The University of British Columbia

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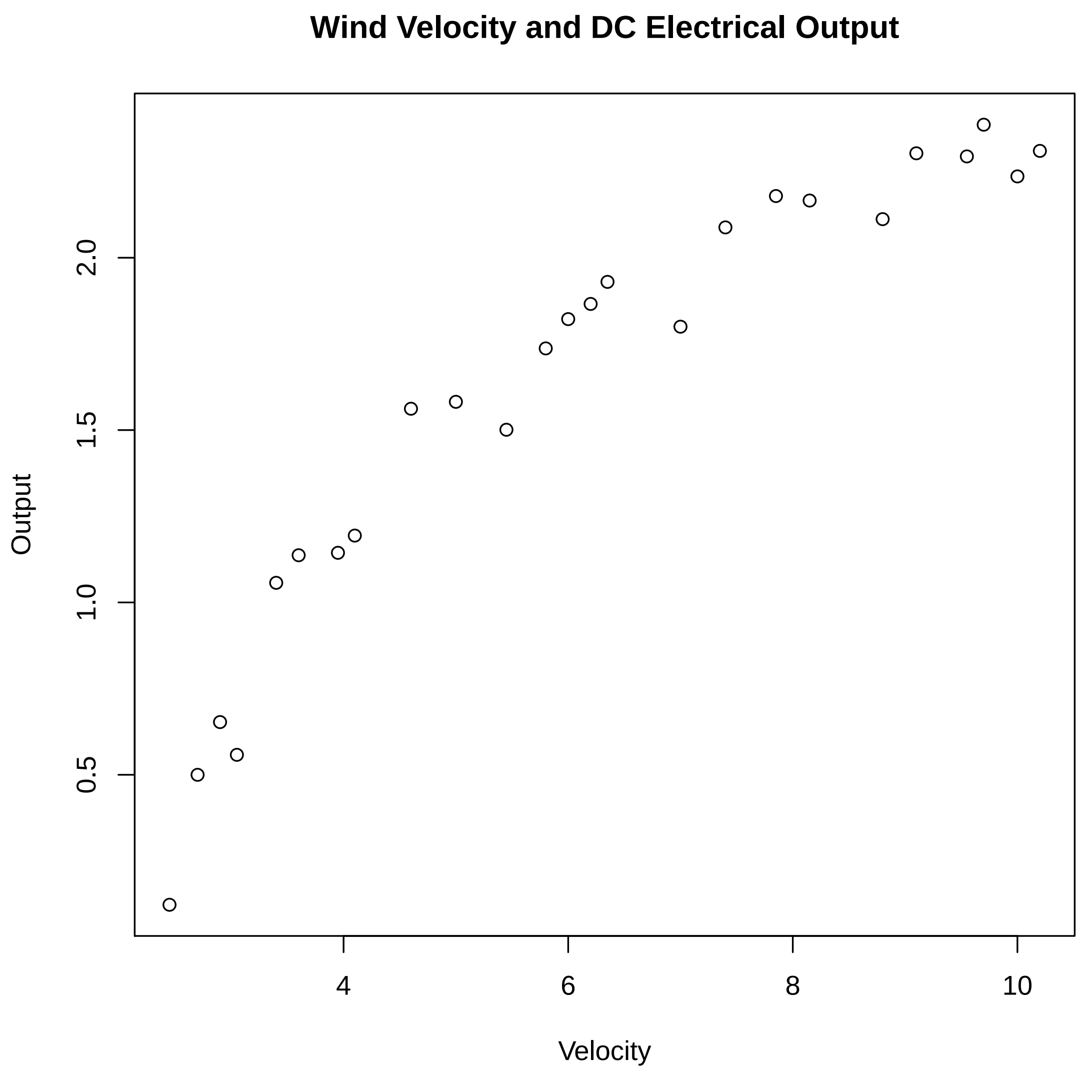
DATA 101

Lab 5 Part 2 Solution

1. Copy the file `windmill.txt` (windmill data) to a folder on your computer. This file contains observations on wind velocity and the corresponding DC electrical output.

   (a) Construct a graph which effectively displays the information in this data set.

```
windmill<-read.table("windmill.txt", header=TRUE)
plot(windmill,main="Wind Velocity and DC Electrical Output")
```

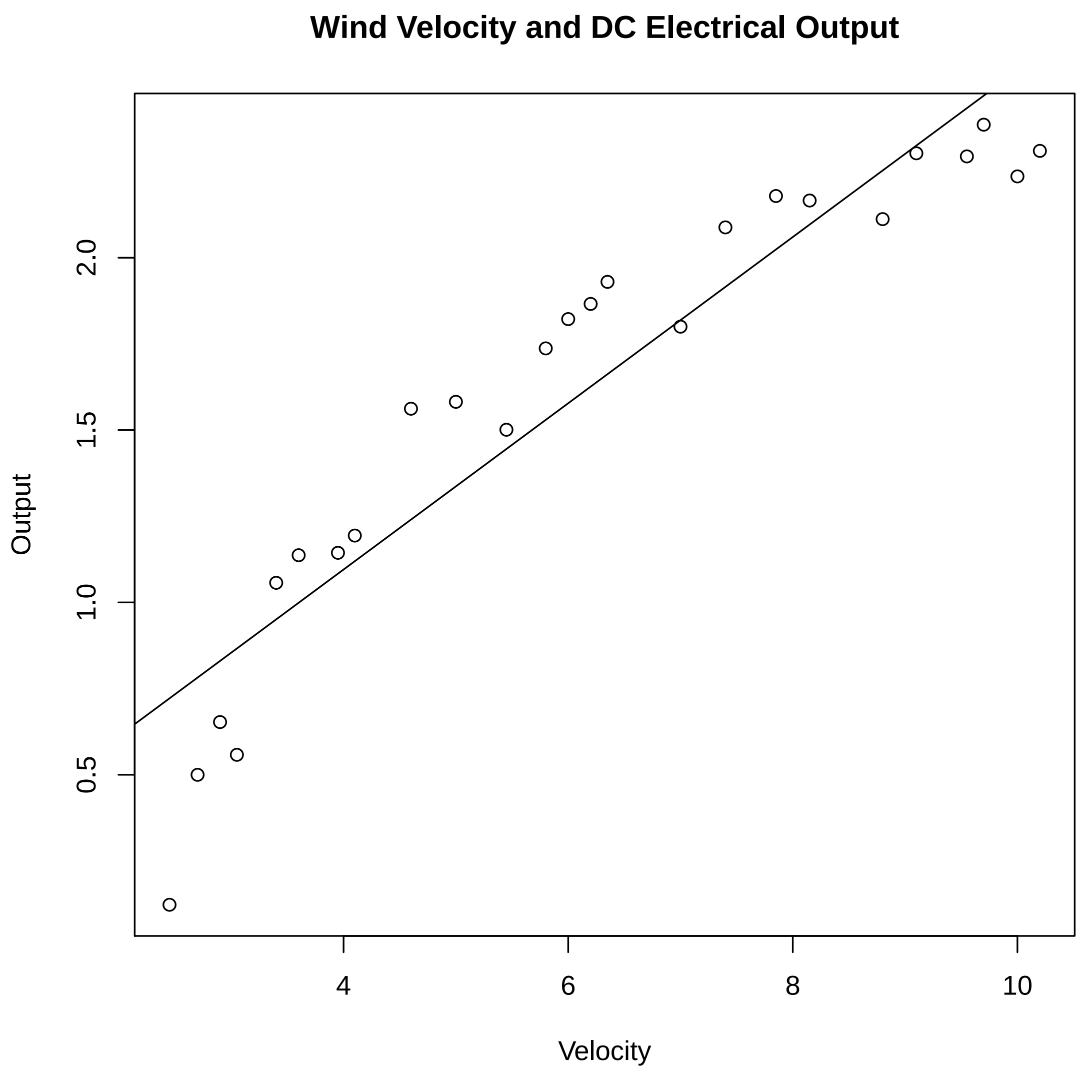


   (b) Find the best fit line for electrical output is produced by the wind velocity. And add this line in the plot you draw in previous question.

```r
windmill.lm <- lm(Output ~ Velocity, data=windmill)
summary(windmill.lm)
```

```
##
## Call:
## lm(formula = Output ~ Velocity, data = windmill)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.59869 -0.14099  0.06059  0.17262  0.32184
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.13088    0.12599   1.039     0.31
## Velocity     0.24115    0.01905  12.659 7.55e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2361 on 23 degrees of freedom
## Multiple R-squared:  0.8745,Adjusted R-squared:  0.869
## F-statistic: 160.3 on 1 and 23 DF,  p-value: 7.546e-12
```

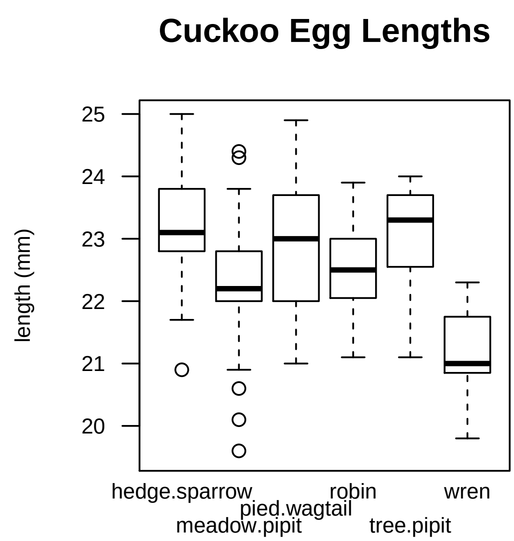
```r
plot(windmill,main="Wind Velocity and DC Electrical Output")
abline(windmill.lm)
```

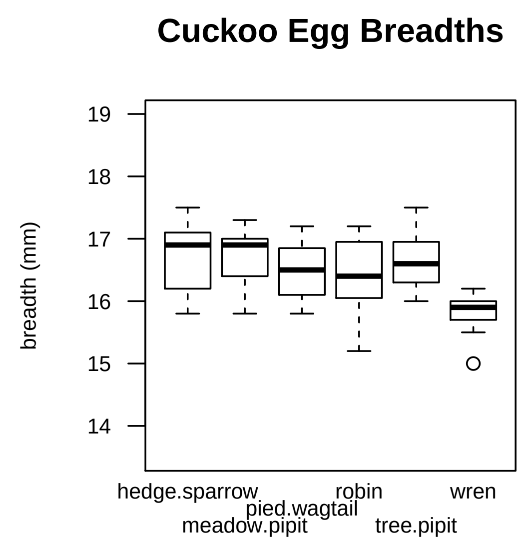


2. Using data `cuckoos` that contains observations on the lengths and breadths of cuckoo eggs left in the nests of various other bird species. Construct the following two sets of graphs. Note that in the second set of graphs, the respective lines are least-squares lines obtained using the `lm()` function.

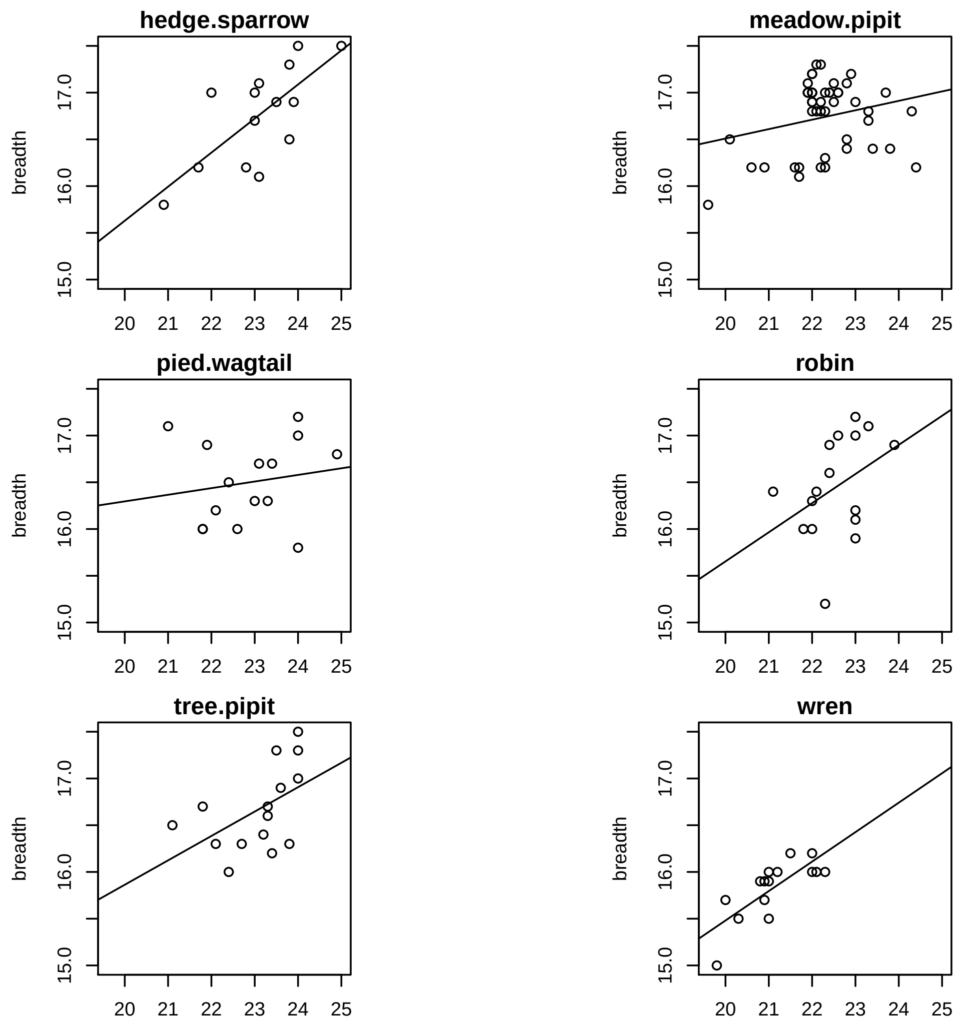
```
cuckoos <- read.table('cuckoos.txt', header=TRUE)
par(mfrow=c(1,2), pty='s')
cuckoos <- cuckoos[order(cuckoos$species),]
boxplot(length ~ species, data=cuckoos, axes=FALSE,ylim=c(19.5,25),
    ylab='length (mm)', cex.lab=.75)
title('Cuckoo Egg Lengths')
box()
axis(side=2, at=seq(20,25,1), label=seq(20,25,1), las=2, cex.axis=.75)
labels1 <- unique(cuckoos$species)[c(1,4,6)]
labels2 <- unique(cuckoos$species)[c(2,5)]
```

```
labels3 <- unique(cuckoos$species)[c(3)]
mtext(labels1, side=1, at=c(1,4,6), cex=.75, line=0)
mtext(labels2, side=1, at=c(2,5), cex=.75, line=1)
mtext(labels3, side=1, at=c(3), cex=.75, line=0.5)
boxplot(breadth ~ species, data=cuckoos, axes=FALSE, ylim=c(13.5,19),
    ylab='breadth (mm)', cex.lab=.75)
title('Cuckoo Egg Breadths')
box()
axis(side=2, at=seq(14,19,1), label=seq(14,19,1), las=2, cex.axis=.75)
labels1 <- unique(cuckoos$species)[c(1,4,6)]
labels2 <- unique(cuckoos$species)[c(2,5)]
labels3 <- unique(cuckoos$species)[c(3)]
mtext(labels1, side=1, at=c(1,4,6), cex=.75, line=0)
mtext(labels2, side=1, at=c(2,5), cex=.75, line=1)
mtext(labels3, side=1, at=c(3), cex=.75, line=0.5)
```






```
par(mfrow=c(3,2), pty='s', mar=c(2.5,1.5,1.5,1))
for (i in 1:6) {
    lengths <- split(cuckoos$length, cuckoos$species)
    widths <- split(cuckoos$breadth, cuckoos$species)
    lenwid.lm <- lm(widths[[i]] ~ lengths[[i]])
x.range <- range(cuckoos$length)
y.range <- range(cuckoos$breadth)
plot(widths[[i]]~lengths[[i]], xlab='length', ylab='breadth',
    main=names(lengths)[i], ylim=y.range, xlim=x.range)
abline(lenwid.lm)
}
```


hedge.sparrow
meadow.pipit
pied.wagtail
robin
tree.pipit
wren
breadth
15.0
16.0
17.0
20
21
22
23
24
25