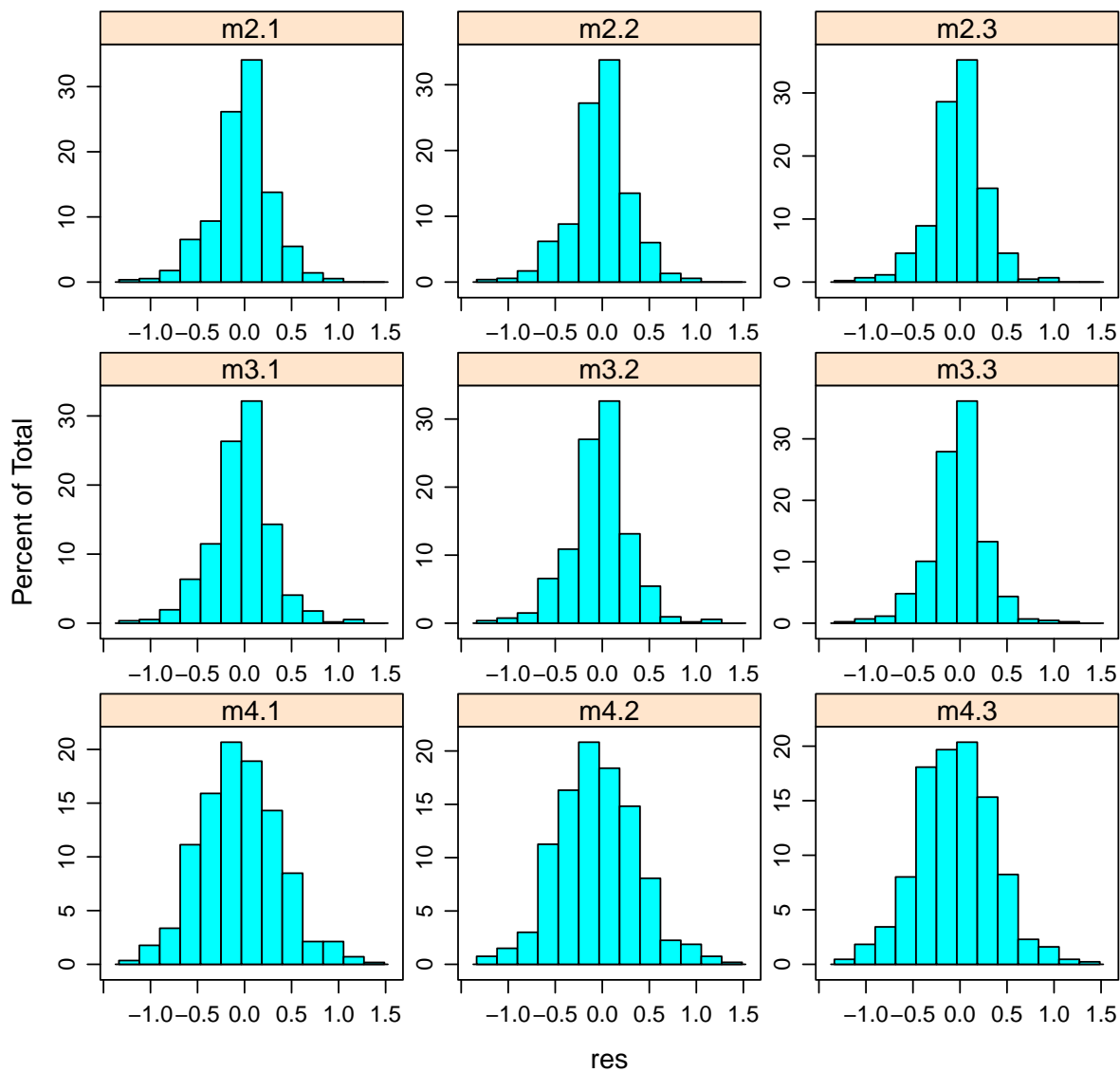


GAM term residuals versus predictions by model

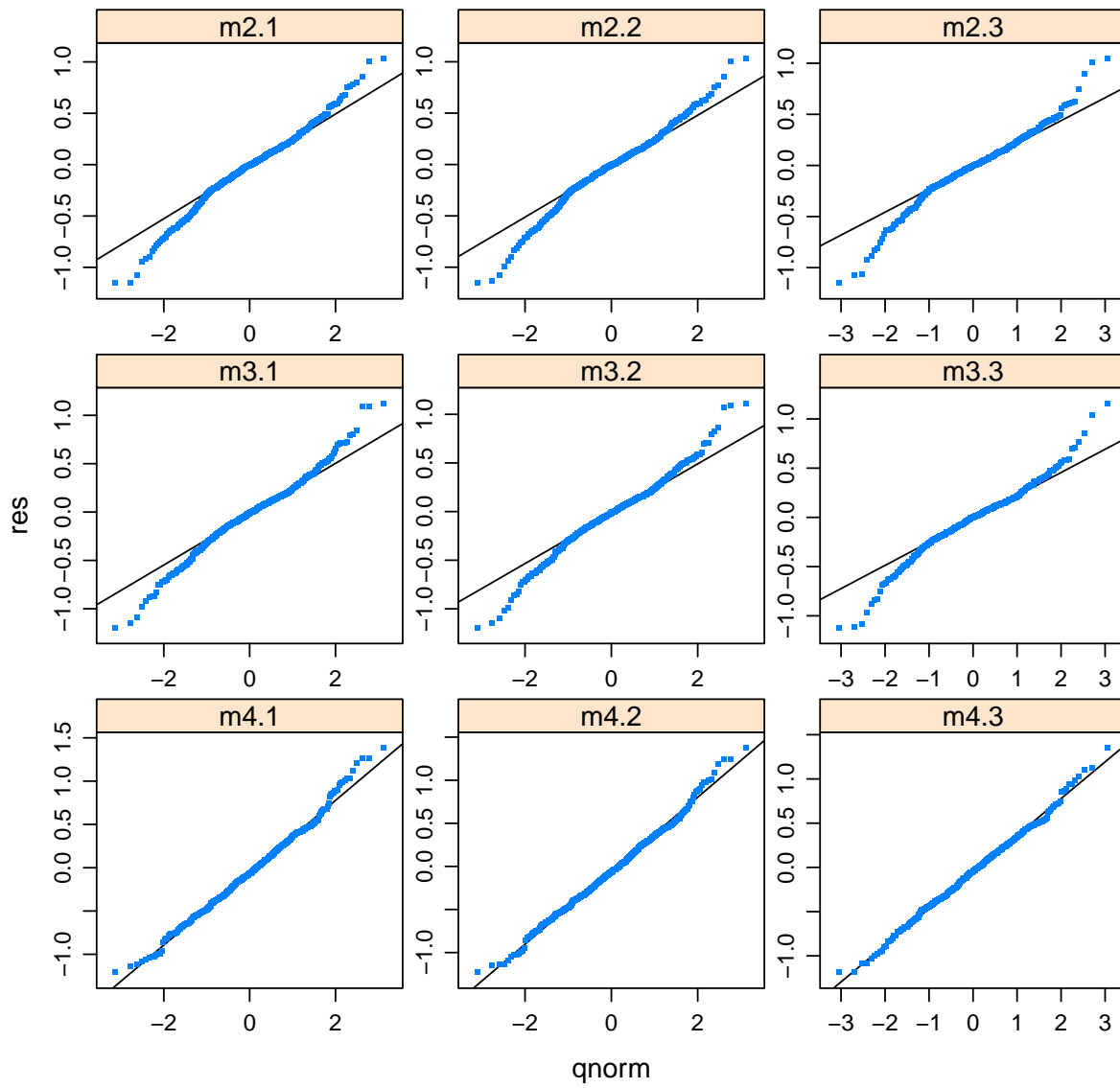


```
res <- lapply(mods[-gamms], function(x) data.frame(res = residuals(x$mer),
  pred = predict(x$mer)))
mod <- rep(names(mods)[-gamms], unlist(lapply(res, nrow)))
res <- do.call("rbind", res)
res$mod <- mod
```

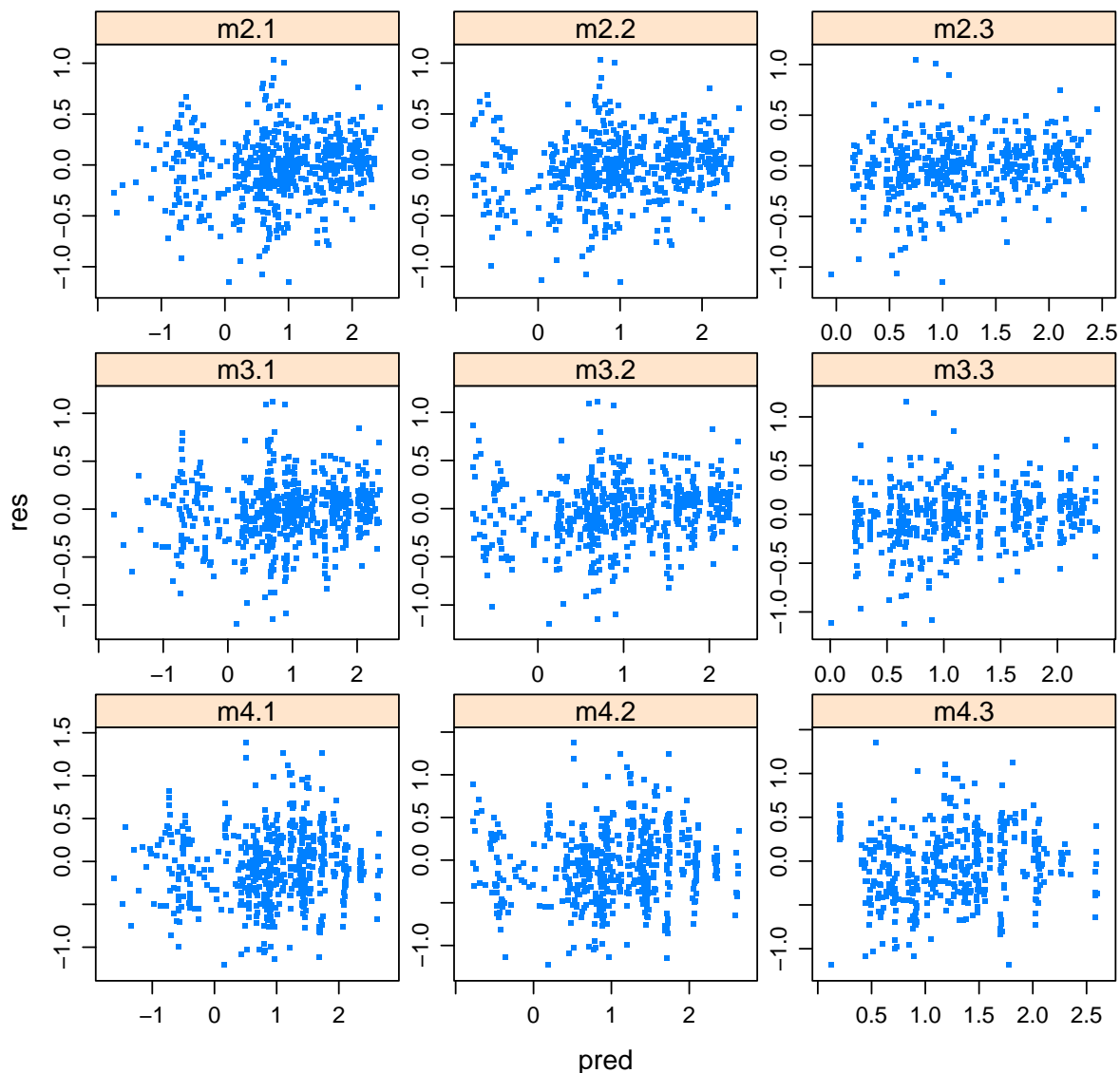
Random effect residuals distribution by model



Random effect residuals quantile plot by model



Random effect residuals versus predictions by model



3.2.2 Robustness to time window

```
pred <- list()
length(pred) <- length(mods)
names(pred) <- names(mods)

pred[-gamms] <- lapply(mods[-gamms], function(x) {
  data.frame(year = 2003:2013, pred = predict(x$gam, newdata = data.frame(Year = yrs),
    type = "response"))
})

pred[gamms] <- lapply(mods[gamms], function(x) {
  data.frame(year = 2003:2013, pred = predict(x, newdata = data.frame(Year = yrs),
    type = "response"))
})

mod <- rep(names(mods), unlist(lapply(pred, nrow)))
pred <- do.call("rbind", pred)
```

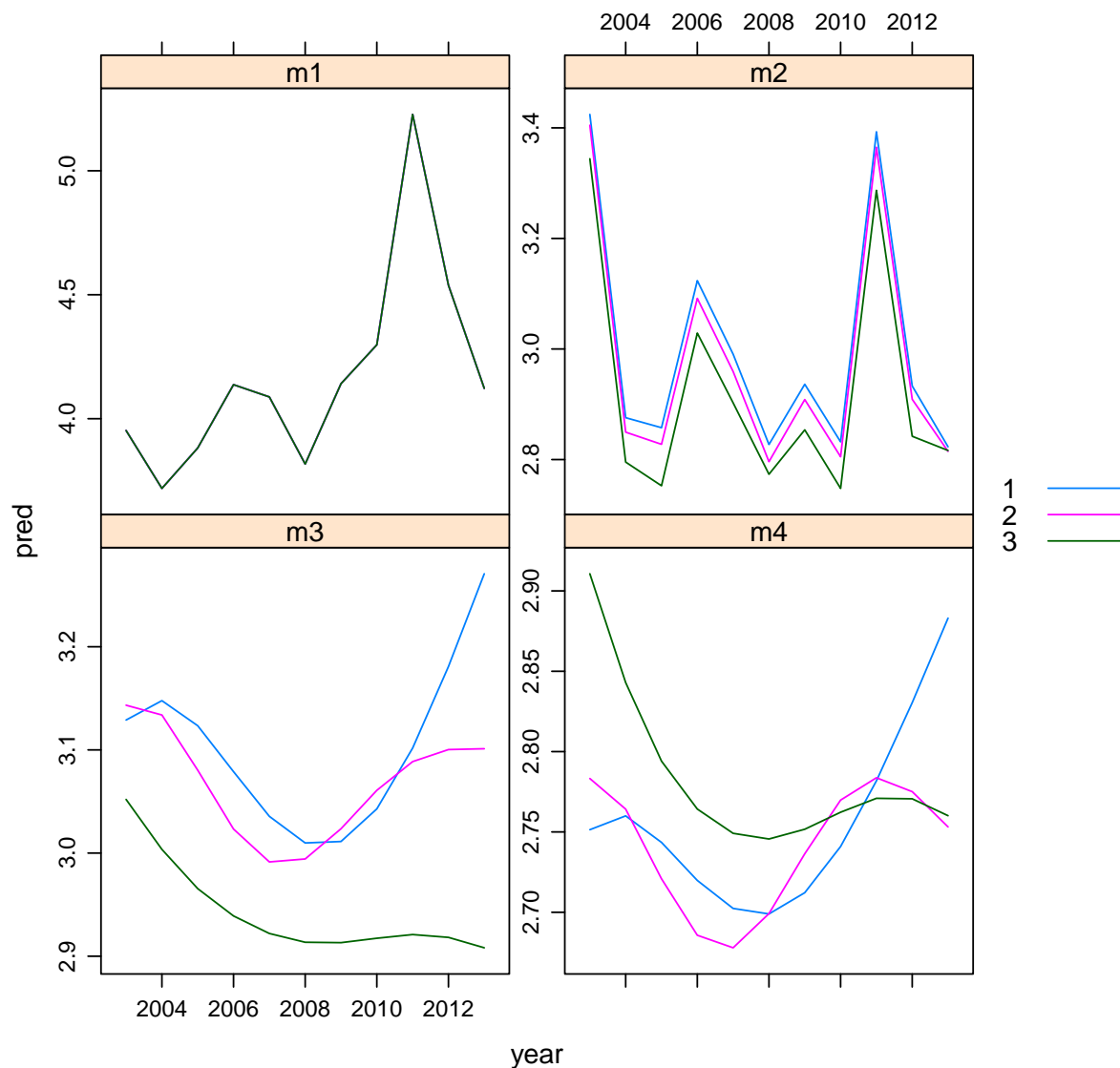


```

pred$mod <- mod
pred$twinn <- unlist(lapply(strsplit(mod, "\\."), "[", 2))
pred$mod <- unlist(lapply(strsplit(mod, "\\."), "[", 1))

```

Stability of the indicator to different time series lengths



3.2.3 AIC and BIC of random effects term

```

aic <- rbind(AIC(m1.1, m2.1$mer, m3.1$mer, m4.1$mer), AIC(m1.2, m2.2$mer,
  m3.2$mer, m4.2$mer), AIC(m1.3, m2.3$mer, m3.3$mer, m4.3$mer))

aic$BIC <- rbind(BIC(m1.1, m2.1$mer, m3.1$mer, m4.1$mer), BIC(m1.2, m2.2$mer,
  m3.2$mer, m4.2$mer), BIC(m1.3, m2.3$mer, m3.3$mer, m4.3$mer))$BIC

```

```

kable(aic[order(aic$BIC), ])

```

	df	AIC	BIC
m3.3\$mer	5	1364.462	1384.861
m2.3\$mer	15	1364.731	1425.930
m3.1\$mer	5	1459.819	1481.512
m3.2\$mer	5	1490.123	1511.515
m4.3\$mer	6	1599.659	1624.139
m2.2\$mer	35	1504.983	1654.731
m2.1\$mer	46	1487.484	1687.059
m4.1\$mer	6	1715.015	1741.046
m4.2\$mer	6	1735.549	1761.221
m1.3	14	2021.274	2078.393
m1.2	34	2213.645	2359.114
m1.1	45	2221.482	2416.719

3.3 Predict

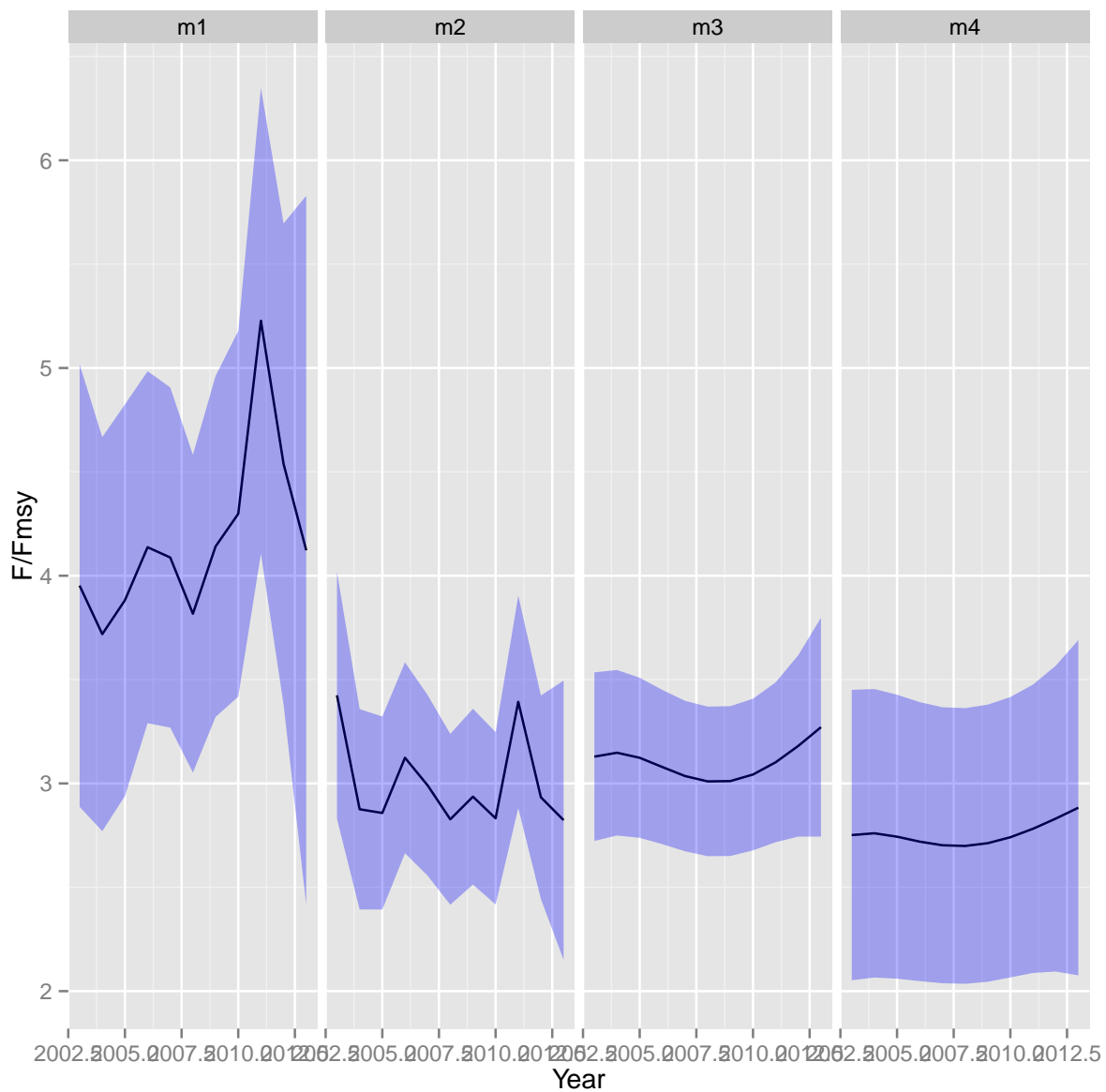
To output model fits on the scale of F/Fmsy it is necessary to predict on the responde scale and at popolation level. Here the prediction, for the specific sake of monitoring the implementation of the CFP, is restricted to the period 2003-2013.

```
newdata <- expand.grid(Year = seq(2003, 2013, 1), dum1 = 0)

mvec <- list(m1 = m1.1, m2 = m2.1$gam, m3 = m3.1$gam, m4 = m4.1$gam)
res <- mvec

for (i in 1:length(mvec)) {
  # i <-2
  frpred <- predict(mvec[[i]], newdata, type = "response", se.fit = TRUE,
    re.form = NA)
  fit <- frpred$fit
  SE <- frpred$se.fit
  new <- cbind(fit, newdata)
  new$se.up <- (fit + (1.96 * SE))
  new$se.lo <- (fit - (1.96 * SE))
  new$model <- names(mvec[i])
  res[[i]] <- new
}

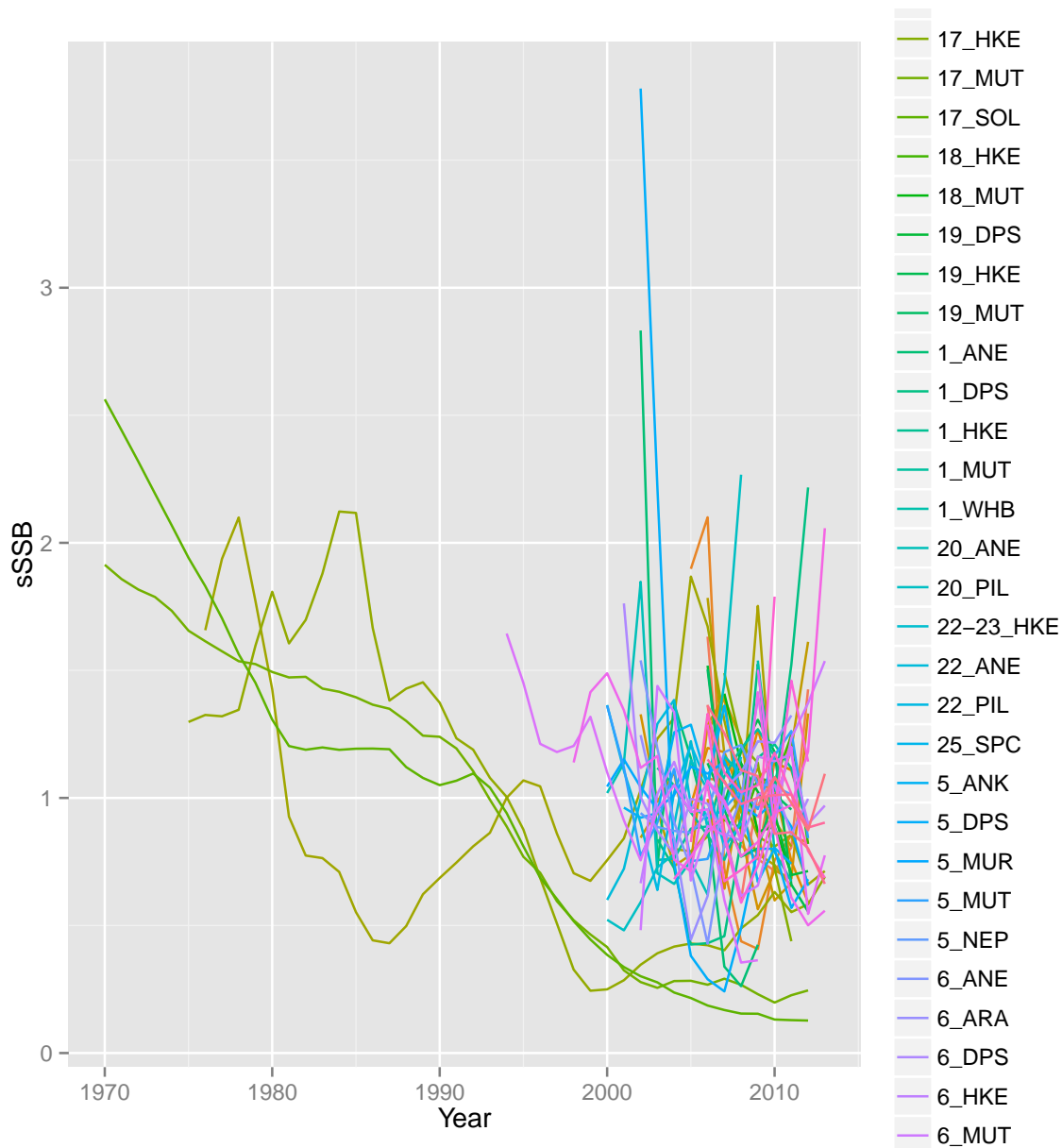
res.df2 <- do.call(rbind, res)
```



4 Model based indicator for SSB

The second set of model based indicators is applied to the Spawning Stock Biomass (SSB). The objective is understanding if trends in SSB can be reliably detected. Since no reference points for SSB (SSB_{msy}) are available for the Mediterranean stocks it is not possible to determine the level of SSB depletion.

```
# take the groups data frame and scale the SSB/mean(SSB) by stock
groupsSSB <- ddply(groups, .(Stock2), transform, sSSB = (SSB/mean(SSB,
  na.rm = TRUE)))
```



```
group1ssb <- groupsSSB[groupsSSB$Year > 1950, ]
group2ssb <- groupsSSB[groupsSSB$Year > 1980, ]
group3ssb <- groupsSSB[groupsSSB$Year > 2000, ]
```

Fit

```
# -----

# linear model
m1.1sb <- glm(sSSB ~ factor(Year), data = group1ssb)
m1.2sb <- glm(sSSB ~ factor(Year), data = group2ssb)
m1.3sb <- glm(sSSB ~ factor(Year), data = group3ssb)

# -----

# linear mixed effects model with random intercept by stock
m2.1sb <- gamm4(sSSB ~ factor(Year), random = ~(1 | Stock2), data = group1ssb)
```

```

m2.2sb <- gamm4(sSSB ~ factor(Year), random = ~(1 | Stock2), data = group2ssb)
m2.3sb <- gamm4(sSSB ~ factor(Year), random = ~(1 | Stock2), data = group3ssb)

# -----

# GAMM with random intercept by stock
m3.1sb <- gamm4(sSSB ~ s(Year), random = ~(1 | Stock2), data = group1ssb)
m3.2sb <- gamm4(sSSB ~ s(Year), random = ~(1 | Stock2), data = group2ssb)
m3.3sb <- gamm4(sSSB ~ s(Year), random = ~(1 | Stock2), data = group3ssb)

# -----

# GAMM with random intercept by GSA and species
m4.1sb <- gamm4(sSSB ~ s(Year), random = ~(1 | GSA) + (1 | species), data = group1ssb)
m4.2sb <- gamm4(sSSB ~ s(Year), random = ~(1 | GSA) + (1 | species), data = group2ssb)
m4.3sb <- gamm4(sSSB ~ s(Year), random = ~(1 | GSA) + (1 | species), data = group3ssb)

# -----

# all together !
mods <- list(m1.1sb, m2.1sb, m3.1sb, m4.1sb, m1.2sb, m2.2sb, m3.2sb, m4.2sb,
            m1.3sb, m2.3sb, m3.3sb, m4.3sb)
names(mods) <- c("m1.1", "m2.1", "m3.1", "m4.1", "m1.2", "m2.2", "m3.2",
               "m4.2", "m1.3", "m2.3", "m3.3", "m4.3")

```

4.1 Compare

```

gamms <- grep("m1.", names(mods))
yrs <- 2003:2013

```

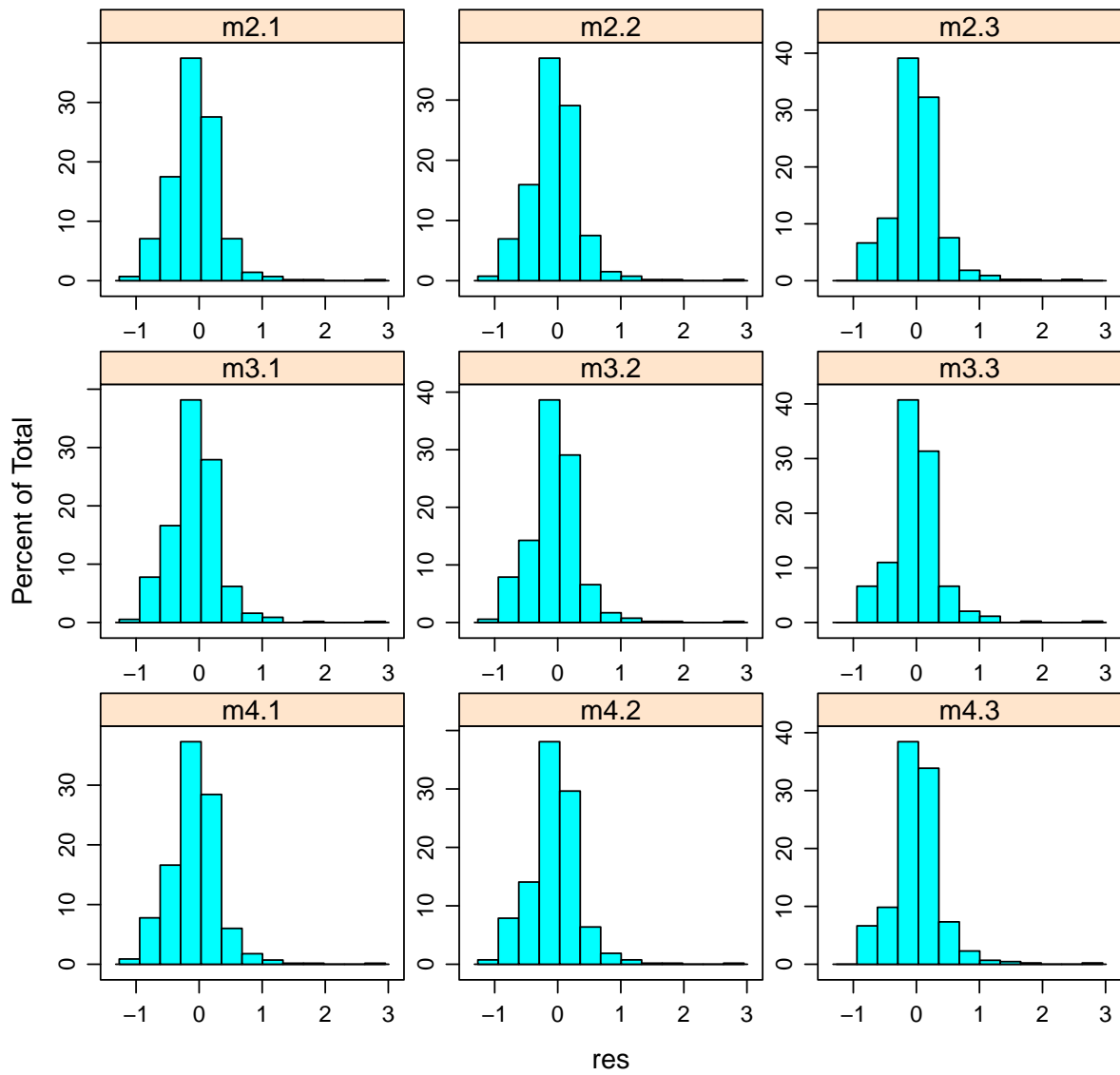
4.1.1 Residuals

```

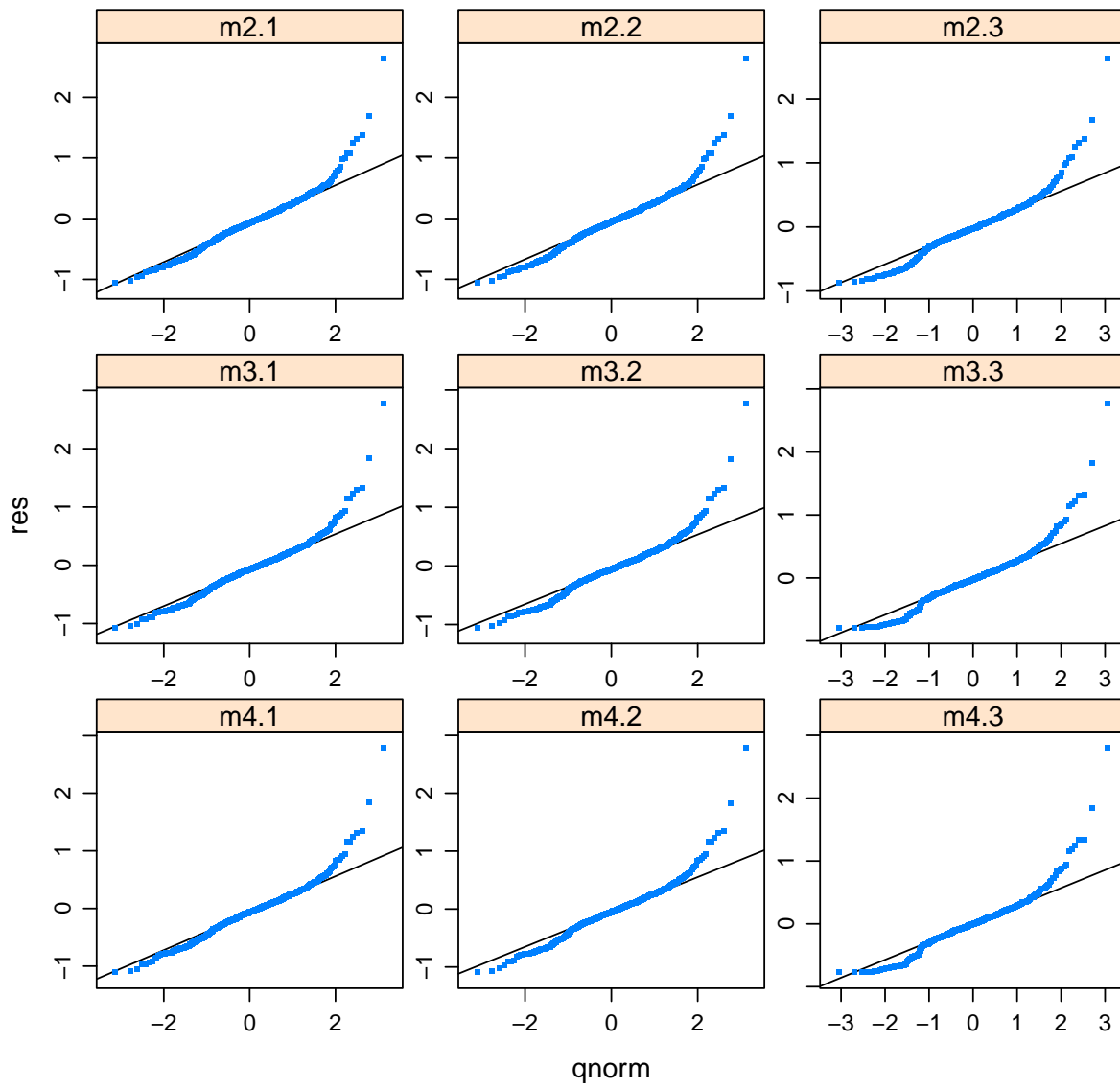
res <- lapply(mods[-gamms], function(x) data.frame(res = residuals(x$gam),
            pred = predict(x$gam)))
mod <- rep(names(mods)[-gamms], unlist(lapply(res, nrow)))
res <- do.call("rbind", res)
res$mod <- mod

```

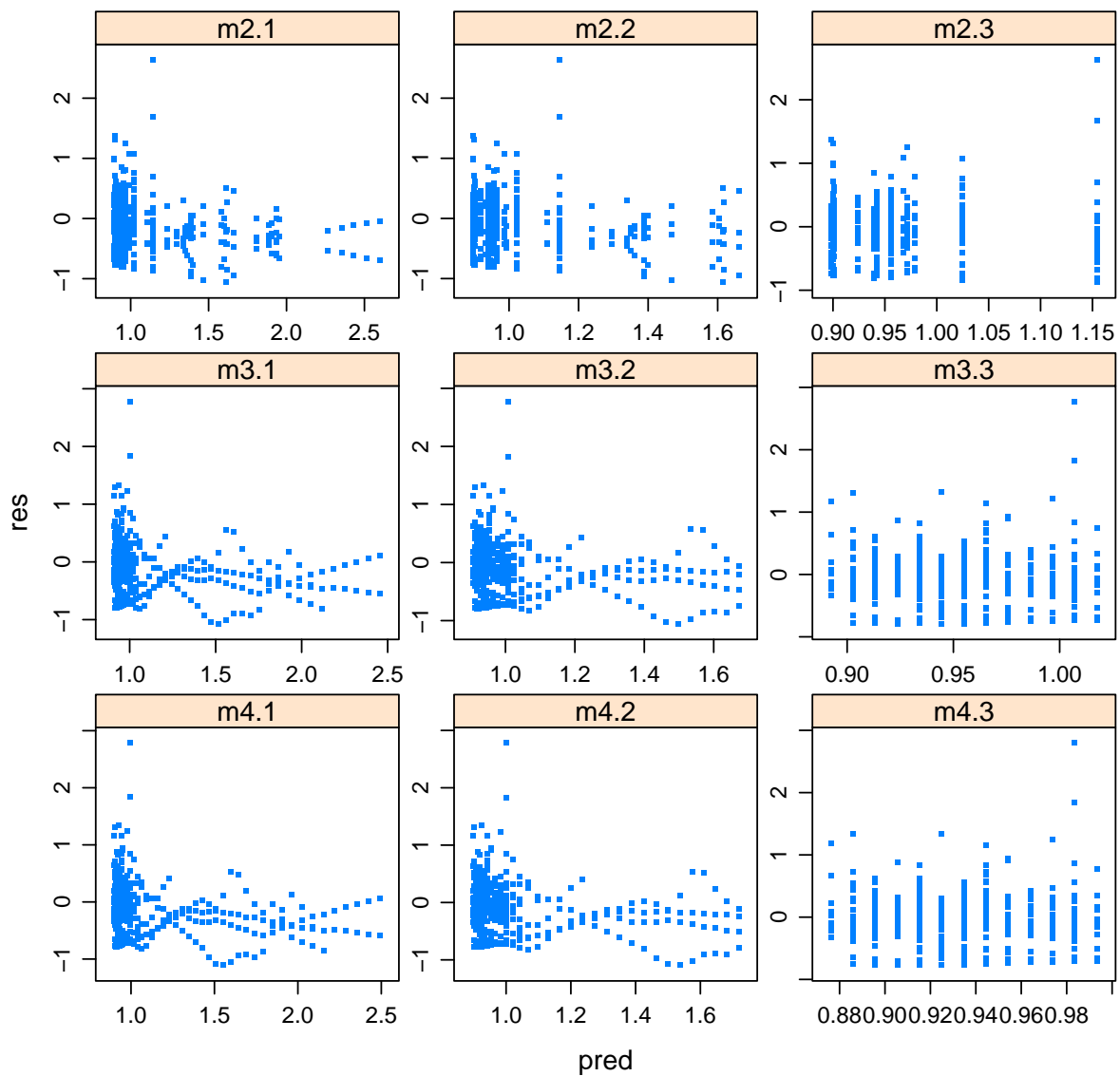
GAM term residuals distribution by model



GAM term residuals quantile plot by model

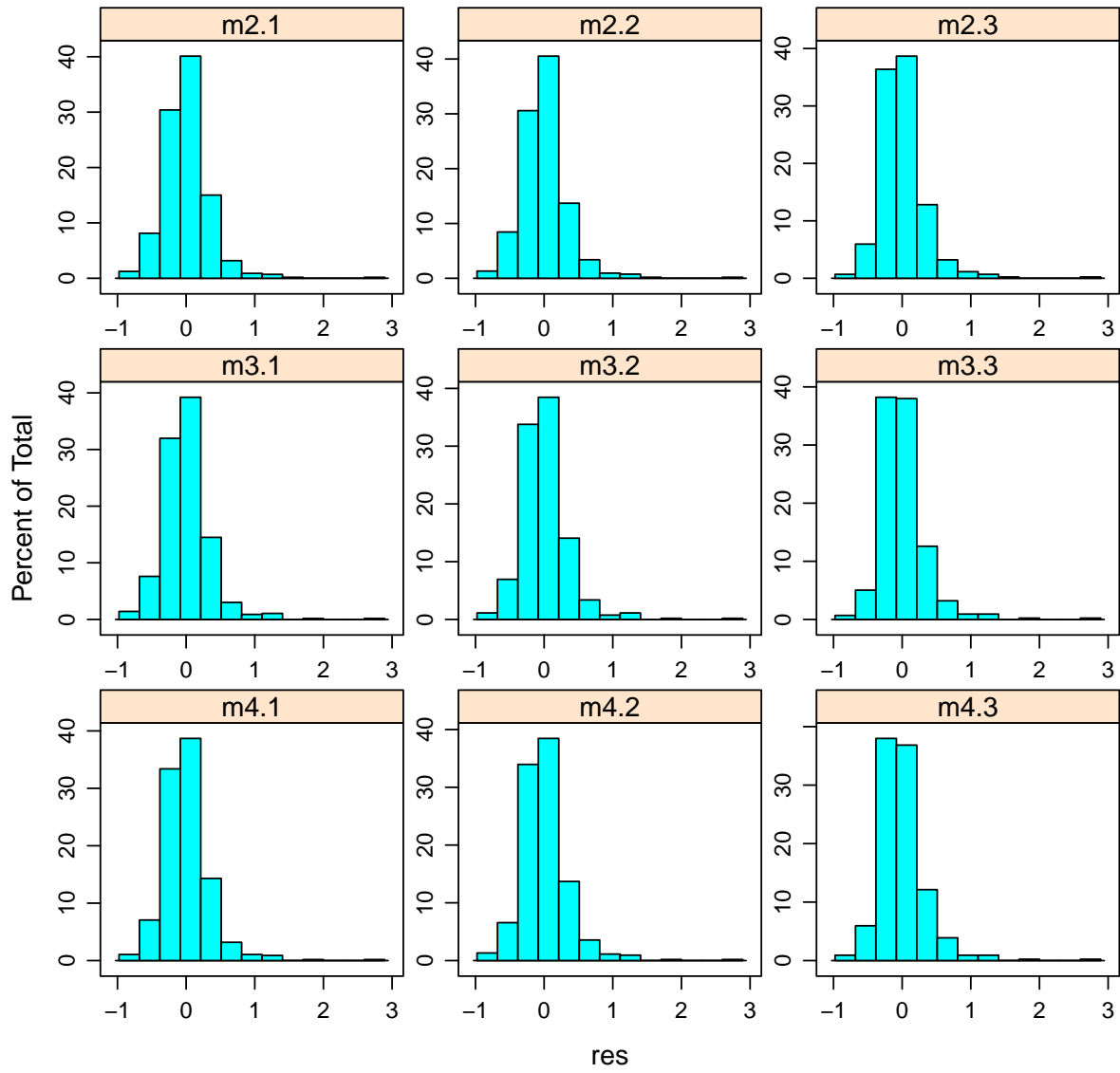


GAM term residuals versus predictions by model

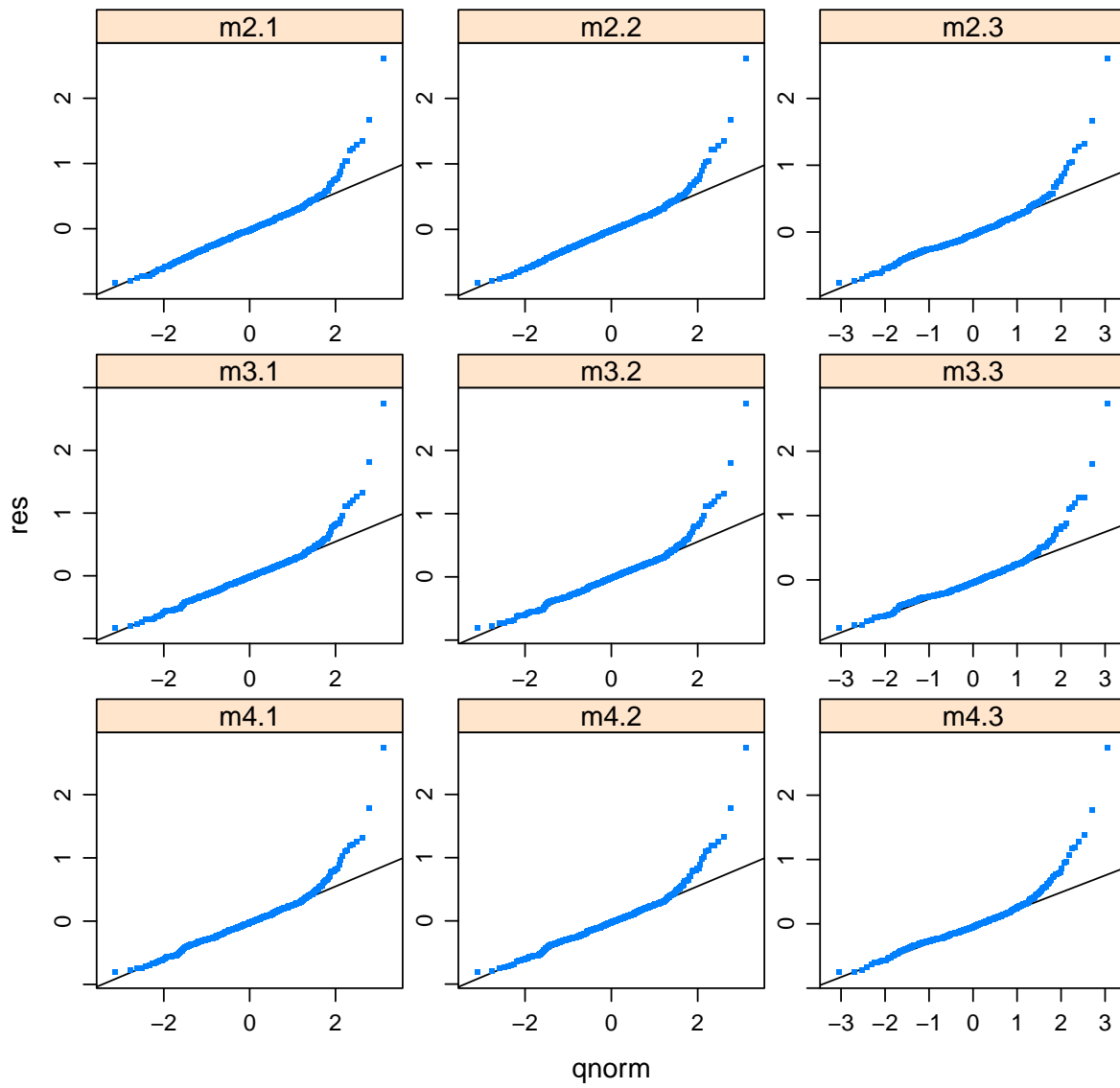


```
res <- lapply(mods[-gamms], function(x) data.frame(res = residuals(x$mer),
  pred = predict(x$mer)))
mod <- rep(names(mods)[-gamms], unlist(lapply(res, nrow)))
res <- do.call("rbind", res)
res$mod <- mod
```

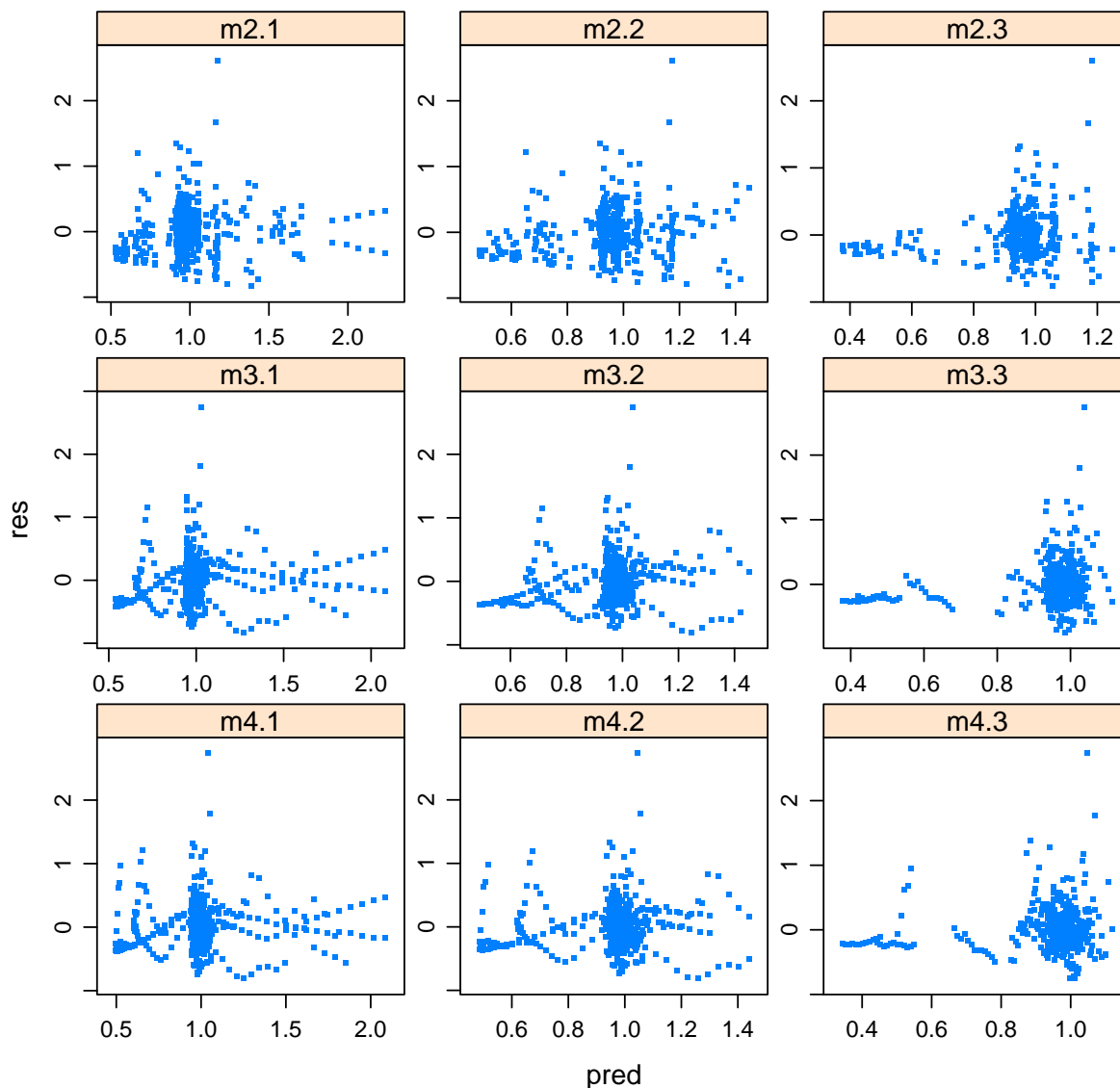

Random effect residuals distribution by model



Random effect residuals quantile plot by model



Random effect residuals versus predictions by model



4.1.2 Robustness to time window

```

pred <- list()
length(pred) <- length(mods)
names(pred) <- names(mods)

pred[-gamms] <- lapply(mods[-gamms], function(x) {
  data.frame(year = 2003:2013, pred = predict(x$gam, newdata = data.frame(Year = yrs),
    type = "response"))
})

pred[gamms] <- lapply(mods[gamms], function(x) {
  data.frame(year = 2003:2013, pred = predict(x, newdata = data.frame(Year = yrs),
    type = "response"))
})

mod <- rep(names(mods), unlist(lapply(pred, nrow)))
pred <- do.call("rbind", pred)

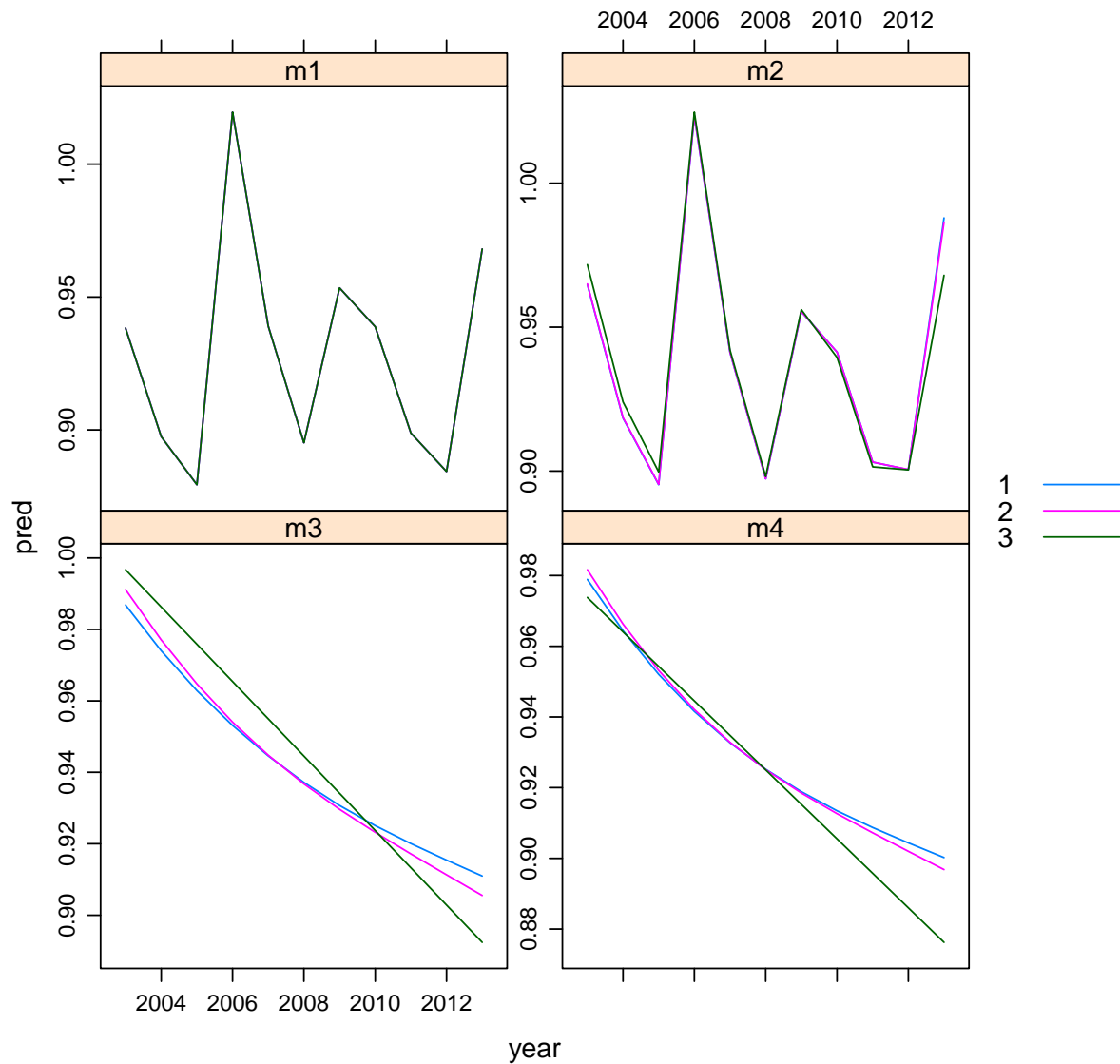
```

```

pred$mod <- mod
pred$twinn <- unlist(lapply(strsplit(mod, "\\."), "[", 2))
pred$mod <- unlist(lapply(strsplit(mod, "\\."), "[", 1))

```

Stability of the indicator to different time series lengths



4.1.3 AIC and BIC of random effects term

```

aic <- rbind(AIC(m1.1, m2.1$mer, m3.1$mer, m4.1$mer), AIC(m1.2, m2.2$mer,
  m3.2$mer, m4.2$mer), AIC(m1.3, m2.3$mer, m3.3$mer, m4.3$mer))

aic$BIC <- rbind(BIC(m1.1, m2.1$mer, m3.1$mer, m4.1$mer), BIC(m1.2, m2.2$mer,
  m3.2$mer, m4.2$mer), BIC(m1.3, m2.3$mer, m3.3$mer, m4.3$mer))$BIC

```

```

kable(aic[order(aic$BIC), ])

```

	df	AIC	BIC
m3.3\$mer	5	1364.462	1384.861
m2.3\$mer	15	1364.731	1425.930
m3.1\$mer	5	1459.819	1481.512
m3.2\$mer	5	1490.123	1511.515
m4.3\$mer	6	1599.659	1624.139
m2.2\$mer	35	1504.983	1654.731
m2.1\$mer	46	1487.484	1687.059
m4.1\$mer	6	1715.015	1741.046
m4.2\$mer	6	1735.549	1761.221
m1.3	14	2021.274	2078.393
m1.2	34	2213.645	2359.114
m1.1	45	2221.482	2416.719

4.2 Predict

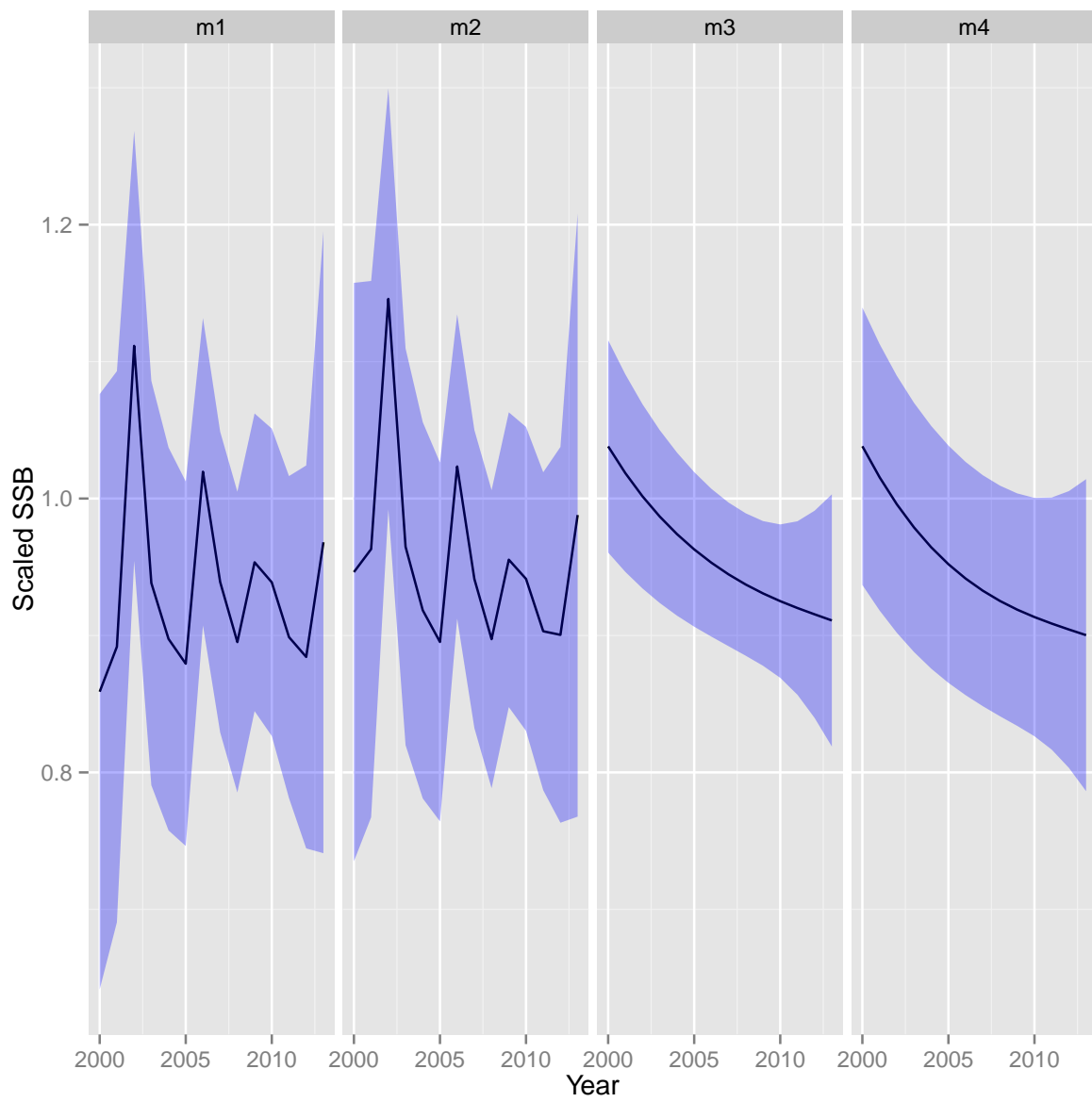
```

newdata <- expand.grid(Year = seq(2000, 2013, 1), dum1 = 0)
mvec_ssb <- list(m1 = m1.1sb, m2 = m2.1sb$gam, m3 = m3.1sb$gam, m4 = m4.1sb$gam)
res_ssb <- mvec_ssb

for (i in 1:length(mvec_ssb)) {
  # i <-2
  frpred <- predict(mvec_ssb[[i]], newdata, type = "response", se.fit = TRUE,
    re.form = NA)
  fit <- frpred$fit
  SE <- frpred$se.fit
  new <- cbind(fit, newdata)
  new$se.up <- (fit + (1.96 * SE))
  new$se.lo <- (fit - (1.96 * SE))
  new$model <- names(mvec[i])
  res_ssb[[i]] <- new
}

res_ssb <- do.call(rbind, res_ssb)
res_ssb <- res_ssb[res_ssb$model %in% c("m1", "m2", "m3", "m4"), ]

```



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