

Linear Regression Review

FW8051 Statistics for Ecologists

Department of Fisheries, Wildlife and Conservation Biology

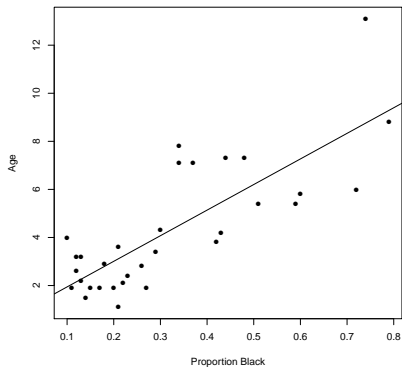


Confidence and Prediction Intervals for Regression

Learning Objectives

Understand the difference between a confidence interval and a prediction interval

The Lion's Nose (from W & S)



Regression Model

$$\widehat{age} = 0.879 + 10.65\text{Proportion.black}$$

```
summary(lm.nose)
```

Call:

```
lm(formula = age ~ proportion.black, data = LionNoses)
```

Residuals:

Min	1Q	Median	3Q	Max
-2.5449	-1.1117	-0.5285	0.9635	4.3421

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.8790	0.5688	1.545	0.133
proportion.black	10.6471	1.5095	7.053	7.68e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.669 on 30 degrees of freedom

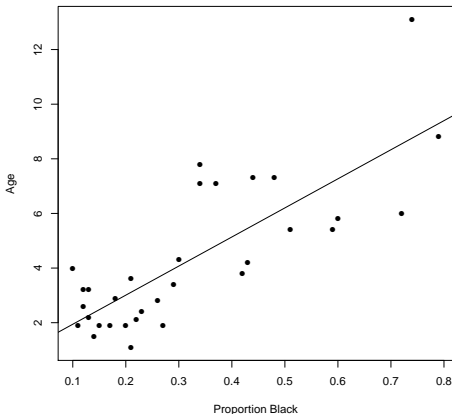
Multiple R-squared: 0.6238, Adjusted R-squared: 0.6113

F-statistic: 49.75 on 1 and 30 DF, p-value: 7.677e-08

Predictions

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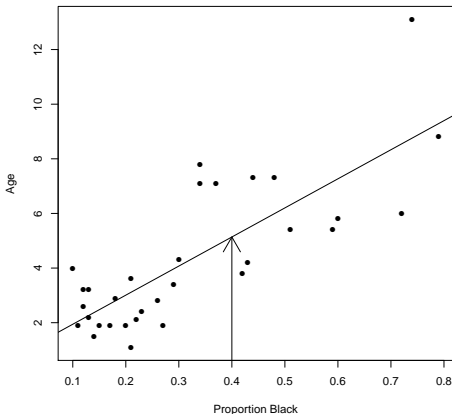
If we see a lion with a nose that is 40% black, what age would we predict?



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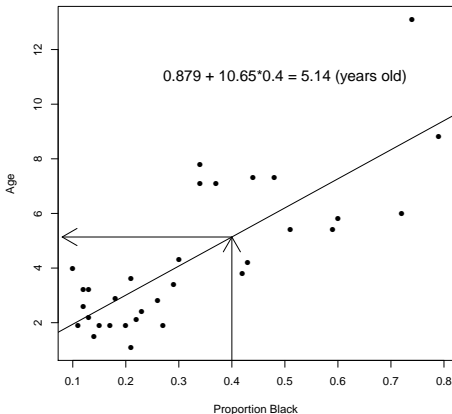
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For a single predictor model and a particular value ($X = x$) of the predictor, the predicted response (Y) is:

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Two types of intervals:

- Confidence Interval for Mean Y (at $X = x$)
- Prediction Interval for Individual Y 's (at $X = x$)

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Goal: 95% sure we capture the **average** age of lions with noses that are 40% black:

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A confidence interval only addresses uncertainty about the line, a prediction interval also includes the scatter of the points around the line

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Lets start by considering how much the fitted line might vary from sample to sample. How can we explore this question?

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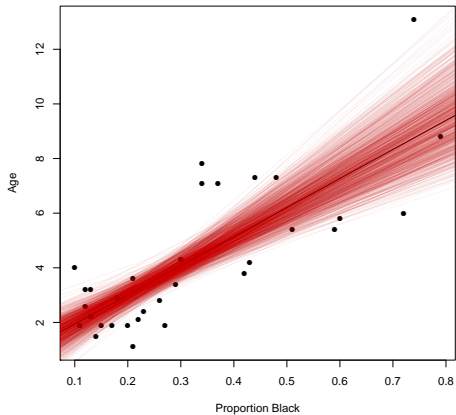
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Bootstrap!

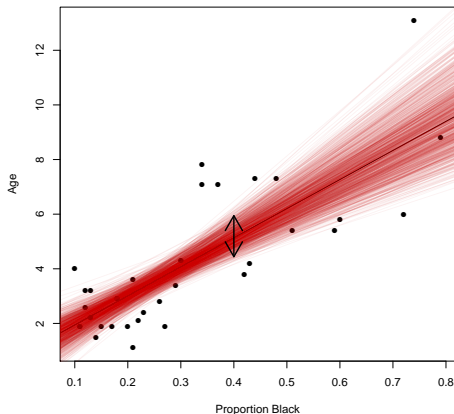
Lets fit 1000 lines to bootstrap samples

```
nboots<-1000
betas<-matrix(NA, nboots,2)
nobs<-nrow(LionNoses)
for(i in 1:nboots){
  bootdat<-LionNoses[sample(1:nobs, nobs,replace=T),]
  lmfit<-lm(age~proportion.black, data=bootdat)
  betas[i,]<-coef(lmfit)
}
```


Now, lets plot them!



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Middle 95% of predicted values gives the CI for the mean age when proportion black is 0.40.

R code

```
with(LionNoses,plot(proportion.black,age, xlab="Proportion Black", ylab="Age", pch=16))
lm.nose<-lm(age~proportion.black, data=LionNoses)
abline(lm.nose) # best fit line, now add bootstrap lines (below)
for(i in 1:1000){abline(a=betas[i,1],b=betas[i,2], col=rgb(0.8,0,0, alpha=0.05))}
phats<-betas[,1]+ 0.4*betas[,2] # Predicted MEAN values for x = 0.4
arrows(0.4, quantile(phats, prob=0.025), 0.4, quantile(phats, prob=0.975), code=3, lwd=2)
```

Using R: predict function

```
quantile(phats, prob=c(0.025, 0.975)) # Bootstrap CI
```

```
      2.5%      97.5%  
4.395015 5.952447
```

If we want to relax the normality assumption: We are 95% sure that the mean age of lions with noses that are 40% black is between 4.44 and 5.94.

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```
newdata<-data.frame(proportion.black=0.4)  
predict(lm.nose, newdata, interval="confidence")
```

```
      fit      lwr      upr  
1 5.137854 4.489386 5.786322
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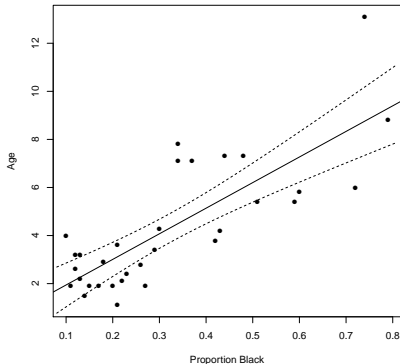
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If we believe our assumptions (HILG): We are 95% sure that the mean age of lions with noses that are 40% black is between 4.49 and 5.79.

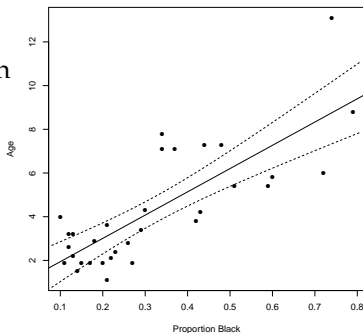
Confidence Interval for mean Y at each X

```
newdata<-data.frame(proportion.black=seq(0.08, 0.81, length=100))
predict.mean<-as.data.frame(predict(lm.nose, newdata, interval="confidence"))
with(LionNoses,plot(proportion.black,age, xlab="Proportion Black", ylab="Age", pch=16))
abline(lm.nose)
lines(newdata$proportion.black, predict.mean$lwr, lty=2)
lines(newdata$proportion.black, predict.mean$upr, lty=2)
```



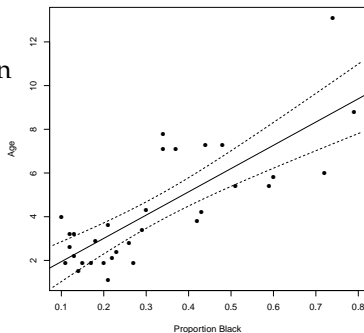
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- Captures uncertainty regarding the “true” population line
- Does NOT capture uncertainty in individual data values
- CI gets wider for more extreme predictor values



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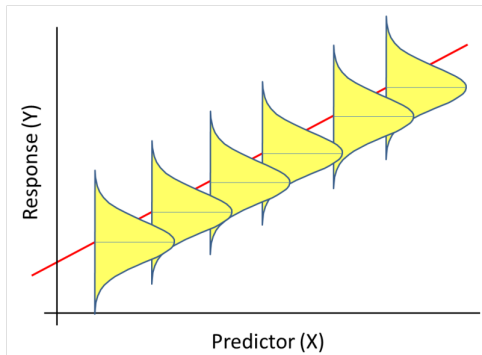
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We find a lion that has a nose that is 40% black, and we estimate its age. Can we construct an interval that will contain this animal's true age 95% of the time?

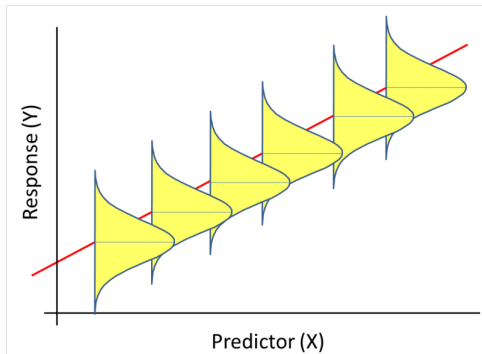
Prediction Interval for Individual Y

Need to account for the random variability (error) around the line.



Prediction Interval for Individual Y

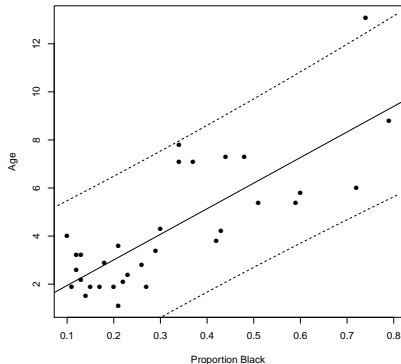
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Remember: $\epsilon \sim N(0, \sigma^2)$. $\hat{\sigma} = s_{\epsilon} = \sqrt{\sum_{i=1}^n \frac{(y_i - \hat{y}_i)^2}{n-2}}$

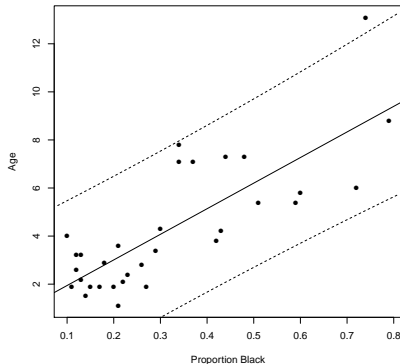
Prediction Intervals in R:

```
predict.ind<-as.data.frame(predict(lm.nose, newdata, interval="prediction"))  
with(LionNoses,plot(proportion.black,age, xlab="Proportion Black", ylab="Age", pch=16))  
abline(lm.nose)  
lines(newdata$proportion.black, predict.ind$lower, lty=2)  
lines(newdata$proportion.black, predict.ind$upper, lty=2)
```



Prediction Intervals in R:

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```



Captures $31/32 = 96\%$ of the data values.

CI and PI

Two forms of intervals for regression predictions:

- CI for mean Y at a particular x
- PI for individual Y 's at a particular x

