

Evolution of age at primiparity in pinnipeds in the absence of the quality-quantity trade-off in reproduction

Kalberer S., DeRango E., Trillmich T., Krüger O.

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Packages needed

```
library(ape)
library(caper)
library(ggplot2)
```

Data

```
# set working directory
setwd("M:/Bielefeld - PhD/Data/Projects/Kalberer et al. 2019_Ecol_Evol/01_Data and Analyses")

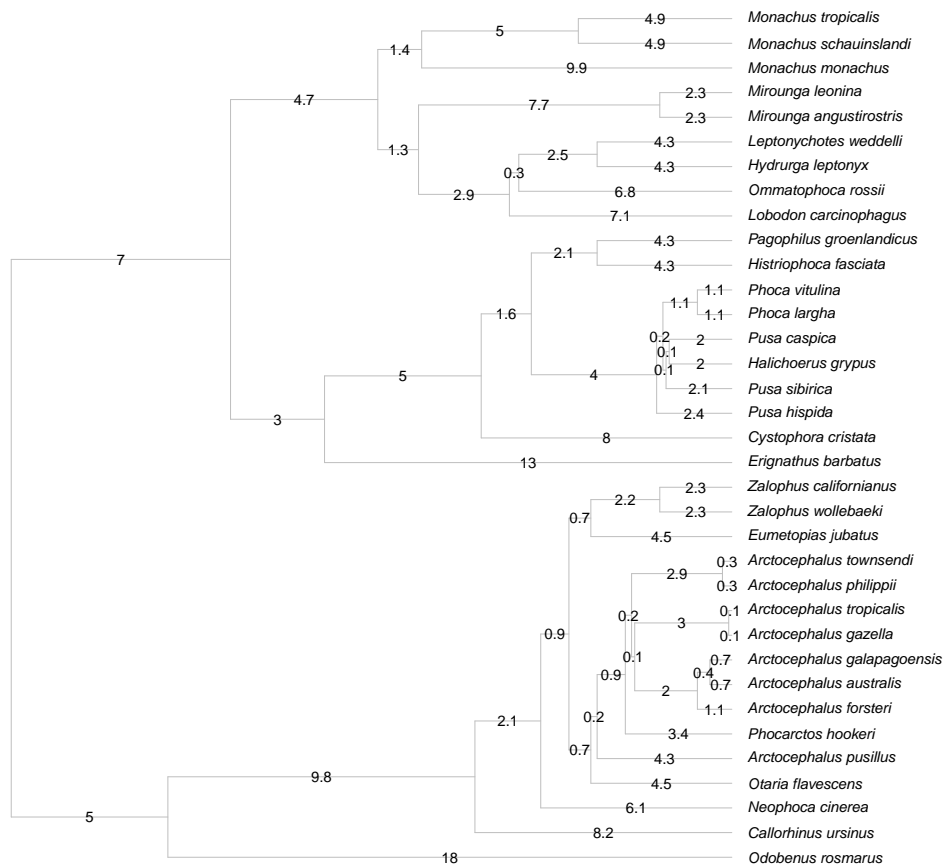
# Tree adjusted from Higdon et al. 2007
pinnipeds.tree <- read.tree(file="seal_tree_SK_PGLS.tre")

# Life history variables
pinnipeds.data <- read.delim("Data_for_PGLS.txt", header=TRUE)
pinnipeds.data$Birth.weight.log <- log(pinnipeds.data$Birth.weight)
rownames(pinnipeds.data) <- pinnipeds.data[,1]
pinnipeds.data <- pinnipeds.data[,c(1:18,21,23)]

# create one data set for PGLS
pinnipeds <- comparative.data(pinnipeds.tree,pinnipeds.data, Species, vcv=TRUE)
```

Cladogram

```
plot.phylo(pinnipeds.tree,edge.color = "grey",type = "phylogram",label.offset = 0.5, cex = 1)
edgelabels(pinnipeds.tree$edge.length, font=1,frame = "none", bg = "none", cex=1)
```



PGLS:

Lactation length and rel. BM

```
lact_BM <- pglis(Lactation.length ~ Rel.birth.weight, pinnipeds, lambda='ML')
print(lact_BM)
```

```
##
## Call:
## pglis(formula = Lactation.length ~ Rel.birth.weight, data = pinnipeds,
##       lambda = "ML")
##
## Coefficients:
##      (Intercept)  Rel.birth.weight
##           2.271          -3.463
```

```
summary(lact_BM)
```

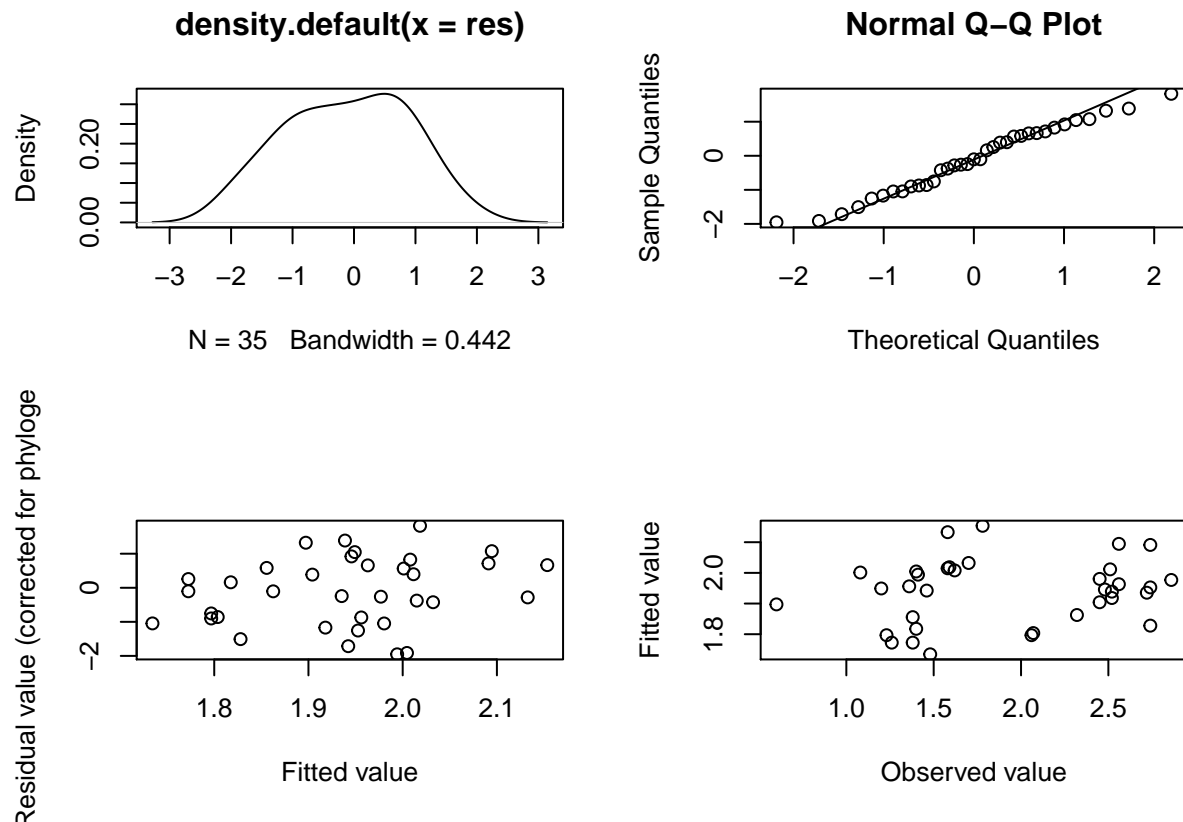
```
##
## Call:
## pglis(formula = Lactation.length ~ Rel.birth.weight, data = pinnipeds,
##       lambda = "ML")
```

```
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.17571 -0.07975 -0.00940  0.05946  0.16361
##
## Branch length transformations:
##
## kappa  [Fix]   : 1.000
## lambda [ ML]   : 0.930
##   lower bound : 0.000, p = 4.4409e-14
##   upper bound : 1.000, p = 0.00026941
##   95.0% CI    : (0.762, 0.985)
## delta  [Fix]   : 1.000
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.27120    0.29062   7.8150 5.248e-09 ***
## Rel.birth.weight -3.46297    1.26420  -2.7392 0.009854 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.09192 on 33 degrees of freedom
## Multiple R-squared:  0.1853,    Adjusted R-squared:  0.1606
## F-statistic: 7.503 on 1 and 33 DF,  p-value: 0.009854

coef(lact_BM)

##      (Intercept) Rel.birth.weight
##      2.271199      -3.462968

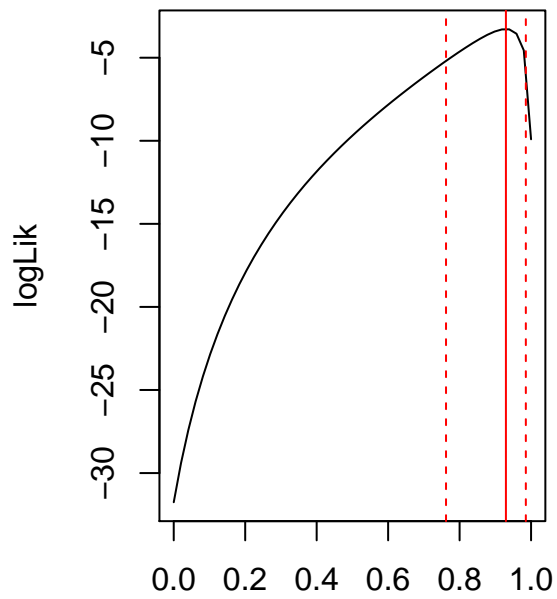
par(mfrow=c(2,2))
plot(lact_BM)
```



```
par(mfrow=c(1,1))

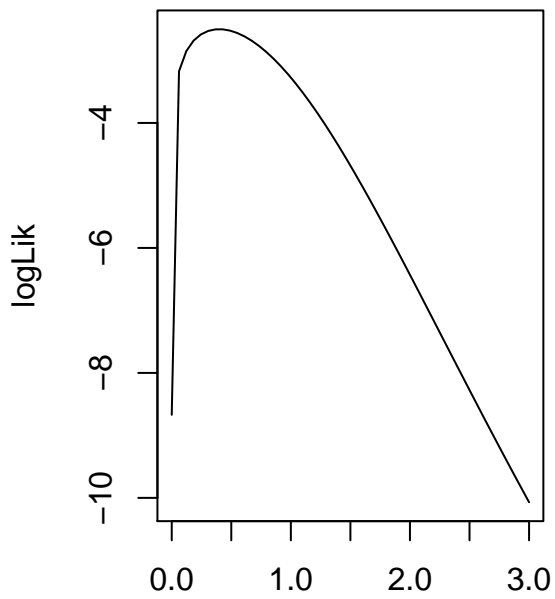
lact_BM.l <- pglS.profile(lact_BM, 'lambda')
lact_BM.d <- pglS.profile(lact_BM, 'delta')

par(mfrow=c(1,2))
plot(lact_BM.l); plot(lact_BM.d)
```



lambda

Data: pinnipeds; Model: Lactation.length ~ Rel.birth.weight
kappa 1.00; lambda 0.03; delta 1.00

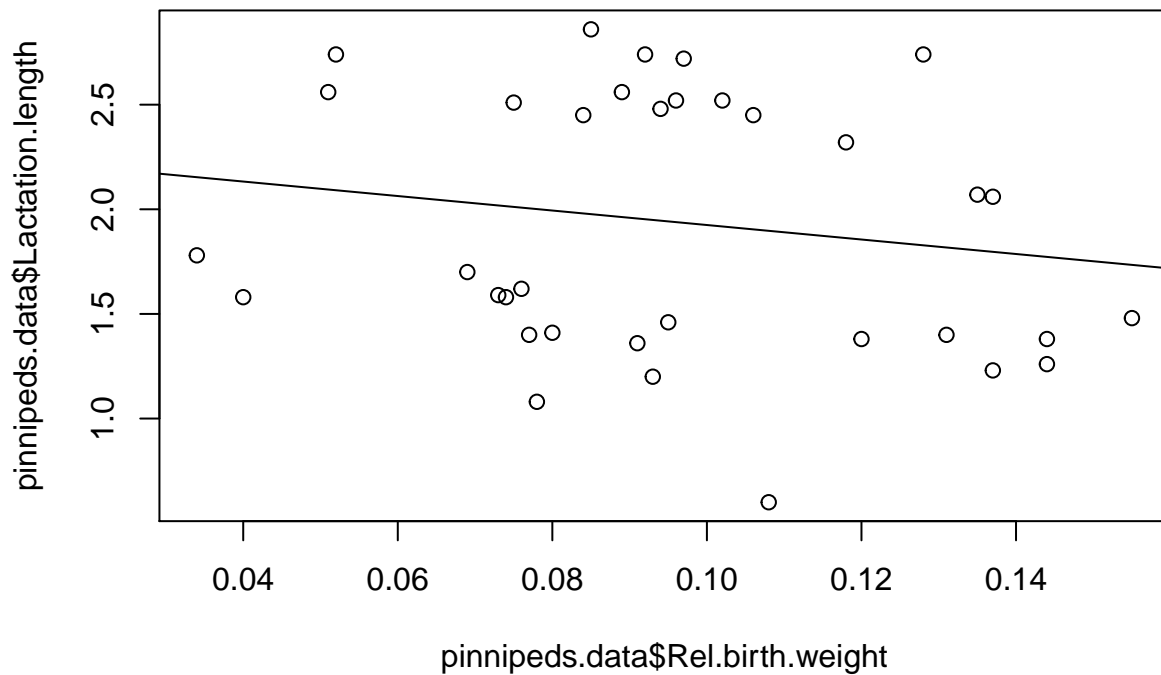


delta

Data: pinnipeds; Model: Lactation.length ~ Rel.birth.weight
kappa 1.00; lambda 0.03; delta 1.00

```
par(mfrow=c(1,1))
```

```
plot(pinnipeds.data$Lactation.length ~ pinnipeds.data$Rel.birth.weight)
abline(a = coef(lact_BM)[1], b = coef(lact_BM)[2])
```



Sexual size dimorphism (SSD)

```
SSD <- pglis(AFR.Encyclop.Female ~ SSD, pinnipeds, lambda='ML')
print(SSD)
```

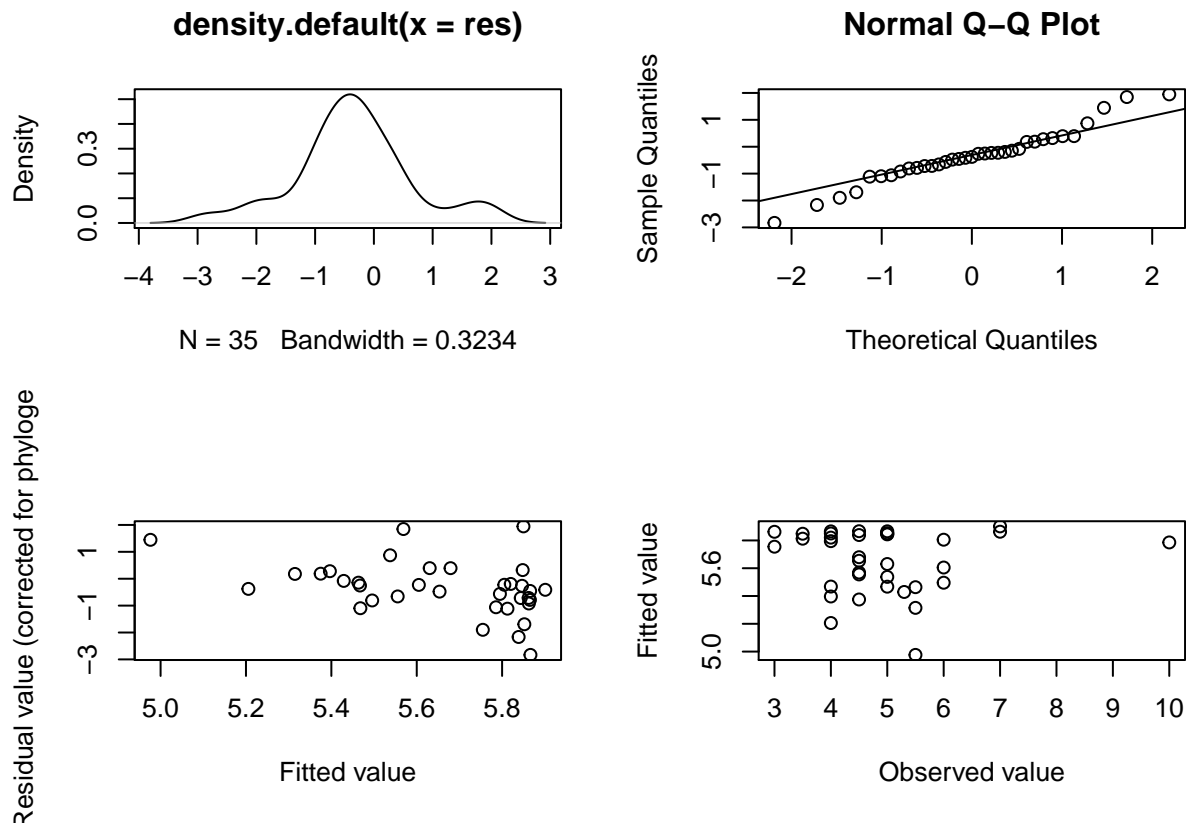
```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ SSD, data = pinnipeds, lambda = "ML")
##
## Coefficients:
## (Intercept)      SSD
##      5.9979      -0.1503
```

```
summary(SSD)
```

```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ SSD, data = pinnipeds, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.02212 -0.28789 -0.13642  0.06596  0.70239
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.961
## lower bound : 0.000, p = 0.00018856
```

```
## upper bound : 1.000, p = 0.0097095
## 95.0% CI : (0.804, 0.997)
## delta [Fix] : 1.000
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 5.99791 1.19031 5.0390 1.645e-05 ***
## SSD -0.15033 0.17212 -0.8734 0.3887
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3889 on 33 degrees of freedom
## Multiple R-squared: 0.02259, Adjusted R-squared: -0.007024
## F-statistic: 0.7629 on 1 and 33 DF, p-value: 0.3887
```

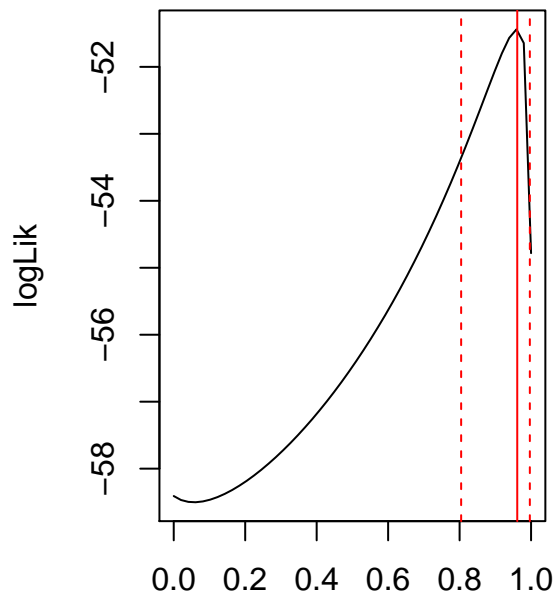
```
par(mfrow=c(2,2))
plot(SSD)
```



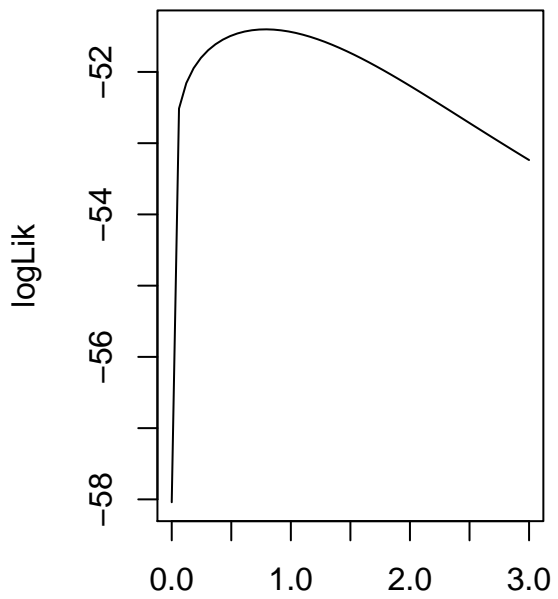
```
par(mfrow=c(1,1))

SSD.l <- pglis.profile(SSD, 'lambda')
SSD.d <- pglis.profile(SSD, 'delta')

par(mfrow=c(1,2))
plot(SSD.l); plot(SSD.d)
```



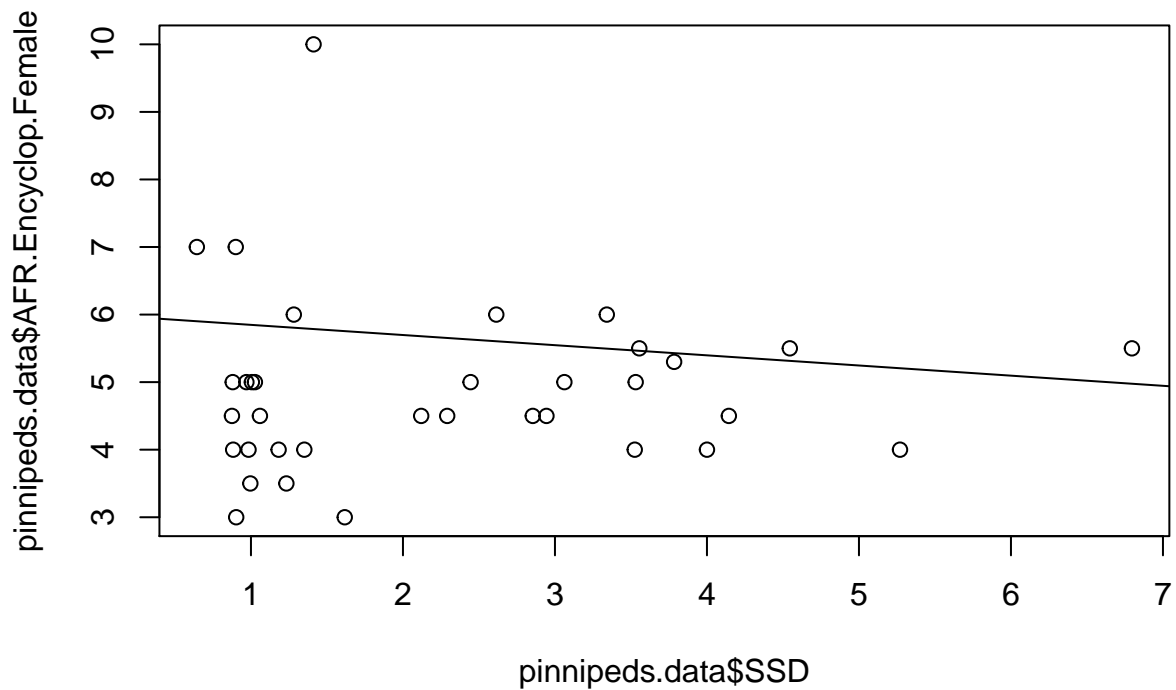
lambda
Data: pinnipeds; Model: AFR.Encyclop.Female ~ SSD
kappa 1.00; lambda 0.96; delta 1.00



delta
Data: pinnipeds; Model: AFR.Encyclop.Female ~ SSD
kappa 1.00; lambda 0.96; delta 1.00

```
par(mfrow=c(1,1))

plot(pinnipeds.data$AFR.Encyclop.Female ~ pinnipeds.data$SSD)
abline(a = coef(SSD)[1], b = coef(SSD)[2])
```

Lactation length (log)

```
lact <- pglis(AFR.Encyclop.Female ~ Lactation.length, pinnipeds, lambda='ML')
print(lact)
```

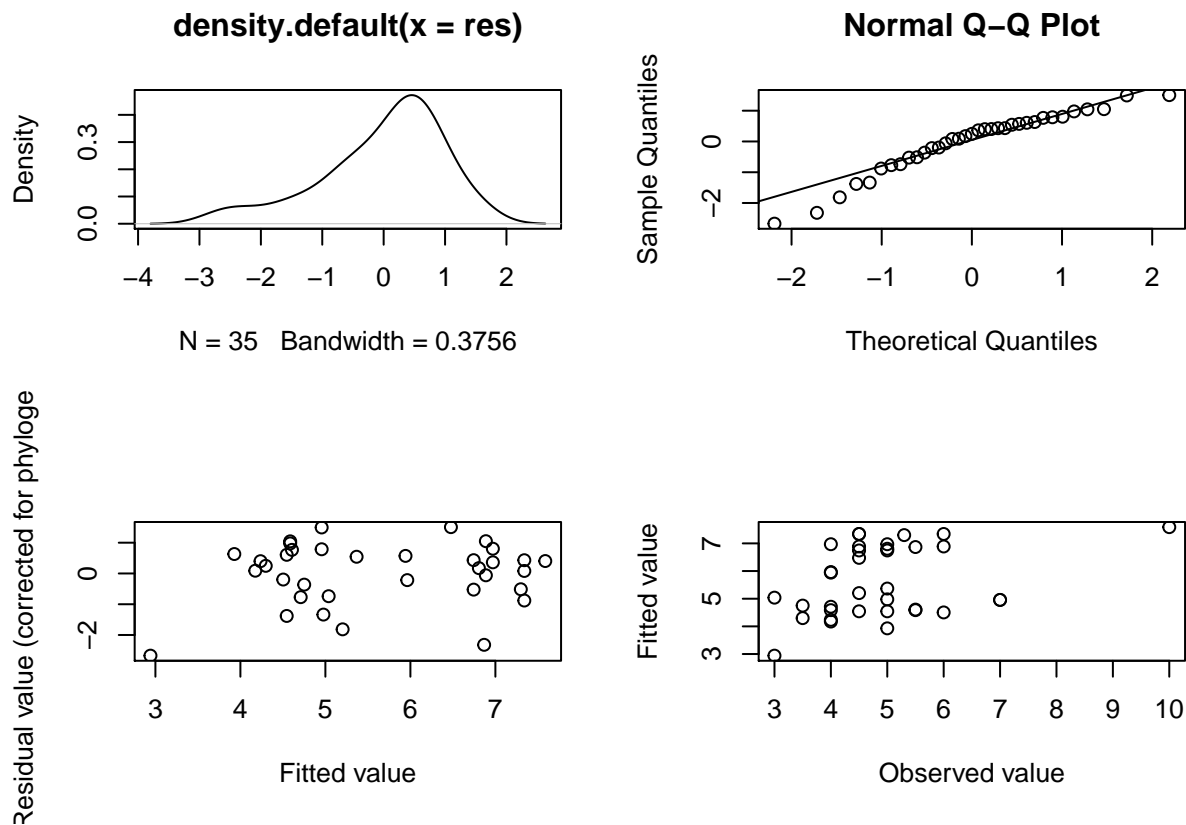
```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Lactation.length, data = pinnipeds,
##       lambda = "ML")
##
## Coefficients:
##      (Intercept)  Lactation.length
##           1.709           2.055
```

```
summary(lact)
```

```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Lactation.length, data = pinnipeds,
##       lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.03925 -0.20217  0.09631  0.24078  0.58566
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
```

```
## lambda [ ML] : 1.000
## lower bound : 0.000, p = 1.849e-05
## upper bound : 1.000, p = 1
## 95.0% CI : (0.821, NA)
## delta [Fix] : 1.000
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.70872 1.34671 1.2688 0.2134
## Lactation.length 2.05535 0.34591 5.9419 1.145e-06 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3949 on 33 degrees of freedom
## Multiple R-squared: 0.5169, Adjusted R-squared: 0.5022
## F-statistic: 35.31 on 1 and 33 DF, p-value: 1.145e-06
```

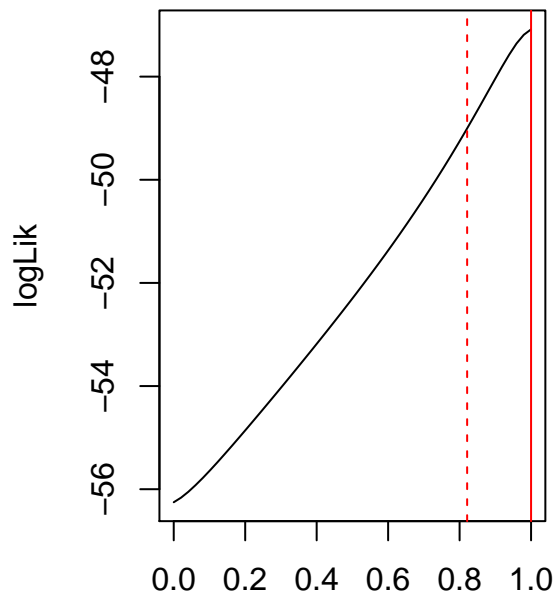
```
par(mfrow=c(2,2))
plot(lact)
```



```
par(mfrow=c(1,1))

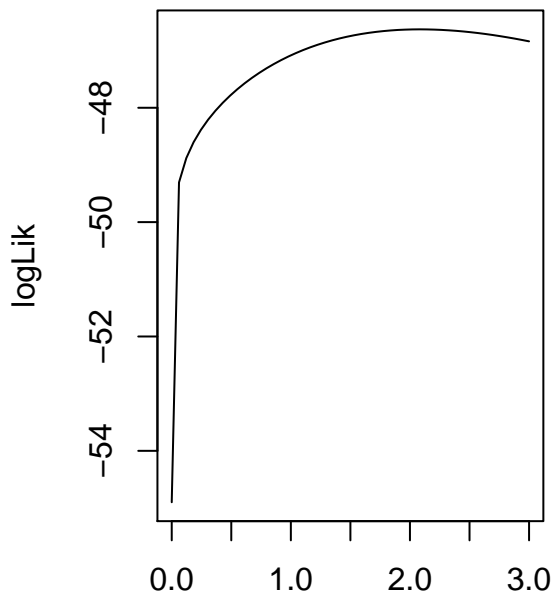
lact.l <- pglis.profile(lact, 'lambda')
lact.d <- pglis.profile(lact, 'delta')

par(mfrow=c(1,2))
plot(lact.l); plot(lact.d)
```



lambda

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Lactation.ler
kappa 1.00; lambda 1.00; delta 1.00

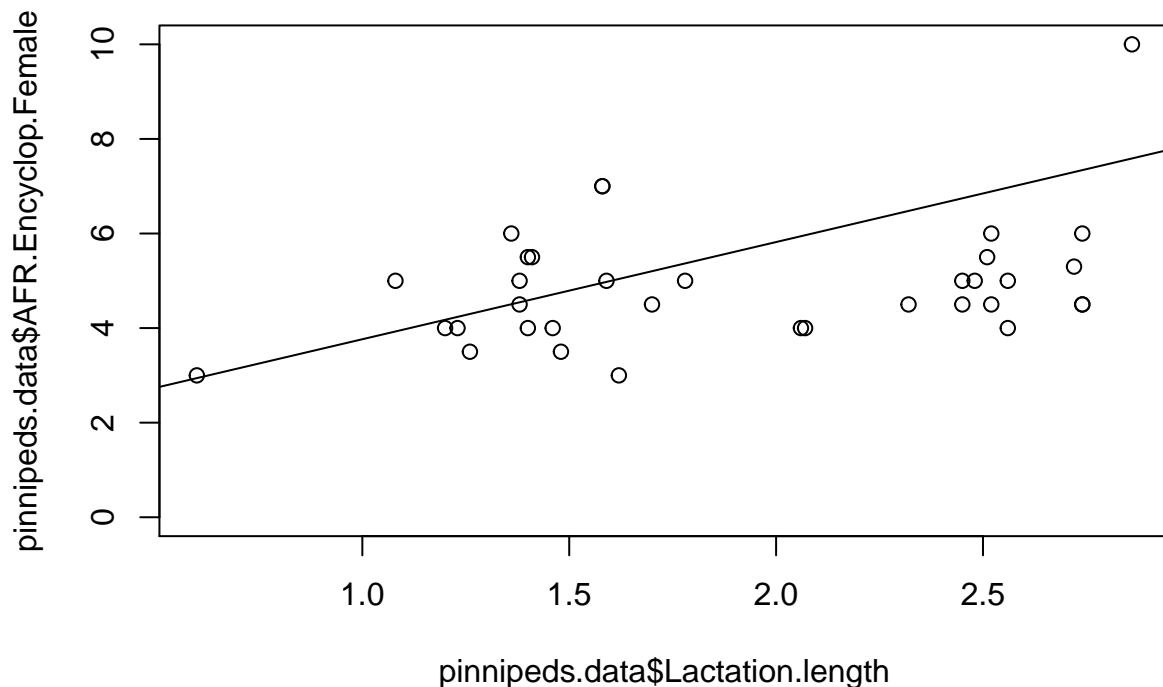


delta

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Lactation.ler
kappa 1.00; lambda 1.00; delta 1.00

```
par(mfrow=c(1,1))
```

```
plot(pinnipeds.data$AFR.Encyclop.Female ~ pinnipeds.data$Lactation.length,ylim=c(0,10))
abline(a = coef(lact)[1], b = coef(lact)[2])
```



ggPlot

```
# Lactation length
pinnipeds.data.plot <- pinnipeds.data
pinnipeds.data.plot <- pinnipeds.data.plot[,c(1:3,8,10,19)]

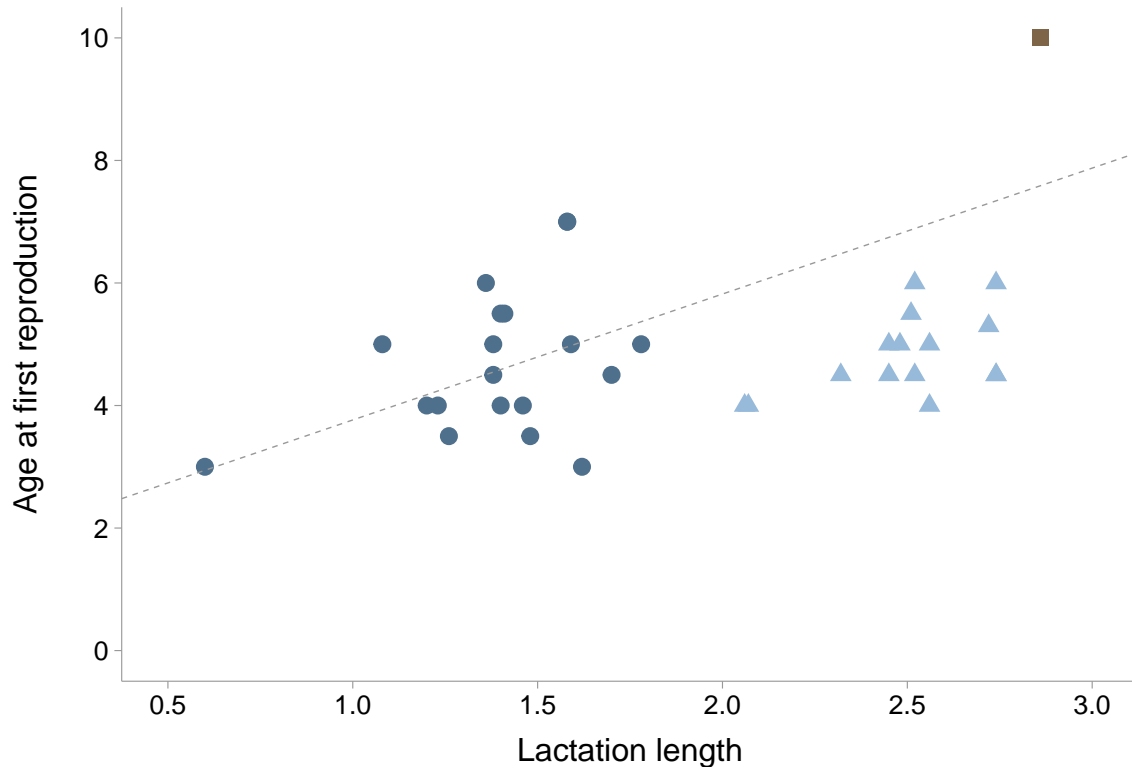
regr_lact <- pglms(AFR.Encyclop.Female~Lactation.length,pinnipeds,lambda='ML')

ggplot(data=pinnipeds.data.plot, aes(x=Lactation.length, y=AFR.Encyclop.Female))+
  geom_point(size=2.5, aes(shape=Group,colour=Group))+
  # geom_smooth(method='pgls',formula=y~x, se=FALSE,alpha=0.2,linetype = "dashed",color="#999999",size=
  # geom_segment(aes(x = -0.923, xend = 0.277, y = regr_lact$coefficients[1]*(-0.923),
  # yend = 0+regr_lact$coefficients[1]*(0.277)), color='#999999', size=0.25,linetype =
  geom_abline(intercept= regr_lact$model$coef[1],slope=regr_lact$model$coef[2], color="#999999",size=0.
  scale_shape_manual(values=c(15,17,19))+
  scale_color_manual(values=c('#7F6548', '#98BADA', '#4E708C'))+
  theme(axis.text.x=element_text(colour="black",size=10, hjust = 0.5))+
  theme(axis.title.x=element_text(colour="black",size=12,vjust= -0.5)) +
  theme(panel.background = element_blank()) +
  theme(axis.line = element_line(colour = "#999999",size=0.2))+
  theme(axis.ticks=element_line(colour="#999999",size=0.2))+
  scale_y_continuous("Age at first reproduction",
    breaks = seq(0,10,2), limits = c(0,10))+
  scale_x_continuous("Lactation length",breaks = seq(0.5,3,0.5),limits = c(0.5,3))+
  theme(axis.text.y=element_text(colour="black",size=10))+
  theme(axis.title.y=element_text(colour="black",size=12,vjust= 5))+
  # ggtitle("Predicted influence of SST on survival estimates")+
```

```

theme(plot.title=element_text(size=12, face="bold", vjust=2,hjust = 0.5))+
theme(legend.text=element_text(colour="black", size=12))+
theme(legend.title=element_blank()+
theme(legend.key = element_rect(fill = NA, color = NA))+
theme(plot.margin = unit(c(1,1,0.5,1), "cm"))+ #t, r, b, l
guides(colour = guide_legend(nrow = 1))+
# theme(legend.position="bottom")
theme(legend.position="none")

```



```
dev.copy2pdf(file="AFR_Lactation.pdf",out.type="cairo", width=5.54, height=5.54)
```

```
## pdf
## 2
```

```
dev.copy2pdf(file="AFR_Lactation_wo_legend.pdf",out.type="cairo", width=5.54, height=4.54)
```

```
## pdf
## 2
```

Harem size

```

Harem <- pglis(AFR.Encyclop.Female ~ Harem.size, pinnipeds,lambda='ML')
print(Harem)

```

```

##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Harem.size, data = pinnipeds,
##       lambda = "ML")

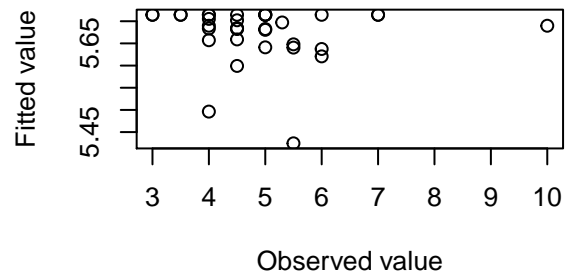
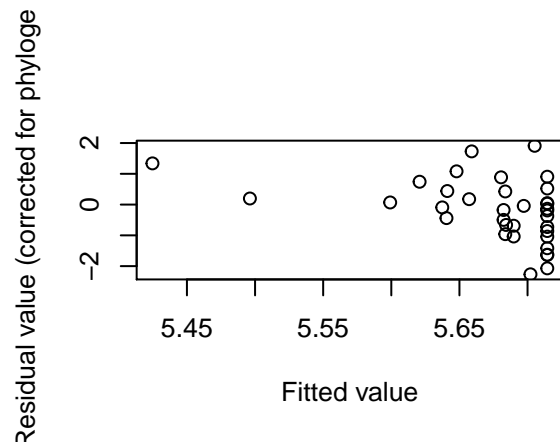
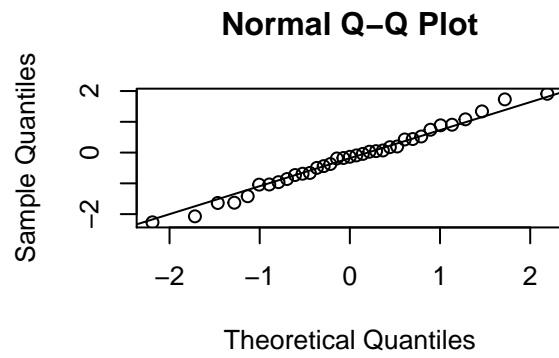
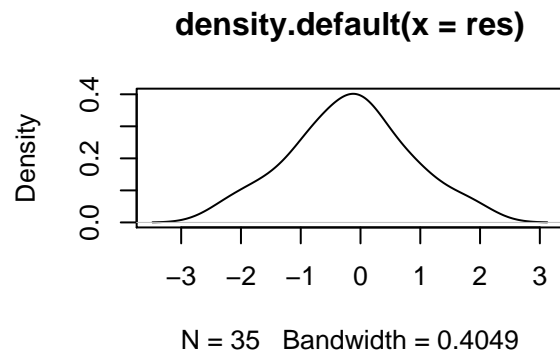
```

```
##
## Coefficients:
## (Intercept)    Harem.size
##      5.720644    -0.006165

summary(Harem)

##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Harem.size, data = pinnipeds,
##       lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.84494 -0.29631 -0.05067  0.16149  0.71221
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.953
##   lower bound : 0.000, p = 0.00028485
##   upper bound : 1.000, p = 0.00023161
##   95.0% CI   : (0.789, 0.992)
## delta [Fix] : 1.000
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  5.7206440  1.1286299  5.0687 1.507e-05 ***
## Harem.size  -0.0061654  0.0200204 -0.3080  0.7601
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3851 on 33 degrees of freedom
## Multiple R-squared:  0.002866,    Adjusted R-squared: -0.02735
## F-statistic: 0.09484 on 1 and 33 DF,  p-value: 0.7601

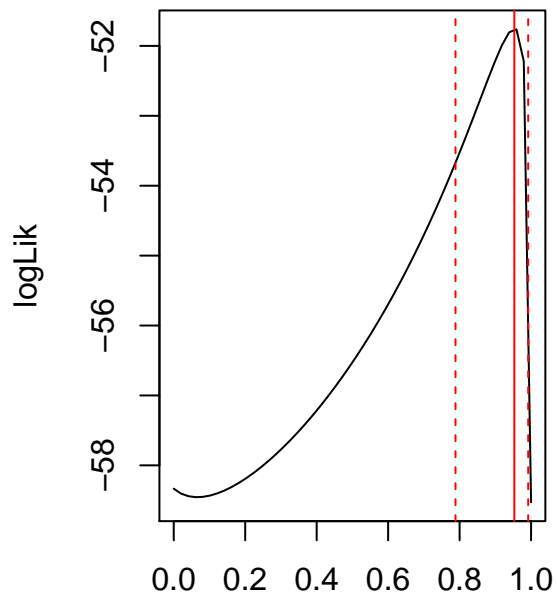
par(mfrow=c(2,2))
plot(Harem)
```



```
par(mfrow=c(1,1))

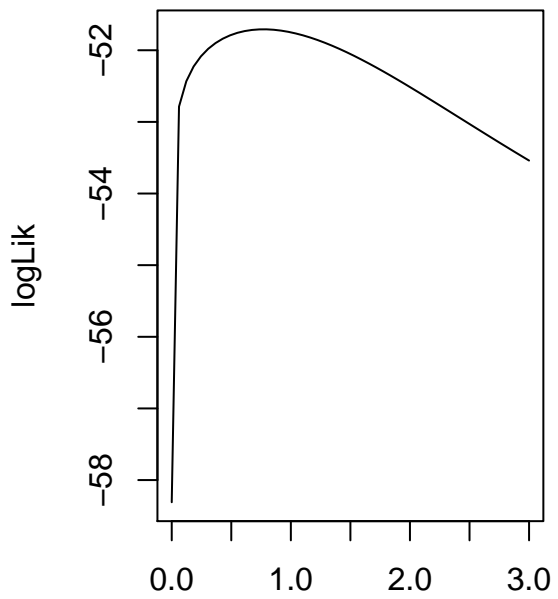
Harem.l <- pglS.profile(Harem, 'lambda')
Harem.d <- pglS.profile(Harem, 'delta')

par(mfrow=c(1,2))
plot(Harem.l); plot(Harem.d)
```



lambda

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Harem.size
kappa 1.00; lambda 0.95; delta 1.00

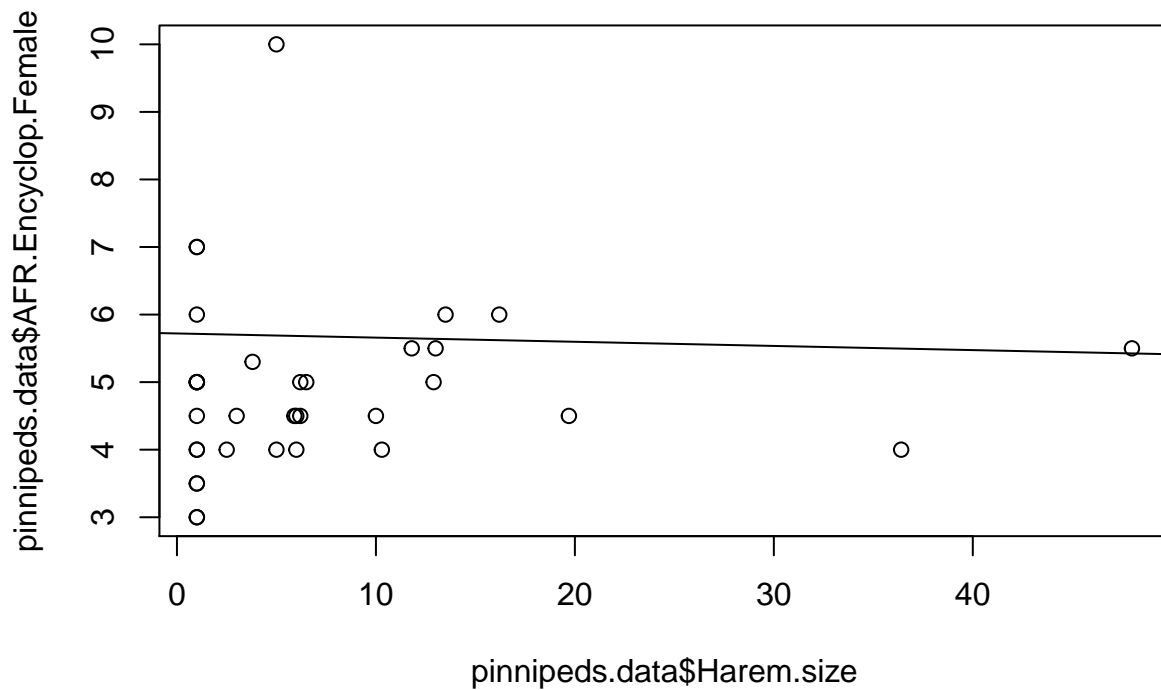


delta

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Harem.size
kappa 1.00; lambda 0.95; delta 1.00

```
par(mfrow=c(1,1))
```

```
plot(pinnipeds.data$AFR.Encyclop.Female ~ pinnipeds.data$Harem.size)
abline(a = coef(Harem)[1], b = coef(Harem)[2])
```

Latitude

```
Latitude <- pglis(AFR.Encyclop.Female ~ Latitude, pinnipeds, lambda='ML')
print(Latitude)
```

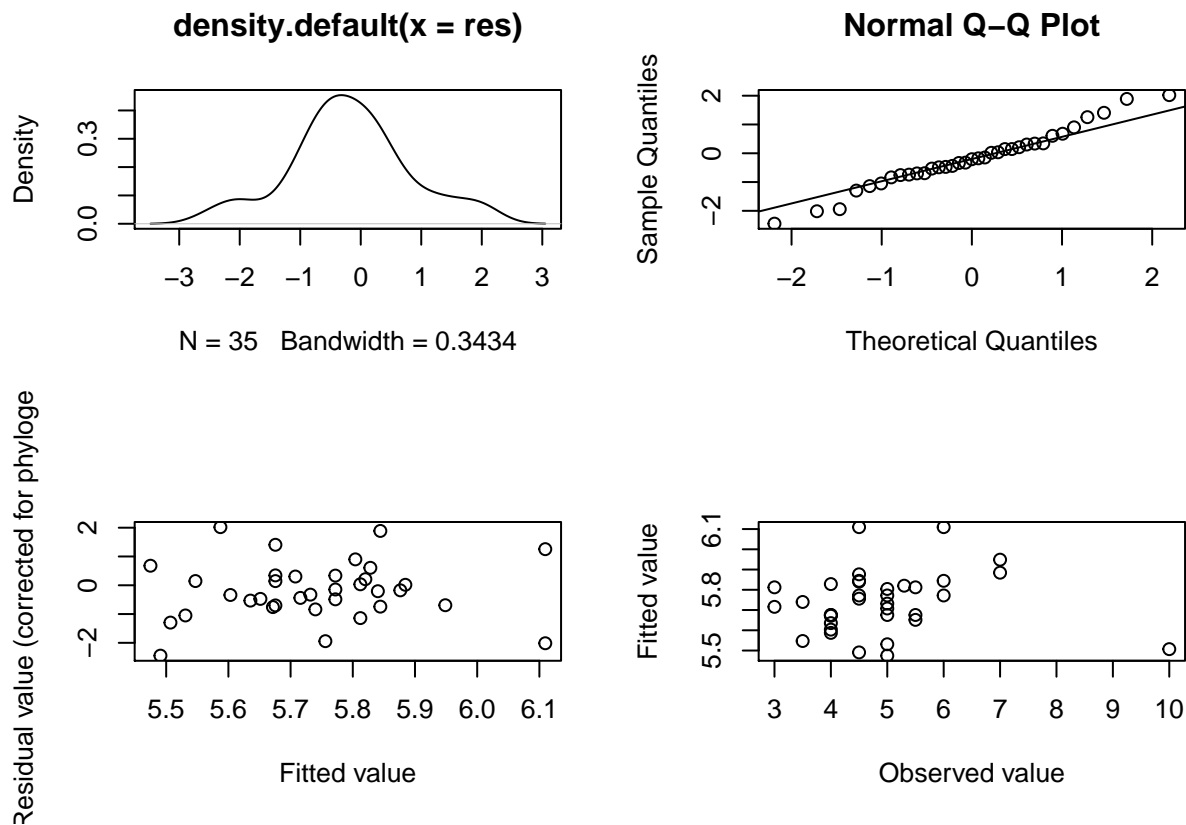
```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Latitude, data = pinnipeds,
##       lambda = "ML")
##
## Coefficients:
## (Intercept)      Latitude
##    6.109453    -0.008035
```

```
summary(Latitude)
```

```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Latitude, data = pinnipeds,
##       lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.9170 -0.2704 -0.0775  0.1200  0.7572
##
## Branch length transformations:
##
## kappa  [Fix]   : 1.000
```

```
## lambda [ ML] : 0.959
## lower bound : 0.000, p = 0.00020818
## upper bound : 1.000, p = 0.0037008
## 95.0% CI : (0.800, 0.995)
## delta [Fix] : 1.000
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 6.1094532 1.2368600 4.9395 2.204e-05 ***
## Latitude -0.0080347 0.0094571 -0.8496 0.4017
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3872 on 33 degrees of freedom
## Multiple R-squared: 0.0214, Adjusted R-squared: -0.00825
## F-statistic: 0.7218 on 1 and 33 DF, p-value: 0.4017
```

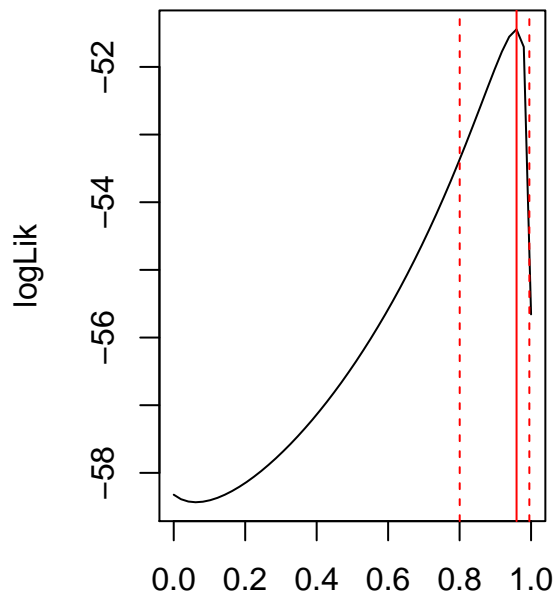
```
par(mfrow=c(2,2))
plot(Latitude)
```



```
par(mfrow=c(1,1))

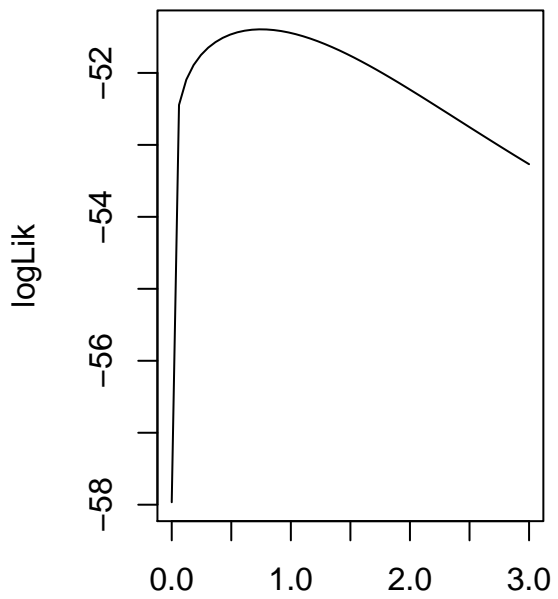
Latitude.l <- pgls.profile(Latitude, 'lambda')
Latitude.d <- pgls.profile(Latitude, 'delta')

par(mfrow=c(1,2))
plot(Latitude.l); plot(Latitude.d)
```



lambda

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Latitude
kappa 1.00; lambda 0.96; delta 1.00



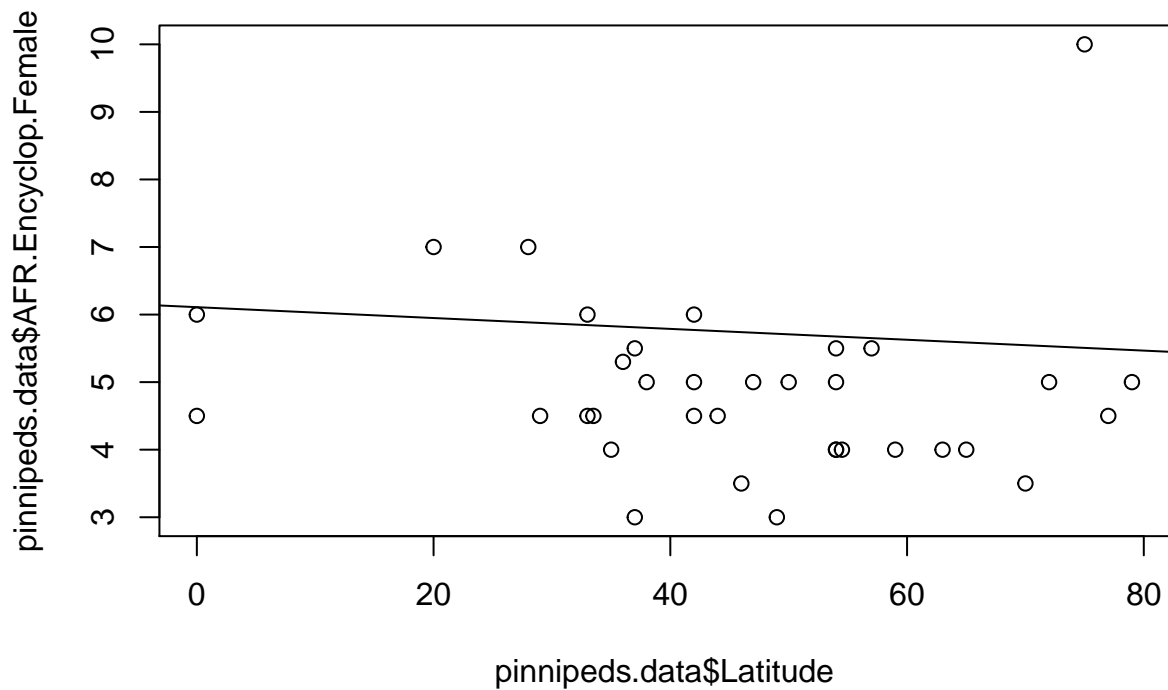
delta

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Latitude
kappa 1.00; lambda 0.96; delta 1.00

```
par(mfrow=c(1,1))
```

```
plot(pinnipeds.data$AFR.Encyclop.Female ~ pinnipeds.data$Latitude)
```

```
abline(a = coef(Latitude)[1], b = coef(Latitude)[2])
```



Season Length (log)

```
Season <- pglis(AFR. Encyclop. Female ~ Season.length, pinnipeds, lambda='ML')
print(Season)
```

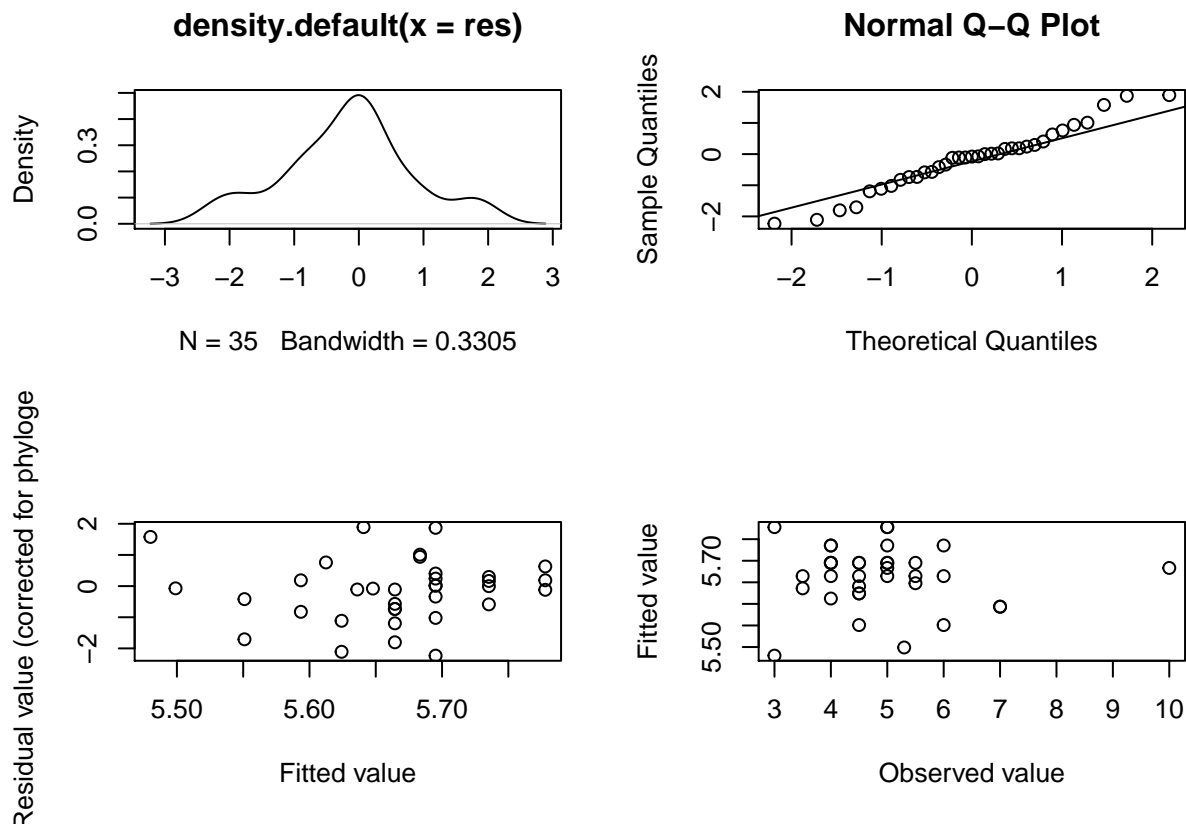
```
##
## Call:
## pglis(formula = AFR. Encyclop. Female ~ Season.length, data = pinnipeds,
##       lambda = "ML")
##
## Coefficients:
## (Intercept) Season.length
##      6.0851      -0.2363
```

```
summary(Season)
```

```
##
## Call:
## pglis(formula = AFR. Encyclop. Female ~ Season.length, data = pinnipeds,
##       lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.82802 -0.27245 -0.02954  0.09924  0.70189
##
## Branch length transformations:
##
## kappa  [Fix]   : 1.000
```

```
## lambda [ ML] : 0.949
## lower bound : 0.000, p = 0.00027483
## upper bound : 1.000, p = 0.00036329
## 95.0% CI : (0.787, 0.991)
## delta [Fix] : 1.000
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 6.08509 1.56923 3.8778 0.0004754 ***
## Season.length -0.23634 0.63133 -0.3743 0.7105398
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3816 on 33 degrees of freedom
## Multiple R-squared: 0.004229, Adjusted R-squared: -0.02595
## F-statistic: 0.1401 on 1 and 33 DF, p-value: 0.7105
```

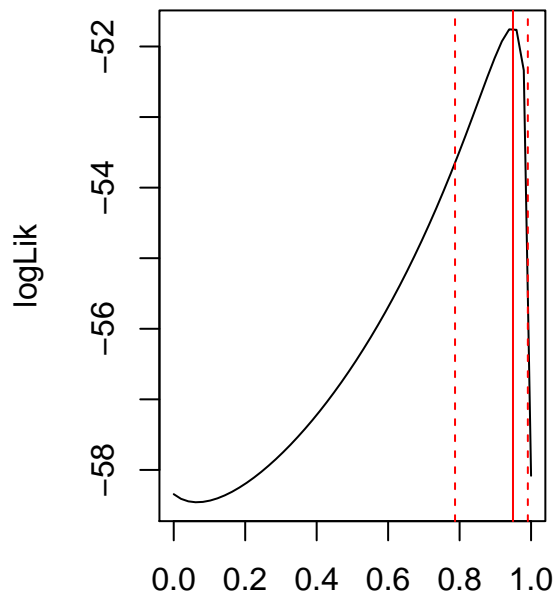
```
par(mfrow=c(2,2))
plot(Season)
```



```
par(mfrow=c(1,1))

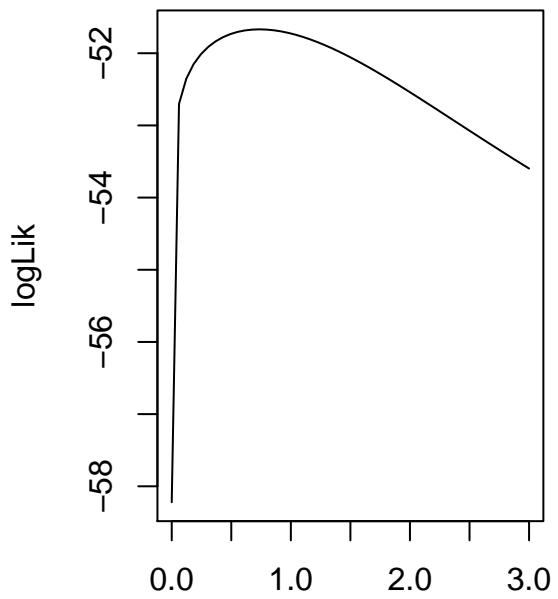
Season.l <- pglis.profile(Season, 'lambda')
Season.d <- pglis.profile(Season, 'delta')

par(mfrow=c(1,2))
plot(Season.l); plot(Season.d)
```



lambda

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Season.len;
kappa 1.00; lambda 0.95; delta 1.00

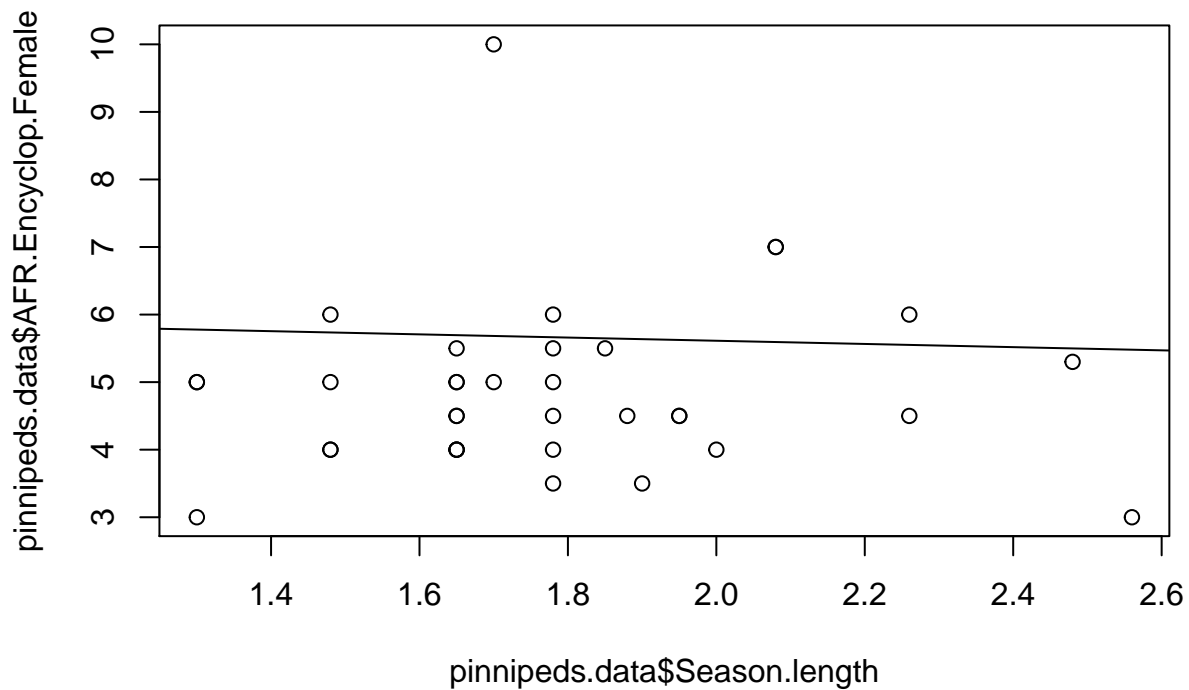


delta

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Season.len;
kappa 1.00; lambda 0.95; delta 1.00

```
par(mfrow=c(1,1))
```

```
plot(pinnipeds.data$AFR.Encyclop.Female ~ pinnipeds.data$Season.length)
abline(a = coef(Season)[1], b = coef(Season)[2])
```



Life span

```
Lifespan <- pglis(AFR.Encyclop.Female ~ Life.span, pinnipeds, lambda='ML')
print(Lifespan)
```

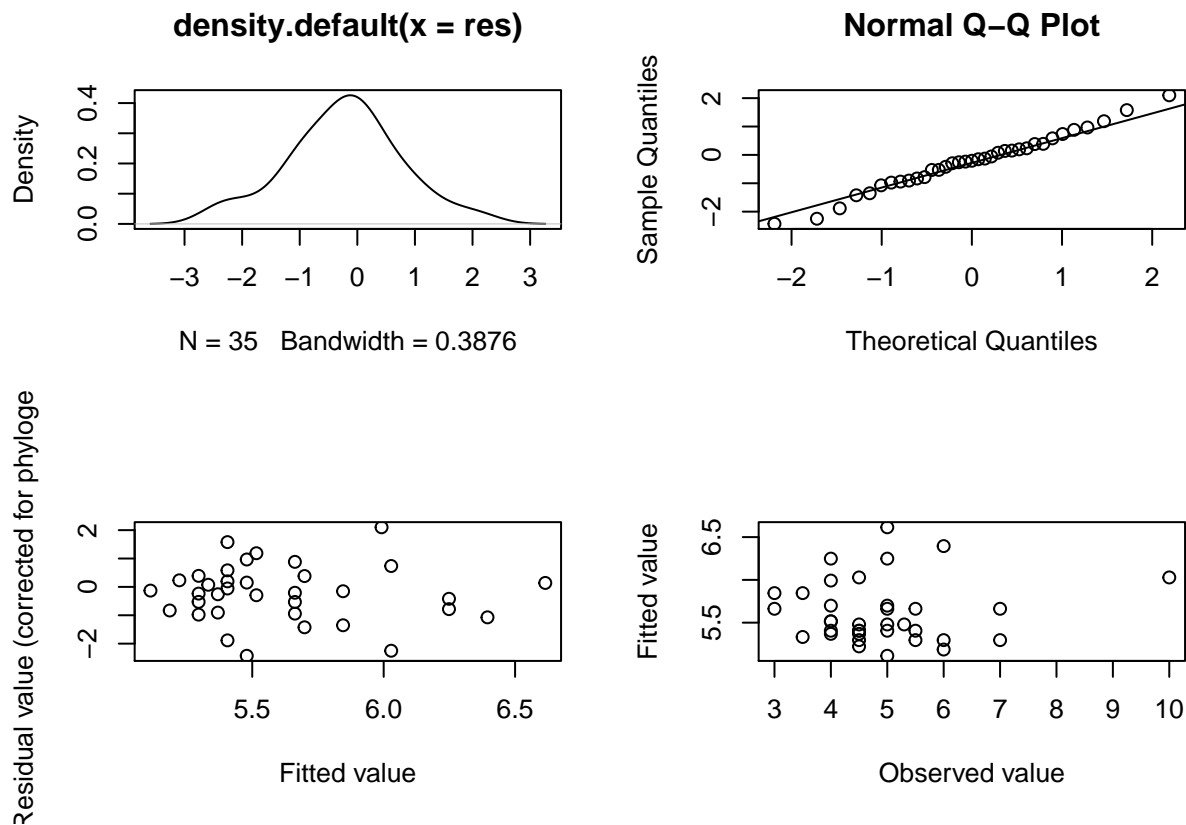
```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Life.span, data = pinnipeds,
##       lambda = "ML")
##
## Coefficients:
## (Intercept)    Life.span
##      4.56320      0.03664
```

```
summary(Lifespan)
```

```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Life.span, data = pinnipeds,
##       lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.88111 -0.31507 -0.07519  0.11128  0.76202
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
```

```
## lambda [ ML] : 0.957
## lower bound : 0.000, p = 0.00010761
## upper bound : 1.000, p = 0.00022483
## 95.0% CI : (0.805, 0.992)
## delta [Fix] : 1.000
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 4.563197 1.368695 3.3340 0.002124 **
## Life.span 0.036636 0.026966 1.3586 0.183483
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3782 on 33 degrees of freedom
## Multiple R-squared: 0.05297, Adjusted R-squared: 0.02427
## F-statistic: 1.846 on 1 and 33 DF, p-value: 0.1835
```

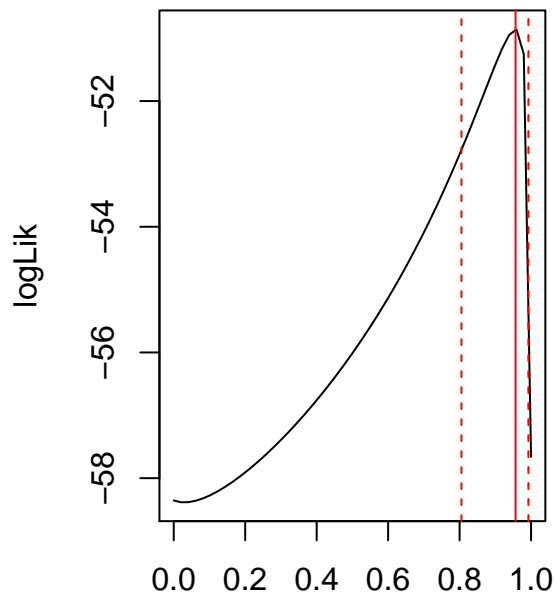
```
par(mfrow=c(2,2))
plot(Lifespan)
```



```
par(mfrow=c(1,1))

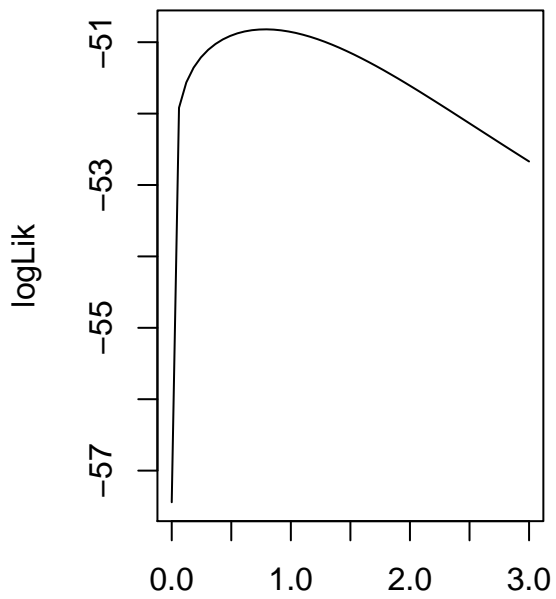
Lifespan.l <- pgls.profile(Lifespan, 'lambda')
Lifespan.d <- pgls.profile(Lifespan, 'delta')

par(mfrow=c(1,2))
plot(Lifespan.l); plot(Lifespan.d)
```

lambda

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Life.span
kappa 1.00; lambda 0.96; delta 1.00



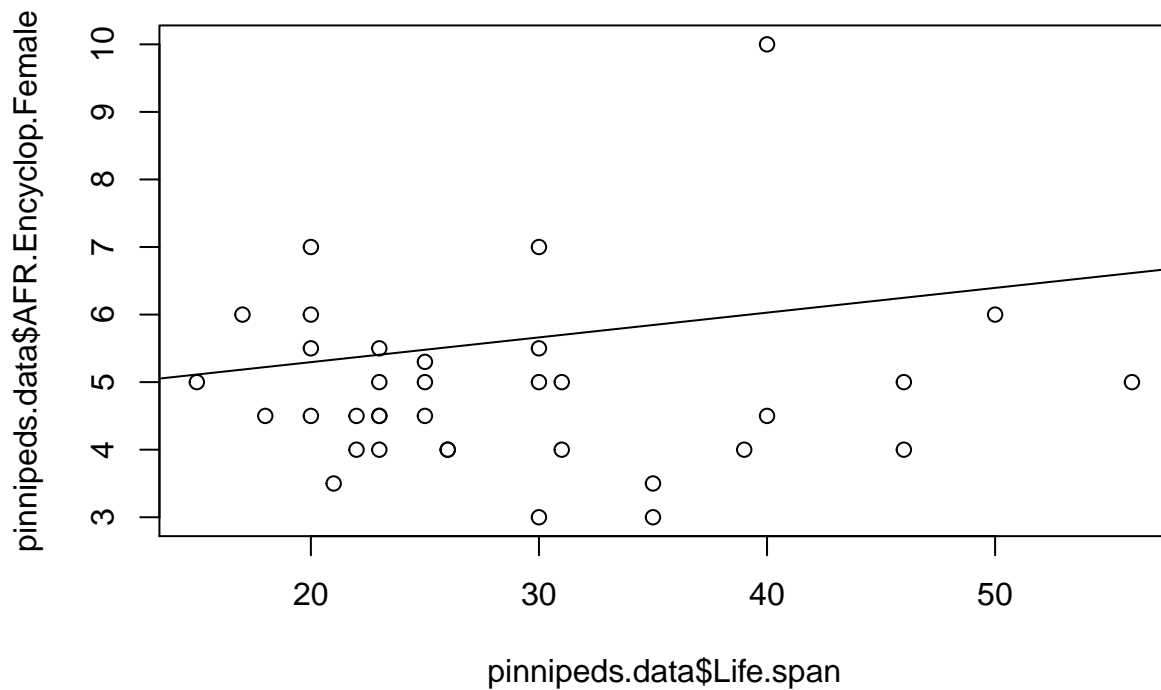
delta

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Life.span
kappa 1.00; lambda 0.96; delta 1.00

```
par(mfrow=c(1,1))
```

```
plot(pinnipeds.data$AFR.Encyclop.Female ~ pinnipeds.data$Life.span)
```

```
abline(a = coef(Lifespan)[1], b = coef(Lifespan)[2])
```



Relative birth mass

```
Rel_BM <- pglis(AFR. Encyclop. Female ~ Rel. birth. weight, pinnipeds, lambda = 'ML')
print(Rel_BM)
```

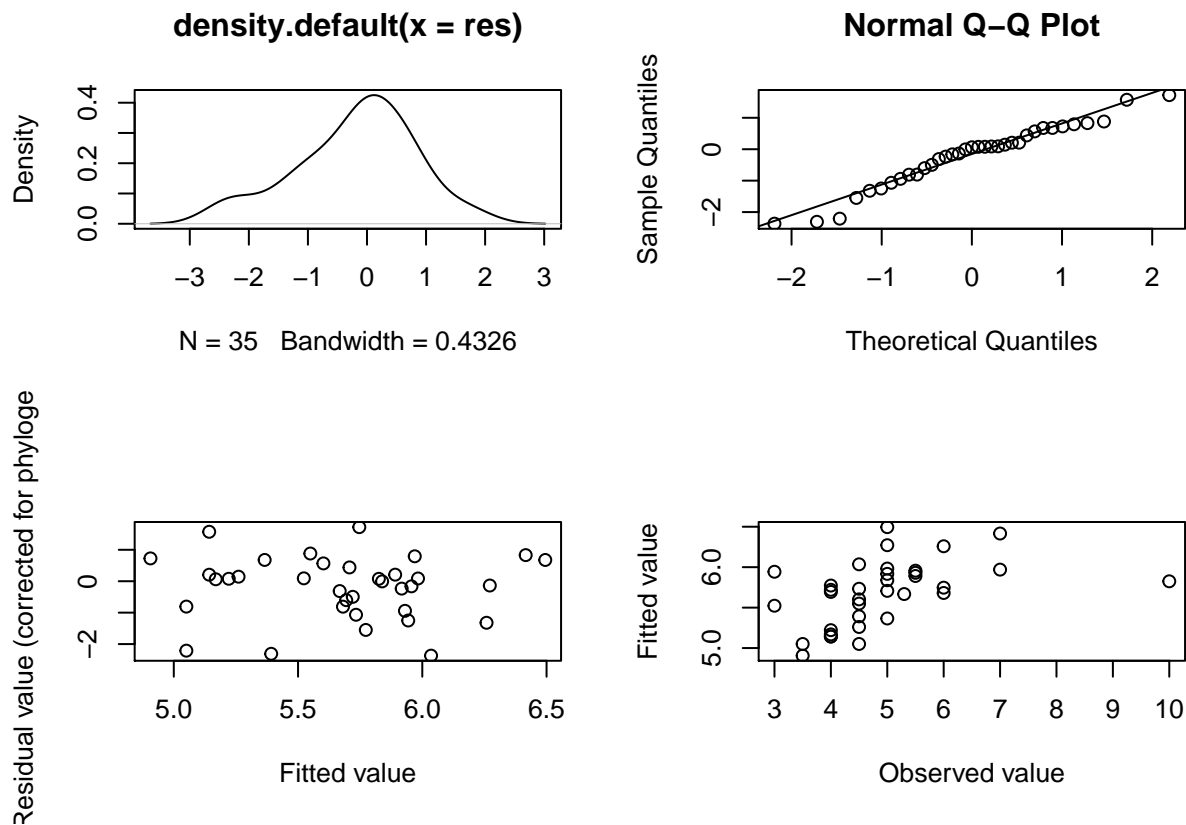
```
##
## Call:
## pglis(formula = AFR. Encyclop. Female ~ Rel. birth. weight, data = pinnipeds,
##       lambda = "ML")
##
## Coefficients:
##      (Intercept)  Rel. birth. weight
##           6.941         -13.129
```

```
summary(Rel_BM)
```

```
##
## Call:
## pglis(formula = AFR. Encyclop. Female ~ Rel. birth. weight, data = pinnipeds,
##       lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.79656 -0.27207  0.02084  0.16915  0.57871
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
```

```
## lambda [ ML] : 0.962
## lower bound : 0.000, p = 0.00024074
## upper bound : 1.000, p = 0.067636
## 95.0% CI : (0.794, NA)
## delta [Fix] : 1.000
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 6.9412 1.0941 6.3444 3.513e-07 ***
## Rel.birth.weight -13.1295 4.2974 -3.0552 0.004429 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3479 on 33 degrees of freedom
## Multiple R-squared: 0.2205, Adjusted R-squared: 0.1969
## F-statistic: 9.334 on 1 and 33 DF, p-value: 0.004429
```

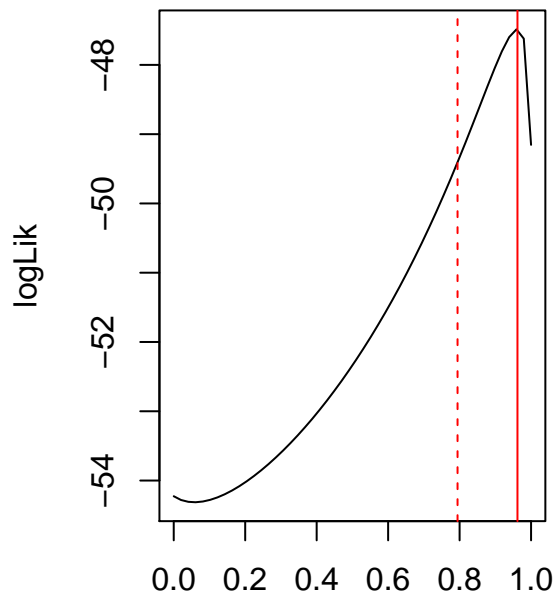
```
par(mfrow=c(2,2))
plot(Rel_BM)
```



```
par(mfrow=c(1,1))

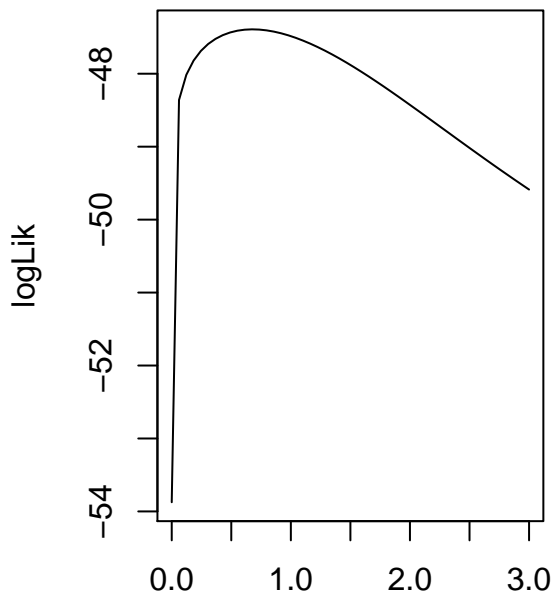
Rel_BM.l <- pglis.profile(Rel_BM, 'lambda')
Rel_BM.d <- pglis.profile(Rel_BM, 'delta')

par(mfrow=c(1,2))
plot(Rel_BM.l); plot(Rel_BM.d)
```



lambda

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Rel.birth.weight
kappa 1.00; lambda 0.96; delta 1.00

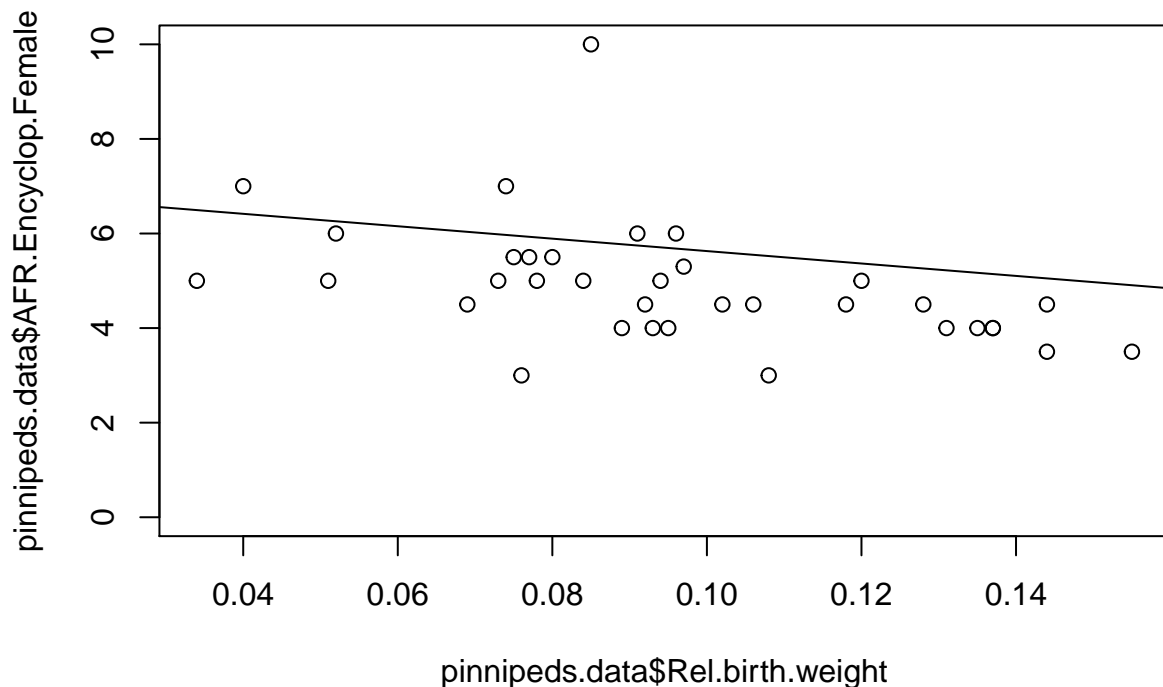


delta

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Rel.birth.weight
kappa 1.00; lambda 0.96; delta 1.00

```
par(mfrow=c(1,1))
```

```
plot(pinnipeds.data$AFR.Encyclop.Female ~ pinnipeds.data$Rel.birth.weight, ylim=c(0,10))
abline(a = coef(Rel_BM)[1], b = coef(Rel_BM)[2])
```



ggPlot

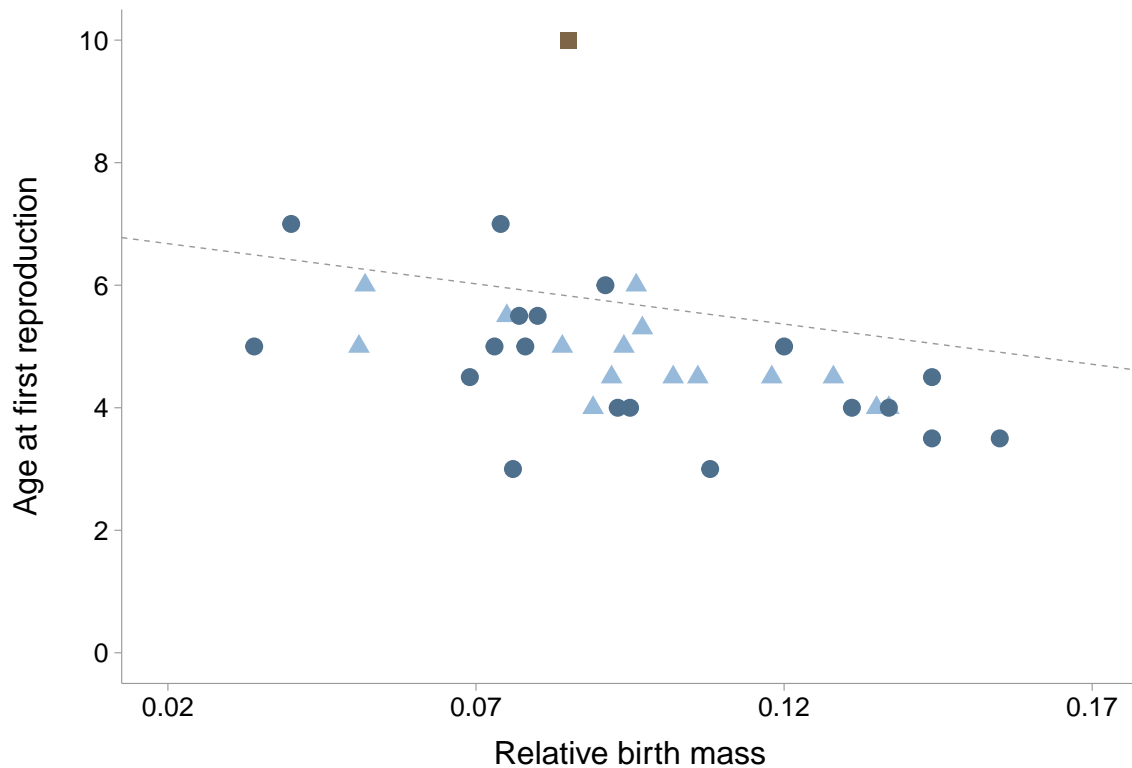
```
# rel birth mass
regr_BM <- pglis(AFR.Encyclop.Female~Rel.birth.weight, pinnipeds,lambda='ML')

ggplot(data=pinnipeds.data.plot, aes(x=Rel.birth.weight, y=AFR.Encyclop.Female))+
  geom_point(size=2.5, aes(shape=Group,colour=Group))+
  # geom_smooth(method='lm',formula=y~x, se=FALSE,alpha=0.2,linetype = "dashed",color="#999999",size=0.25)+
  # geom_segment(aes(x = -0.923, xend = 0.277, y = regr_lact$coefficients[1]*(-0.923),
  # yend = 0+regr_lact$coefficients[1]*(0.277)), color='#999999', size=0.25,linetype = "dashed")+
  # geom_abline(intercept=0, slope=regr_BM$coefficients[1], color='black', size=0.5,linetype = "dashed")+
  geom_abline(intercept= regr_BM$model$coef[1],slope=regr_BM$model$coef[2], color="#999999",size=0.25,linetype = "dashed")+
  scale_shape_manual(values=c(15,17,19))+
  scale_color_manual(values=c('#7F6548', '#98BADA', '#4E708C'))+
  theme(axis.text.x=element_text(colour="black",size=10, hjust = 0.5))+
  theme(axis.title.x=element_text(colour="black",size=12,vjust= -0.5)) +
  theme(panel.background = element_blank()) +
  theme(axis.line = element_line(colour = "#999999",size=0.2))+
  theme(axis.ticks=element_line(colour="#999999",size=0.2))+
  scale_y_continuous("Age at first reproduction",
    breaks = seq(0,10,2), limits = c(0,10))+
  scale_x_continuous("Relative birth mass",breaks = seq(0.02,0.17,0.05),limits = c(0.02,0.17))+
  theme(axis.text.y=element_text(colour="black",size=10))+
  theme(axis.title.y=element_text(colour="black",size=12,vjust= 5))+
  # ggtitle("Predicted influence of SST on survival estimates")+
  theme(plot.title=element_text(size=12, face="bold", vjust=2,hjust = 0.5))+
  theme(legend.text=element_text(colour="black", size=12))+
```

```

theme(legend.title=element_blank())+
theme(legend.key = element_rect(fill = NA, color = NA))+
theme(plot.margin = unit(c(1,1,0.5,1), "cm"))+ #t, r, b, l
guides(colour = guide_legend(nrow = 1))+
# theme(legend.position="bottom")
theme(legend.position="none")

```



```
dev.copy2pdf(file="AFR_BM.pdf",out.type="cairo", width=5.54, height=5.54)
```

```
## pdf
## 2
```

```
dev.copy2pdf(file="AFR_BM_wo_legend.pdf",out.type="cairo", width=5.54, height=4.54)
```

```
## pdf
## 2
```

Male body mass (log)

```

Male_BodyMass <- pglis(AFR.Encyclop.Female ~ Male.weight, pinnipeds)
print(Male_BodyMass)

```

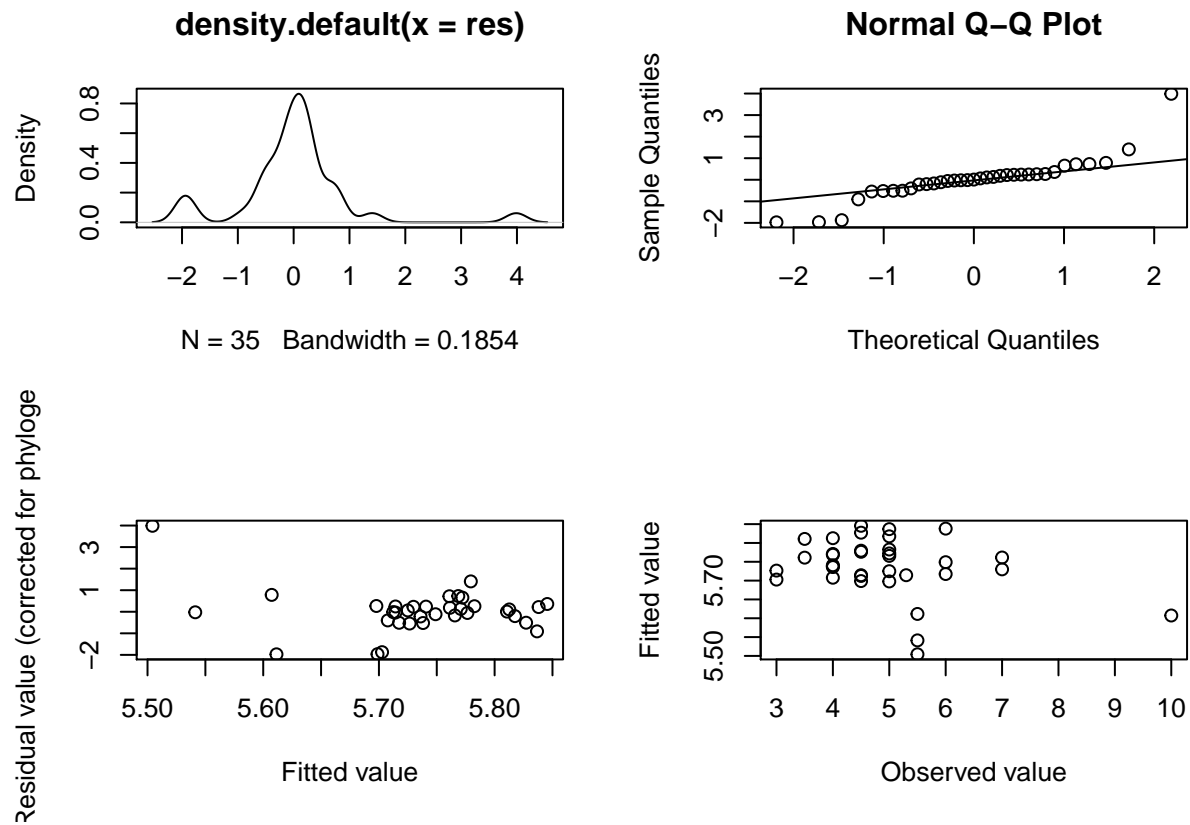
```

##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Male.weight, data = pinnipeds)
##
## Coefficients:
## (Intercept)  Male.weight

```

```
##      6.2015      -0.1967
summary(Male_BodyMass)

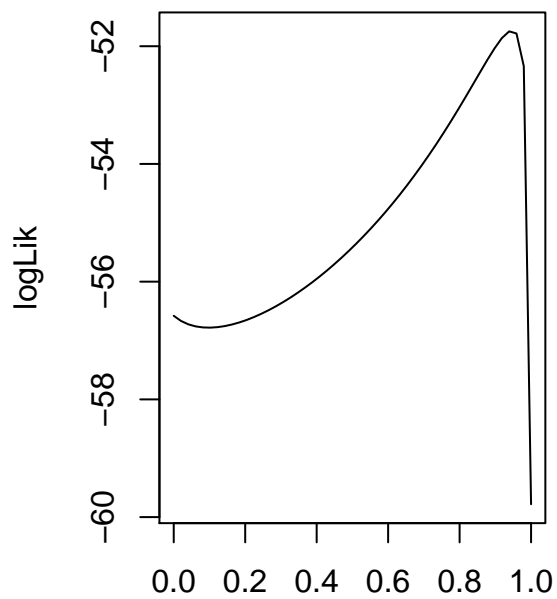
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Male.weight, data = pinnipeds)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.10328 -0.17353  0.00485  0.14082  2.22928
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [Fix] : 1.000
## delta [Fix] : 1.000
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  6.20150     2.61592  2.3707  0.02375 *
## Male.weight -0.19668     0.78752 -0.2497  0.80433
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5676 on 33 degrees of freedom
## Multiple R-squared:  0.001887,    Adjusted R-squared: -0.02836
## F-statistic: 0.06237 on 1 and 33 DF,  p-value: 0.8043
par(mfrow=c(2,2))
plot(Male_BodyMass)
```



```
par(mfrow=c(1,1))

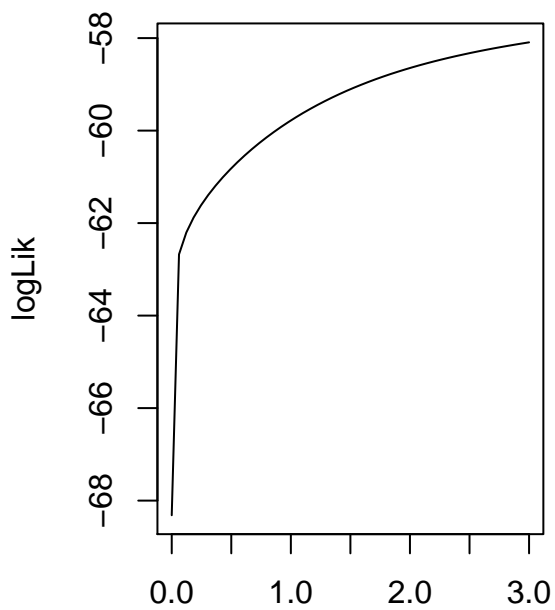
Male_BodyMass.l <- pgls.profile(Male_BodyMass, 'lambda')
Male_BodyMass.d <- pgls.profile(Male_BodyMass, 'delta')

par(mfrow=c(1,2))
plot(Male_BodyMass.l); plot(Male_BodyMass.d)
```

lambda

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Male.weight
kappa 1.00; lambda 1.00; delta 1.00

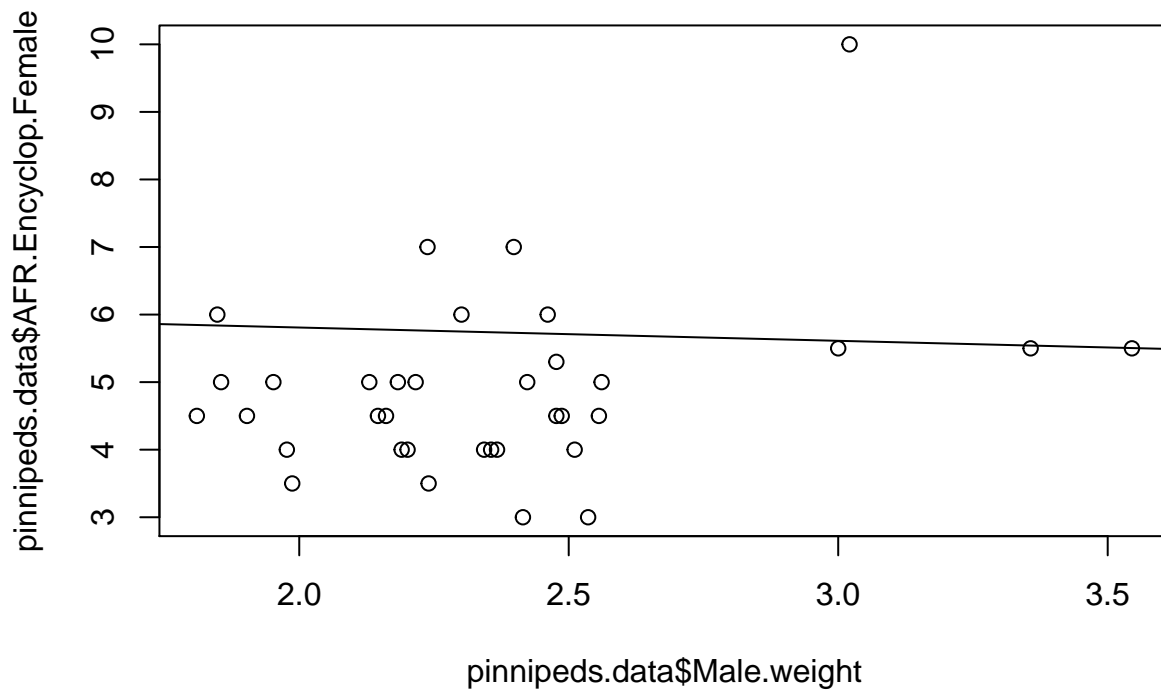


delta

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Male.weight
kappa 1.00; lambda 1.00; delta 1.00

```
par(mfrow=c(1,1))
```

```
plot(pinnipeds.data$AFR.Encyclop.Female ~ pinnipeds.data$Male.weight)
abline(a = coef(Male_BodyMass)[1], b = coef(Male_BodyMass)[2])
```



Female body mass (log)

```
Female_BodyMass <- pglis(AFR.Encyclop.Female ~ Fem.weight, pinnipeds, lambda='ML')
print(Female_BodyMass)
```

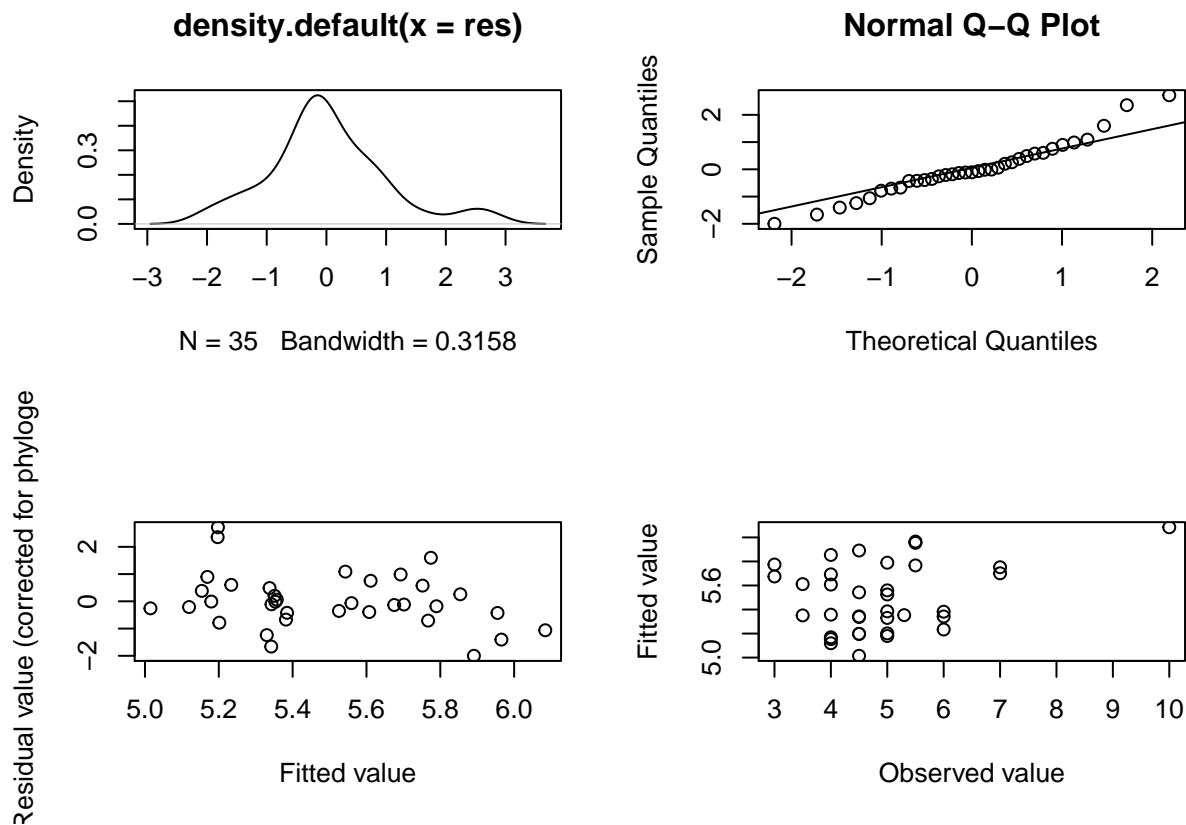
```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Fem.weight, data = pinnipeds,
##       lambda = "ML")
##
## Coefficients:
## (Intercept)    Fem.weight
##      3.9251      0.7521
```

```
summary(Female_BodyMass)
```

```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Fem.weight, data = pinnipeds,
##       lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.7283 -0.1547 -0.0397  0.1939  0.9899
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
```

```
## lambda [ ML] : 0.940
## lower bound : 0.000, p = 0.0012092
## upper bound : 1.000, p = 0.00018668
## 95.0% CI : (0.683, 0.991)
## delta [Fix] : 1.000
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.92508 1.99672 1.9658 0.05779 .
## Fem.weight 0.75210 0.73092 1.0290 0.31097
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3698 on 33 degrees of freedom
## Multiple R-squared: 0.03109, Adjusted R-squared: 0.001727
## F-statistic: 1.059 on 1 and 33 DF, p-value: 0.311
```

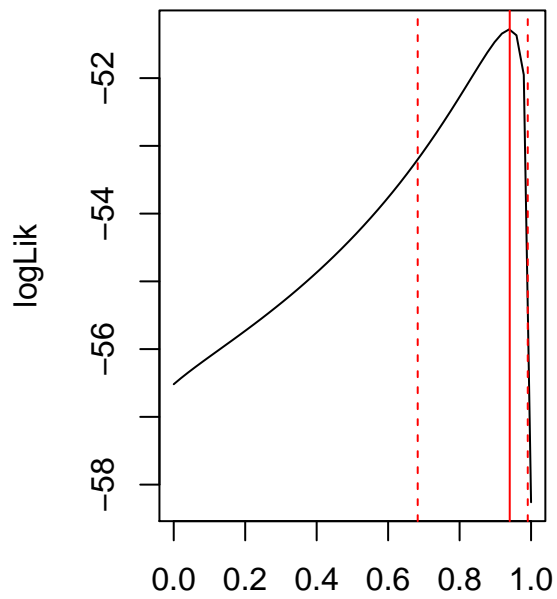
```
par(mfrow=c(2,2))
plot(Female_BodyMass)
```



```
par(mfrow=c(1,1))

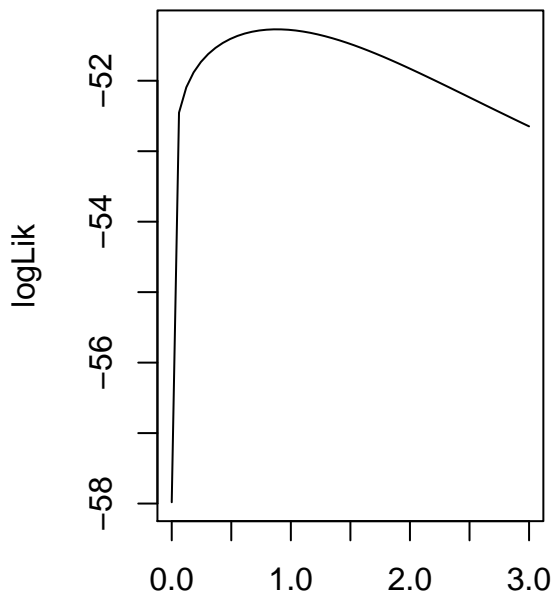
Female_BodyMass.l <- pgls.profile(Female_BodyMass, 'lambda')
Female_BodyMass.d <- pgls.profile(Female_BodyMass, 'delta')

par(mfrow=c(1,2))
plot(Female_BodyMass.l); plot(Female_BodyMass.d)
```



lambda

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Fem.weight
kappa 1.00; lambda 0.94; delta 1.00

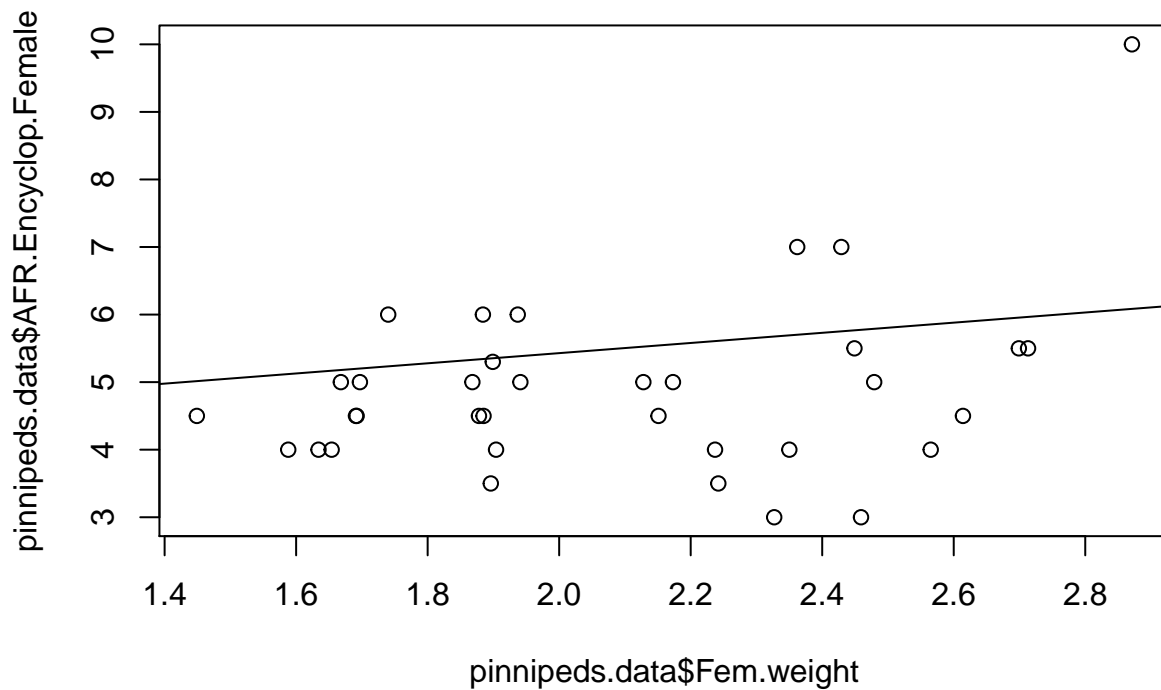


delta

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Fem.weight
kappa 1.00; lambda 0.94; delta 1.00

```
par(mfrow=c(1,1))
```

```
plot(pinnipeds.data$AFR.Encyclop.Female ~ pinnipeds.data$Fem.weight)
abline(a = coef(Female_BodyMass)[1], b = coef(Female_BodyMass)[2])
```



Generation time

```
GTime <- pglis(AFR.Encyclop.Female ~ Gen.time, pinnipeds, lambda='ML')
print(GTime)
```

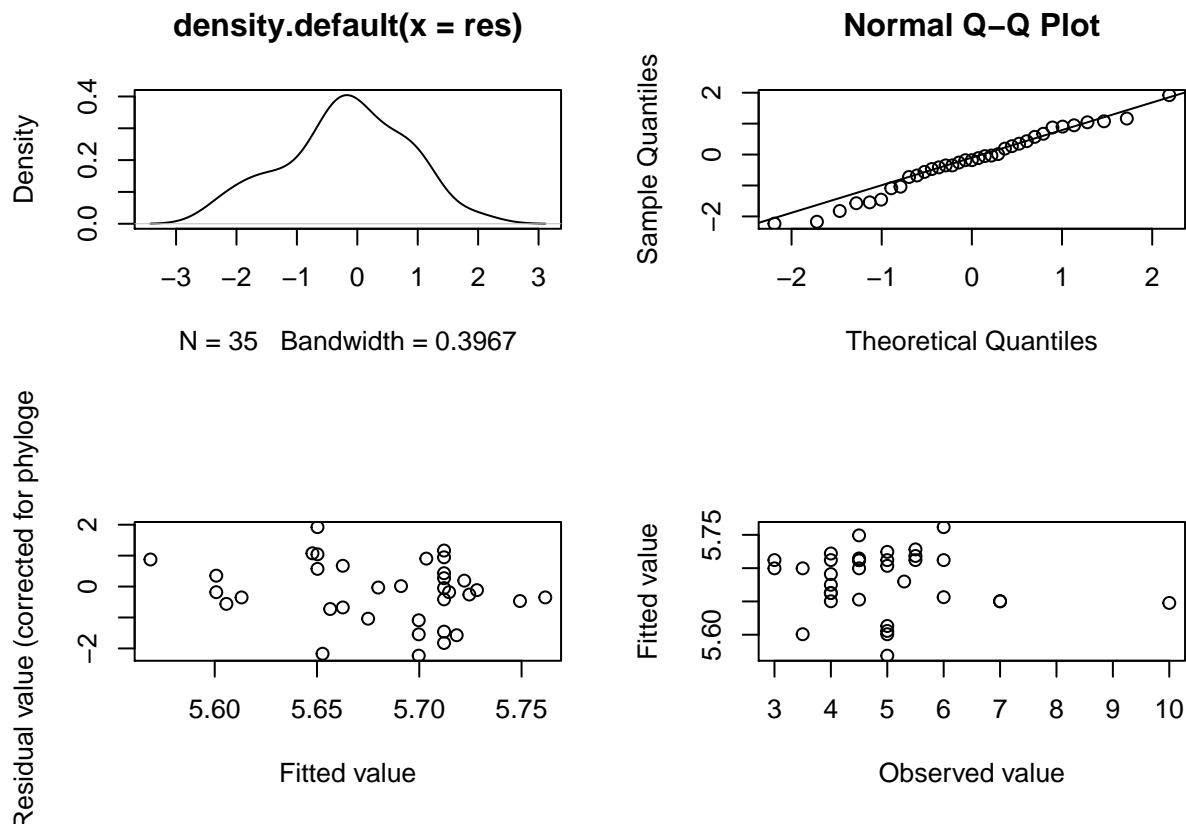
```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Gen.time, data = pinnipeds,
##       lambda = "ML")
##
## Coefficients:
## (Intercept)      Gen.time
##      5.83582      -0.01237
```

```
summary(GTime)
```

```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Gen.time, data = pinnipeds,
##       lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.83235 -0.26112 -0.06757  0.18701  0.71588
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
```

```
## lambda [ ML] : 0.954
## lower bound : 0.000, p = 0.00035295
## upper bound : 1.000, p = 6.883e-05
## 95.0% CI : (0.782, 0.991)
## delta [Fix] : 1.000
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 5.835821 1.272576 4.5858 6.217e-05 ***
## Gen.time -0.012372 0.045486 -0.2720 0.7873
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3856 on 33 degrees of freedom
## Multiple R-squared: 0.002237, Adjusted R-squared: -0.028
## F-statistic: 0.07398 on 1 and 33 DF, p-value: 0.7873
```

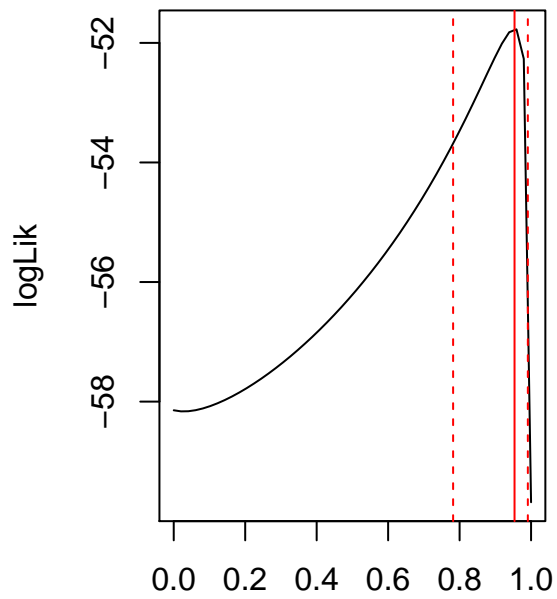
```
par(mfrow=c(2,2))
plot(GTime)
```



```
par(mfrow=c(1,1))

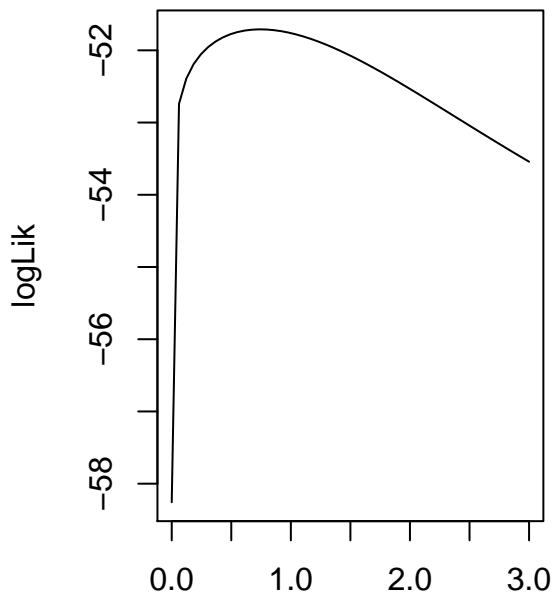
GTime.l <- pgl.profile(GTime, 'lambda')
GTime.d <- pgl.profile(GTime, 'delta')

par(mfrow=c(1,2))
plot(GTime.l); plot(GTime.d)
```



lambda

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Gen.time
kappa 1.00; lambda 0.95; delta 1.00

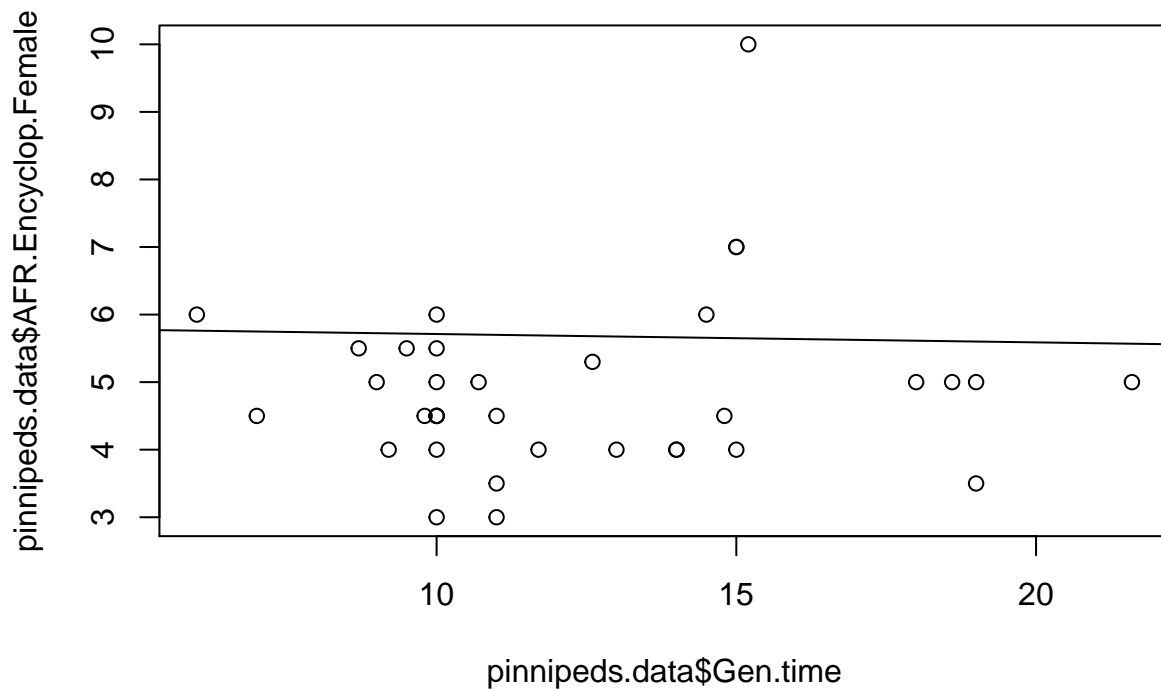


delta

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Gen.time
kappa 1.00; lambda 0.95; delta 1.00

```
par(mfrow=c(1,1))
```

```
plot(pinnipeds.data$AFR.Encyclop.Female ~ pinnipeds.data$Gen.time)
abline(a = coef(GTime)[1], b = coef(GTime)[2])
```



Birth mass

```
BM <- pglis(AFR.Encyclop.Female ~ Birth.weight, pinnipeds, lambda='ML')
print(BM)
```

```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Birth.weight, data = pinnipeds,
##       lambda = "ML")
##
## Coefficients:
## (Intercept) Birth.weight
##      5.32252      0.01281
```

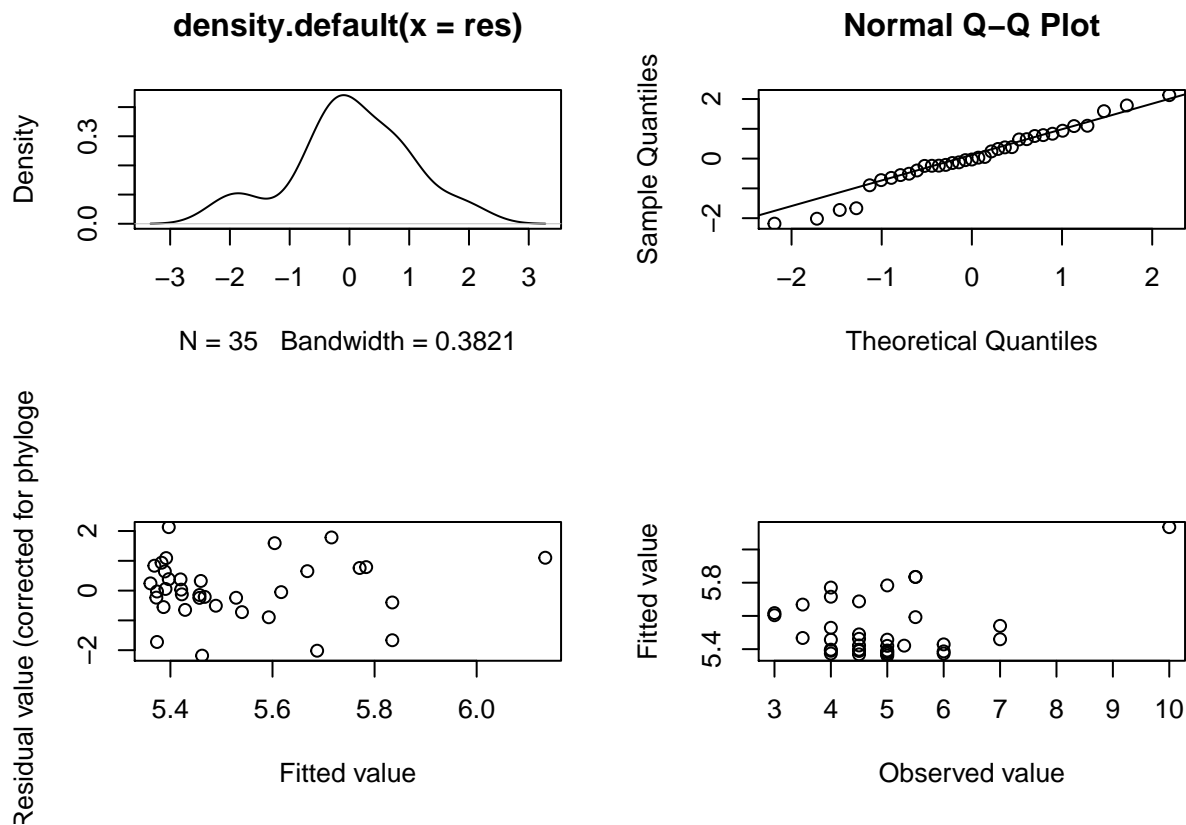
```
summary(BM)
```

```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Birth.weight, data = pinnipeds,
##       lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.80792 -0.16767 -0.01114  0.26110  0.78835
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
```



```
## lambda [ ML] : 0.943
## lower bound : 0.000, p = 0.0022421
## upper bound : 1.000, p = 5.5675e-05
## 95.0% CI : (0.694, 0.990)
## delta [Fix] : 1.000
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 5.322522 1.248045 4.2647 0.0001578 ***
## Birth.weight 0.012805 0.023110 0.5541 0.5832336
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3759 on 33 degrees of freedom
## Multiple R-squared: 0.009219, Adjusted R-squared: -0.0208
## F-statistic: 0.307 on 1 and 33 DF, p-value: 0.5832
```

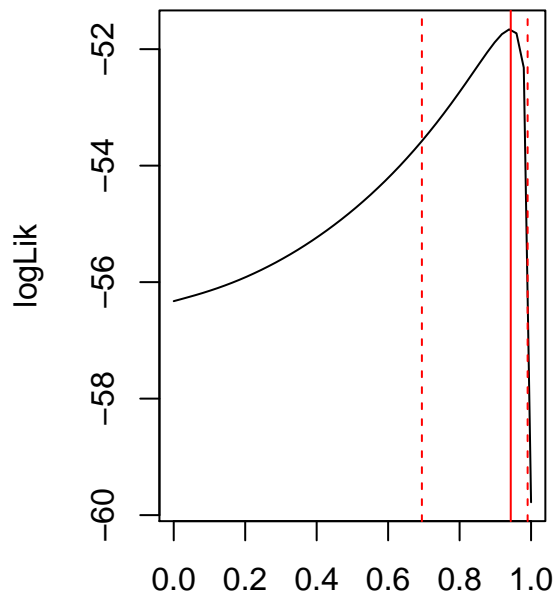
```
par(mfrow=c(2,2))
plot(BM)
```



```
par(mfrow=c(1,1))

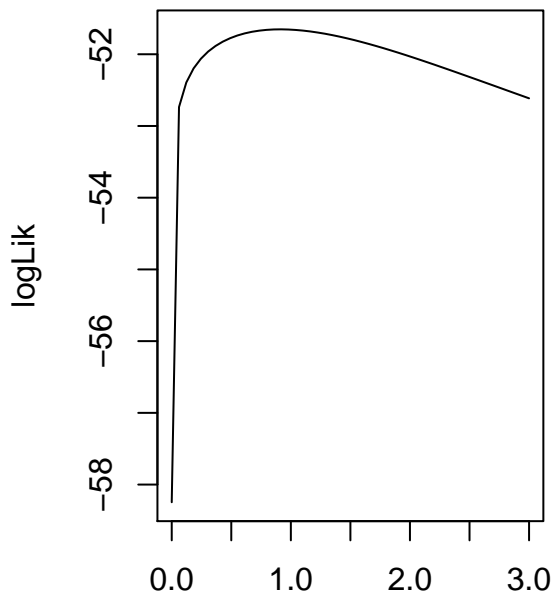
BM.l <- pglis.profile(BM, 'lambda')
BM.d <- pglis.profile(BM, 'delta')

par(mfrow=c(1,2))
plot(BM.l); plot(BM.d)
```



lambda

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Birth.weigl
kappa 1.00; lambda 0.94; delta 1.00

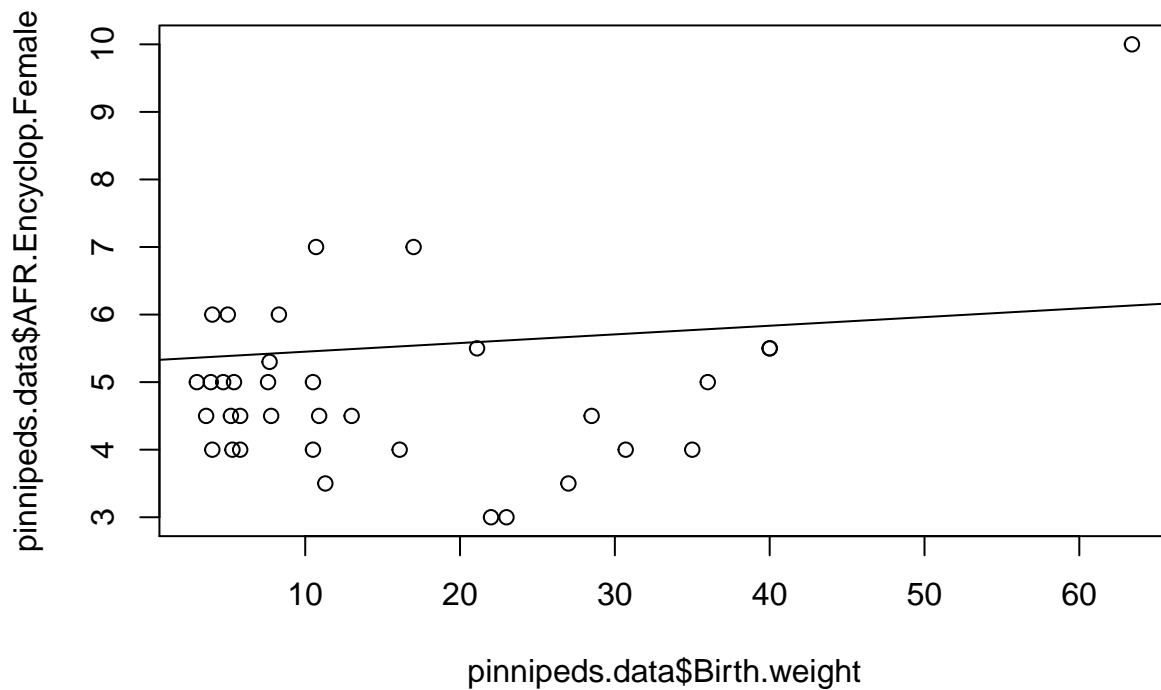


delta

Data: pinnipeds; Model: AFR.Encyclop.Female ~ Birth.weigl
kappa 1.00; lambda 0.94; delta 1.00

```
par(mfrow=c(1,1))
```

```
plot(pinnipeds.data$AFR.Encyclop.Female ~ pinnipeds.data$Birth.weight)
abline(a = coef(BM)[1], b = coef(BM)[2])
```



Birth mass (log)

```
BM_log <- pglis(AFR.Encyclop.Female ~ Birth.weight.log, pinnipeds, lambda='ML')
print(BM_log)
```

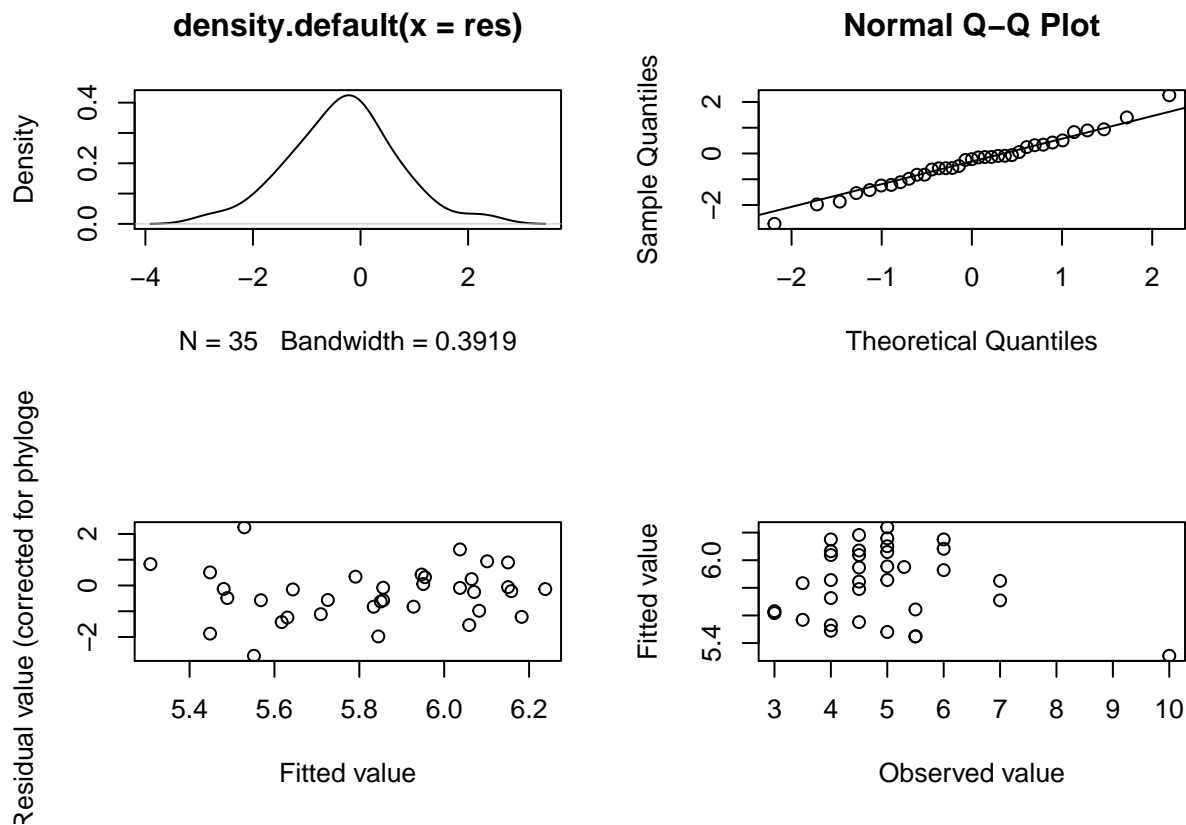
```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Birth.weight.log, data = pinnipeds,
##       lambda = "ML")
##
## Coefficients:
##      (Intercept)  Birth.weight.log
##           6.5731          -0.3049
```

```
summary(BM_log)
```

```
##
## Call:
## pglis(formula = AFR.Encyclop.Female ~ Birth.weight.log, data = pinnipeds,
##       lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.98952 -0.32748 -0.08013  0.10328  0.81881
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
```

```
## lambda [ ML] : 0.961
## lower bound : 0.000, p = 0.00025756
## upper bound : 1.000, p = 0.00018281
## 95.0% CI : (0.819, 0.993)
## delta [Fix] : 1.000
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 6.57312 1.45540 4.5164 7.612e-05 ***
## Birth.weight.log -0.30492 0.31226 -0.9765 0.3359
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3878 on 33 degrees of freedom
## Multiple R-squared: 0.02808, Adjusted R-squared: -0.001369
## F-statistic: 0.9535 on 1 and 33 DF, p-value: 0.3359
```

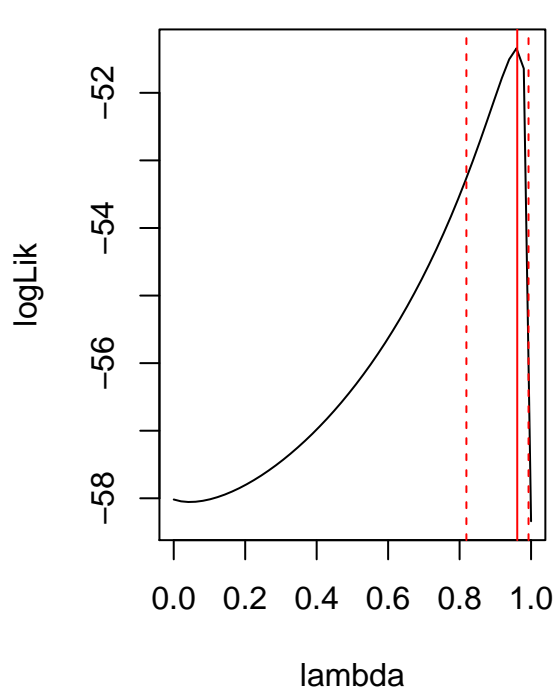
```
par(mfrow=c(2,2))
plot(BM_log)
```



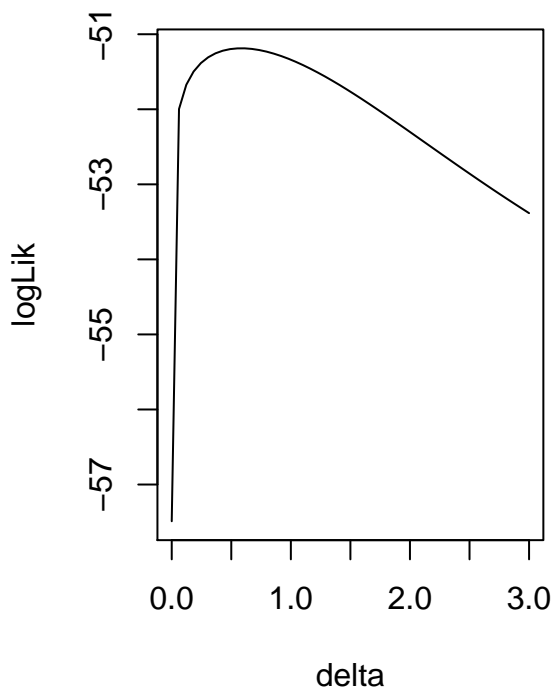
```
par(mfrow=c(1,1))

BM_log.l <- pgl.s.profile(BM_log, 'lambda')
BM_log.d <- pgl.s.profile(BM_log, 'delta')

par(mfrow=c(1,2))
plot(BM_log.l); plot(BM_log.d)
```



Data: pinnipeds; Model: AFR.Encyclop.Female ~ Birth.weight
kappa 1.00; lambda 0.96; delta 1.00



Data: pinnipeds; Model: AFR.Encyclop.Female ~ Birth.weight
kappa 1.00; lambda 0.96; delta 1.00

```
plot(pinnipeds.data$AFR.Encyclop.Female ~ pinnipeds.data$Birth.weight.log)
abline(a = coef(BM_log)[1], b = coef(BM_log)[2])
```

