Linear Regression Review

FW8051 Statistics for Ecologists

Department of Fisheries, Wildlife and Conservation Biology

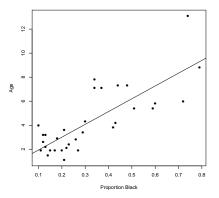


Confidence and Prediction Intervals for Regression	



Understand the difference between a confidence interval and a prediction interval

The Lion's Nose (from W & S)



Regression Model

summary(lm.nose)

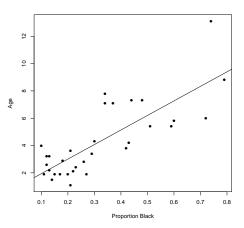
$\widehat{age} = 0.879 + 10.65$ Proportion.black

```
Call:
lm(formula = age ~ proportion.black, data = LionNoses)
Residuals:
   Min 10 Median 30 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

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

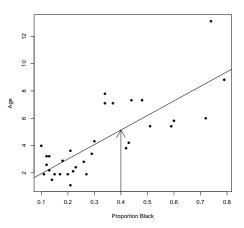
If we see a lion with a nose that is 40% black, what age would we predict?



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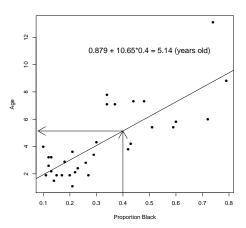
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For a single predictor model and a particular value (X = x) of the predictor, the predicted response (Y) is:

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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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 \Rightarrow Prediction interval for individual Y

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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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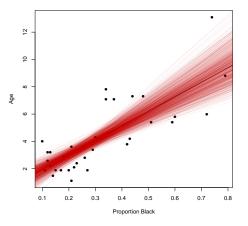
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Bootstrap!

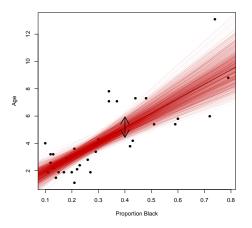
Lets fit 1000 lines to bootstrap samples

```
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)
}</pre>
```

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)</pre>
```

Using R: predict function

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.

Using R: predict function

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

2.5% 97.5%
4.395015 5.952447
```

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

fit    lwr    upr</pre>
```

```
fit lwr upr
1 5.137854 4.489386 5.786322
```

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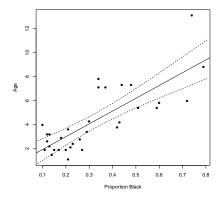
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```

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.

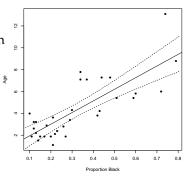
Confidence Interval for mean *Y* at each *X*

```
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$1wr, lty=2)
lines(newdata$proportion.black, predict.mean$upr, lty=2)</pre>
```



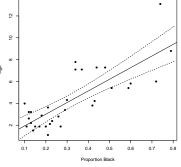
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- Does NOT capture uncertainty in individual data values
- CI gets wider for more extreme predictor values



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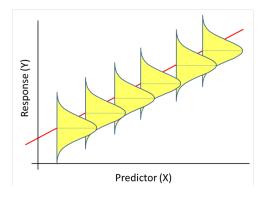
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We find a lion that has a nose that is 40% black, and we estimate its age. Can we construct an interval that will contain this animal's true age 95% of the time?

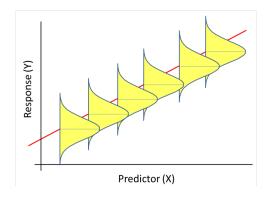
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Need to account for the random variability (error) around the line.



Prediction Interval for Individual *Y*

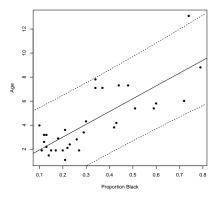
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Remember:
$$\epsilon \sim N(0, \sigma^2)$$
. $\hat{\sigma} = s_{\epsilon} = \sqrt{\sum_{i=1}^n \frac{(y_i - \hat{y}_i)^2}{n-2}}$

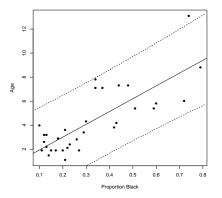
Prediction Intervals in R:

```
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$proportion.black, predict.ind$lwr, lty=2)
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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*
- ullet PI for individual Y's at a particular x

