eda

2022-08-26

An analysis of LWR data was conducted.

```
setwd("C:\\Users\\goodk\\Desktop")
fish = read.table("fish.txt", header=T,fileEncoding = "euc-kr")
str(fish)
```

```
## 'data.frame':    4904 obs. of  3 variables:
##  $ 종명: chr  "고등어" "고등어" "고등어" "고등어" ...
##  $ TL  : num  28 21 28.7 29.3 21.5 ...
##  $ BW  : num  150 70 192 206 84 77 83 172 82 136 ...
```

```
head(fish)
```

```
##     종명    TL  BW
## 1 고등어 27.98 150
## 2 고등어 21.00  70
## 3 고등어 28.70 192
## 4 고등어 29.30 206
## 5 고등어 21.50  84
## 6 고등어 21.70  77
```

```
fishsplit = split(fish, fish$종명)
attach(fishsplit)
go = 고등어
nun = 눈볼대
duck = 덕대
myul = 멸치
ban = 밴댕이
bo = 보구치
bul = 붉은메기
sat = 샛멸
sung = 성대
jeon = 전갱이
ju = 주둥치
cham = 참돔
hwangd = 황돔
hwanga = 황아귀
```
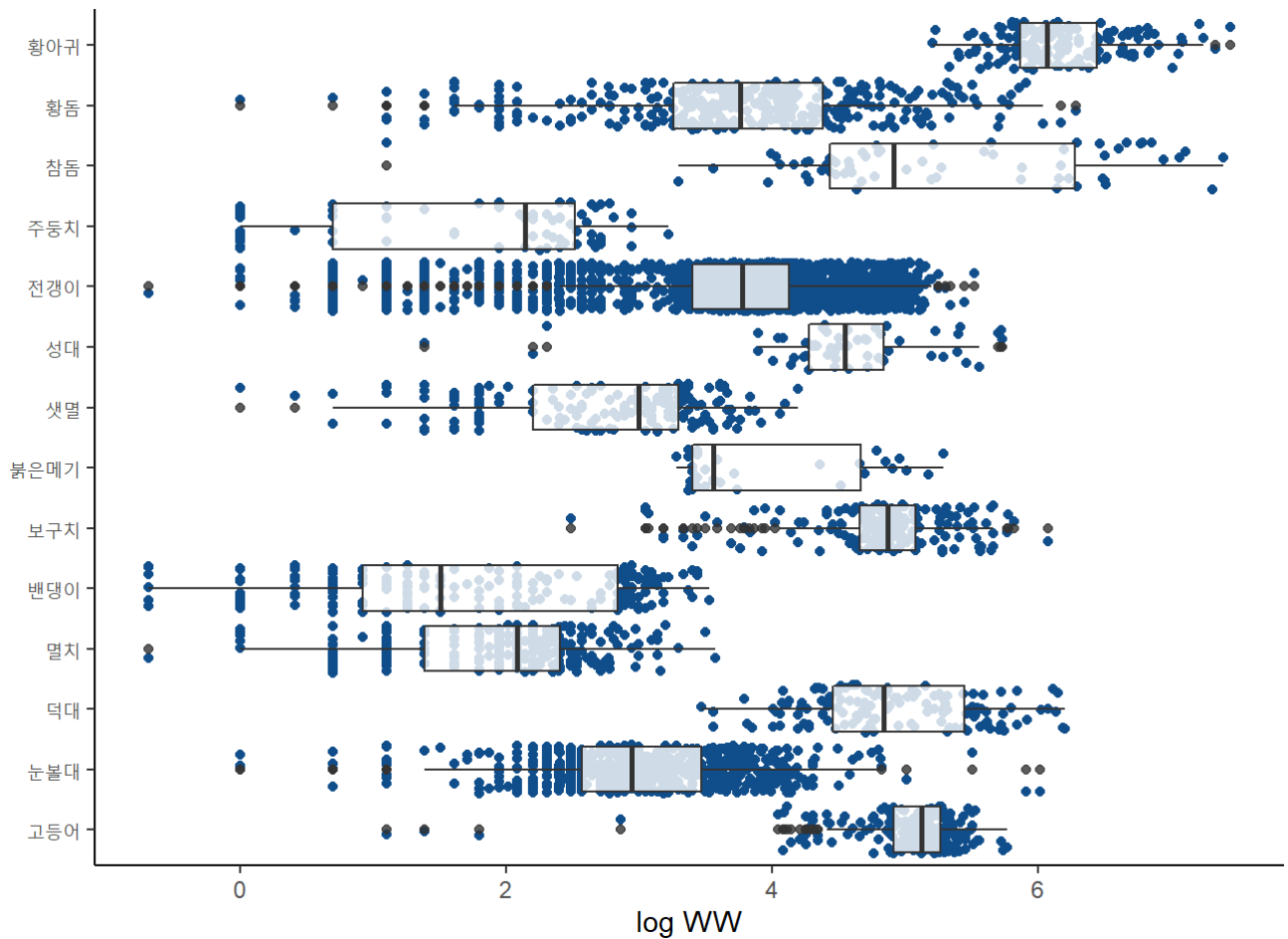
boxplot

```
library(ggplot2)
library(dplyr)
library(gridExtra)
library(tidyverse)
```

```
fish %>% ggplot(aes(종명,TL)) + geom_jitter(col='dodgerblue4') + geom_boxplot(alpha=.8) + theme
_classic()+ coord_flip()
```
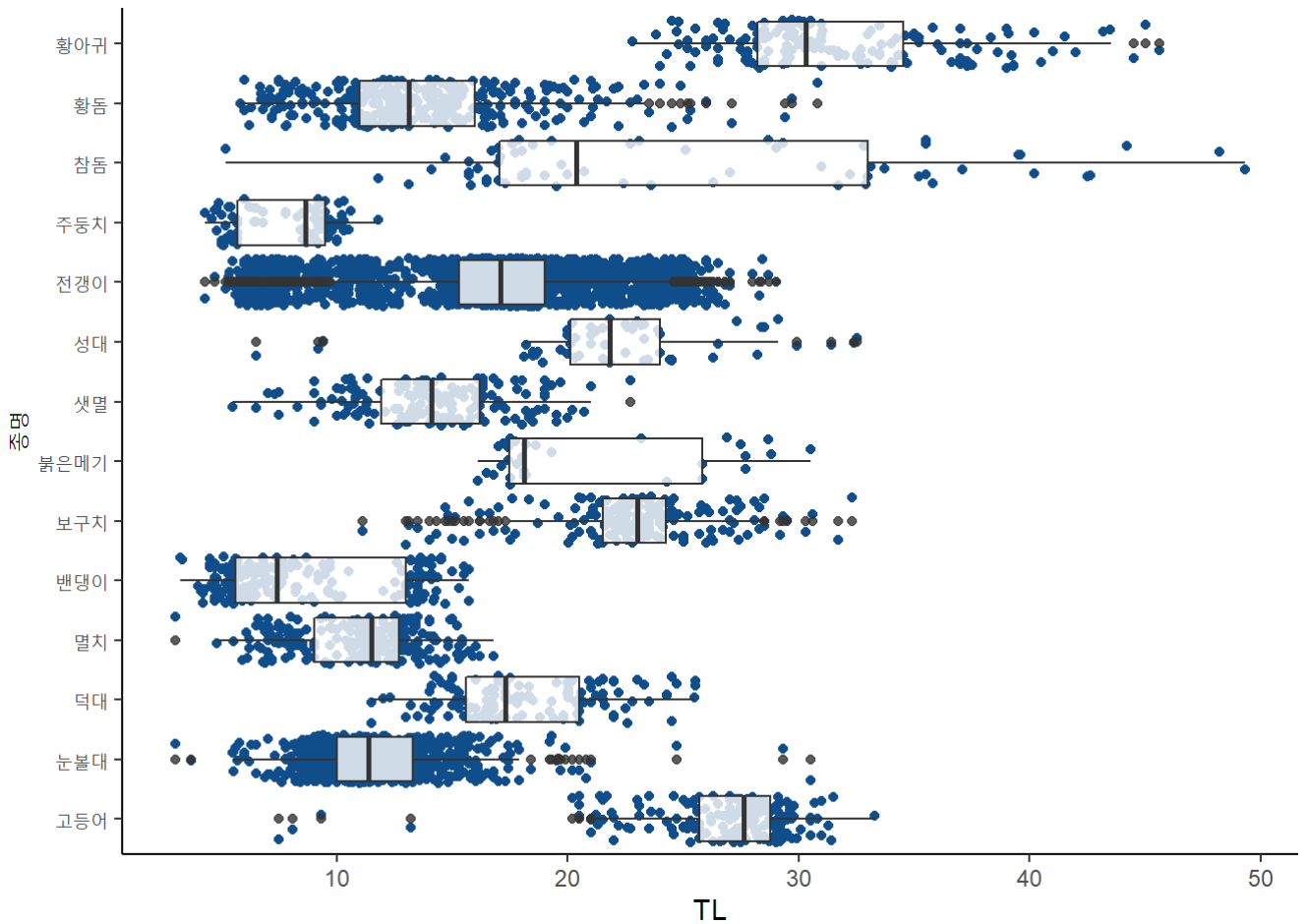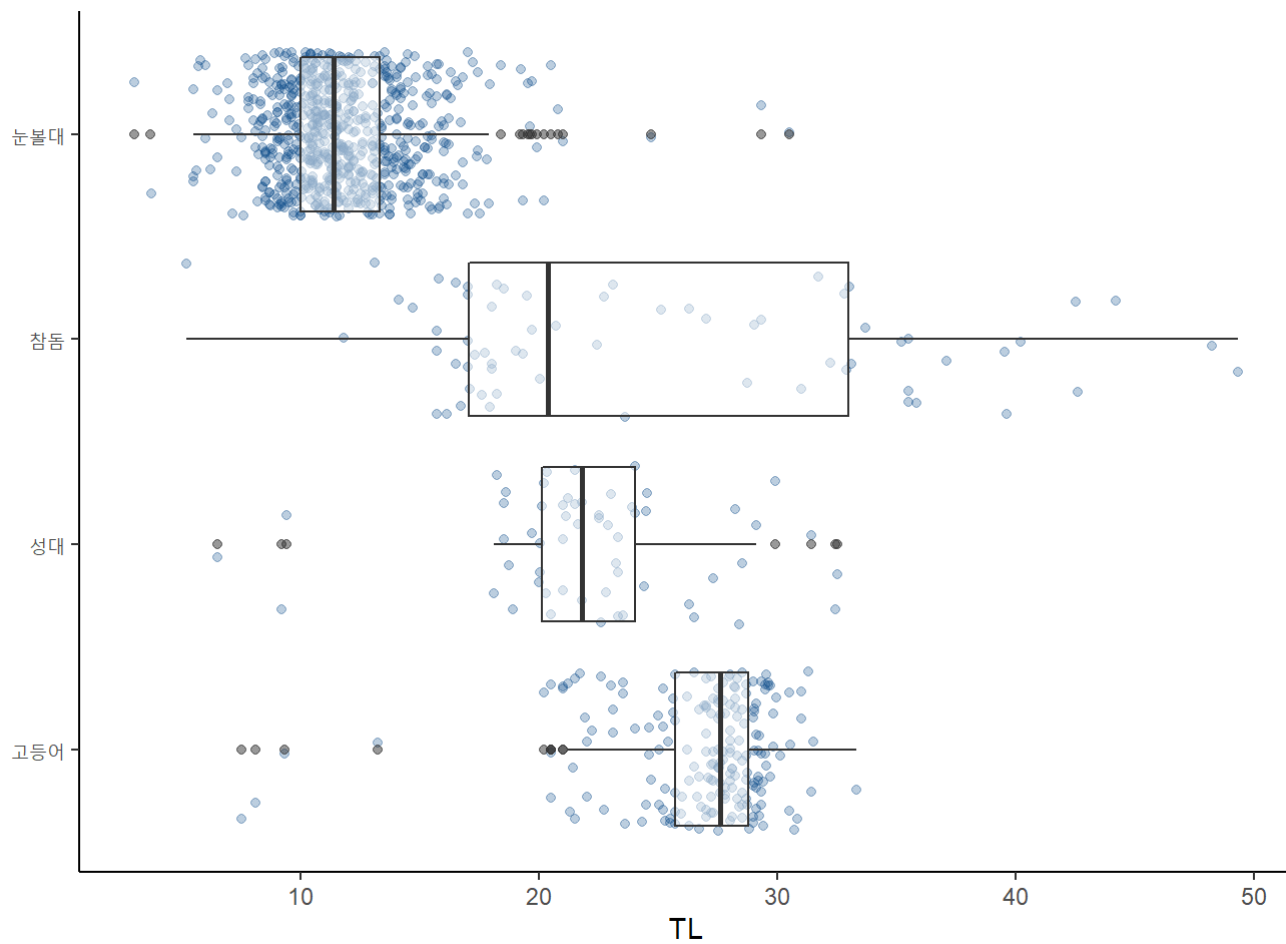


```
fish %>% ggplot(aes(종명,log(BW))) + geom_jitter(col='dodgerblue4') + geom_boxplot(alpha=.8) +
 theme_classic()+ coord_flip()+ labs(x="",y="log WW")
```

이제부터는 6가지 기준에 의하여 선정된 고등어, 눈볼대, 참돔, 성대 4종에 관하여 살펴보겠다.

```
a = merge(go,cham,all=T)
b = merge(a, nun,all=T)
c = merge(b, sung, all=T)
c %>% ggplot(aes(fct_reorder(종명, TL,.desc=T),TL)) + geom_jitter(col='dodgerblue4',alpha=0.28)
+ geom_boxplot(alpha=.5) + theme_classic()+ coord_flip() + labs(x="",y="TL")
```

```
c %>% ggplot(aes(fct_reorder(종명, BW,.desc=T),log(BW))) + geom_jitter(col='dodgerblue4',alpha=
0.28) + geom_boxplot(alpha=.5) + theme_classic()+ coord_flip() + labs(x="",y="log WW")
```
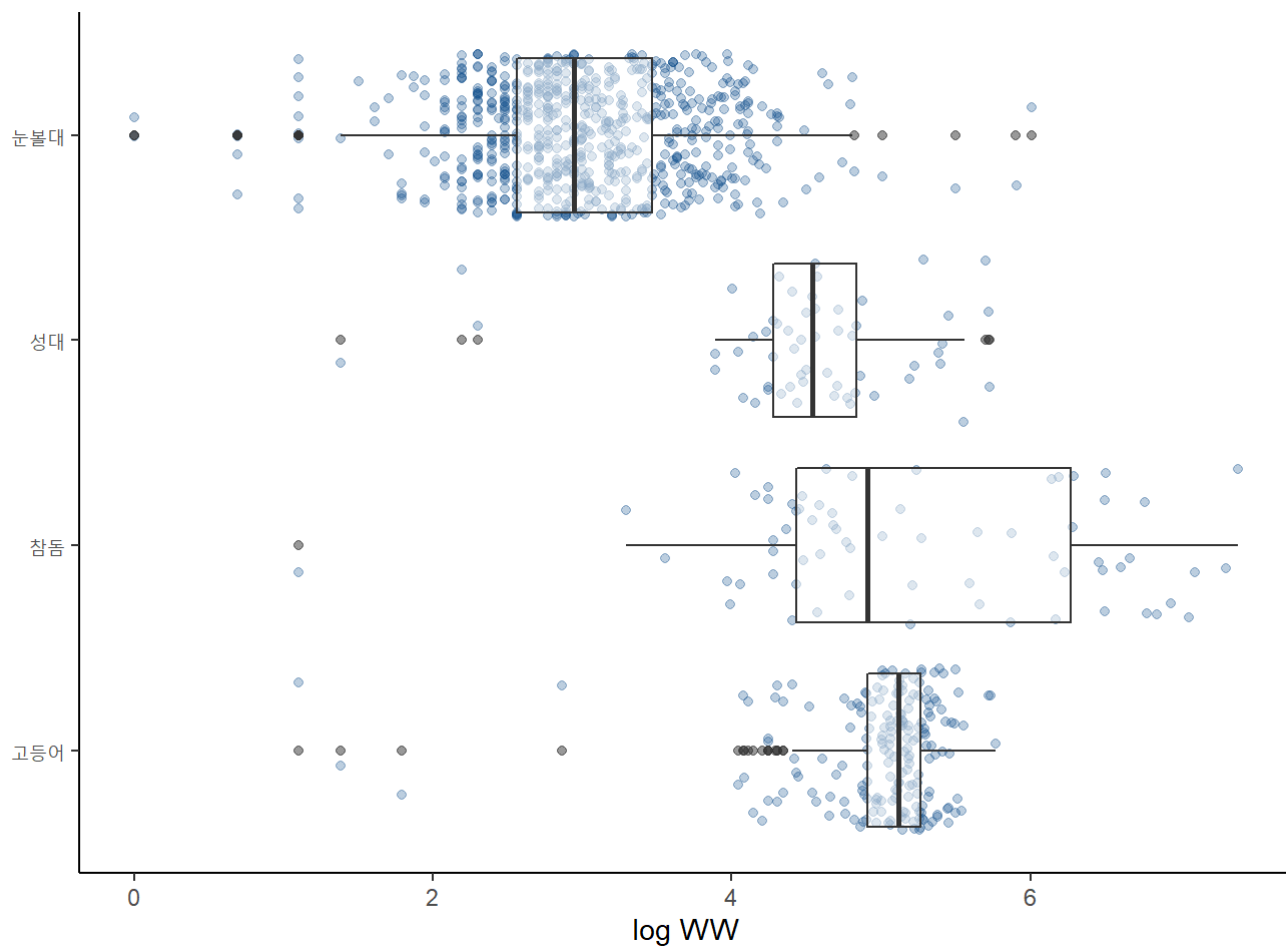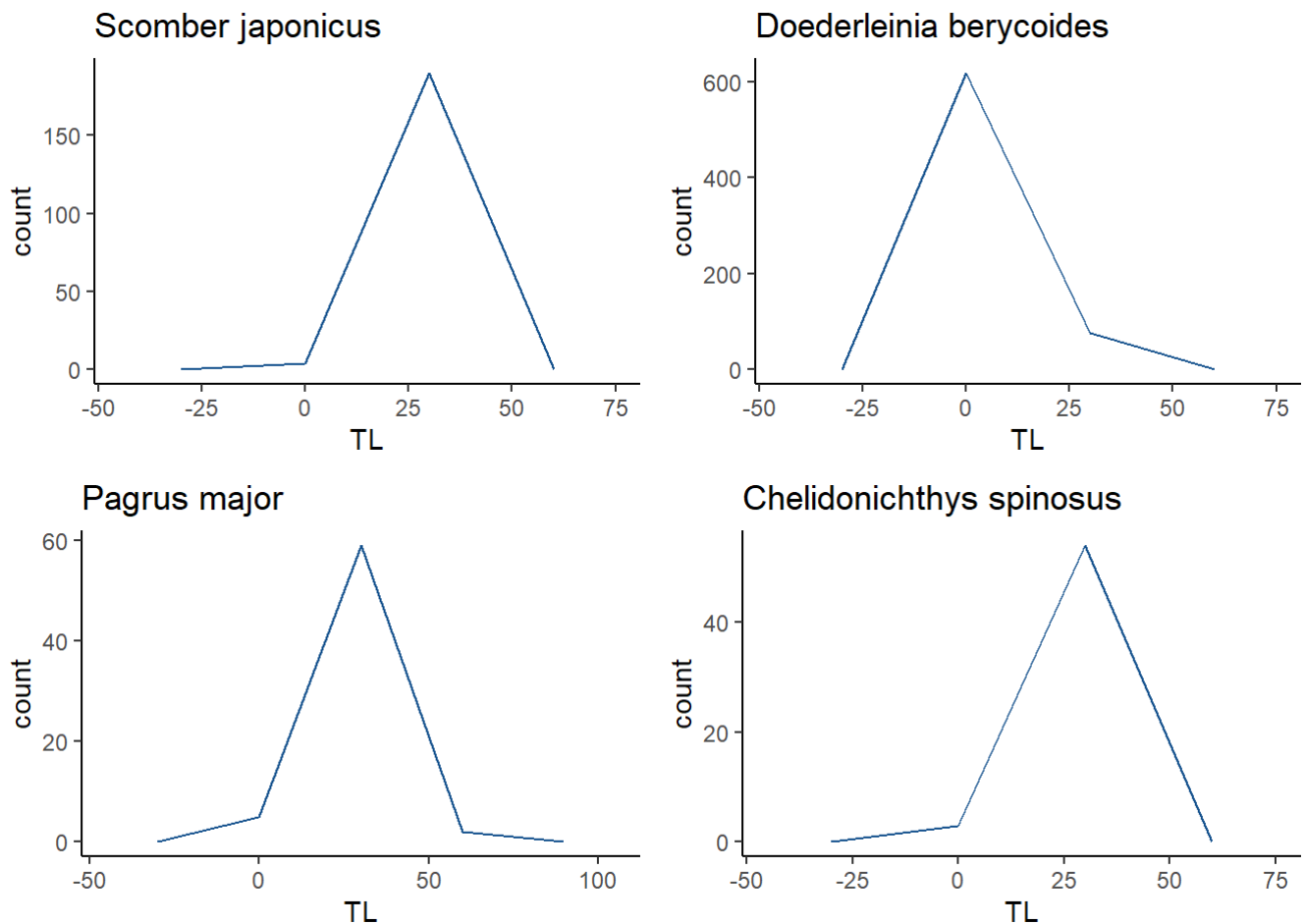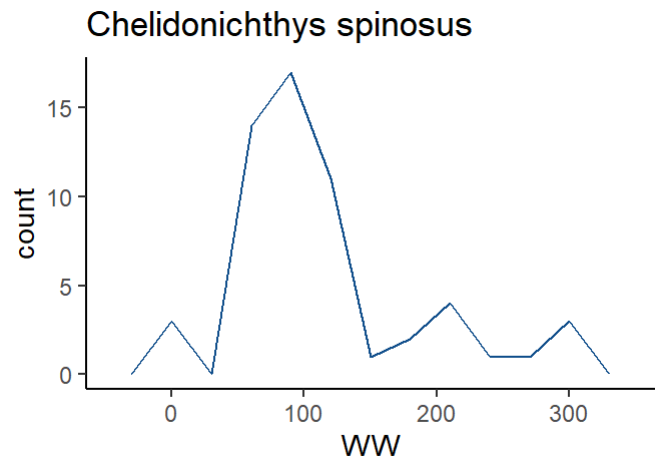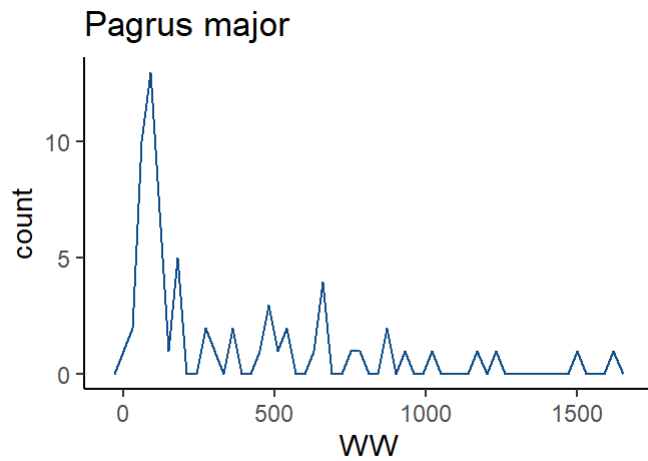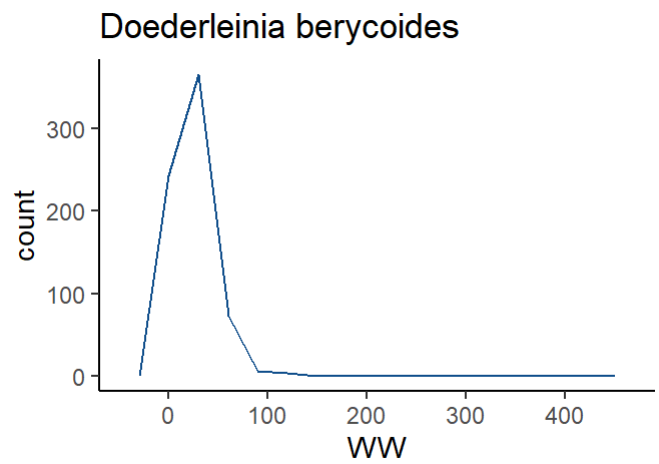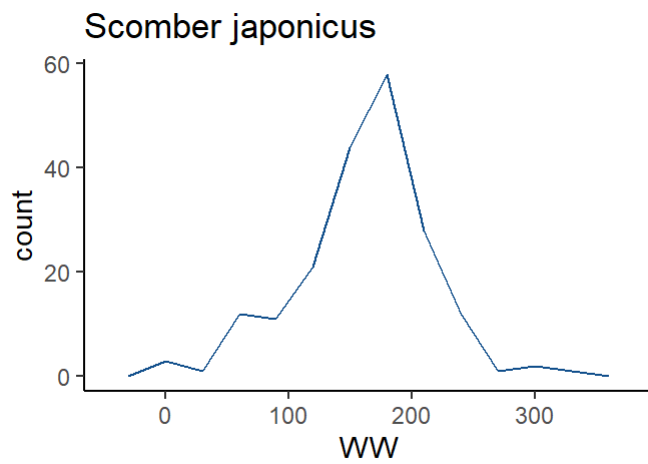
frequency polygon

```
p1 <- go %>% ggplot(aes(TL)) + geom_freqpoly(col="dodgerblue4",binwidth=30) + theme_classic() +
labs(title="Scomber japonicus")
p2 <- nun %>% ggplot(aes(TL)) + geom_freqpoly(col="dodgerblue4",binwidth=30) + theme_classic()
 + labs(title="Doederleinia berycoides")
p3 <- cham %>% ggplot(aes(TL)) + geom_freqpoly(col="dodgerblue4",binwidth=30) + theme_classic()
+ labs(title="Pagrus major")
p4 <- sung %>% ggplot(aes(TL)) + geom_freqpoly(col="dodgerblue4",binwidth=30) + theme_classic()
+ labs(title="Chelidonichthys spinosus")
grid.arrange(p1,p2,p3,p4,ncol=2)
```



```
p1 <- go %>% ggplot(aes(BW)) + geom_freqpoly(col="dodgerblue4",binwidth=30) + theme_classic()+
 labs(title="Scomber japonicus",x="WW")
p2 <- nun %>% ggplot(aes(BW)) + geom_freqpoly(col="dodgerblue4",binwidth=30) + theme_classic()+
labs(title="Doederleinia berycoides",x="WW")
p3 <- cham %>% ggplot(aes(BW)) + geom_freqpoly(col="dodgerblue4",binwidth=30) + theme_classic()
+ labs(title="Pagrus major",x="WW")
p4 <- sung %>% ggplot(aes(BW)) + geom_freqpoly(col="dodgerblue4",binwidth=30) + theme_classic()
+ labs(title="Chelidonichthys spinosus",x="WW")
grid.arrange(p1,p2,p3,p4,ncol=2)
```
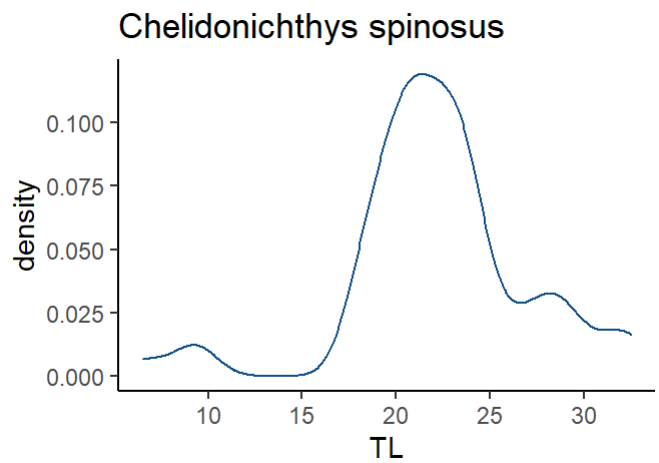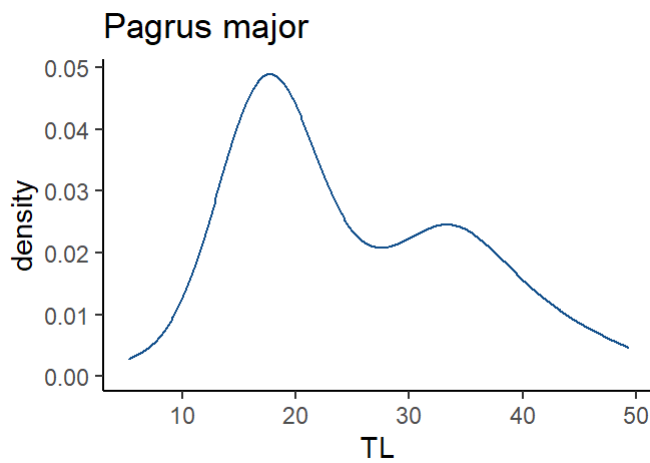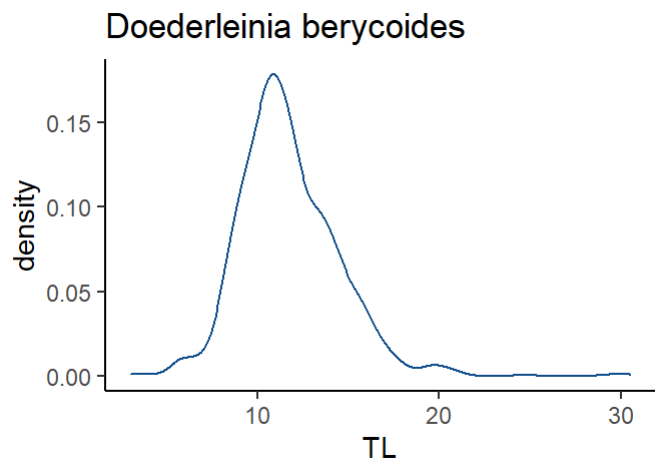
Scomber japonicus

Doederleinia berycoides

Pagrus major

Chelidonichthys spinosus

kernel density estimator

```
p1 <- go %>% ggplot(aes(TL)) + geom_density(col="dodgerblue4") + theme_classic()+ labs(title="S
comber japonicus")
p2 <- nun %>% ggplot(aes(TL)) + geom_density(col="dodgerblue4") + theme_classic()+ theme_classi
c()+ labs(title="Doederleinia berycoides")
p3 <- cham %>% ggplot(aes(TL)) + geom_density(col="dodgerblue4") + theme_classic()+ theme_class
ic()+ labs(title="Pagrus major")
p4 <- sung %>% ggplot(aes(TL)) + geom_density(col="dodgerblue4") + theme_classic()+ theme_class
ic()+ labs(title="Chelidonichthys spinosus")
grid.arrange(p1,p2,p3,p4,ncol=2)
```
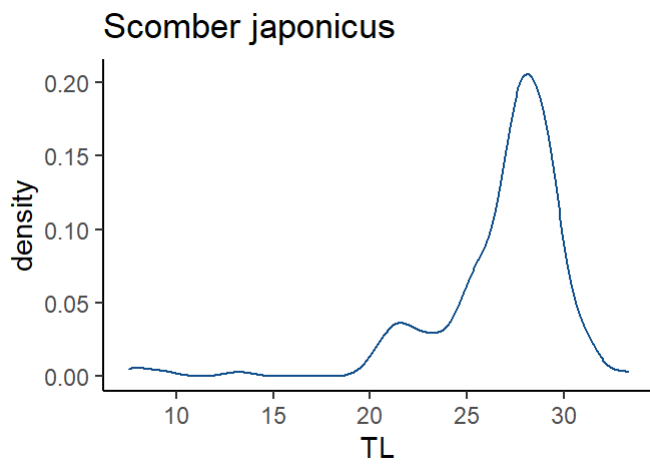
```
p1 <- go %>% ggplot(aes(BW)) + geom_density(col="dodgerblue4") + theme_classic()+ labs(title="S
comber japonicus",x="WW")
p2 <- nun %>% ggplot(aes(BW)) + geom_density(col="dodgerblue4") + theme_classic()+ theme_classi
c()+ labs(title="Doederleinia berycoides",x="WW")
p3 <- cham %>% ggplot(aes(BW)) + geom_density(col="dodgerblue4") + theme_classic()+ theme_class
ic()+ labs(title="Pagrus major",x="WW")
p4 <- sung %>% ggplot(aes(BW)) + geom_density(col="dodgerblue4") + theme_classic()+ theme_class
ic()+ labs(title="Chelidonichthys spinosus",x="WW")
grid.arrange(p1,p2,p3,p4,ncol=2)
```
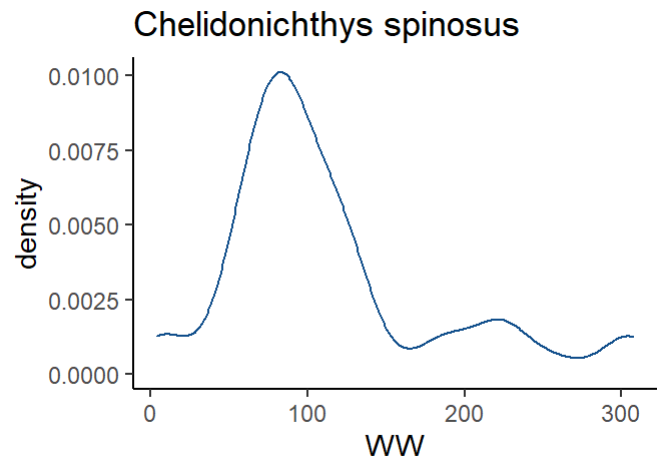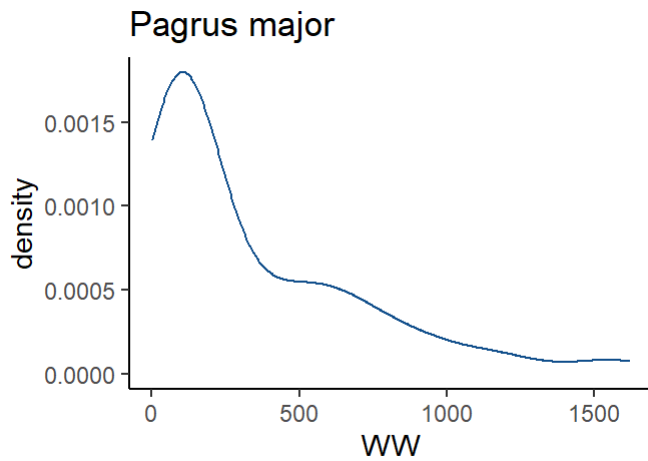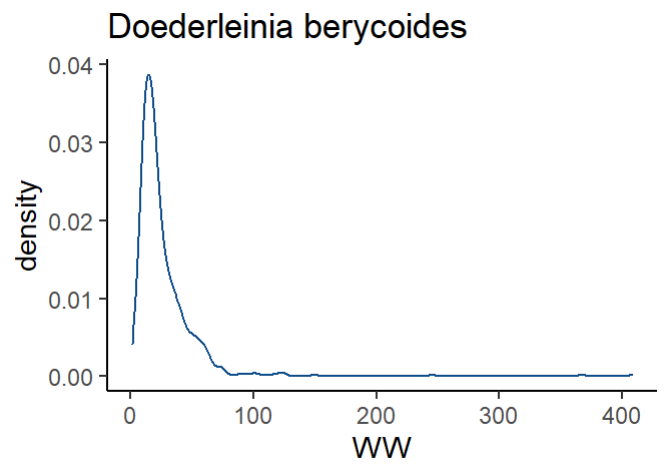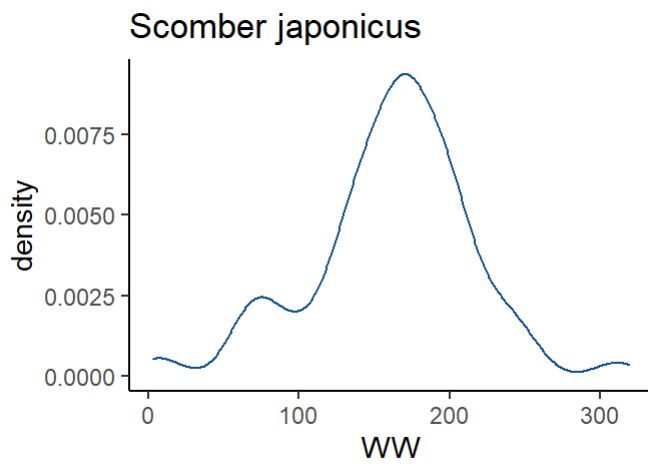
Scomber japonicus

Doederleinia berycoides

Pagrus major

Chelidonichthys spinosus

scatterplot

```
par(mfrow=c(2,2))
plot(go$TL ,go$BW, xlab="TL", ylab="WW", pch=19, cex=0.7,main="Scomber japonicus")
plot(nun$TL ,nun$BW, xlab="TL", ylab="WW", pch=19, cex=0.7,main="Doederleinia berycoides")
plot(cham$TL ,cham$BW, xlab="TL", ylab="WW", pch=19, cex=0.7,main="Pagrus major")
plot(sung$TL ,sung$BW, xlab="TL", ylab="WW", pch=19, cex=0.7,main="Chelidonichthys spinosus")
```

Scomber japonicus

Doederleinia berycoides

Pagrus major

Chelidonichthys spinosus
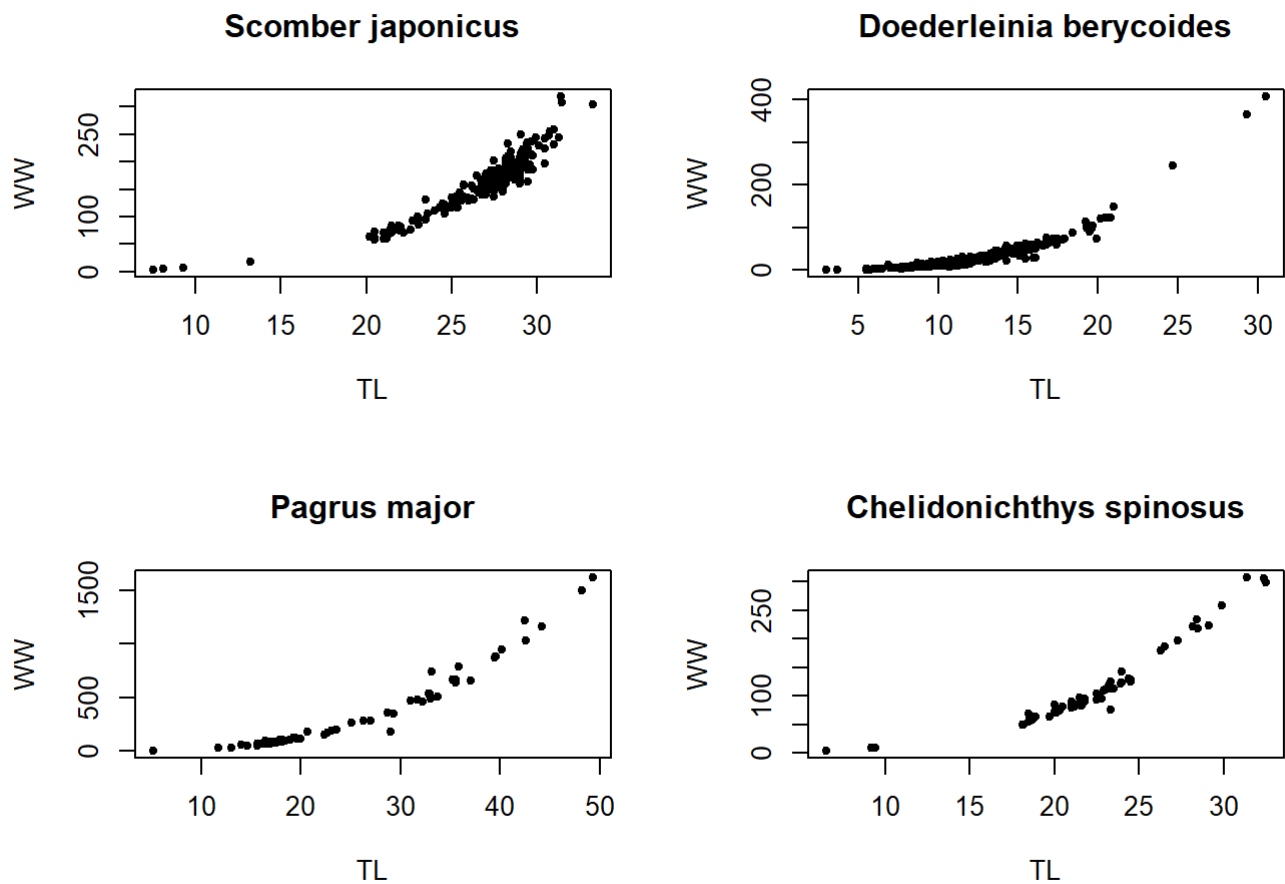
지금까지 데이터의 전체적인 분포를 살펴보았다. 이제부터는 모델 적합에 관하여 살펴보겠다.

linear regression

```
fit_go = lm(log(BW)~log(TL), data=go)
summary(fit_go)
```

```
##
## Call:
## lm(formula = log(BW) ~ log(TL), data = go)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.23335 -0.07535  0.01035  0.06340  0.24977
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -5.24566    0.12435  -42.19   <2e-16 ***
## log(TL)      3.12579    0.03792   82.43   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.09662 on 192 degrees of freedom
## Multiple R-squared:  0.9725, Adjusted R-squared:  0.9724
## F-statistic:  6795 on 1 and 192 DF,  p-value: < 2.2e-16
```

log a = -5.24566, b = 3.12579, R-squared : 0.9725

outlier 검토

```
# Scomber japonicus
go2 <- go
par(mfrow=c(1,2))
boxplot(go2$TL,main="TL",col="dodgerblue4")
boxplot(go2$BW,main="WW",col="dodgerblue4")
```
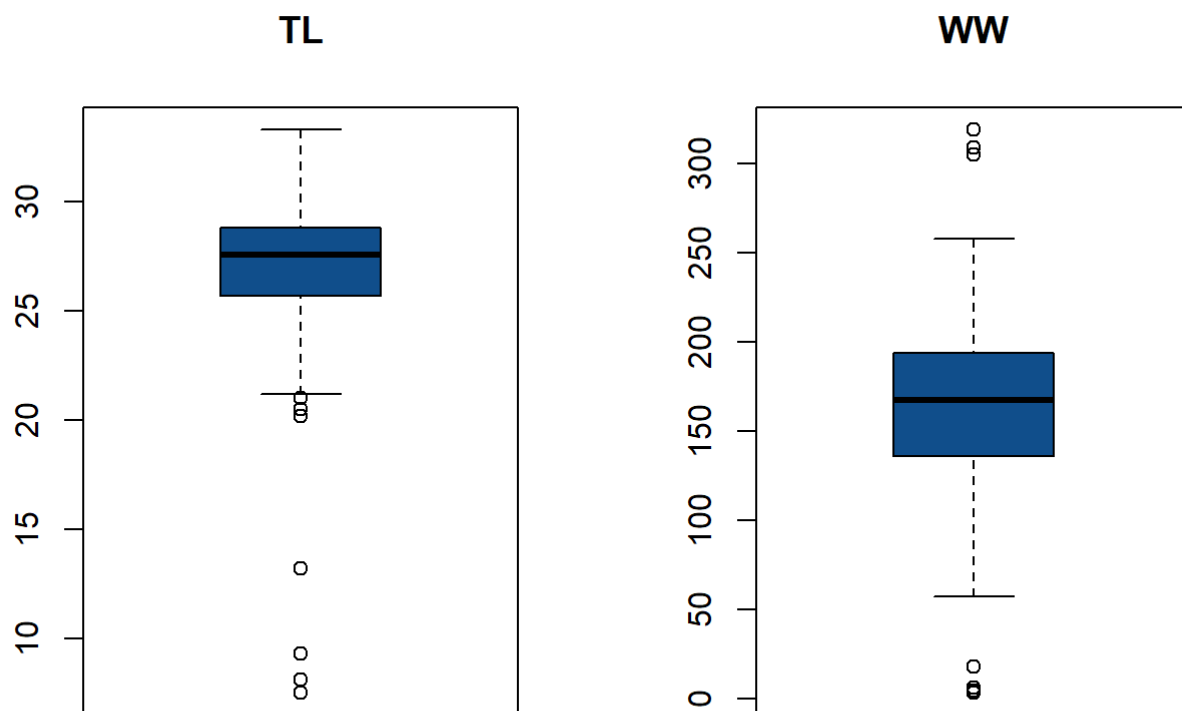


```
boxplot.stats(go2$BW)$out
```

```
## [1]    6.0    4.0    3.0 305.0 319.0 309.0   17.5
```

```
boxplot.stats(go2$TL)$out
```

```
##  [1] 21.0 20.5 21.0 20.5 20.5  9.3  8.1  7.5 13.2 20.2
```

```
out.val <- boxplot.stats(go2$BW)$out
go2$BW[go2$BW %in% out.val] <- NA
go2 <- go2[complete.cases(go2),]

out.val <- boxplot.stats(go2$TL)$out
go2$TL[go2$TL %in% out.val] <- NA
go2 <- go2[complete.cases(go2),]

boxplot(go2$TL, horizontal=F,main="TL",col="dodgerblue4")
boxplot(go2$BW, horizontal=F,main="BW", col="dodgerblue4")
```
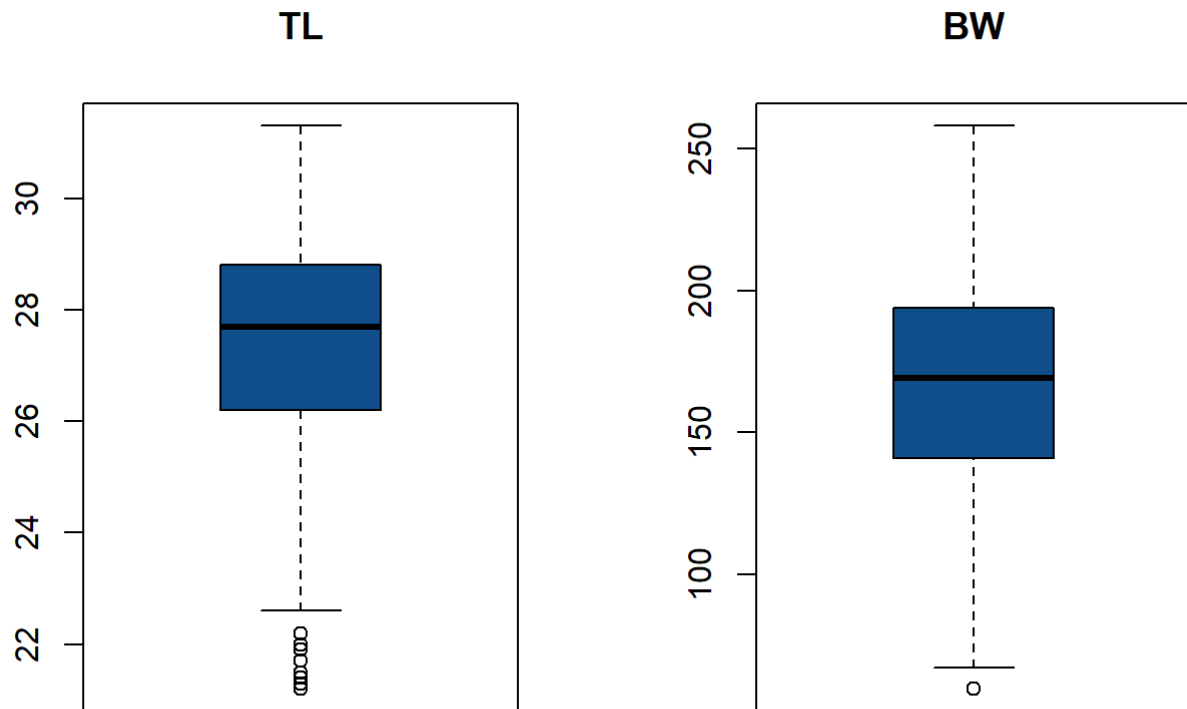


```
dev.off()
```

```
## null device
##            1
```

```
plot(log(go2$TL),log(go2$BW),xlab="log TL",ylab="log WW",main="Scomber japonicus",pch=19,cex=0.
7,col="gray48")
abline(lm(log(go2$BW)~log(go2$TL)), col="dodgerblue4",lwd=2,pch=19,cex=0.8)
```

```
summary(lm(log(go2$BW)~log(go2$TL)))
```

```
##
## Call:
## lm(formula = log(go2$BW) ~ log(go2$TL))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.23861 -0.07396  0.01171  0.06169  0.26321
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -5.53128    0.27248  -20.30   <2e-16 ***
## log(go2$TL)  3.21173    0.08248   38.94   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.09435 on 179 degrees of freedom
## Multiple R-squared:  0.8944, Adjusted R-squared:  0.8938
## F-statistic:  1516 on 1 and 179 DF,  p-value: < 2.2e-16
```

특이값(치어)을 제거한 결과 결정계수가 0.8944로 낮아짐을 확인할 수 있다.

parametric regression vs non-parametric regression

```
# example : Scomber japonicus TL = 8.1
# lowess curve
library(msir)
low_go <- loess.sd(go$TL,go$BW, nsigma = 1.96)
plot(go$TL,go$BW,xlab="TL",ylab="WW",pch=19,cex=0.7,col="gray48",main="Scomber japonicus")
lines(low_go$x, low_go$y)
lines(low_go$x, low_go$upper, lty="dashed",col="dodgerblue4",lwd=2)
lines(low_go$x, low_go$lower, lty="dashed",col="dodgerblue4",lwd=2)
```

Scomber japonicus
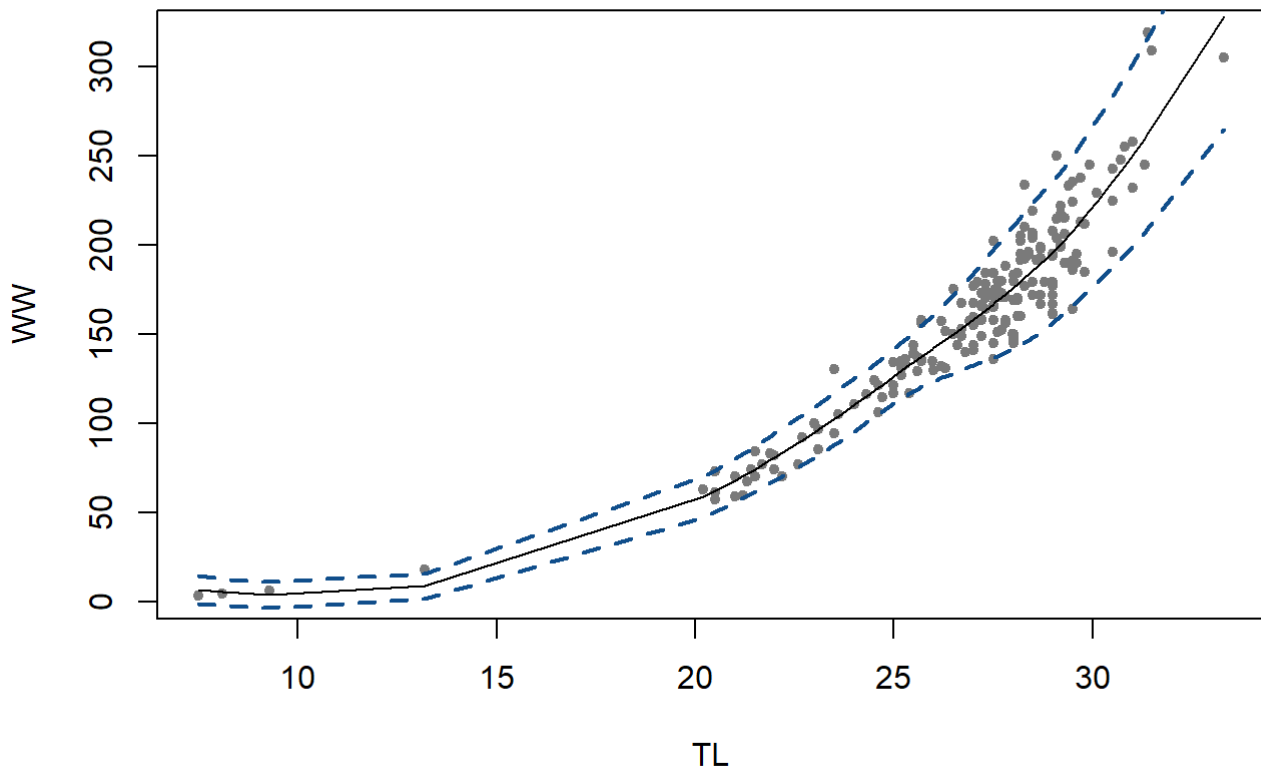

```
# confidence interval for lowess
golow = loess(BW~TL,data=go)
plx <- predict(golow, newdata = data.frame(TL=21), se=T)
lowe_fit <- c(plx$fit)
lowe_lwr <- c(plx$fit - qt(0.975,plx$df)*plx$se)
lowe_upr <- c(plx$fit + qt(0.975,plx$df)*plx$se)
lowe_conf <- data.frame(lowe_fit,lowe_lwr,lowe_upr)
lowe_conf
```

```
##   lowe_fit lowe_lwr lowe_upr
## 1 67.94269 61.17197 74.71342
```

```
# confidence interval for linear regression
exp(predict(fit_go, newdata = data.frame(TL=21), interval="confidence"))
```

```
##        fit      lwr      upr
## 1 71.58341 70.02853 73.17282
```

lowess가 linear regression보다 더 큰 신뢰구간을 보인다. 또한 linear regression 결과 적합이 잘 된 것을 확인할 수 있으므로 체장-체중 데이터에 대한 linear regression을 수행한다.

linear regression with ANOVA

Scomber japonicus

```
fit_go = lm(log(BW)~log(TL), data=go)
summary(fit_go)
```

```
##
## Call:
## lm(formula = log(BW) ~ log(TL), data = go)
##
## Residuals:
##       Min       1Q   Median       3Q      Max
## -0.23335 -0.07535  0.01035  0.06340  0.24977
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -5.24566    0.12435  -42.19   <2e-16 ***
## log(TL)      3.12579    0.03792   82.43   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.09662 on 192 degrees of freedom
## Multiple R-squared:  0.9725, Adjusted R-squared:  0.9724
## F-statistic:  6795 on 1 and 192 DF,  p-value: < 2.2e-16
```

```
anova(fit_go)
```

```
## Analysis of Variance Table
##
## Response: log(BW)
##            Df Sum Sq Mean Sq F value     Pr(>F)
## log(TL)     1 63.431  63.431  6795.3 < 2.2e-16 ***
## Residuals 192  1.792   0.009
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

log a = -5.24566, b = 3.12579, R-squared : 0.9725

Doederleinia berycoides

```
fit_nun = lm(log(BW)~log(TL), data=nun)
summary(fit_nun)
```

```
##
## Call:
## lm(formula = log(BW) ~ log(TL), data = nun)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.75730 -0.07620  0.00915  0.08819  0.96007
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -4.13102    0.06628  -62.33   <2e-16 ***
## log(TL)      2.92819    0.02708  108.15   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1682 on 692 degrees of freedom
## Multiple R-squared:  0.9441, Adjusted R-squared:  0.9441
## F-statistic: 1.17e+04 on 1 and 692 DF,  p-value: < 2.2e-16
```

```
anova(fit_nun)
```

```
## Analysis of Variance Table
##
## Response: log(BW)
##            Df Sum Sq Mean Sq F value    Pr(>F)
## log(TL)     1 330.76  330.76   11696 < 2.2e-16 ***
## Residuals 692  19.57    0.03
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

log a = -4.13102, b = 2.92819, R-squared : 0.9441

Pagrus major

```
fit_cham = lm(log(BW)~log(TL), data=cham)
summary(fit_cham)
```

```
##
## Call:
## lm(formula = log(BW) ~ log(TL), data = cham)
##
## Residuals:
##      Min      1Q   Median      3Q     Max
## -0.69655 -0.04677 -0.00224  0.04322  0.34016
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -3.59768    0.12280  -29.30   <2e-16 ***
## log(TL)      2.81910    0.03881   72.63   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1301 on 64 degrees of freedom
## Multiple R-squared:  0.988,  Adjusted R-squared:  0.9878
## F-statistic:  5275 on 1 and 64 DF,  p-value: < 2.2e-16
```

```
anova(fit_cham)
```

```
## Analysis of Variance Table
##
## Response: log(BW)
##           Df Sum Sq Mean Sq F value    Pr(>F)
## log(TL)    1 89.248  89.248  5275.3 < 2.2e-16 ***
## Residuals 64  1.083   0.017
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

log a = -3.59768, b = 2.81910, R-squared : 0.988

Chelidonichthys spinosus

```
fit_sung = lm(log(BW)~log(TL), data=sung)
summary(fit_sung)
```

```
##
## Call:
## lm(formula = log(BW) ~ log(TL), data = sung)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.40974 -0.06524  0.00145  0.06271  0.20972
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -4.04875    0.15522  -26.08   <2e-16 ***
## log(TL)      2.79160    0.05034   55.45   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1035 on 55 degrees of freedom
## Multiple R-squared:  0.9824, Adjusted R-squared:  0.9821
## F-statistic:  3075 on 1 and 55 DF,  p-value: < 2.2e-16
```

```
anova(fit_sung)
```

```
## Analysis of Variance Table
##
## Response: log(BW)
##           Df Sum Sq Mean Sq F value    Pr(>F)
## log(TL)    1 32.967  32.967  3074.8 < 2.2e-16 ***
## Residuals 55  0.590   0.011
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
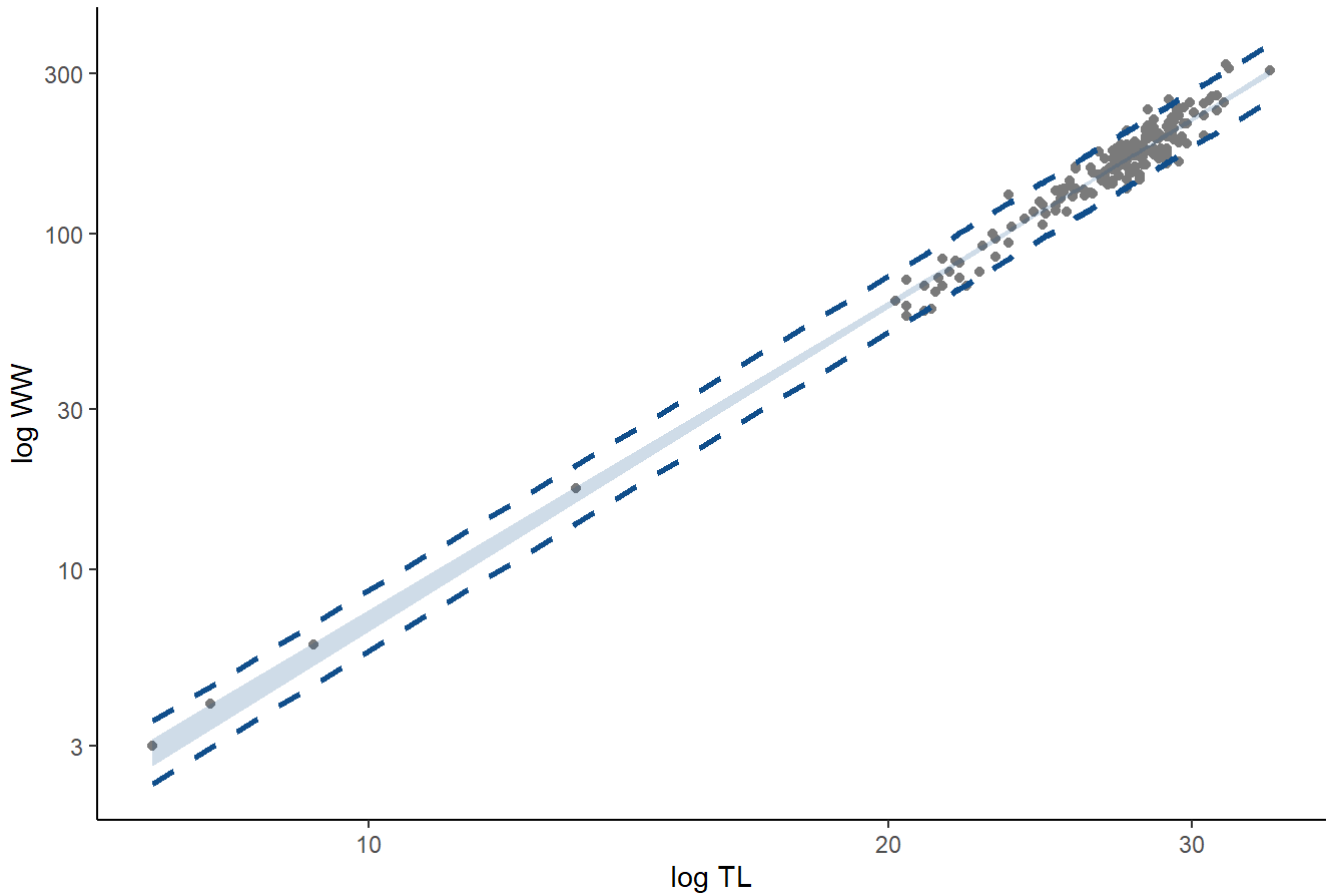
log a = -4.04875, b = 2.79160, R-squared : 0.9824

confidence interval and prediction interval

Scomber japonicus

```
go$pred.lwr<-predict(fit_go, interval="prediction")[,2]
go$pred.upr<-predict(fit_go, interval="prediction")[,3]
go$conf.lwr<-predict(fit_go, interval="confidence")[,2]
go$conf.upr<-predict(fit_go, interval="confidence")[,3]
z = seq(0, 33.3, length = 194)
coef = fit_go$coefficients
ahat = coef[1]
bhat = coef[2]
ggplot(data = go,aes(x=TL,y=BW))+
  geom_point(col="gray48")+ theme_classic()+
  geom_ribbon(aes(ymin=exp(conf.lwr),ymax=exp(conf.upr)),fill="dodgerblue4",alpha=0.2)+
  geom_line(aes(y=exp(pred.lwr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  geom_line(aes(y=exp(pred.upr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  scale_x_log10() + scale_y_log10()+ labs(x="log TL",y="log WW",title="Scomber japonicus")
```

Scomber japonicus

```
z = seq(0, 33.3, length = 194)
coef = fit_go$coefficients
ahat = exp(coef[1])
bhat = coef[2]

go$pred.lwr<-predict(fit_go, interval="prediction")[,2]
go$pred.upr<-predict(fit_go, interval="prediction")[,3]
go$conf.lwr<-predict(fit_go, interval="confidence")[,2]
go$conf.upr<-predict(fit_go, interval="confidence")[,3]

ggplot(data = go, aes(TL,BW)) + geom_point(col="gray48")+
  theme_classic()+ labs(x="TL",y="WW",title="Scomber japonicus")+
  geom_line(aes(z, ahat*z^(bhat)),col="black",size=0.8)+
  geom_line(aes(y=exp(pred.lwr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  geom_line(aes(y=exp(pred.upr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  geom_ribbon(aes(ymin=exp(conf.lwr),ymax=exp(conf.upr)),fill="dodgerblue4",alpha=0.3)
```
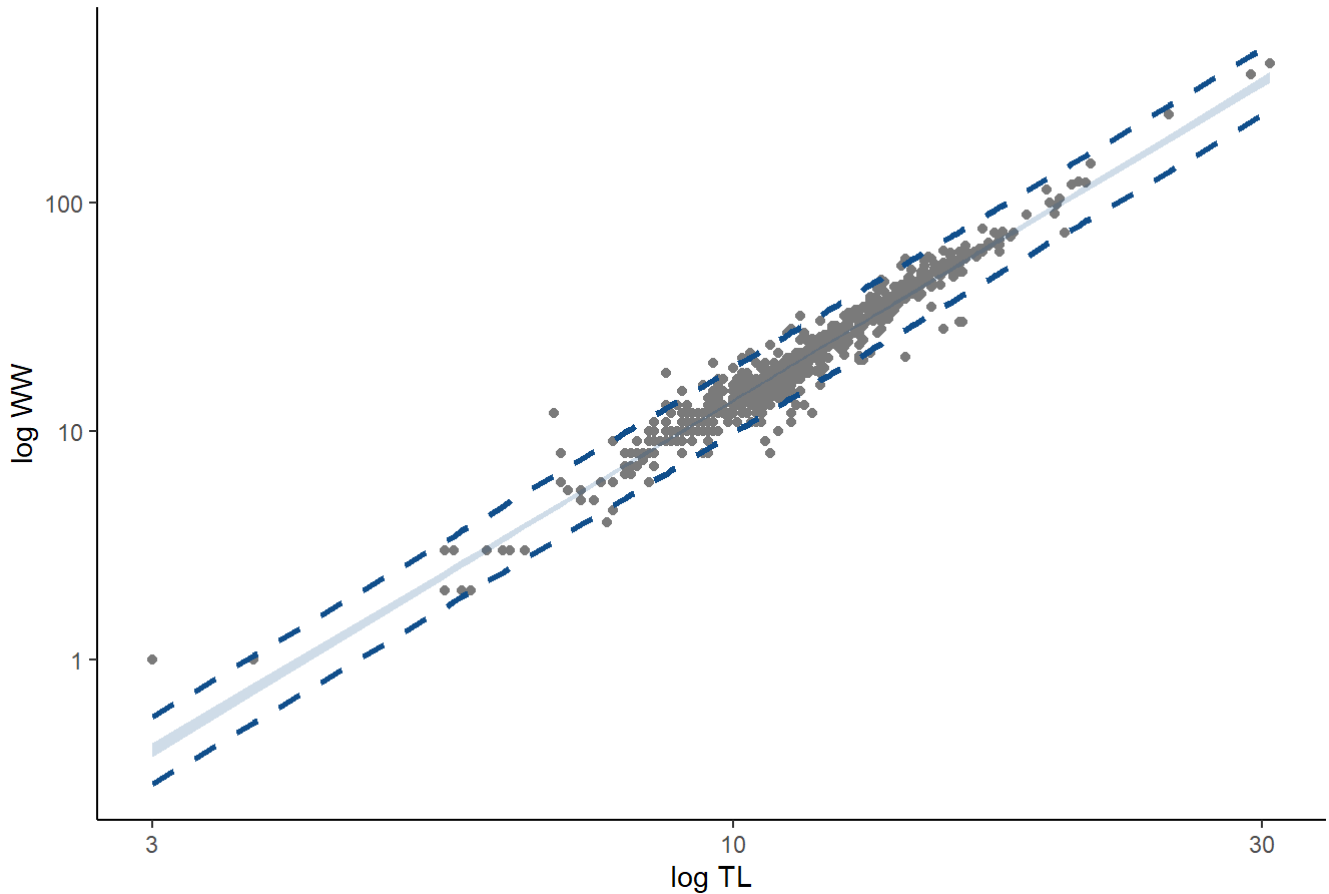
Scomber japonicus
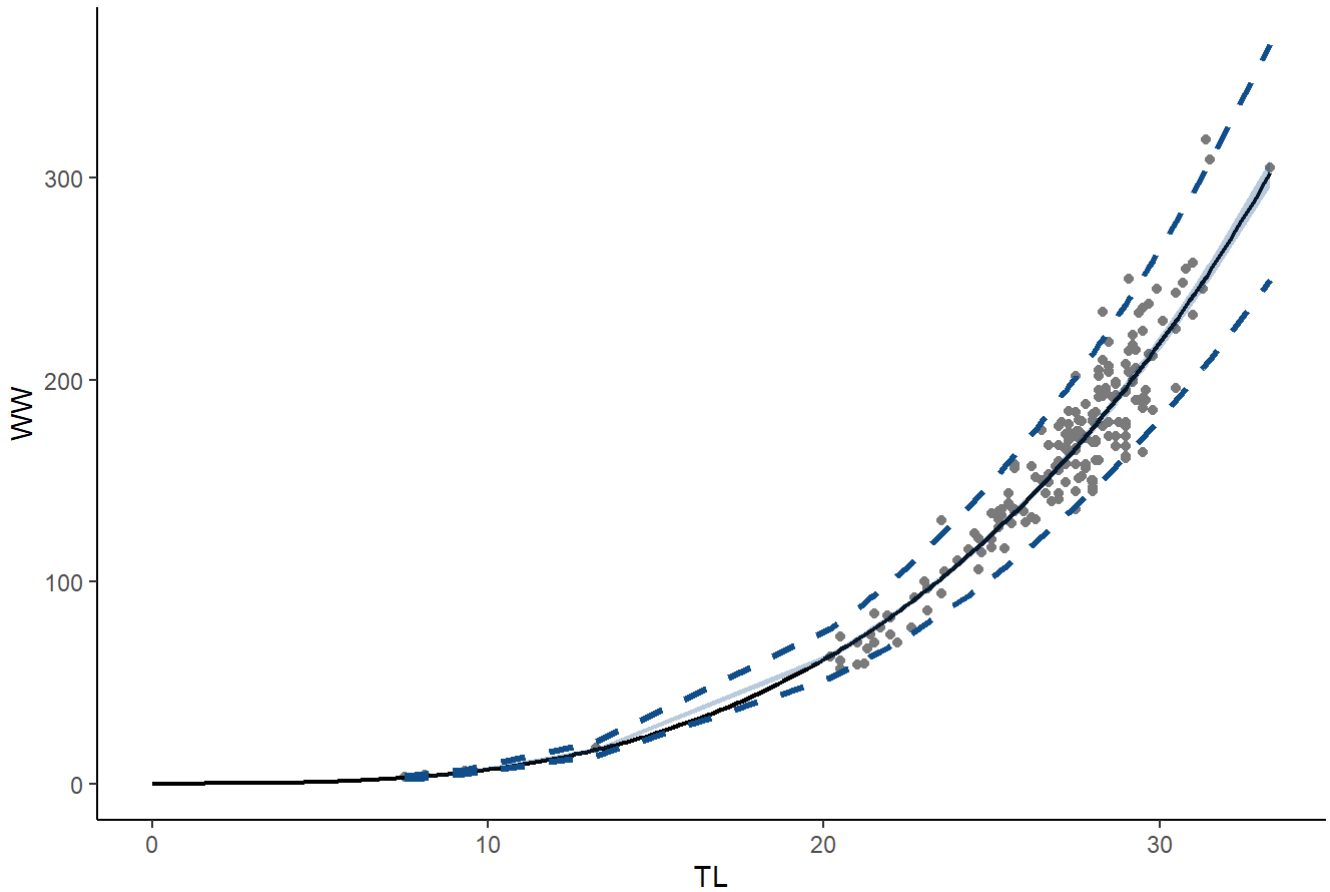
Doederleinia berycoides

```
nun$pred.lwr<-predict(fit_nun, interval="prediction")[,2]
nun$pred.upr<-predict(fit_nun, interval="prediction")[,3]
nun$conf.lwr<-predict(fit_nun, interval="confidence")[,2]
nun$conf.upr<-predict(fit_nun, interval="confidence")[,3]

coef = fit_nun$coefficients
ahat = coef[1]
bhat = coef[2]

ggplot(data = nun,aes(x=TL,y=BW))+
  geom_point(col="gray48")+
  geom_ribbon(aes(ymin=exp(conf.lwr),ymax=exp(conf.upr)),fill="dodgerblue4",alpha=0.2)+
  geom_line(aes(y=exp(pred.lwr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  geom_line(aes(y=exp(pred.upr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  scale_x_log10() + scale_y_log10() + theme_classic() +labs(x="log TL",y="log WW",title="Doeder
leinia berycoides")
```

Doederleinia berycoides


```
z = seq(0, 30.5, length = 694)
coef = fit_nun$coefficients
ahat = exp(coef[1])
bhat = coef[2]

nun$pred.lwr<-predict(fit_nun, interval="prediction")[,2]
nun$pred.upr<-predict(fit_nun, interval="prediction")[,3]
nun$conf.lwr<-predict(fit_nun, interval="confidence")[,2]
nun$conf.upr<-predict(fit_nun, interval="confidence")[,3]

ggplot(data = nun, aes(TL,BW)) + geom_point(col="gray48")+
  theme_classic()+ labs(x="TL",y="WW",title="Doederleinia berycoides")+
  geom_line(aes(z, ahat*z^(bhat)),col="black",size=0.8)+
  geom_line(aes(y=exp(pred.lwr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  geom_line(aes(y=exp(pred.upr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  geom_ribbon(aes(ymin=exp(conf.lwr),ymax=exp(conf.upr)),fill="dodgerblue4",alpha=0.3)
```
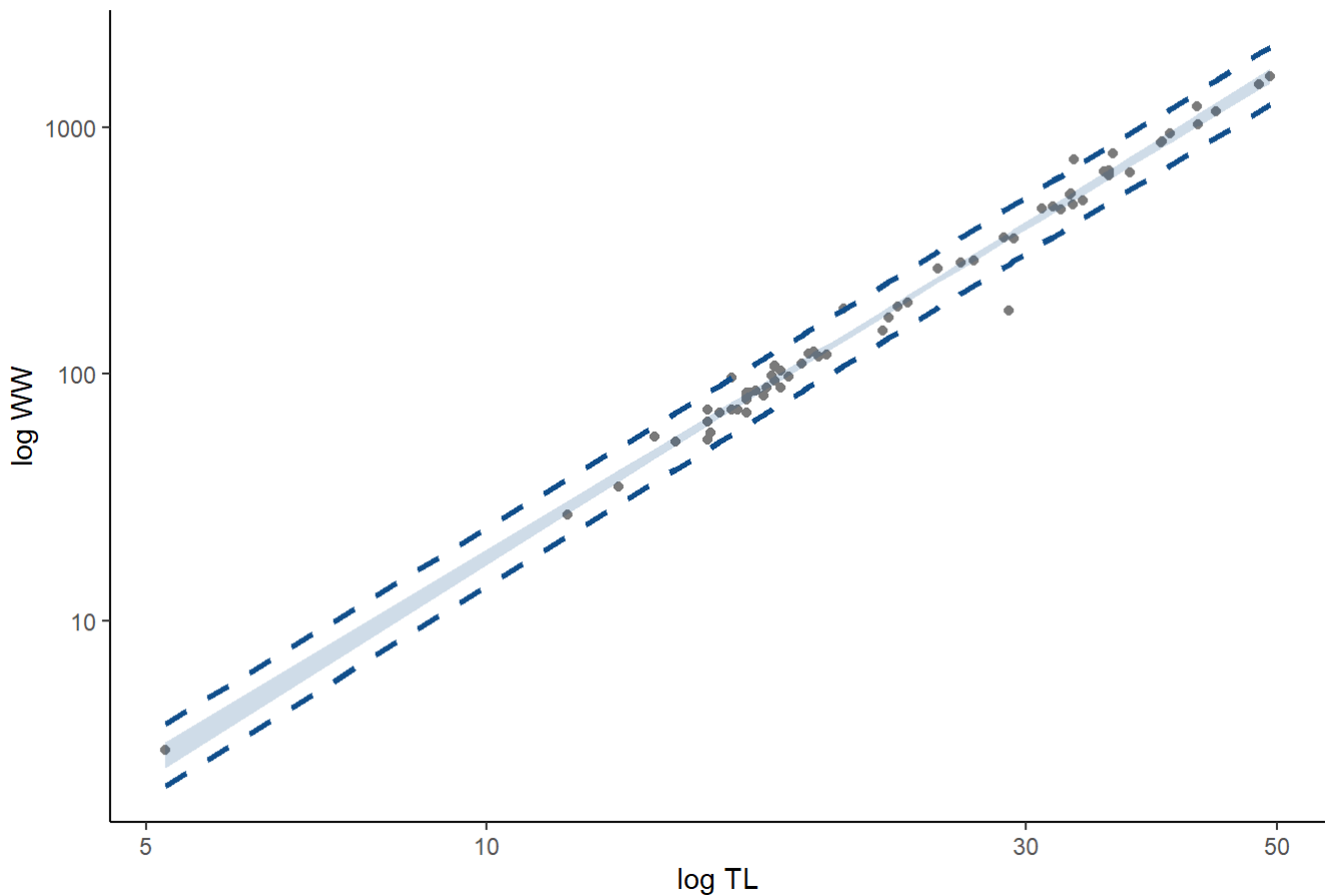
Doederleinia berycoides
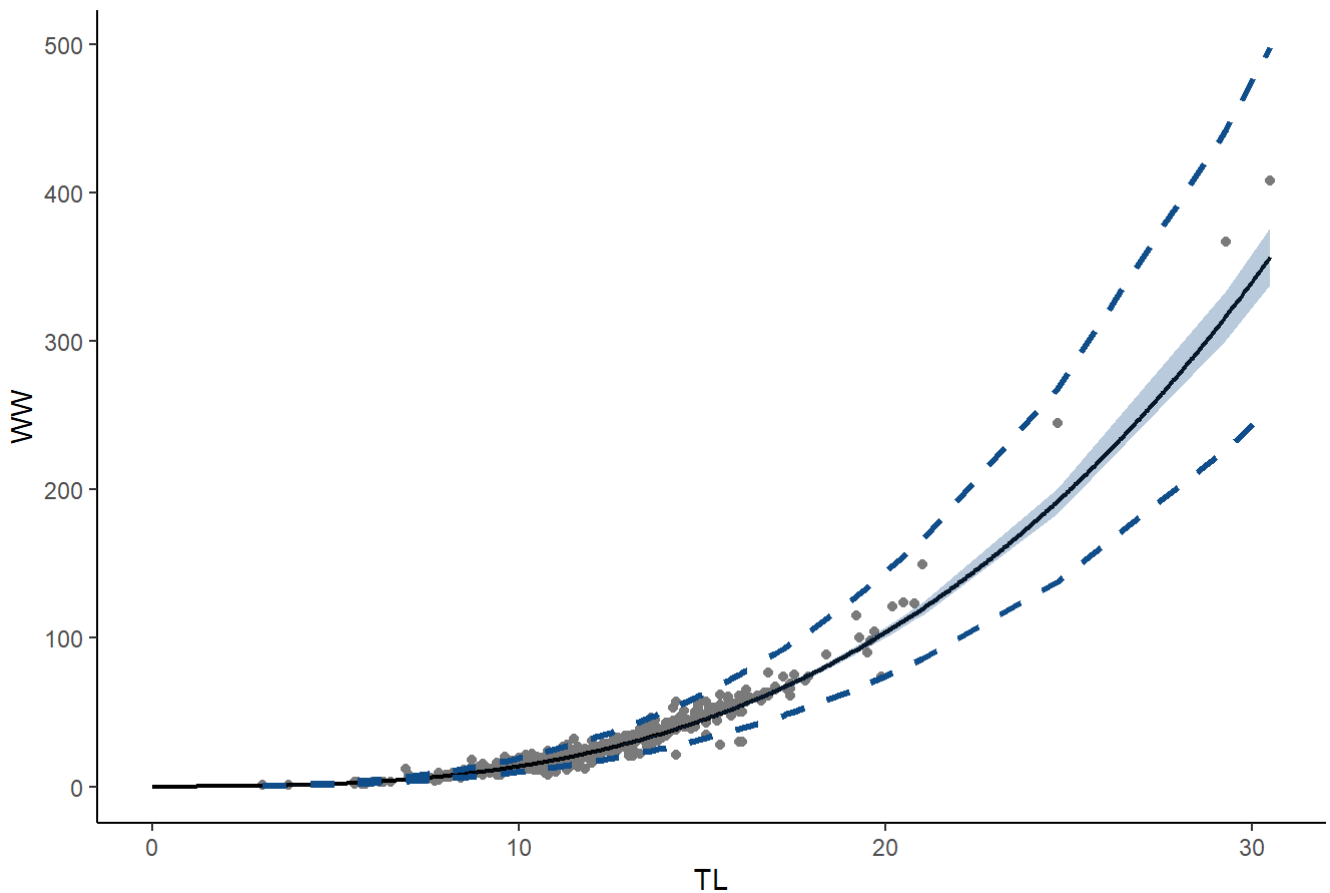
Pagrus major

```
cham$pred.lwr<-predict(fit_cham, interval="prediction")[,2]
cham$pred.upr<-predict(fit_cham, interval="prediction")[,3]
cham$conf.lwr<-predict(fit_cham, interval="confidence")[,2]
cham$conf.upr<-predict(fit_cham, interval="confidence")[,3]

z = seq(0, 30.5, length = 66)
coef = fit_cham$coefficients
ahat = coef[1]
bhat = coef[2]

ggplot(data = cham,aes(x=TL,y=BW))+
  geom_point(col="gray48")+
  geom_ribbon(aes(ymin=exp(conf.lwr),ymax=exp(conf.upr)),fill="dodgerblue4",alpha=0.2)+
  geom_line(aes(y=exp(pred.lwr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  geom_line(aes(y=exp(pred.upr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  scale_x_log10() + scale_y_log10() + theme_classic() +labs(x="log TL",y="log WW",title="Pagrus
major")
```

Pagrus major


```
z = seq(0, 49.3, length = 66)
coef = fit_cham$coefficients
ahat = exp(coef[1])
bhat = coef[2]
cham$pred.lwr<-predict(fit_cham, interval="prediction")[,2]
cham$pred.upr<-predict(fit_cham, interval="prediction")[,3]
cham$conf.lwr<-predict(fit_cham, interval="confidence")[,2]
cham$conf.upr<-predict(fit_cham, interval="confidence")[,3]
ggplot(data = cham, aes(TL,BW)) + geom_point(col="gray48")+
  theme_classic()+ labs(x="TL",y="WW",title="Pagrus major")+
  geom_line(aes(z, ahat*z^(bhat)),col="black",size=0.8)+
  geom_line(aes(y=exp(pred.lwr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  geom_line(aes(y=exp(pred.upr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  geom_ribbon(aes(ymin=exp(conf.lwr),ymax=exp(conf.upr)),fill="dodgerblue4",alpha=0.3)
```
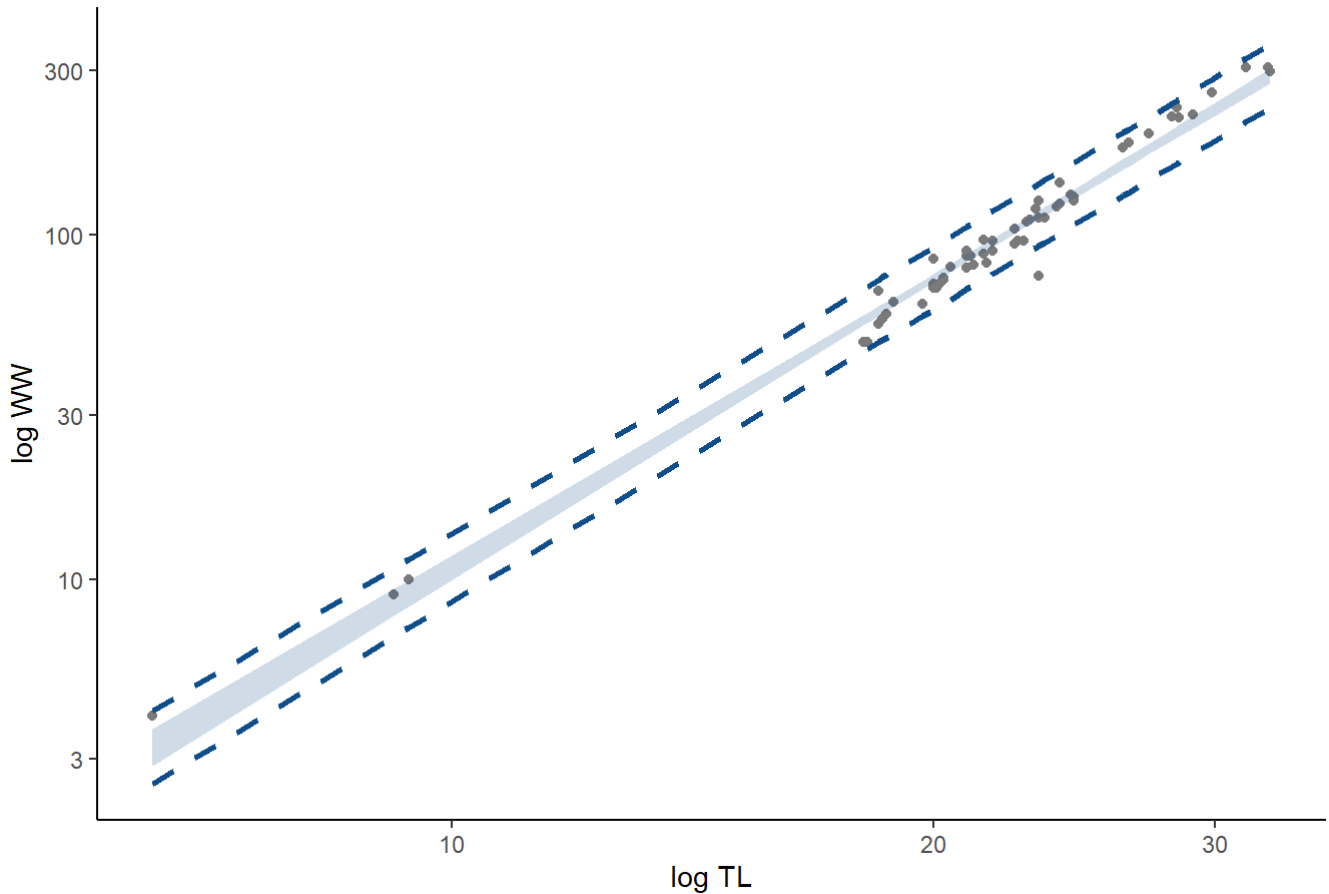
Pagrus major
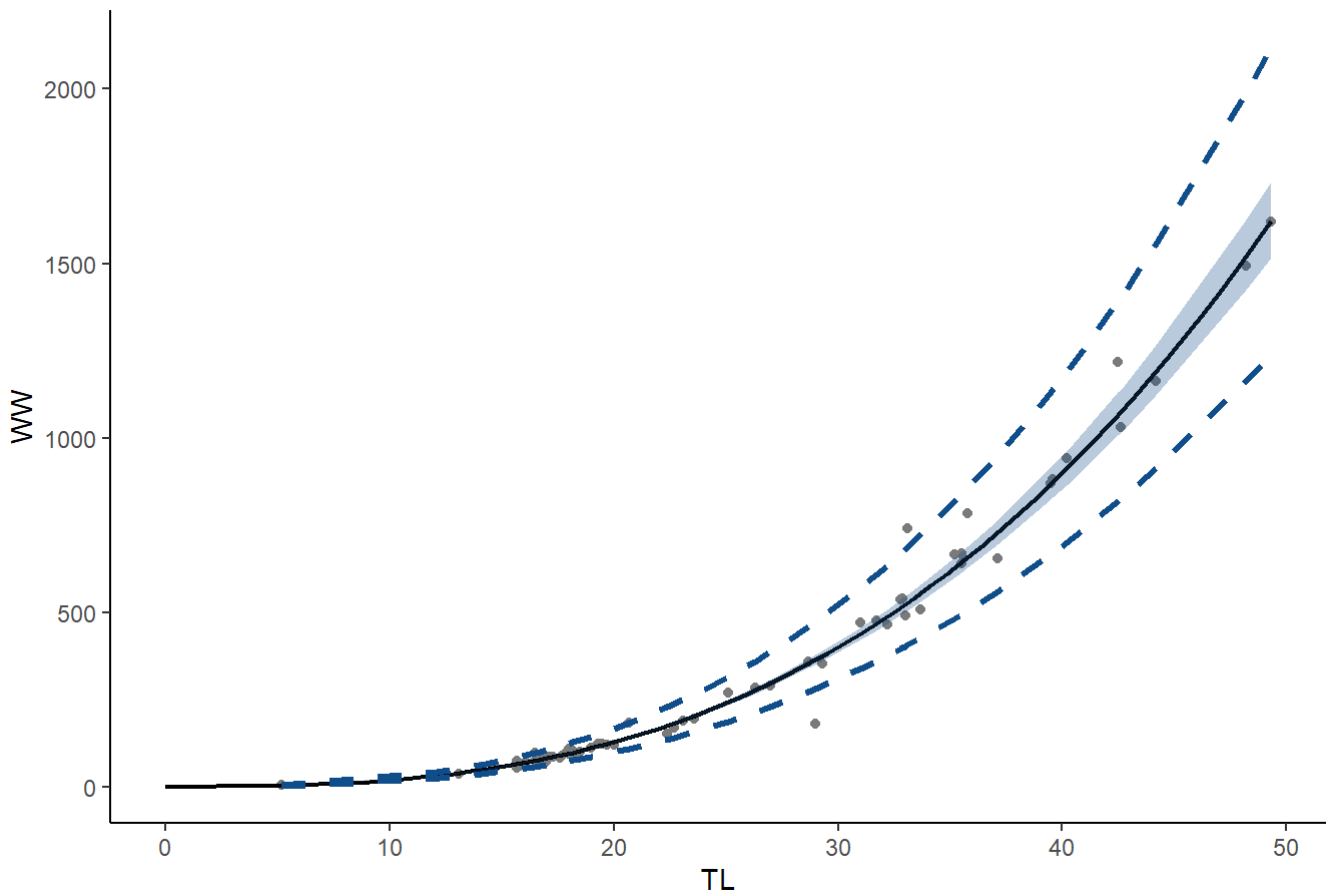
Chelidonichthys spinosus

```
sung$pred.lwr<-predict(fit_sung, interval="prediction")[,2]
sung$pred.upr<-predict(fit_sung, interval="prediction")[,3]
sung$conf.lwr<-predict(fit_sung, interval="confidence")[,2]
sung$conf.upr<-predict(fit_sung, interval="confidence")[,3]

coef = fit_sung$coefficients
ahat = coef[1]
bhat = coef[2]

ggplot(data = sung,aes(x=TL,y=BW))+
  geom_point(col="gray48")+ labs(x="log TL",y="log WW",title="Chelidonichthys spinosus")+
  geom_ribbon(aes(ymin=exp(conf.lwr),ymax=exp(conf.upr)),fill="dodgerblue4",alpha=0.2)+
  geom_line(aes(y=exp(pred.lwr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  geom_line(aes(y=exp(pred.upr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  scale_x_log10() + scale_y_log10() + theme_classic()
```

Chelidonichthys spinosus


```
z = seq(0, 32.5, length = 57)
coef = fit_sung$coefficients
ahat = exp(coef[1])
bhat = coef[2]

sung$pred.lwr<-predict(fit_sung, interval="prediction")[,2]
sung$pred.upr<-predict(fit_sung, interval="prediction")[,3]
sung$conf.lwr<-predict(fit_sung, interval="confidence")[,2]
sung$conf.upr<-predict(fit_sung, interval="confidence")[,3]

ggplot(data = sung, aes(TL,BW)) + geom_point(col="gray48")+
  theme_classic()+ labs(x="TL",y="WW",title="Chelidonichthys spinosus")+
  geom_line(aes(z, ahat*z^(bhat)),col="black",size=0.8)+
  geom_line(aes(y=exp(pred.lwr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  geom_line(aes(y=exp(pred.upr)),col="dodgerblue4",linetype="dashed",size=1.2)+
  geom_ribbon(aes(ymin=exp(conf.lwr),ymax=exp(conf.upr)),fill="dodgerblue4",alpha=0.3)
```

Chelidonichthys spinosus
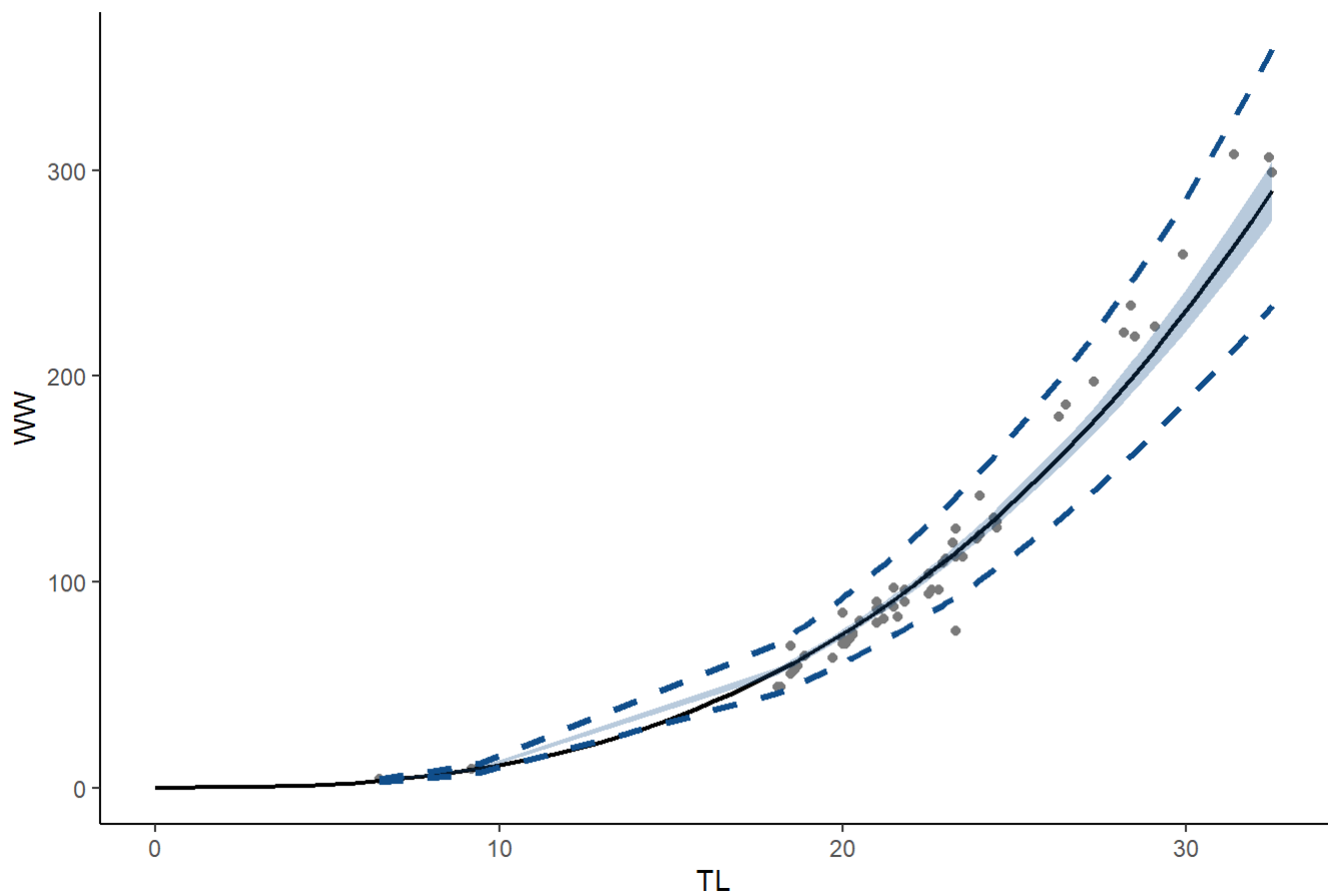
prediction example

```
exp(predict(fit_go, newdata = data.frame(TL=25), interval="prediction"))
```

```
##        fit      lwr      upr
## 1 123.4523 101.9778 149.4489
```