

Comparing von Bertalanffy Growth Functions

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Preliminaries

```
> library(FSAdata)      # for Croaker2 data
> library(FSA)          # for vbStarts(), residPlot(), extraSS(), lrt(), vbFuns(), filterD(), col2rbgt()
> library(dplyr)        # for mutate()
```

Loading the Data and Some Preparations

```
> data(Croaker2)
> str(Croaker2)
'data.frame':   318 obs. of  3 variables:
 $ age: int   1 1 1 2 2 2 2 2 2 2 ...
 $ t1 : int  243 247 248 330 320 285 280 265 260 248 ...
 $ sex: Factor w/ 2 levels "F","M": 1 1 2 1 1 1 1 1 1 1 ...

> Croaker2 <- mutate(Croaker2, logTL=log(t1))
```

Fitting Most Complex Model and Checking Assumptions

```
> ( sv0m <- vbStarts(t1~age, data=Croaker2) )
$Linf
[1] 434.697

$K
[1] 0.1837369

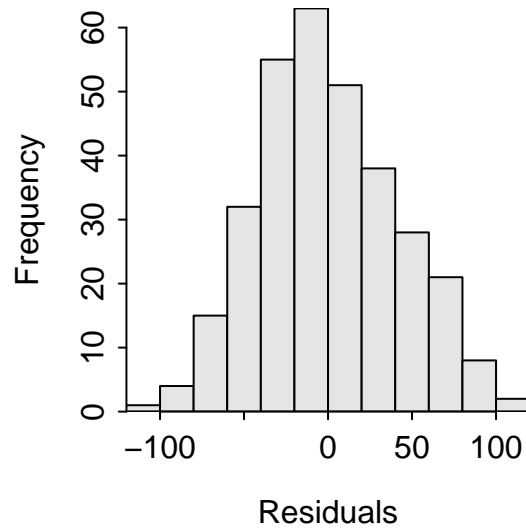
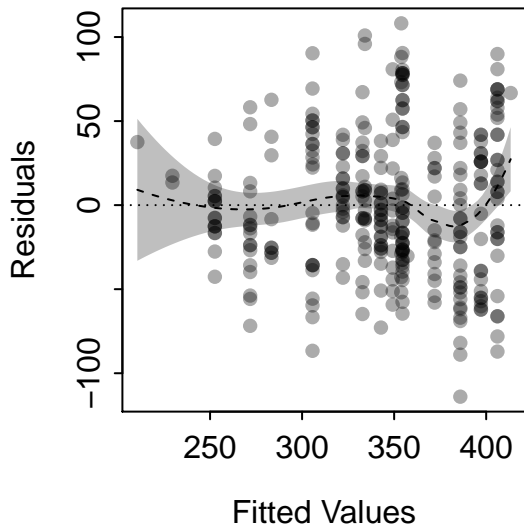
$t0
[1] -3.541856

> ( svLKt <- Map(rep, sv0m, c(2,2,2)) )
$Linf
[1] 434.697 434.697

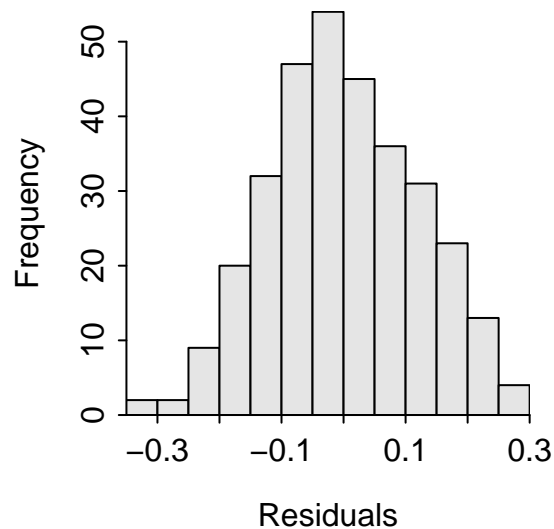
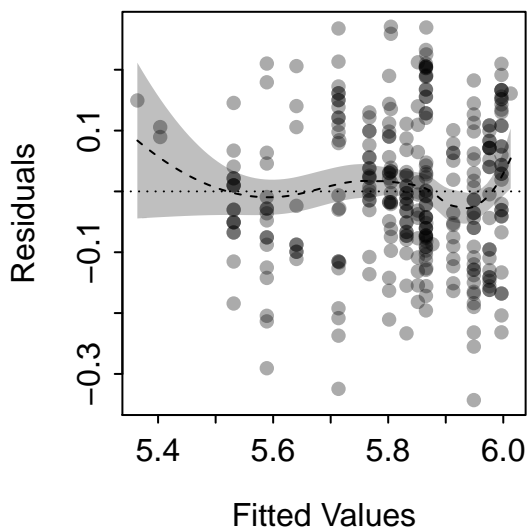
$K
[1] 0.1837369 0.1837369

$t0
[1] -3.541856 -3.541856

> vbLKt <- t1~Linf[sex]*(1-exp(-K[sex]*(age-t0[sex])))
> fitLKt <- nls(vbLKt, data=Croaker2, start=svLKt)
> residPlot(fitLKt, col=rgb(0,0,0,1/3))
```



```
> vbLKt <- logTL~log(Linf[sex]*(1-exp(-K[sex]*(age-t0[sex]))))
> fitLKt <- nls(vbLKt,data=Croaker2,start=svLKt)
> residPlot(fitLKt,col=col2rgb("black",1/3))
```



Are There Any Differences?

```
> vb0m <- logTL~log(Linf*(1-exp(-K*(age-t0))))
> fit0m <- nls(vb0m,data=Croaker2,start=sv0m)

> extraSS(fit0m,com=fitLKt,sim.name="{Omega}",com.name="{Linf,K,t0}")
Model 1: {Omega}
Model A: {Linf,K,t0}
```

	Df0	RSS0	DfA	RSSA	Df	SS	F	Pr(>F)
1vA	315	5.23971	312	4.44264	3	0.79707	18.659	3.705e-11

```
> lrt(fit0m,com=fitLKt,sim.name="{Omega}",com.name="{Linf,K,t0}")
Model 1: {Omega}
Model A: {Linf,K,t0}
```

	Df0	logLik0	DfA	logLikA	Df	logLik	Chisq	Pr(>Chisq)
1vA	315	201.597	312	227.835	3	-26.238	52.476	2.372e-11

Is the Most Complex Model Warranted?

```
> vbLK <- logTL~log(Linf[sex]*(1-exp(-K[sex]*(age-t0))))
> ( svLK <- Map(rep,sv0m,c(2,2,1)) )
$Linf
[1] 434.697 434.697

$K
[1] 0.1837369 0.1837369

$t0
[1] -3.541856

> fitLK <- nls(vbLK,data=Croaker2,start=svLK)
> vbLt <- logTL~log(Linf[sex]*(1-exp(-K*(age-t0[sex]))))
> svLt <- Map(rep,sv0m,c(2,1,2))
> fitLt <- nls(vbLt,data=Croaker2,start=svLt)
> vbKt <- logTL~log(Linf*(1-exp(-K[sex]*(age-t0[sex]))))
> svKt <- Map(rep,sv0m,c(1,2,2))
> fitKt <- nls(vbKt,data=Croaker2,start=svKt)
> extraSS(fitLK,fitLt,fitKt,com=fitLKt,com.name="{Linf,K,t0}",
          sim.names=c("{Linf,K}", "{Linf,t0}", "{K,t0}"))
Model 1: {Linf,K}
Model 2: {Linf,t0}
Model 3: {K,t0}
Model A: {Linf,K,t0}
```

	Df0	RSS0	Dfa	RSSA	Df	SS	F	Pr(>F)
1vA	313	4.442641	312	4.442639	1	0.000002	0.0001	0.9916
2vA	313	4.444957	312	4.442639	1	0.002318	0.1628	0.6869
3vA	313	4.476736	312	4.442639	1	0.034097	2.3946	0.1228

Can the Model be Reduced to Only One Parameter that Differs?

```
> vbL <- logTL~log(Linf[sex]*(1-exp(-K*(age-t0))))
> ( svL <- Map(rep,sv0m,c(2,1,1)) )
$Linf
[1] 434.697 434.697

$K
[1] 0.1837369

$t0
[1] -3.541856

> fitL <- nls(vbL,data=Croaker2,start=svL)
> vbK <- logTL~log(Linf*(1-exp(-K[sex]*(age-t0))))
> svK <- Map(rep,sv0m,c(1,2,1))
> fitK <- nls(vbK,data=Croaker2,start=svK)
> extraSS(fitL,fitK,com=fitLK,com.name="{Linf,K}",sim.names=c("{Linf}", "{K}"))
Model 1: {Linf}
Model 2: {K}
Model A: {Linf,K}
```

	Df0	RSS0	Dfa	RSSA	Df	SS	F	Pr(>F)
1vA	314	4.484252	313	4.442641	1	0.041612	2.9317	0.087847
2vA	314	4.621667	313	4.442641	1	0.179027	12.6131	0.000442

Summarize Final Model

```
> summary(fitL,correlation=TRUE)
```

Formula: $\log TL \sim \log(\text{Linf}[\text{sex}] * (1 - \exp(-K * (\text{age} - t_0))))$

Parameters:

	Estimate	Std. Error	t value	Pr(> t)
Linf1	425.37158	17.13519	24.824	< 2e-16
Linf2	384.21649	15.65097	24.549	< 2e-16
K	0.24825	0.05315	4.671	4.45e-06
t0	-2.12303	0.66226	-3.206	0.00149

Residual standard error: 0.1195 on 314 degrees of freedom

Correlation of Parameter Estimates:

	Linf1	Linf2	K
Linf2	0.94		
K	-0.95	-0.93	
t0	-0.87	-0.85	0.97

Number of iterations to convergence: 4

Achieved convergence tolerance: 1.809e-06

```
> round(cbind(coef(fitL),confint(fitL)),3)
```

Waiting for profiling to be done...

	2.5%	97.5%	
Linf1	425.372	400.090	481.671
Linf2	384.216	360.721	435.082
K	0.248	0.144	0.357
t0	-2.123	-3.986	-1.108

```
> vb <- vbFuns("typical")
```

```
> # Females
```

```
> crF <- filterD(Croaker2,sex=="F")
```

```
> svF <- list(Linf=425,K=0.25,t0=-2)
```

```
> fitF <- nls(logTL~log(vb(age,Linf,K,t0)),data=crF,start=svF)
```

```
> # Males
```

```
> crM <- filterD(Croaker2,sex=="M")
```

```
> svM <- list(Linf=385,K=0.25,t0=-2)
```

```
> fitM <- nls(logTL~log(vb(age,Linf,K,t0)),data=crM,start=svM)
```

```
> clr1 <- c("black","red")
```

```
> clr2 <- col2rgbt(clr1,1/5)
```

```
> offset <- 0.04
```

```
> # Females
```

```
> plot(tl~I(age-offset),data=crF,pch=19,col=clr2[1],ylim=c(200,500),
```

```
      xlab="Age (yrs)",ylab="Total Length (mm)")
```

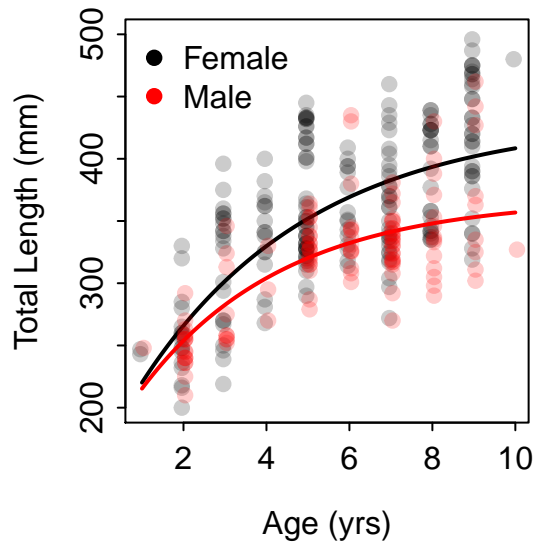
```
> curve(vb(x-offset,coef(fitF)),from=1,to=10,col=clr1[1],lwd=2,add=TRUE)
```

```
> # Males
```

```
> points(tl~I(age+offset),data=crM,pch=19,col=clr2[2])
```

```
> curve(vb(x+offset,coef(fitM)),from=1,to=10,col=clr1[2],lwd=2,add=TRUE)
```

```
> legend("topleft",c("Female","Male"),pch=19,col=clr1,bty="n")
```



Using Information Criterion

Fit the Only Other Model not Fit Above

```
> vbt <- logTL~log(Linf*(1-exp(-K*(age-t0[sex]))))
> svt <- Map(rep,sv0m,c(1,1,2))
> fitt <- nls(vbt,data=Croaker2,start=svt)
```

AICc Table

```
> library(AICcmodavg)
> ms <- list(fitOm,fitL,fitK,fitt,fitLK,fitLt,fitKt,fitLKt)
> mnames <- c("{Omega}","{Linf}","{K}","{t0}","{Linf,K}","{Linf,t0}","{K,t0}","{Linf,K,t0}")
> aictab(ms,mnames)
```

Model selection based on AICc:

	K	AICc	Delta_AICc	AICcWt	Cum.Wt	LL
{Linf,K}	6	-443.40	0.00	0.31	0.31	227.84
{Linf,t0}	6	-443.23	0.17	0.29	0.60	227.75
{Linf}	5	-442.51	0.89	0.20	0.80	226.35
{Linf,K,t0}	7	-441.31	2.09	0.11	0.91	227.84
{K,t0}	6	-440.97	2.43	0.09	1.00	226.62
{K}	5	-432.91	10.49	0.00	1.00	221.55
{t0}	5	-422.44	20.96	0.00	1.00	216.31
{Omega}	4	-395.07	48.33	0.00	1.00	201.60