The Jack Knife

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Introduction

The jack knife can be used to estimate the variance and bias of parameter estimates and derived quantities.

Estimation

The jackknife estimate of a parameter is derived by omitting in turn the i^{th} observation from the sample data set then re-estimating the parameters and calculating the mean $\overline{\theta}_i$.

$$f(X) \simeq \overline{f} \equiv \frac{1}{N} \sum_{i=1}^{N} f_i^J$$

Variance estimation

The variance can then be calculated i.e.

$$\sigma_{f(\bar{x})} = \sqrt{N-1}\sigma_{f^J}$$

where

$$\sigma_{f^J}^2 \equiv \overline{(f^J)^2} - (\overline{f^J})^2$$

Th covariance for the α^{th} and β^{th} parameters is given by

$$COV_{\alpha,\beta} = \frac{N-1}{N} \sum_{i=1}^{N} [\theta_i^J - \overline{\theta^J}]_a [\theta_i^J - \overline{\theta^J}]_b$$

where

$$\overline{\theta_\alpha^J} = \frac{1}{N} \sum i = 1 N \theta_J^{i,\alpha}$$

The reason the sample covariance matrix has $N-1$ as the denominator rather than N is because the population mean $E(x)$ is not known and is replaced by the sample mean.

Bias estimation and correction

The bias of the estimator, calculated over the entire sample, can be estimated by

$$f(X) \simeq Nf(\bar{x}) - (N-1)\overline{f^J}$$

This reduces bias by an order of magnitude, from $O(N^{-1})$ to $O(N^{-2})$.

Simulation

Simulate an object with known properties using the biodyn package

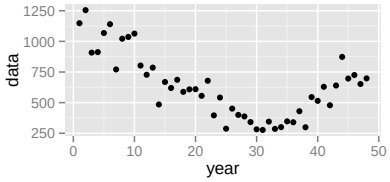
```
library(plyr)
library(biodyn)

bd=simBiodyn()
bd=window(bd,end=49)
```

A proxy for stock abundance is also required, therefore an unbiased catch per effort (CPUE) series is generated from mid year stock biomass.

```
cpue=(stock(bd)[,-dims(bd)$year]+stock(bd)[,-1])/2
cpue=rlnorm(1,log(cpue),.2)

ggplot(cpue)+geom_point(aes(year,data))
```



Perform an assessment

```
#set parameters
setParams(bd) =cpue
setControl(bd)=params(bd)
control(bd)[3:4,"phase"]=-1

#fit
bdHat=fit(bd,cpue)
```

```
[1] TRUE
```

```
plot(biodyns("Estimate"=bdHat,"Actual"=bd))+
  theme(legend.position="bottom")
```

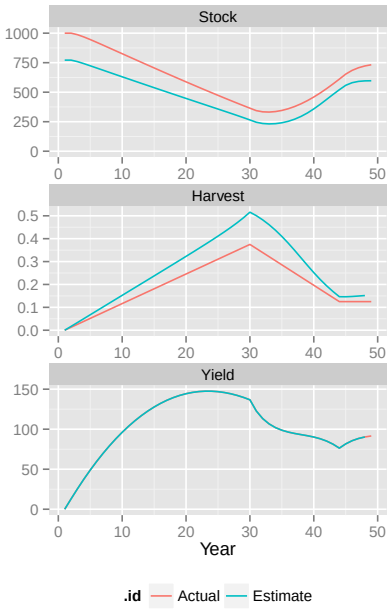


Figure 1: Fitted compared to actual time series

Jack knife procedure

```
bdJK=fit(bdHat,jackknife(cpue))

plotJack(bdHat,bdJK)


library(ggplotFL)
true=stock(bd   )[,49]
hat =stock(bdHat)[,49]
jack=stock(bdJK )[,49]
```

FLQuant

```
n   =dims(jack)$iter
mn  =apply(jack, 1:5, mean)
rsdl=sweep(jack,1:5,mn,"-")
ss  =apply(rsdl^2,1:5,sum)

bias         =(n-1)*(hat-mn)
biasCorrected=n*hat-(n-1)*mn

se  =sqrt(((n-1)/n)*ss)
```

FLPar

```
true=bmsy(bd   )
hat =bmsy(bdHat)
jack=bmsy(bdJK )

n   =dims(jack)$iter
mn  =apply(jack,  seq(length(dim(jack))-1), mean)
rsdl=sweep(jack,  seq(length(dim(jack))-1), mn,"-")
ss  =apply(rsdl^2,seq(length(dim(jack))-1),sum)

bias         =(n-1)*(hat-mn)
biasCorrected=n*hat-(n-1)*mn

se  =sqrt(((n-1)/n)*ss)
```

FLPars

```
true=refpts(bd   )
hat =refpts(bdHat)
jack=refpts(bdJK )

n   =dims(jack)$iter
```

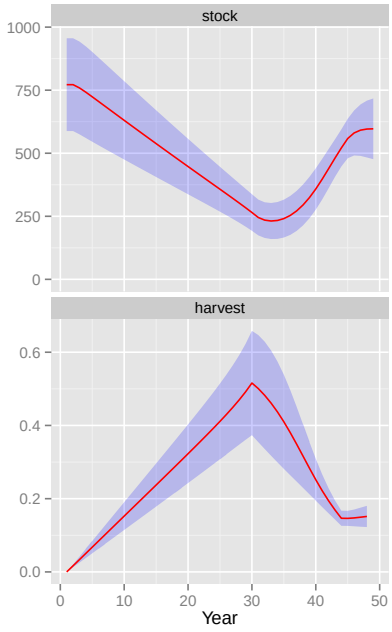


Figure 2: Jack knife error bars

```
mn  =apply(jack,  seq(length(dim(jack))-1), mean)
rsdl=sweep(jack,  seq(length(dim(jack))-1), mn,"-")
ss  =apply(rsdl^2,seq(length(dim(jack))-1),sum)

bias         =(n-1)*(hat-mn)
biasCorrected=n*hat-(n-1)*mn
se           =sqrt(((n-1)/n)*ss)
cov          =FLPar(cov(model.frame(rsdl)[,dimnames(rsdl)[[1]]])*(n-1)*(n-1)/n)
```

Perform an assessment with Monte Carlo simulation of CPUE series

Maybe perform a Monte Carlo simulation of the Jack knife to see how well it works.

Simulations

```
library(ggplotFL)
bd=simBiodyn()
bd=window(bd,end=49)

cpue=(stock(bd)[,-dims(bd)$year]+stock(bd)[,-1])/2
cpue=rlnorm(250,log(cpue),.2)

plot(cpue)


#set parameters
setParams(bd) =cpue
setControl(bd)=params(bd)
control(bd)[3:4,"phase"]=-1

#fit
catch(bd)=propagate(catch(bd),250)
bdHat=fit(bd,cpue)

plot(biodyns("Hat"=bdHat,"True"=bd))

median(stock(bd)[,49])
median(stock(bdHat)[,49])
```

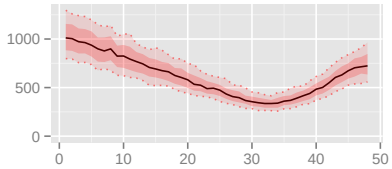


Figure 3: Simulated CPUE series