

fishR Vignette - Von Bertalanffy Growth Model, Mixed Effects

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XXX THIS IS A WORK IN PROGRESS XXX

The functions required to perform growth analyses in R are contained in the packages loaded below,

```
> library(FSA)
> library(lattice)
> library(nlme)
```

1 The Data

The “data” used in this vignette will be simulated individual length-at-age data as described in [Vigliola and Meekan \(2009\)](#). These data may be thought of as back-calculated lengths-at-age. Ten individuals aged 4 to 12 will be simulated with mean $L_{\infty}=30$, $K=0.2$, and $t_0=-0.02$ with the code below (see [Vigliola and Meekan \(2009\)](#) and `?vbDataGen` for more details). The random seed was set to allow reproducibility.

```
> ### Set seed to make reproducible
> set.seed(158936)
> ### Make some data -- 10 individuals
> dw <- vbDataGen(10,Linf=30,K=0.2,t0=-0.02,minAge=4,maxAge=12,CV=0.05,undf=10,dataType="wide")
> head(dw)
```

	id	agecap	anu1	anu2	anu3	anu4	anu5	anu6	anu7	anu8	anu9	anu10	anu11	anu12
1	1	8	5.885	10.832	14.46	18.03	20.05	22.86	23.37	23.33	NA	NA	NA	NA
2	2	9	5.862	10.440	13.96	15.55	19.06	20.06	22.65	24.67	25.68	NA	NA	NA
3	3	9	5.452	9.868	13.64	19.03	21.73	23.58	24.99	24.84	26.18	NA	NA	NA
4	4	7	5.360	8.306	11.94	14.75	18.54	20.01	21.22	NA	NA	NA	NA	NA
5	5	11	5.022	9.117	12.41	15.45	17.18	18.38	20.51	22.83	23.99	22.25	24.16	NA
6	6	8	4.993	9.589	11.85	16.63	18.29	21.72	20.71	26.36	NA	NA	NA	NA

The data in `dw` are in “wide” format but need to be in “long” format for the modeling. The conversion from “wide” to “long” format is accomplished with `gReshape()` as shown below. Finally, the long format data can be put into a “groupedData” format with `groupedData()` for ease of graphing and modeling.

```
> dl <- gReshape(dw,in.pre="anu",id.var=c("id","agecap"),na.rm=TRUE)
> head(dl)
```

	id	agecap	age	anu
1	1	8	1	5.885
2	2	9	1	5.862
3	3	9	1	5.452
4	4	7	1	5.360
5	5	11	1	5.022
6	6	8	1	4.993

```
> dg <- groupedData(anu~age|id,data=dl,labels=list(x="Age",y="Size"),units=list(x="(Years)",
      y="(cm)"))
> head(dg)
```

Grouped Data: anu ~ age | id

	id	agecap	age	anu
1	1	8	1	5.885

```

2 2      9  1 5.862
3 3      9  1 5.452
4 4      7  1 5.360
5 5     11  1 5.022
6 6      8  1 4.993

> str(dg)
Classes 'nfnGroupedData', 'nfGroupedData', 'groupedData' and 'data.frame': 78 obs. of  4 variables:
 $ id      : Ord.factor w/ 10 levels "8"<"10"<"4"<"7"<...: 5 7 8 3 6 9 4 1 10 2 ...
 $ agecap: int   8 9 9 7 11 8 6 4 11 5 ...
 $ age     : num   1 1 1 1 1 1 1 1 1 1 ...
 $ anu     : num   5.88 5.86 5.45 5.36 5.02 ...
- attr(*, "formula")=Class 'formula' length 3 anu ~ age | id
.. ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
- attr(*, "labels")=List of 2
..$ x: chr "Age"
..$ y: chr "Size"
- attr(*, "units")=List of 2
..$ x: chr "(Years)"
..$ y: chr "(cm)"
- attr(*, "FUN")=function (x)
- attr(*, "order.groups")= logi TRUE

```

The individual data are observed (Figure 1) by plotting the groupedData data frame `dg`,

```
> plot(dg)
```

A plot of length-at-age ignoring the repeated measures nature of the data (Figure 2) is created by plotting *anu* versus *agecap* from either the long or groupedData data frame,

```
> plot(anu~age,data=dg,ylab="Length (cm)",xlab="Age (years)")
```

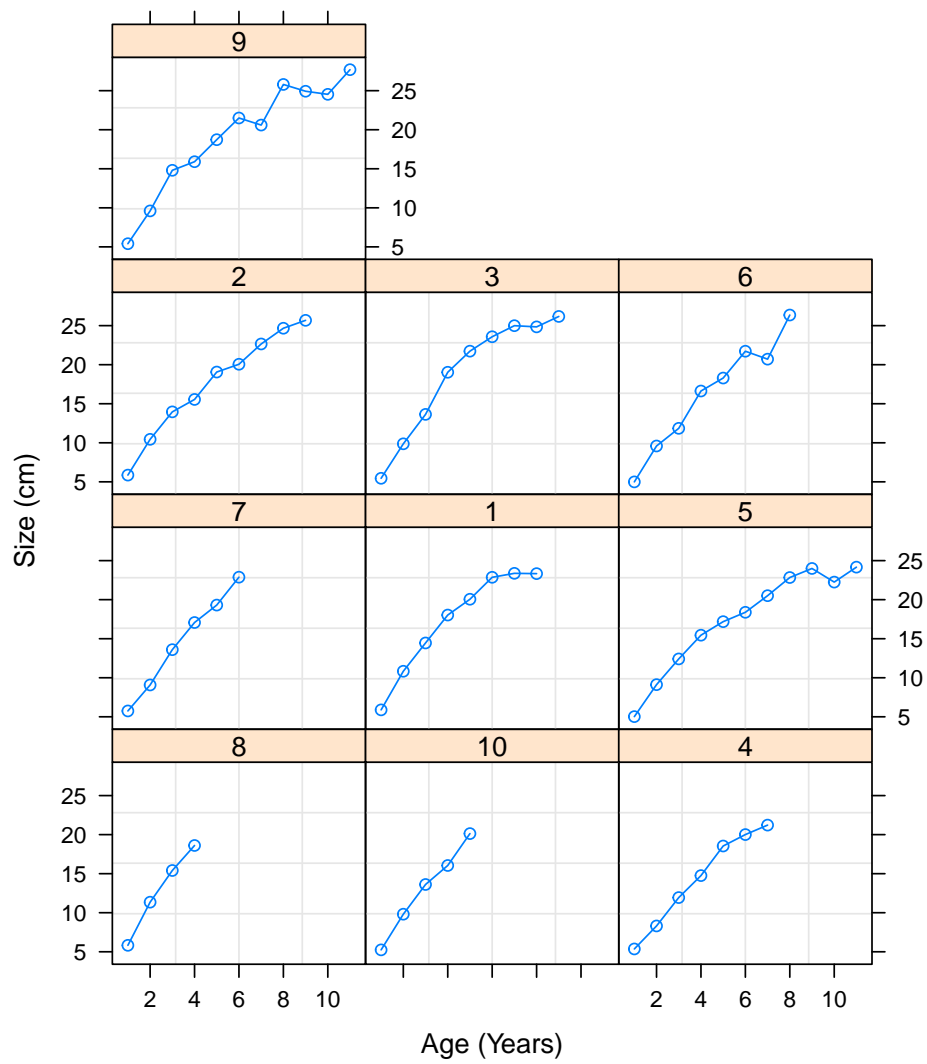


Figure 1. Individual lengths-at-age for ten simulated individuals.

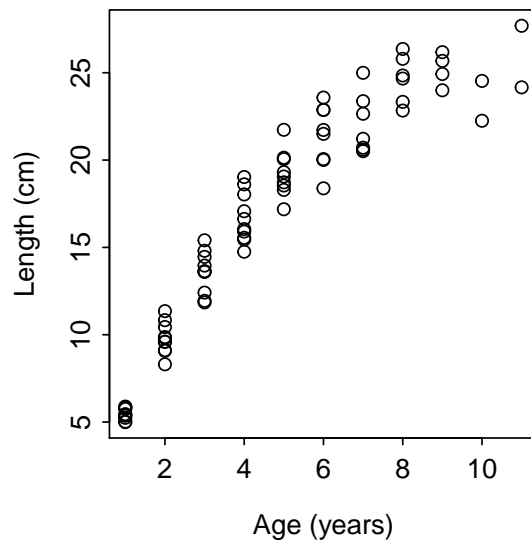


Figure 2. Lengths-at-age for ten simulated individuals ignoring the repeated-measures natures of the data.

2 Fitting Individual von Bertalanffy Models

A function for the “typical” or “traditional” von Bertalanffy model is created with `vbFuns()` as follows,

```
> ### Create a vonB function for ease of use
> ( vb <- vbFuns("typical",simple=TRUE) )
function (t, Linf, K, t0)
{
  Linf * (1 - exp(-K * (t - t0)))
}
<environment: 0x09c58748>
```

Starting values are obtained by fitting the typical von Bertalanffy to “all” of the data ignoring the repeated-measures nature. This is most easily accomplished with `vbStarts()` as follows,

```
> ## get started values for all fish together
> vbs <- vbStarts(anu~age,data=dg,"typical")
> unlist(vbs) # unlist is only used for the presentation
      Linf      K      t0
27.7027  0.2405 -0.7484
```

The typical von Bertalanffy model found in the `vb` object is fit to each individual fish with `nlsList()` as follows,

```
> ## Fit all of the nls models at once
> resAll <- nlsList(anu~vb(age,Linf,K,t0),data=dg,start=vbs)
```

with the individual coefficients obtained with `coef()` as follows,

```
> # get coefficient results
> ( cfAll <- coef(resAll) )
      Linf      K      t0
8  28.36 0.27844  0.17266
10 49.06 0.10021 -0.16349
4  34.62 0.13867 -0.11952
7  56.37 0.08232 -0.26460
1  26.96 0.28632  0.17498
5  26.93 0.20817  0.01643
2  34.77 0.14297 -0.38377
3  29.41 0.26829  0.34090
6  40.78 0.11648 -0.17408
9  30.23 0.19473 -0.04533
```

The means, standard deviation, and coefficient of variation for each coefficient can be obtained with,

```
> # average coefficients over all fish
> ( cfMean <- apply(cfAll,2,mean,na.rm=TRUE) )
      Linf      K      t0
35.74886  0.18166 -0.04458
> # SD coefficients over all fish
> ( cfSd <- apply(cfAll,2,sd,na.rm=TRUE) )
      Linf      K      t0
10.05766  0.07659  0.22304
```

```

> # CV of coefficients over all fish
> ( cfCV <- apply(cfAll,2,function(x) sd(x,na.rm=TRUE)/mean(x,na.rm=TRUE) ) )
      Linf      K      t0
0.2813  0.4216 -5.0030

```

Finally, a plot of the model fits for each individual can be put on one figure (Figure 3) to get a feel of where the individual variation occurs,

```

> ### Put all model fits on one graph to observe where variation is
> plot(-1,-1,xlab="Age",ylab="Length",xlim=c(1.1*cfMean[3],max(dw$agecap)),
      ylim=c(0,1.1*cfMean[1]))
> for (i in 1:nrow(cfAll)) {
  curve(vb(x,cfAll[i,1],cfAll[i,2],cfAll[i,3]),from=floor(cfMean[3]),to=11,add=TRUE)
}

```

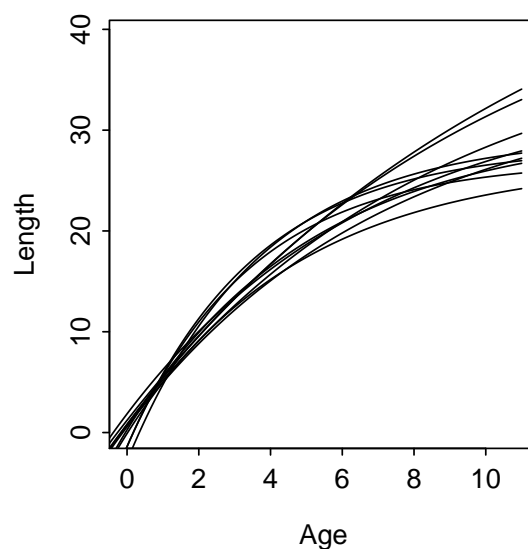


Figure 3. Fitted line plots for the typical von Bertalanffy model fit to the lengths-at-age separately for each of ten simulated individuals.

3 Fitting Mixed-Effect von Bertalanffy Models

All models below use the same list for starting values of the fixed-effects. Thus, this list is saved to an object as follows,

```
> vbMEs <- list(fixed=c(Linf=cfMean[1],K=cfMean[2],t0=cfMean[3]))
```

The mixed effects model with fixed-effect estimates of the population mean value for each parameter and random effects for each parameter (i.e., estimates of the individual variability around each mean parameter) would be fit with `nlme()` as shown below. However, this model did not converge.

```
> vbME0 <- nlme(anu~Linf*(1-exp(-K*(age-t0))),data=dg,start=vbMEs,  
>               fixed=list(Linf~1,K~1,t0~1),random=Linf+K+t0~1|id)
```

The mixed effects model with fixed-effect estimates of the population mean value for each parameter and random effects for L_∞ and K was fit with `nlme()` as shown below.

```
> vbME2LK <- nlme(anu~vb(age,Linf,K,t0),data=dg,start=vbMEs,fixed=list(Linf~1,K~1,t0~1),  
                  random=Linf+K~1|id)
```

```
> summary(vbME2LK)
```

Nonlinear mixed-effects model fit by maximum likelihood

Model: anu ~ vb(age, Linf, K, t0)

Data: dg

	AIC	BIC	logLik
	239.9	256.4	-112.9

Random effects:

Formula: list(Linf ~ 1, K ~ 1)

Level: id

Structure: General positive-definite, Log-Cholesky parametrization

	StdDev	Corr
Linf	1.139718	Linf
K	0.006659	0.97
Residual	0.891817	

Fixed effects: list(Linf ~ 1, K ~ 1, t0 ~ 1)

	Value	Std.Error	DF	t-value	p-value
Linf	29.945	0.9801	66	30.555	0.0000
K	0.208	0.0149	66	13.972	0.0000
t0	0.054	0.0797	66	0.681	0.4983

Correlation:

	Linf	K
K	-0.823	
t0	-0.597	0.795

Standardized Within-Group Residuals:

	Min	Q1	Med	Q3	Max
	-2.28790	-0.63733	-0.01915	0.60505	2.81729

Number of Observations: 78

Number of Groups: 10

```
> fixME2LK <- fixef(vbME2LK)
```

```
> ( ranME2LK <- ranef(vbME2LK) )
```

```

      Linf      K
8   1.63765  0.0094939
10  0.03053  0.0001583
4  -1.41791 -0.0082333
7   0.37757  0.0021307
1   0.67002  0.0039769
5  -2.00944 -0.0114958
2  -0.13126 -0.0007856
3   1.37544  0.0079487
6  -0.31591 -0.0019440
9  -0.21669 -0.0012497
> ( cfME2LK <- coef(vbME2LK) )
      Linf      K      t0
8  31.58 0.2171 0.05429
10 29.98 0.2078 0.05429
4  28.53 0.1994 0.05429
7  30.32 0.2097 0.05429
1  30.62 0.2116 0.05429
5  27.94 0.1961 0.05429
2  29.81 0.2068 0.05429
3  31.32 0.2156 0.05429
6  29.63 0.2057 0.05429
9  29.73 0.2064 0.05429

```

Similar models for L_∞ and t_0 and K and t_0 with random effects are fit with,

```

> vbME2LT <- nlme(anu~vb(age,Linf,K,t0),data=dg,start=vbMEs,fixed=list(Linf~1,K~1,t0~1),
                  random=Linf+t0~1|id)
> summary(vbME2LT)
Nonlinear mixed-effects model fit by maximum likelihood
  Model: anu ~ vb(age, Linf, K, t0)
  Data: dg
        AIC BIC logLik
    240.5 257 -113.3

Random effects:
Formula: list(Linf ~ 1, t0 ~ 1)
Level: id
Structure: General positive-definite, Log-Cholesky parametrization
      StdDev   Corr
Linf   1.608e+00 Linf
t0     1.711e-05 -0.001
Residual 8.983e-01

Fixed effects: list(Linf ~ 1, K ~ 1, t0 ~ 1)
      Value Std.Error DF t-value p-value
Linf 29.848   1.0615 66  28.118  0.0000
K      0.210   0.0151 66  13.898  0.0000
t0     0.066   0.0799 66   0.821  0.4144
Correlation:
      Linf      K
K    -0.832
t0   -0.557  0.801

Standardized Within-Group Residuals:

```


Min	Q1	Med	Q3	Max
-2.2857	-0.6841	-0.0464	0.6435	2.7858

Number of Observations: 78

Number of Groups: 10

```
> fixME2LT <- fixef(vbME2LT)
```

```
> ( ranME2LT <- ranef(vbME2LT) )
```

	Linf	t0
8	2.39327	-2.054e-08
10	0.02497	4.101e-10
4	-2.06272	1.750e-08
7	0.55805	-3.244e-09
1	0.86989	-9.531e-09
5	-2.74018	2.090e-08
2	-0.20350	6.799e-10
3	1.90034	-1.423e-08
6	-0.42970	5.968e-09
9	-0.31043	2.097e-09

```
> ( cfME2LT <- coef(vbME2LT) )
```

	Linf	K	t0
8	32.24	0.21	0.06562
10	29.87	0.21	0.06562
4	27.79	0.21	0.06562
7	30.41	0.21	0.06562
1	30.72	0.21	0.06562
5	27.11	0.21	0.06562
2	29.64	0.21	0.06562
3	31.75	0.21	0.06562
6	29.42	0.21	0.06562
9	29.54	0.21	0.06562

```
> vbME2KT <- nlme(anu~vb(age,Linf,K,t0),data=dg,start=vbMEs,fixed=list(Linf~1,K~1,t0~1),
  random=K+t0~1|id)
```

```
> summary(vbME2KT)
```

Nonlinear mixed-effects model fit by maximum likelihood

Model: anu ~ vb(age, Linf, K, t0)

Data: dg

AIC	BIC	logLik
241	257.5	-113.5

Random effects:

Formula: list(K ~ 1, t0 ~ 1)

Level: id

Structure: General positive-definite, Log-Cholesky parametrization

	StdDev	Corr
K	0.02422	K
t0	0.10836	1

Residual 0.89823

Fixed effects: list(Linf ~ 1, K ~ 1, t0 ~ 1)

	Value	Std.Error	DF	t-value	p-value
Linf	30.786	0.9543	66	32.26	0.0000
K	0.195	0.0157	66	12.44	0.0000
t0	-0.019	0.0862	66	-0.23	0.8224

```

Correlation:
  Linf    K
K -0.827
t0 -0.566  0.822

Standardized Within-Group Residuals:
      Min      Q1      Med      Q3      Max
-2.36468 -0.57776  0.01856  0.65837  2.68652

Number of Observations: 78
Number of Groups: 10
> fixME2KT <- fixef(vbME2KT)
> ( ranME2KT <- ranef(vbME2KT) )
      K      t0
8  0.0339145  0.151640
10 0.0008034  0.003613
4 -0.0280368 -0.125373
7  0.0076106  0.034065
1  0.0144838  0.064740
5 -0.0410571 -0.183660
2 -0.0051706 -0.023145
3  0.0328098  0.146772
6 -0.0080594 -0.036000
9 -0.0072983 -0.032651
> ( cfME2KT <- coef(vbME2KT) )
      Linf      K      t0
8  30.79 0.2287  0.13223
10 30.79 0.1956 -0.01580
4  30.79 0.1668 -0.14478
7  30.79 0.2024  0.01465
1  30.79 0.2093  0.04533
5  30.79 0.1538 -0.20307
2  30.79 0.1897 -0.04256
3  30.79 0.2276  0.12736
6  30.79 0.1868 -0.05541
9  30.79 0.1875 -0.05206

```

The three models with only one parameter as a random effect is then fit with,

```

> vbME1L <- nlme(anu~vb(age,Linf,K,t0),data=dg,start=vbMEs,fixed=list(Linf~1,K~1,t0~1),
  random=Linf~1|id)
> summary(vbME1L)

Nonlinear mixed-effects model fit by maximum likelihood
  Model: anu ~ vb(age, Linf, K, t0)
  Data: dg
      AIC      BIC logLik
  236.5  248.3 -113.3

Random effects:
  Formula: Linf ~ 1 | id
      Linf Residual
StdDev: 1.608   0.8983

Fixed effects: list(Linf ~ 1, K ~ 1, t0 ~ 1)

```

	Value	Std.Error	DF	t-value	p-value
Linf	29.848	1.0615	66	28.118	0.0000
K	0.210	0.0151	66	13.898	0.0000
t0	0.066	0.0799	66	0.821	0.4144

Correlation:

	Linf	K
K	-0.832	
t0	-0.557	0.801

Standardized Within-Group Residuals:

	Min	Q1	Med	Q3	Max
	-2.2857	-0.6841	-0.0464	0.6435	2.7858

Number of Observations: 78

Number of Groups: 10

```
> fixME1L <- fixef(vbME1L)
> ( ranME1L <- ranef(vbME1L) )
```

	Linf
8	2.39327
10	0.02497
4	-2.06272
7	0.55805
1	0.86989
5	-2.74018
2	-0.20350
3	1.90034
6	-0.42970
9	-0.31043

```
> ( cfME1L <- coef(vbME1L) )
```

	Linf	K	t0
8	32.24	0.21	0.06562
10	29.87	0.21	0.06562
4	27.79	0.21	0.06562
7	30.41	0.21	0.06562
1	30.72	0.21	0.06562
5	27.11	0.21	0.06562
2	29.64	0.21	0.06562
3	31.75	0.21	0.06562
6	29.42	0.21	0.06562
9	29.54	0.21	0.06562

```
> vbME1K <- nlme(anu~vb(age,Linf,K,t0),data=dg,start=vbMEs,fixed=list(Linf~1,K~1,t0~1),
  random=K~1|id)
```

```
> summary(vbME1K)
```

Nonlinear mixed-effects model fit by maximum likelihood

Model: anu ~ vb(age, Linf, K, t0)

Data: dg

AIC	BIC	logLik
239.5	251.3	-114.8

Random effects:

Formula: K ~ 1 | id

K Residual

StdDev: 0.01942 0.9155

```
Fixed effects: list(Linf ~ 1, K ~ 1, t0 ~ 1)
      Value Std.Error DF   t-value p-value
Linf 30.465    0.9582 66    31.79  0.0000
K      0.199    0.0157 66    12.62  0.0000
t0      0.008    0.0838 66     0.10  0.9245
```

```
Correlation:
      Linf   K
K   -0.879
t0  -0.656  0.740
```

```
Standardized Within-Group Residuals:
      Min      Q1      Med      Q3      Max
-2.52490 -0.56743  0.08409  0.61463  2.69275
```

```
Number of Observations: 78
```

```
Number of Groups: 10
```

```
> fixME1K <- fixef(vbME1K)
> ( ranME1K <- ranef(vbME1K) )
```

```
      K
8   0.026084
10  0.000470
4  -0.022674
7   0.005496
1   0.013648
5  -0.034471
2  -0.002648
3   0.025324
6  -0.006748
9  -0.004483
```

```
> ( cfME1K <- coef(vbME1K) )
```

```
      Linf      K      t0
8  30.46 0.2248 0.007969
10 30.46 0.1992 0.007969
4  30.46 0.1760 0.007969
7  30.46 0.2042 0.007969
1  30.46 0.2124 0.007969
5  30.46 0.1642 0.007969
2  30.46 0.1961 0.007969
3  30.46 0.2240 0.007969
6  30.46 0.1920 0.007969
9  30.46 0.1942 0.007969
```

```
> vbME1T <- nlme(anu~vb(age,Linf,K,t0),data=dg,start=vbMEs,fixed=list(Linf~1,K~1,t0~1),
  random=t0~1|id)
```

```
> summary(vbME1T)
```

```
Nonlinear mixed-effects model fit by maximum likelihood
```

```
Model: anu ~ vb(age, Linf, K, t0)
```

```
Data: dg
```

```
      AIC      BIC logLik
267.4 279.2 -128.7
```

```
Random effects:
```

```
Formula: t0 ~ 1 | id
```

```

          t0 Residual
StdDev: 0.1821    1.182

Fixed effects: list(Linf ~ 1, K ~ 1, t0 ~ 1)
      Value Std.Error DF t-value p-value
Linf 28.952    0.9750 66  29.695  0.0000
K      0.219    0.0188 66  11.652  0.0000
t0     0.070    0.1183 66   0.592  0.5557
Correlation:
  Linf  K
K  -0.953
t0 -0.568  0.703

Standardized Within-Group Residuals:
      Min      Q1      Med      Q3      Max
-2.724562 -0.605583  0.000533  0.666876  2.204906

Number of Observations: 78
Number of Groups: 10
> fixME1T <- fixef(vbME1T)
> ( ranME1T <- ranef(vbME1T) )

          t0
8  -0.180597
10 0.010206
4   0.201811
7  -0.022324
1  -0.155891
5   0.259007
2  -0.018754
3  -0.186262
6   0.089482
9   0.003323

> ( cfME1T <- coef(vbME1T) )

      Linf      K      t0
8 28.95 0.219 -0.11052
10 28.95 0.219  0.08028
4 28.95 0.219  0.27189
7 28.95 0.219  0.04775
1 28.95 0.219 -0.08582
5 28.95 0.219  0.32908
2 28.95 0.219  0.05132
3 28.95 0.219 -0.11619
6 28.95 0.219  0.15956
9 28.95 0.219  0.07340

```

Finally fit the model with no random effects using the usual `nls()`,

```

> vbNLS <- nls(anu~vb(age,Linf,K,t0),data=dg,start=vbs)
> fixNLS <- coef(vbNLS)

```

4 Model Selection

Compare all models?

```
> AIC(vbME2LK,vbME2LT,vbME2KT,vbME1L,vbME1K,vbME1T,vbNLS)
      df    AIC
vbME2LK  7 239.9
vbME2LT  7 240.5
vbME2KT  7 241.0
vbME1L   5 236.5
vbME1K   5 239.5
vbME1T   5 267.4
vbNLS    4 270.7
```

How much different do the predictions using the mean parameter values look?

```
> cols <- chooseColors("rich",7)
> curve(vb(x,fixNLS[1],fixNLS[2],fixNLS[3]),from=floor(cfMean[3]),to=11,col=cols[1],
      lwd=2,xlab="Age (years)",ylab="TL (cm)")
> curve(vb(x,fixME2LK[1],fixME2LK[2],fixME2LK[3]),from=floor(cfMean[3]),to=11,
      add=TRUE,col=cols[2],lwd=2)
> curve(vb(x,fixME2LT[1],fixME2LT[2],fixME2LT[3]),from=floor(cfMean[3]),to=11,
      add=TRUE,col=cols[3],lwd=2)
> curve(vb(x,fixME2KT[1],fixME2KT[2],fixME2KT[3]),from=floor(cfMean[3]),to=11,
      add=TRUE,col=cols[4],lwd=2)
> curve(vb(x,fixME1L[1],fixME1L[2],fixME1L[3]),from=floor(cfMean[3]),to=11,add=TRUE,
      col=cols[5],lwd=2)
> curve(vb(x,fixME1K[1],fixME1K[2],fixME1K[3]),from=floor(cfMean[3]),to=11,add=TRUE,
      col=cols[6],lwd=2)
> curve(vb(x,fixME1T[1],fixME1T[2],fixME1T[3]),from=floor(cfMean[3]),to=11,add=TRUE,
      col=cols[7],lwd=2)
> legend("topleft",legend=c("NLS","LK","LT","KT","L","K","T"),col=cols,lwd=2,lty=1)
```

How different do the fixed effects look?

```
> fixFits <- rbind(fixNLS,fixME2LK,fixME2LT,fixME2KT,fixME1L,fixME1K,fixME1T)
> rownames(fixFits) <- c("NLS","LK","LT","KT","L","K","T")
> fixFits
      Linf      K      t0
NLS 28.52 0.2266 0.094994
LK  29.95 0.2076 0.054293
LT  29.85 0.2100 0.065623
KT  30.79 0.1948 -0.019412
L   29.85 0.2100 0.065623
K   30.46 0.1987 0.007969
T   28.95 0.2190 0.070075
```

What does the model fit look like with the “best” model?

```
> plot(augPred(vbME1L,level=0:1))
```

What does the residual plot and histogram of residuals look like?

heteroscedasticity

```
> plot(vbME1L,resid(.,type="p")~fitted(.))
```

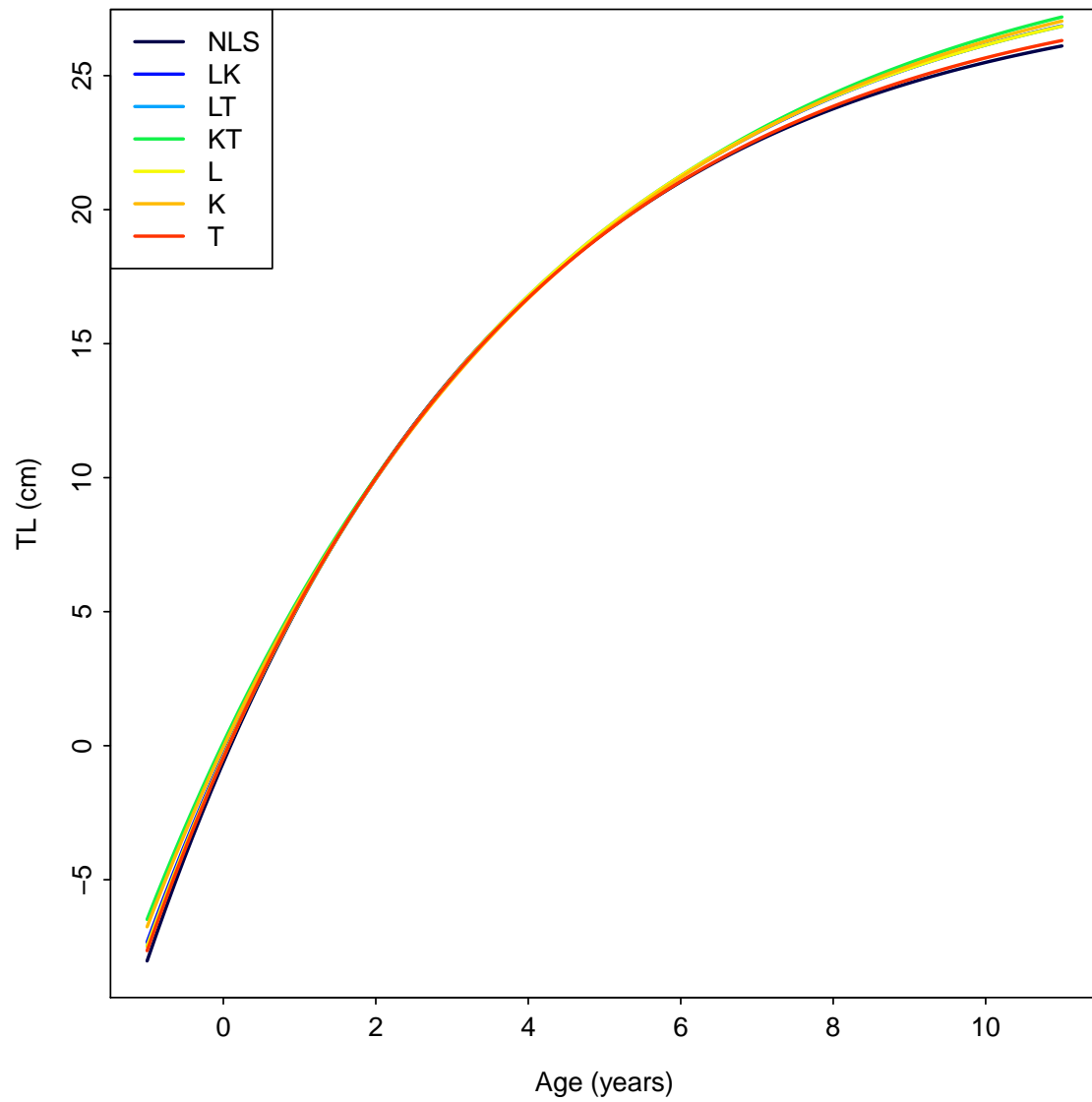


Figure 4. Predicted lengths-at-age for each typical von Bertalanffy model fit to the lengths-at-age of ten simulated individuals.

```
> plot(vbME1L, resid(., type="p") ~ fitted(.) | id)
```

```
> qqnorm(vbME1L, ~ resid(., type="p") | id)
```

```
> qqnorm(vbME1L, ~ ranef(., level=1))
```

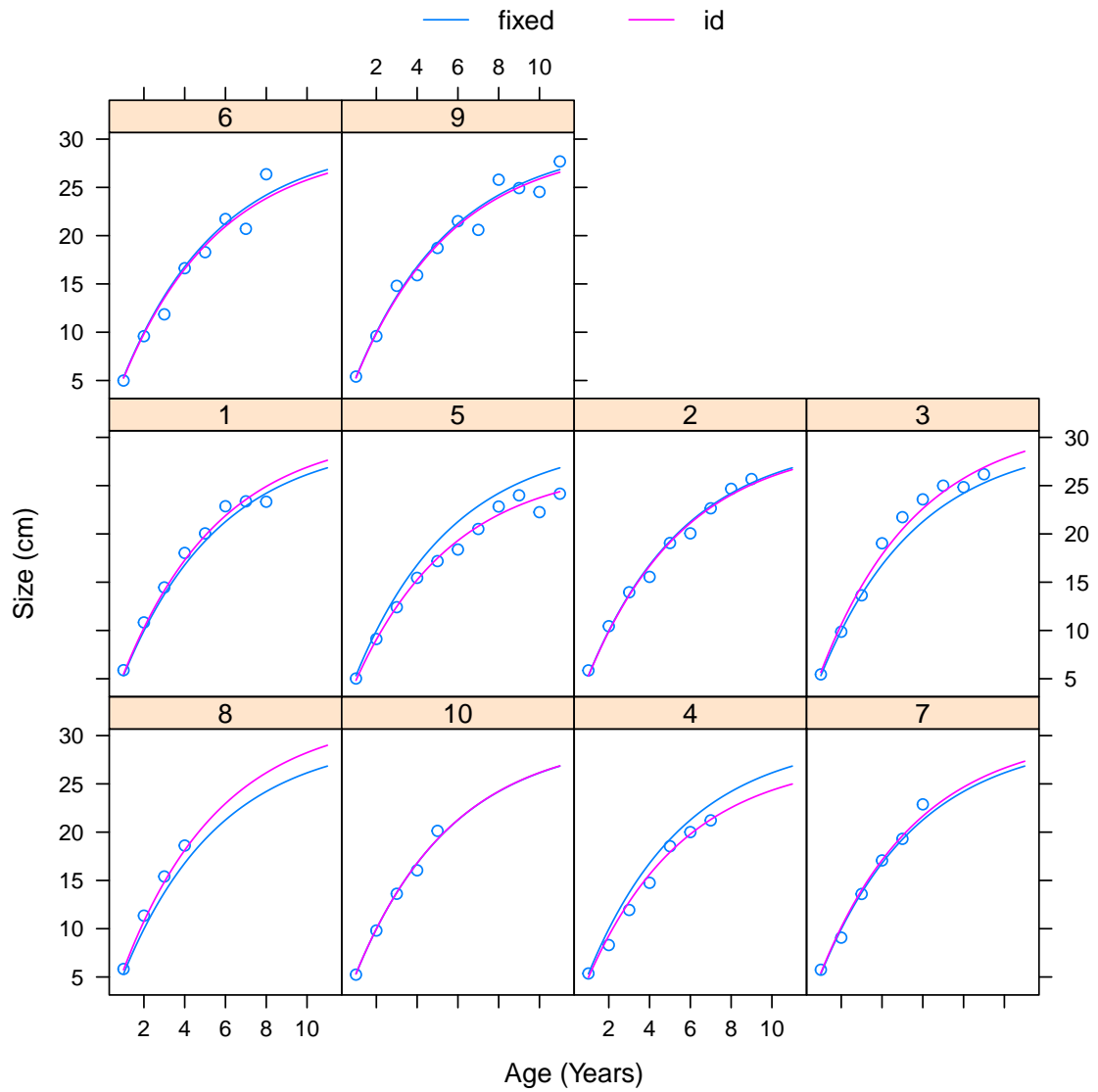


Figure 5. Fitted line plots to lengths-at-age using only the fixed effects (blue) and fixed and random effects (red) from the fit of the mixed-effect model with only a random effect for L_{∞} for each of ten simulated individuals.

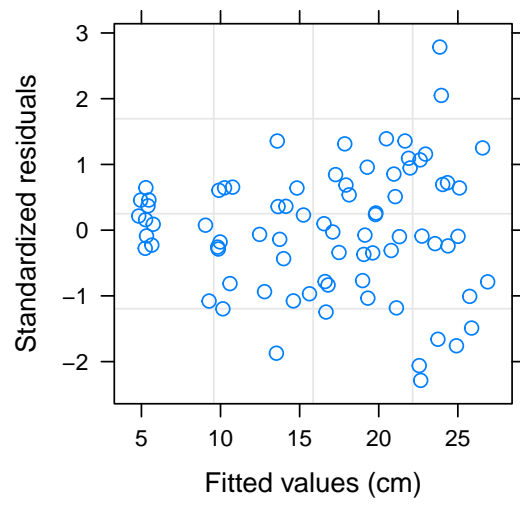


Figure 6. Residual plot from the fit of the mixed-effect model with only a random effect for L_{∞} for each of ten simulated individuals.

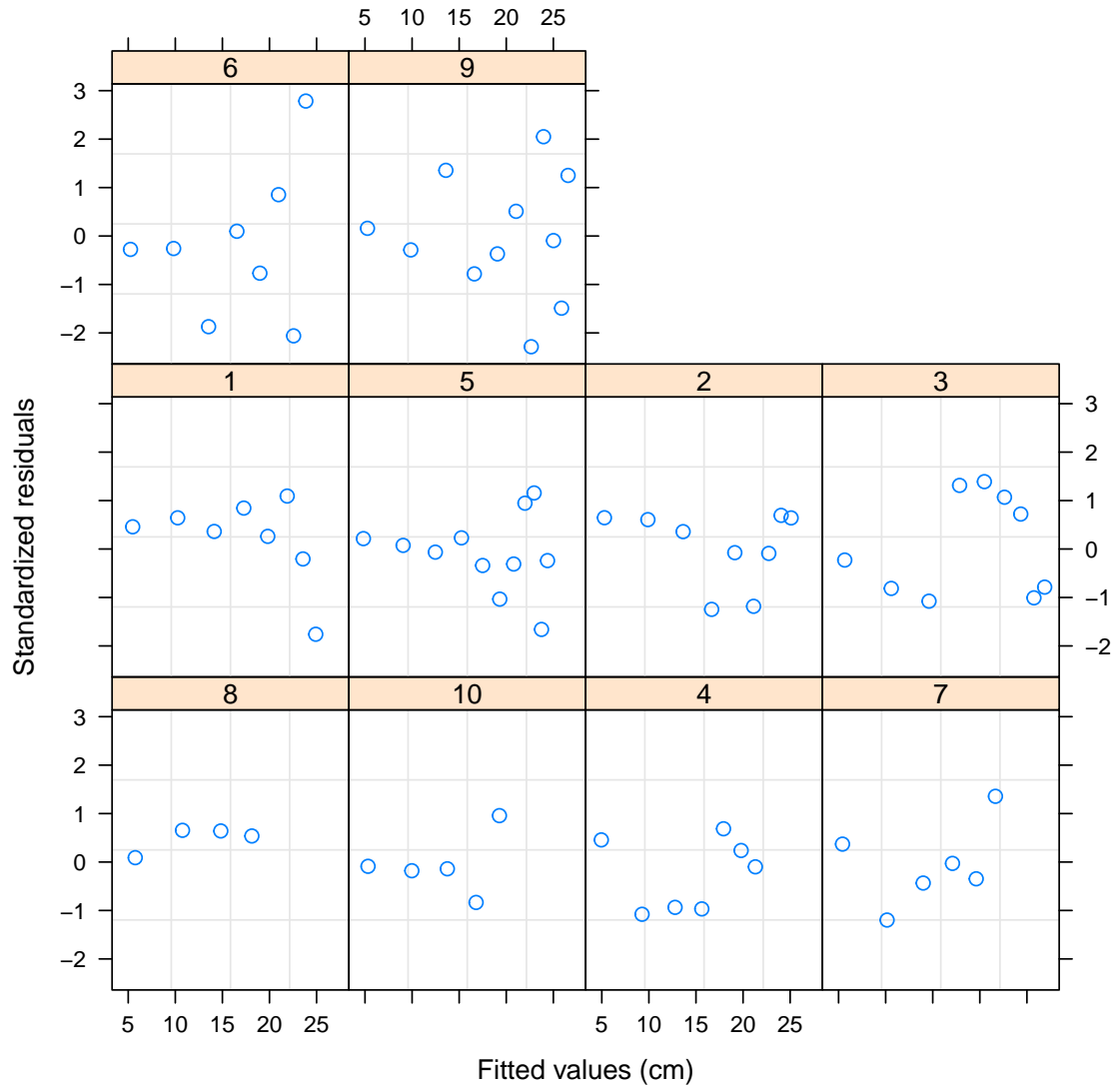


Figure 7. Residual plot for each individual from the fit of the mixed-effect model with only a random effect for L_∞ for each of ten simulated individuals.

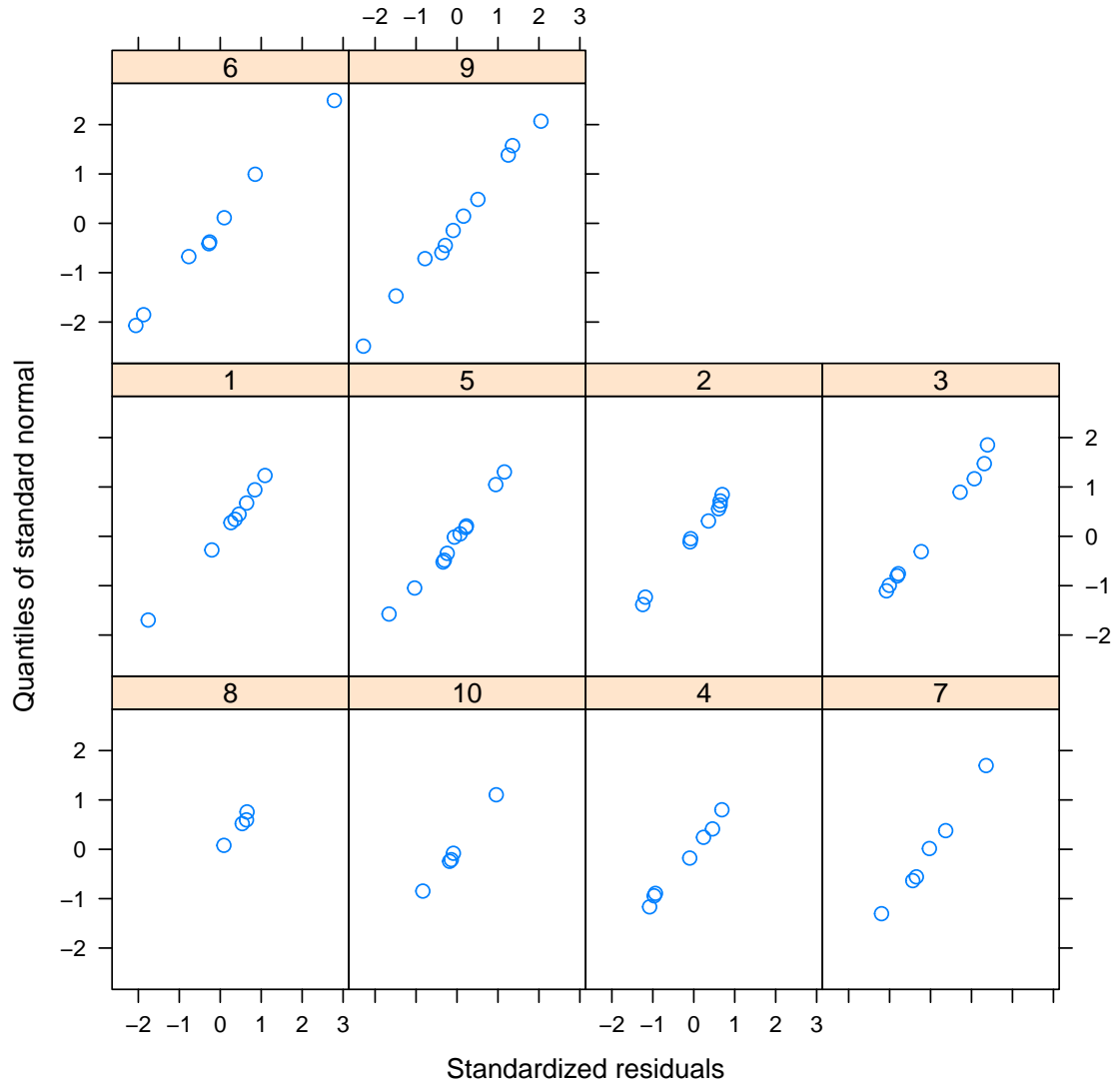


Figure 8. Normal quantile plot of residuals for each individual from the fit of the mixed-effect model with only a random effect for L_∞ for each of ten simulated individuals.

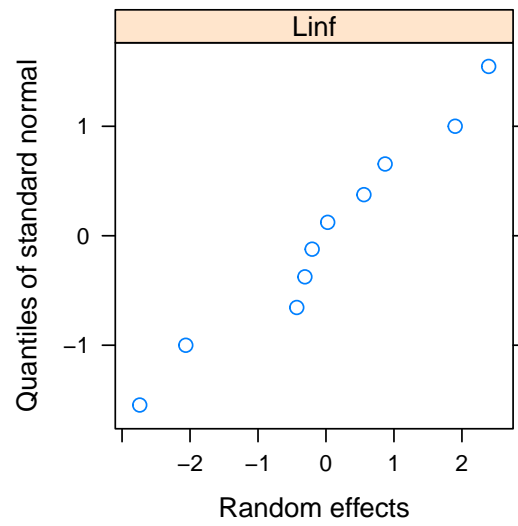


Figure 9. Normal quantile plot of random effects from the fit of the mixed-effect model with only a random effect for L_∞ for each of ten simulated individuals.

5 Fitting Mixed-Effect with Power Variance Function von Bertalanffy Models

```
> vbMEP2LK <- update(vbME2LK,weights=varPower(form=~anu))
> vbMEP2LT <- update(vbME2LT,weights=varPower(form=~anu))
> vbMEP2KT <- update(vbME2KT,weights=varPower(form=~anu))
> vbMEP1L <- update(vbME1L,weights=varPower(form=~anu))
> vbMEP1K <- update(vbME1K,weights=varPower(form=~anu))
> vbMEP1T <- update(vbME1T,weights=varPower(form=~anu))
```

```
> AIC(vbMEP2LK,vbMEP2LT,vbMEP2KT,vbMEP1L,vbMEP1K,vbMEP1T)
```

	df	AIC
vbMEP2LK	8	220.2
vbMEP2LT	8	220.7
vbMEP2KT	8	220.5
vbMEP1L	6	216.7
vbMEP1K	6	222.1
vbMEP1T	6	247.2

```
> plot(vbMEP1L,resid(.,type="p")~fitted(.))
```

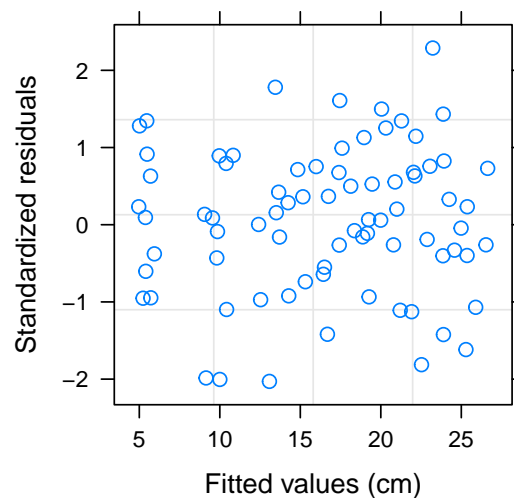


Figure 10. Residual plot from the fit of the mixed-effect model using a power variance function with only a random effect for L_{∞} for each of ten simulated individuals.

```
> plot(vbMEP1L,resid(.,type="p")~fitted(.)|id)
```

```
> qqnorm(vbMEP1L,~resid(.,type="p")|id)
```

```
> qqnorm(vbMEP1L,~ranef(.,level=1))
```

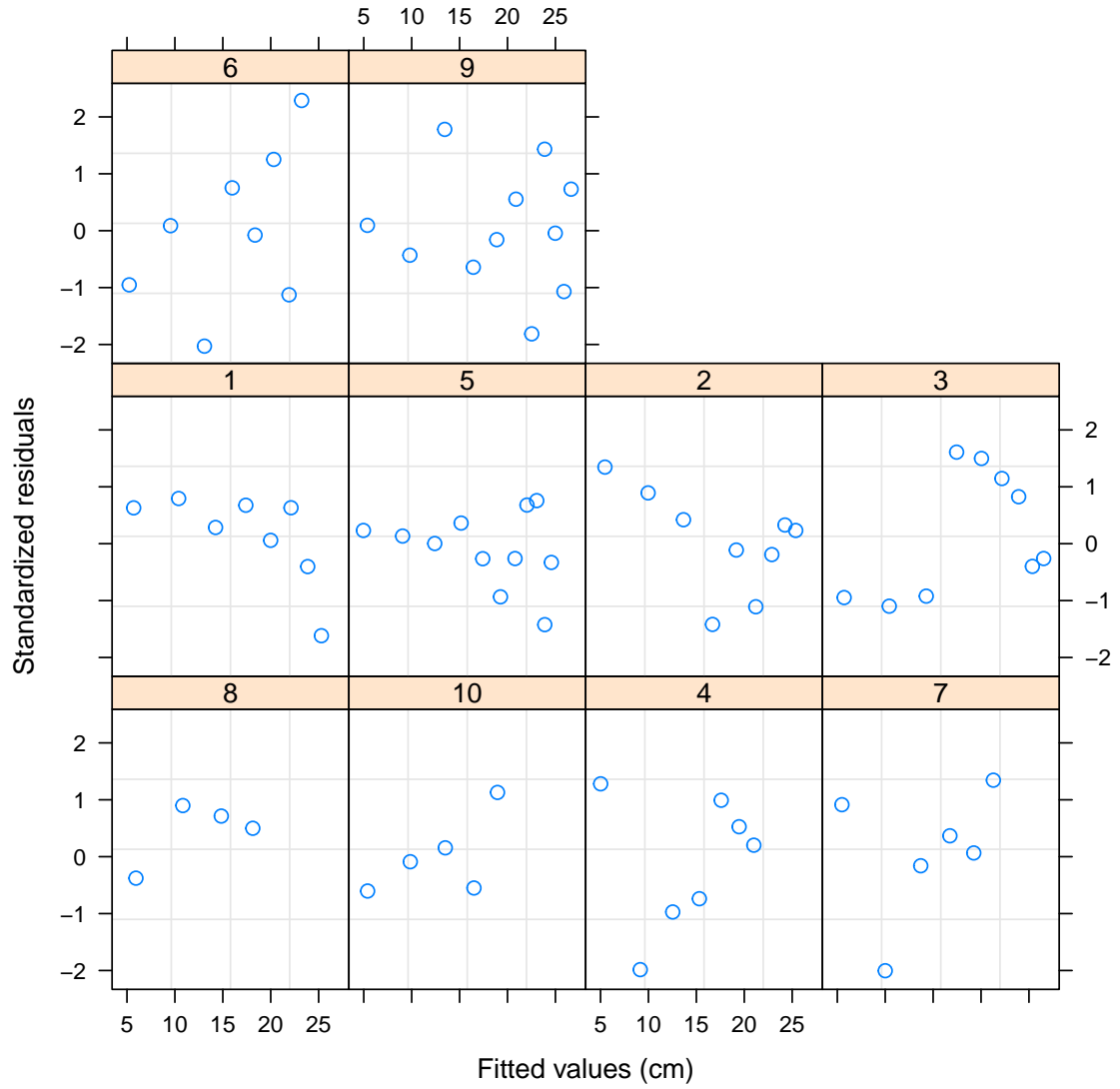


Figure 11. Residual plot for each individual from the fit of the mixed-effect model using a power variance function with only a random effect for L_∞ for each of ten simulated individuals.

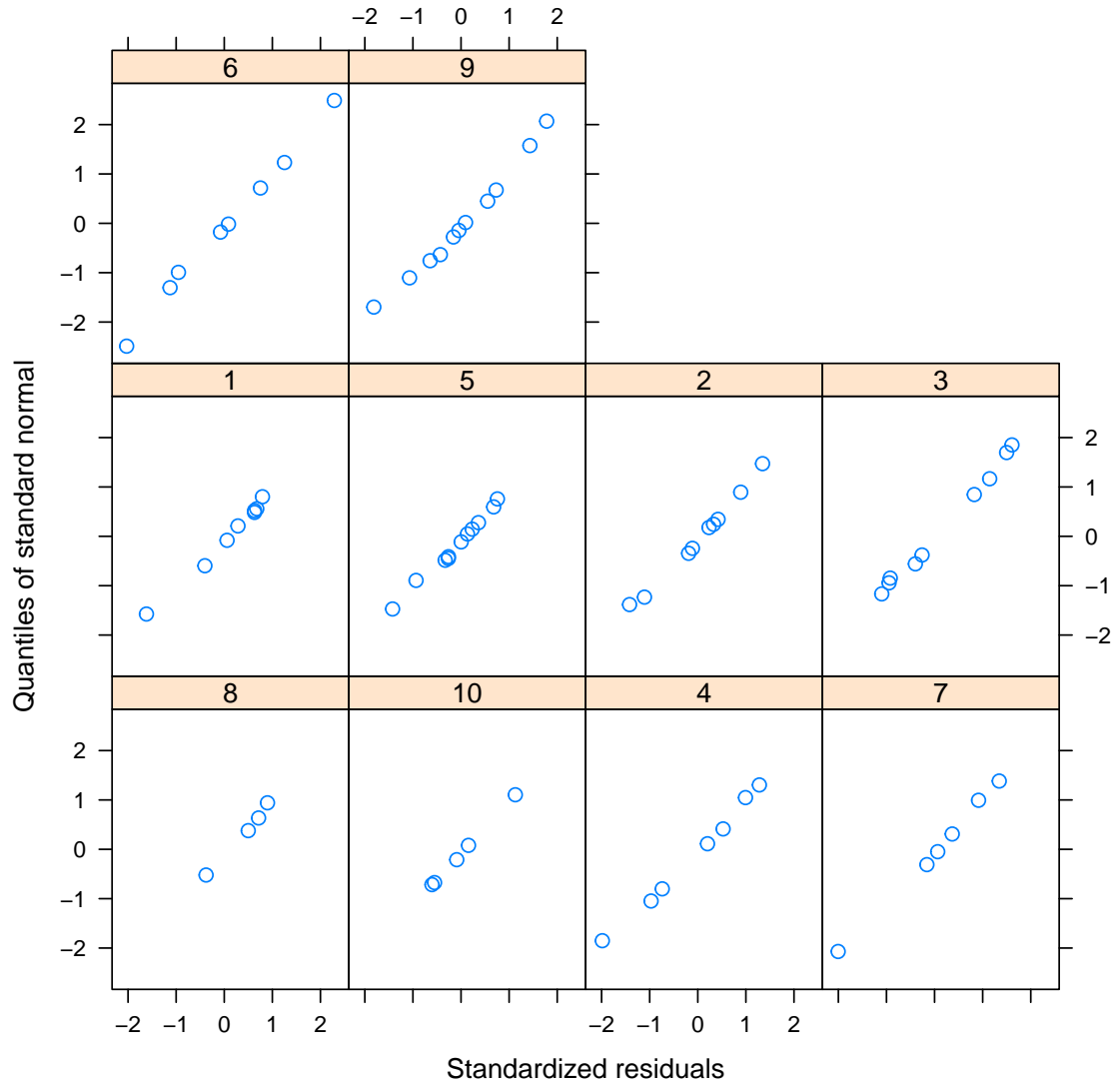


Figure 12. Normal quantile plot of residuals for each individual from the fit of the mixed-effect model using a power variance function with only a random effect for L_∞ for each of ten simulated individuals.

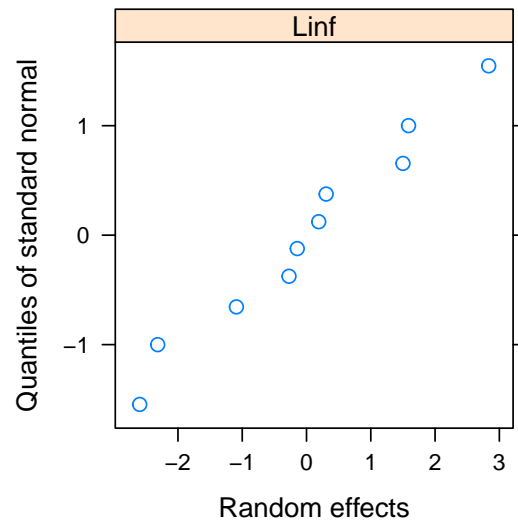


Figure 13. Normal quantile plot of random effects from the fit of the mixed-effect model using a power variance function with only a random effect for L_∞ for each of ten simulated individuals.

References

Vigliola, L. and M. Meekan. 2009. Tropical Fish Otoliths: Information for Assessment, Management, and Ecology, chapter The back-calculation of fish growth from otoliths, pp. 174–211. Number 11 in Reviews: Methods and Technologies in Fish Biology and Fisheries, Springer. [1](#)

Reproducibility Information

Version Information

- **Compiled Date:** Fri Jun 21 2013
- **Compiled Time:** 7:26:37 PM
- **Code Execution Time:** 8.96 s

R Information

- **R Version:** R version 3.0.0 (2013-04-03)
- **System:** Windows, i386-w64-mingw32/i386 (32-bit)
- **Base Packages:** base, datasets, graphics, grDevices, methods, stats, tcltk, utils
- **Other Packages:** FSA_0.3.5, knitr_1.2, lattice_0.20-15, nlme_3.1-109, plyr_1.8, reshape_0.8.4
- **Loaded-Only Packages:** car_2.0-16, cluster_1.14.4, digest_0.6.3, evaluate_0.4.3, formatR_0.7, gdata_2.12.0.2, gplots_2.11.0.1, grid_3.0.0, gtools_2.7.1, Hmisc_3.10-1, multcomp_1.2-17, plotrix_3.4-7, quantreg_4.98, relax_1.3.13, sciplot_1.1-0, SparseM_0.99, stringr_0.6.2, TeachingDemos_2.9, tools_3.0.0
- **Required Packages:** FSA, lattice, nlme and their dependencies (car, gdata, gplots, graphics, grDevices, grid, Hmisc, knitr, multcomp, plotrix, quantreg, relax, reshape, sciplot, stats, tcltk, TeachingDemos, utils)