

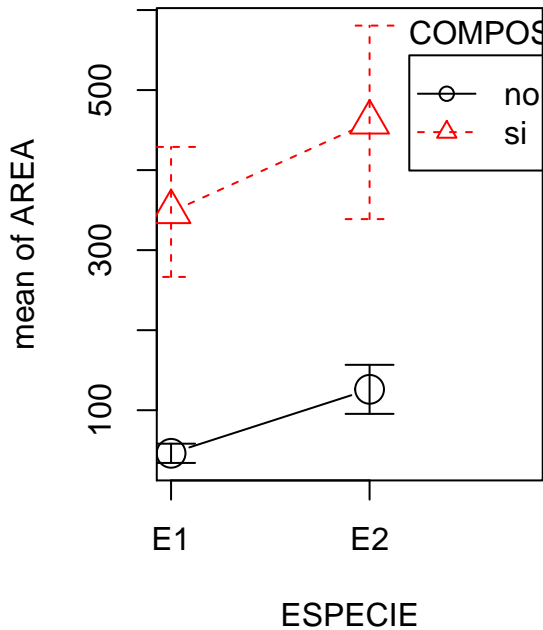
4 - AREA

```
## Loading required package: car
## Loading required package: sandwich
## Loading required package: survival
## Loading required package: estimability
```

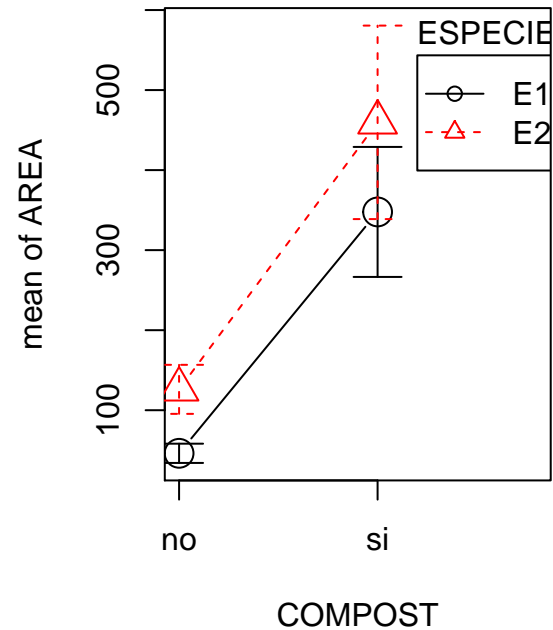
Descriptiva

```
#dd <- read.csv("area.csv", sep=";", dec=",")
cv<-function(x) {sd(x)/mean(x)}
oldpar <- par(oma=c(0,0,1,0), mfrow=c(1,2))
with(dd,plotMeans(AREA,ESPECIE,COMPOST,error.bars="conf.int",level=0.95))
with(dd,plotMeans(AREA,COMPOST,ESPECIE,error.bars="conf.int",level=0.95))
```

Plot of Means



Plot of Means



```
par(oldpar)
summaryBy(AREA~ESPECIE*COMPOST,data=dd,FUN= c(length,mean,sd,cv))
```

	ESPECIE	COMPOST	AREA.length	AREA.mean	AREA.sd	AREA.cv
1	E1	no	6	46.14624	11.46092	0.2483608
2	E1	si	6	347.74374	77.38105	0.2225232
3	E2	no	6	126.07049	29.18922	0.2315310
4	E2	si	6	459.68379	115.19088	0.2505872

A)1)

```
m01<-lm(AREA~ESPECIE+COMPOST,data=dd)
summary(m01)
```

Call:

```
lm(formula = AREA ~ ESPECIE + COMPOST, data = dd)
```

Residuals:

Min	1Q	Median	3Q	Max
-145.076	-35.260	8.457	19.232	163.636

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	244.91	14.28	17.15	7.88e-14 ***
ESPECIE1	47.97	14.28	3.36	0.00297 **
COMPOST1	158.80	14.28	11.12	2.91e-10 ***

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

Residual standard error: 69.94 on 21 degrees of freedom

Multiple R-squared: 0.8654, Adjusted R-squared: 0.8526

F-statistic: 67.5 on 2 and 21 DF, p-value: 7.17e-10

```
Anova(m01,type=3)
```

Anova Table (Type III tests)

Response: AREA

	Sum Sq	Df	F value	Pr(>F)
(Intercept)	1439554	1	294.249	7.884e-14 ***
ESPECIE	55218	1	11.287	0.002966 **
COMPOST	605239	1	123.713	2.914e-10 ***
Residuals	102738	21		

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

```
cld(lsmmeans(m01,c("ESPECIE","COMPOST")))
```

ESPECIE	COMPOST	lsmean	SE	df	lower.CL	upper.CL	.group
E1	no	38.14229	24.72927	21	-13.28504	89.56962	1
E2	no	134.07444	24.72927	21	82.64711	185.50177	2
E1	si	355.74769	24.72927	21	304.32037	407.17502	3
E2	si	451.67984	24.72927	21	400.25251	503.10717	4

Confidence level used: 0.95

P value adjustment: tukey method for comparing a family of 4 estimates

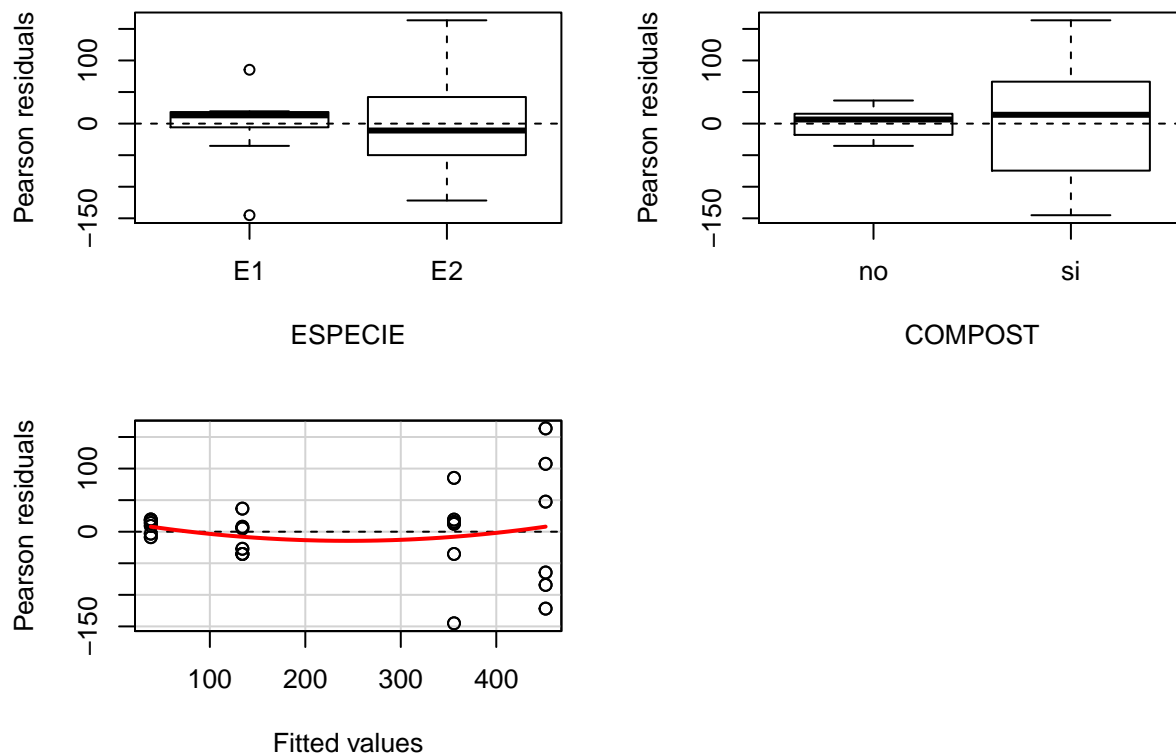
significance level used: alpha = 0.05

```
pairs(lsmmeans(m01,c("ESPECIE","COMPOST")))
```

contrast	estimate	SE	df	t.ratio	p.value
E1,no - E2,no	-95.93215	28.55490	21	-3.360	0.0145
E1,no - E1,si	-317.60540	28.55490	21	-11.123	<.0001
E1,no - E2,si	-413.53755	40.38273	21	-10.240	<.0001
E2,no - E1,si	-221.67325	40.38273	21	-5.489	0.0001
E2,no - E2,si	-317.60540	28.55490	21	-11.123	<.0001
E1,si - E2,si	-95.93215	28.55490	21	-3.360	0.0145

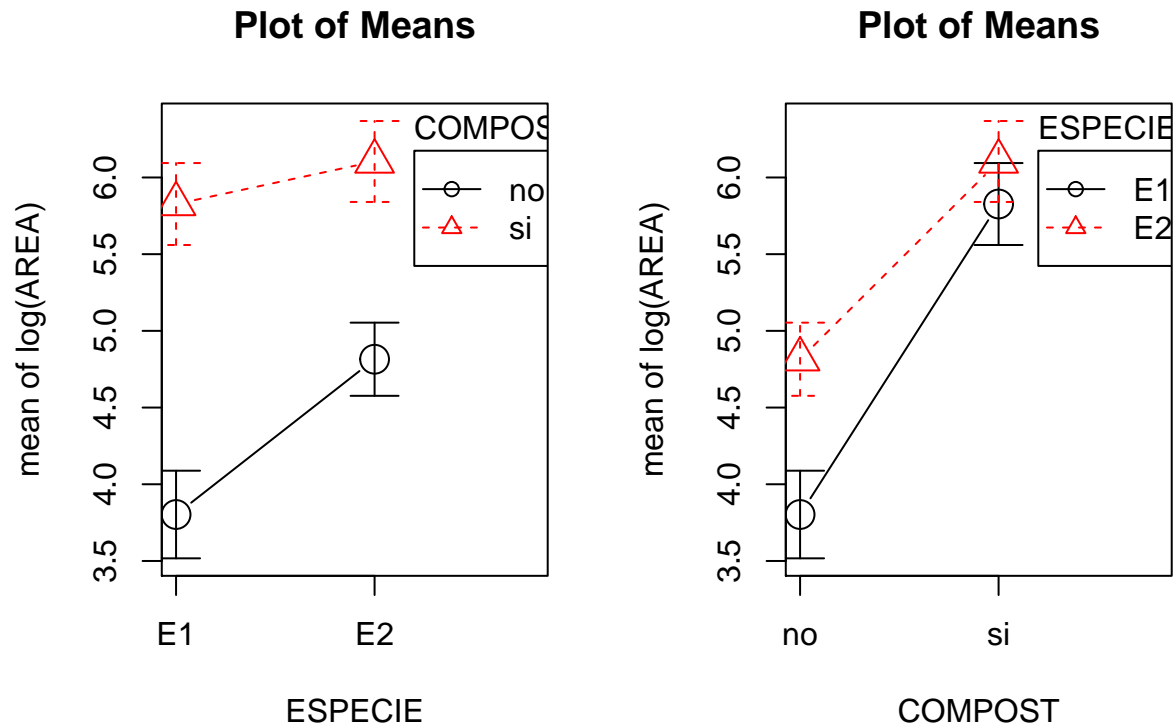
P value adjustment: tukey method for comparing a family of 4 estimates

```
residualPlots(m01,test=F)
```



A)2)

```
oldpar <- par(oma=c(0,0,1,0), mfrow=c(1,2))
with(dd,plotMeans(log(AREA), ESPECIE, COMPOST, error.bars="conf.int", level=0.95))
with(dd,plotMeans(log(AREA), COMPOST, ESPECIE, error.bars="conf.int", level=0.95))
```



```
par(oldpar)
summaryBy(log(AREA)~ESPECIE*COMPOST,data=dd,FUN= c(mean,sd,cv))
```

	ESPECIE	COMPOST	log(AREA).mean	log(AREA).sd	log(AREA).cv
1	E1	no	3.802768	0.2721619	0.07156943
2	E1	si	5.826868	0.2545030	0.04367750
3	E2	no	4.815052	0.2272472	0.04719518
4	E2	si	6.104243	0.2514310	0.04118955

```
m01<-lm(log(AREA)~ESPECIE*COMPOST,data=dd)
summary(m01)
```

Call:

```
lm(formula = log(AREA) ~ ESPECIE * COMPOST, data = dd)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-0.47657	-0.20381	0.08585	0.16359	0.32458

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	5.13723	0.05141	99.931	< 2e-16 ***
ESPECIE1	0.32241	0.05141	6.272	4.01e-06 ***
COMPOST1	0.82832	0.05141	16.113	6.38e-13 ***
ESPECIE1:COMPOST1	-0.18373	0.05141	-3.574	0.0019 **

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

Residual standard error: 0.2518 on 20 degrees of freedom
 Multiple R-squared: 0.9397, Adjusted R-squared: 0.9307
 F-statistic: 103.9 on 3 and 20 DF, p-value: 2.282e-12

```
Anova(m01,type=3)
```

Anova Table (Type III tests)

Response: log(AREA)

	Sum Sq	Df	F value	Pr(>F)
(Intercept)	633.39	1	9986.297	< 2.2e-16 ***
ESPECIE	2.49	1	39.335	4.008e-06 ***
COMPOST	16.47	1	259.624	6.385e-13 ***
ESPECIE:COMPOST	0.81	1	12.773	0.0019 **
Residuals	1.27	20		

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

```
lsmeans(m01,c("ESPECIE","COMPOST"))
```

ESPECIE	COMPOST	lsmean	SE	df	lower.CL	upper.CL
E1	no	3.802768	0.1028151	20	3.588299	4.017236
E2	no	4.815052	0.1028151	20	4.600583	5.029521
E1	si	5.826868	0.1028151	20	5.612399	6.041336
E2	si	6.104243	0.1028151	20	5.889774	6.318711

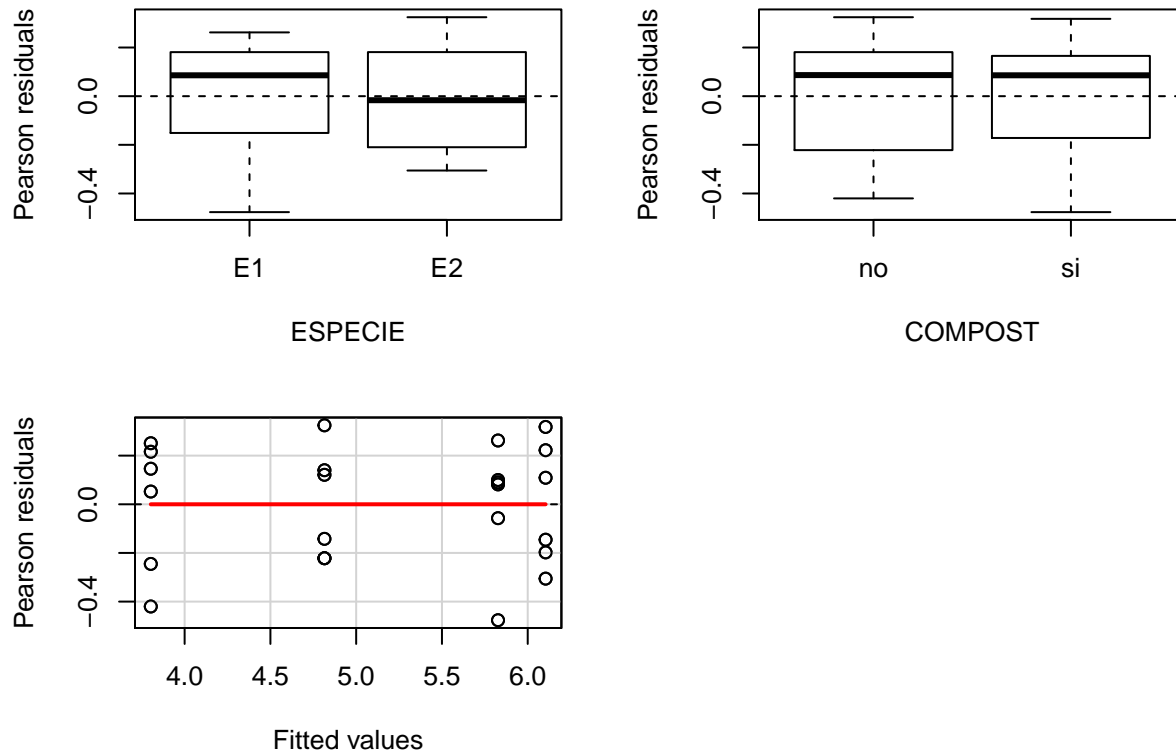
Confidence level used: 0.95

```
pairs(lsmeans(m01,c("ESPECIE","COMPOST")))
```

contrast	estimate	SE	df	t.ratio	p.value
E1,no - E2,no	-1.0122845	0.1454025	20	-6.962	<.0001
E1,no - E1,si	-2.0241003	0.1454025	20	-13.921	<.0001
E1,no - E2,si	-2.3014754	0.1454025	20	-15.828	<.0001
E2,no - E1,si	-1.0118158	0.1454025	20	-6.959	<.0001
E2,no - E2,si	-1.2891909	0.1454025	20	-8.866	<.0001
E1,si - E2,si	-0.2773751	0.1454025	20	-1.908	0.2565

P value adjustment: tukey method for comparing a family of 4 estimates

```
residualPlots(m01,test=F)
```



B)1)

```
m1<-glm(AREA~ESPECIE+COMPOST,family=gaussian(link="identity"),data=dd)
summary(m1)
```

Call:

```
glm(formula = AREA ~ ESPECIE + COMPOST, family = gaussian(link = "identity"),
    data = dd)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-145.076	-35.260	8.457	19.232	163.636

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	244.91	14.28	17.15	7.88e-14 ***
ESPECIE1	47.97	14.28	3.36	0.00297 **
COMPOST1	158.80	14.28	11.12	2.91e-10 ***

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

(Dispersion parameter for gaussian family taken to be 4892.294)

```
Null deviance: 763195  on 23  degrees of freedom
Residual deviance: 102738  on 21  degrees of freedom
AIC: 276.79
```

```
Number of Fisher Scoring iterations: 2
```

```
logLik(m1)
```

```
'log Lik.' -134.3971 (df=4)
```

```
(scale<-sqrt(summary(m1)$disp))
```

```
[1] 69.94493
```

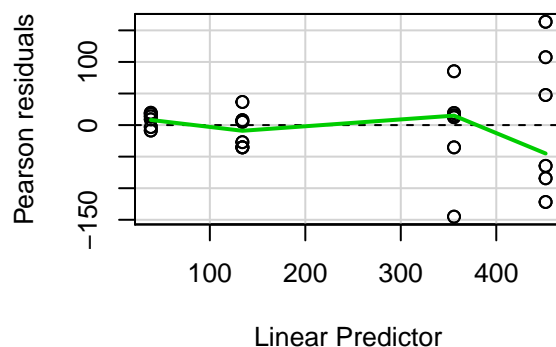
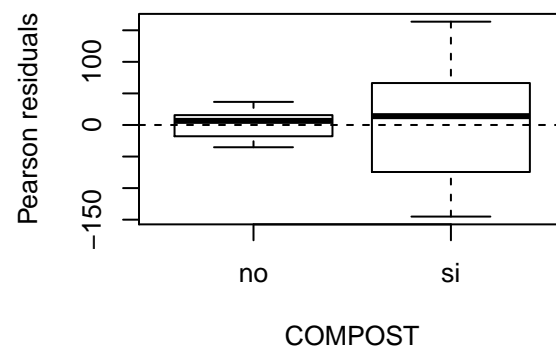
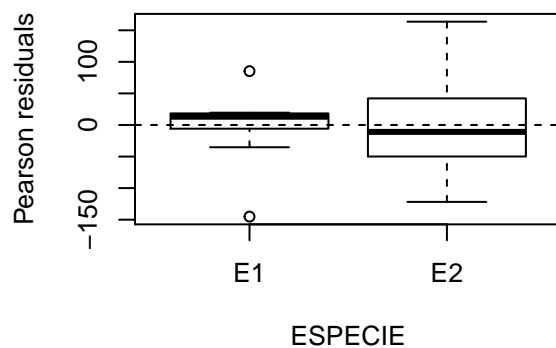
```
sum(residuals(m1,type="pearson")^2)/m1$df.res
```

```
[1] 4892.294
```

```
sum(residuals(m1,type="deviance")^2)/m1$df.res
```

```
[1] 4892.294
```

```
residualPlots(m1,test=F)
```



```
Anova(m1,type=3,error.estimate="pearson",test="LR")
```

Analysis of Deviance Table (Type III tests)

Response: AREA

	LR	Chisq	Df	Pr(>Chisq)
ESPECIE	11.287	1	0.0007806	***
COMPOST	123.713	1	< 2.2e-16	***

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

```
Anova(m1,type=3,error.estimate="pearson",test="F")
```

Analysis of Deviance Table (Type III tests)

Response: AREA

	SS	Df	F	Pr(>F)
ESPECIE	55218	1	11.287	0.002966 **
COMPOST	605239	1	123.713	2.914e-10 ***
Residuals	102738	21		

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

```
cld(lsmeans(m1,c("ESPECIE","COMPOST")))
```

	ESPECIE	COMPOST	lsmean	SE	df	asympt.LCL	asympt.UCL	.group
E1	no		38.14229	24.72927	NA	-10.32618	86.61077	1
E2	no		134.07444	24.72927	NA	85.60596	182.54291	2
E1	si		355.74769	24.72927	NA	307.27922	404.21617	3
E2	si		451.67984	24.72927	NA	403.21137	500.14832	4

Confidence level used: 0.95

P value adjustment: tukey method for comparing a family of 4 estimates

significance level used: alpha = 0.05

```
pairs(lsmeans(m1,c("ESPECIE","COMPOST")))
```

contrast	estimate	SE	df	z.ratio	p.value
E1,no - E2,no	-95.93215	28.55490	NA	-3.359569	0.0043
E1,no - E1,si	-317.60540	28.55490	NA	-11.122624	<.0001
E1,no - E2,si	-413.53755	40.38273	NA	-10.240457	<.0001
E2,no - E1,si	-221.67325	40.38273	NA	-5.489309	<.0001
E2,no - E2,si	-317.60540	28.55490	NA	-11.122624	<.0001
E1,si - E2,si	-95.93215	28.55490	NA	-3.359569	0.0043

P value adjustment: tukey method for comparing a family of 4 estimates

```
Anova(glm(AREA~ESPECIE*COMPOST,family=gaussian(link="identity"),data=dd),type=3,error.estimate="pearson")
```


Analysis of Deviance Table (Type III tests)

Response: AREA

	SS	Df	F	Pr(>F)
ESPECIE	55218	1	10.9126	0.003548 **
COMPOST	605239	1	119.6117	6.877e-10 ***
ESPECIE:COMPOST	1538	1	0.3039	0.587582
Residuals	101201	20		

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

B)2)

```
m2<-glm(AREA~ESPECIE+COMPOST,family=Gamma(link="identity"),data=dd)
summary(m2)
```

Call:

```
glm(formula = AREA ~ ESPECIE + COMPOST, family = Gamma(link = "identity"),
    data = dd)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.49156	-0.19497	0.02953	0.14363	0.35144

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	243.714	13.900	17.534	5.12e-14 ***
ESPECIE1	40.821	6.335	6.443	2.19e-06 ***
COMPOST1	156.944	13.674	11.478	1.65e-10 ***

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

(Dispersion parameter for Gamma family taken to be 0.05534811)

Null deviance: 17.4558 on 23 degrees of freedom

Residual deviance: 1.2386 on 21 degrees of freedom

AIC: 251.77

Number of Fisher Scoring iterations: 4

```
logLik(m2)
```

'log Lik.' -121.8825 (df=4)

```
sum(residuals(m2,type="pearson")^2)/m2$df.res
```

[1] 0.05534808

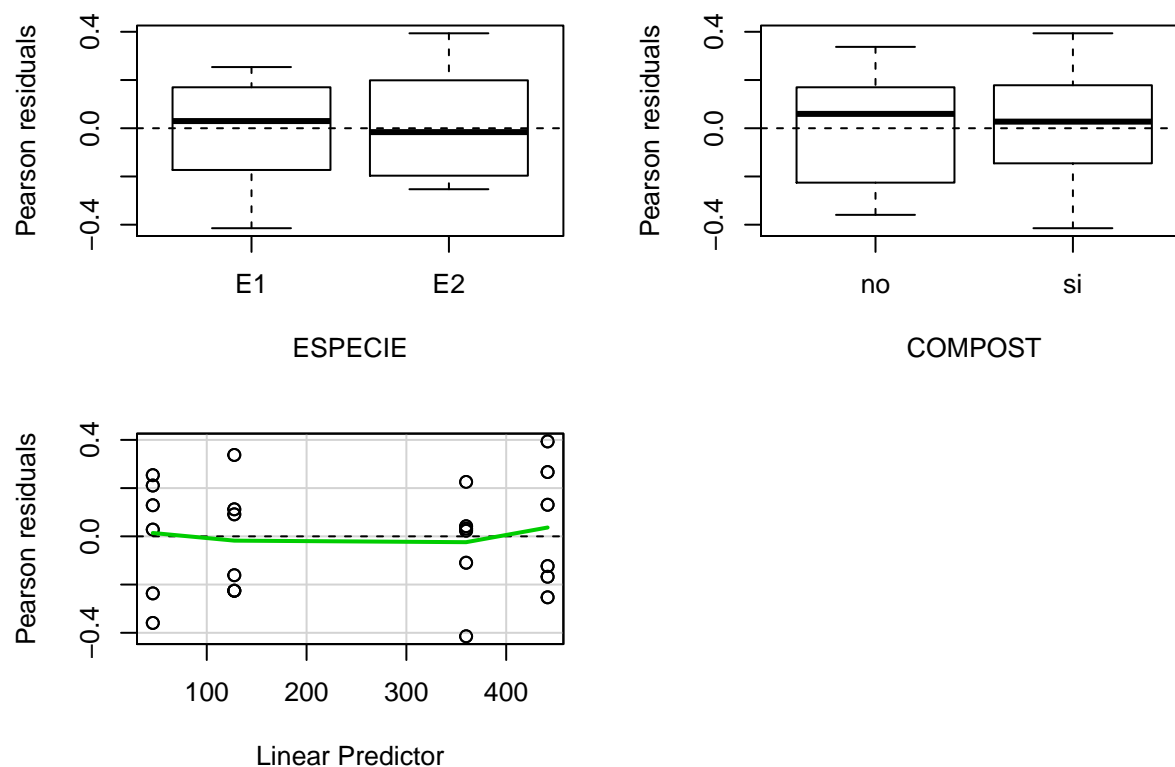
```
(scale<-1/summary(m2)$disp)
```

```
[1] 18.06747
```

```
print(dispdev<-sum(residuals(m2,type="deviance")^2)/m1$df.res)
```

```
[1] 0.05898123
```

```
residualPlots(m2,test=F)
```



```
Anova(m2,type=2,error.estimate="pearson",test="F")
```

Analysis of Deviance Table (Type II tests)

Response: AREA

	SS	Df	F	Pr(>F)
ESPECIE	3.1257	1	56.474	2.212e-07 ***
COMPOST	15.2785	1	276.044	1.475e-13 ***
Residuals	1.1623	21		

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

```
Anova(glm(AREA~ESPECIE*COMPOST,family=Gamma(link="identity"),data=dd),type=2,error.estimate="pearson",t
```

Analysis of Deviance Table (Type II tests)

Response: AREA

	SS	Df	F	Pr(>F)
ESPECIE	3.1257	1	54.9338	3.715e-07 ***
COMPOST	15.2785	1	268.5146	4.664e-13 ***
ESPECIE:COMPOST	0.0178	1	0.3134	0.5818
Residuals	1.1380	20		

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

```
cld(lsmmeans(m2,c("ESPECIE","COMPOST")))
```

ESPECIE	COMPOST	lsmean	SE	df	asympt.LCL	asympt.UCL	.group
E1	no	45.94904	4.399555	NA	37.32608	54.57201	1
E2	no	127.59111	11.960266	NA	104.14942	151.03280	2
E1	si	359.83738	27.262208	NA	306.40444	413.27033	3
E2	si	441.47945	27.849768	NA	386.89491	496.06399	4

Confidence level used: 0.95

P value adjustment: tukey method for comparing a family of 4 estimates

significance level used: alpha = 0.05

```
pairs(lsmmeans(m2,c("ESPECIE","COMPOST")))
```

contrast	estimate	SE	df	z.ratio	p.value
E1,no - E2,no	-81.64207	12.67099	NA	-6.443227	<.0001
E1,no - E1,si	-313.88834	27.34722	NA	-11.477889	<.0001
E1,no - E2,si	-395.53041	28.58521	NA	-13.836892	<.0001
E2,no - E1,si	-232.24627	31.61858	NA	-7.345247	<.0001
E2,no - E2,si	-313.88834	27.34722	NA	-11.477889	<.0001
E1,si - E2,si	-81.64207	12.67099	NA	-6.443227	<.0001

P value adjustment: tukey method for comparing a family of 4 estimates

B)3)

```
m3<-glm(AREA~ESPECIE+COMPOST,family=quasi(link="identity",var="mu^2"),data=dd)
summary(m3)
```

Call:

```
glm(formula = AREA ~ ESPECIE + COMPOST, family = quasi(link = "identity",
  var = "mu^2"), data = dd)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.49156	-0.19497	0.02953	0.14363	0.35144

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	243.714	13.900	17.534	5.12e-14 ***
ESPECIE1	40.821	6.335	6.443	2.19e-06 ***
COMPOST1	156.944	13.674	11.478	1.65e-10 ***

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

(Dispersion parameter for quasi family taken to be 0.05534811)

Null deviance: 17.4558 on 23 degrees of freedom
 Residual deviance: 1.2386 on 21 degrees of freedom
 AIC: NA

Number of Fisher Scoring iterations: 4

```
logLik(m3)
```

'log Lik.' NA (df=3)

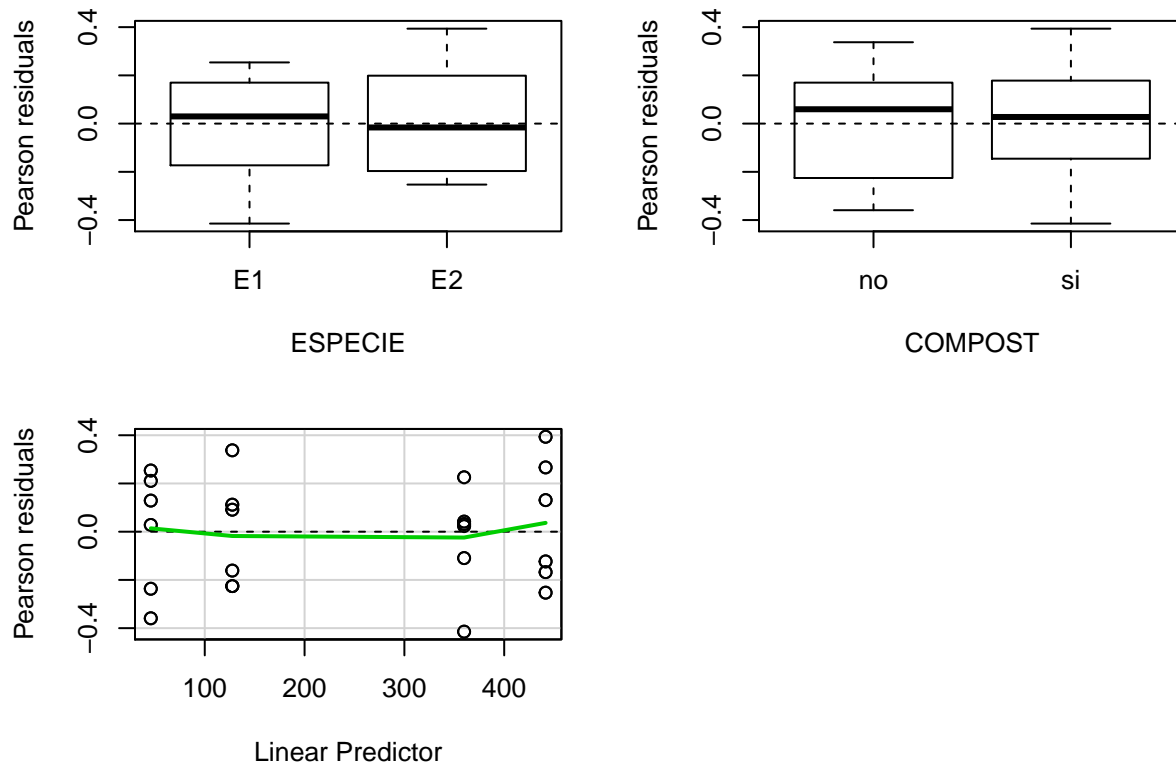
```
sum(residuals(m3,type="pearson")^2)/m1$df.res
```

[1] 0.05534808

```
print(dispdev<-sum(residuals(m3,type="deviance")^2)/m1$df.res)
```

[1] 0.05898123

```
residualPlots(m3,test=F)
```



```
Anova(m3,type=3,error.estimate="pearson",test="F")
```

Analysis of Deviance Table (Type III tests)

Response: AREA

	SS	Df	F	Pr(>F)
ESPECIE	3.1257	1	56.474	2.212e-07 ***
COMPOST	15.2785	1	276.044	1.475e-13 ***
Residuals	1.1623	21		

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

```
Anova(glm(AREA~ESPECIE*COMPOST,family=quasi(link="identity",var="mu^2"),data=dd),type=2,error.estimate=
```

Analysis of Deviance Table (Type II tests)

Response: AREA

	SS	Df	F	Pr(>F)
ESPECIE	3.1257	1	54.9338	3.715e-07 ***
COMPOST	15.2785	1	268.5146	4.664e-13 ***
ESPECIE:COMPOST	0.0178	1	0.3134	0.5818
Residuals	1.1380	20		

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

```
cld(lsmmeans(m3,c("ESPECIE","COMPOST")))
```

ESPECIE	COMPOST	lsmean	SE	df	asympt.LCL	asympt.UCL	.group
E1	no	45.94904	4.399555	NA	37.32608	54.57201	1
E2	no	127.59111	11.960266	NA	104.14942	151.03280	2
E1	si	359.83738	27.262208	NA	306.40444	413.27033	3
E2	si	441.47945	27.849768	NA	386.89491	496.06399	4

Confidence level used: 0.95

P value adjustment: tukey method for comparing a family of 4 estimates

significance level used: alpha = 0.05

```
pairs(lsmmeans(m3,c("ESPECIE","COMPOST")))
```

contrast	estimate	SE	df	z.ratio	p.value
E1,no - E2,no	-81.64207	12.67099	NA	-6.443227	<.0001
E1,no - E1,si	-313.88834	27.34722	NA	-11.477889	<.0001
E1,no - E2,si	-395.53041	28.58521	NA	-13.836892	<.0001
E2,no - E1,si	-232.24627	31.61858	NA	-7.345247	<.0001
E2,no - E2,si	-313.88834	27.34722	NA	-11.477889	<.0001
E1,si - E2,si	-81.64207	12.67099	NA	-6.443227	<.0001

P value adjustment: tukey method for comparing a family of 4 estimates