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a4a short research project

# **Stock Assessment of Hellenic Small Pelagic Stocks**

Ernesto JARDIM (Editor), Marianna GIANNOULAKI, Maria-Mirto PIROUNAKI,  
Konstantinos TSAGARAKIS, Giacomo-Chato OSIO, Finlay SCOTT, and Dimitrios DAMALAS

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Institute for the Protection and Security of the Citizen (IPSC)

#### Contact information

Ernesto Jardim

Address: Maritime Affairs Unit, Via Enrico Fermi 2749, 21027Ispra VA, Italy

E-mail: [ernesto.jardim@jrc.ec.europa.eu](mailto:ernesto.jardim@jrc.ec.europa.eu)

Tel.: 0039 0332 785311

Fax: 0039 0332 789658

<https://stecf.jrc.ec.europa.eu/home>

<http://ipsc.jrc.ec.europa.eu/>

<http://www.jrc.ec.europa.eu/>

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#### Abstract

With the objective of applying the a4a methods to real life situations the JRC held a Workshop on stock assessment for the Hellenic small pelagic stocks in the Aegean Sea (JRC, Italy) between the 4th and 7th of May 2015. The main objectives were to compare assessment models and incorporate environmental indices into stock forecasts.

a4a short research project  
Stock Assessment of Hellenic Small Pelagic Stocks

Ernesto Jardim (Editor)<sup>1</sup>, Marianna Giannoulaki<sup>2</sup>, Maria-Mirto Pirounaki<sup>2</sup>,  
Konstantinos Tsagarakis<sup>3</sup>, Giacomo-Chato Osio<sup>1</sup>, Finlay Scott<sup>1</sup>, and  
Dimitrios Damalas<sup>1</sup>

<sup>1</sup>*European Commission, Joint Research Centre, IPSC / Maritime Affairs  
Unit, 21027 Ispra (VA), Italy*

<sup>2</sup>*HCMR, Institute for Marine Biological Resources, Herakleion-Crete,  
GREECE*

<sup>3</sup>*HCMR, Institute for Marine Biological Resources, Athens, GREECE*

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# 1 Introduction

Under the scope of the a4a Initiative, the JRC is promoting cooperative activities between fisheries scientists with the aim to test, disseminate and promote a4a methods. These Small Research Projects (SRP) are focus on comparing the results of assessments from other models to assessments obtained from the a4a statistical catch-at-age model, and explore research questions using case studies.

The Workshop dedicated to the Hellenic small pelagic stocks took place in Ispra, Italy, the 4th to the 7th of May 2015. The main objectives were to investigate the performance of a4a on poor data stocks, like the ones under study, and furthermore fill data gaps in the time series by incorporating information from other potentially influential external indices.

## 1.1 ToRs and Agenda

The terms of reference of the workshop were:

1. Assess the stocks of sardine and anchovy in GSAs 20 & 22 with a4a and compare results with other stock assessment models.
2. Develop forecast scenario considering requirements of multi-annual management plans.
3. Report to STECF and other relevant management bodies.

The first day of the workshop was dedicated to identify which of the historical data series were worth including in the analyses and examine the pros and cons of each one. In the second day a thorough investigation of all available environmental indices allowed for identifying the correlations amongst them and exclude redundant ones. The initial inspection of the data series revealed that only sardine and anchovy in the Aegean sea (GSA 22) were feasible to assess, while the Ionian sea stocks (GSA 20) were dropped due to great deficiencies in the data series. The first runs with the a4a statistical catch-at-age method on the stocks of sardine and anchovy were made possible. The third and fourth day were dedicated in tweaking the models assuming different catchability and fishing mortalities scenarios as well as using the most relevant environmental index. As an outcome long and short-term model runs were compared for consistency in results.

## 1.2 The a4a Initiative

The volume and availability of data useful for fisheries stock assessment is continually increasing. Time series of traditional sources of information, such as surveys and landings data are not only getting longer, but also cover an increasing number of species.

For example, in Europe the 2009 revision of the Data Collection Regulation (EU, 2008a) has changed the focus of fisheries sampling programmes away from providing data for individual assessments of key stocks (i.e. those that are economically important) to documenting fishing trips, thereby shifting the perspective to a large marine monitoring

programme. The result has been that data on growth and reproduction of fish stocks are being collected for more than 300 stocks in waters where the European fleets operate.

Recognizing that the context above required new methodological developments, the European Commission Joint Research Centre (JRC) started its Assessment for All Initiative (a4a), with the aim to develop, test, and distribute methods to assess large numbers of stocks in an operational time frame, and to build the necessary capacity/expertise on stock assessment and advice provision.

The long-term strategy of a4a is to increase the number of stock assessments while simultaneously promoting the inclusion of the major sources of uncertainty in scientific advice. Our tactic is to reduce the required workload, by developing a software framework with the methods required to run the analysis a stock assessment needs (Jardim, et.al, 2014), including methods to deal with recognized bottlenecks, *e.g.* model averaging to deal with model selection (Millar, et.al, 2014). Moreover, we aim to make the analysis more intuitive, thereby attracting more experts to join stock assessment teams. Having more scientists/analysts working in fisheries management advice will increase the human resource basis, which is currently recognized to be limited. Regarding the former, a4a promotes a risk analysis approach to scientific advice through a wider usage of Operating Model/MSE approaches. We're focused on developing methods that can deal with the most common settings these type of analysis require, and creating the conditions for scientists to develop their own methods. Our expectation is that having a common framework, with clear data structures and workflows, will promote research in this area and make it simpler to implement and share methods.

To achieve these objectives, the Initiative identified a series of tasks, which were or are being carried out, namely:

- define a moderate data stock;
- develop a stock assessment framework;
- develop a forecasting algorithm based on MSE;
- organize training courses for marine scientists.

### 1.3 The a4a approach to stock assessment and management advice

As stated before, one of the main objectives of a4a is to promote a risk type of analysis, so that scientific advice provides policy and decision makers a perspective of the uncertainty existing on stock assessments and its propagation into the scenarios being analyzed.

The sources of uncertainty implemented so far are related to the processes of growth, natural mortality and reproduction (stock-recruitment); and to the estimation of population abundance and fishing mortality by the stock assessment model. In all cases the framework can include sampling error.

The approach is split into 4 steps: (i) converting length data to age data using a growth model, (ii) modeling natural mortality, (iii) assessing the stock, and (iv) MSE.

These steps may be followed in sequence or independently, depending on the user's preferences. All that is needed is to use the objects provided by the previous step and provide

the objects required by the next, so that data flows between steps smoothly. One can make the analogy with building with Lego, where for each layer the builder may use the pieces provided by a particular boxset, or make use of pieces from other boxsets. Figure 1 shows the process, including the class of the objects that carry the data (in black).

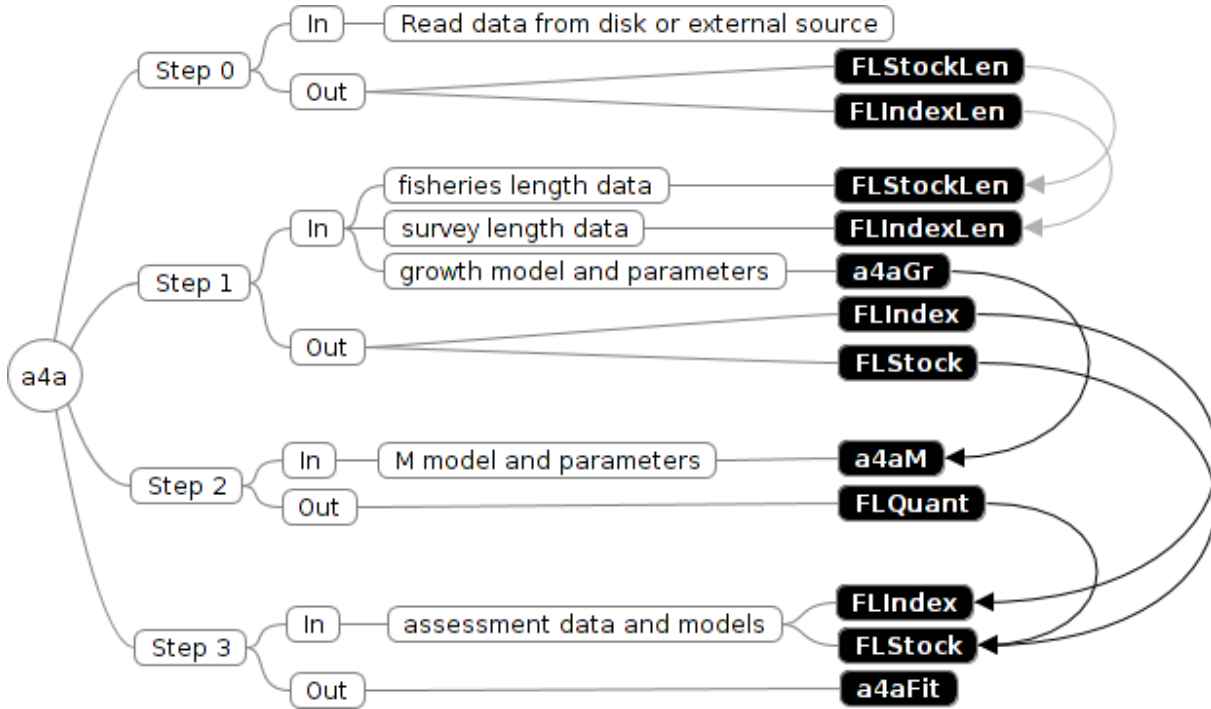


Figure 1: In/out process of the a4a approach. The boxes in black represent the classes of the objects that carry the information in and out of each step.

Analysis related to projections and biological reference points are dealt with by the FLR packages `FLash` and `FLBRP`.

In Steps 1 and 2 there is no fitting of growth models or natural mortality models. The rationale is to provide tools that allow the uncertainty associated with these processes to be carried on into the stock assessment, e.g. through parameter uncertainty. This approach allows the users to pick up the required information from other sources of information such as papers, PhDs, Fishbase, other stocks, etc. If the stock under analysis does not have specific information on the growth or natural mortality processes, generic information about life history invariants may be used such as the generic priors suggested by Bentley, (2014).

Note that an environment like the one distributed by a4a promotes the exploration of different models for each process, giving the analyst a lot of flexibility. It also opens the possibility to efficiently include distinct models in the analysis. For example, a stock assessment using two growth, or several models for natural mortality could be performed. Our suggestion to streamline the assessment process is to combine the final outcomes using model averaging (Miller, et. al, 2014). Other solutions may be implemented, like scenario analysis, etc. What is important is to keep the data flowing smoothly and the models clear. R (R Core Team, 2014) and FLR (Kell, et.al, 200) provide powerful platforms for this approach.



## 1.4 How to read this document

The target audience for this document are stock assessment experts. It presents a mixture of text and code that shows how the analysis can be run with R/FLR/FLa4a. The chapters are as independent as possible, so they can be extracted and run individually.

## 1.5 Software packages - FLR & FLa4a

To run the FLa4a methods the reader will need to install the package and its dependencies and load them, together with a couple of other packages. The data sets can be made available upon request.

```
# from CRAN
install.packages(c("copula", "triangle"))
# from FLR
install.packages(c("FLCore", "FLa4a"), repos = "http://flr-project.org/R")
```

To replicate the analysis carried out in this document the user will need the following additional packages:

```
# from CRAN
install.packages(c("plyr", "xtable", "plot3D", "gridExtra", "ggplot2"))
# from FLR
pkgs <- c("FLXSA", "FLAssess", "FLSAM", "FLash", "FLBRP")
install.packages(pkgs, repos = "http://flr-project.org/R")
```

After installing the reader will have to load the packages into one's R session.

```
library(FLa4a)
library(FLBRP)
library(FLXSA)
library(xtable)
library(plyr)
library(plot3D)
library(gridExtra)
library(corrplot)
library(energy)
library(ggplot2)
```

## 2 The context of small pelagics in Hellenic waters

Anchovy (*Engraulis encrasicolus*) and sardine (*Sardina pilchardus*) are two of the most important target species for the purse seine fishery in GSA 22. Pelagic trawls are banned and benthic trawls are allowed to fish small pelagics in percentages less than 5% of their total catch. Commonly anchovy and sardine are caught from shallow waters about 30 m to 100 m depth.

Regarding the management regulations enforced they concern a closed period from the mid December till the end of February and technical measures, such as minimum distance from shore (300 m), minimum bottom depth (30 m), gear and mesh size, engine, GRT restrictions etc.

The assessment of the anchovy and sardine stocks in [GSA 22](#) has been based on information derived from the Greek part of the Aegean Sea. The main distribution area of the two stocks in Aegean Sea is located in the continental shelf of the northern Aegean Sea. Their spatial distribution is strongly related to semi closed gulfs, shallow waters (less than 100 m depth) with high productivity, often related to areas of rivers outflows (e.g. [Tsagarakis et al., 2007](#); [Tsagarakis et al., 2008](#); [Giannoulaki et al., 2011](#); [Giannoulaki et al., 2013](#)).

## 2.1 Historical catches

Historical catches going back to 1970 are available from [FAO GFCM Fisheries Statistics Dataset](#) for Aegean and Ionian Seas. Historical catches however do not include any age or length structure information.

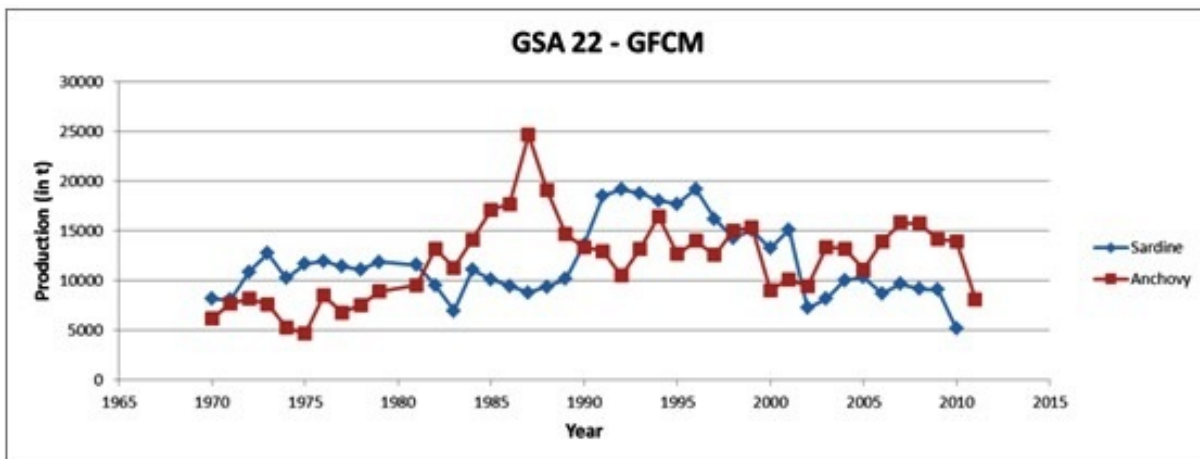


Figure 2: Historical catches going back to 1970 are available from [FAO GFCM Fisheries Statistics Dataset](#) for the Greek part of Aegean Sea.

The number of vessels officially reported by the Hellenic Statistical Service for the period 1970-2014 is shown below.

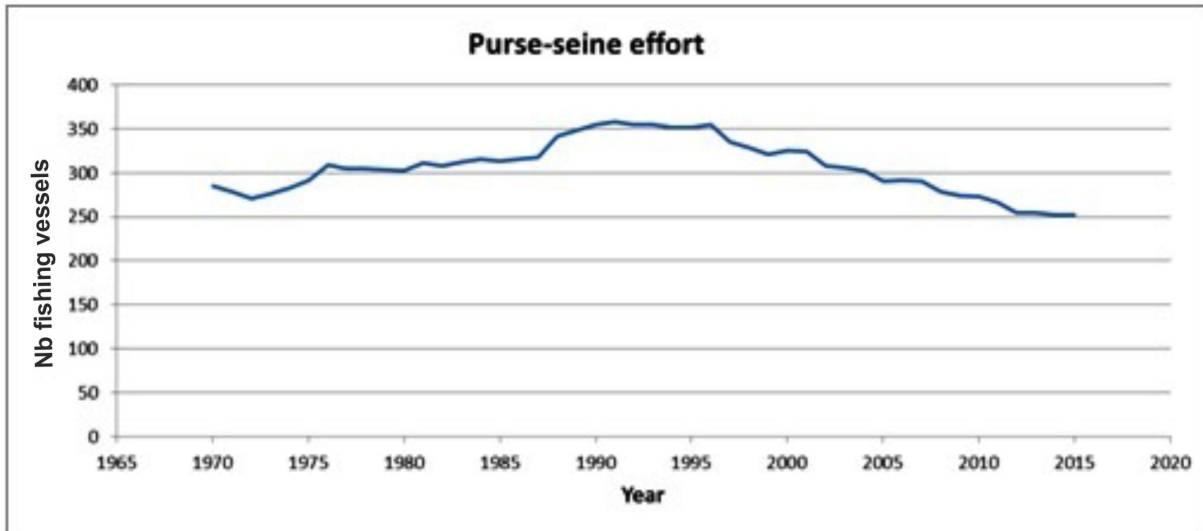


Figure 3: The evolution of the purse seine fleet in Greek part of GSAs 20 and 22.

## 2.2 DCR/DCF catches

The Hellenic Centre for Marine Research is responsible for the collection of data for the Greek part of GSA 22. Since the European data collection frameworks were implemented, early 2000's, sampling was carried out in GSA 22 for the period 2003-2006, 2008 and 2013-2014. The information available includes anchovy and sardine monthly landings, and length frequency information based on sampling on-board commercial vessels. Discards are estimated to be negligible, <1% of the total catch of the purse seine fishery. The trend in reported landings for both species as well as the landings per age group (number of individuals in thousands) is shown below for GSA 22. Gaps in the fisheries information result into a series of limiting data issues for stock assessment purposes.

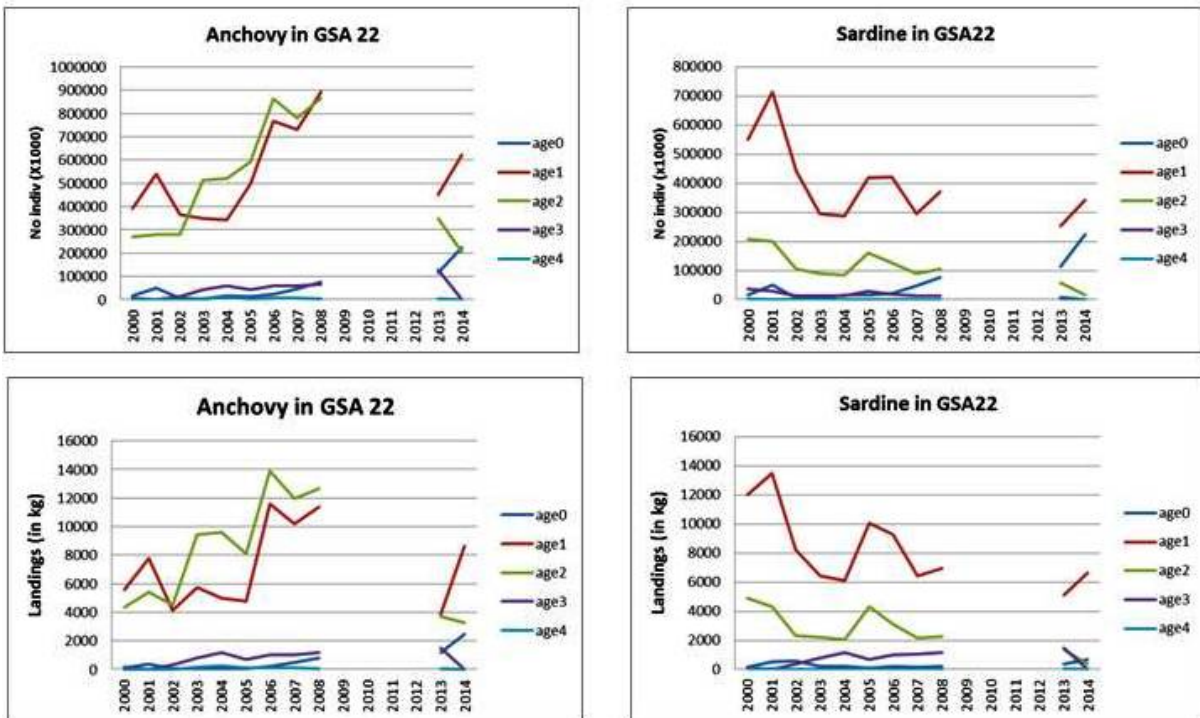
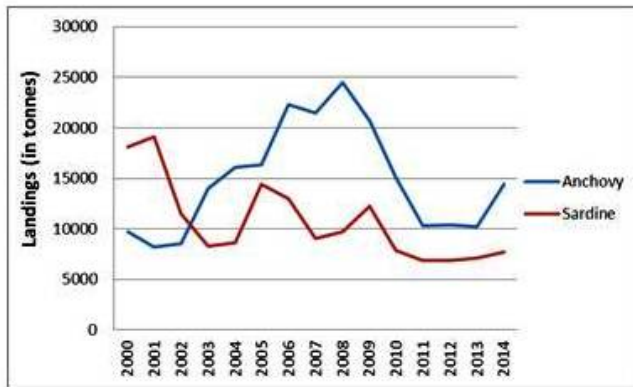


Figure 4: The trend in reported landings for sardine and anchovy, as well as the landings per age group (number of individuals in thousands) for GSAs 20 and 22.

### 2.3 Surveys

Total biomass, abundance, length and age composition for anchovy and sardine stocks in the Greek part of GSA 22 were estimated by acoustics from 2003 to 2008 and 2014. The survey takes place usually in June-July (spawning period for anchovy and recruitment period for sardine) and complies with the MEDIAS protocol. No acoustic survey took place in 2007 and 2009-2012. An acoustic survey took place in September-October 2013 but it was not considered appropriate to use it for stock assessment purposes for neither stock as it was referring to a different sampling period.

### 2.4 Limiting data issues

Specific limiting data issues were revealed in the exploratory analysis.

- Historical catches do not include any age or length structure information. The mean weight in the catch and in the stock for the period 1970-2000 was considered equal to the average values of the 2000-2008 and 2014 period.
- The lack of length frequencies and catch at age information for the period 2009-2012 impaired problems in the stock assessment. In addition the mean weight at age in the catch and in the stock for 2013 is very low compared to 2014 and 2008. This is explainable as the DCF/DCR was carried out in 2013 for covering only August 2013-December 2013 instead of all year. Thus the mean weight in the catch and in the stock for the period 2009-2013 was considered equal to the average values of the 2008-2014.
- Deviations were observed between the historical landings and the ones reported based on the DCF/DCR for the period 2000-2008 and 2014 with DCF/DCR being higher. Based on the observed differences the entire historical data series was adjusted.
- Due to the gaps in the data series we considered appropriate to use environmental indices i.e. mean satellite SST and Chla values from the main distribution area of the stocks as well as oscillation indices like the NAO and MOI as additional indices for stock assessment purposes (see next section).

### 3 Filling the gaps

There were two sets of gaps that required attention, (i) the historical lack of biological information, and (ii) the recent (2009-2013) missing of the same data. As such two datasets for each stock were built, including or not the historical information.

For both periods, the data missing were catch-at-age, mean weight-at-age in the catch and in the stock, maturity ogive and natural mortality. To run stock assessment models on these datasets some assumptions were made to rebuild the time series.

Furthermore, there was a mismatch between the landings reported by GFCM for the Aegean Sea when compared with the DCF estimates. As such it was necessary to adjust the historical time series to account for these differences.

#### 3.1 Reconstructing the time series of age structured information

In order to reconstruct the time series of catch data for the application of the assessment method, we assumed that for the period 1970-1999 mean weight-at-age in the catch and in the stock, the maturity ogive and natural mortality follow the average values of the period 2000-2008.

For the period 2009-2013 the following assumptions were made. Mean weight-at-age in the catch and in the stock, the maturity ogive and natural mortality in 2009, was assumed to be the same as in 2008. In 2013 equal to the one in 2014. For the years 2010-2012 the average values of 2008 and 2014 were used.

Catch-at-age was derived by scaling the average age composition to the historical catches in weight, after adjusting (see next section). For the recent missing years the same data allocation as for mean weights were taken (described above).

### 3.2 Adjusting catches by year by linking historical and contemporary

A relationship was modeled between historical and recent catch data for anchovy and sardine in GSA 22 (Figure 5). Based on this relationship historical catch data were adjusted to account for potential misreporting.

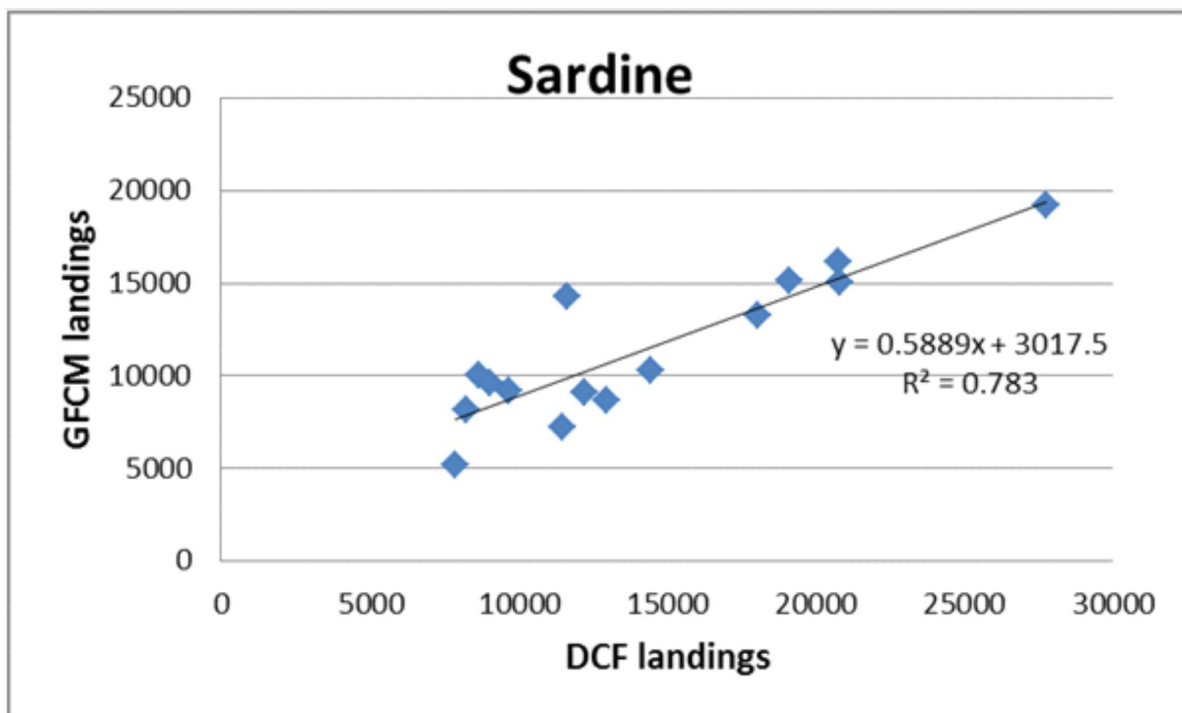
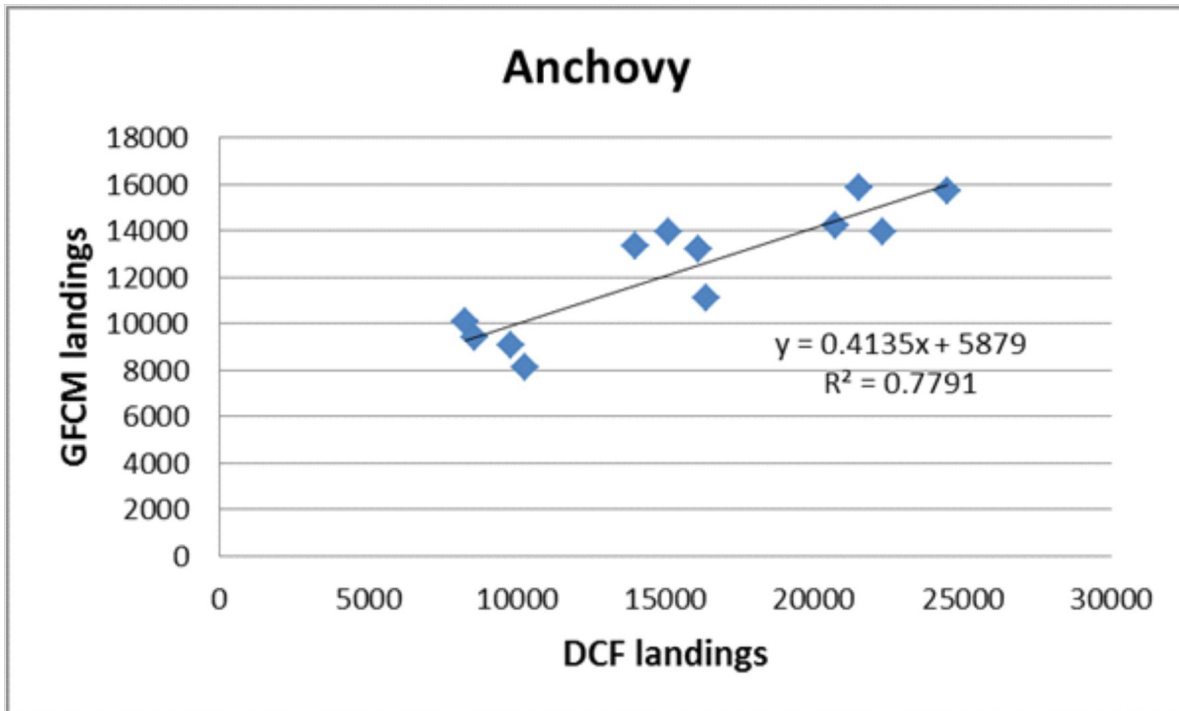


Figure 5: The relationship between historical and recent catch data for anchovy and sardine in GSA 22.

## 4 Investigating the use of environmental indices

A range of environmental indices were available that could be included as covariates in the stock-recruitment relationship, or as indices of abundances (Table 1). Many of the indices record similar information. For example, the NAO index contains information that is included in the SST.

Table 1. List of the environmental and oscillation indices examined for inclusion in the stock assessment models for the Greek small pelagic stocks.

Name of indicator	Abbreviation	Period available	Comments	Source
Atlantic Multidecadal	AMO	1856-present	Related to the patterns of SST variability in the North Atlantic	<a href="http://www.esrl.noaa.gov/psd/data/timeseries/AMO/">http://www.esrl.noaa.gov/psd/data/timeseries/AMO/</a>
Mediterranean Oscillation Index (Gibraltar/Israel)	MOI	1948-2013	Associated with Temperature and Precipitation Patterns	<a href="http://www.cru.uea.ac.uk/cru/data/moi/">http://www.cru.uea.ac.uk/cru/data/moi/</a>
Mediterranean Oscillation Index (Algiers/Cairo)	MOIAL	1948-2013	Associated with Temperature and Precipitation Patterns	<a href="http://www.cru.uea.ac.uk/cru/data/moi/">http://www.cru.uea.ac.uk/cru/data/moi/</a>
Western Mediterranean Oscillation Index	WEMOI	1821-2013	WeMOi has been correlated with sunshine variability and winter rainfall trends in the Western Mediterranean	<a href="http://www.ub.edu/gc/English/wemo.htm">http://www.ub.edu/gc/English/wemo.htm</a>
North Atlantic Oscillation	NAO	1950-present	Associated with Temperature and Precipitation Patterns	<a href="http://www.cpc.ncep.noaa.gov/data/teledoc/nao.shtml">http://www.cpc.ncep.noaa.gov/data/teledoc/nao.shtml</a>
satellite Chl-a concentration	CHL-A	1998 onward from MODISA	Associated with primary production and can be adjusted to provide 'rates'.	<a href="http://www.oceancolor.gsfc.nasa.gov">http://www.oceancolor.gsfc.nasa.gov</a>
satellite Sea Surface Temperature	SST	1994 onward from AVHRR		<a href="http://www.eoweb.dlr.de:8080">http://www.eoweb.dlr.de:8080</a>

Including multiple sources of similar information may not improve the assessment model fit and may create a problem of multi-collinearity. It was therefore important to only include indices that contained information not included by other sources.

The relationships between the indices were explored. Of particular interest is the association between pairs of indices. Many methods are available to quantify the strength of

association between a pair of variables. The most familiar method is correlation. However, correlation is only for quantifying the strength of a linear relationship. In the real world, most relationships are non-linear and are only approximately linear over a small range, meaning that correlation must be used with care.

It must be remembered that *correlation does not imply causation*.

Here, each pair of environmental indices is analysed using distance correlation. Of particular interest is pairs of indices that appear to be independent (have low values of distance correlation) as these will each contain new information.

Previous analyses ([Scott and Jardim, 2015](#)) has suggested that the power of distance correlation is enough to avoid Type II errors for many relationship types.

However, it is possible that the distance correlation score between two independent data sets can be greater than 0, implying dependence i.e. the chance of a Type I error (a false positive).

The `dcov.test()` function provides a test of multivariate independence using a permutation bootstrap method. It returns a p-value that can be used for significance testing. The null hypothesis is that the data are independent. Performing this test will help avoid Type I errors i.e. avoid mistakenly rejecting the null (independence) hypothesis.

## 4.1 Identify the effect of environment on species biology

All available environmental indices were investigated to identify the ones actually having an effect on the species biology. The following figures provide a synoptic overview of the work exerted, linking environmental variables with specific biological processes (spawning, recruitment) and time of the year (in quarters).



Sardine									
					ENV				
Year	Season	Spawning	Recruitment	Fishing period	Chl-a	SST	nao	moi	
X	Qtr1	Yellow		Grey					
	Qtr2		Yellow	Grey				Red	
	Qtr3		Yellow	Black				Red	
	Qtr4	Yellow		Grey	Red				
X+1	Qtr1	Yellow		Grey					
	Qtr2		Yellow	Grey				Red	
	Qtr3		Yellow	Black				Red	
	Qtr4	Yellow		Grey	Red				
<b>EFFECT ON</b>					larvae surv.	spawn conditions		recr mortality or surv.	spawn conditions ?fecundity ~SSB

Figure 6: Linkage of environmental parameters with biological processes for Sardine in Greek waters.

Anchovy									
					ENV				
Year	Season	Spawning	Recruitment	Fishing period	Chl-a	SST	nao	moi	
X	Qtr1								
	Qtr2	Yellow		Grey	Red				Red
	Qtr3	Yellow		Black	Red	Light Red			
	Qtr4		Yellow	Grey				Red	
X+1	Qtr1								
	Qtr2	Yellow		Grey	Red				Red
	Qtr3	Yellow		Black	Red	Light Red			
	Qtr4		Yellow	Grey				Red	
<b>EFFECT ON</b>					larvae	spawn		recr	spawn
					surv.	conditions		mortality	conditions
								or surv.	?fecundity
									~SSB

Figure 7: Linkage of environmental parameters with biological processes for Anchovy in Greek waters.

## 4.2 Reading in the data

First we read in all of the indices and put them in one big data.frame.

```
indices <- data.frame()

# Load in indices Oscillation indices
osc_files <- list.files(".././data/oscillation_indices", pattern = "Rdata")
for (i in osc_files) {
  load(paste(".././data/oscillation_indices/", i, sep = ""))
  object <- unlist(strsplit(i, ".Rdata"))
  # get index
  indices <- rbind(indices, cbind(index = object, melt(index=get(object))[,
    c("year", "value")]))
}

# Ionian
ion_files <- list.files(".././data/ionian", pattern = "Rdata")
# Remove stock object from list
ion_files <- ion_files[!(ion_files %in% c("Ane14iostk.Rdata",
  "Saio14stk.Rdata"))]
for (i in ion_files) {
  load(paste(".././data/ionian/", i, sep = ""))
}
```

```

    object <- unlist(strsplit(i, ".Rdata"))
    # get index
    indices <- rbind(indices, cbind(index = object, melt(index(get(object)))[,
      c("year", "value")]))
  }

aeg_files <- list.files(".././data/aegean", pattern = "Rdata")
# Remove stock object from list
aeg_files <- aeg_files[!(aeg_files %in% c("AneG14index.Rdata",
  "AneG14stk.Rdata", "SaeG14index.Rdata", "SaeG14stk.Rdata"))]
for (i in aeg_files) {
  load(paste(".././data/aegean/", i, sep = ""))
  object <- unlist(strsplit(i, ".Rdata"))
  # get index
  indices <- rbind(indices, cbind(index = object, melt(index(get(object)))[,
    c("year", "value")]))
}

```

### 4.3 Analysis

The values are then transformed by scaling by the maximum of each time series (Figure 8).

```

indices <- ddply(indices, .(index), transform, scvalue = value/max(value,
  na.rm = TRUE))
ggplot(indices) + geom_line(aes(x = year, y = scvalue, colour = index)) +
  theme(legend.position = "none")

```

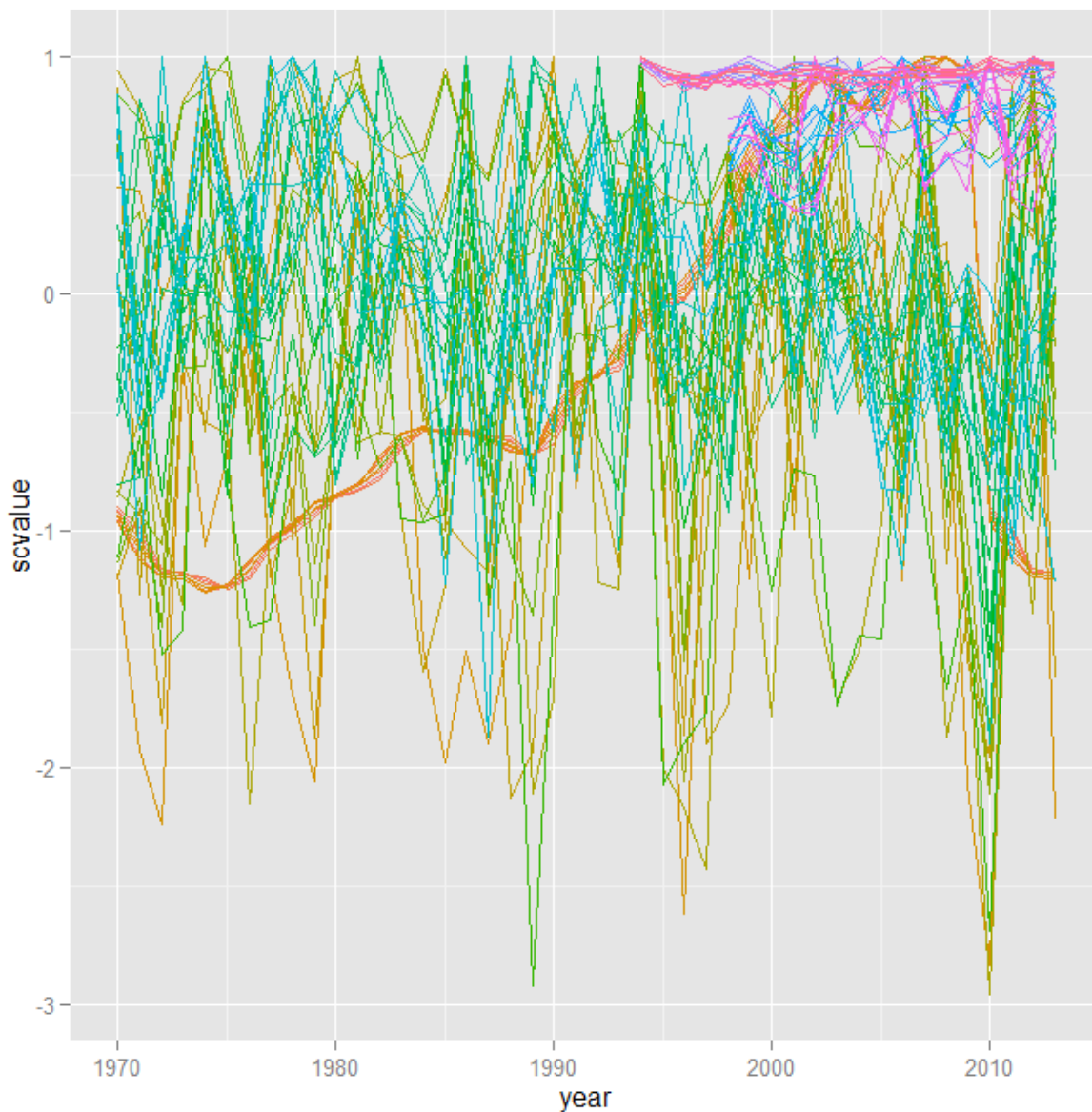


Figure 8: Scaled indices values (legend not shown due to number of indices).

We perform distance correlation on each pair of indices and also the p-value for significance testing.

```
# Rename the indices for plotting
indices$index <- as.character(indices$index)
indices$index <- unlist(strsplit(indices$index, "_index"))
ind_names <- as.character(unique(indices$index))
# Matrices for storing the results
co <- matrix(NA, nrow = length(ind_names), ncol = length(ind_names),
  dimnames = list(x = ind_names, y = ind_names))
dc <- matrix(NA, nrow = length(ind_names), ncol = length(ind_names),
  dimnames = list(x = ind_names, y = ind_names))
dcp <- matrix(NA, nrow = length(ind_names), ncol = length(ind_names),
  dimnames = list(x = ind_names, y = ind_names))
for (ind1 in ind_names) {
```

```

for (ind2 in ind_names) {
  # NAs not allowed so trim indices to common length
  x <- indices[indices$index == ind1, "scvalue"]
  y <- indices[indices$index == ind2, "scvalue"]
  non_na <- !is.na(x) & !is.na(y)
  x <- x[non_na]
  y <- y[non_na]
  # Calculate
  dc[ind1, ind2] <- dcor(x, y)
  dcp[ind1, ind2] <- dcov.test(x, y)$p.value
  co[ind1, ind2] <- cor(x, y)
}
}

```

## 4.4 Results

We can plot the distance correlation matrix of results (Figure 9).

```

# Set colours
colv <- colorRampPalette(c("white", "white", "white", "white",
  "yellow", "green", "blue", "red"))
colp <- colorRampPalette(c("white", "white", "white", "red"))

corrplot(dc, cl.lim = c(0, 1), col = colv(8))

```

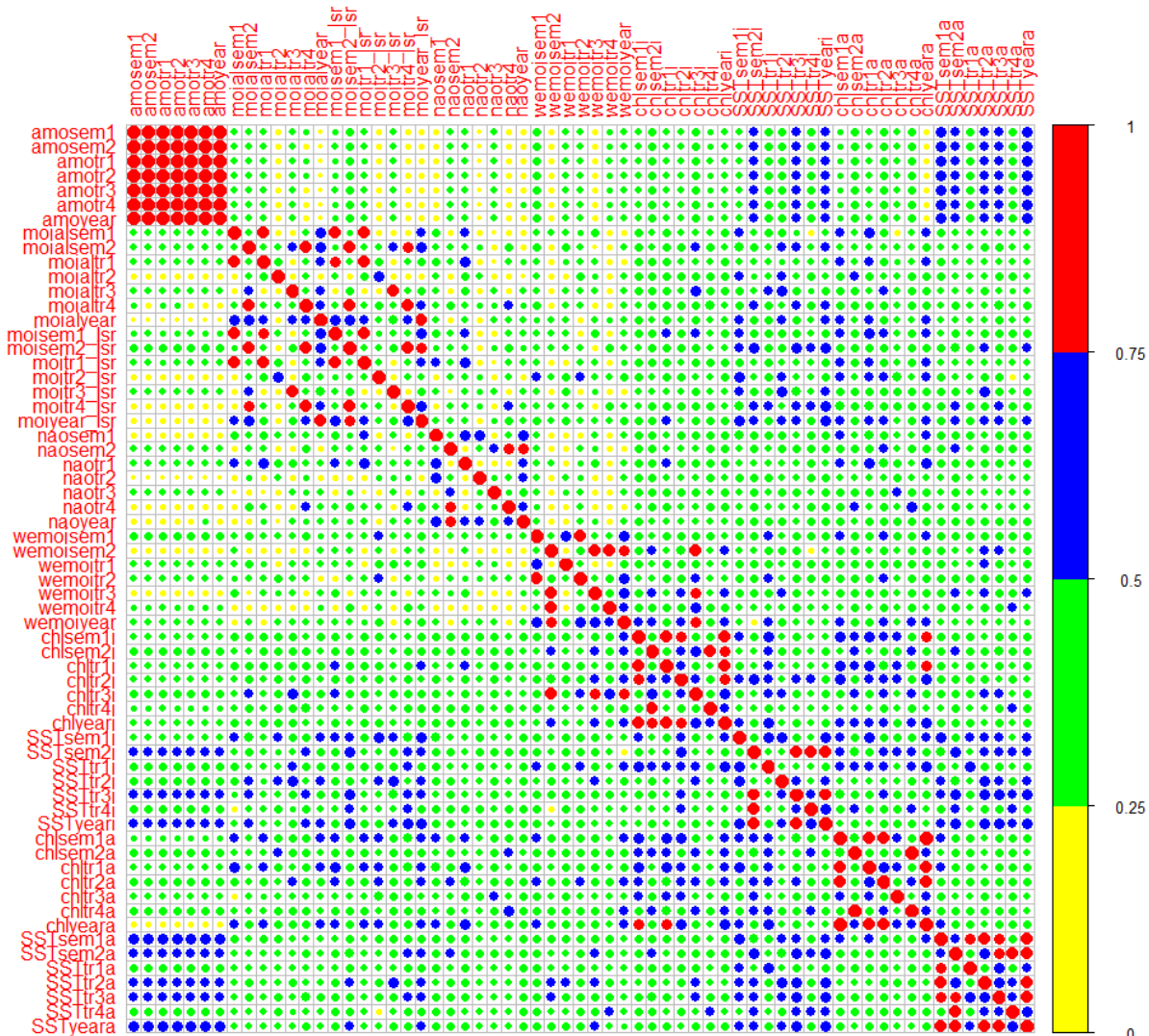


Figure 9: Distance correlation of the environmental indices. Data are independent only if the distance correlation is 0. However, significance testing should also be performed.

We can also look at the results of the significance test. The null hypothesis is that the data are independent. Here we set a significance level and plot whether or not the data are independent (Figure 10).

```
# Can we reject the null hypothesis of independence?
sig_level <- 0.05
corrplot(dcp <= sig_level, cl.lim = c(0, 1), col = colp(4))
```

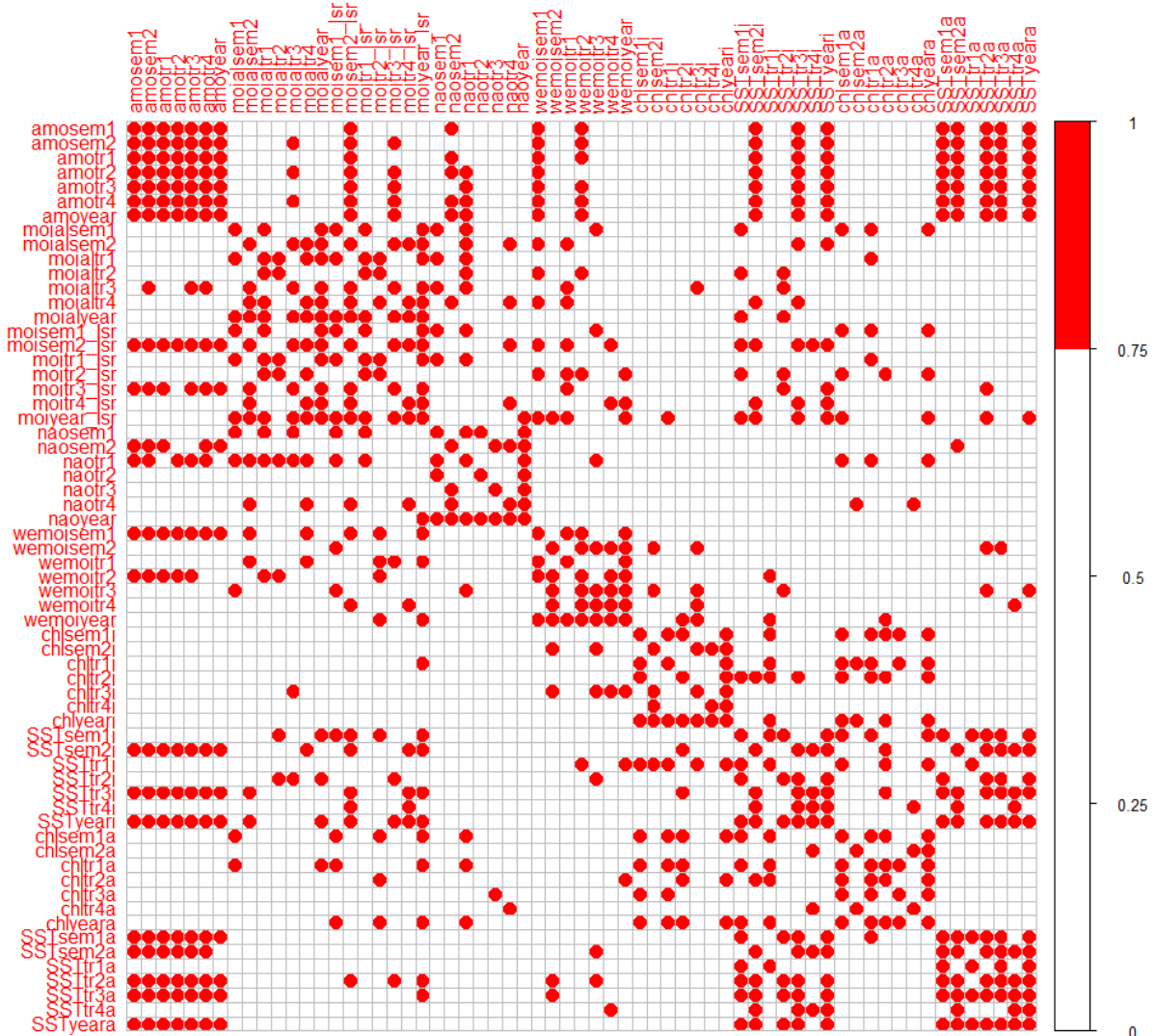


Figure 10: Results of the significance test. The significance level is set at 0.05. Red points are significant at this level, i.e. we can reject the null hypothesis of independence, implying a level of dependence between the indices. The plot is not perfectly symmetric as the significance test is nonparametric and the result is obtained through 199 replicates.

As mentioned above, we are interested in combinations of indices that bring new information, i.e. indices that are independent of each other. For this reason we are interested in index combinations that have 'white squares' in Figure 10. The level of dependence (from Figure 9) is of less interest than whether there is independence or not.

Finally, the indices to assist model fit were chosen based on a) their independence and b) the season corresponding to the period prior/beginning spawning for each species (See Table 2).

Table 2. Environmental indices used in the a4a stock assessment model applied for anchovy and sardine stock in GSA 22.

A4A assessment model	Auxilliary abundance Index	Covariate in SR relationship
<b>Anchovy short time series</b>	CHl-a 2 <sup>nd</sup> trimester	SST 2 <sup>nd</sup> trimester
<b>Sardine short time series</b>	CHl-a 4 <sup>th</sup> trimester	SST 4 <sup>th</sup> trimester
<b>Anchovy long time series</b>	CHl-a 2 <sup>nd</sup> trimester	MOI 2 <sup>nd</sup> trimester
<b>Sardine long time series</b>	SST 4 <sup>th</sup> trimester	MOI 2 <sup>nd</sup> trimester

Concerning the long time series MOI was chosen as a covariate for the SR relationship as this index was the only one available for the entire time series. This index is known to be associated with SST and precipitation.

## 5 Running assessments with the statistical catch-at-age method

### 5.1 Anchovy in GSA 22 (Aegean Sea)

#### 5.1.1 Data and input

```
# stock and acoustic survey objects
load("../..../data/aegean/AneG14stk.Rdata")
load("../..../data/aegean/AneG14index.Rdata")
```

```
# stock and acoustic survey objects historical data
yh <- ac(1970:1999)
yNA <- ac(2009:2012)
yd <- ac(2004:2008, 2013, 2014)
lndHist.orig <- read.csv("../..../data/historical/Historical_landings.csv")
load("../..../data/historical/PScapacity.RData")
```

```
# build objects
ane22.stk <- window(AneG14.stk, start = 1970)
ane22.stk <- setPlusGroup(ane22.stk, 4)
```

```
## [1] "maxfbar has been changed to accomodate new plusgroup"
```



```

catch(ane22.stk) <- landings(ane22.stk) <- lndHist.orig$anchovy22
catch.wt(ane22.stk)[, yd] <- yearMeans(catch.wt(ane22.stk)[, yd])
stock.wt(ane22.stk)[, yh] <- yearMeans(stock.wt(ane22.stk))
m(ane22.stk)[, yh] <- yearMeans(m(ane22.stk))
mat(ane22.stk)[, yh] <- yearMeans(mat(ane22.stk))
harvest.spwn(ane22.stk)[, yh] <- yearMeans(harvest.spwn(ane22.stk))
m.spwn(ane22.stk)[, yh] <- yearMeans(m.spwn(ane22.stk))
ane22.ind <- AneG14.ind
ane22a.ind <- AneG14.ind
ane22b.ind <- AneG14.ind
ane22c.ind <- AneG14.ind
ane22d.ind <- AneG14.ind
ane22e.ind <- AneG14.ind
ane22f.ind <- AneG14.ind
index.var(ane22.ind[[1]])[] <- 0.3

# rebuild catch at age
flq <- catch.wt(ane22.stk)
flq[] <- apply(catch.wt(ane22.stk) * catch.n(ane22.stk), 2, function(x) x/sum(x))
flq[, "2009"] <- flq[, "2008"]
flq[, "2012"] <- yearMeans(flq[, c("2014", "2013")])
flq[, "2010"] <- yearMeans(flq[, c("2008", "2014")])
flq[, "2011"] <- yearMeans(flq[, c("2008", "2014")])
flq[, ac(1970:1999)] <- yearMeans(flq[, ac(2000:2008)])
flq <- flq * catch(ane22.stk)[rep(1, 5)]/catch.wt(ane22.stk)
ane22rbld.stk <- ane22.stk
flq <- FLQuantDistr(flq, flq)
flq@var[] <- 0.3
flq@var[, ac(1970:1999, 2009:2012)] <- 0.5
catch.n(ane22rbld.stk) <- flq

```

```

load("../..../data/aegean/chltr2a_index.Rdata")
load("../..../data/aegean/chltr3a_index.Rdata")
load("../..../data/aegean/SSTtr2a_index.Rdata")
load("../..../data/oscillation_indices/naotr4_index.Rdata")
load("../..../data/oscillation_indices/moitr2_Isr_index.Rdata")

```

```

flq <- index(chltr2a_index)
dimnames(flq)[1] <- 0
quant(flq) <- "age"
ane22.ind$chlQ2 <- FLIndex(index = flq)
range(ane22.ind$chlQ2)[c("startf", "endf")] <- c(0.25, 0.5)
index.var(ane22.ind$chlQ2)[] <- 0.4

flq <- index(chltr3a_index)
dimnames(flq)[1] <- 0
quant(flq) <- "age"
ane22.ind$chlQ3 <- FLIndex(index = flq)
range(ane22.ind$chlQ3)[c("startf", "endf")] <- c(0.5, 0.75)

```

```

index.var(ane22.ind$chlQ3)[] <- 0.4

flq <- index(naotr4_index) + 3
dimnames(flq)[1] <- 0
quant(flq) <- "age"
ane22.ind$naoQ4 <- FLIndex(index = flq)
range(ane22.ind$naoQ4)[c("startf", "endf")] <- c(0.75, 1)
index.var(ane22.ind$naoQ4)[] <- 0.4

flq <- index(SSTtr2a_index)
dimnames(flq)[1] <- 0
quant(flq) <- "age"
ane22.ind$sstQ2 <- FLIndex(index = flq)
range(ane22.ind$sstQ2)[c("startf", "endf")] <- c(0.25, 0.5)
index.var(ane22.ind$sstQ2)[] <- 0.4

flq <- index(moitr2_Isr_index) + 3
dimnames(flq)[1] <- 0
quant(flq) <- "age"
ane22.ind$moiQ2 <- FLIndex(index = flq)
range(ane22.ind$moiQ2)[c("startf", "endf")] <- c(0.25, 0.5)
index.var(ane22.ind$moiQ2)[] <- 0.4

# cha2 only
flq <- index(chltr2a_index)
dimnames(flq)[1] <- 0
quant(flq) <- "age"
ane22a.ind$chlQ2 <- FLIndex(index = flq)
range(ane22a.ind$chlQ2)[c("startf", "endf")] <- c(0.25, 0.5)
index.var(ane22a.ind$chlQ2)[] <- 0.4
index.var(ane22a.ind[[1]])[] <- 0.3

# cha3 only
flq <- index(chltr3a_index)
dimnames(flq)[1] <- 0
quant(flq) <- "age"
ane22b.ind$chlQ3 <- FLIndex(index = flq)
range(ane22b.ind$chlQ3)[c("startf", "endf")] <- c(0.25, 0.5)
index.var(ane22b.ind$chlQ3)[] <- 0.4
index.var(ane22b.ind[[1]])[] <- 0.3

# nao4 only
flq <- index(naotr4_index) + 3
dimnames(flq)[1] <- 0
quant(flq) <- "age"
ane22c.ind$naoQ4 <- FLIndex(index = flq)
range(ane22c.ind$naoQ4)[c("startf", "endf")] <- c(0.25, 0.5)
index.var(ane22c.ind$naoQ4)[] <- 0.4
index.var(ane22c.ind[[1]])[] <- 0.3

# sst only

```

```

flq <- index(SSTtr2a_index)
dimnames(flq)[1] <- 0
quant(flq) <- "age"
ane22d.ind$sstQ2 <- FLIndex(index = flq)
range(ane22d.ind$sstQ2)[c("startf", "endf")] <- c(0.25, 0.5)
index.var(ane22d.ind$sstQ2)[,] <- 0.4
index.var(ane22d.ind[[1]])[,] <- 0.3

# moi2 only
flq <- index(moittr2_Isr_index) + 3
dimnames(flq)[1] <- 0
quant(flq) <- "age"
ane22e.ind$moiQ2 <- FLIndex(index = flq)
range(ane22e.ind$moiQ2)[c("startf", "endf")] <- c(0.25, 0.5)
index.var(ane22e.ind$moiQ2)[,] <- 0.4
index.var(ane22e.ind[[1]])[,] <- 0.3

##### chla and sst
flq <- index(chltr2a_index)
dimnames(flq)[1] <- 0
quant(flq) <- "age"
ane22f.ind$chlQ2 <- FLIndex(index = flq)
range(ane22f.ind$chlQ2)[c("startf", "endf")] <- c(0.25, 0.5)
index.var(ane22f.ind$chlQ2)[,] <- 0.4
index.var(ane22f.ind[[1]])[,] <- 0.3

flq <- index(SSTtr2a_index)
dimnames(flq)[1] <- 0
quant(flq) <- "age"
ane22f.ind$sstQ2 <- FLIndex(index = flq)
range(ane22f.ind$sstQ2)[c("startf", "endf")] <- c(0.25, 0.5)
index.var(ane22f.ind$sstQ2)[,] <- 0.4

```

## 5.1.2 Initial model runs

```

## =====
## assessments - Short time series
## =====
## sst as a covariate in the ricker and chla used as index F
## in the years after 2008 are replaced by the F of 2014
fmod <- ~te(age, replace(year, year > 2008, 2014), k = c(4, 7))
qmod <- list(~s(age, k = 3), ~s(year, k = 5))

#### sst as covariate for ricker
cov <- c(index(window(ane22d.ind[[2]], start = 2000)))
cov <- c(cov, mean(cov))
srmod <- ~ricker(CV = 0.3, a = ~s(cov, k = 4))

```

```

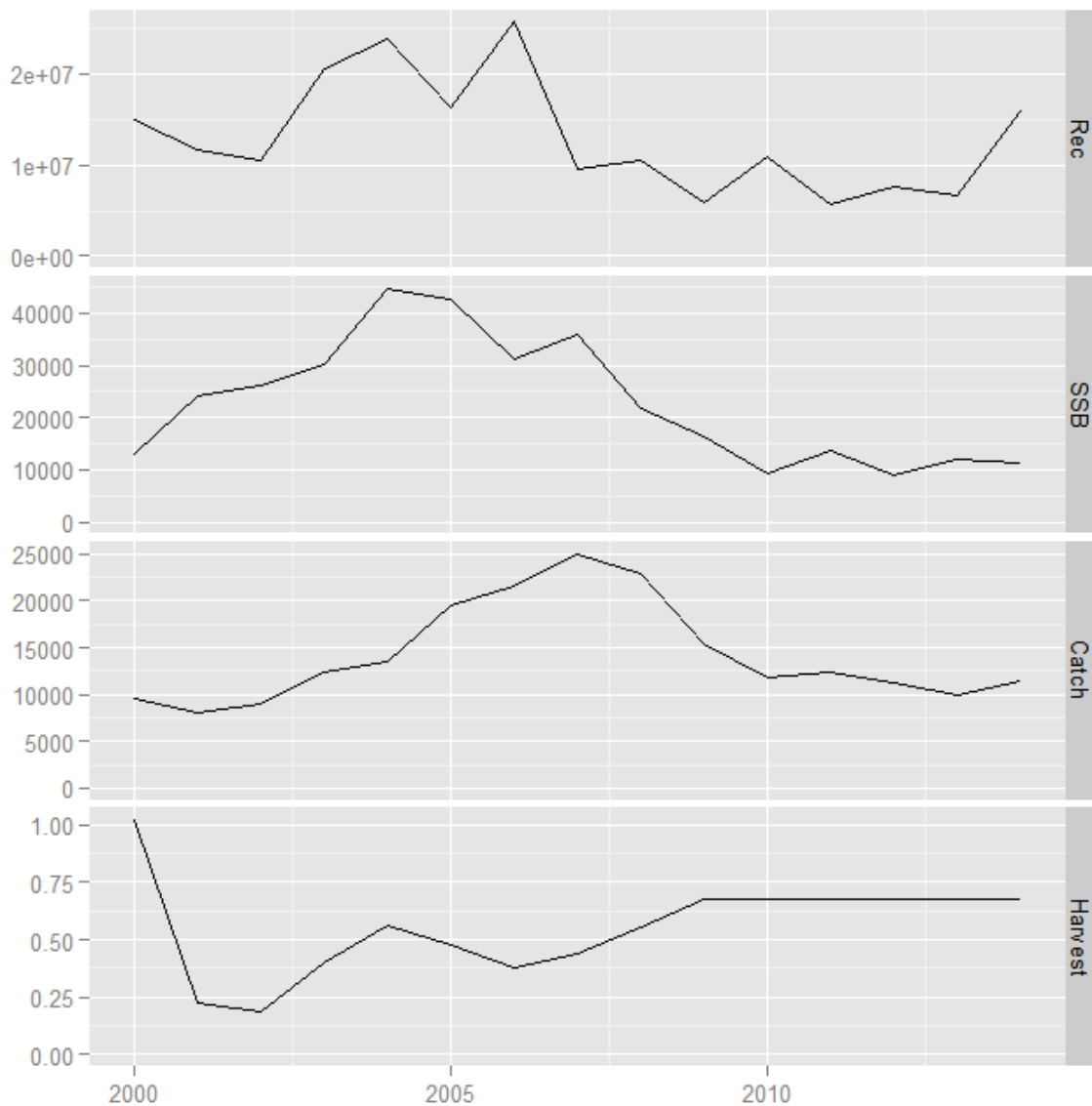
### using
fit41 <- sca(trim(ane22rbld.stk, year = 2000:2014), window(ane22a.ind,
  start = 2000), qmodel = qmod, fmodel = fmod, srmodel = srmod,
  fit = "assessment")

ane22.stk.a4a.41 <- trim(ane22rbld.stk, year = 2000:2014) + fit41

plot(ane22.stk.a4a.41) #####much worse catch and landinds fit

```

### Short time series

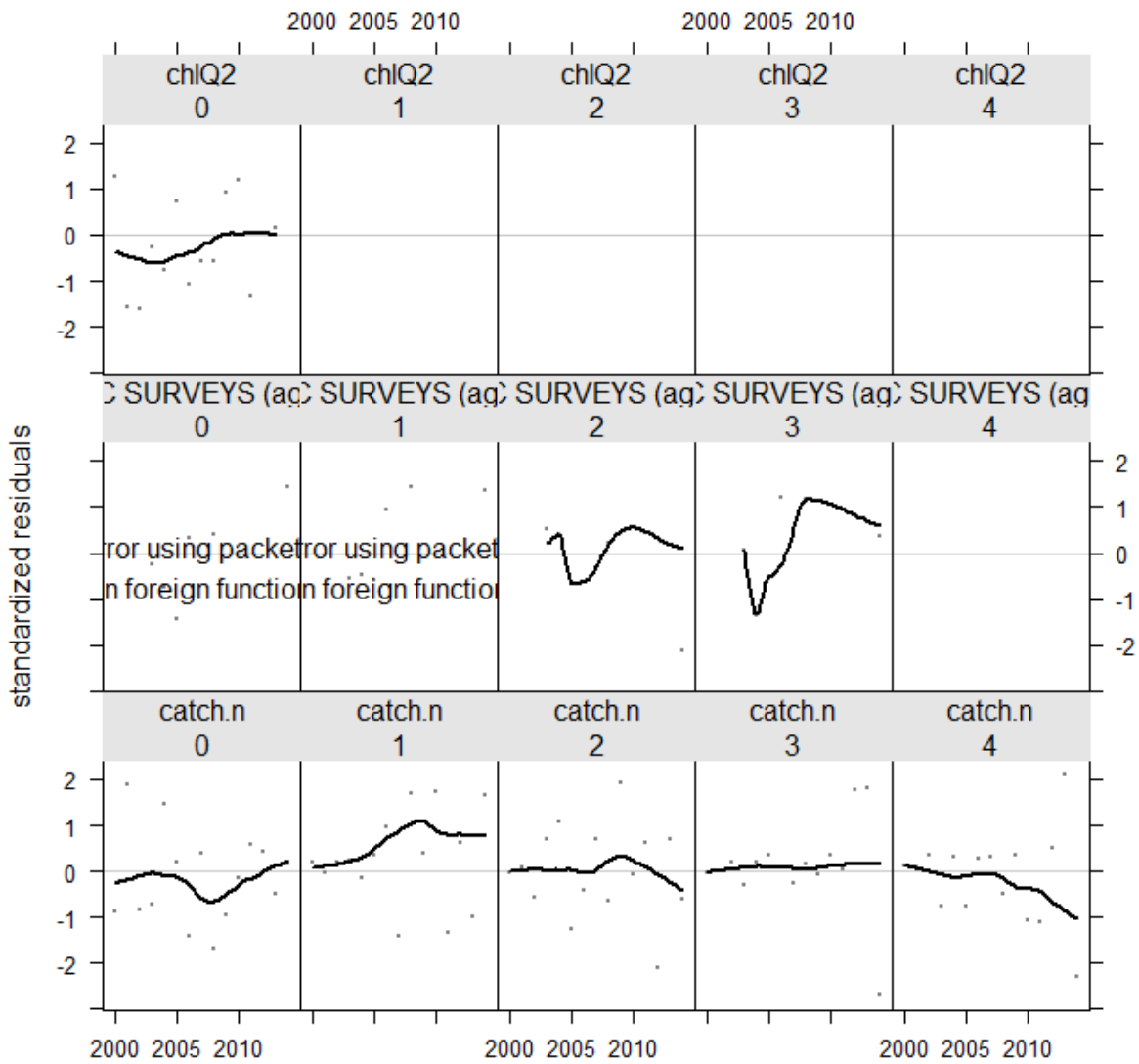


```

res <- residuals(fit41, trim(ane22rbld.stk, year = 2000:2014),
  window(ane22a.ind, start = 2000))
plot(res) ###ok

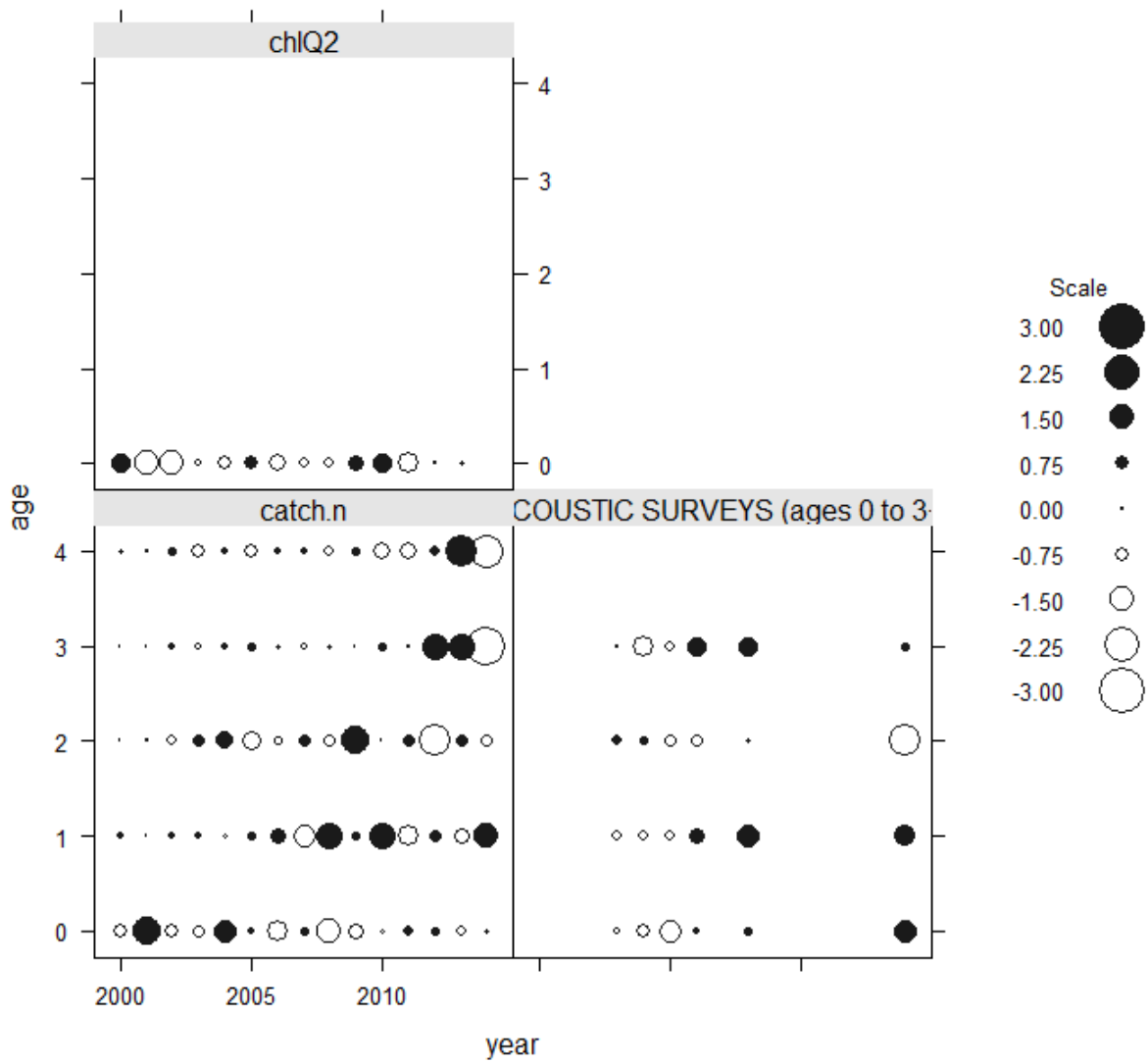
```

## log residuals of catch and abundance indices



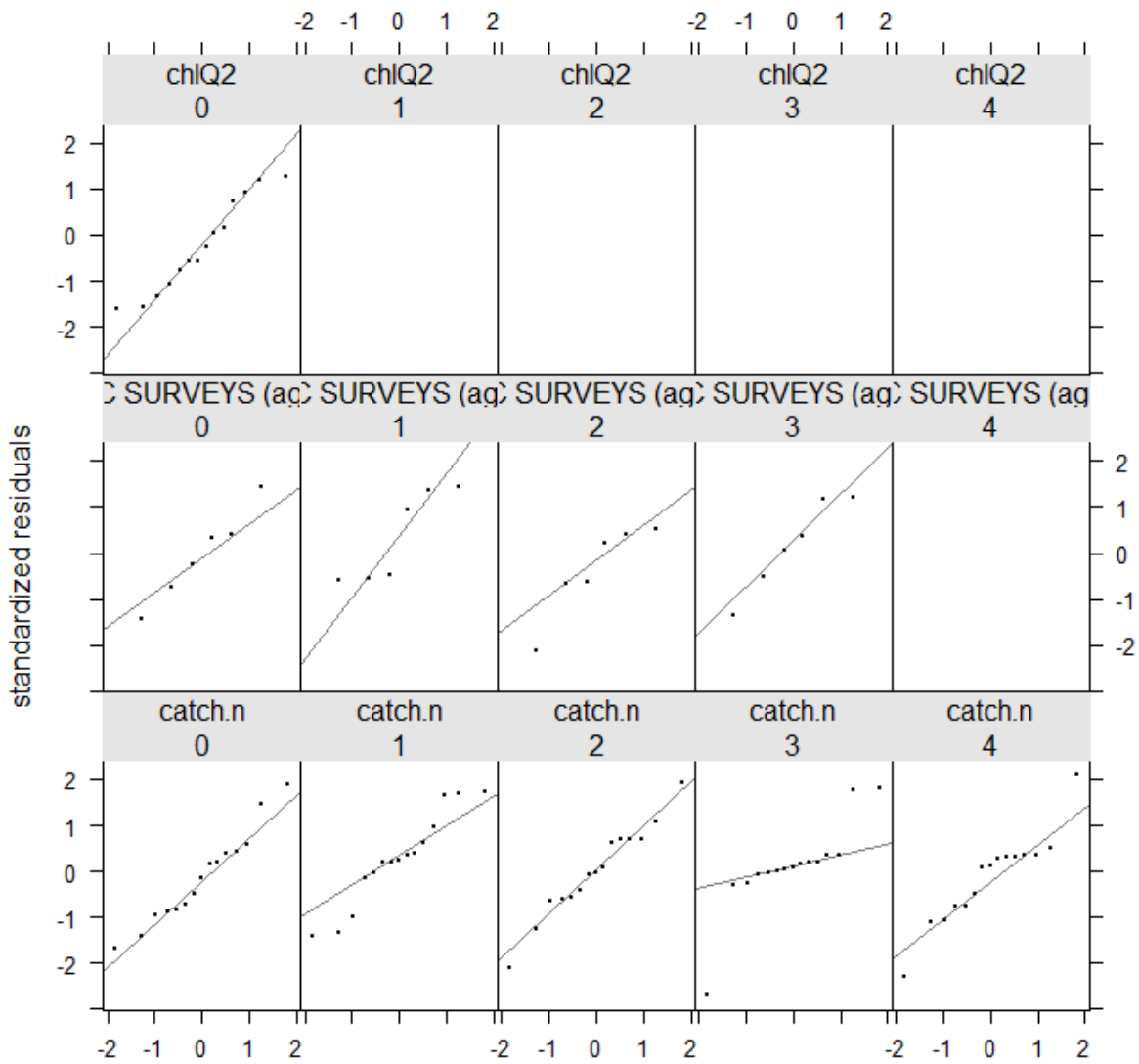
```
bubbles(res) # check the residuals plot
```

## log residuals of catch and abundance indices

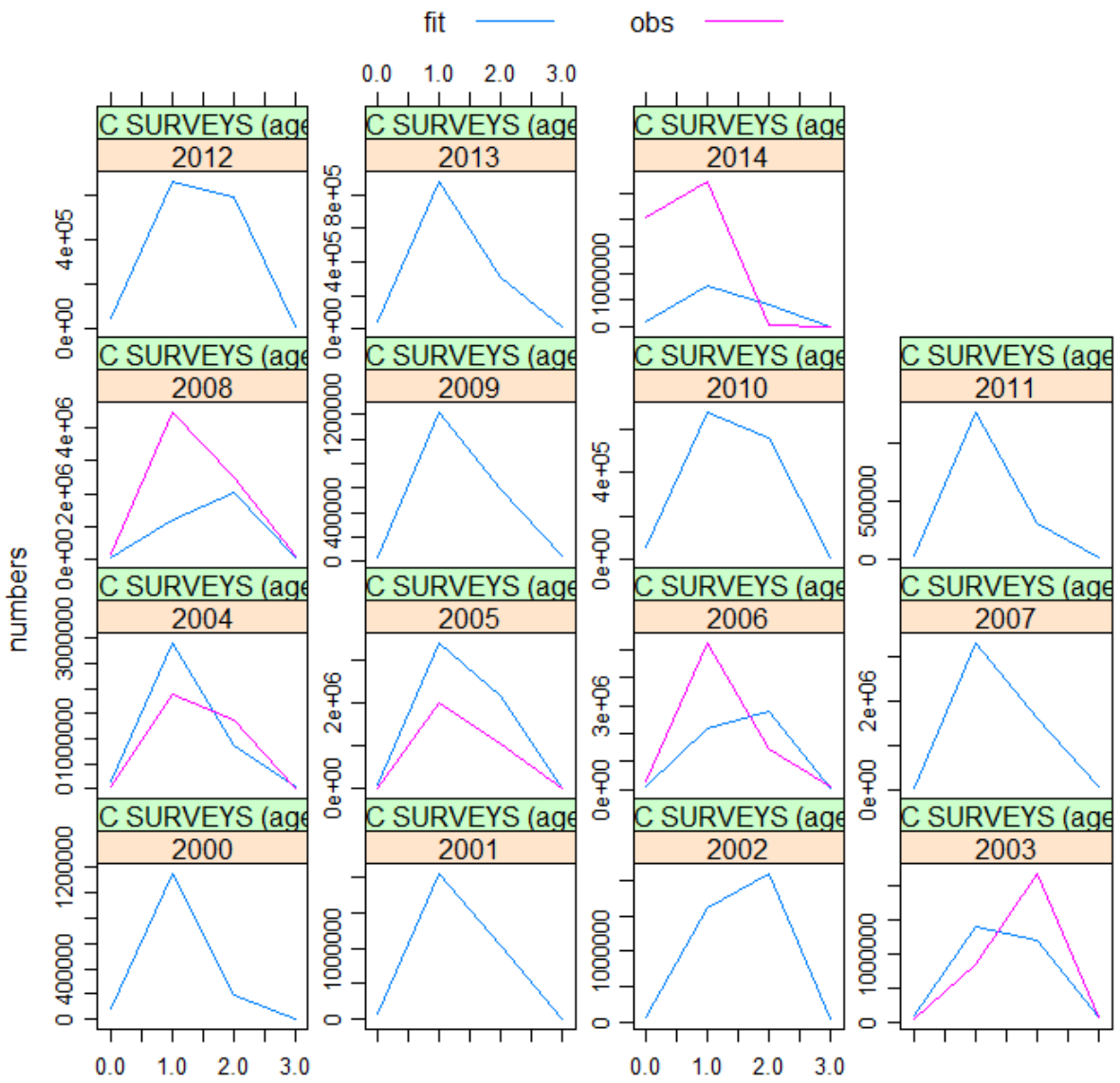


```
qqmath(res) # quantile plots rather ok output
```

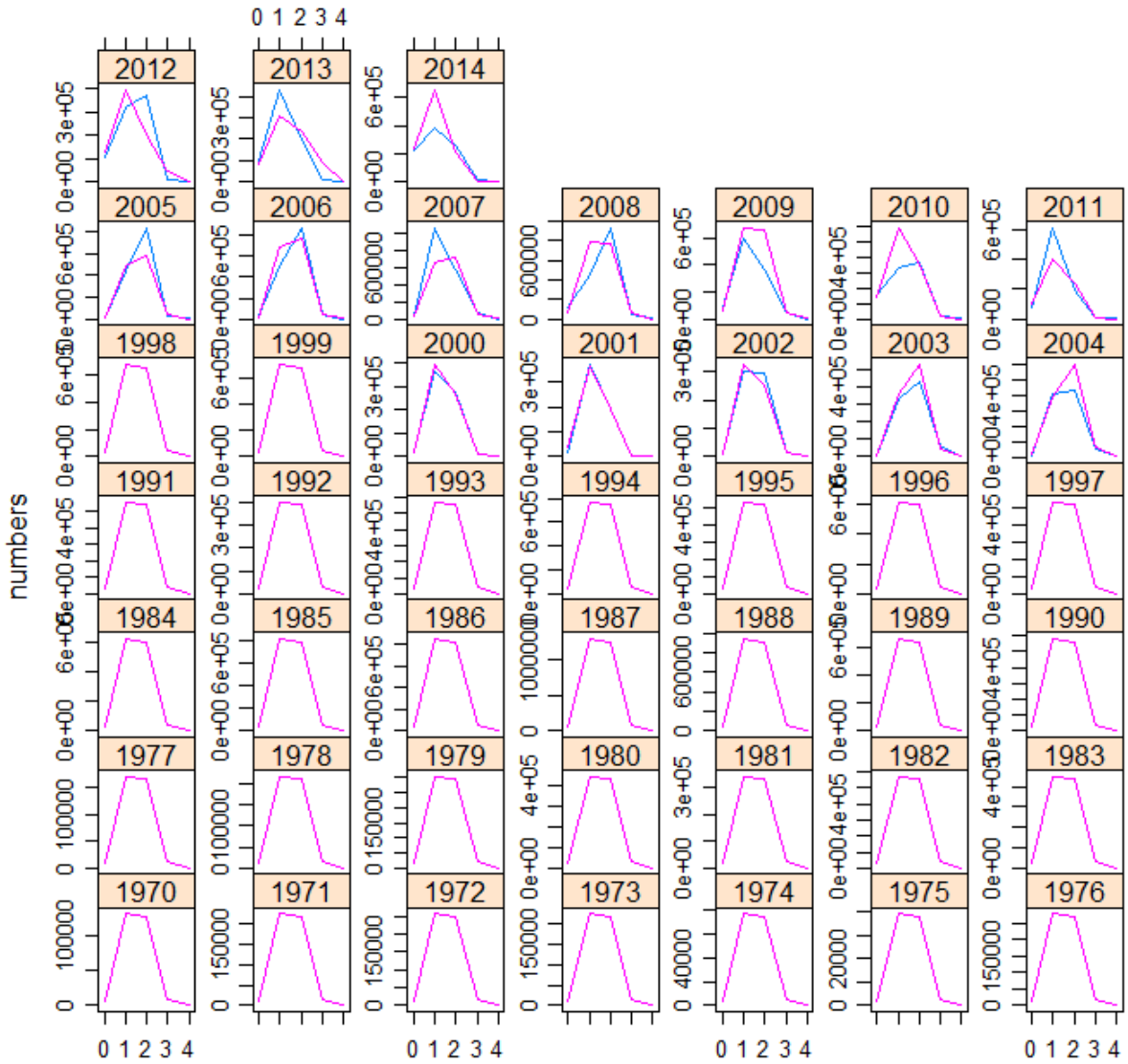
## quantile-quantile plot of log residuals of catch and abundance indices



```
# Plot fitted against observed for survey
plot(fit41, AneG14.ind) ### good
# Plot fitted against observed for catch at age
plot(fit41, ane22rbld.stk) ###good
```







```
AIC(fit41)
## [1] -1441.566

BIC(fit41)
## [1] -1264.286
```

```
# =====
# assessments
# =====
# MOI as a covar for recruitment and Chla along with surveys
```

```

# for an index
fmod <- ~te(age, replace(year, year > 2008, 2014), k = c(4, 7))
qmod <- list(~s(age, k = 3), ~s(year, k = 4))

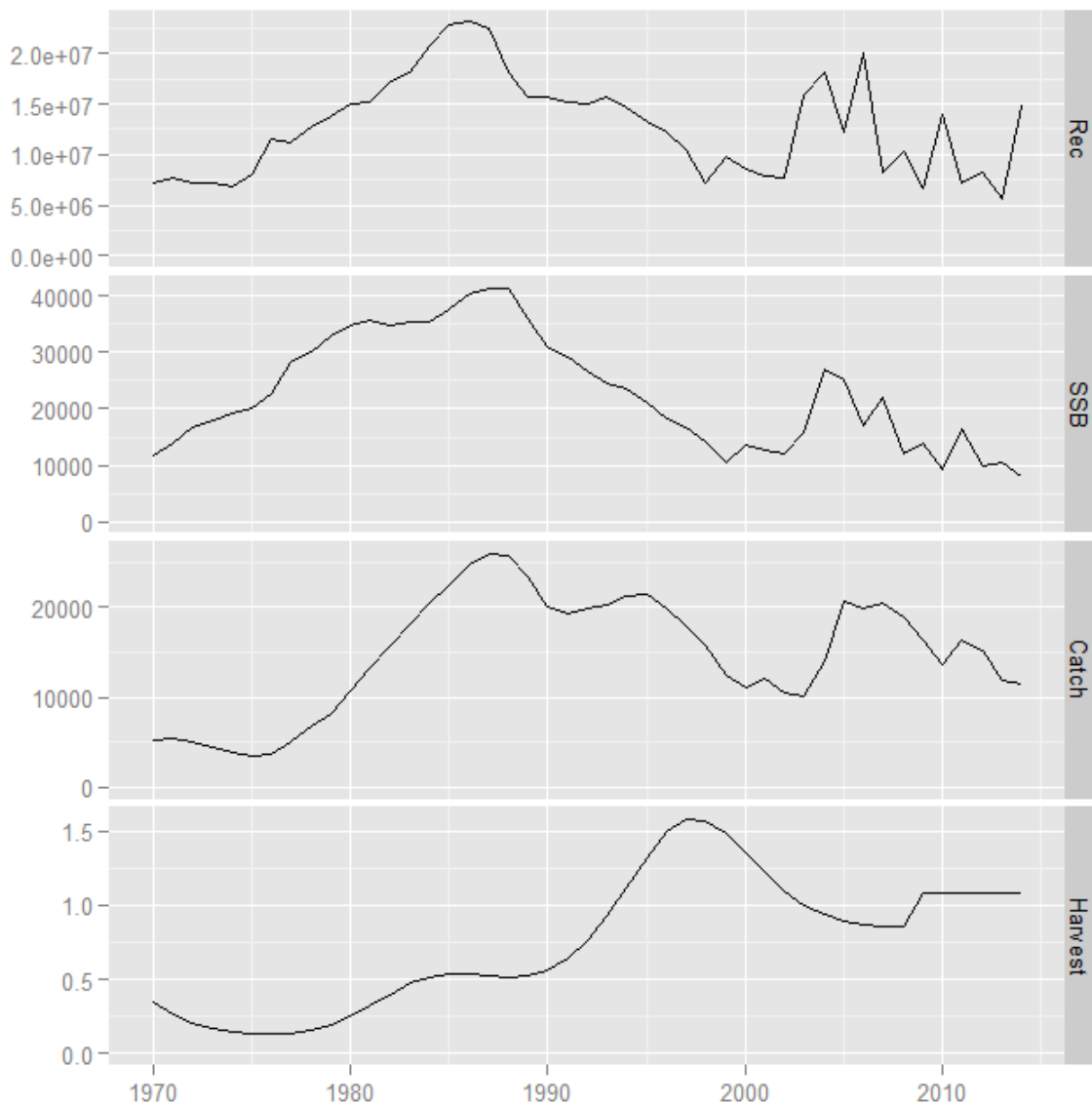
#### sst as covariate for ricker
cov <- c(index(ane22e.ind[[2]]))
cov <- c(cov, mean(cov))
srmod <- ~ricker(CV = 0.3, a = ~s(cov, k = 4))

### using
fit42 <- sca(ane22rbld.stk, ane22a.ind, qmodel = qmod, fmodel = fmod,
  srmodel = srmod, fit = "assessment") ####it converges
ane22.stk.a4a.42 <- ane22rbld.stk + fit42

plot(ane22.stk.a4a.42) #### very good

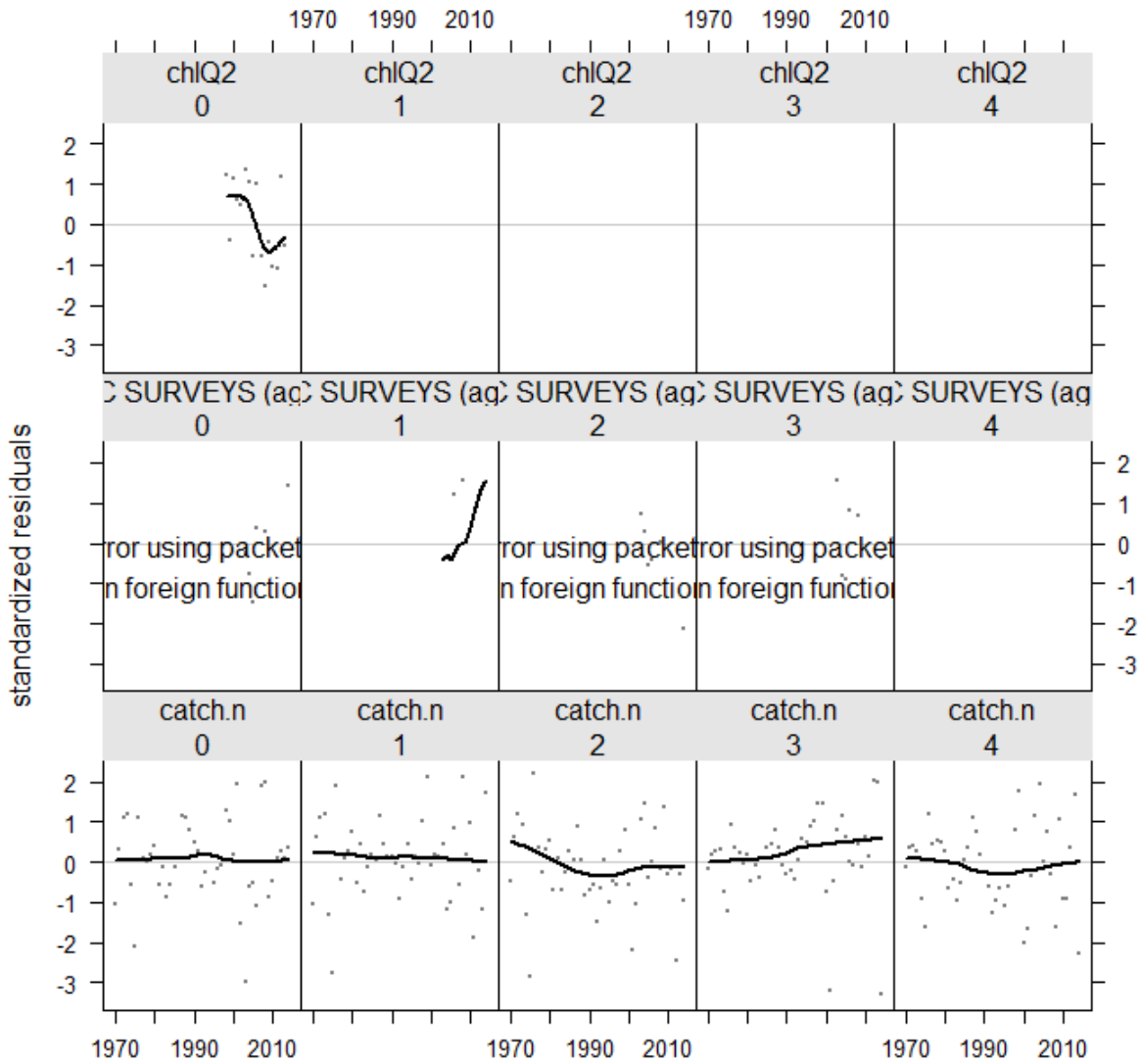
```

### Long time series



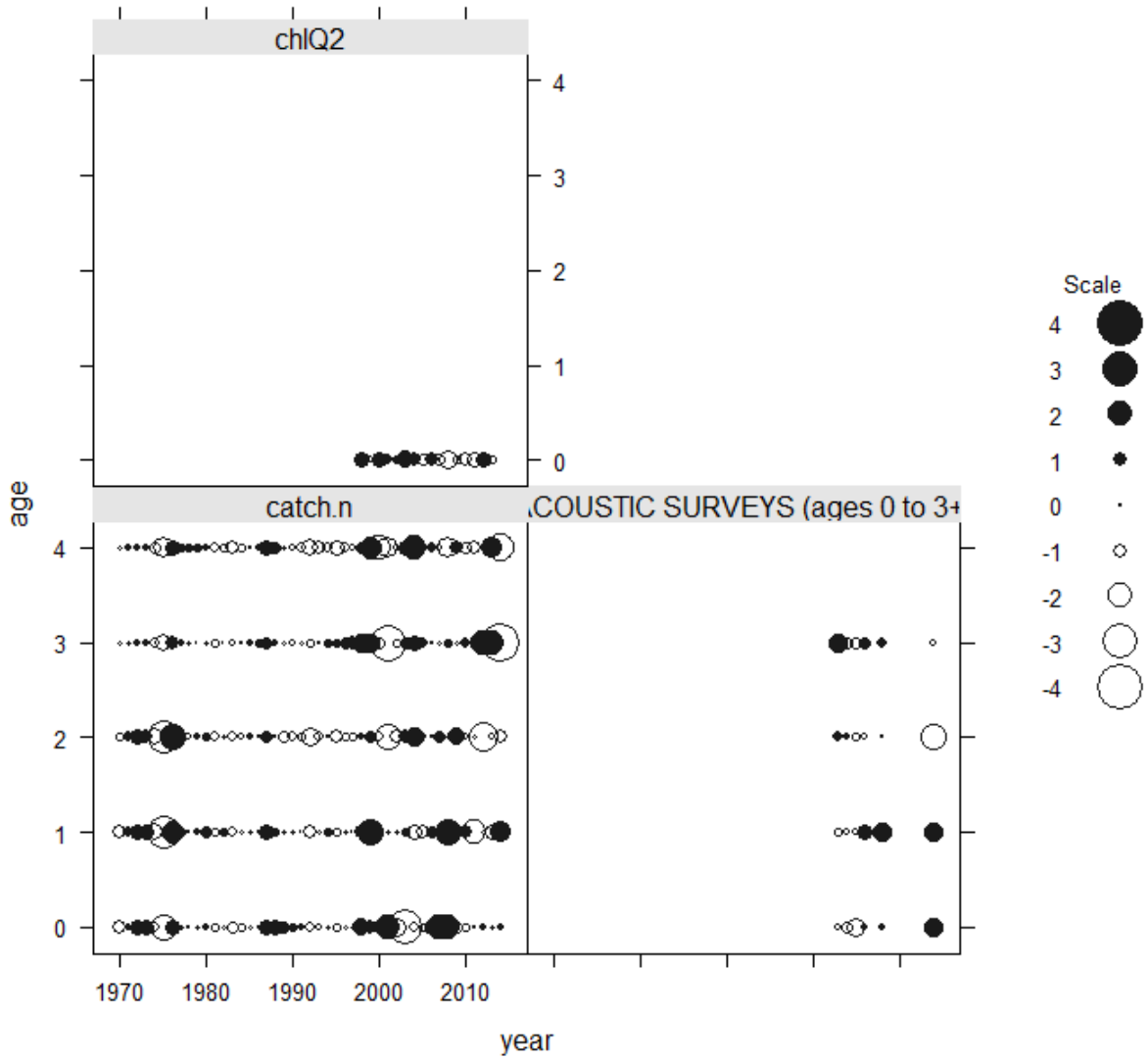
```
res <- residuals(fit42, ane22rbld.stk, ane22a.ind)
plot(res) ###ok!!!
```

### log residuals of catch and abundance indices



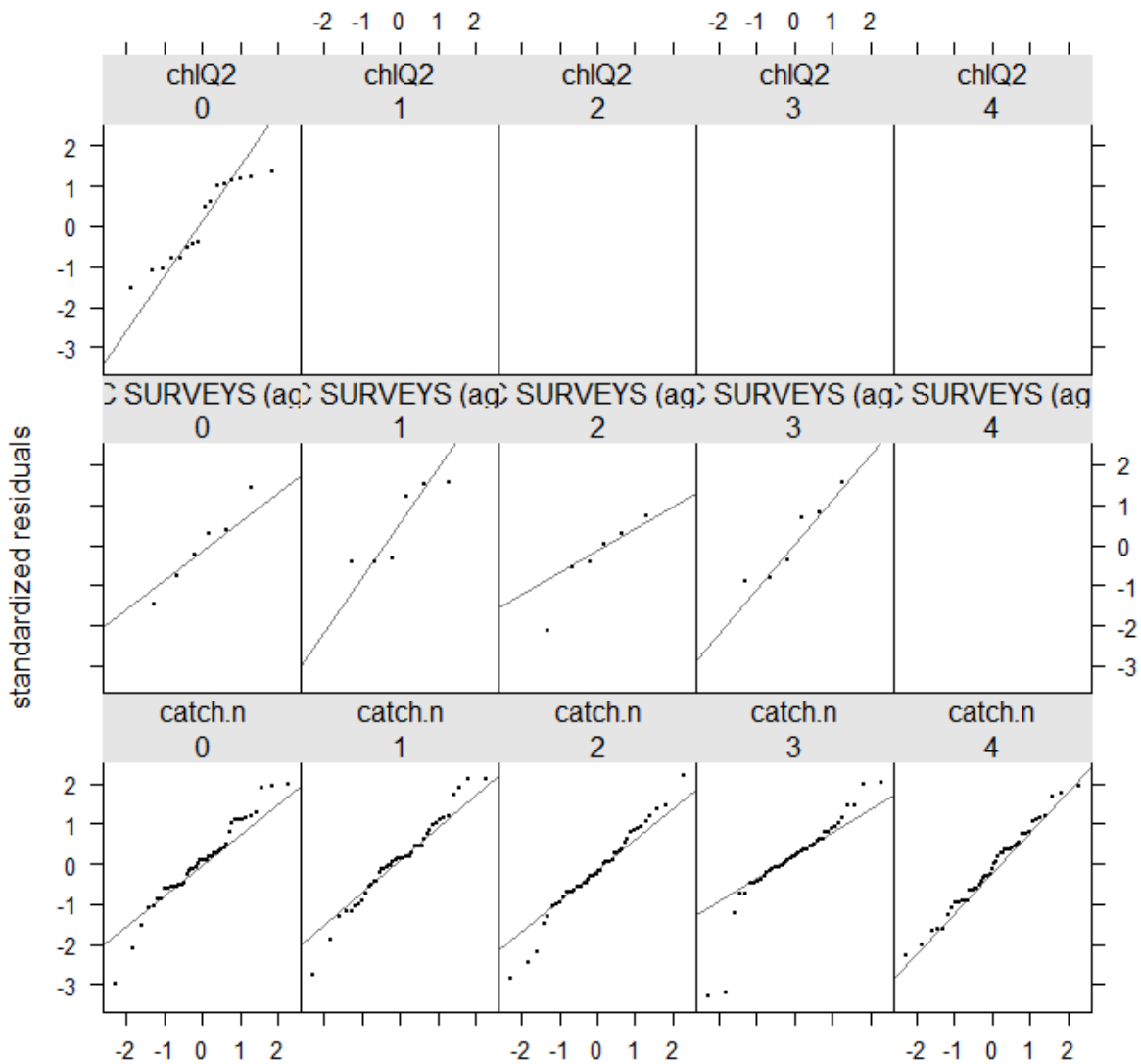
```
bubbles(res) # they look ok
```

## log residuals of catch and abundance indices

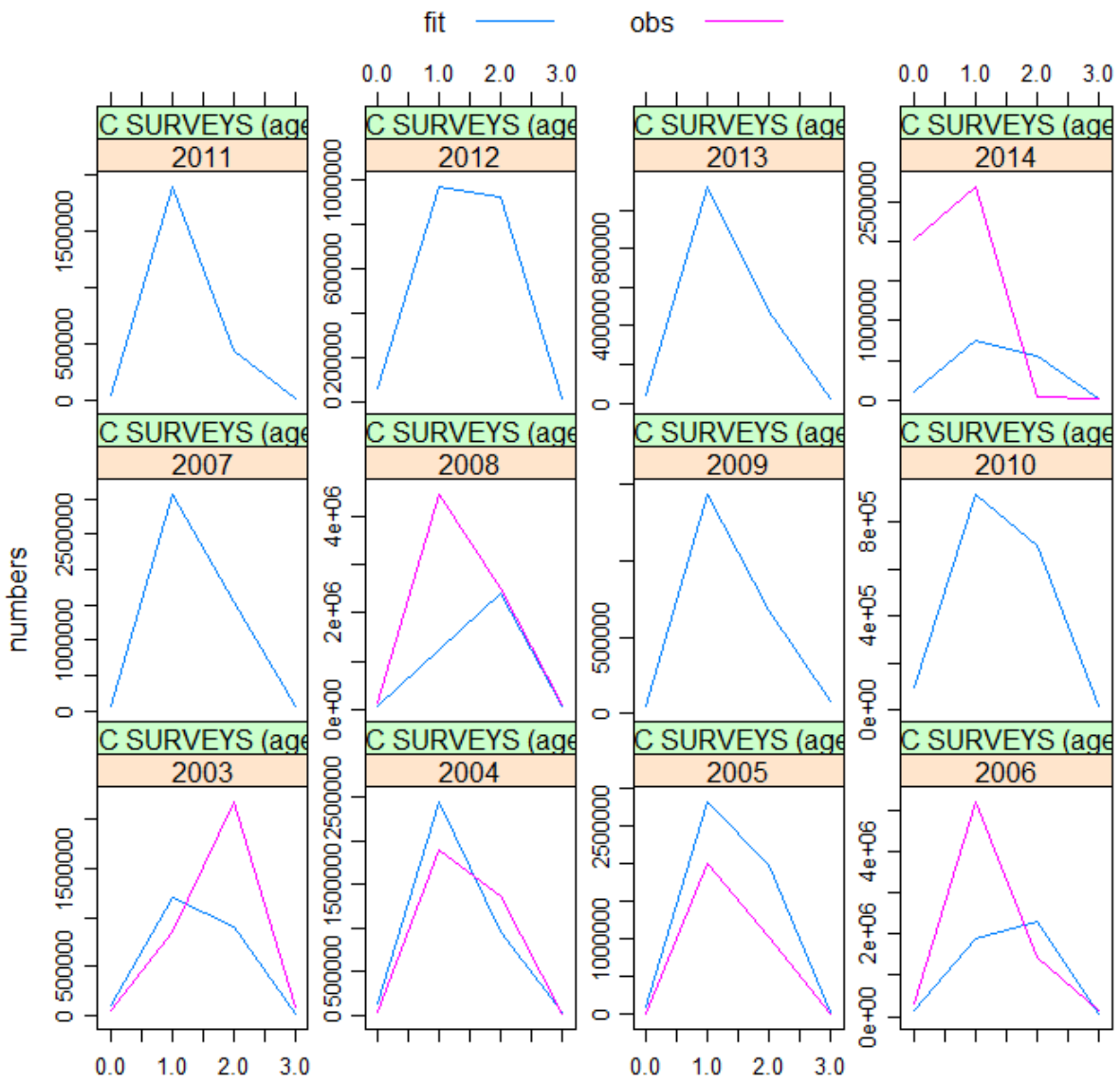


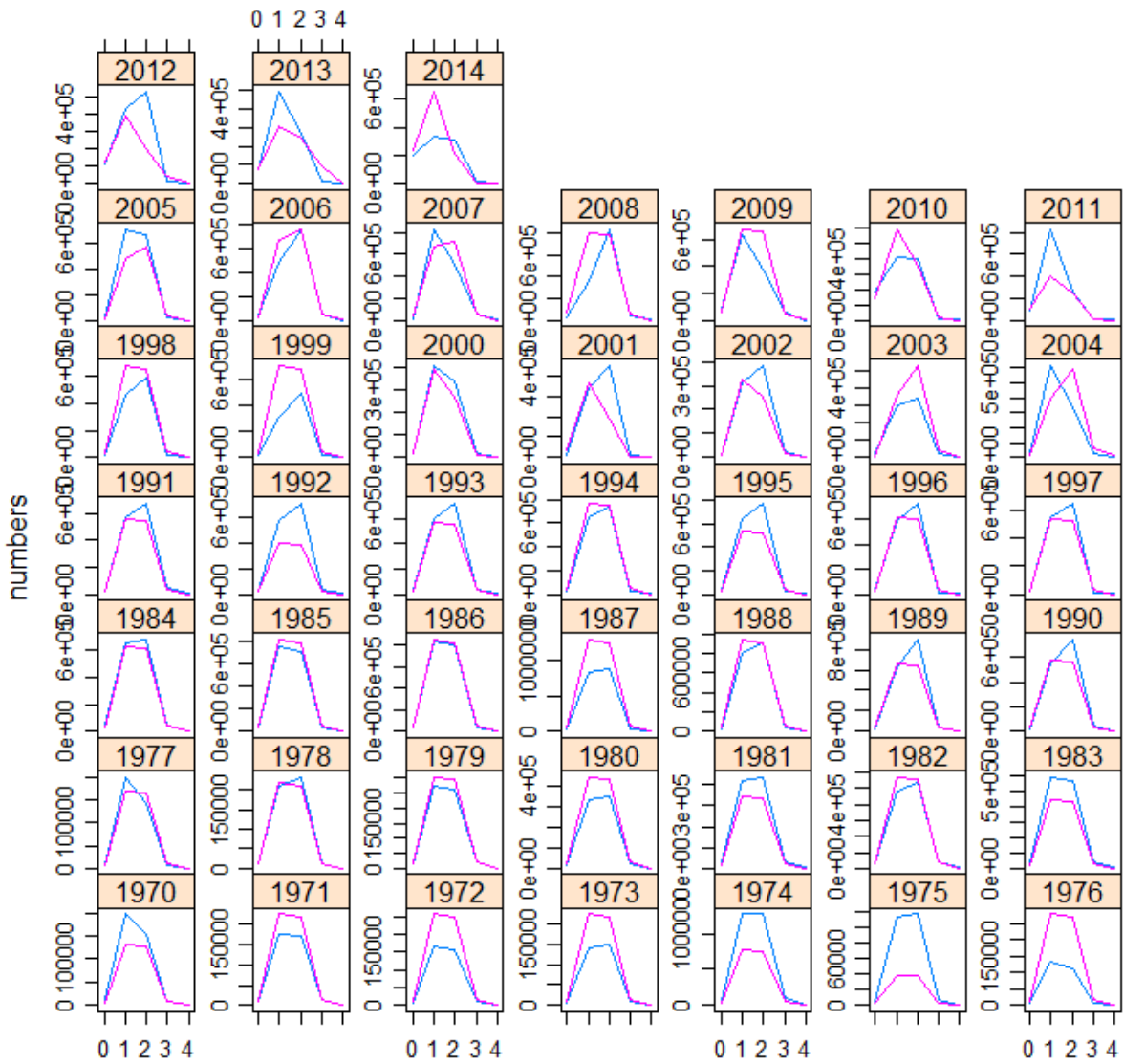
```
qqmath(res) # quantile plots rather ok, age 2 seems to have an outlier
```

### quantile-quantile plot of log residuals of catch and abundance indices



```
# Plot fitted against observed for survey
plot(fit42, AneG14.ind) ###can be improved, issue for the 2014 survey
# Plot fitted against observed for catch at age
plot(fit42, ane22rbld.stk) ### ok
```





```
AIC(fit42)
## [1] -1007.706

BIC(fit42)
## [1] -671.2114
```

### 5.1.3 Final model runs

```
##### Final models after numerous trials... ##### MOI instead of
##### Chla as an index
```

```

fmod <- ~te(age, replace(year, year > 2008, 2014), k = c(4, 7))
qmod <- list(~s(age, k = 3), ~s(year))

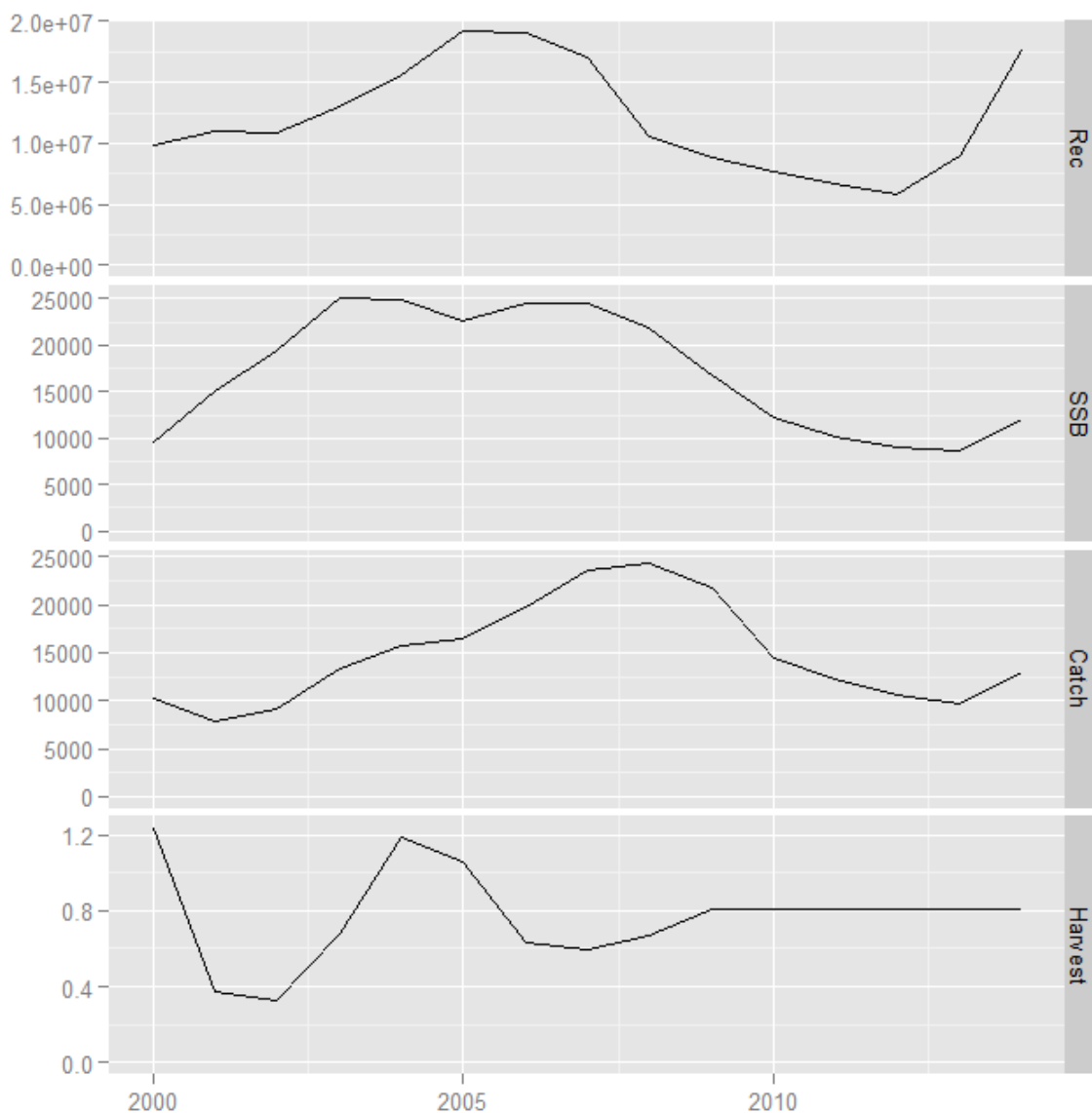
#### sst as covariate for ricker
cov <- c(index(window(ane22d.ind[[2]], start = 2000)))
cov <- c(cov, mean(cov))
srmod <- ~ricker(CV = 0.3, a = ~s(cov, k = 4))

### fit
fit40 <- sca(trim(ane22rbld.stk, year = 2000:2014), window(ane22e.ind,
  start = 2000), qmodel = qmod, fmodel = fmod, srmodel = srmod,
  fit = "assessment")
ane22.stk.a4a.40 <- trim(ane22rbld.stk, year = 2000:2014) + fit40

plot(ane22.stk.a4a.40) #### very good

```

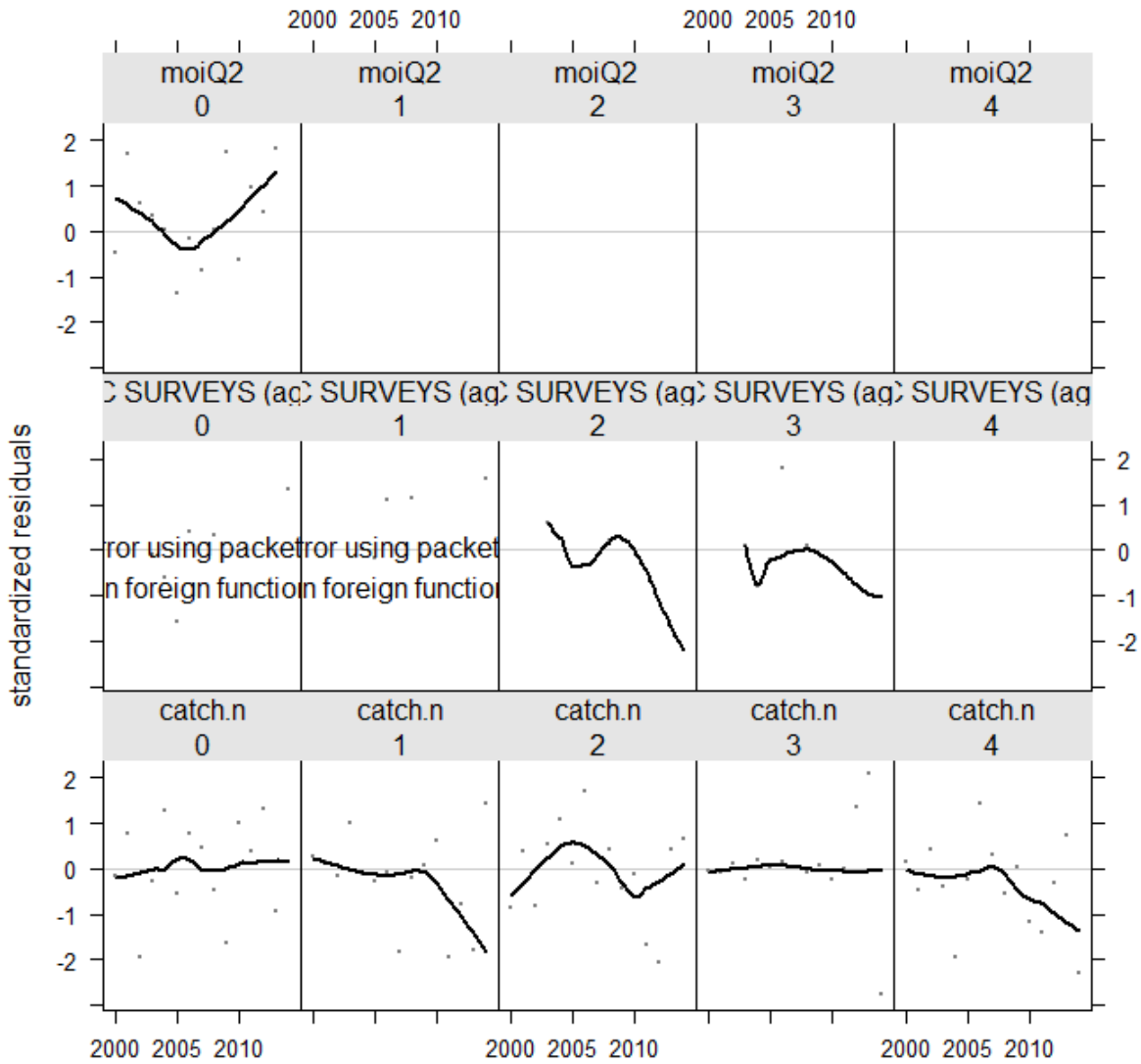
### Short time series





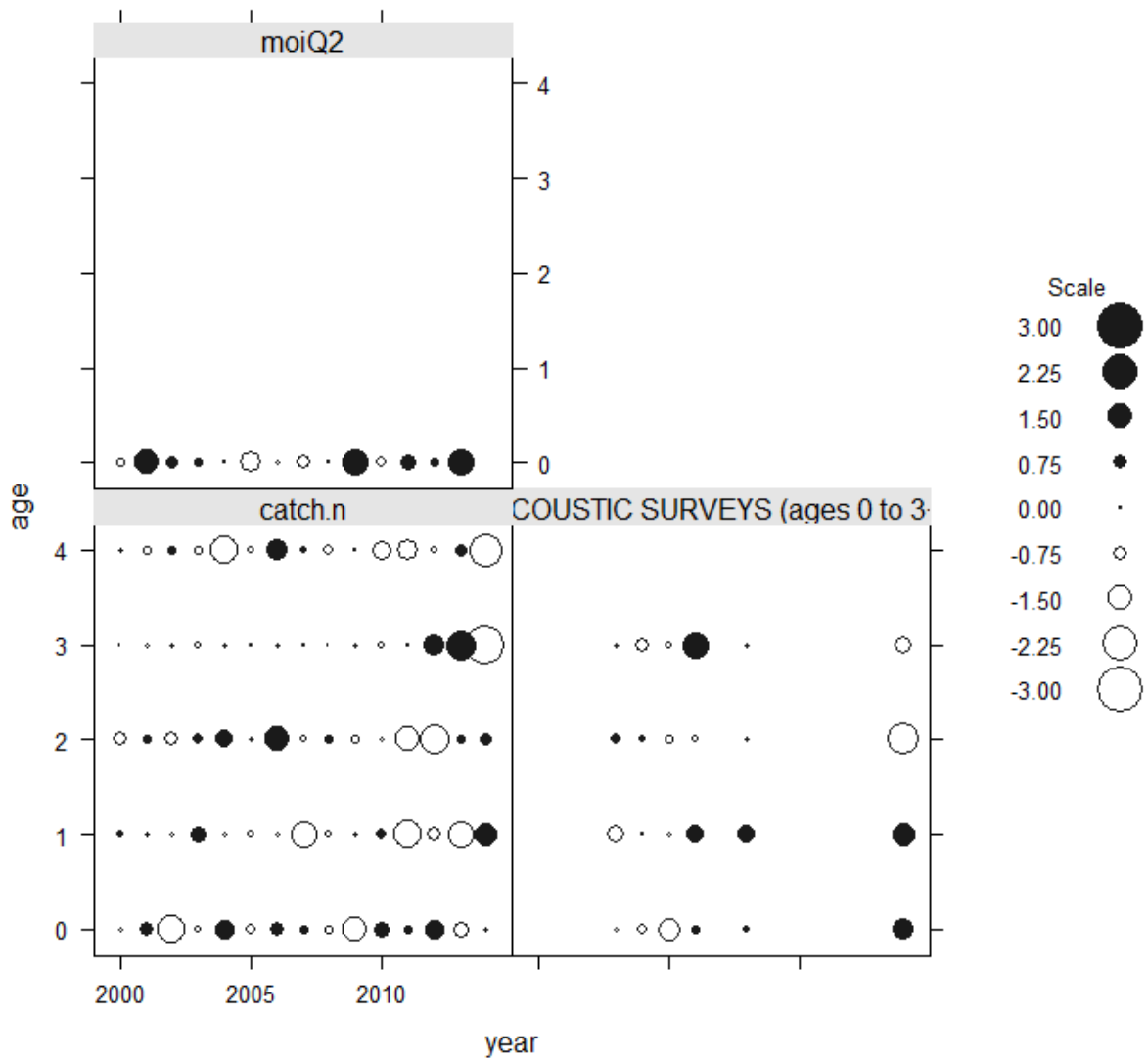
```
res <- residuals(fit40, trim(ane22rbld.stk, year = 2000:2014),
  window(ane22e.ind, start = 2000))
plot(res) ###ok!!!
```

### log residuals of catch and abundance indices



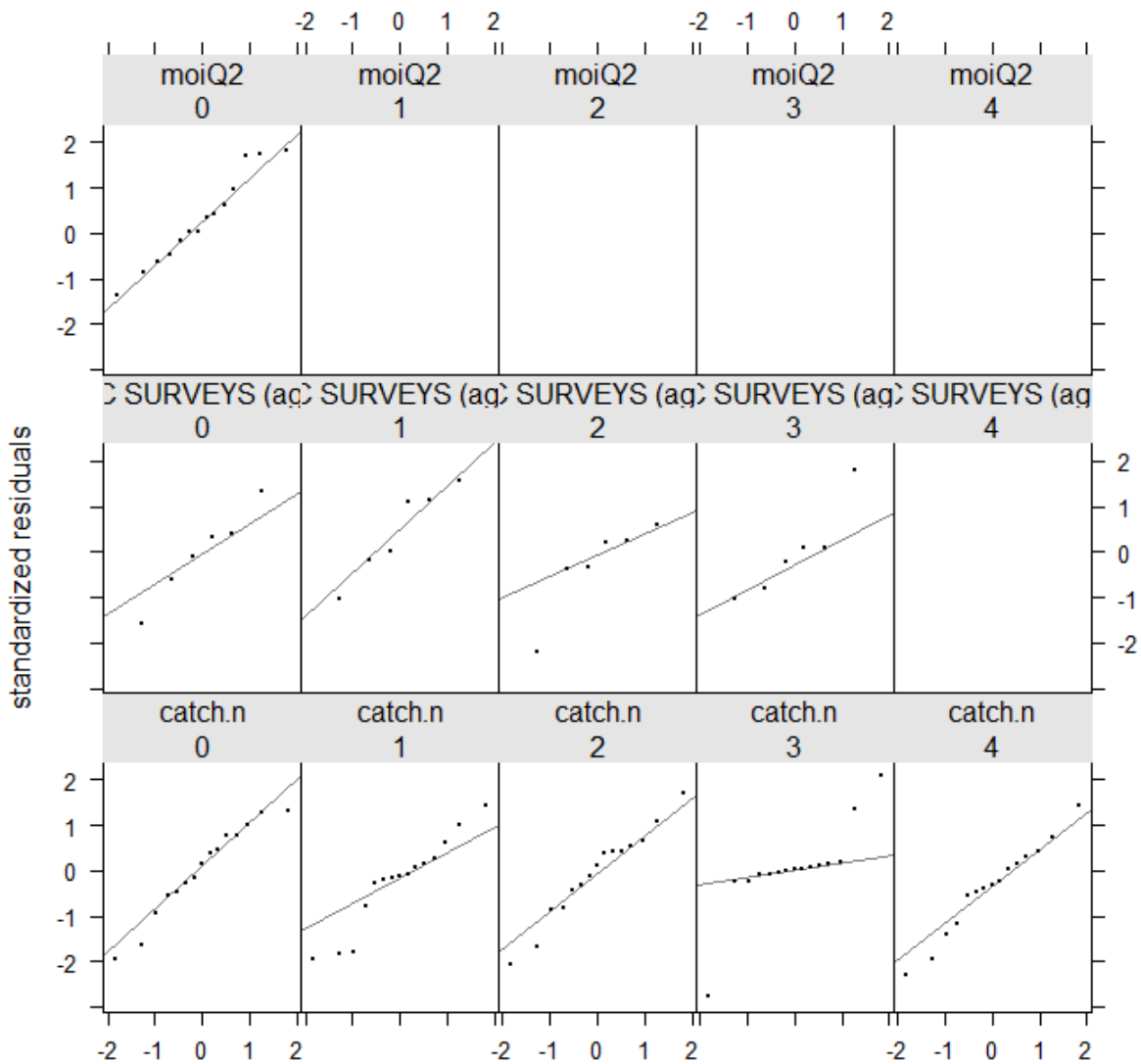
```
bubbles(res) # check the residuals plot
```

## log residuals of catch and abundance indices

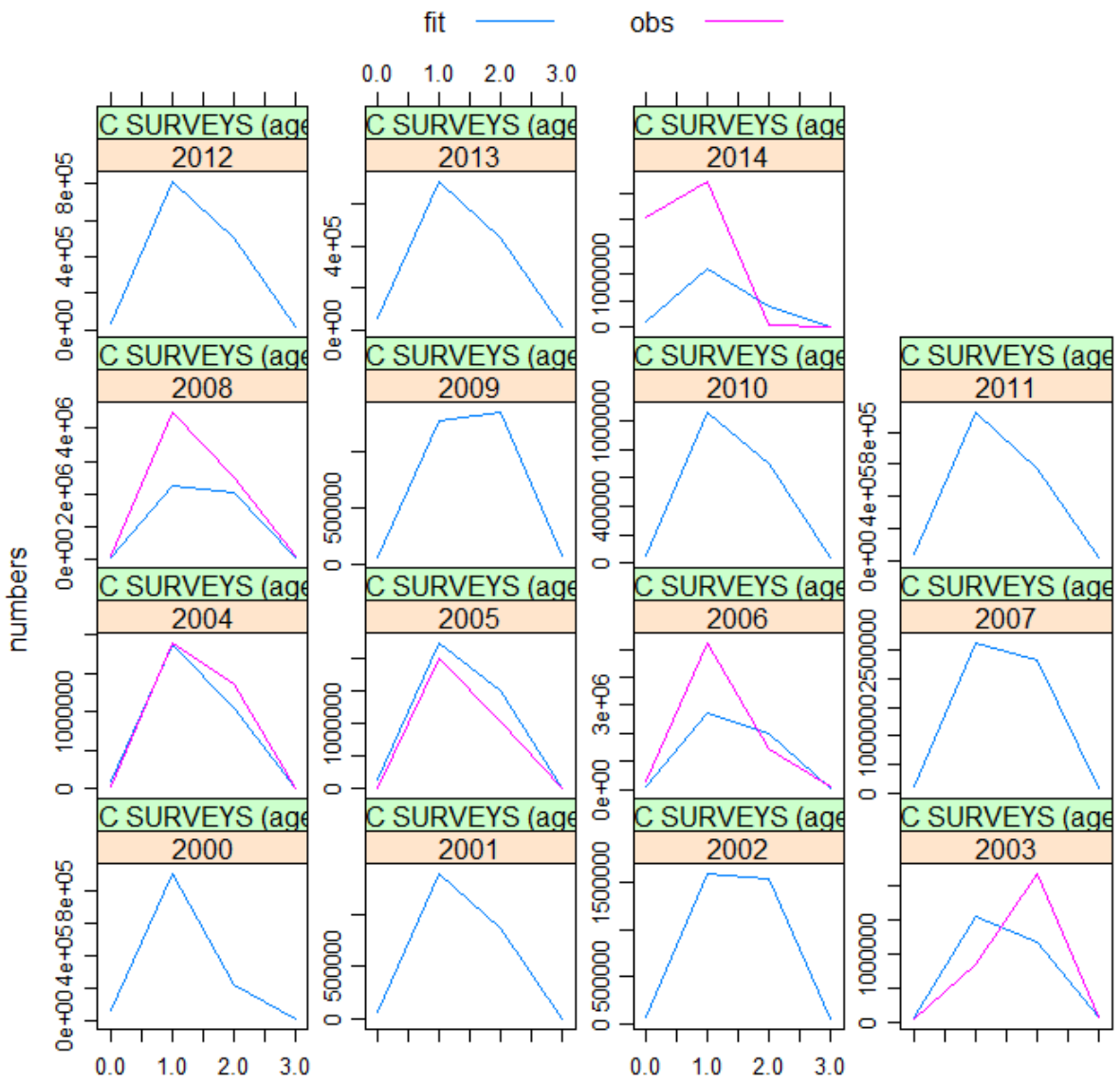


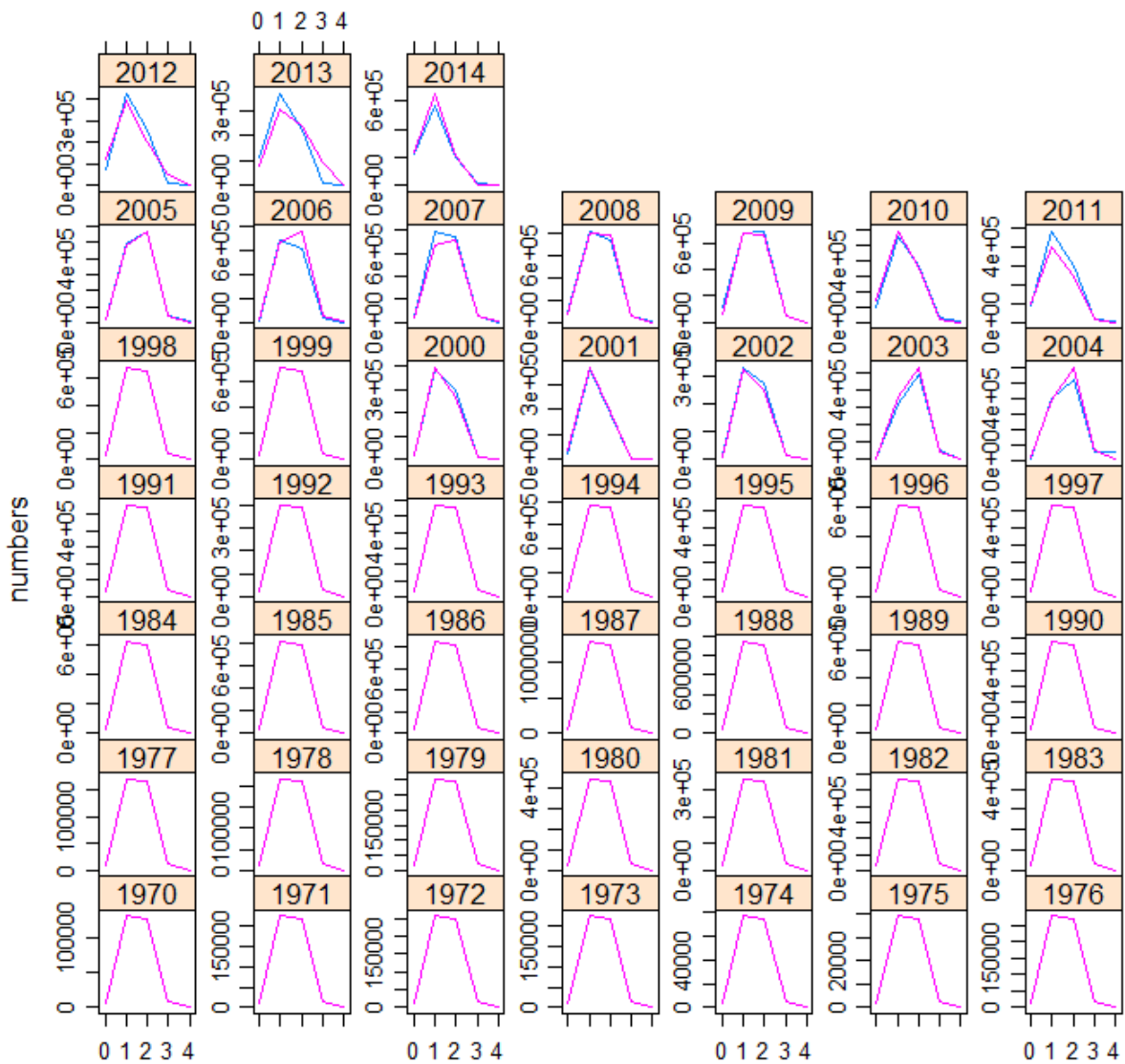
```
qqmath(res) # quantile plots rather ok output besides age 2
```

## quantile-quantile plot of log residuals of catch and abundance indices



```
# Plot fitted against observed for survey
plot(fit40, AneG14.ind) ###can be improved for 2014 survey
# Plot fitted against observed for catch at age
plot(fit40, ane22rbld.stk) ###good
```





```
AIC(fit40) ##-1495.196
```

```
## [1] -1495.196
```

```
BIC(fit40) ###-1304.279
```

```
## [1] -1304.279
```

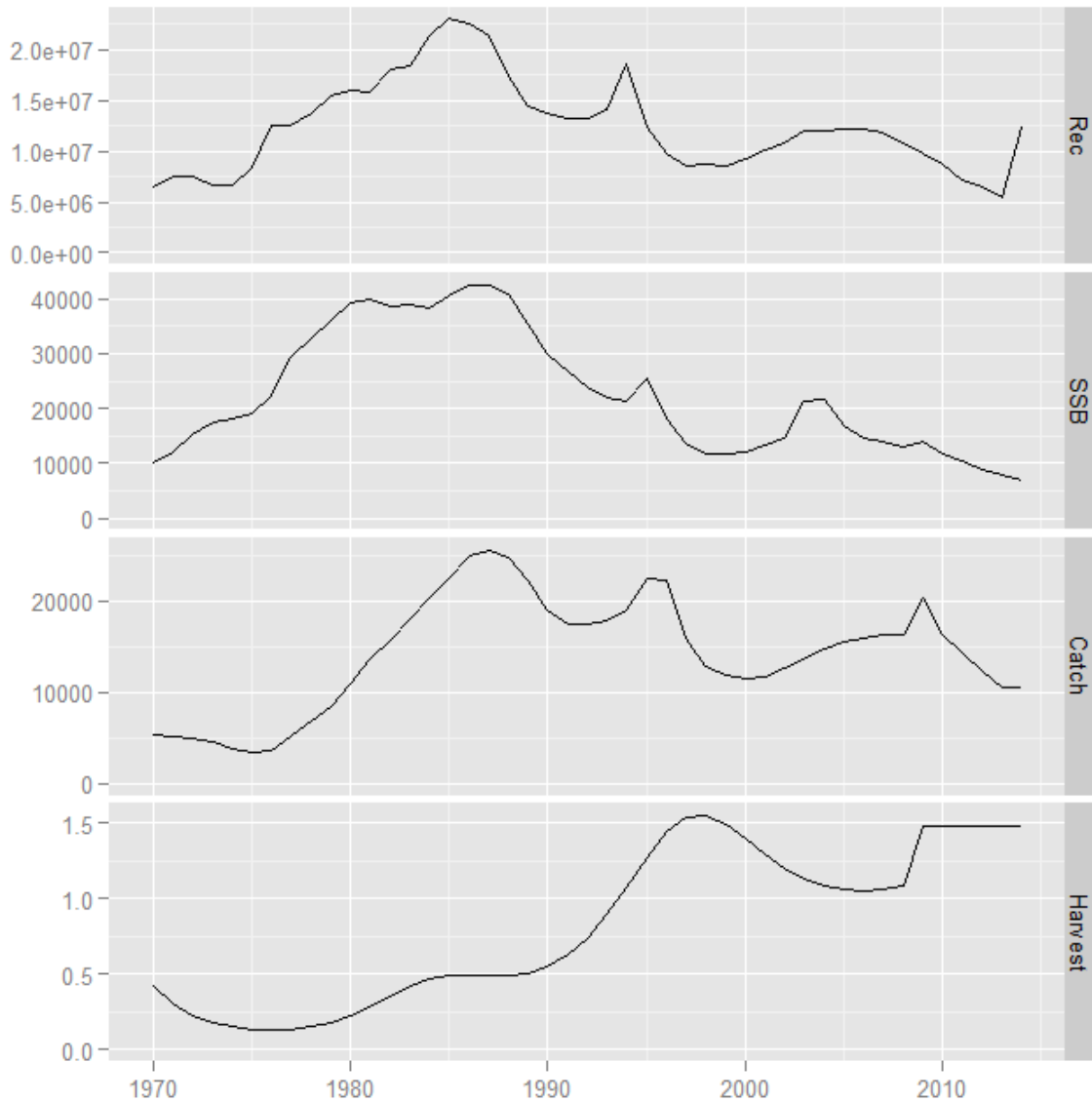
```
##### MOI as a covar for recruitment and sst along with surveys
##### for an index
fmod <- ~te(age, replace(year, year > 2008, 2014), k = c(4, 7))
qmod <- list(~s(age, k = 3), ~s(year, k = 4))
```

```
#### moi as covariate for ricker
cov <- c(index(ane22e.ind[[2]]))
cov <- c(cov, mean(cov))
srmod <- ~ricker(CV = 0.3, a = ~s(cov, k = 4))

### fit
fit51 <- sca(ane22rbld.stk, ane22d.ind, qmodel = qmod, fmodel = fmod,
            srmodel = srmod, fit = "assessment") ####it converges

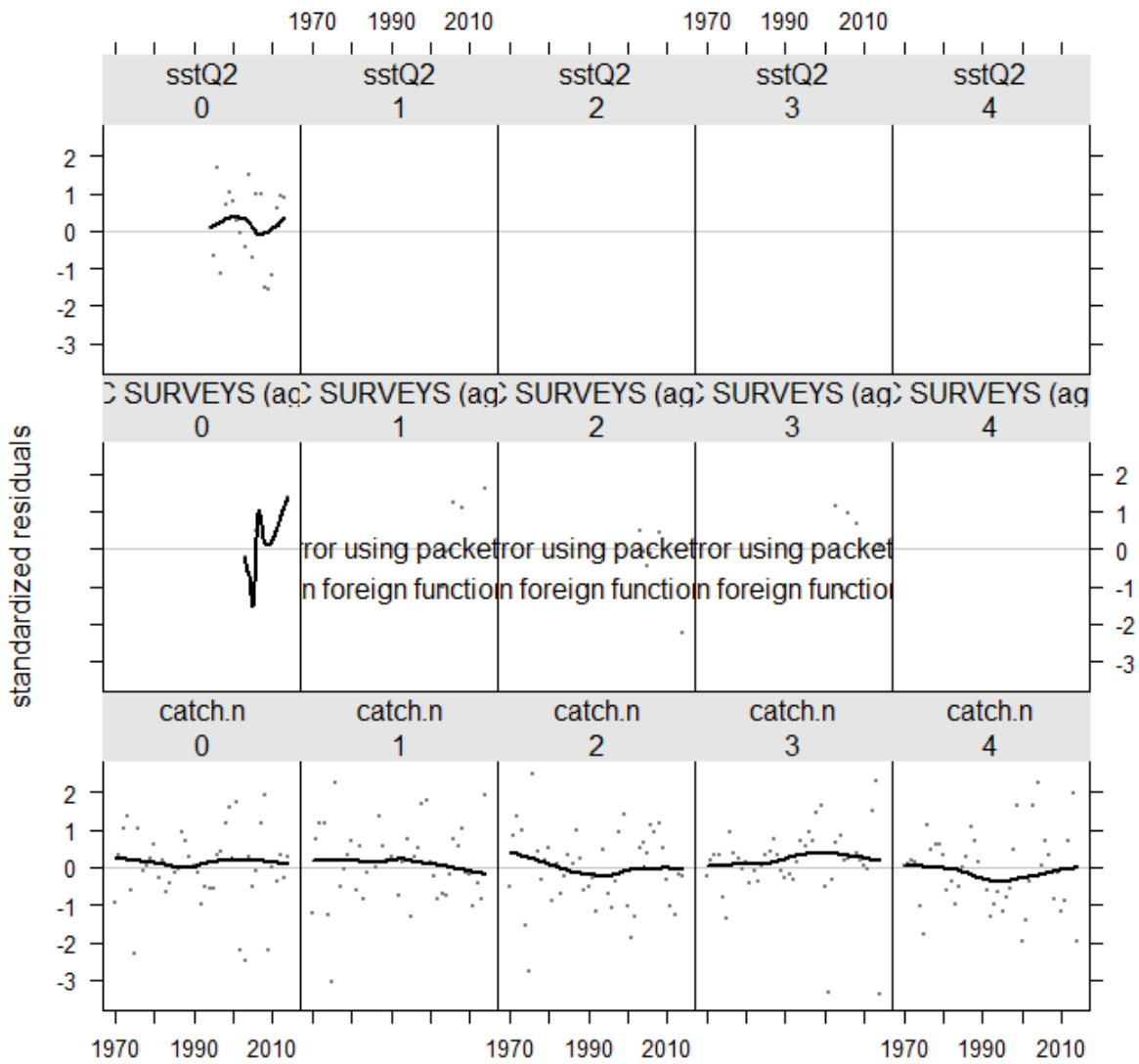
ane22.stk.a4a.51 <- ane22rbld.stk + fit51
plot(ane22.stk.a4a.51) #### very good
```

### Long time series



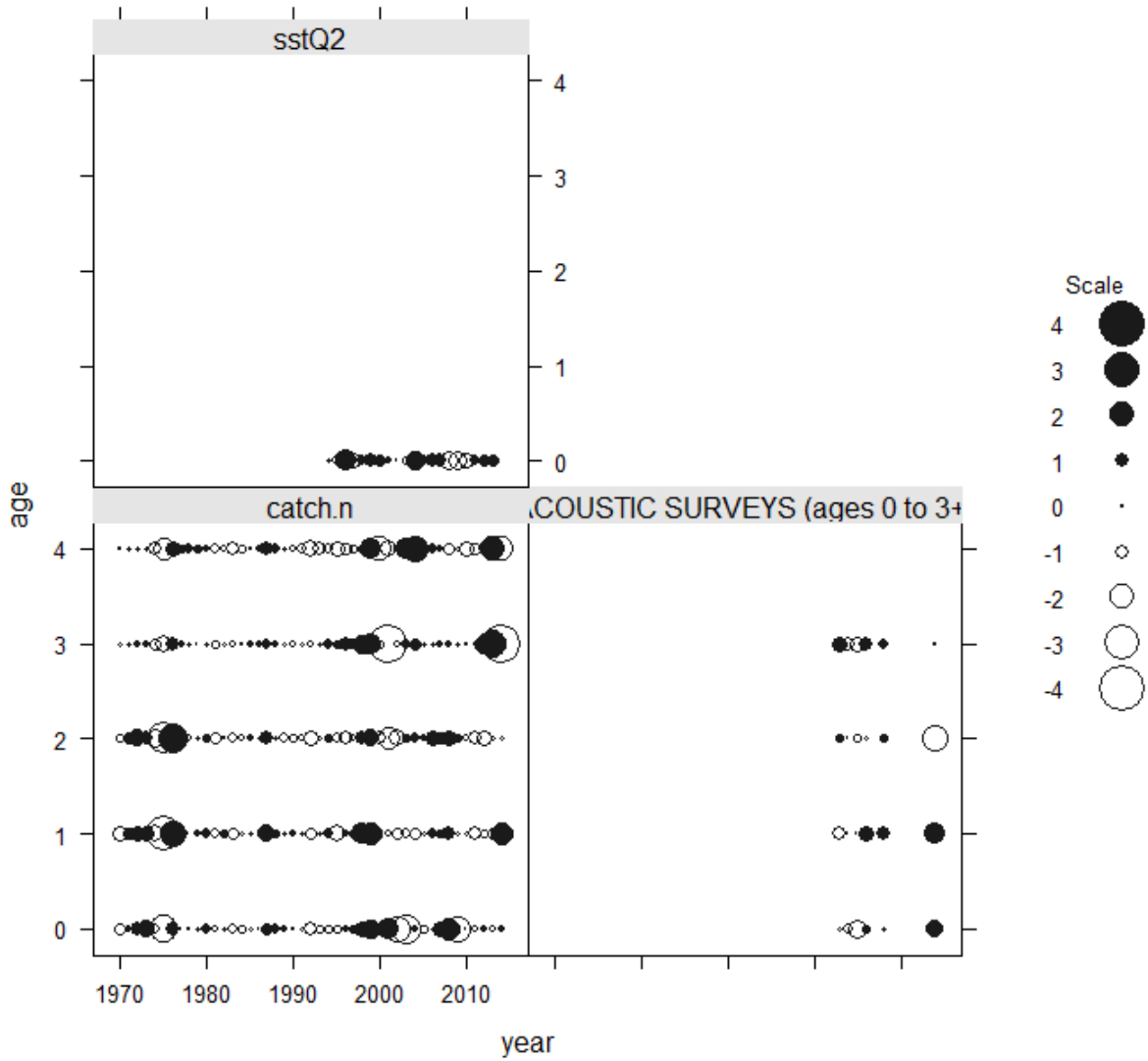
```
res <- residuals(fit51, ane22rbld.stk, ane22d.ind)
plot(res) ####ok!!!
```

## log residuals of catch and abundance indices



```
bubbles(res) # check the residuals, res have increased
```

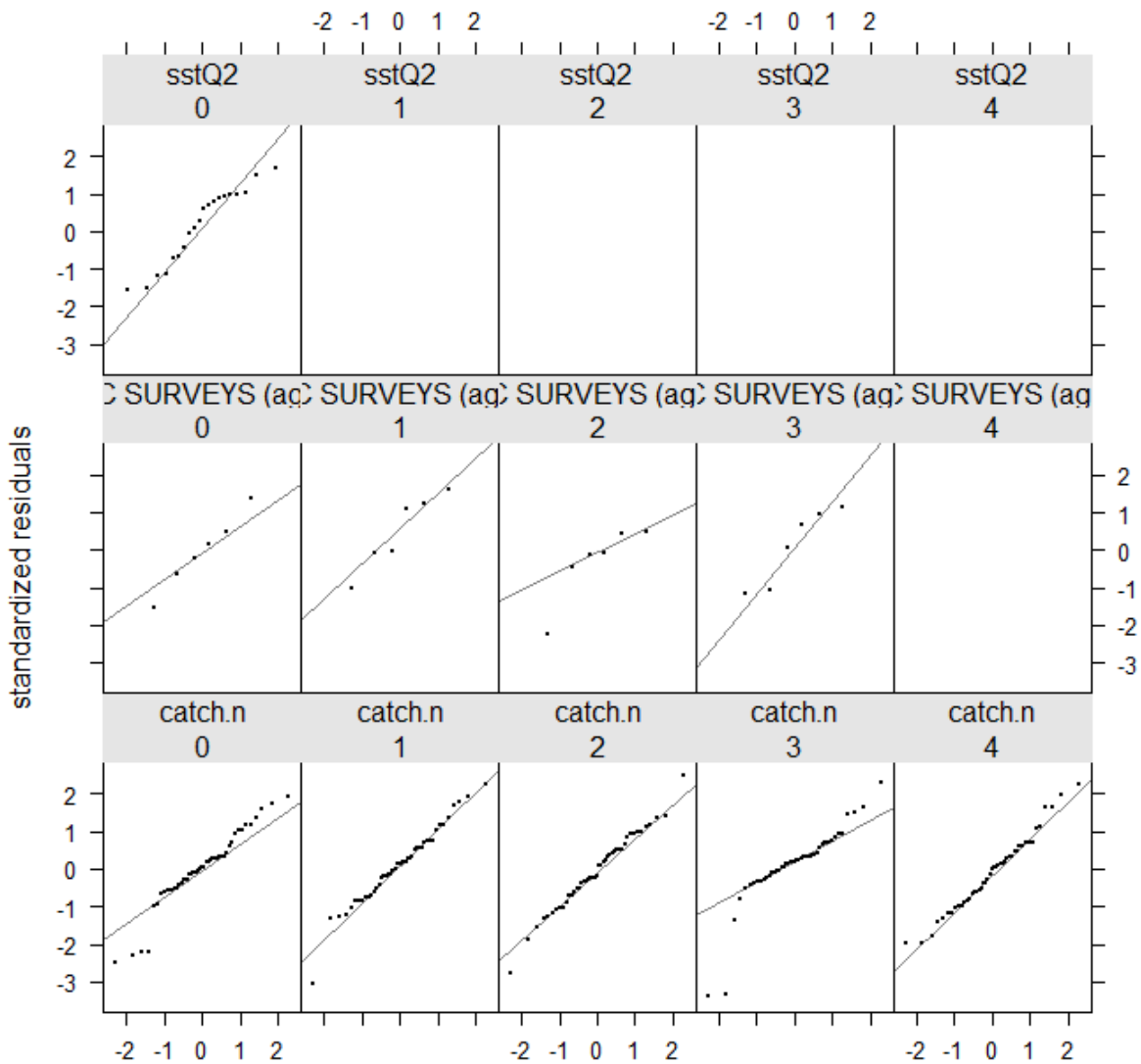
## log residuals of catch and abundance indices



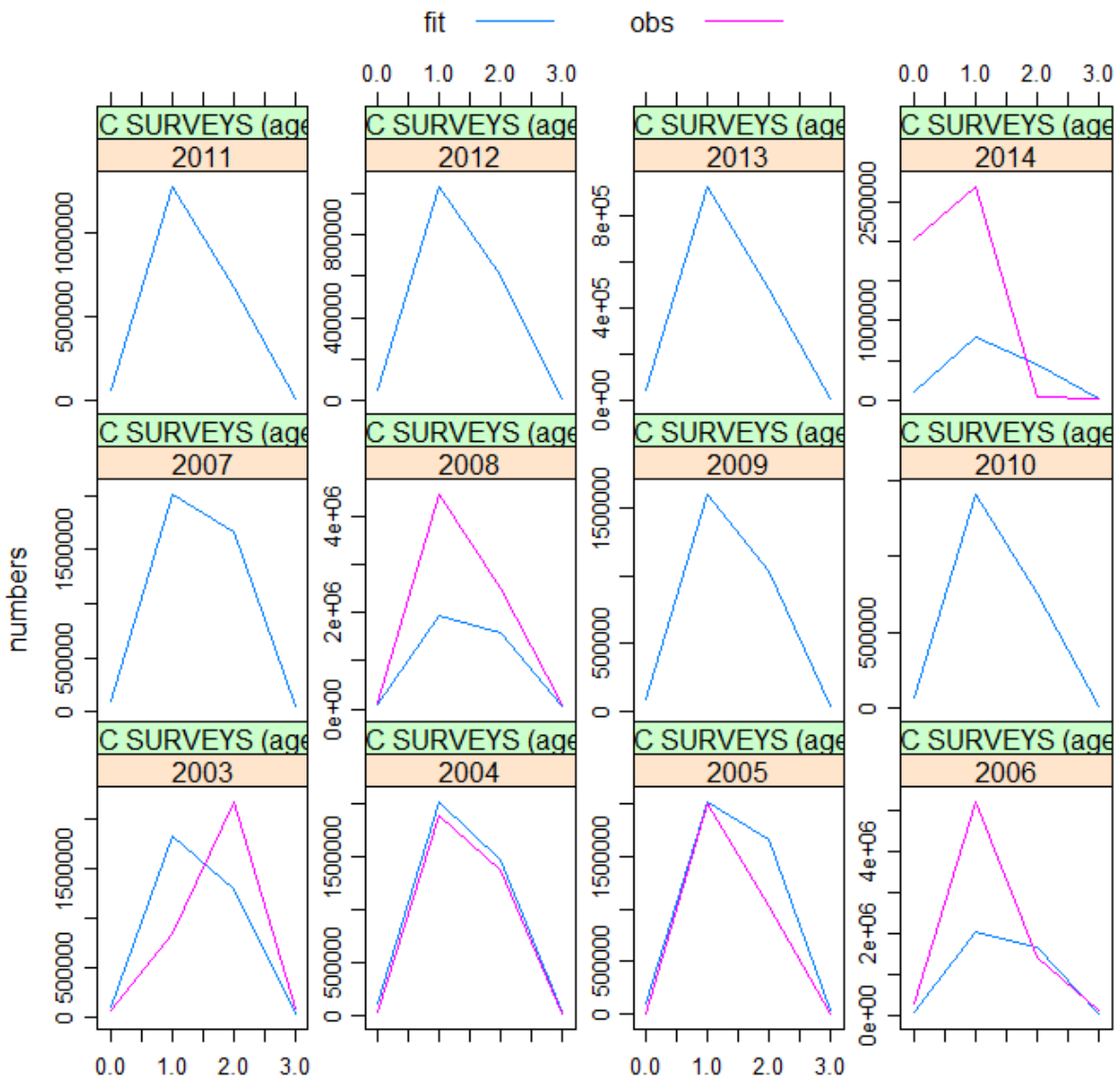
```
qqmath(res) # quantile plots rather ok, age 2 seems to have an outlier
```

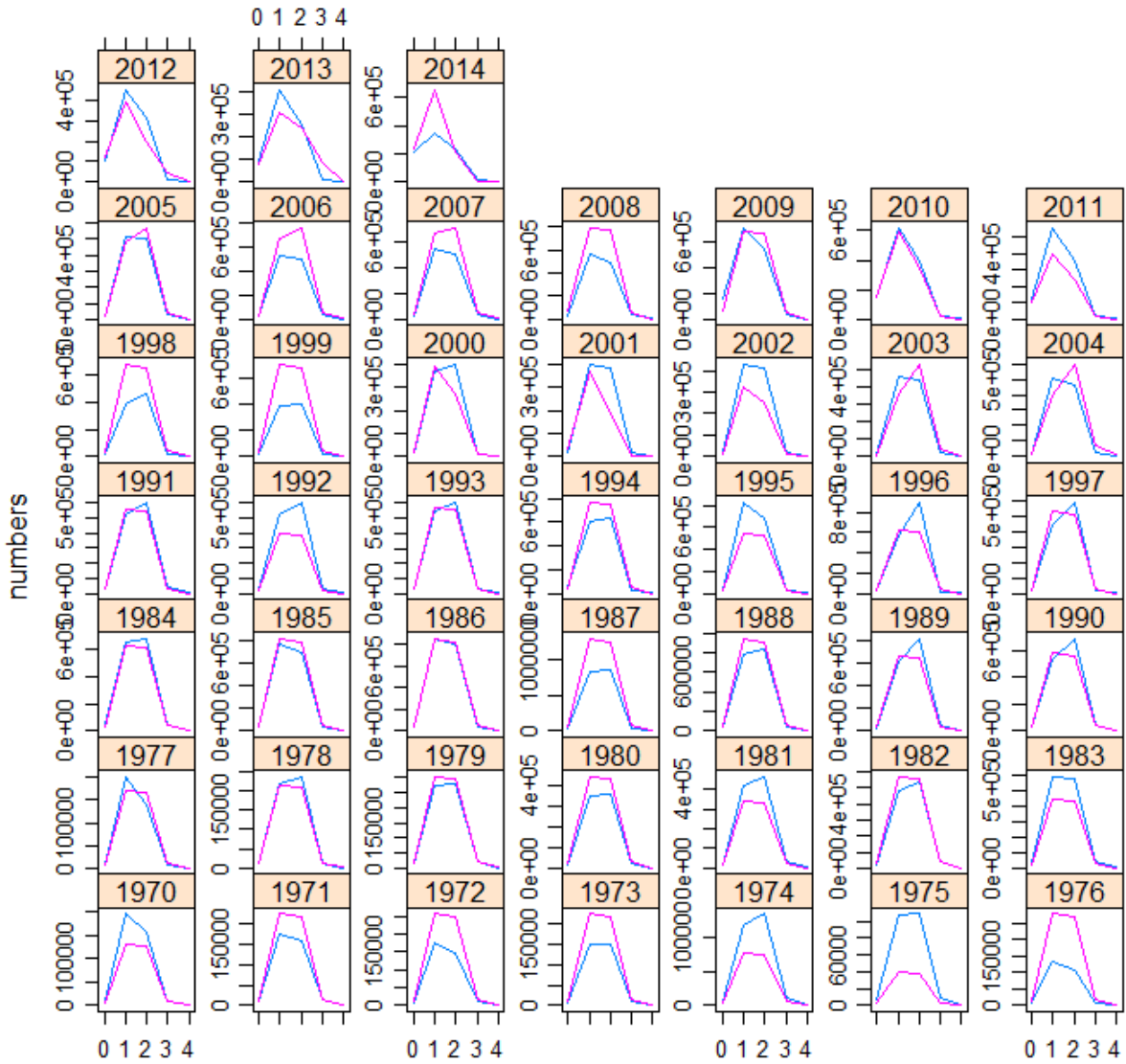


## quantile-quantile plot of log residuals of catch and abundance indices



```
# Plot fitted against observed for survey
plot(fit51, AneG14.ind) ###can be improved, issue for the 2014 survey
# Plot fitted against observed for catch at age
plot(fit51, ane22rbld.stk) ### better fit compared to chla
```





```
AIC(fit51)  ##-1738.902
```

```
## [1] -1738.902
```

```
BIC(fit51)  ###-1400.999
```

```
## [1] -1400.999
```

## 5.2 Sardine in GSA 22 (Aegean Sea)

### 5.2.1 Data and input

```

# stock and acoustic survey objects
load(".././data/aegean/SaeG14stk.Rdata")
load(".././data/aegean/SaeG14index.Rdata")
load(".././data/aegean/AneG14stk.Rdata")
load(".././data/aegean/AneG14index.Rdata")

# historical data
yh <- ac(1970:1999)
yNA <- ac(2009:2012)
yd <- ac(2004:2008, 2013, 2014)
lndHist.orig <- read.csv(".././data/historical/Historical_landings.csv")
load(".././data/historical/PScapacity.RData")

# build objects
pil22.stk <- window(Saeg14.stk, start = 2000)
pil22.stk <- window(Saeg14.stk, start = 1970)
catch(pil22.stk) <- landings(pil22.stk) <- lndHist.orig$sardine22
catch.wt(pil22.stk)[] <- yearMeans(catch.wt(pil22.stk)[, yd])
stock.wt(pil22.stk)[] <- yearMeans(stock.wt(pil22.stk)[, yd])
stock.wt(pil22.stk)[, yd] <- stock.wt(pil22.stk)[, yd]
m(pil22.stk)[, yh] <- yearMeans(m(pil22.stk))
mat(pil22.stk)[, yh] <- yearMeans(mat(pil22.stk))
harvest.spwn(pil22.stk)[, yh] <- yearMeans(harvest.spwn(pil22.stk))
m.spwn(pil22.stk)[, yh] <- yearMeans(m.spwn(pil22.stk))
pil22.ind <- Saeg14.ind
index.var(pil22.ind[[1]])[] <- 0.3
pil22.ind@.Data[[1]]@index[4, 12] <- 1

# rebuild catch at age
flq <- catch.wt(pil22.stk)
flq[] <- apply(catch.wt(pil22.stk) * catch.n(pil22.stk), 2, function(x) x/sum(x))
flq[, "2009"] <- flq[, "2008"]
flq[, "2012"] <- flq[, "2013"]
flq[, "2010"] <- yearMeans(flq[, c("2008", "2013")])
flq[, "2011"] <- yearMeans(flq[, c("2008", "2013")])
flq[, ac(1970:1999)] <- yearMeans(flq[, ac(2000:2008)])
flq <- flq * catch(pil22.stk)[rep(1, 5)]/catch.wt(pil22.stk)
pil22rbld.stk <- pil22.stk
flq <- FLQuantDistr(flq, flq)
flq@var[] <- 0.3
flq@var[, ac(1970:1999, 2009:2012)] <- 0.5
catch.n(pil22rbld.stk) <- flq

# environmental indices
load(".././data/aegean/chltr4a_index.Rdata")
load(".././data/aegean/SSTtr4a_index.Rdata")
load(".././data/oscillation_indices/naotr3_index.Rdata")
load(".././data/oscillation_indices/moitr2_Isr_index.Rdata")

```

```

flq <- index(chltr4a_index)
dimnames(flq)[1] <- 0
quant(flq) <- "age"
pil22.ind$chlQ4 <- FLIndex(index = flq)
range(pil22.ind$chlQ4)[c("startf", "endf")] <- c(0.75, 1)
index.var(pil22.ind$chlQ4)[] <- 0.4

flq <- index(naotr3_index) + 3
dimnames(flq)[1] <- 0
quant(flq) <- "age"
pil22.ind$naoQ3 <- FLIndex(index = flq)
range(pil22.ind$naoQ3)[c("startf", "endf")] <- c(0.5, 0.75)
index.var(pil22.ind$naoQ3)[] <- 0.4

flq <- index(SSTtr4a_index)
dimnames(flq)[1] <- 0
quant(flq) <- "age"
pil22.ind$sstQ4 <- FLIndex(index = flq)
range(pil22.ind$sstQ4)[c("startf", "endf")] <- c(0.75, 1)
index.var(pil22.ind$sstQ4)[] <- 0.4

flq <- index(moitr2_Isr_index) + 3
dimnames(flq)[1] <- 0
quant(flq) <- "age"
pil22.ind$moiQ2 <- FLIndex(index = flq)
range(pil22.ind$moiQ2)[c("startf", "endf")] <- c(0.25, 0.5)
index.var(pil22.ind$moiQ2)[] <- 0.4

## build separate FLIndices with fewer indices
flq1 <- index(chltr4a_index)
dimnames(flq1)[1] <- 0
quant(flq1) <- "age"

flq2 <- index(naotr3_index) + 3
dimnames(flq2)[1] <- 0
quant(flq2) <- "age"

flq3 <- index(SSTtr4a_index)
dimnames(flq3)[1] <- 0
quant(flq3) <- "age"

flq4 <- index(moitr2_Isr_index) + 3
dimnames(flq4)[1] <- 0
quant(flq4) <- "age"

# -chla4 only
pil22a.ind <- Saeg14.ind
pil22a.ind$chlQ4 <- FLIndex(index = flq1)
range(pil22a.ind$chlQ4)[c("startf", "endf")] <- c(0.75, 1)
index.var(pil22a.ind$chlQ4)[] <- 0.4
index.var(pil22a.ind[[1]])[] <- 0.3

```

```

pil22a.ind@.Data[[1]]@index[4, 12] <- 1

# -SST4 only
pil22b.ind <- Saeg14.ind
pil22b.ind$sstQ4 <- FLIndex(index = flq3)
range(pil22b.ind$sstQ4)[c("startf", "endf")] <- c(0.75, 1)
index.var(pil22b.ind$sstQ4)[] <- 0.4
index.var(pil22b.ind[[1]])[] <- 0.3
pil22b.ind@.Data[[1]]@index[4, 12] <- 1

# -nao3 only
pil22c.ind <- Saeg14.ind
pil22c.ind$naoQ3 <- FLIndex(index = flq2)
range(pil22c.ind$naoQ3)[c("startf", "endf")] <- c(0.5, 0.75)
index.var(pil22c.ind$naoQ3)[] <- 0.4
index.var(pil22c.ind[[1]])[] <- 0.3
pil22c.ind@.Data[[1]]@index[4, 12] <- 1

# -moi2 only
pil22d.ind <- Saeg14.ind
pil22d.ind$moiQ2 <- FLIndex(index = flq4)
range(pil22d.ind$moiQ2)[c("startf", "endf")] <- c(0.25, 0.5)
index.var(pil22d.ind$moiQ2)[] <- 0.4
index.var(pil22d.ind[[1]])[] <- 0.3
pil22d.ind@.Data[[1]]@index[4, 12] <- 1

# -chl4 & SST4
pil22e.ind <- Saeg14.ind
pil22e.ind$chlQ4 <- FLIndex(index = flq1)
range(pil22e.ind$chlQ4)[c("startf", "endf")] <- c(0.75, 1)
index.var(pil22e.ind$chlQ4)[] <- 0.4

pil22e.ind$sstQ4 <- FLIndex(index = flq3)
range(pil22e.ind$sstQ4)[c("startf", "endf")] <- c(0.75, 1)
index.var(pil22e.ind$sstQ4)[] <- 0.4
index.var(pil22e.ind[[1]])[] <- 0.3
pil22e.ind@.Data[[1]]@index[4, 12] <- 1

# -chl4 & nao3
pil22f.ind <- Saeg14.ind
pil22f.ind$chlQ4 <- FLIndex(index = flq1)
range(pil22f.ind$chlQ4)[c("startf", "endf")] <- c(0.75, 1)
index.var(pil22f.ind$chlQ4)[] <- 0.4

pil22f.ind$naoQ3 <- FLIndex(index = flq2)
range(pil22f.ind$naoQ3)[c("startf", "endf")] <- c(0.5, 0.75)
index.var(pil22f.ind$naoQ3)[] <- 0.4
index.var(pil22f.ind[[1]])[] <- 0.3
pil22f.ind@.Data[[1]]@index[4, 12] <- 1

# -sst 4& nao3

```

```

pil22g.ind <- Saeg14.ind
pil22g.ind$sstQ4 <- FLIndex(index = flq3)
range(pil22g.ind$sstQ4)[c("startf", "endf")] <- c(0.75, 1)
index.var(pil22g.ind$sstQ4)[] <- 0.4

pil22g.ind$naoQ3 <- FLIndex(index = flq2)
range(pil22g.ind$naoQ3)[c("startf", "endf")] <- c(0.5, 0.75)
index.var(pil22g.ind$naoQ3)[] <- 0.4
# -index.var(pil22g.ind[[1]])[] <- 0.3
index.var(pil22g.ind[[1]])[] <- 0.3
pil22g.ind@.Data[[1]]@index[4, 12] <- 1

# -chl4 & sst4 & nao3
pil22h.ind <- Saeg14.ind
pil22h.ind$chlQ4 <- FLIndex(index = flq1)
range(pil22h.ind$chlQ4)[c("startf", "endf")] <- c(0.75, 1)
index.var(pil22h.ind$chlQ4)[] <- 0.4

pil22h.ind$sstQ4 <- FLIndex(index = flq3)
range(pil22h.ind$sstQ4)[c("startf", "endf")] <- c(0.75, 1)
index.var(pil22h.ind$sstQ4)[] <- 0.4

pil22h.ind$naoQ3 <- FLIndex(index = flq2)
range(pil22h.ind$naoQ3)[c("startf", "endf")] <- c(0.5, 0.75)
index.var(pil22h.ind$naoQ3)[] <- 0.4
index.var(pil22h.ind[[1]])[] <- 0.3
pil22h.ind@.Data[[1]]@index[4, 12] <- 1

```

## 5.2.2 Initial model runs

```

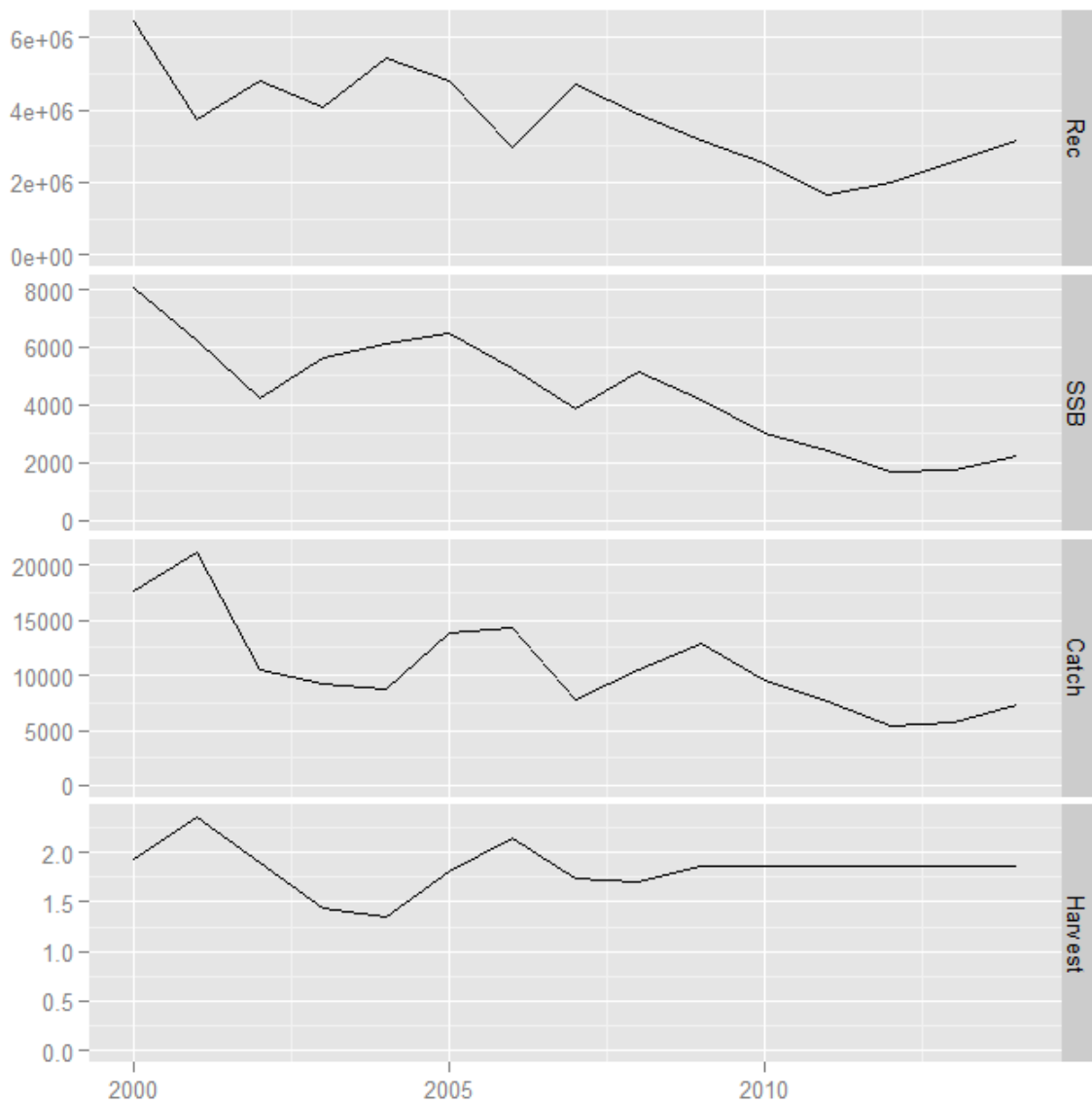
#### sst as covariate for ricker+Chla as an index along with
#### surveys
fmod <- ~te(age, replace(year, year > 2008, 2014), k = c(4, 9))
qmod <- list(~s(age, k = 3), ~s(year))
### set the SST as a covariate
cov <- c(index(window(pil22b.ind[[2]], start = 2000)))
cov <- c(cov, mean(cov))
srmod <- ~ricker(CV = 0.3, a = ~s(cov, k = 4))

fit42 <- sca(trim(pil22rbld.stk, year = 2000:2014), window(pil22a.ind,
  start = 2000), qmodel = qmod, fmodel = fmod, srmodel = srmod,
  fit = "assessment") ###it converges
pil22.stk.a4a.42 <- trim(pil22rbld.stk, year = 2000:2014) + fit42

plot(pil22.stk.a4a.42) # harvest up to 2.4, catches good

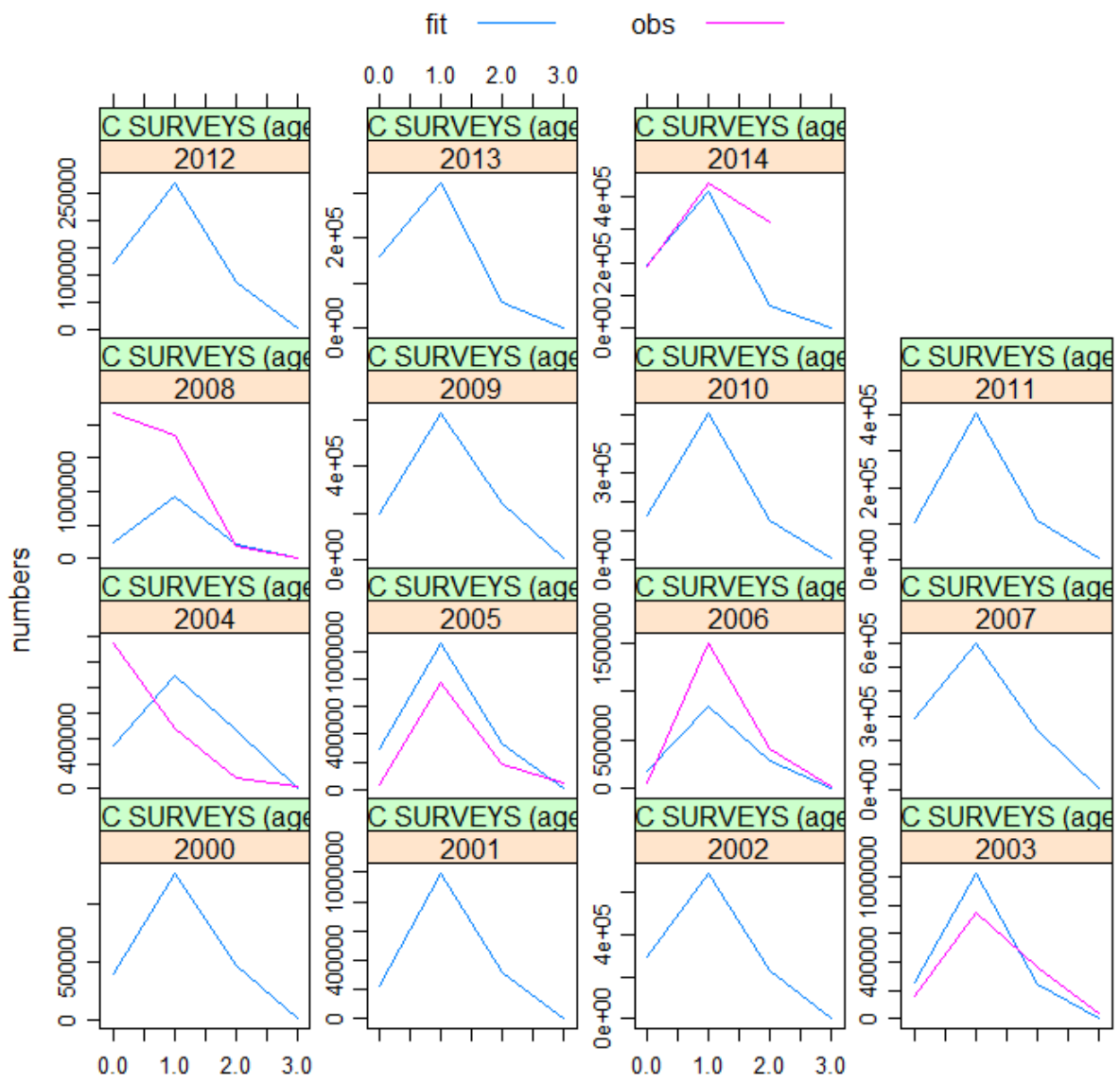
```

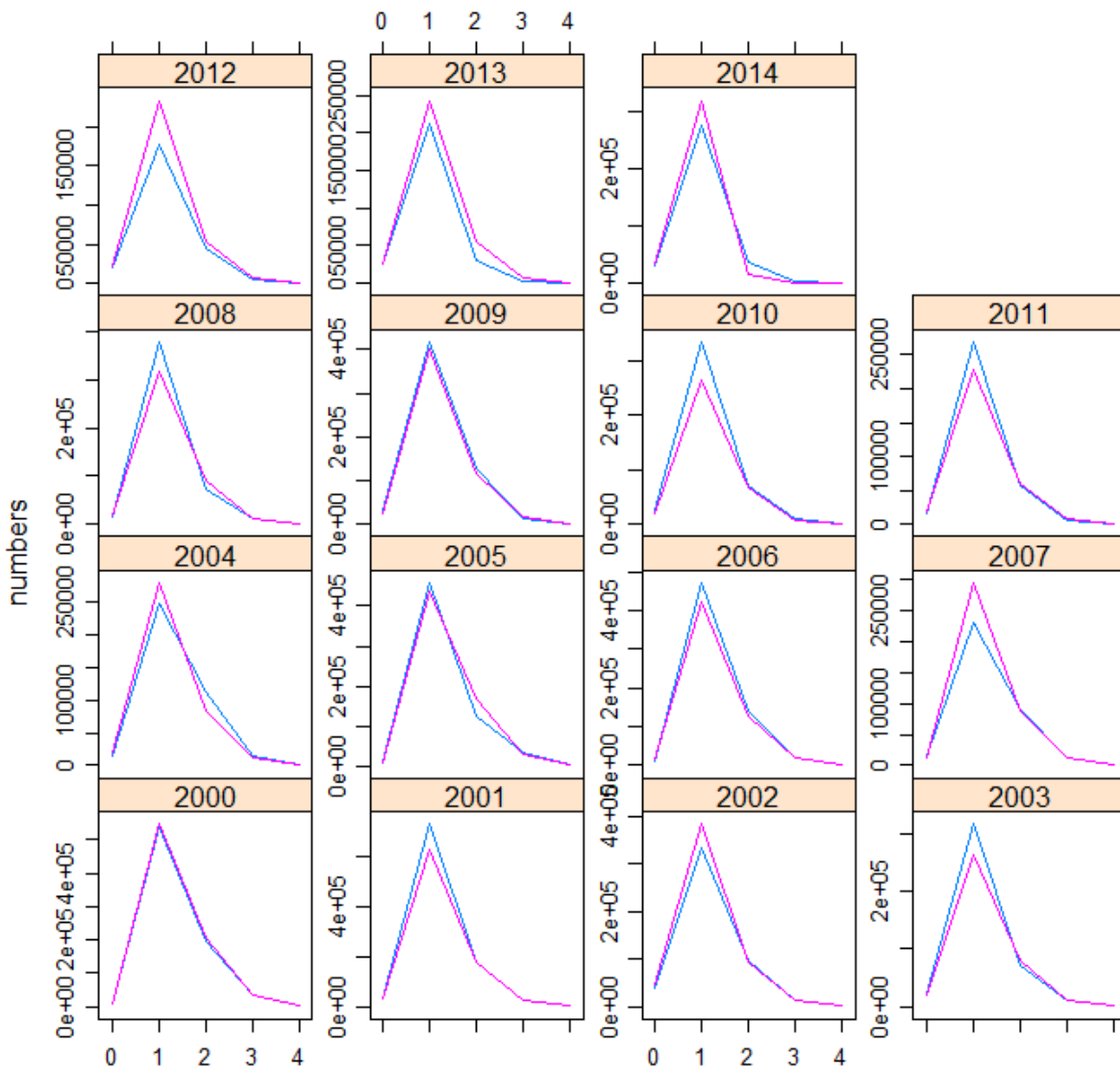
## Short time series



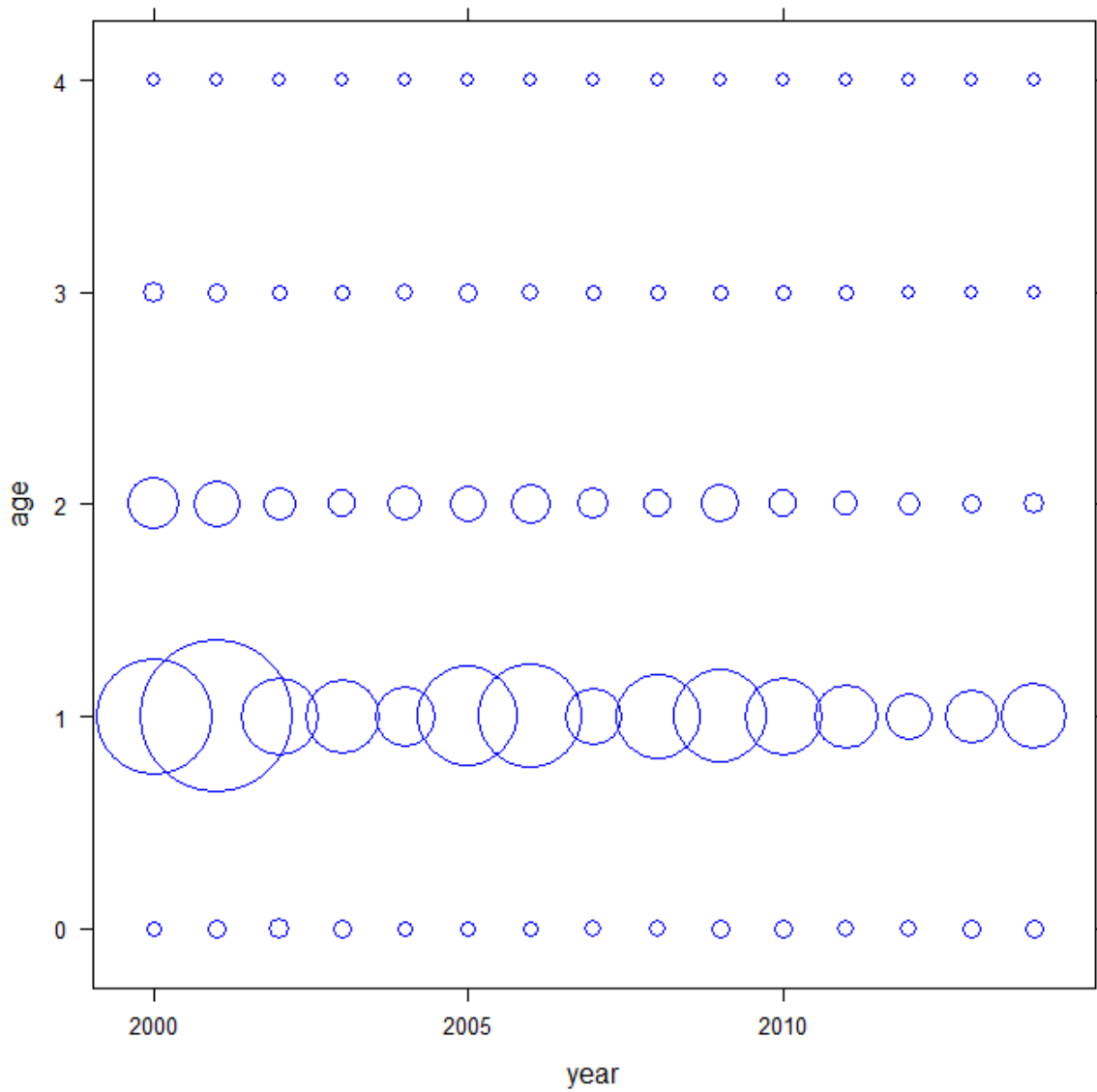
```
plot(fit42, Saeg14.ind)
plot(fit42, trim(pil22rbld.stk, year = 2000:2014)) ###very good fit!!!!
```





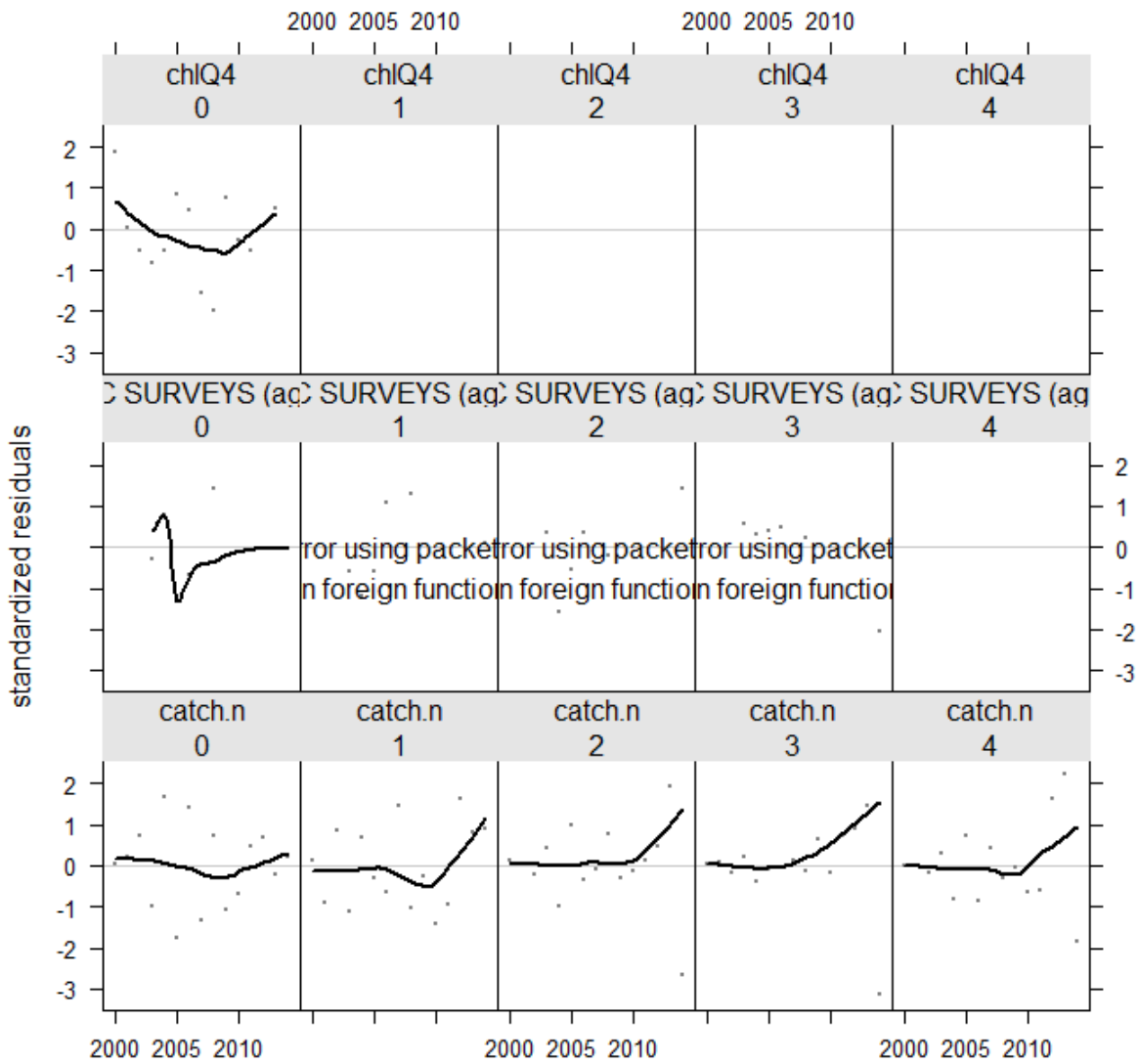


```
bubbles(age ~ year, data = catch.n(pil22.stk.a4a.42), bub.scale = 10)
```



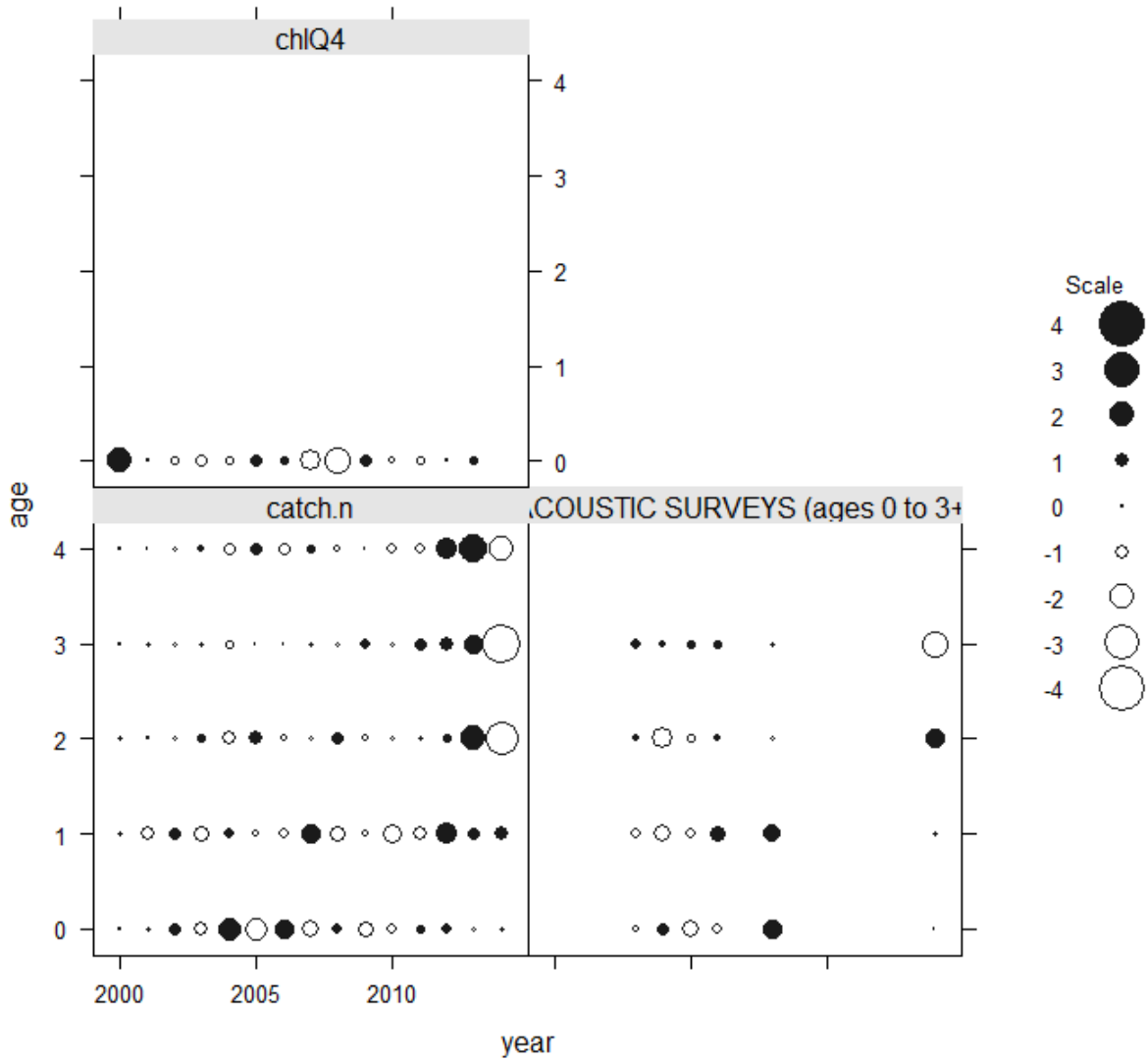
```
res <- residuals(fit42, trim(pil22rbld.stk, year = 2000:2014),  
  window(pil22a.ind, start = 2000))  
plot(res)
```

## log residuals of catch and abundance indices



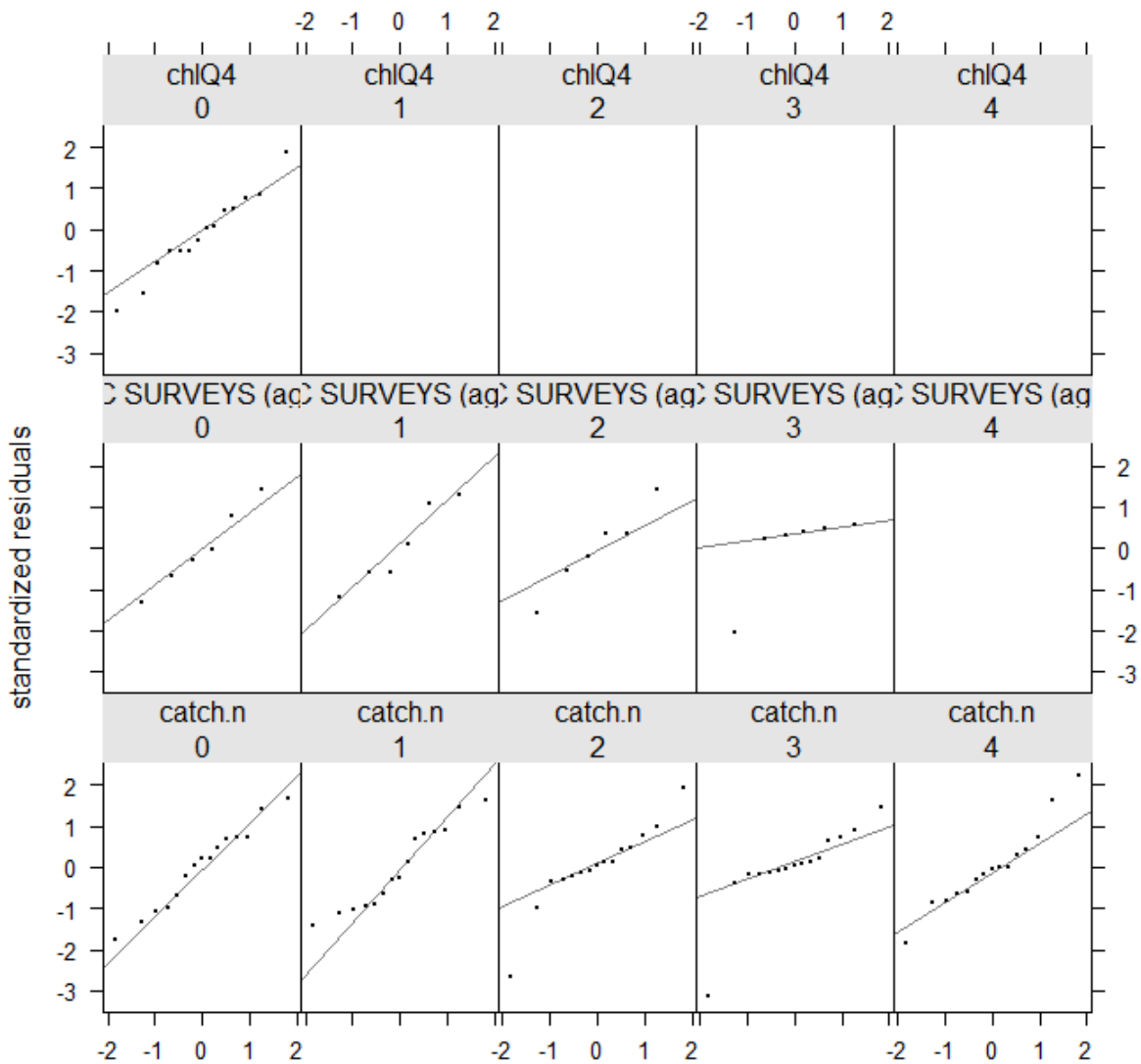
```
bubbles(res) # check the residuals plot, chla has greatly improved
```

## log residuals of catch and abundance indices



`qqmath(res)` # quantile plots, fit is generally ok, age 3 in the surveys, ages 2 and 3 in the ca

## quantile-quantile plot of log residuals of catch and abundance indices



```
AIC(fit42) ## -1604.01
```

```
## [1] -1604.01
```

```
BIC(fit42) ###-1391.274
```

```
## [1] -1391.274
```

```
### MOI as a covar for recruitment and ChlaTr4 along with
### surveys for an index ### Trials fmod5 <- ~ te(age, year,
### k=c(4,5), by=breakpts(year, seq(1969, 2020, 10))) qmod5 <-
### list(~s(age, k=3), ~1) moi<- c(index(pil22.ind[[5]])) moi
```

```

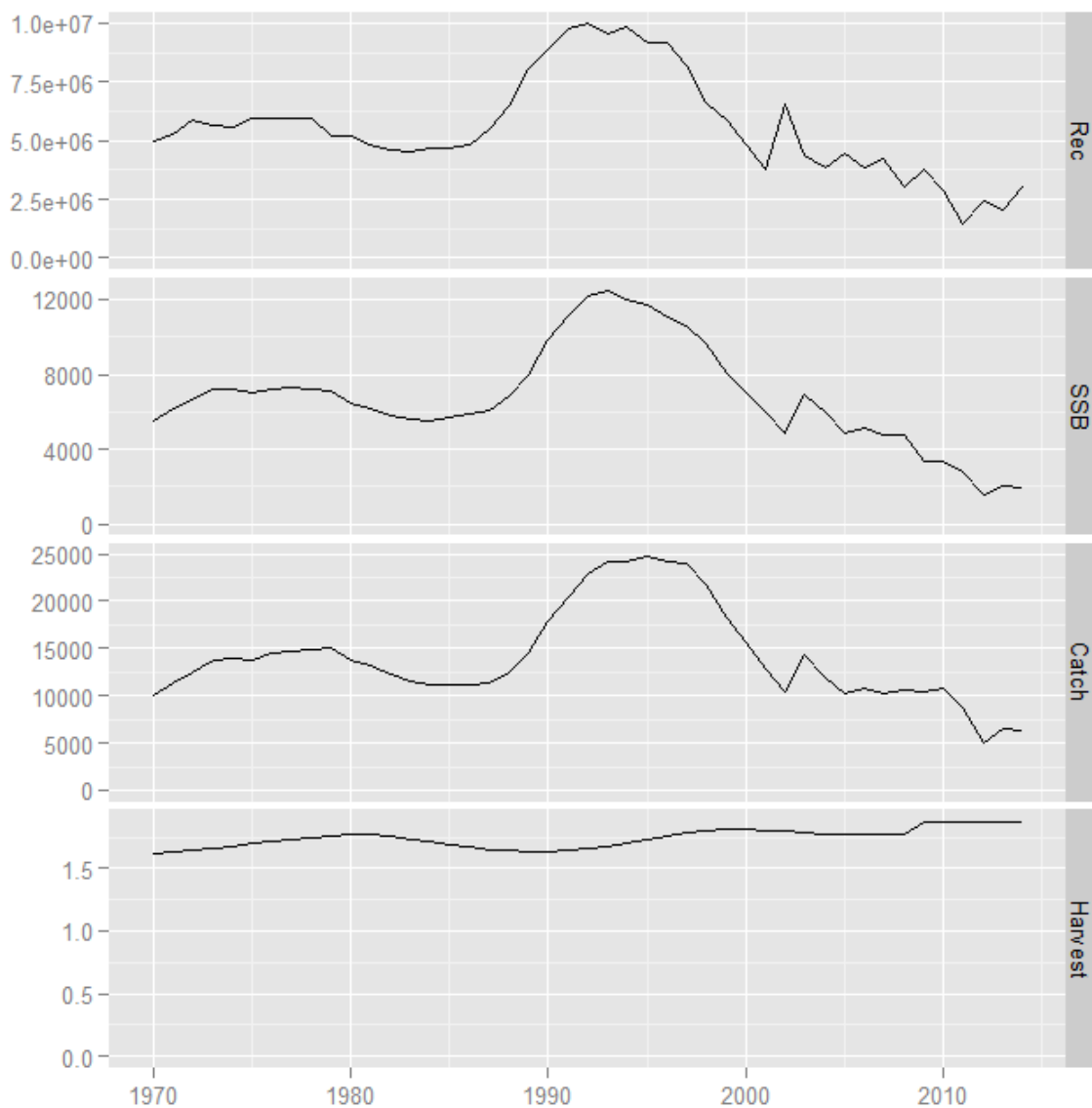
### <- c(moi, mean(moi)) srmod5 <- ~ricker(a=~moi,CV=0.3)

fmod5 <- ~te(age, replace(year, year > 2008, 2014), k = c(4,
8))
qmod5 <- list(~s(age, k = 3), ~s(year, k = 10))
moi <- c(index(pil22.ind[[5]]))
moi <- c(moi, mean(moi))
srmod5 <- ~ricker(a = ~moi, CV = 0.3)

fit5 <- sca(pil22rbld.stk, pil22a.ind, fmodel = fmod5, qmodel = qmod5,
srmodel = srmod5, fit = "assessment")
pil22.stk.a4a.5 <- pil22rbld.stk + fit5
plot(pil22.stk.a4a.5)

```

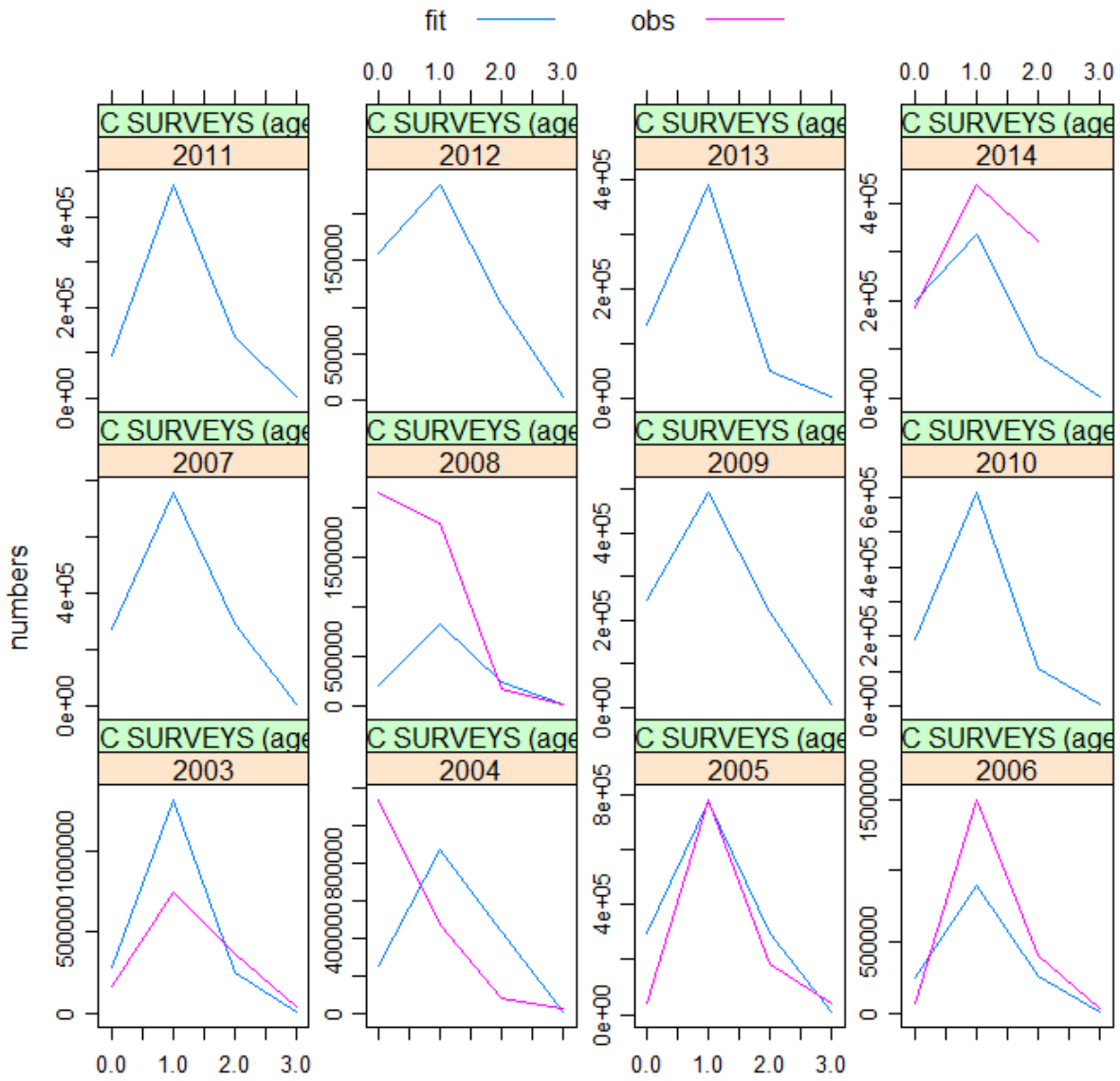
### Long time series



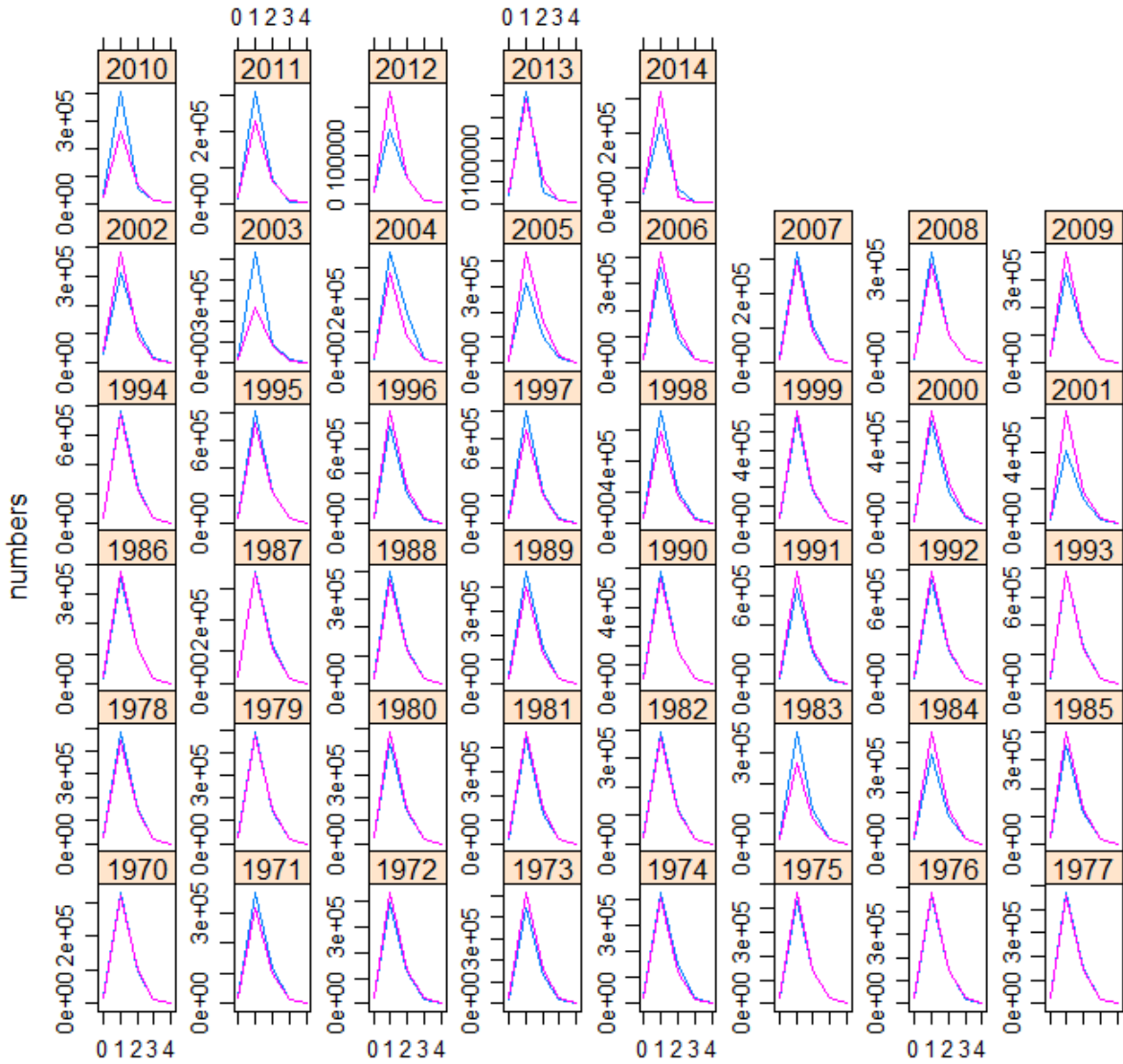
```

plot(fit5, Saeg14.ind)
plot(fit5, pil22rbld.stk)

```

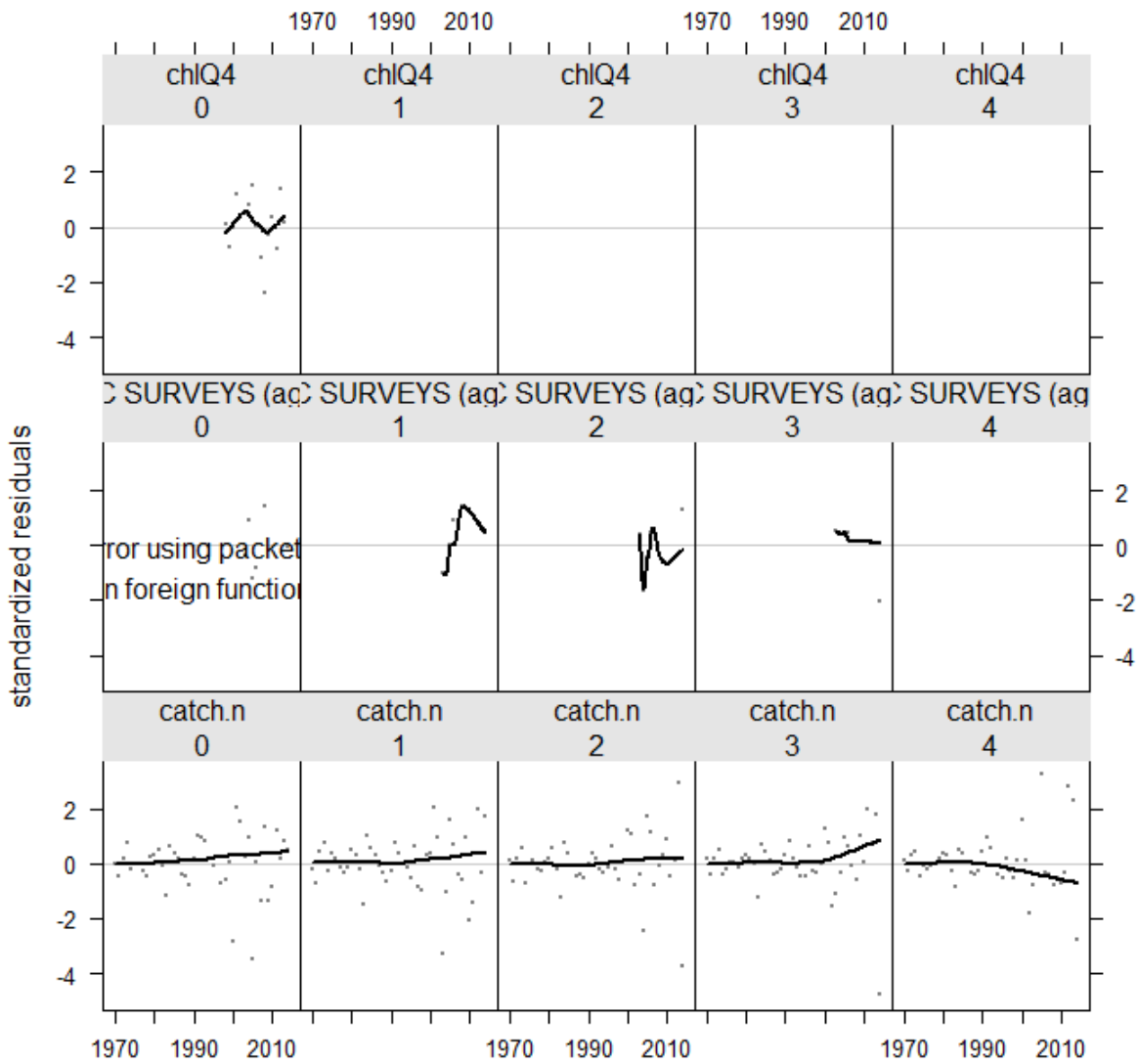






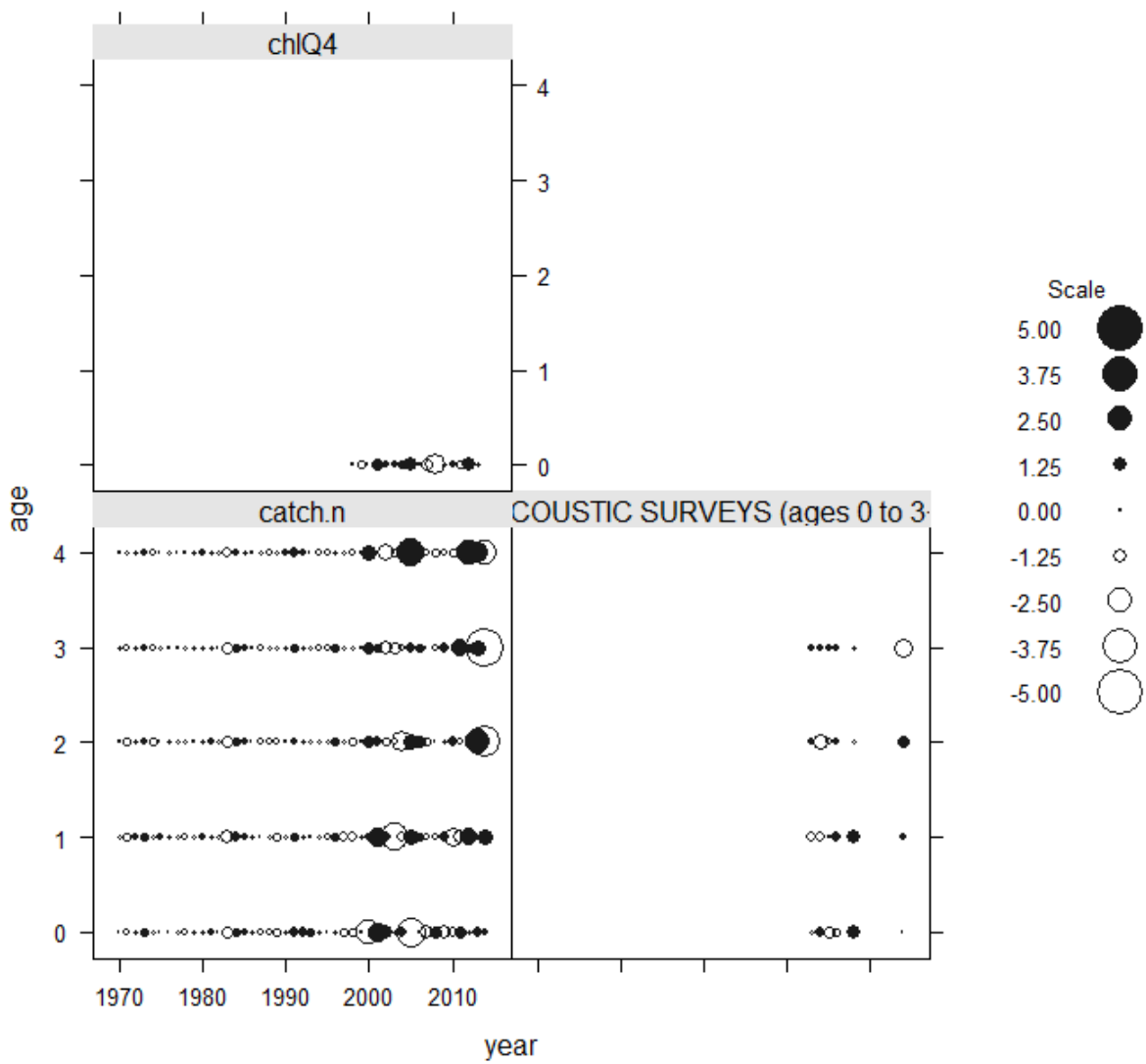
```
res5 <- residuals(fit5, pil22rbld.stk, pil22a.ind)
plot(res5)
```

### log residuals of catch and abundance indices



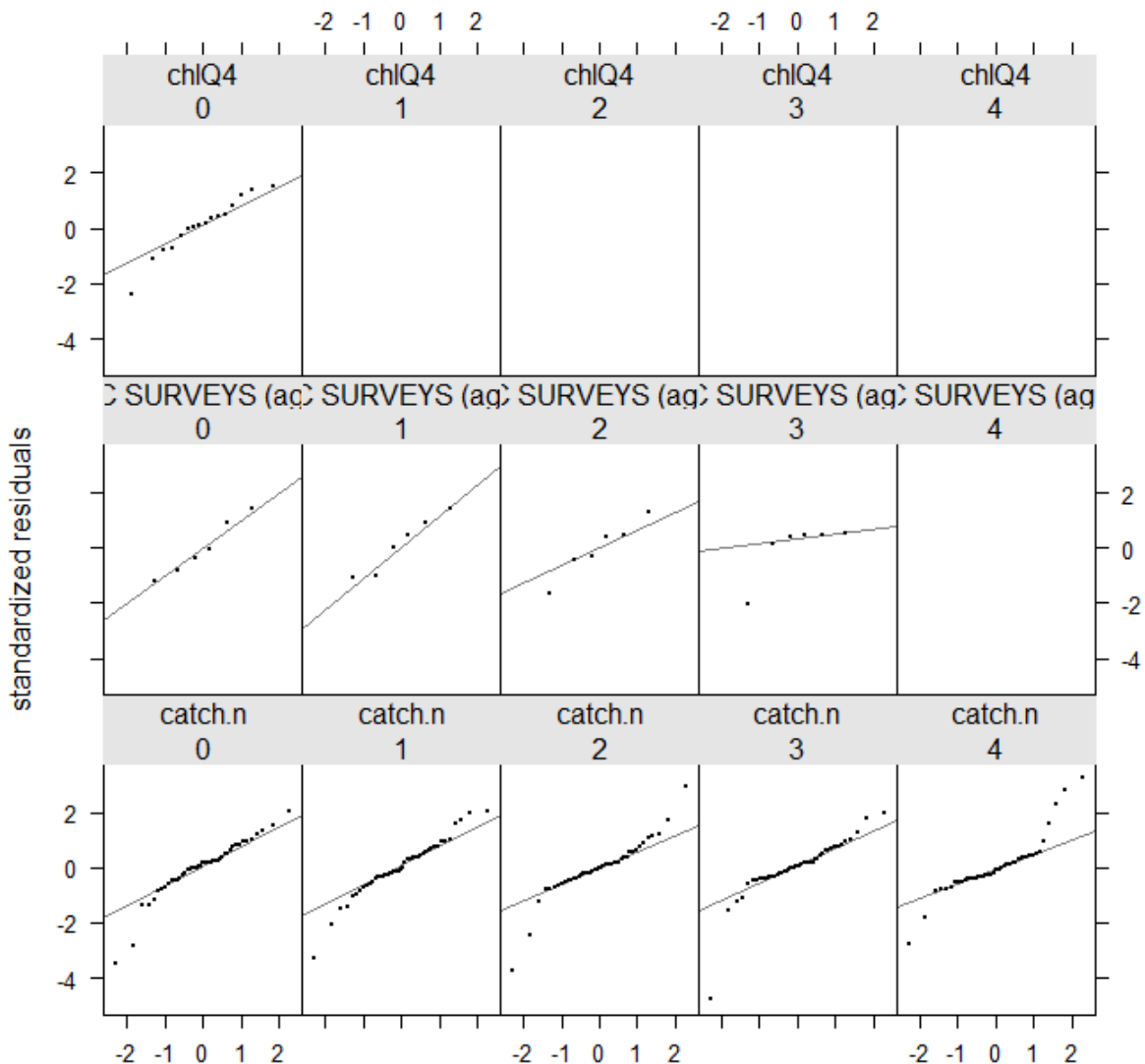
```
bubbles(res5)
```

## log residuals of catch and abundance indices



qqmath(res5)

## quantile-quantile plot of log residuals of catch and abundance indices



### 5.2.3 Final model runs

```
##### SST as a covariate for Ricker and Moitr2 instead of Chlatr4
##### as an index
fmod <- ~te(age, replace(year, year > 2008, 2014), k = c(4, 7))
qmod <- list(~s(age, k = 3), ~s(year))

#### sst as covariate for ricker
cov <- c(index(window(pil22b.ind[[2]], start = 2000)))
cov <- c(cov, mean(cov))
srmod <- ~ricker(CV = 0.3, a = ~s(cov, k = 4))

### moi instead of chla
fit43 <- sca(trim(pil22rbld.stk, year = 2000:2014), window(pil22d.ind,
```

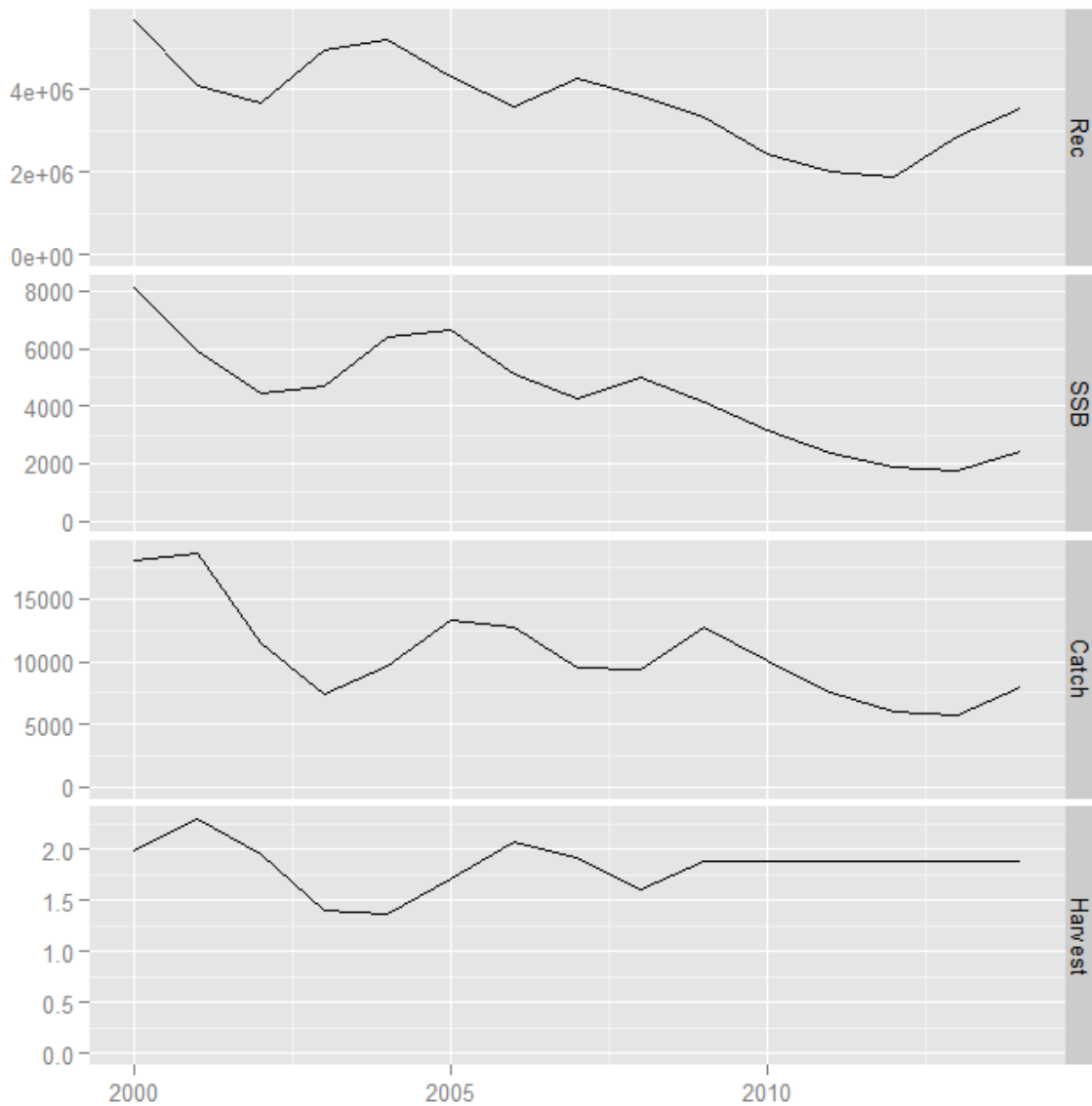
```

    start = 2000), qmodel = qmod, fmodel = fmod, srmodel = srmod,
    fit = "assessment") ###it converges
pil22.stk.a4a.43 <- trim(pil22rbld.stk, year = 2000:2014) + fit43

plot(pil22.stk.a4a.43) # harvest up to 2.4, catches good

```

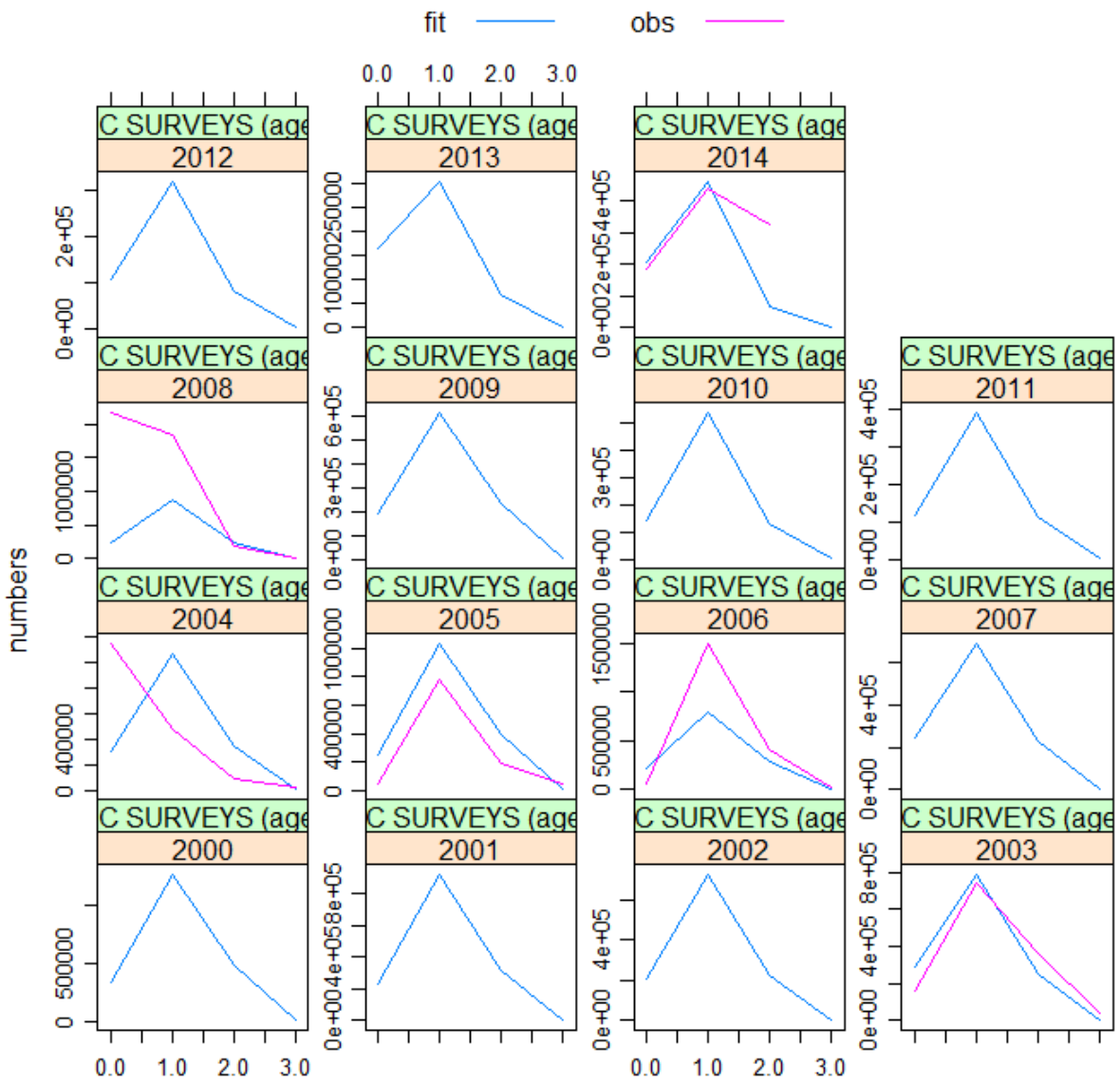
### Short time series

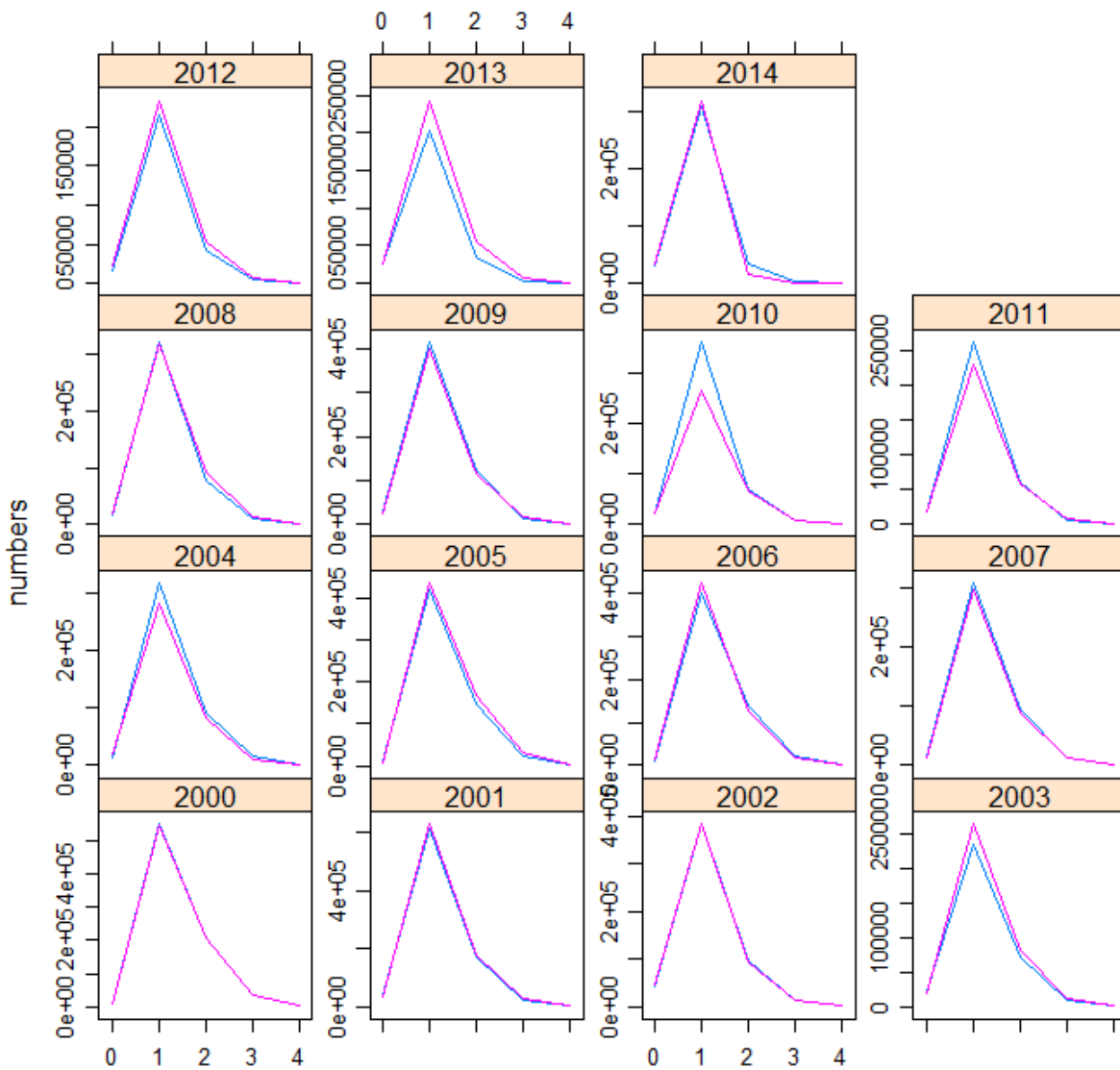


```

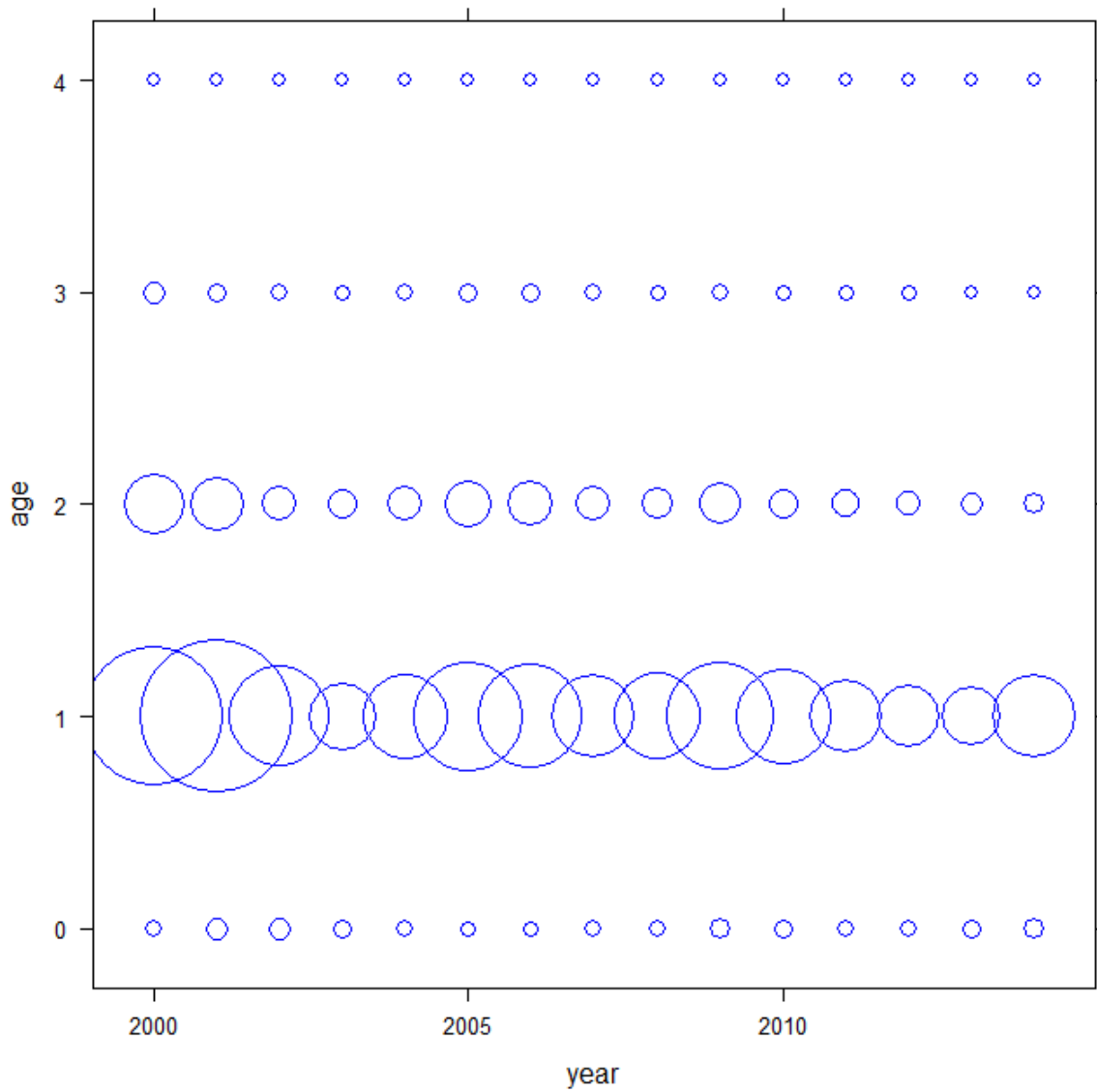
plot(fit43, Saeg14.ind)
plot(fit43, trim(pil22rbld.stk, year = 2000:2014)) ###very good fit!!!!

```





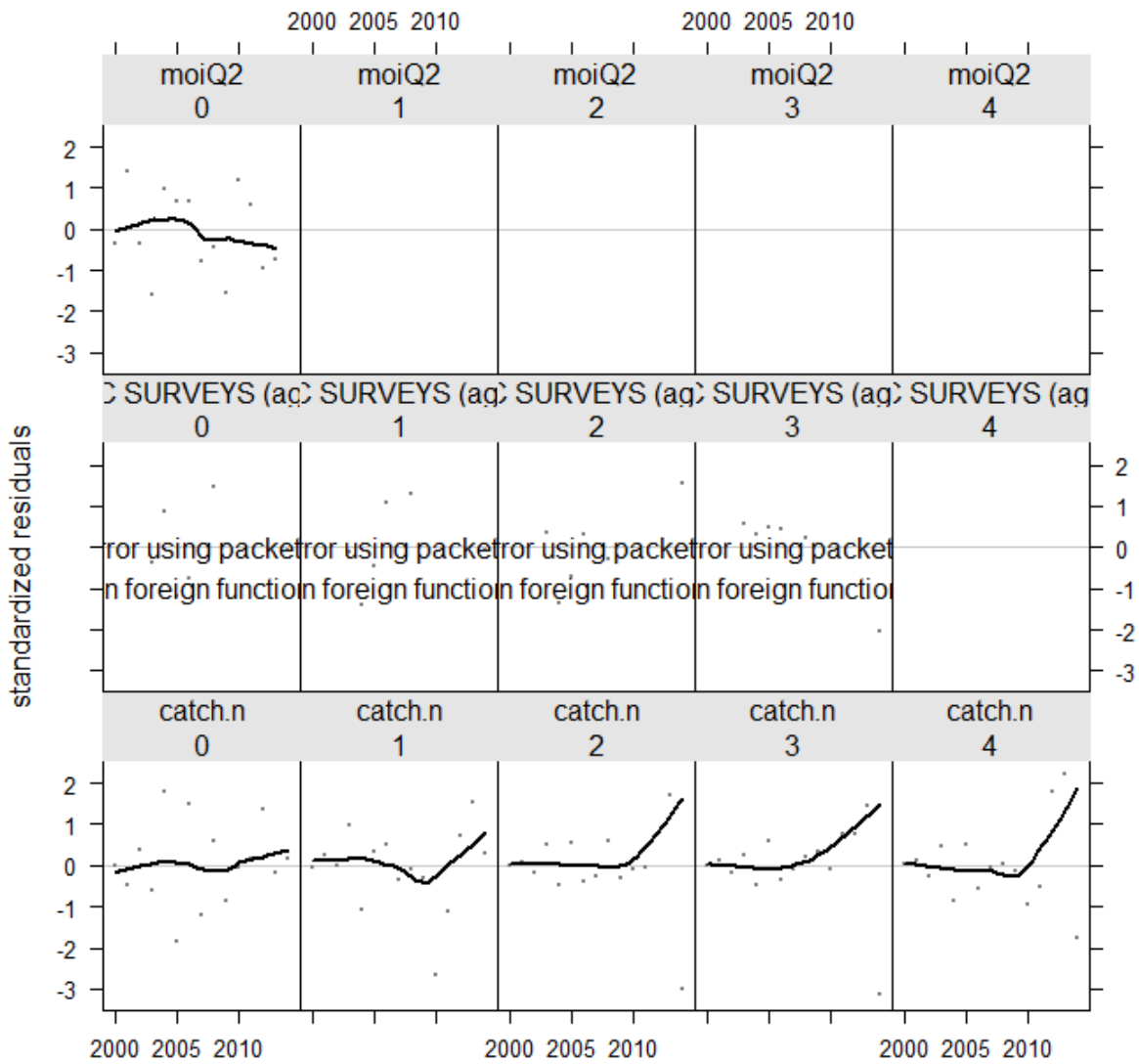
```
bubbles(age ~ year, data = catch.n(pil22.stk.a4a.43), bub.scale = 10)
```



```
res <- residuals(fit43, trim(pil22rbld.stk, year = 2000:2014),  
  window(pil22d.ind, start = 2000))  
plot(res)
```

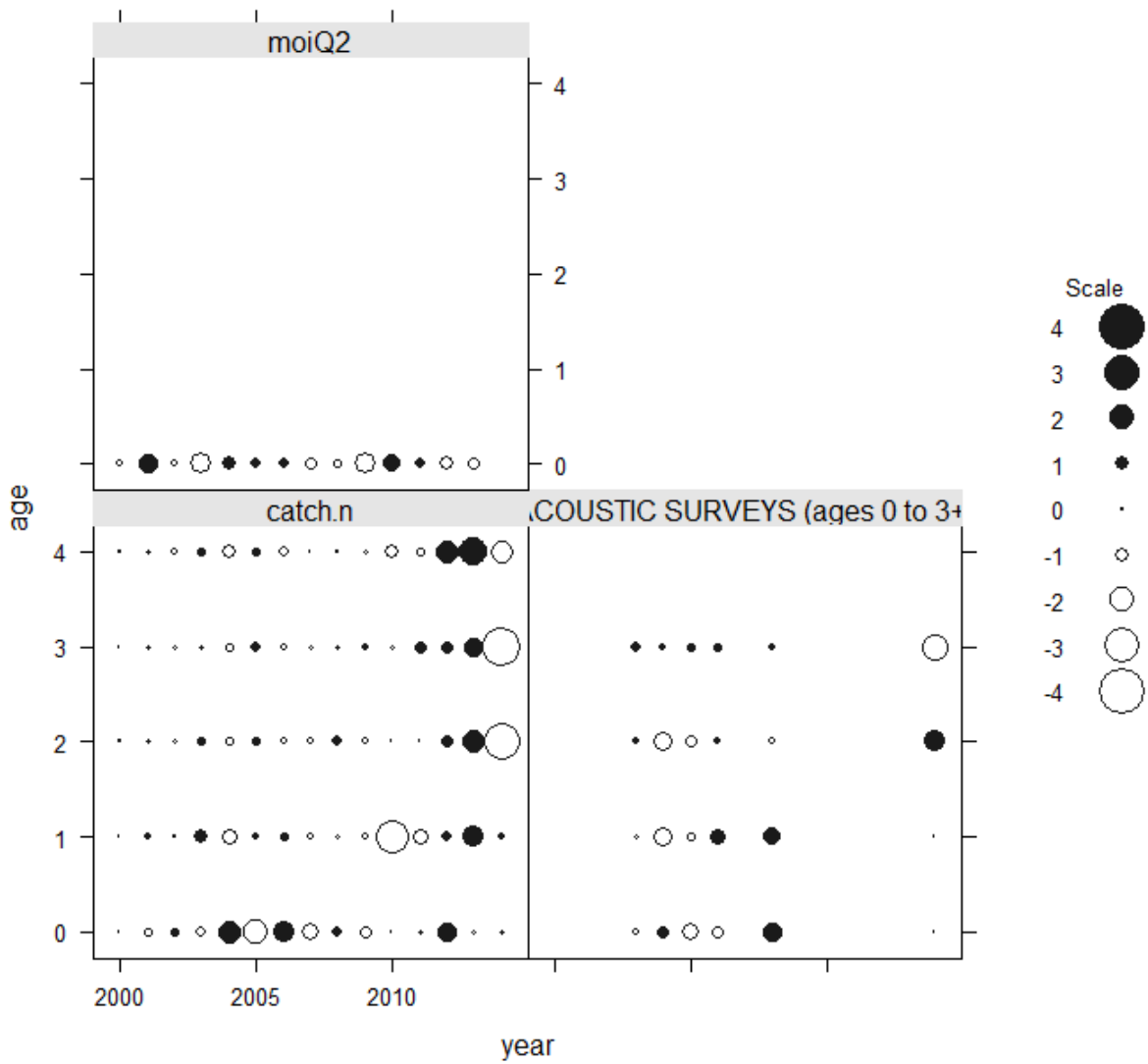


## log residuals of catch and abundance indices



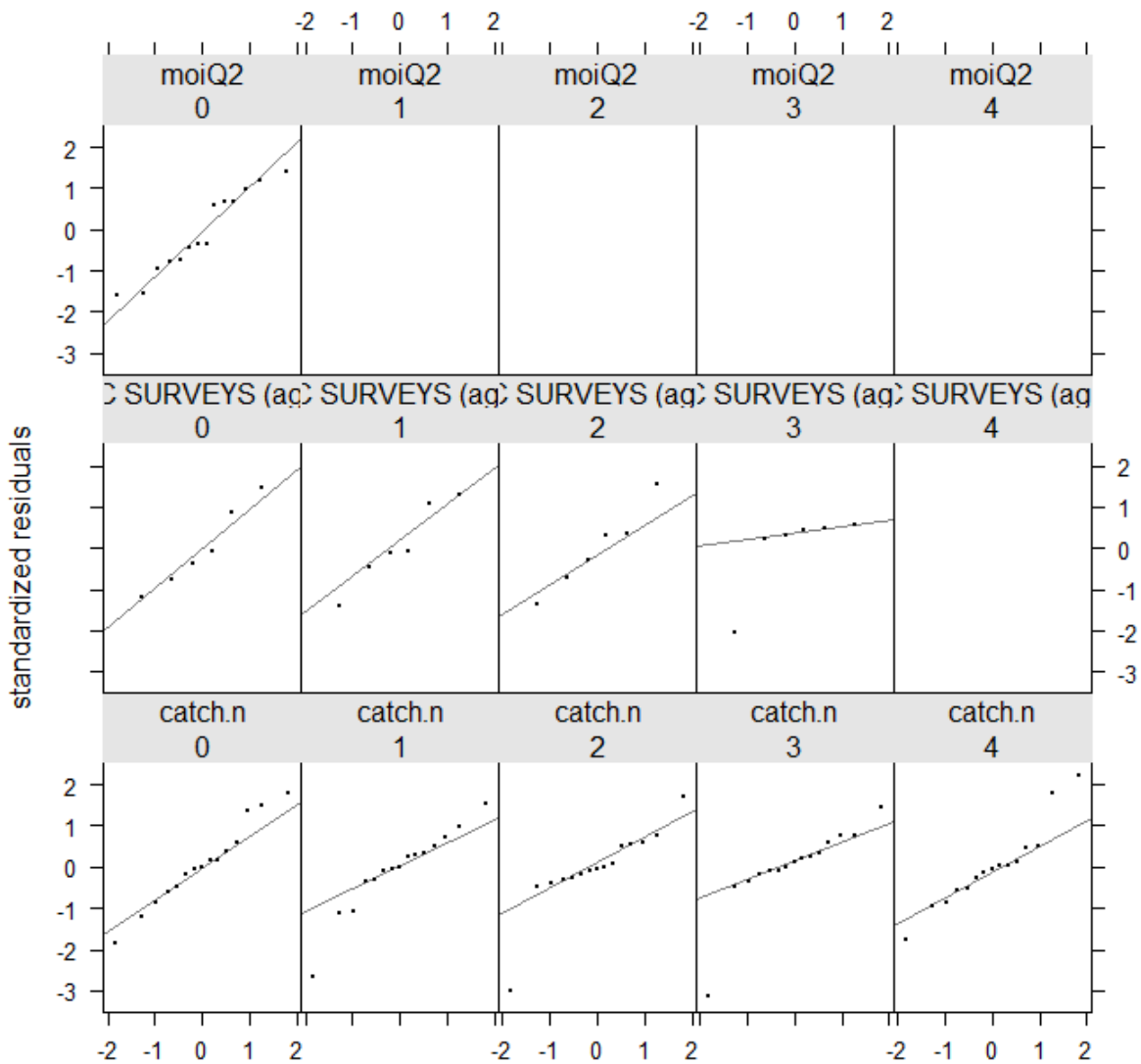
```
bubbles(res) # check the residuals plot, chla has greatly improved
```

## log residuals of catch and abundance indices



`qqmath(res)` # quantile plots, fit is generally ok, age 3 in the surveys, ages 2 and 3 in the ca

## quantile-quantile plot of log residuals of catch and abundance indices



```
AIC(fit43) ## -1651.432
```

```
## [1] -1651.432
```

```
BIC(fit43) ## -1460.515
```

```
## [1] -1460.515
```

```
##### MOITr2 as a covar for recruitment and sstTr4 along with
##### surveys for an index
fmod6 <- ~te(age, replace(year, year > 2008, 2014), k = c(4,
8))
```

```

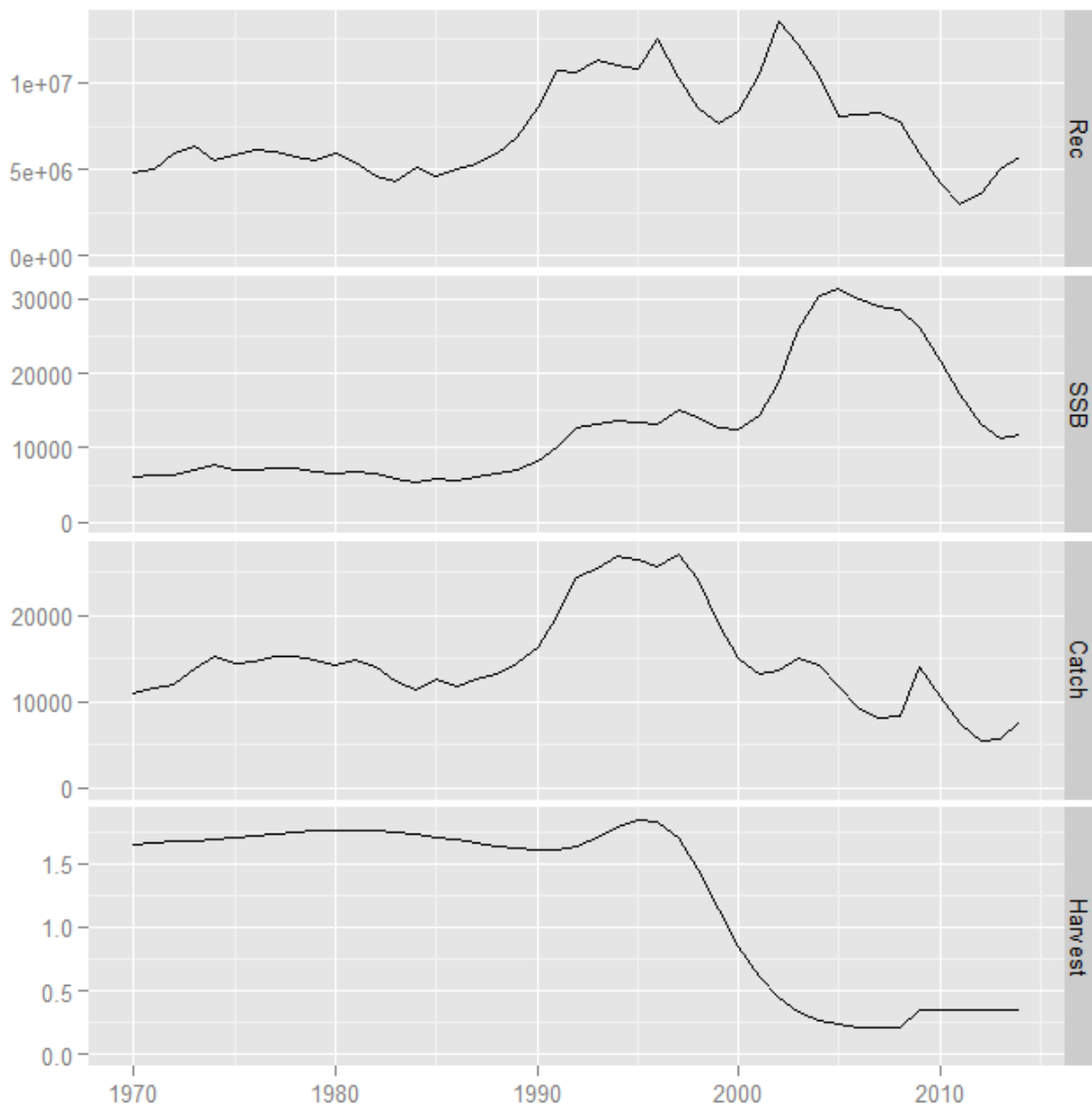
qmod6 <- list(~s(age, k = 3), ~s(year, k = 15))
moi <- c(index(pil22.ind[[5]]))
moi <- c(moi, mean(moi))
srmod6 <- ~ricker(a = ~moi, CV = 0.3)

fit6 <- sca(pil22rbld.stk, pil22b.ind, fmodel = fmod6, qmodel = qmod6,
           srmodel = srmod6, fit = "assessment")
pil22.stk.a4a.6 <- pil22rbld.stk + fit6

plot(pil22.stk.a4a.6)

```

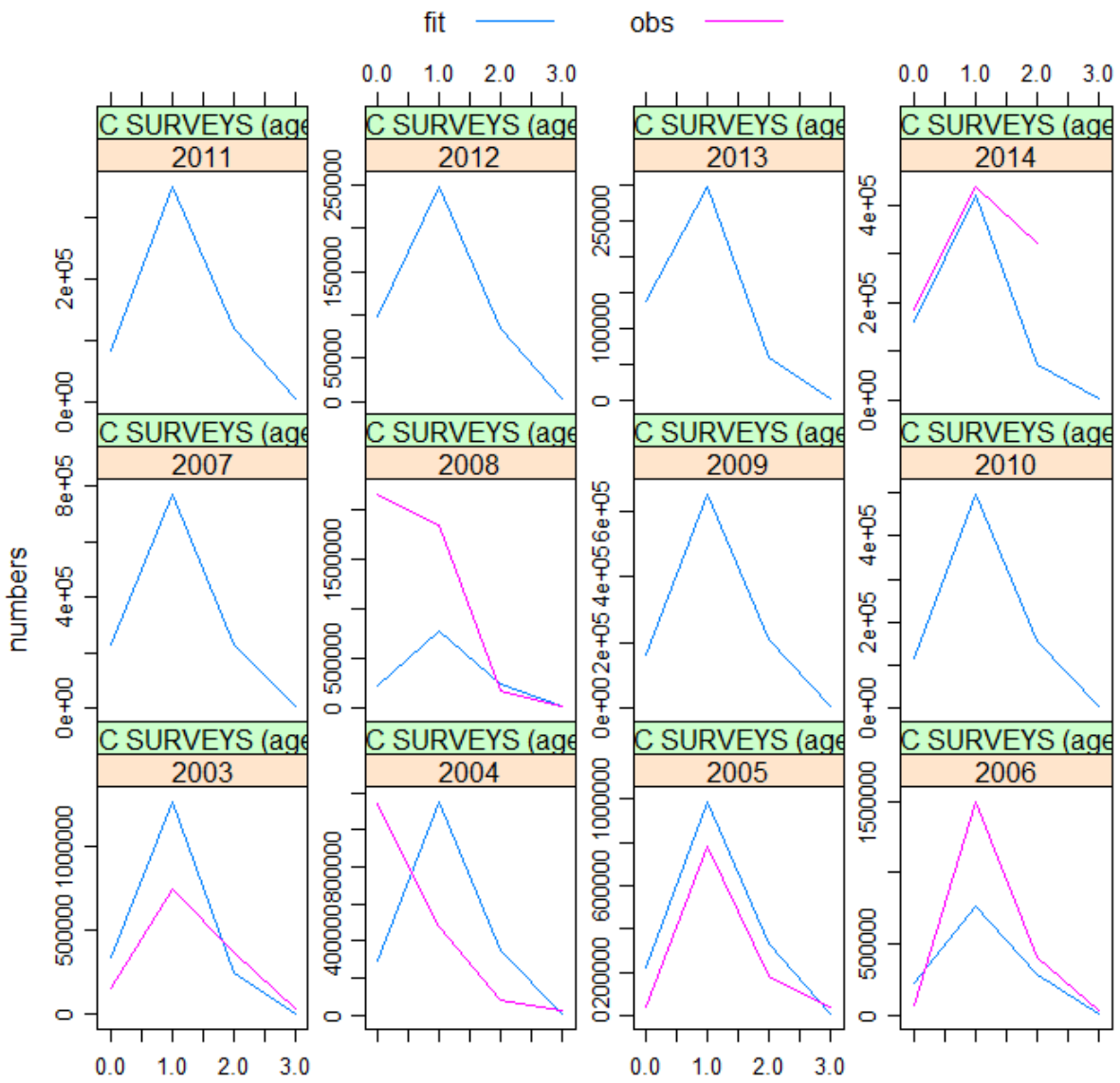
### Long time series

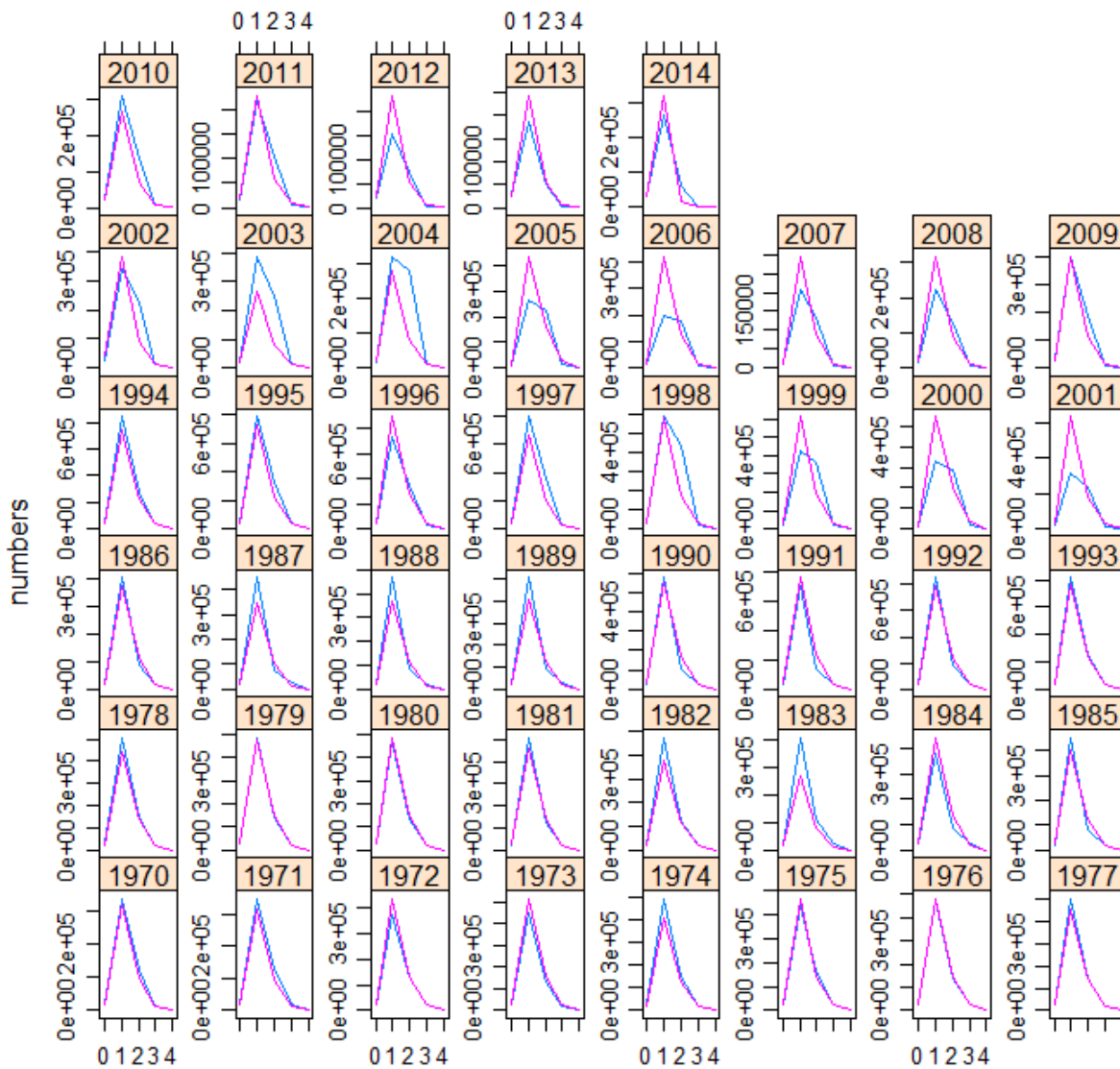


```

plot(fit6, Saeg14.ind)
plot(fit6, pil22rbld.stk)

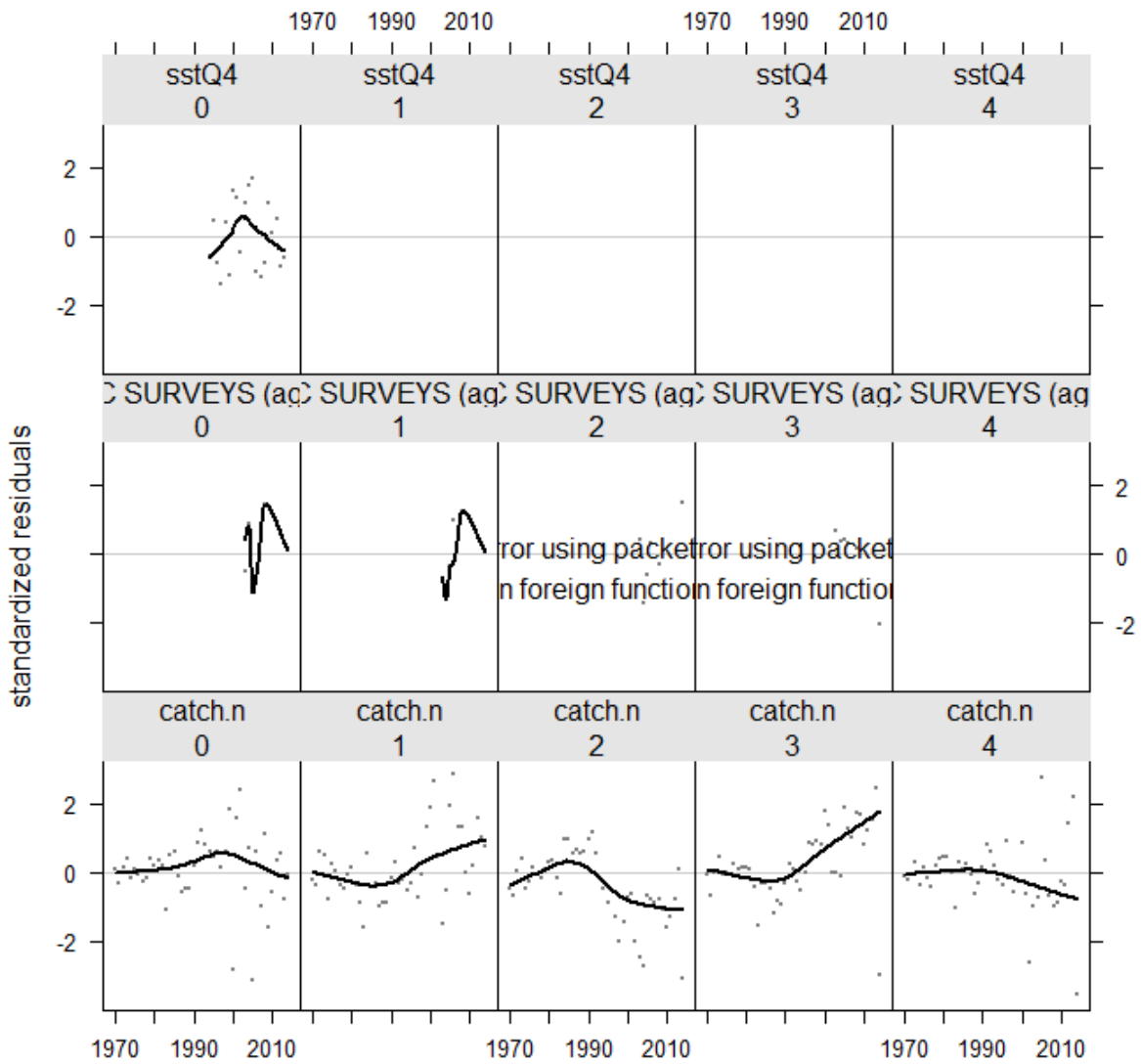
```





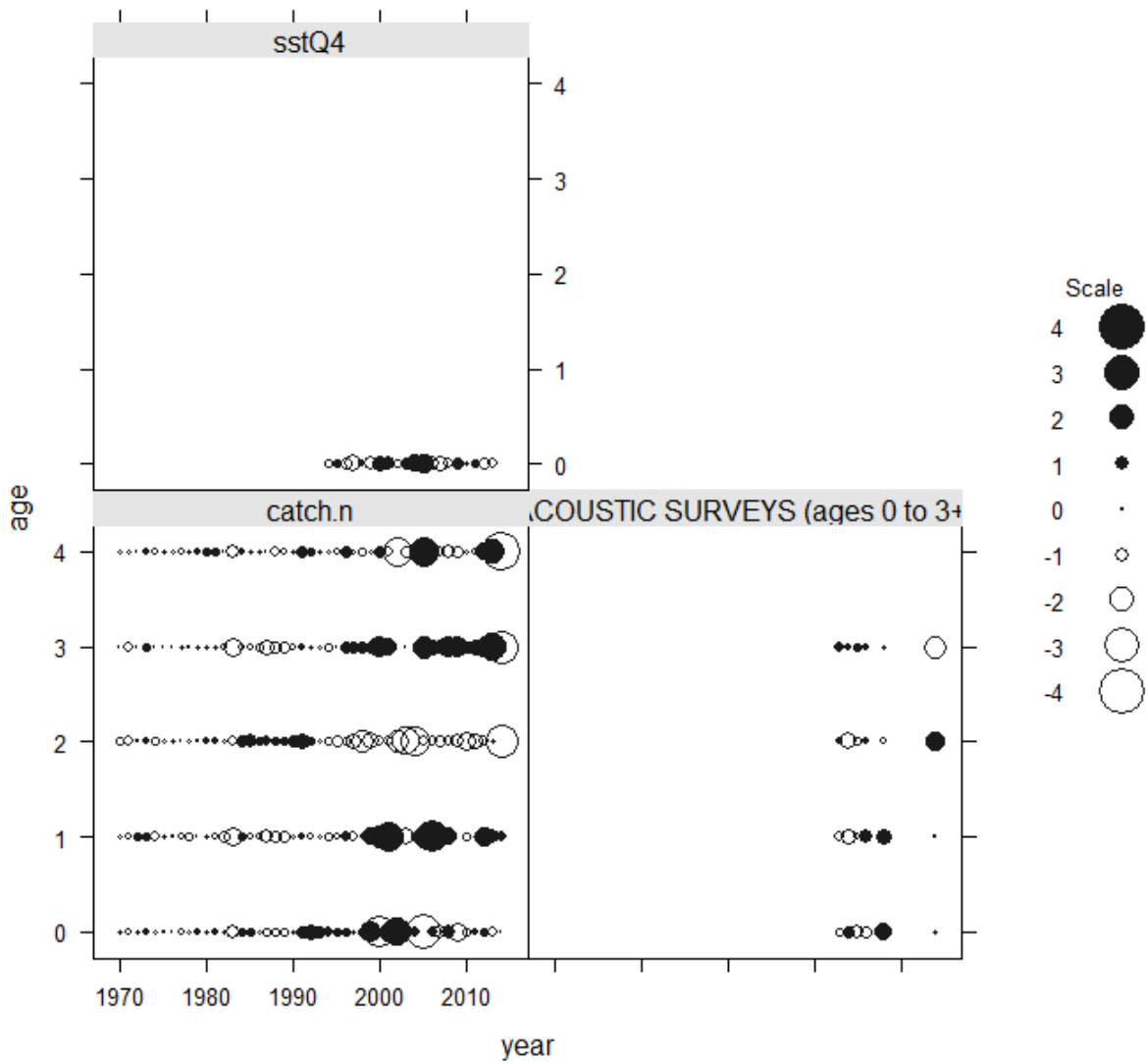
```
res6 <- residuals(fit6, pil22rbld.stk, pil22b.ind)
plot(res6)
```

### log residuals of catch and abundance indices



bubbles(res6)

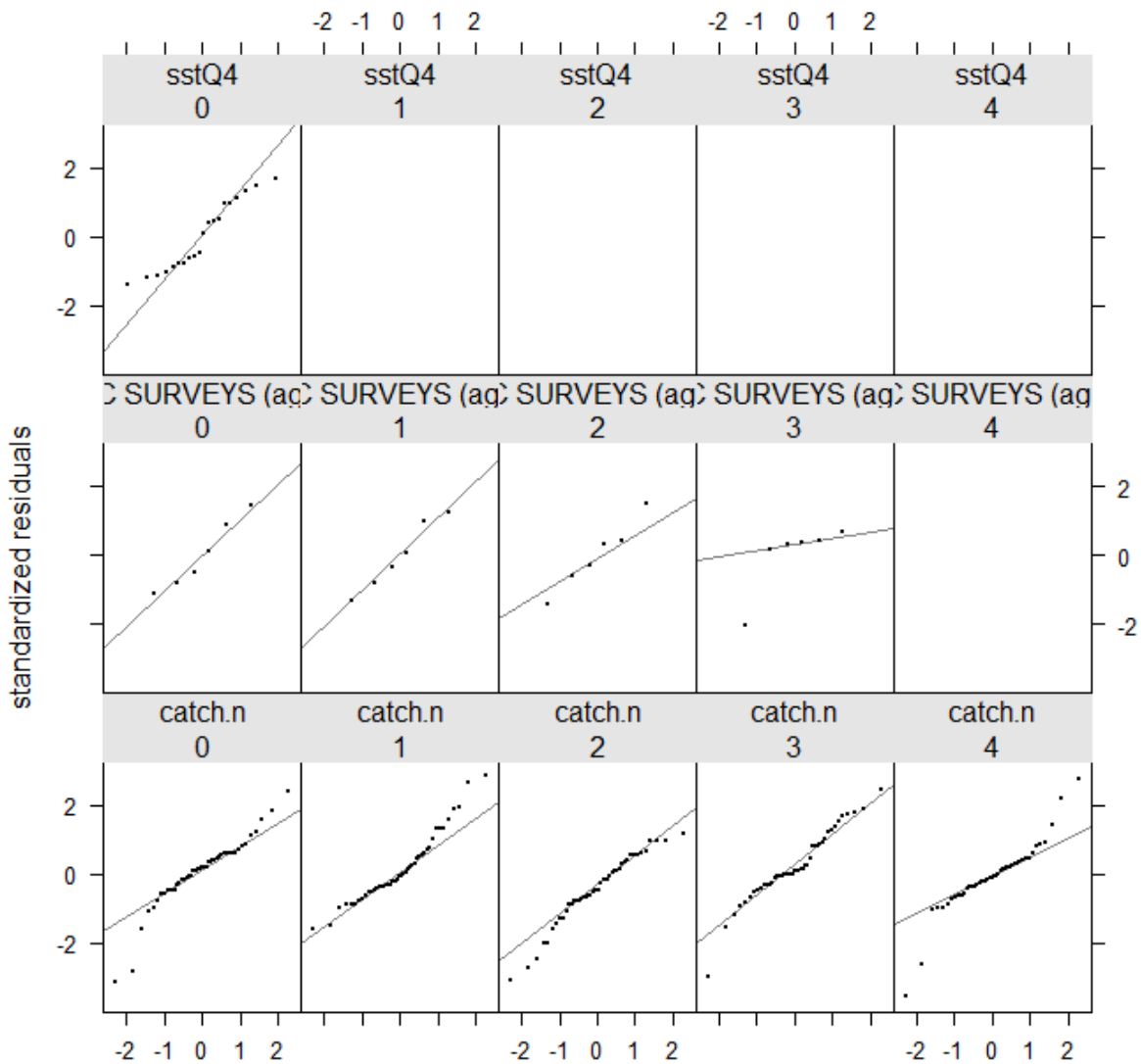
## log residuals of catch and abundance indices



```
qqmath(res6) ###age 3 presents an outlier
```



## quantile-quantile plot of log residuals of catch and abundance indices



```
AIC(fit6) ## -2113.38
```

```
## [1] -2113.38
```

```
BIC(fit6) ###-1728.746
```

```
## [1] -1728.746
```

## 5.3 Exploring the assessment results

### 5.3.1 Anchovy

```
##### COMPARE a4a fits

# HARVEST RATES F COMPARISON
par(mfrow = c(1, 2)) # create a 1 x 2 window

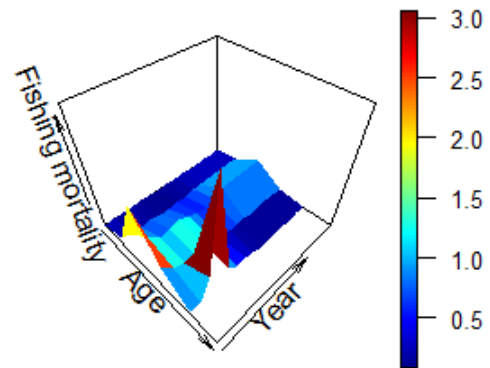
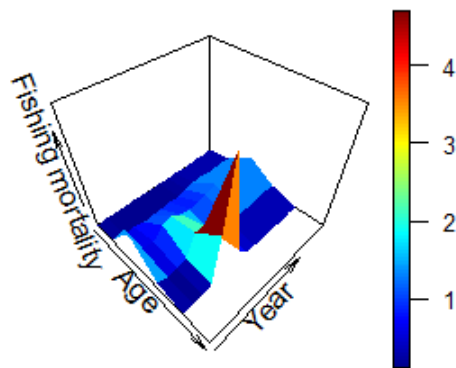
persp3D(z = harvest(ane22.stk.a4a.40)[drop = TRUE], x = as.numeric(dimnames(harvest(ane22.stk.a4a.40))[[1]]),
  y = as.numeric(dimnames(harvest(ane22.stk.a4a.40))[[2]]),
  expand = 0.9, space = 0.3, along = "xy", colkey = list(side = 4,
    width = 0.9, length = 0.4, cex.axis = 0.8), box = TRUE,
  col.var = harvest(ane22.stk.a4a.40)[drop = TRUE], zlab = "Fishing mortality",
  ylab = "Year", xlab = "Age", theta = 45, phi = 45, xlim = c(0,
    5), main = "F-Final model fit40")

persp3D(z = harvest(ane22.stk.a4a.41)[drop = TRUE], x = as.numeric(dimnames(harvest(ane22.stk.a4a.41))[[1]]),
  y = as.numeric(dimnames(harvest(ane22.stk.a4a.41))[[2]]),
  expand = 0.9, space = 0.3, along = "xy", colkey = list(side = 4,
    width = 0.9, length = 0.4, cex.axis = 0.8), box = TRUE,
  col.var = harvest(ane22.stk.a4a.41)[drop = TRUE], zlab = "Fishing mortality",
  ylab = "Year", xlab = "Age", theta = 45, phi = 45, xlim = c(0,
    5), main = "F-Initial model fit41")
```

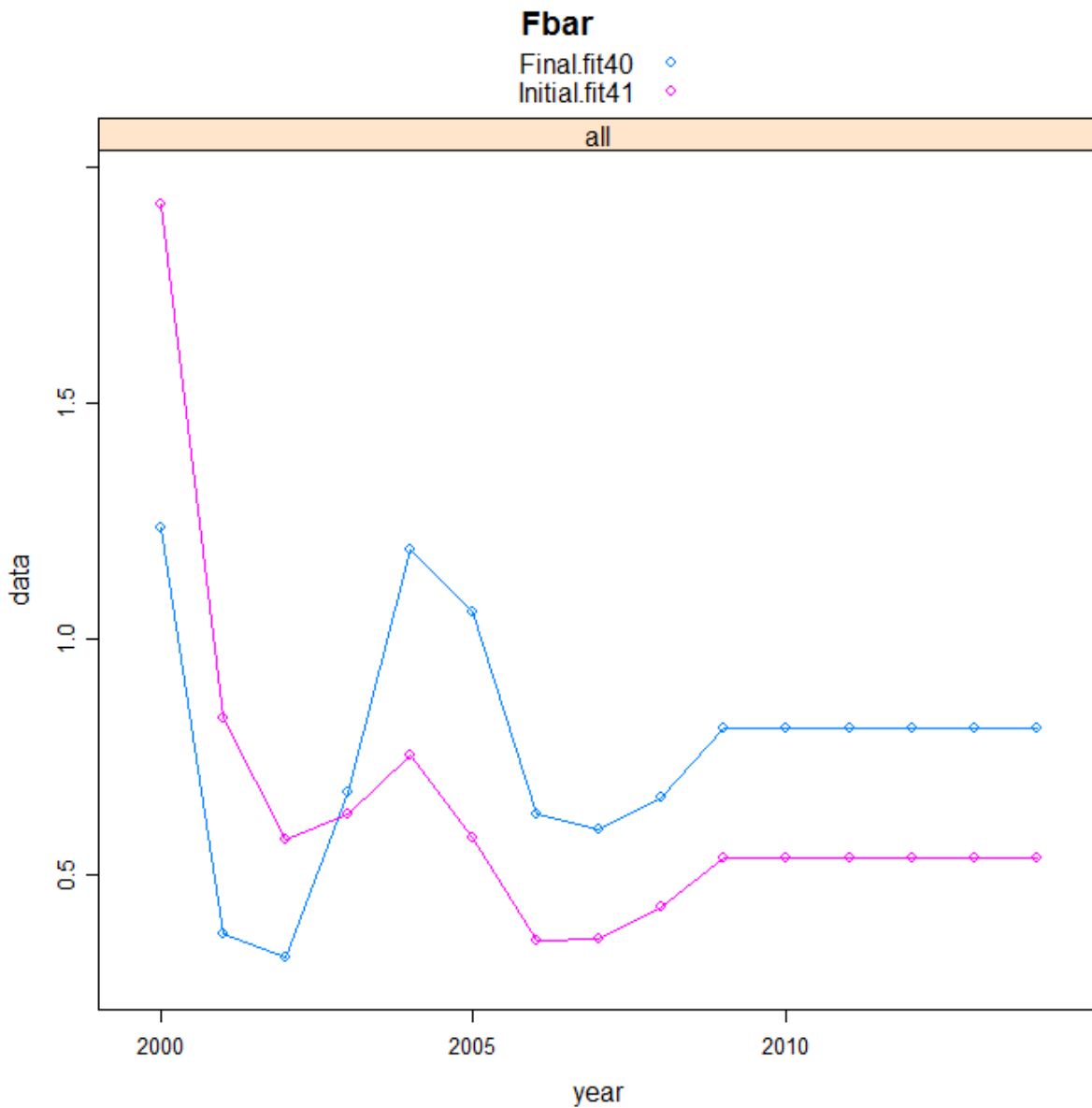
### Short time series

**F-Final model fit40**

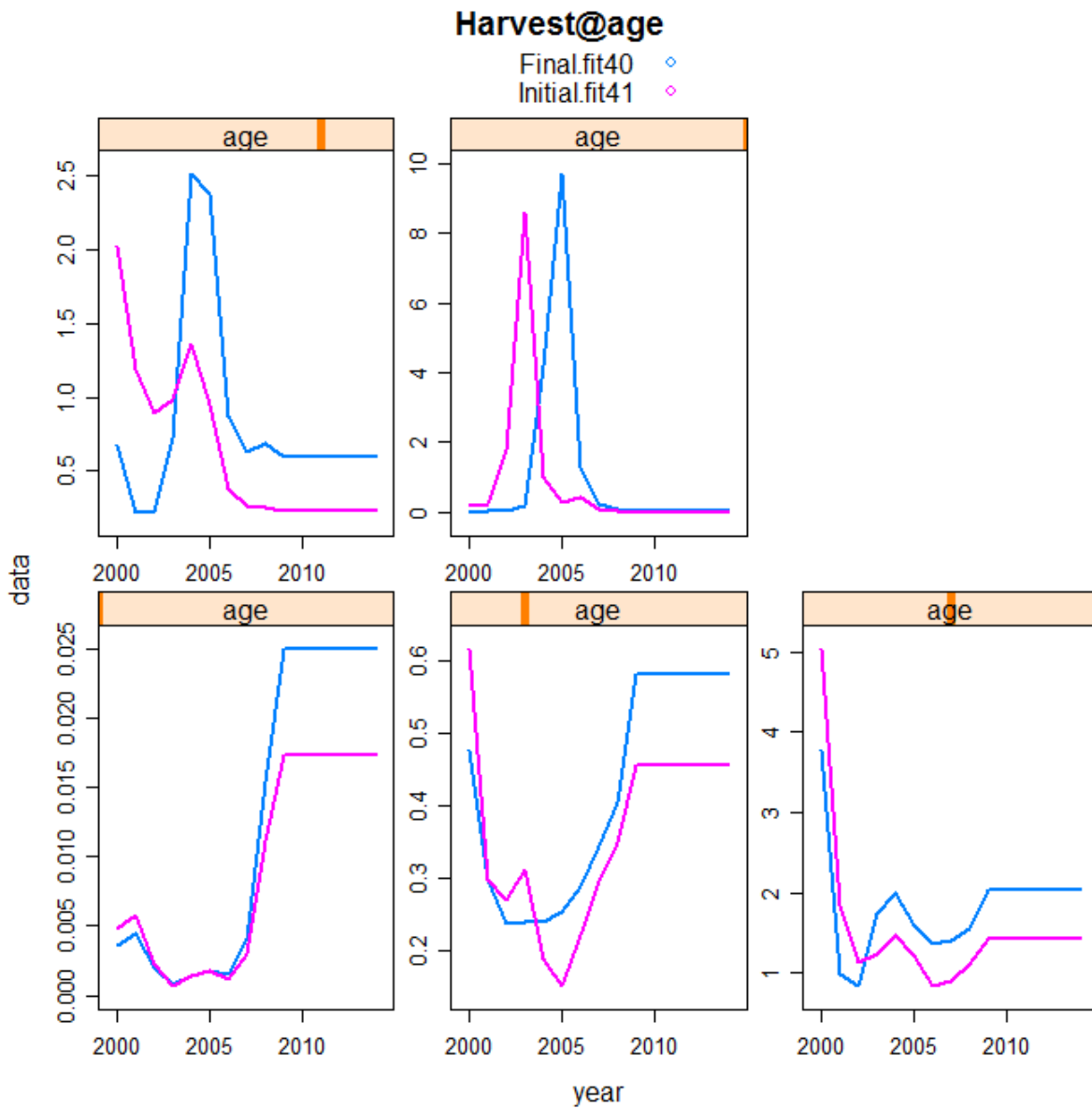
**F-Initial model fit41**



```
# Compare F's by Year Pass all harvest slots in an FLQuant
comp.mods.Fbar <- FLQuants(Final.fit40 = fbar(ane22.stk.a4a.40),
  Initial.fit41 = fbar(ane22.stk.a4a.41))
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.Fbar,
  type = "b", auto.key = T, main = "Fbar", scale = "free")
```



```
# Compare harvest by Year Pass all harvest slots in an
# FLQuant
comp.mods.harvest <- FLQuants(Final.fit40 = harvest(ane22.stk.a4a.40),
  Initial.fit41 = harvest(ane22.stk.a4a.41))
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.harvest,
  type = "l", auto.key = T, main = "Harvest@age", scale = "free",
  lwd = 2)
```



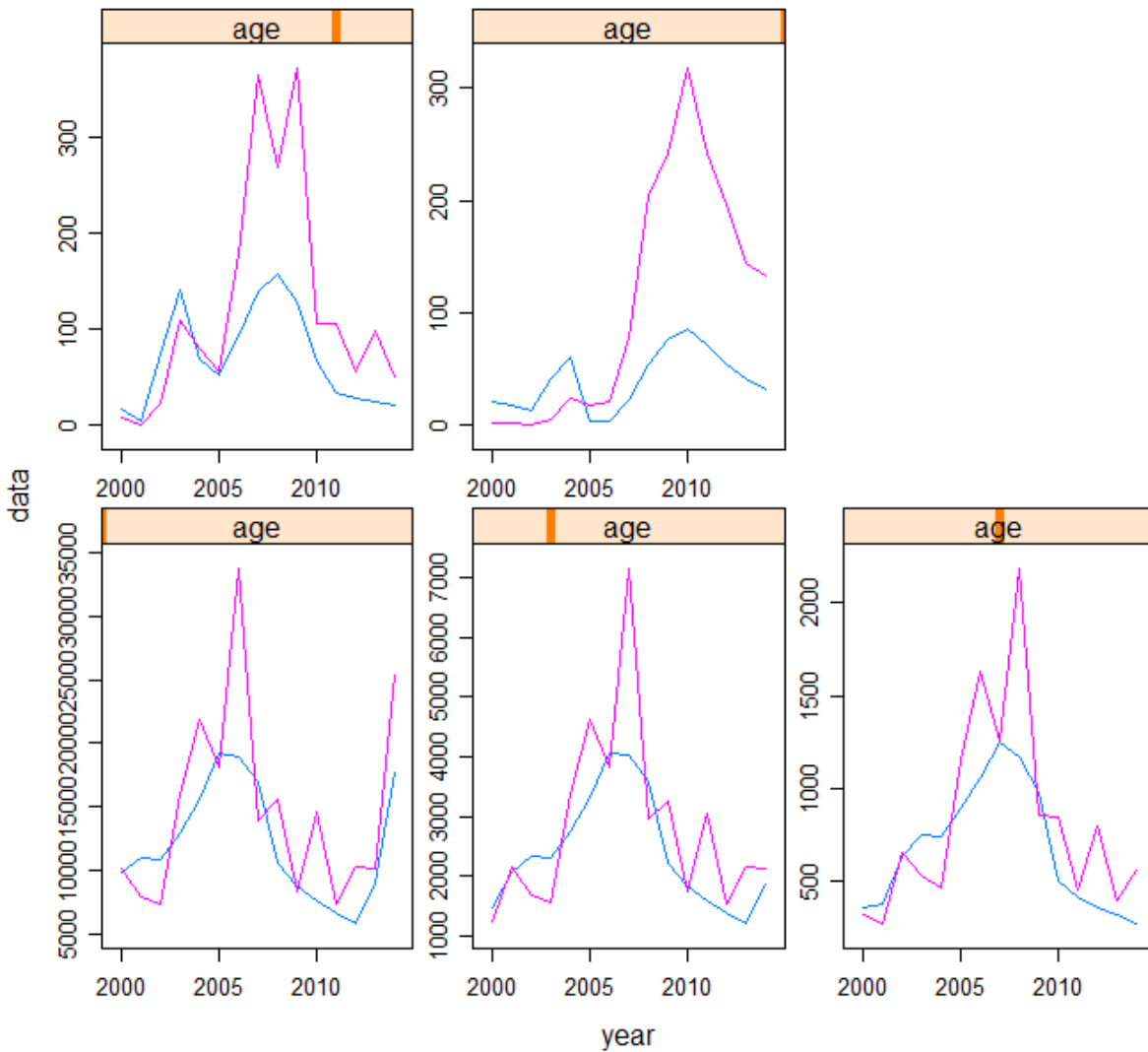
```

# Compare Stock abundances Pass all stock.n slots in an
# FLQuant
comp.mods.stock.n <- FLQuants(Final.fit40 = ane22.stk.a4a.40@stock.n/1000,
  Initial.fit41 = ane22.stk.a4a.41@stock.n/1000)
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.stock.n,
  type = "l", auto.key = T, main = "Stock Nb@age", scale = "free")

```

### Stock Nb@age

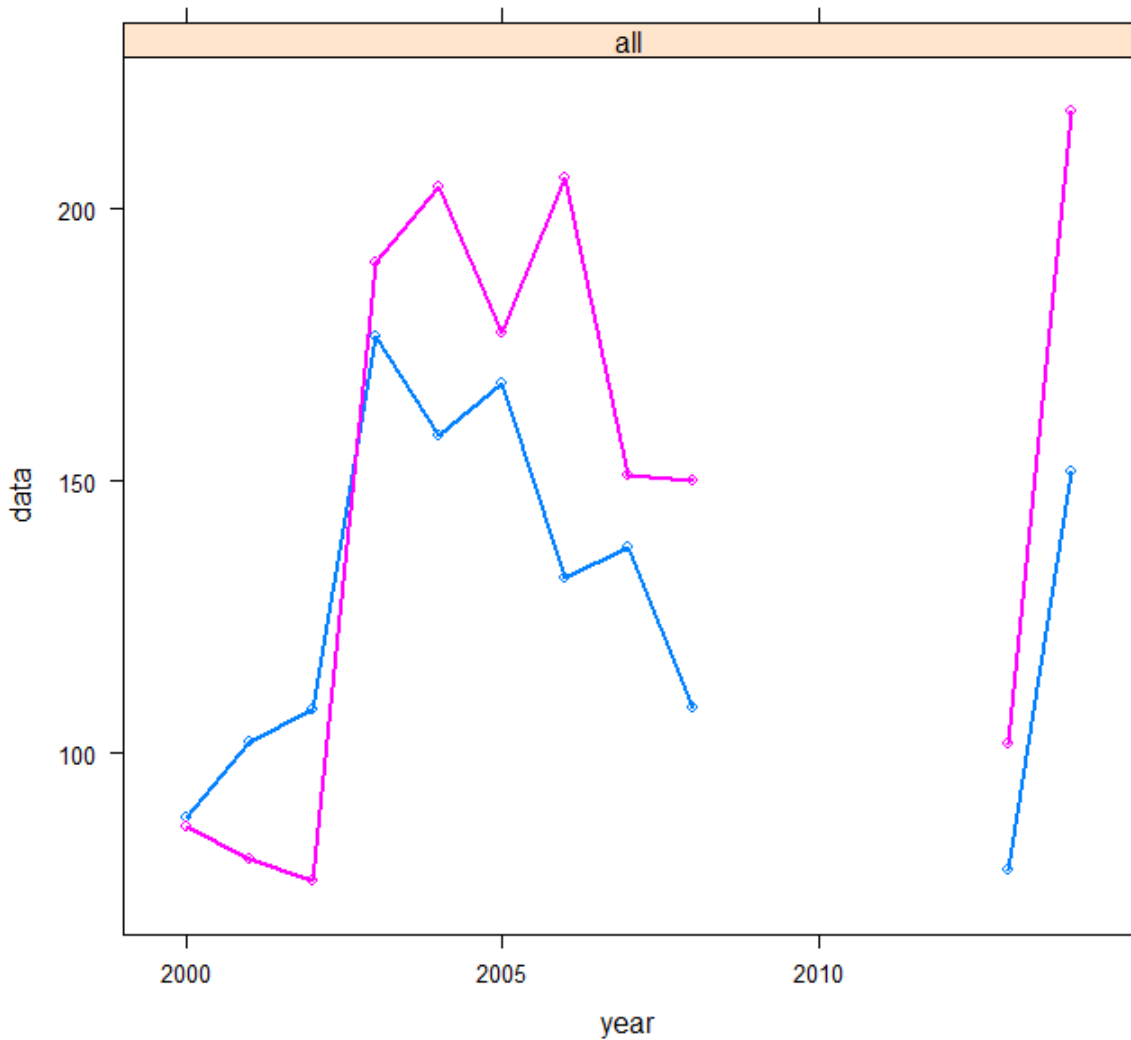
Final.fit40 ◊  
Initial.fit41 ◊



```
# Compare Stock Biomass Pass all stock slots in an FLQuant
comp.mods.stock <- FLQuants(Final.fit40 = ane22.stk.a4a.40@stock/1000,
  Initial.fit41 = ane22.stk.a4a.41@stock/1000)
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.stock,
  type = "b", auto.key = T, main = "Stock Biomass (tons)",
  lwd = 2)
```

## Stock Biomass (tons)

Final.fit40 ◊  
Initial.fit41 ◊



```
##### COMPARE a4a fits
```

```
# HARVEST RATES F COMPARISON
```

```
par(mfrow = c(1, 2)) # create a 1 x 2 window
```

```
persp3D(z = harvest(ane22.stk.a4a.51)[drop = TRUE], x = as.numeric(dimnames(harvest(ane22.stk.a4a.51))[[1]]),
y = as.numeric(dimnames(harvest(ane22.stk.a4a.51))[[2]]),
expand = 0.9, space = 0.3, along = "xy", colkey = list(side = 4,
width = 0.9, length = 0.4, cex.axis = 0.8), box = TRUE,
col.var = harvest(ane22.stk.a4a.51)[drop = TRUE], zlab = "Fishing mortality",
ylab = "Year", xlab = "Age", theta = 45, phi = 45, xlim = c(0,
5), main = "F-Final model fit51")
```

```
persp3D(z = harvest(ane22.stk.a4a.42)[drop = TRUE], x = as.numeric(dimnames(harvest(ane22.stk.a4a.42))[[1]]),
```

```

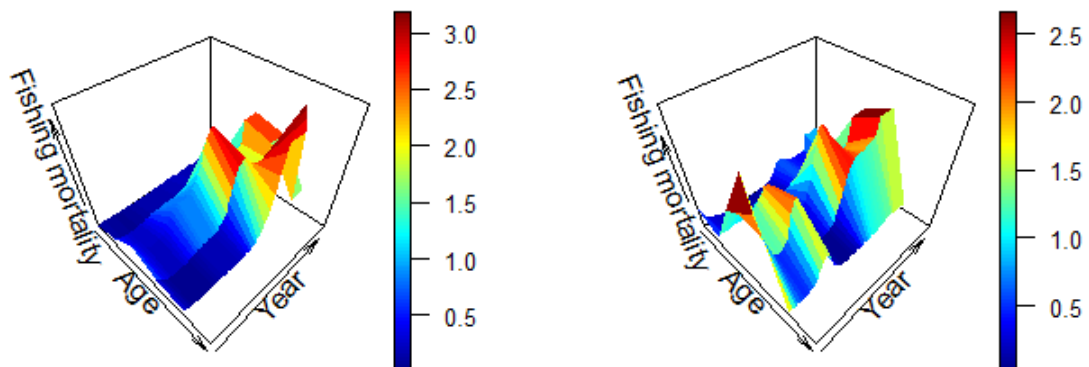
y = as.numeric(dimnames(harvest(ane22.stk.a4a.42))[[2]]),
expand = 0.9, space = 0.3, along = "xy", colkey = list(side = 4,
  width = 0.9, length = 0.4, cex.axis = 0.8), box = TRUE,
col.var = harvest(ane22.stk.a4a.42)[drop = TRUE], zlab = "Fishing mortality",
ylab = "Year", xlab = "Age", theta = 45, phi = 45, xlim = c(0,
  5), main = "F-Initial model fit42")

```

## Long time series

**F-Final model fit51**

**F-Initial model fit42**

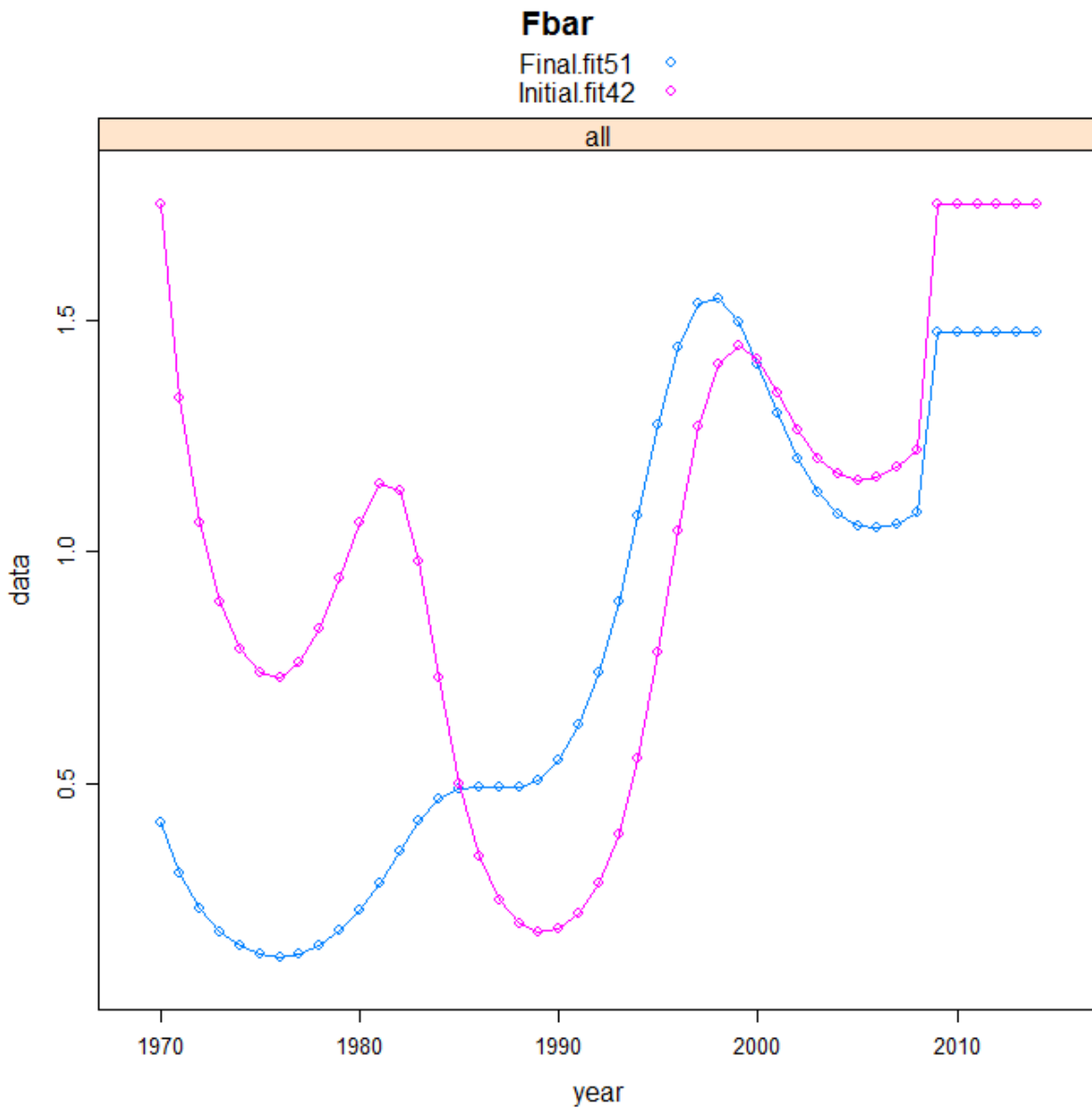


```

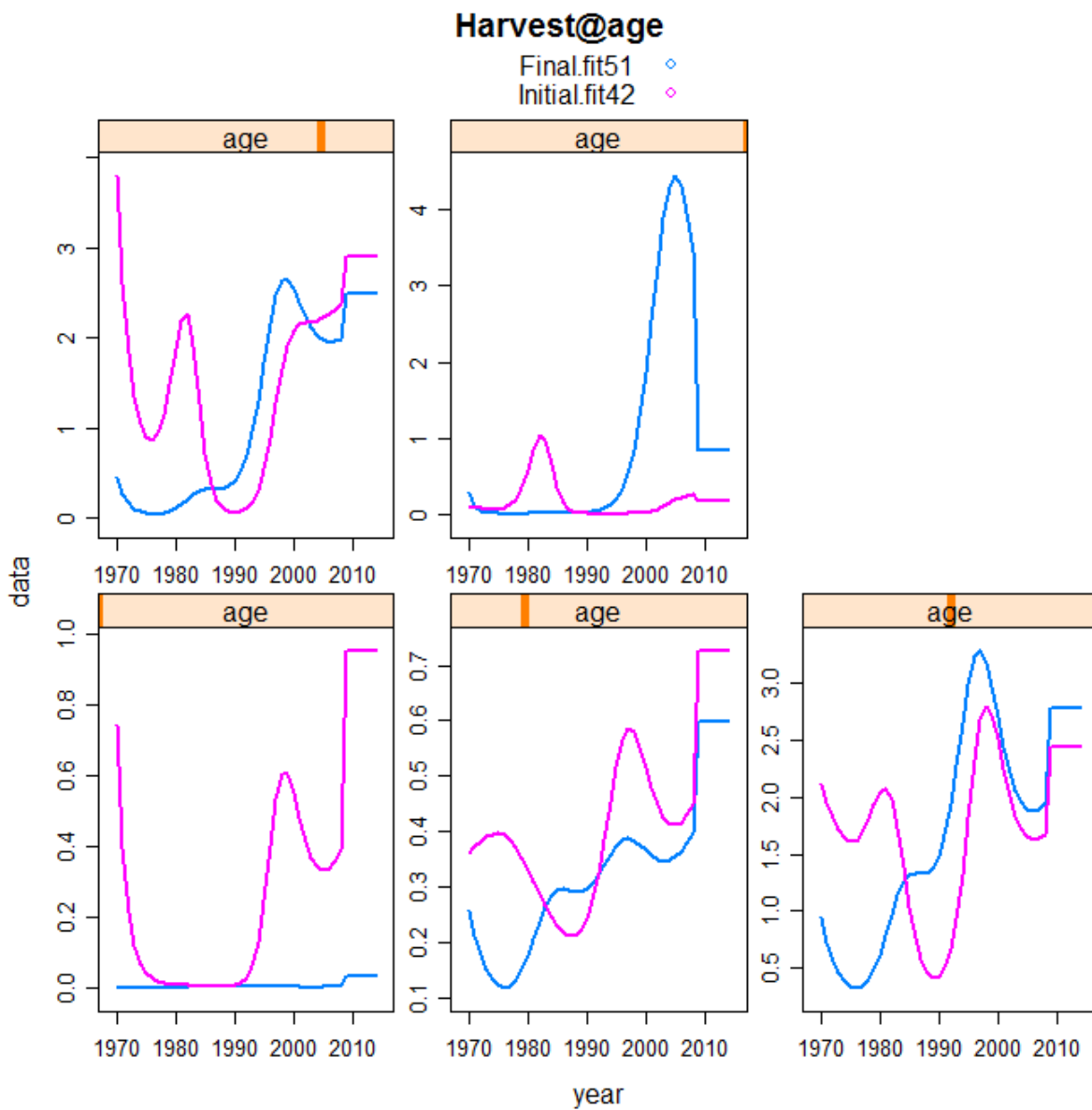
# Compare F's by Year Pass all harvest slots in an FLQuant
comp.mods.Fbar <- FLQuants(Final.fit51 = fbar(ane22.stk.a4a.51),
  Initial.fit42 = fbar(ane22.stk.a4a.42))
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.Fbar,
  type = "b", auto.key = T, main = "Fbar", scale = "free")

```





```
# Compare harvest by Year Pass all harvest slots in an
# FLQuant
comp.mods.harvest <- FLQuants(Final.fit51 = harvest(ane22.stk.a4a.51),
  Initial.fit42 = harvest(ane22.stk.a4a.42))
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.harvest,
  type = "l", auto.key = T, main = "Harvest@age", scale = "free",
  lwd = 2)
```



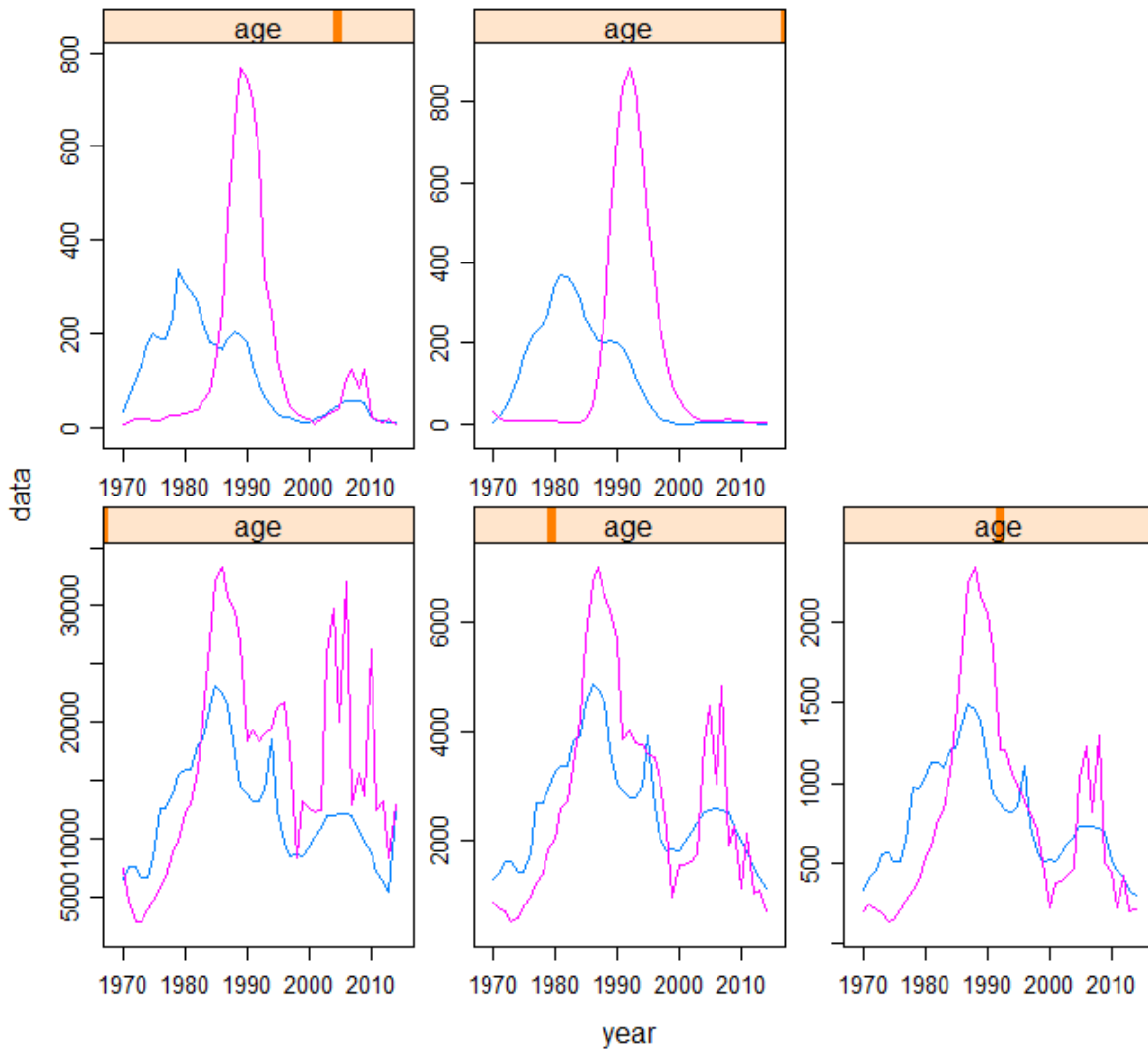
```

# Compare Stock abundances Pass all stock.n slots in an
# FLQuant
comp.mods.stock.n <- FLQuants(Final.fit51 = ane22.stk.a4a.51@stock.n/1000,
  Initial.fit42 = ane22.stk.a4a.42@stock.n/1000)
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.stock.n,
  type = "l", auto.key = T, main = "Stock Nb@age", scale = "free")

```

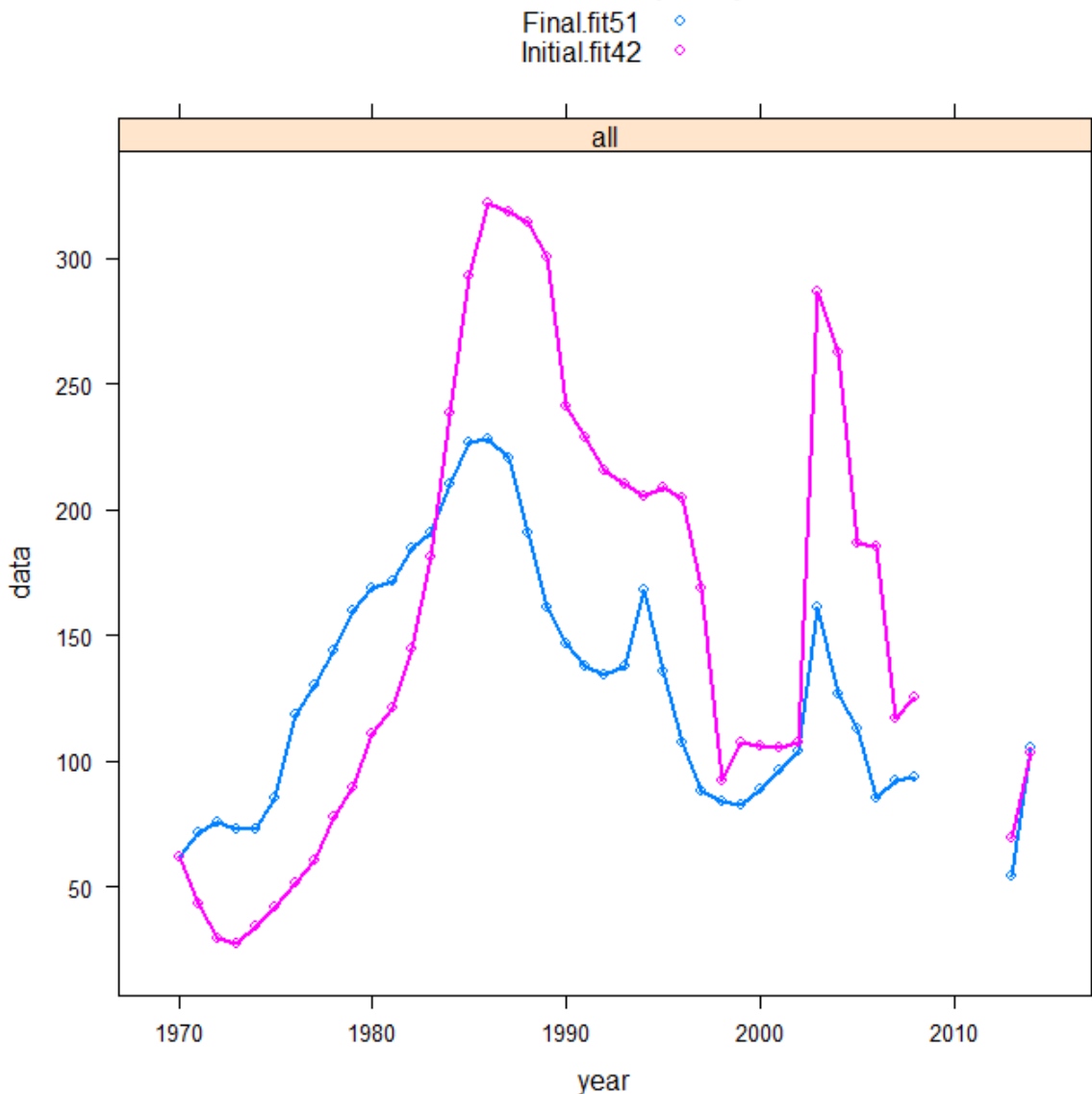
### Stock Nb@age

Final.fit51 ◊  
Initial.fit42 ◊



```
# Compare Stock Biomass Pass all stock slots in an FLQuant
comp.mods.stock <- FLQuants(Final.fit51 = ane22.stk.a4a.51@stock/1000,
  Initial.fit42 = ane22.stk.a4a.42@stock/1000)
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.stock,
  type = "b", auto.key = T, main = "Stock Biomass (tons)",
  lwd = 2)
```

## Stock Biomass (tons)



### 5.3.2 Sardine

```
##### COMPARE a4a fits HAR
par(mfrow = c(1, 2)) # create a 1 x 2 window

persp3D(z = harvest(pil22.stk.a4a.42)[drop = TRUE], x = as.numeric(dimnames(harvest(pil22.stk.a4a.42))[[1]]),
        y = as.numeric(dimnames(harvest(pil22.stk.a4a.42))[[2]]),
        expand = 0.9, space = 0.3, along = "xy", colkey = list(side = 4,
        width = 0.9, length = 0.4, cex.axis = 0.8), box = TRUE,
        col.var = harvest(pil22.stk.a4a.42)[drop = TRUE], zlab = "Fishing mortality",
        ylab = "Year", xlab = "Age", theta = 45, phi = 45, xlim = c(0,
        5), main = "F-Initial model fit42")

persp3D(z = harvest(pil22.stk.a4a.43)[drop = TRUE], x = as.numeric(dimnames(harvest(pil22.stk.a4a.43))[[1]]),
        y = as.numeric(dimnames(harvest(pil22.stk.a4a.43))[[2]]),
        expand = 0.9, space = 0.3, along = "xy", colkey = list(side = 4,
        width = 0.9, length = 0.4, cex.axis = 0.8), box = TRUE,
        col.var = harvest(pil22.stk.a4a.43)[drop = TRUE], zlab = "Fishing mortality",
        ylab = "Year", xlab = "Age", theta = 45, phi = 45, xlim = c(0,
        5), main = "F-Initial model fit43")
```

```

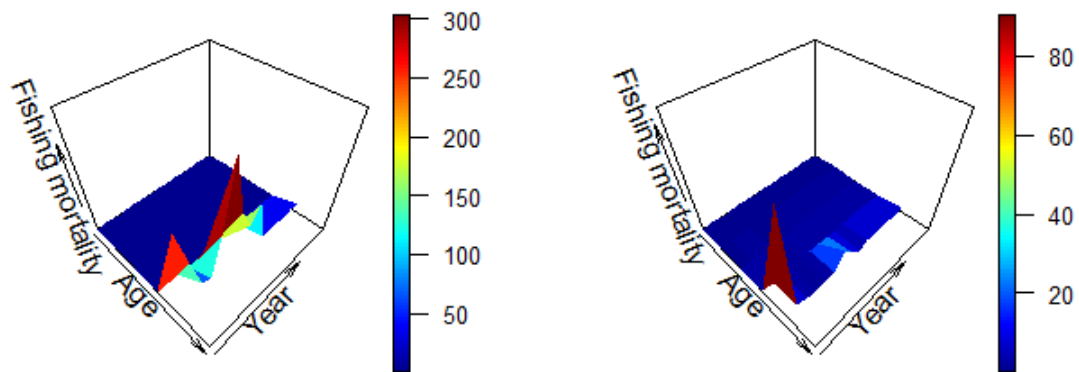
y = as.numeric(dimnames(harvest(pil22.stk.a4a.43))[[2]]),
expand = 0.9, space = 0.3, along = "xy", colkey = list(side = 4,
  width = 0.9, length = 0.4, cex.axis = 0.8), box = TRUE,
col.var = harvest(pil22.stk.a4a.43)[drop = TRUE], zlab = "Fishing mortality",
ylab = "Year", xlab = "Age", theta = 45, phi = 45, xlim = c(0,
  5), main = "F-Final model fit43")

```

### Short time series

**F-Initial model fit42**

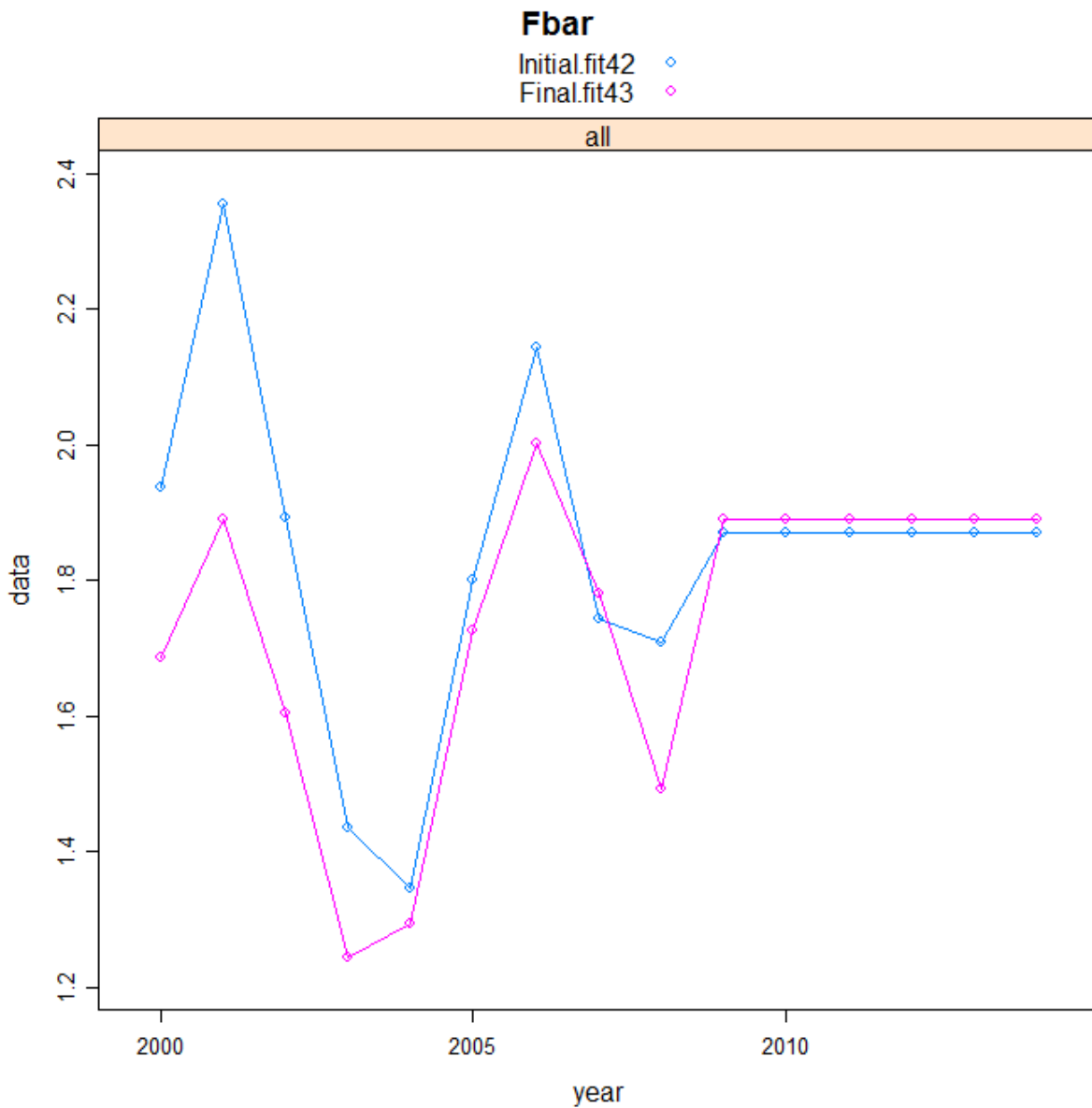
**F-Final model fit43**



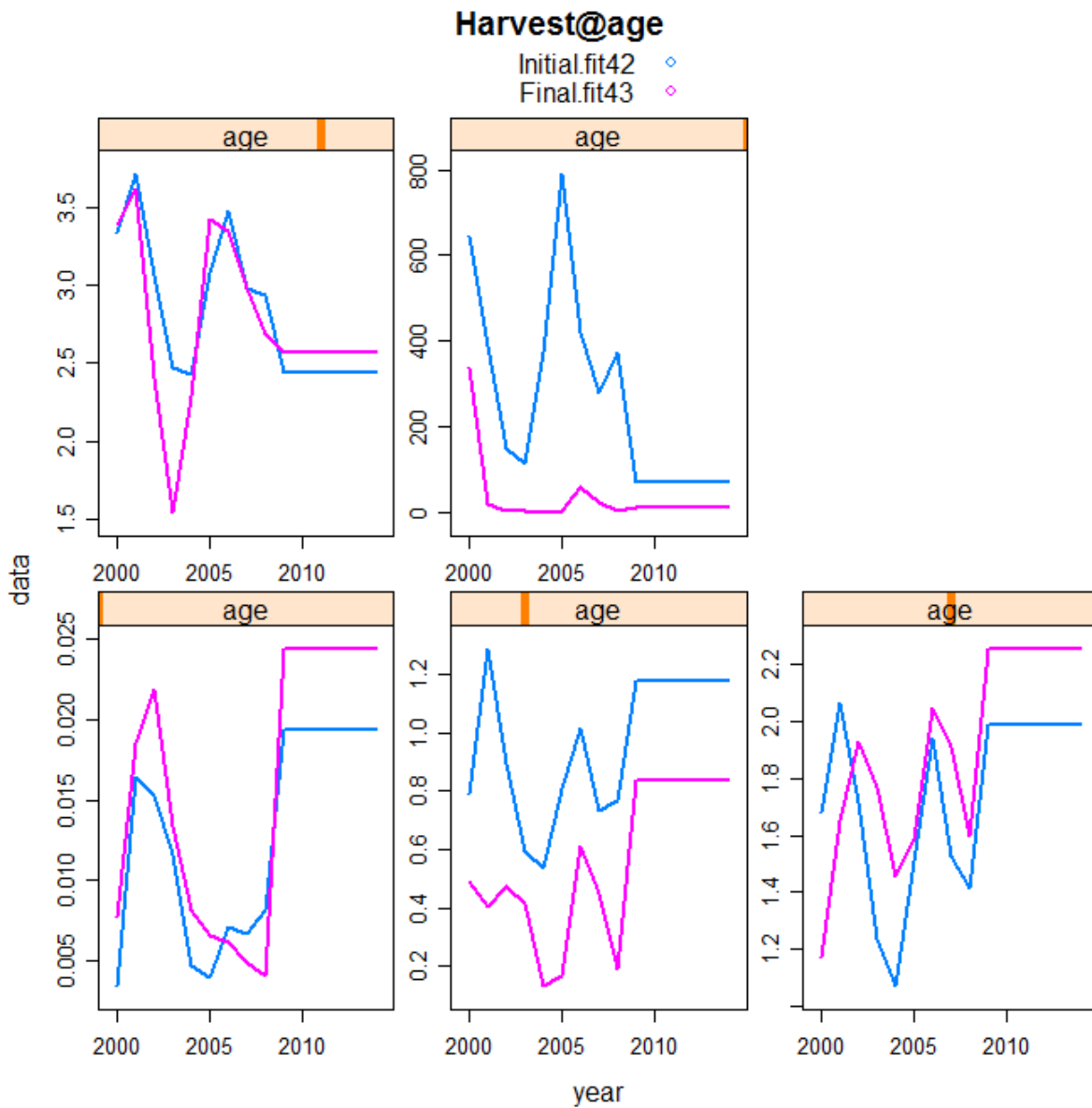
```

# Compare F's by Year Pass all harvest slots in an FLQuant
comp.mods.Fbar <- FLQuants(Initial.fit42 = fbar(pil22.stk.a4a.42),
  Final.fit43 = fbar(pil22.stk.a4a.43))
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.Fbar,
  type = "b", auto.key = T, main = "Fbar", scale = "free")

```



```
# Compare harvest by Year Pass all harvest slots in an
# FLQuant
comp.mods.harvest <- FLQuants(Initial.fit42 = harvest(pil22.stk.a4a.42),
  Final.fit43 = harvest(pil22.stk.a4a.43))
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.harvest,
  type = "l", auto.key = T, main = "Harvest@age", scale = "free",
  lwd = 2)
```



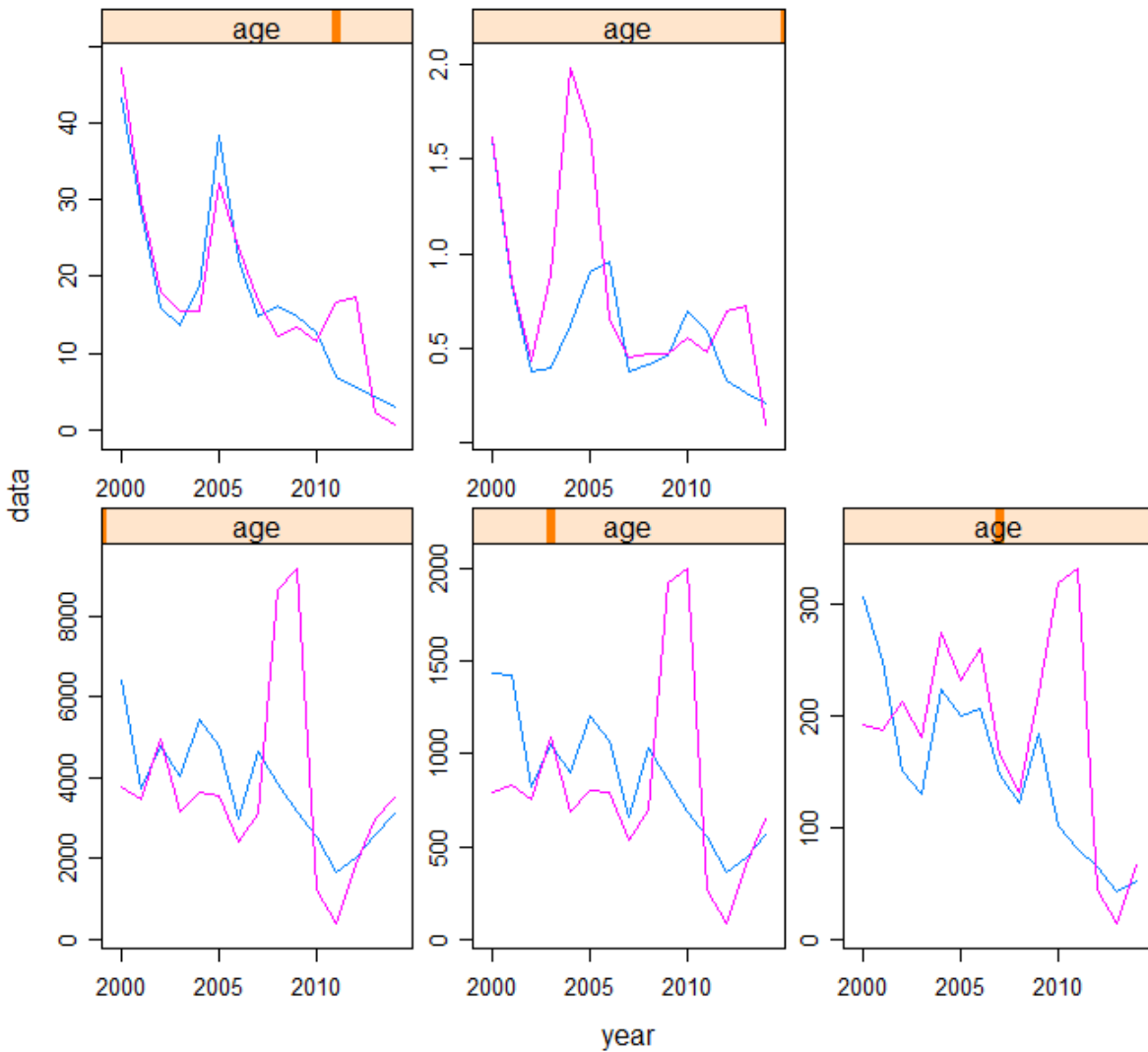
```

# Compare Stock abundances Pass all stock.n slots in an
# FLQuant
comp.mods.stock.n <- FLQuants(Initial.fit42 = pil22.stk.a4a.42@stock.n/1000,
  Final.fit43 = pil22.stk.a4a.43@stock.n/1000)
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.stock.n,
  type = "l", auto.key = T, main = "Stock Nb@age", scale = "free")

```

### Stock Nb@age

Initial.fit42 ◊  
Final.fit43 ◊

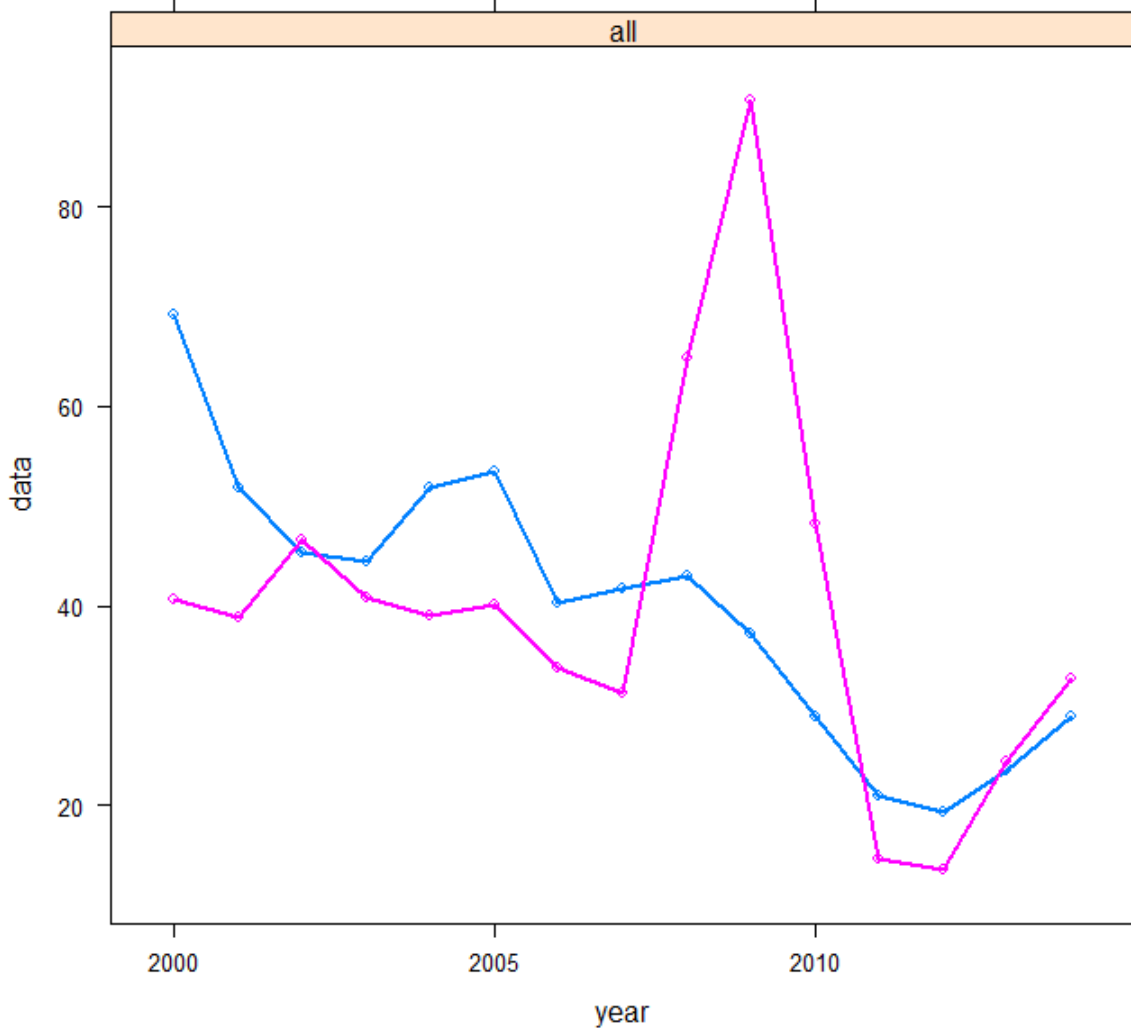


```
# Compare Stock Biomass Pass all stock slots in an FLQuant
comp.mods.stock <- FLQuants(Initial.fit42 = pil22.stk.a4a.42@stock/1000,
  Final.fit43 = pil22.stk.a4a.43@stock/1000)
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.stock,
  type = "b", auto.key = T, main = "Stock Biomass (tons)",
  lwd = 2)
```



## Stock Biomass (tons)

Initial.fit42 ◊  
 Final.fit43 ◊



```
##### COMPARE a4a fits HAR
par(mfrow = c(1, 2)) # create a 1 x 2 window

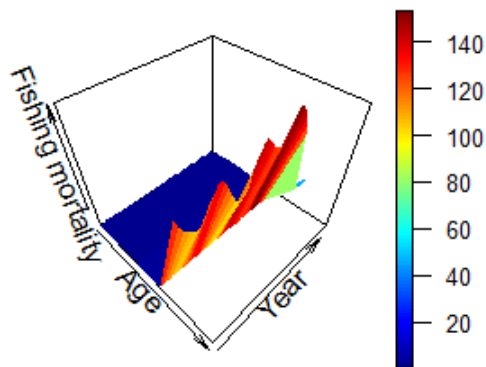
persp3D(z = harvest(pil22.stk.a4a.5)[drop = TRUE], x = as.numeric(dimnames(harvest(pil22.stk.a4a.5))[[1]]),
        y = as.numeric(dimnames(harvest(pil22.stk.a4a.5))[[2]]),
        expand = 0.9, space = 0.3, along = "xy", colkey = list(side = 4,
            width = 0.9, length = 0.4, cex.axis = 0.8), box = TRUE,
        col.var = harvest(pil22.stk.a4a.5)[drop = TRUE], zlab = "Fishing mortality",
        ylab = "Year", xlab = "Age", theta = 45, phi = 45, xlim = c(0,
            5), main = "F-Initial model fit5")

persp3D(z = harvest(pil22.stk.a4a.6)[drop = TRUE], x = as.numeric(dimnames(harvest(pil22.stk.a4a.6))[[1]]),
        y = as.numeric(dimnames(harvest(pil22.stk.a4a.6))[[2]]),
        expand = 0.9, space = 0.3, along = "xy", colkey = list(side = 4,
```

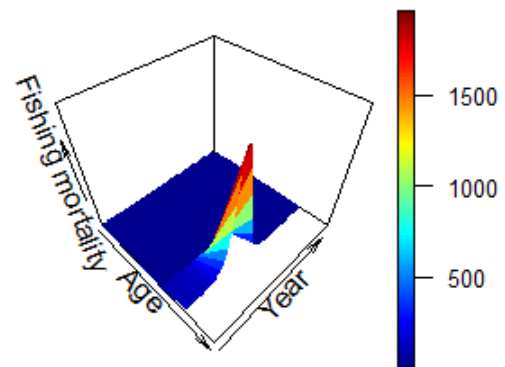
```
width = 0.9, length = 0.4, cex.axis = 0.8), box = TRUE,
col.var = harvest(pil22.stk.a4a.6)[drop = TRUE], zlab = "Fishing mortality",
ylab = "Year", xlab = "Age", theta = 45, phi = 45, xlim = c(0,
5), main = "F-Final model fit6")
```

## Long time series

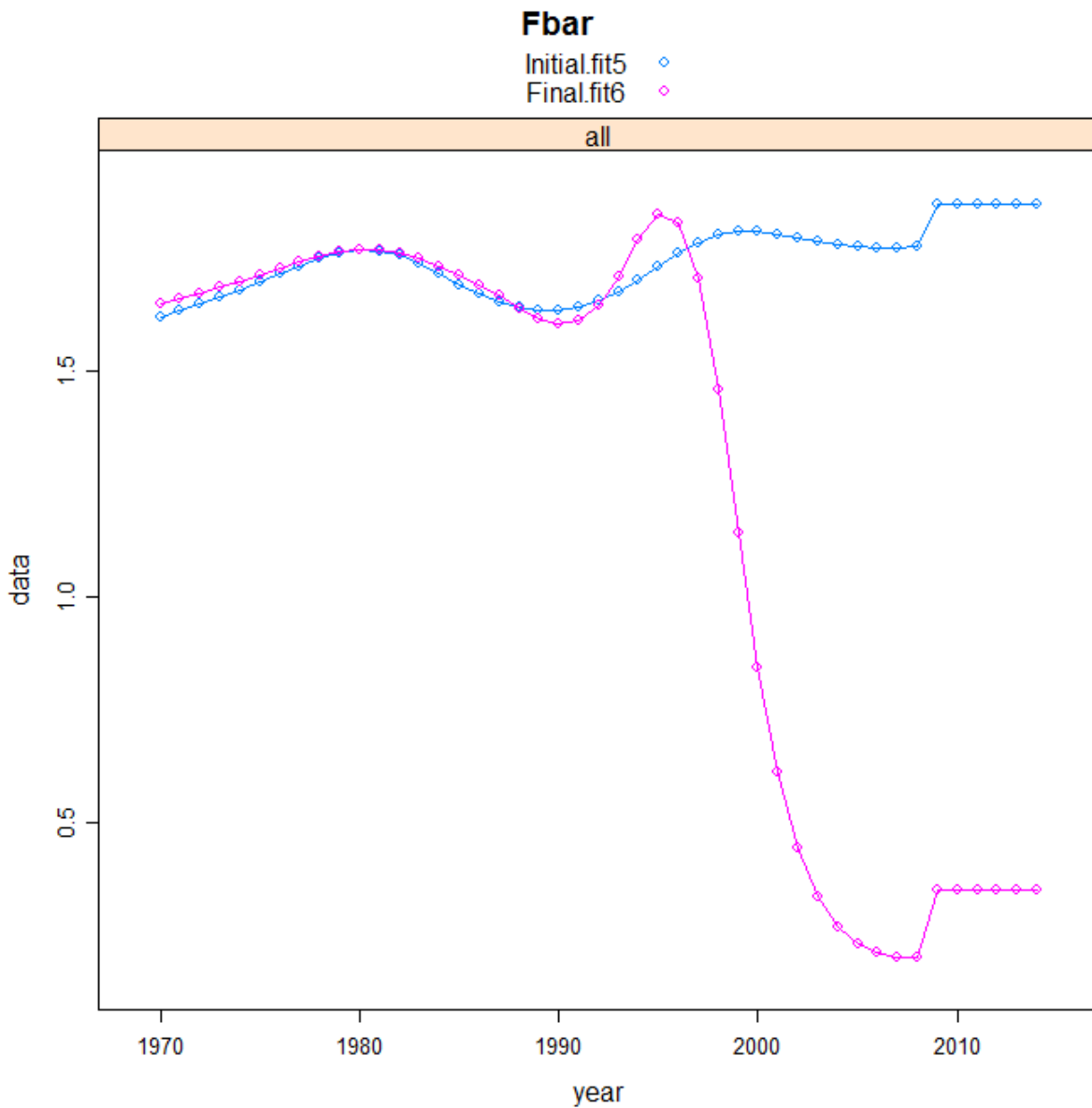
**F-Initial model fit5**



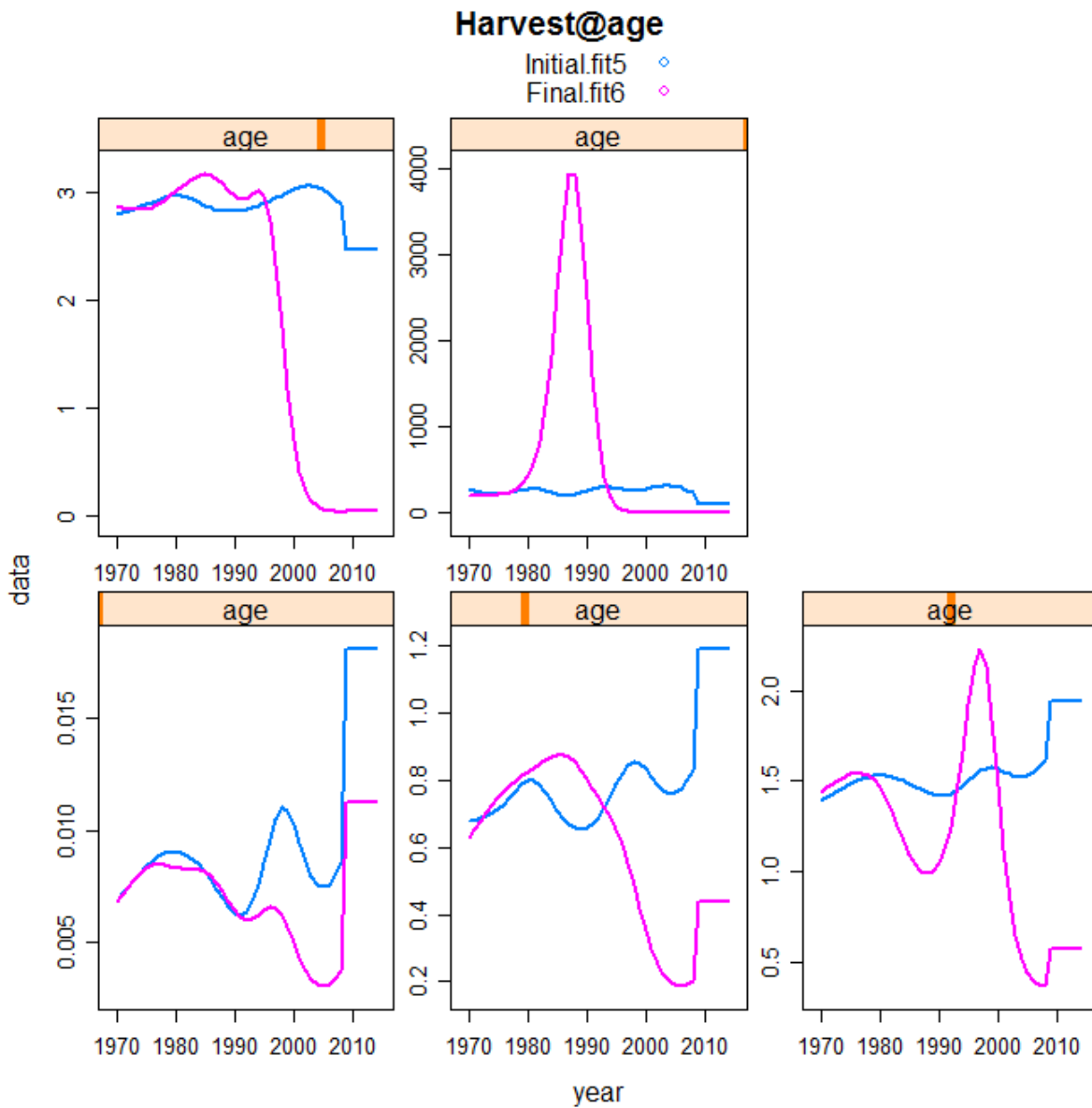
**F-Final model fit6**



```
# Compare F's by Year Pass all harvest slots in an FLQuant
comp.mods.Fbar <- FLQuants(Initial.fit5 = fbar(pil22.stk.a4a.5),
  Final.fit6 = fbar(pil22.stk.a4a.6))
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.Fbar,
  type = "b", auto.key = T, main = "Fbar", scale = "free")
```



```
# Compare harvest by Year Pass all harvest slots in an
# FLQuant
comp.mods.harvest <- FLQuants(Initial.fit5 = harvest(pil22.stk.a4a.5),
  Final.fit6 = harvest(pil22.stk.a4a.6))
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.harvest,
  type = "l", auto.key = T, main = "Harvest@age", scale = "free",
  lwd = 2)
```



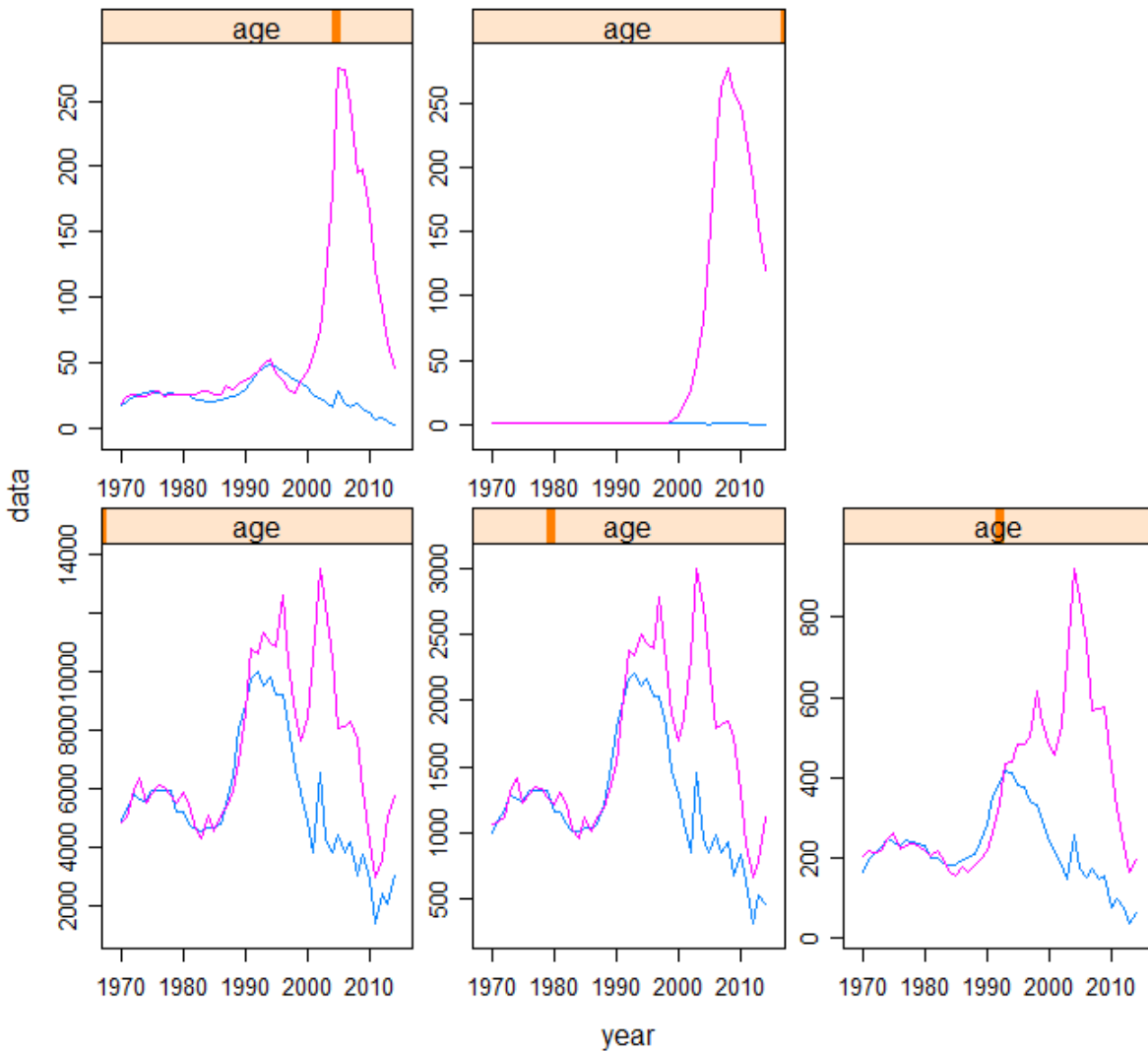
```

# Compare Stock abundances Pass all stock.n slots in an
# FLQuant
comp.mods.stock.n <- FLQuants(Initial.fit5 = pil22.stk.a4a.5@stock.n/1000,
  Final.fit6 = pil22.stk.a4a.6@stock.n/1000)
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.stock.n,
  type = "l", auto.key = T, main = "Stock Nb@age", scale = "free")

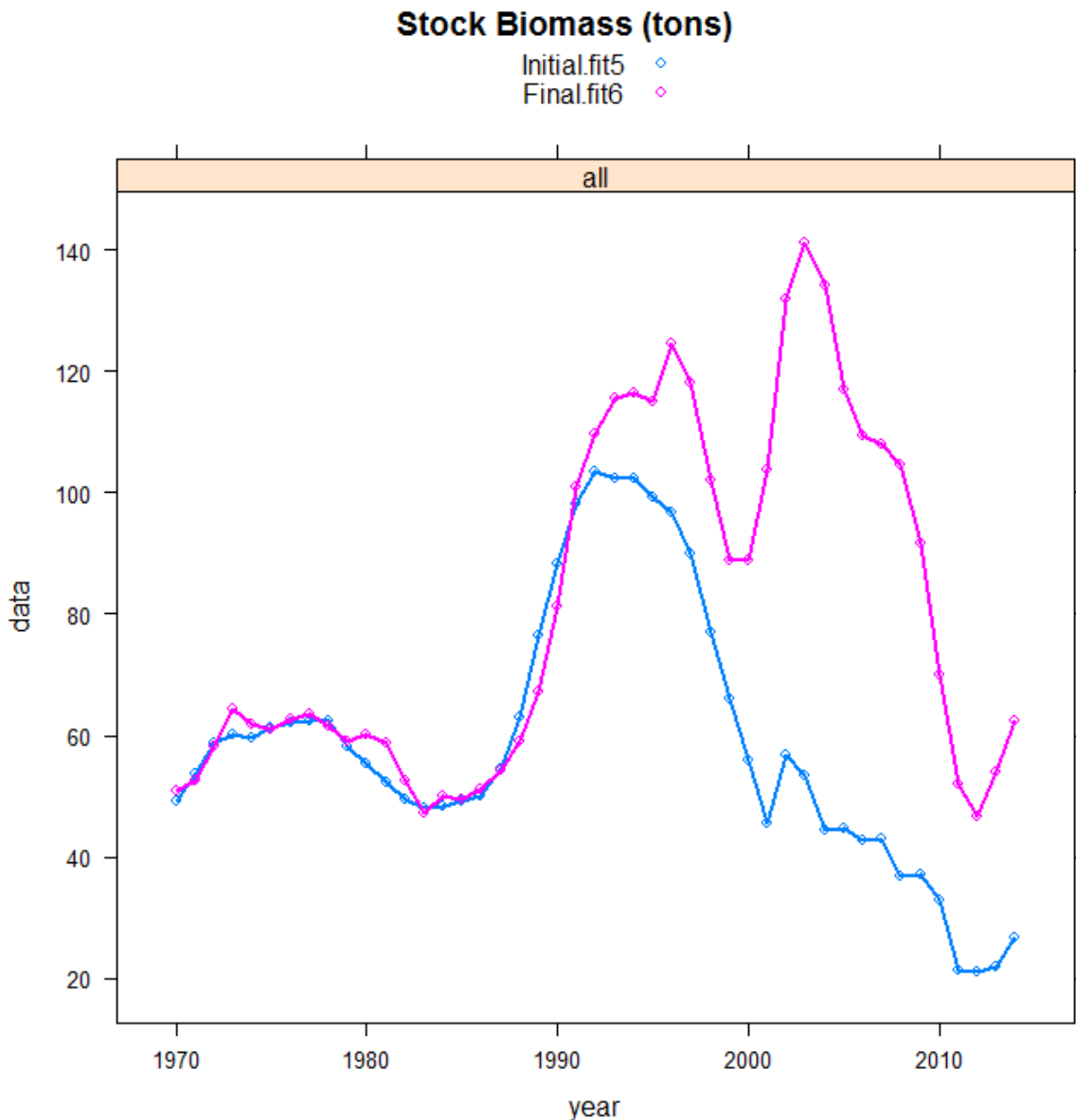
```

### Stock Nb@age

Initial.fit5 ◇  
Final.fit6 ◇



```
# Compare Stock Biomass Pass all stock slots in an FLQuant
comp.mods.stock <- FLQuants(Initial.fit5 = pil22.stk.a4a.5@stock/1000,
  Final.fit6 = pil22.stk.a4a.6@stock/1000)
# comparison plot
xyplot(data ~ year | age, groups = qname, data = comp.mods.stock,
  type = "b", auto.key = T, main = "Stock Biomass (tons)",
  lwd = 2)
```



## 6 Discussion and conclusions

Enlarging the knowledge base of a fishery is always a good idea and effort worth pursuing. Even when the success is not immediate, the compilation of historical information and the exploratory process of understanding the stock and fishery dynamics with relation to the ecosystem, will provide insights that may help making use of limited/sparse datasets for fish stocks management.

Using environmental indicators to anchor estimates for missing years seems to be promising. In the case studies presented here the success of this approach was not brilliant, in part due to the very short time series, which required large parts of the information base to be rebuilt. Environmental indicators have long time series which allow the analyst to defined/model the temporal behavior of the process, largely contributing for the estimation of stock status and identifying how dependent the stock is of externalities.

## 6.1 Comments on rebuilding historical information

- Rebuilding age structure based on recent catch structure smooths the dynamics and doesn't seem to help much the model fit.
- Not having information for tuning the age structure results in the model confounding high/low  $F$  with low/high  $SSB$ .
- Environmental indices helped model mainly in terms of recruitment. Other indices might be suitable to help with other ages.
- Catches in weight are important to get an idea of the level of exploitation. A model that fits the total catches may make use of it.
- Effort/capacity should also be further explored.

## 6.2 Comments on fitting short time series with gaps

- Stock assessment models fits depend on the number of full cohorts in the data. In the case of anchovy and sardine in GSA 22 fitting can be problematic due to the short time series and the existing gaps.
- Fits tend to get very unstable.
- Linking  $F$  in the missing years to observations gives "good" results and allows the estimation of  $F$  and population numbers.
- Most likely constraining more parameters can stabilize the fit and give better results.

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