

T1-E01-Iogurt.R

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```
setwd("~/Desktop/xperiments/Rii")
dd<-read.csv2("Iogurt.csv") # dd es de dades
head(dd)

##   Ferm dia   pH strep lactob
## 1  T42  21 4.10  7.43   7.46
## 2  T42   0 4.44  7.65   7.75
## 3  T42  21 4.02  7.10   7.35
## 4  T42   7 4.24  7.54   7.62
## 5  T42   7 4.27  7.54   7.66
## 6  T42  28 4.01  7.25   7.41

library(car)

## Warning: package 'car' was built under R version 3.4.4
## Loading required package: carData
## Warning: package 'carData' was built under R version 3.4.4

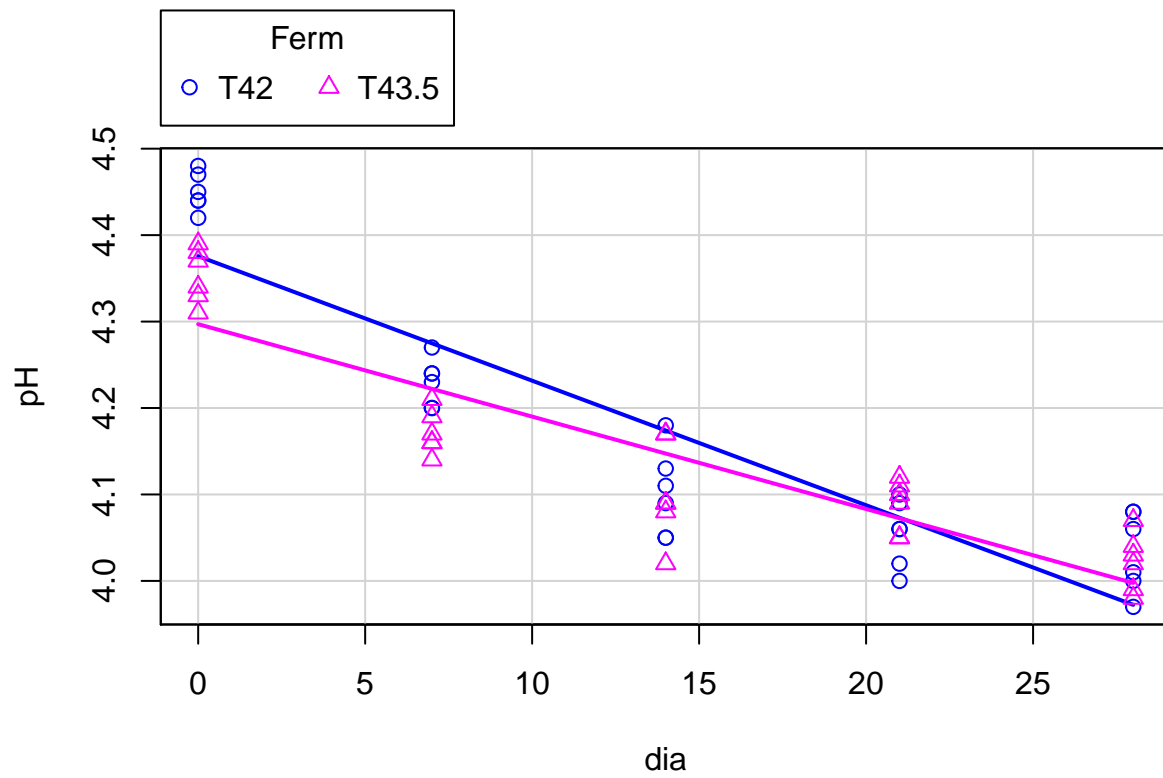
library(tables)

## Warning: package 'tables' was built under R version 3.4.4
## Loading required package: Hmisc
## Loading required package: lattice
## Loading required package: survival
## Loading required package: Formula
## Warning: package 'Formula' was built under R version 3.4.4
## Loading required package: ggplot2
## Warning: package 'ggplot2' was built under R version 3.4.4
##
## Attaching package: 'Hmisc'
## The following objects are masked from 'package:base':
##
##   format.pval, units

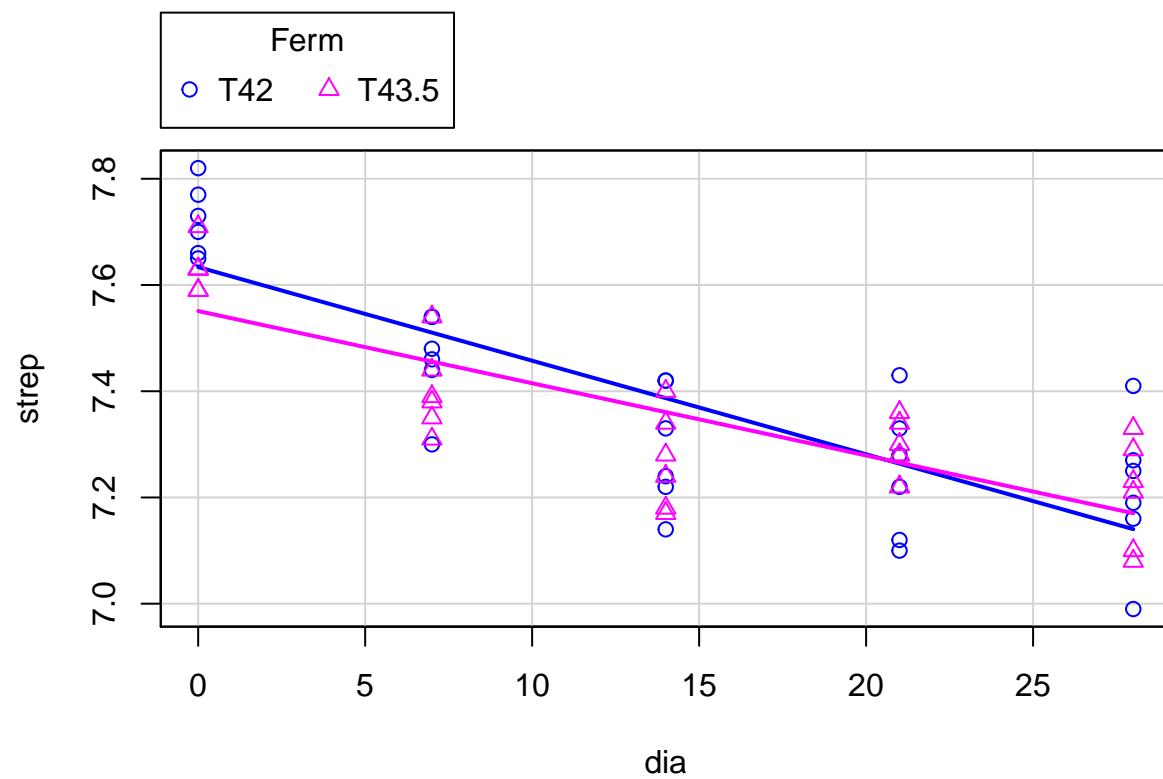
#=====
# (a) Descriptiva

# Gr??fiques

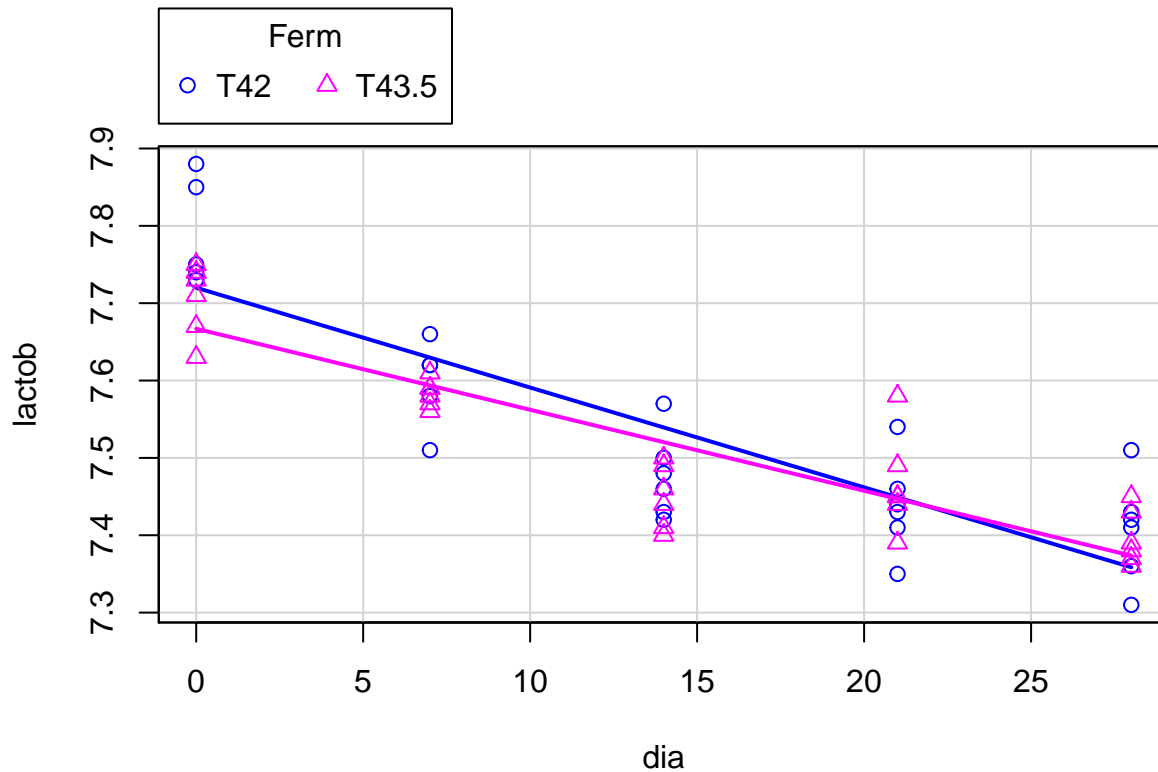
sp(pH~dia|Ferm,dd,smooth=F) # sp es scatter plot
```



```
sp(strep~dia|Ferm, smooth=F, dd)
```



```
sp(lactob~dia|Ferm,smooth=F,dd)
```



Taules

```
dd$Fdia<-as.factor(dd$dia)
tabular((pH+strep+lactob)*Ferm*((n=1)+mean+sd)~Fdia,dd) # n = nombre de dades, repliques i li posem el
```

			Fdia				
	Ferm		0	7	14	21	28
pH	T42	n	6.00000	6.00000	6.00000	6.00000	6.00000
		mean	4.45000	4.23000	4.10167	4.05500	4.03333
		sd	0.02191	0.02683	0.04997	0.03886	0.04633
	T43.5	n	6.00000	6.00000	6.00000	6.00000	6.00000
		mean	4.35333	4.17167	4.10333	4.08667	4.02167
		sd	0.03141	0.02483	0.05785	0.03011	0.03312
strep	T42	n	6.00000	6.00000	6.00000	6.00000	6.00000
		mean	7.72167	7.46000	7.29500	7.24667	7.21167
		sd	0.06555	0.08854	0.11415	0.12644	0.13891
	T43.5	n	6.00000	6.00000	6.00000	6.00000	6.00000
		mean	7.63000	7.40167	7.26833	7.29667	7.20667
		sd	0.04382	0.08035	0.09042	0.04967	0.10013
lactob	T42	n	6.00000	6.00000	6.00000	6.00000	6.00000
		mean	7.78000	7.59500	7.47667	7.43833	7.40667
		sd	0.06693	0.05128	0.05465	0.06242	0.06772
	T43.5	n	6.00000	6.00000	6.00000	6.00000	6.00000
		mean	7.70500	7.58333	7.45000	7.46667	7.39667
		sd	0.04637	0.01751	0.04099	0.06408	0.03559

o b?? per separat tabular(pH*Ferm*((n=1)+mean+sd)~Fdia,dd) ...

#####

(b) Comparacions de 2

```
# pH dia 0
t.test(pH~Ferm,dd[dd$dia==0,]) # test t de dues esperances de variables normals
```

```
##
## Welch Two Sample t-test
##
## data: pH by Ferm
## t = 6.1828, df = 8.9338, p-value = 0.0001673
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.06125851 0.13207482
## sample estimates:
## mean in group T42 mean in group T43.5
## 4.450000 4.353333
```

```
t.test(pH~Ferm,var.equal=T,dd[dd$dia==0,])
```

```
##
## Two Sample t-test
##
## data: pH by Ferm
## t = 6.1828, df = 10, p-value = 0.0001038
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.06183034 0.13150299
## sample estimates:
## mean in group T42 mean in group T43.5
## 4.450000 4.353333
```

```
var.test(pH~Ferm,dd[dd$dia==0,])
```

```
##
## F test to compare two variances
##
## data: pH by Ferm
## F = 0.48649, num df = 5, denom df = 5, p-value = 0.4479
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
## 0.06807452 3.47661819
## sample estimates:
## ratio of variances
## 0.4864865
```

```
t.test(lactob~Ferm,dd[dd$dia==21,])
```

```
##
## Welch Two Sample t-test
##
## data: lactob by Ferm
## t = -0.77578, df = 9.9931, p-value = 0.4558
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.10971800 0.05305134
## sample estimates:
## mean in group T42 mean in group T43.5
```

```

##                7.438333                7.466667
t.test(lactob~Ferm,var.equal=T,dd[dd$dia==21,])

##
## Two Sample t-test
##
## data: lactob by Ferm
## t = -0.77578, df = 10, p-value = 0.4558
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.10971041  0.05304374
## sample estimates:
## mean in group T42 mean in group T43.5
##                7.438333                7.466667

# strep dia 21
t.test(strep~Ferm,dd[dd$dia==21,])

##
## Welch Two Sample t-test
##
## data: strep by Ferm
## t = -0.90159, df = 6.5071, p-value = 0.3994
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.18317752  0.08317752
## sample estimates:
## mean in group T42 mean in group T43.5
##                7.246667                7.296667

t.test(strep~Ferm,var.equal=T,dd[dd$dia==21,])

##
## Two Sample t-test
##
## data: strep by Ferm
## t = -0.90159, df = 10, p-value = 0.3885
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.17356744  0.07356744
## sample estimates:
## mean in group T42 mean in group T43.5
##                7.246667                7.296667

var.test(strep~Ferm,dd[dd$dia==21,])

##
## F test to compare two variances
##
## data: strep by Ferm
## F = 6.4811, num df = 5, denom df = 5, p-value = 0.06108
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  0.9069038 46.3162801
## sample estimates:
## ratio of variances

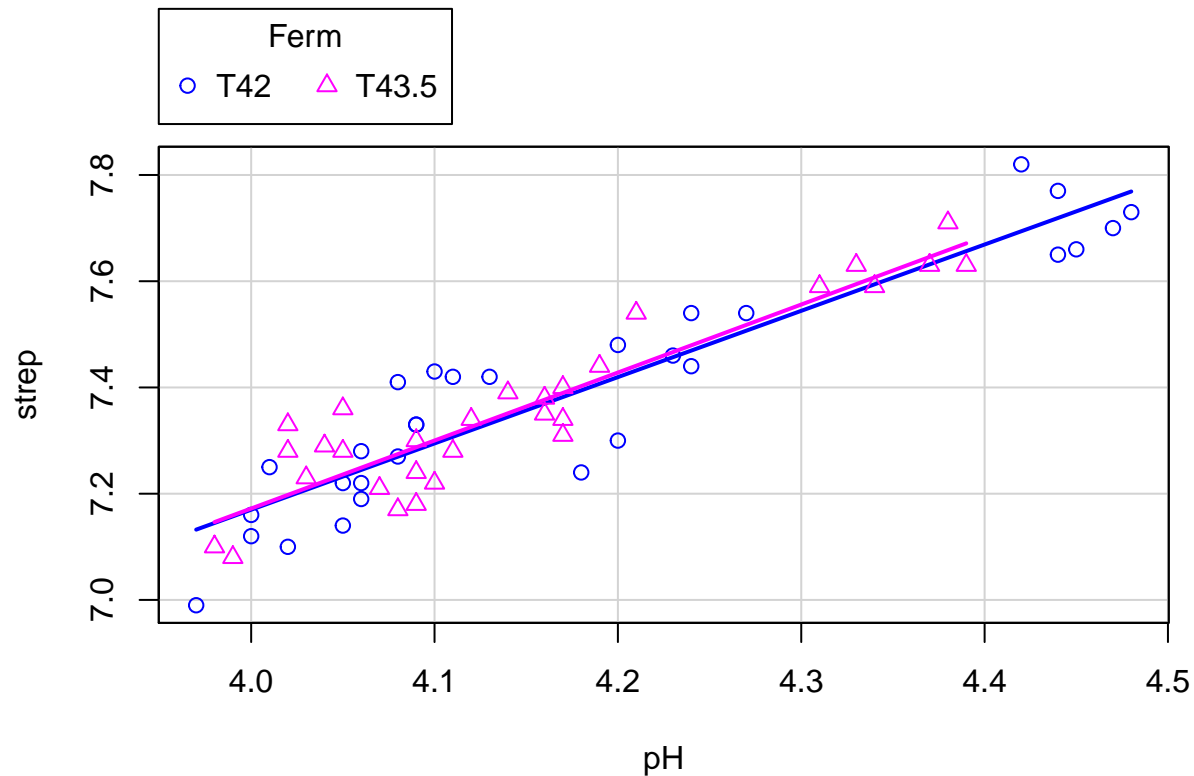
```

```
## 6.481081
```

```
#####  
# (c) Predicci?? a partir del pH
```

```
#strep
```

```
sp(strep~pH|Ferm,dd,smooth=F,boxplot=F)
```



```
sp(strep~pH,dd,smooth=F,boxplot=F) # treiem el condicionat a fermentacio, pq hem vist que no depen
```

```
(mstrep<-lm(strep~pH,dd)) # quan fem assignacio no escriu res a la consola, per això posem en tre paren
```

```
##
```

```
## Call:
```

```
## lm(formula = strep ~ pH, data = dd)
```

```
##
```

```
## Coefficients:
```

```
## (Intercept)      pH
```

```
## 2.143      1.257
```

```
summary(mstrep)
```

```
##
```

```
## Call:
```

```
## lm(formula = strep ~ pH, data = dd)
```

```
##
```

```
## Residuals:
```

```
##      Min       1Q   Median       3Q      Max
```

```
## -0.15814 -0.05035 -0.00171  0.04508  0.13758
```

```
##
```

```
## Coefficients:
```

```
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.14327    0.28205   7.599 2.89e-10 ***
## pH          1.25715    0.06775  18.556 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07359 on 58 degrees of freedom
## Multiple R-squared:  0.8558, Adjusted R-squared:  0.8533
## F-statistic: 344.3 on 1 and 58 DF,  p-value: < 2.2e-16
```

la formula que li hem donat
els residuals son les distancies que hi ha de cada punt a la recta. Per veure com son els residuals,
intercept es el valor alfa.
el pH no es el pH, es el coeficient que multiplica el pH, o sigui, es la beta.
test si lalfa es igual a zero (el test diu que es diferent, ixo vol dir que no pasa per zero)
test de la beta, no es zero i vol dir que la recta no es horitzontal i el lactob depen del pH.
Residual standard error vol dir que la desviacio tipus es petita i ajusta be,
18.556 elevat al quadrat el 344.4 (Tstudent vs Fisher), el p-valor es el mateix.
coeficient de determinacio, si a prop de 1 la relacio es bona (correlacio), si llluny de 1, poca rela
coeficient d e determinacio es el mutiple R-squared. Pero no nhi ha prou
hem der fer ddiagnostics grafics.
el valor predit es el valor de la recta i el residual es el valor predit menys

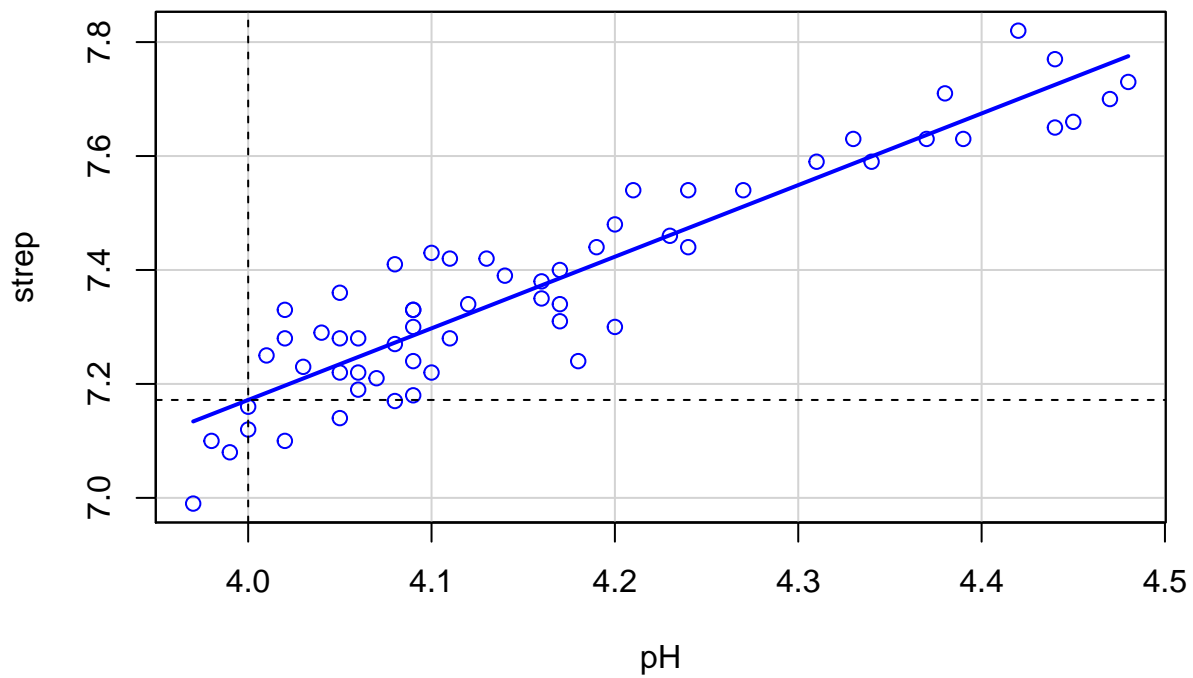
```
summary(mstrep<-lm(strep~pH,dd))

##
## Call:
## lm(formula = strep ~ pH, data = dd)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.15814 -0.05035 -0.00171  0.04508  0.13758
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.14327    0.28205   7.599 2.89e-10 ***
## pH          1.25715    0.06775  18.556 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07359 on 58 degrees of freedom
## Multiple R-squared:  0.8558, Adjusted R-squared:  0.8533
## F-statistic: 344.3 on 1 and 58 DF,  p-value: < 2.2e-16
```

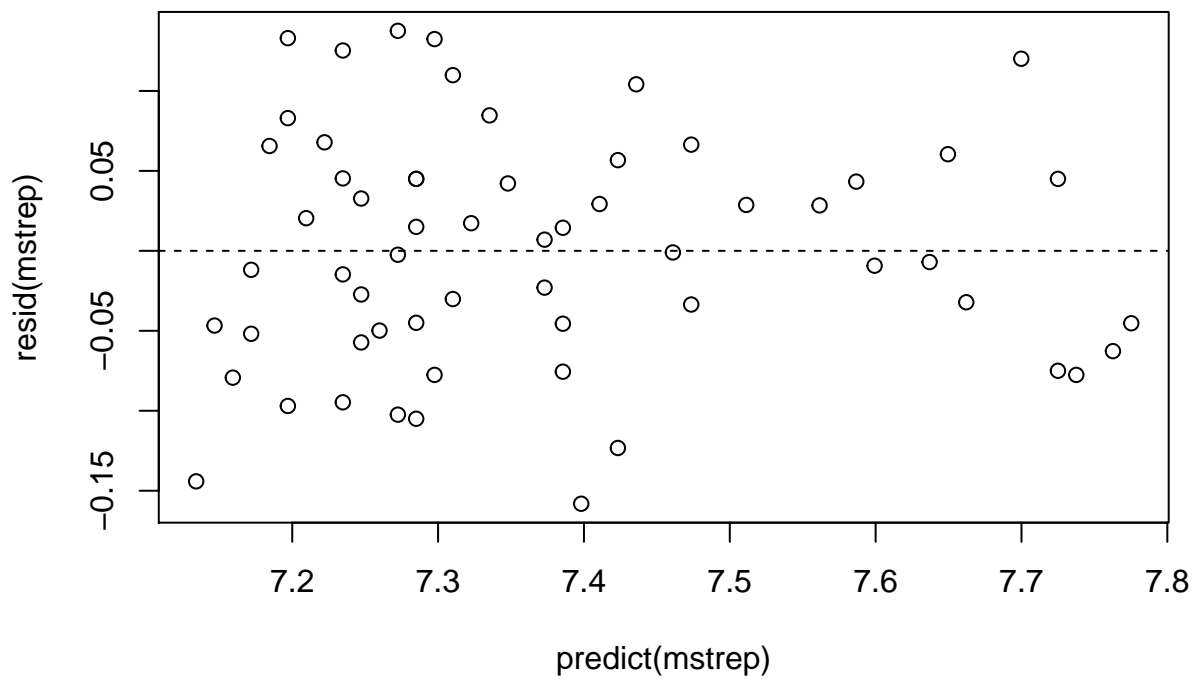
```
(lstrep<-mstrep$coef[1]+mstrep$coef[2]*4)
```

```
## (Intercept)
##      7.171852
```

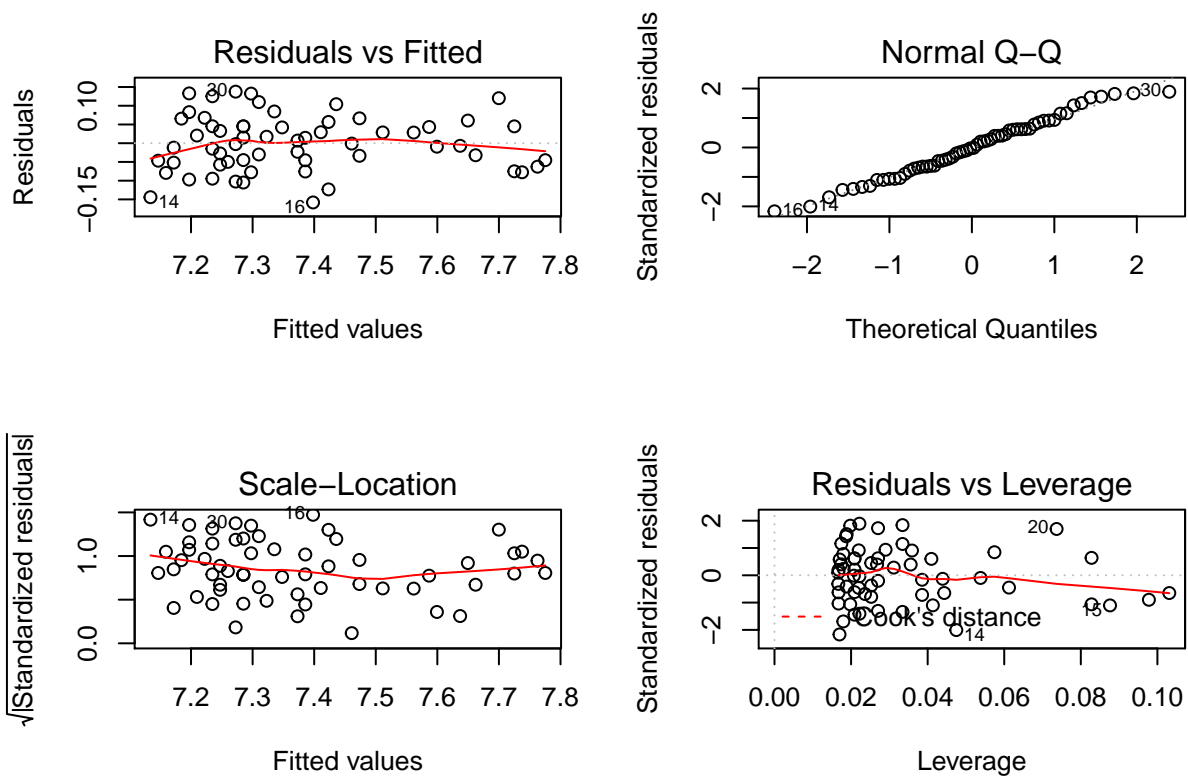
```
sp(strep~pH,dd,smooth=F,boxplot=F)
abline(v=4,h=lstrep,lt=2)
```



```
plot(predict(mstrep), resid(mstrep))
abline(h=0, lt=2)
```

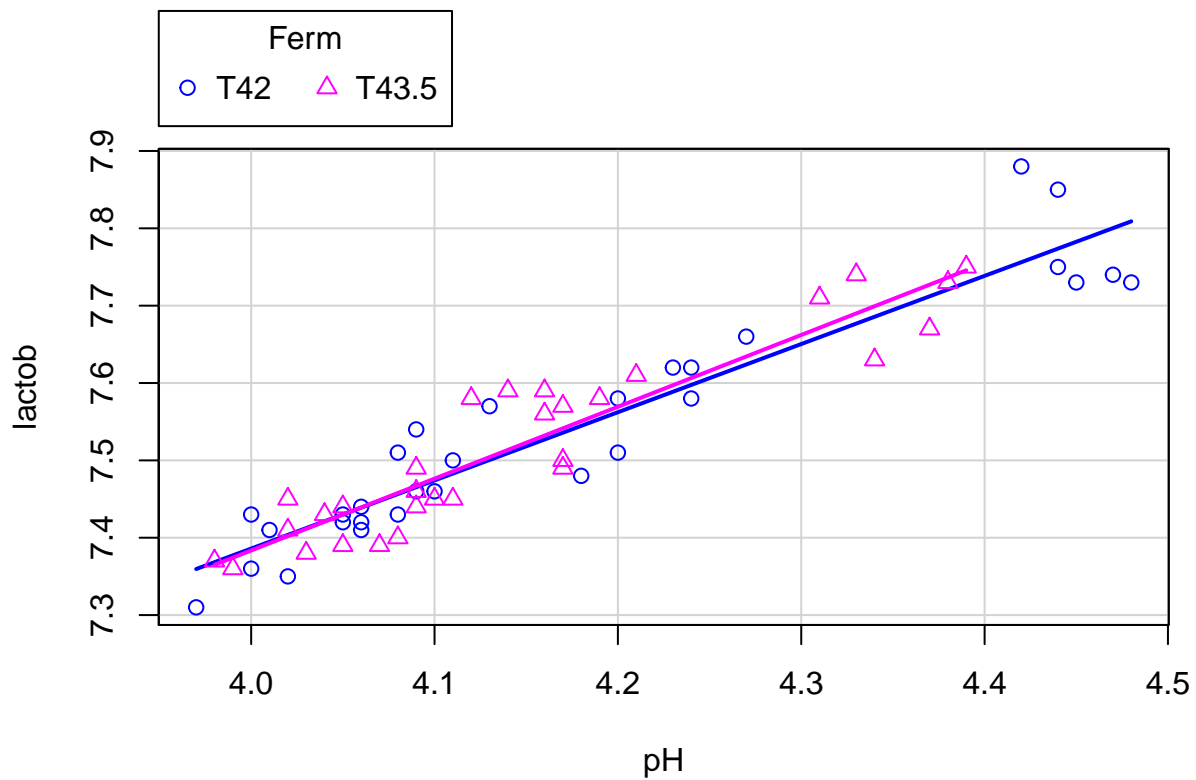


```
oldpar <- par(mfrow=c(2,2))
plot(mstrep, ask=F)
```

```
par(oldpar) # anula la primera comanda

#lactob
sp(lactob~pH|Ferm,dd,smooth=F,boxplot=F)
```



```
sp(lactob~pH,dd,smooth=F,boxplot=F)
```

```
summary(mlactob<-lm(lactob~pH,dd))
```

```
##
## Call:
## lm(formula = lactob ~ pH, data = dd)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.086181 -0.033098 -0.000082  0.031023  0.117622
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  3.79895    0.17497   21.71  <2e-16 ***
## pH           0.89670    0.04203   21.34  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04565 on 58 degrees of freedom
## Multiple R-squared:  0.887, Adjusted R-squared:  0.885
## F-statistic: 455.2 on 1 and 58 DF, p-value: < 2.2e-16
```

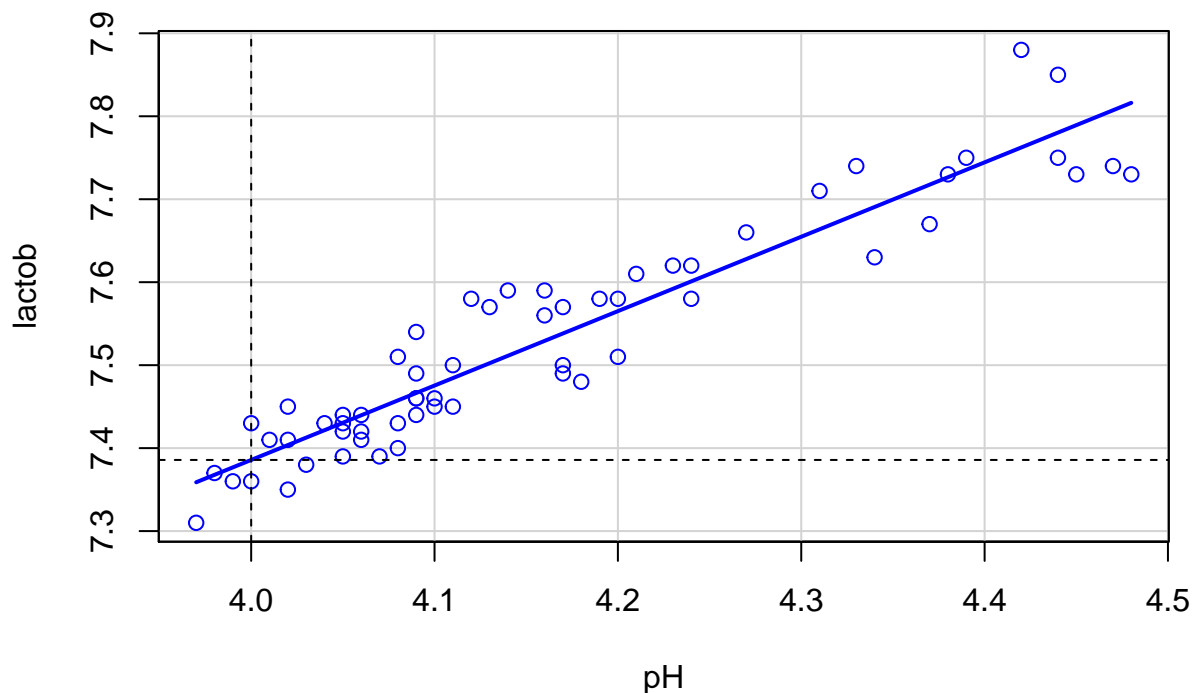
```
(llactob<-mlactob$coef[1]+mlactob$coef[2]*4)
```

```
## (Intercept)
```

```
##      7.385763
```

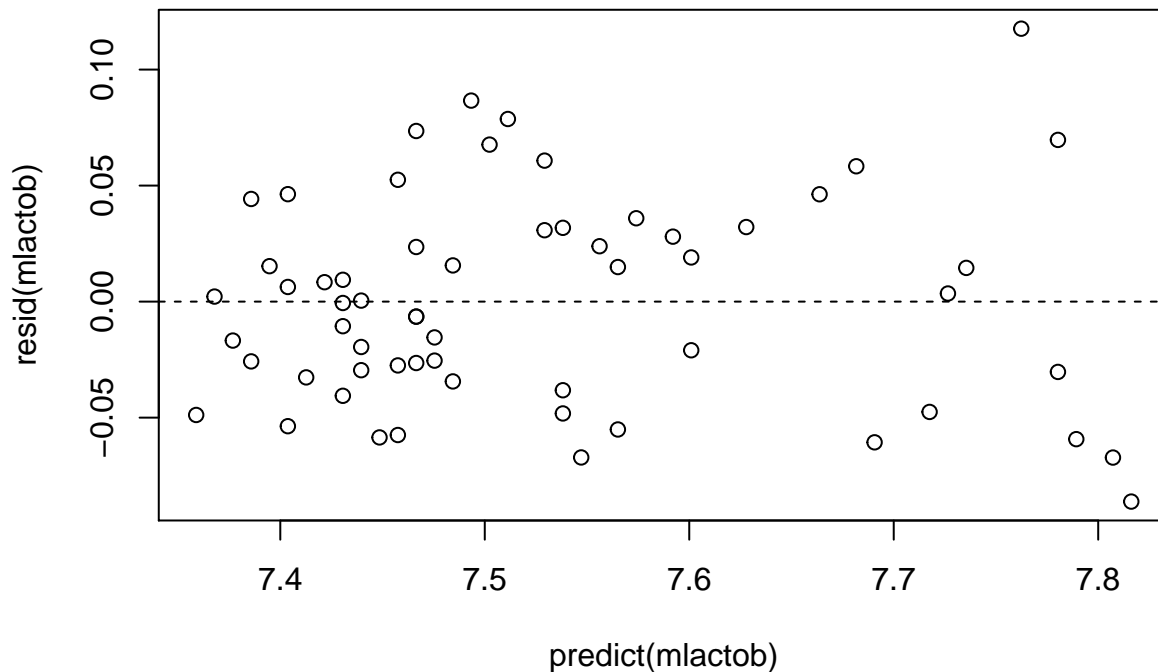
```
sp(lactob~pH,dd,smooth=F,boxplot=F)
```

```
abline(v=4,h=llactob,lt=2)
```



```
plot(predict(mlactob),resid(mlactob))
```

```
abline(h=0,lt=2)
```



```
#oldpar <- par(mfrow=c(2,2))
#plot(mlactob,ask=F)
#par(oldpar)
```

```
# R2 i lv
summary(mstrep)
```

```
##
## Call:
## lm(formula = strep ~ pH, data = dd)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.15814 -0.05035 -0.00171  0.04508  0.13758
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.14327    0.28205   7.599 2.89e-10 ***
## pH           1.25715    0.06775  18.556 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07359 on 58 degrees of freedom
## Multiple R-squared:  0.8558, Adjusted R-squared:  0.8533
## F-statistic: 344.3 on 1 and 58 DF,  p-value: < 2.2e-16
```

```
summary(mlactob)
```

```
##
## Call:
## lm(formula = lactob ~ pH, data = dd)
##
## Residuals:
```

```

##           Min           1Q       Median           3Q           Max
## -0.086181 -0.033098 -0.000082  0.031023  0.117622
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  3.79895    0.17497   21.71  <2e-16 ***
## pH           0.89670    0.04203   21.34  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04565 on 58 degrees of freedom
## Multiple R-squared:  0.887, Adjusted R-squared:  0.885
## F-statistic: 455.2 on 1 and 58 DF, p-value: < 2.2e-16
c(strep=summary(mstrep)$r.squared,lactob=summary(mlactob)$r.squared)

##      strep      lactob
## 0.8558319 0.8869845
c(strep=logLik(mstrep),lactob=logLik(mlactob))

##      strep      lactob
## 72.43656 101.08524

```