### Validation

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Thanks to Anders Nielsen for borrowing course material



### Fish stock assessment models have evolved



#### Advantages with state-space formulation:

- The obvious tool for time series data
- Quantification of observation errors
- Quantification of process errors
- Process formulation of time-varying quantities
- Reasonable (low) number of model parameters
- Prediction as part of model formulation

#### Current validation practice include:

- Residuals
- Retrospective patterns of key outputs
- Leave-fleet-out runs (to check consistency between data sources)
- Jittered starting point analysis



### One-step-ahead residuals

SAM provides functionality for efficiently calculating one-step-ahead residuals

```
library(stockassessment)
  dat <- setup.sam.data(surveys=surveys,
3
        residual.fleet=cn.
4
        prop.mature=mo,
5
        stock.mean.weight=sw.
6
        catch.mean.weight=cw.
7
        dis.mean.weight=dw,
8
        land.mean.weight=lw,
9
        prop.f=pf,
10
        prop.m=pm,
        natural.mortality=nm,
        land.frac=lf)
13
14
  confDef<-defcon(dat)
  par = defpar(dat.confDef)
  fit = sam.fit(dat,confDef,par)
  #Calculate OSA-residuals
  res = residuals(fit)
```

Given the correct model, the residuals should be independent and  $\mathcal{N}(0,1)$  distributed



# In RTMB with your own model

- Inform what are the observations

Calculated one-step-ahead residuals:

```
1 res =oneStepPredict(obj)
```

- method oneStepGeneric
  - Most accurate approximation in general
  - Works in the discrete case

For details, see:

Thygesen, U. H., Albertsen, C. M., Berg, C. W., Kristensen, K., and Nielsen, A. (2017). Validation of ecological state space models using the Laplace approximation. Environmental and Ecological Statistics, 24(2):317–339.

# Simulation study

#### SAM has built-in functionality for simulation experiment

```
library(stockassessment)
  dat<-setup.sam.data(surveys=surveys,
3
        residual.fleet=cn.
       prop.mature=mo,
5
        stock.mean.weight=sw.
6
        catch.mean.weight=cw,
7
       dis.mean.weight=dw,
8
        land.mean.weight=lw.
       prop.f=pf,
       prop.m=pm,
       natural.mortalitv=nm.
        land.frac=lf)
14
  confDef<-defcon(dat)
  par = defpar(dat.confDef)
  fit = sam.fit(dat,confDef,par)
  #Calculate OSA-residuals
  sim = simstudy(fit)
  plot (sim)
```



# **Jitter analysis**

#### SAM has built-in functionality for jitter experiment

```
library(stockassessment)
  dat <- setup.sam.data(surveys=surveys,
        residual.fleet=cn.
       prop.mature=mo,
5
        stock.mean.weight=sw,
6
        catch.mean.weight=cw,
7
       dis.mean.weight=dw,
8
        land.mean.weight=lw,
       prop.f=pf,
       prop.m=pm,
       natural.mortality=nm,
        land.frac=lf)
14
  confDef<-defcon(dat)
  par = defpar(dat,confDef)
 fit = sam.fit(dat.confDef.par)
17 #Do jitter:
  jj = jit(fit)
19|jj
```



# Leave-out analysis

#### SAM has built-in functionality for leave-out analysis

```
library(stockassessment)
  dat <- setup.sam.data(surveys=surveys,
        residual.fleet=cn.
       prop.mature=mo,
5
        stock.mean.weight=sw,
6
        catch.mean.weight=cw,
7
       dis.mean.weight=dw,
8
        land.mean.weight=lw,
       prop.f=pf,
       prop.m=pm,
       natural.mortality=nm,
        land.frac=lf)
14
  confDef<-defcon(dat)
  par = defpar(dat,confDef)
 fit = sam.fit(dat.confDef.par)
  #Do leaveout:
  11 = leaveout(fit)
  plot (11)
```



### **AIC**

#### SAM has built-in functionality for using the AIC function

```
library(stockassessment)
  dat <- setup.sam.data(surveys=surveys,
3
        residual.fleet=cn.
4
       prop.mature=mo,
5
        stock.mean.weight=sw,
6
        catch.mean.weight=cw,
7
       dis.mean.weight=dw,
        land.mean.weight=lw,
       prop.f=pf,
10
       prop.m=pm,
       natural.mortality=nm,
        land.frac=lf)
14
  confDef<-defcon(dat)
15 par = defpar(dat,confDef)
16 fit = sam.fit(dat,confDef,par)
  #Calculate AIC
  AIC(fit)
```



### Likelihood-ratio test

Assume we want to test whether a parameter is significant

- $H_0: \theta \in \Omega_0$
- $H_a: \theta \in \Omega$

A likelihood-ratio test reject  $H_0$  if

$$\mathsf{LR} = \frac{\mathcal{L}(\hat{\theta}_0)}{\mathcal{L}(\hat{\theta})}$$

is small enough.

What is small enough?

- Many standard tests can be derived from the LR principle (e.g., t-test)
- For large sample size we have an approximation for the LR distribution



### The log of the likelihood ratio is

$$\log(\mathsf{LR}) = \log rac{\mathcal{L}(\hat{ heta}_0)}{\mathcal{L}(\hat{ heta})} = \ell(\hat{ heta}_0) - \ell(\hat{ heta})$$

### Asymptotically we have that

$$-2\log(\mathsf{LR}) = 2[\ell(\hat{ heta}) - \ell(\hat{ heta}_0)] \sim \chi_p^2$$

where  $p = dim(\Omega) - dim(\Omega_0)$ 

#### Procedure:

- Calculate -2 log(LR)
- Compare with  $\chi_p^2$

```
1 > qchisq(0.95,df = 1)
2 [1] 6.634897
```



### Liklihood-ratio test and AIC

AIC is defined by  $AIC = 2k - 2\ell(\hat{\theta})$ 

- *k* is the number of model parameters
- $\ell(\hat{\theta})$  is the maximum log-likelihood

We have that for including one parameter:

$$\begin{split} \Delta AIC &= AIC_0 - AIC \\ &= \left(2(k-1) - 2\ell(\hat{\theta}_0)\right) - \left(2k - 2\ell(\hat{\theta})\right) \\ &= 2[\ell(\hat{\theta}) - \ell(\hat{\theta}_0)] - 2 \end{split}$$

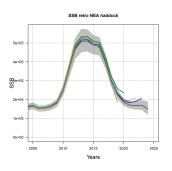
Notice the similarity with a likelihood ratio-test?

The AIC needs to be reduced with approximately 5 to be significant on 0.01-level

• Do not hunt parameters to include based on a small improvement in AIC



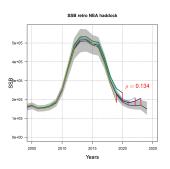
- Average relative difference from terminal estimate



$$\rho = \frac{1}{n} \sum_{y=y_0}^{Y-1} \frac{\hat{X}_{y|y} - \hat{X}_{y|Y}}{\hat{X}_{y|Y}}$$



- Average relative difference from terminal estimate



$$\rho = \frac{1}{n} \sum_{y=y_0}^{Y-1} \frac{\hat{X}_{y|y} - \hat{X}_{y|Y}}{\hat{X}_{y|Y}}$$

#### SAM has built-in functionality for retro analysis

```
library(stockassessment)
  dat <- setup.sam.data(survevs=survevs.
        residual.fleet=cn,
4
        prop.mature=mo,
5
        stock.mean.weight=sw.
6
        catch.mean.weight=cw,
7
        dis.mean.weight=dw,
8
        land.mean.weight=lw.
9
        prop.f=pf,
10
        prop.m=pm,
        natural.mortality=nm,
        land.frac=lf)
14
  confDef<-defcon(dat)
  par = defpar(dat,confDef)
  fit = sam.fit(dat,confDef,par)
17
 #Do retro analysis:
  ret = retro(fit, year = 5)
  #Calculate mohn's rho
  mohn (ret)
```

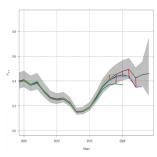


- SAM will by default remove last year of observation from all time series
  - This means that if a survey ended in 2014, SAM will remove year 2014 in first peal
  - This is not what you want
- You can manually set up which year that is removed from each fleet in each peal:

```
1 yearMat = matrix(c(2023, 2024, 2024, 2024, 2024, 2022, 2022, 2023, 2023, 2023, 2021, 2022, 2022, 2022, 2020, 2021, 2021, 2021, 2021, 2021, 2021, 2021, 2021, 2021, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020, 2020
```

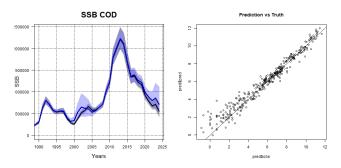
- Fishing mortality is very uncertain without data on catch in year
- If catch is missing in terminal year, default in ICES is to set lag = 1 when calculating Mohn's  $\rho$  for fishing mortality

```
ret = retro(fit,year = 5)
2  #Calculate mohn's rho
mohn(ret,lag = 1)
```



### **Prediction and cross-validations**

- Validate if the model is realistic w.r.t. coverage of confidence intervals
- Of special interest is the 2-3 year ahead predictions



- The only thing that is real is the observations
- When evaluating (and comparing) models we should look at their ability to predict observations.
- With state-space models we can (difficult to compare to other model types).

### Implementing cross validations

Set observations to unobserved. Simple implementation:

```
# function for cross-validation
  xval <- function(fit, year=NULL, fleet=NULL, age=NULL, ...){</pre>
3
       data <- fit$data
       nam <- c("year", "fleet", "age")[c(length(year)>0,length(fleet)>0,length(age)>0)]
5
        if((length(year)==0) & (length(fleet)==0) & (length(age)==0)){
6
             idx <- rep(TRUE, nrow(data$aux))
7
        }else{
8
             idx <- !do.call(paste, as.data.frame(data$aux[,nam,drop=FALSE])) %in% do.call(paste,
                  as.data.frame(cbind(year=year, fleet=fleet, age=age)))
        idx <- !idx
        data$logobs[idx] <- NA
        idx2 <- which (is.na(data$logobs))
13
        conf <- fit$conf
14
       par <- defpar(data,conf)
       thisfit <- sam.fit(data, conf, par, rm.unidentified = TRUE, silent=TRUE,...)
16
        ret <- as.data.frame(cbind(data$aux[idx2,], obs=fit$data$logobs[idx2], pred=thisfit$pl$
             missing, predSd=thisfit$plsd$missing))
        ret <- ret[complete.cases(ret).]
18
        attr(ret, "fit") <- thisfit
        return (ret)
  pred <- xval(fit, year=c(1988:1990,2013:2015))</pre>
```

• Exercise: Try it! See crossvalidation.R to get you started