**Supplementary table 1**. Homologous and heterologous post vaccination neutralising antibody titres (21 or 7 days post vaccination) and clinical observations at 8 days post challenge in cattle vaccinated with a O-3039 + O1 Manisa combination vaccine (Combo) or O-3039 monovalent vaccine and an unvaccinated control group (UVC). Titres are expressed as log10 values at the time of challenge. Combo-21 and O-3039-21 groups were challenged on 21 dpv while Combo-7 and O-3039-7 groups were challenged on 7 dpv. All sera were tested against O1 Manisa, O-3039 and O-ALG virus. Titres ≥1.20 log10 are considered positive and are highlighted in bold. FMD Lesions: + - protected; LF – Left forelimb; BF – Both forelimbs; BH – Both hindlimbs

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Groups | Animal ID | O-3039 | O1 Manisa | O-ALG | Clinical Status |
| Combo-21 | 9658 | **2.40** | **2.10** | **2.40** | + |
| 9659 | **2.40** | **2.10** | **2.40** | + |
| 9660 | **2.40** | **1.95** | **2.40** | + |
| 9661 | **2.25** | **2.10** | **2.40** | + |
| 9662 | **3.00** | **2.40** | **2.10** | + |
| O3039-21 | 9663 | **3.00** | **1.95** | **2.85** | + |
| 9664 | **3.00** | **2.10** | **2.10** | + |
| 9665 | **2.70** | **2.25** | **2.40** | + |
| 9666 | **2.40** | **1.95** | **2.40** | + |
| 9667 | **2.70** | **1.80** | **2.10** | + |
| Combo-7 | 9668 | **2.25** | 0.90 | **1.35** | + |
| 9669 | 1.05 | 0.75 | 0.60 | + |
| 9670 | **2.40** | **1.50** | **2.10** | + |
| 9671 | **1.95** | **1.50** | **1.35** | + |
| 9672 | **2.10** | **1.80** | **1.65** | Not protected; BF |
| O3039-7 | 9673 | **2.10** | **1.35** | **2.10** | + |
| 9674 | **2.10** | **1.80** | **1.35** | Not protected; BH |
| 9675 | **1.95** | 0.75 | **1.80** | + |
| 9676 | **2.10** | 1.05 | **2.40** | + |
| 9677 | **1.80** | **1.50** | 1.05 | Not protected; BF, RH |
| UVC | 9678 | 0.30 | 0.30 | 0.30 | Generalised; LF, BH |
| 9679 | 0.30 | 0.30 | 0.45 | Generalised; BF, BH |
| 9680 | 0.30 | 0.30 | 0.30 | Generalised; BF, BH |

**LVZ194 Type O vaccines linear and linear mixed model analysis using R-Statistics**

R version 4.0.2 (2020-06-22) -- "Taking Off Again"

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Platform: x86\_64-w64-mingw32/x64 (64-bit)

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[Workspace loaded from C:/Data/Type O/.RData]

####################################################################################

> setwd("C:/Data/Type O/New analysis")

> getwd()

[1] "C:/Data/Type O/New analysis"

> library(lme4)

Loading required package: Matrix

**###### protection against challenge #########**

**###### vaccinated vs control against challenge #########**

> pr<-matrix(c(3,17,3,0),byrow=T,ncol=2,dimnames=list(c("vaccinated","control"),c("non-protected","Protected")))

> pr

|  |  |  |
| --- | --- | --- |
|  | non-protected | Protected |
| vaccinated | 3 | 17 |
| control | 3 | 0 |

> fisher.test(pr)

Fisher's Exact Test for Count Data

data: pr

p-value = 0.01129

alternative hypothesis: true odds ratio is not equal to 1

95 percent confidence interval: 0.0000000 0.6866581

sample estimates: odds ratio = 0

**###### day post vaccination against challenge #########**

> table(prot1,day)

|  |  |  |
| --- | --- | --- |
|  | day | |
| prot1 | 21 | 7 |
| 0 | 0 | 3 |
| 1 | 10 | 7 |

> fisher.test(table(prot1,day))

Fisher's Exact Test for Count Data

data: table(prot1, day)

p-value = 0.2105

alternative hypothesis: true odds ratio is not equal to 1

95 percent confidence interval: 0.000000 2.255229

sample estimates: odds ratio = 0

**###### type of vaccine against challenge #########**

> table(prot1,vaccine)

|  |  |  |
| --- | --- | --- |
|  | Vaccine | |
| prot1 | Combo | O3039 |
| 0 | 1 | 2 |
| 1 | 9 | 8 |

> fisher.test(table(prot1,vaccine))

Fisher's Exact Test for Count Data

data: table(prot1, vaccine)

p-value = 1

alternative hypothesis: true odds ratio is not equal to 1

95 percent confidence interval: 0.0067986 10.5137419

sample estimates: odds ratio = 0.4624944

**###### vaccine groups against challenge #########**

> protection.vac<-matrix(c(5,0,5,0,4,1,3,2), byrow=T, ncol=2, dimnames=list(c("Combo-21","O3039-21","Combo-7","O3039-7"), c("Protected","Not protected")))

> protection.vac

|  |  |  |
| --- | --- | --- |
|  | Protected | Not protected |
| Combo-21 | 5 | 0 |
| O3039-21 | 5 | 0 |
| Combo-7 | 4 | 1 |
| O3039-7 | 3 | 2 |

> fisher.test(protection.vac)

Fisher's Exact Test for Count Data

data: protection.vac

p-value = 0.5614

alternative hypothesis: two.sided

**###### vaccine groups against challenge with controls #########**

> protection.uvc<-matrix(c(5,0,5,0,4,1,3,2,0,3),byrow=T,ncol=2,dimnames=list(c("Combo-21","O3039-21","Combo-7","O3039-7","UVC"),c("Protected","Not protected")))

> protection.uvc

|  |  |  |
| --- | --- | --- |
|  | Protected | Not protected |
| Combo-21 | 5 | 0 |
| O3039-21 | 5 | 0 |
| Combo-7 | 4 | 1 |
| O3039-7 | 3 | 2 |
| UVC | 0 | 3 |

> fisher.test(protection.uvc) #only after inclusion of controls significant

Fisher's Exact Test for Count Data

data: protection.uvc

p-value = 0.01359

alternative hypothesis: two.sided

**#############Antibody titres and protective response**

> data<-read.csv('LVZ194.csv',sep=';')

> data$AbOManisa<-ifelse(data$AbOManisa=='<0.3',0.15,as.numeric(as.character(data$AbOManisa)))

> data$AbO3039<-ifelse(data$AbO3039=='<0.3',0.15,as.numeric(as.character(data$AbO3039)))

> data$AbOAlg<-ifelse(data$AbOAlg=='<0.3',0.15,as.numeric(as.character(data$AbOAlg)))

> data$day<-ifelse(is.na(data$day),'control',data$day)

> data$day<-factor(data$day)

> data$group<-factor(data$group)

> summary(data)

> attach(data)

> table(paste(day,vaccine),group)

**########## O Manisa serology between groups 21 day and 7 day**

> t.test(data[group==1|group==3,]$AbOManisa~factor(data[group==1|group==3,]$group),var.equal=T)

Two Sample t-test

data: data[group == 1 | group == 3, ]$AbOManisa by factor(data[group == 1 | group == 3, ]$group)

t = 3.9598, df = 8, p-value = 0.004178

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

0.3508227 1.3291773

sample estimates:

mean in group 1 mean in group 3

2.13 1.29

> t.test(data[group==1|group==3,]$AbOAlg~factor(data[group==1|group==3,]$group),var.equal=T)

Two Sample t-test

data: data[group == 1 | group == 3, ]$AbOAlg by factor(data[group == 1 | group == 3, ]$group)

t = 3.692, df = 8, p-value = 0.006112

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

0.3491341 1.5108659

sample estimates:

mean in group 1 mean in group 3

2.34 1.41

**########## O 3039 serology between groups 21 day and 7 day**

> t.test(data[group==2|group==4,]$AbO3039~factor(data[group==2|group==4,]$group),var.equal=T)

Two Sample t-test

data: data[group == 2 | group == 4, ]$AbO3039 by factor(data[group == 2 | group == 4, ]$group)

t = 5.8926, df = 8, p-value = 0.0003648

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

0.4564936 1.0435064

sample estimates:

mean in group 2 mean in group 4

2.76 2.01

> t.test(data[group==2|group==4,]$AbOAlg~factor(data[group==2|group==4,]$group),var.equal=T)

Two Sample t-test

data: data[group == 2 | group == 4, ]$AbOAlg by factor(data[group == 2 | group == 4, ]$group)

t = 2.245, df = 8, p-value = 0.055

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

-0.01712081 1.27712081

sample estimates:

mean in group 2 mean in group 4

2.37 1.74

**########## O Alg serology between groups 21 day and 7 day**

> t.test(data[group==1|group==2,]$AbOAlg~factor(data[group==1|group==2,]$group),var.equal=T)

Two Sample t-test

data: data[group == 1 | group == 2, ]$AbOAlg by factor(data[group == 1 | group == 2, ]$group)

t = -0.2, df = 8, p-value = 0.8465

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

-0.3759006 0.3159006

sample estimates:

mean in group 1 mean in group 2

2.34 2.37

> t.test(data[group==3|group==4,]$AbOAlg~factor(data[group==3|group==4,]$group),var.equal=T)

Two Sample t-test

data: data[group == 3 | group == 4, ]$AbOAlg by factor(data[group == 3 | group == 4, ]$group)

t = -0.95382, df = 8, p-value = 0.3681

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

-1.1278241 0.4678241

sample estimates:

mean in group 3 mean in group 4

1.41 1.74

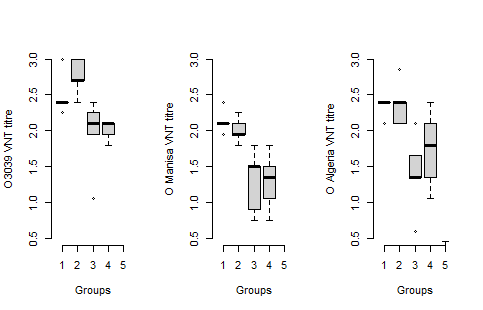
**##### Figure 2 ########**

> par(bty='n',mfrow=c(1,3))

> boxplot(data[group==1|group==2|group==3|group==4|group==5,]$AbO3039~data[group==1|group==2|group==3|group==4|group==5,]$group,ylim=c(0.5,3),ylab="O3039 VNT titre",xlab="Groups")

> boxplot(data[group==1|group==2|group==3|group==4|group==5,]$AbOManisa~data[group==1|group==2|group==3|group==4|group==5,]$group,ylim=c(0.5,3),ylab="O Manisa VNT titre",xlab="Groups")

> boxplot(data[group==1|group==2|group==3|group==4|group==5,]$AbOAlg~data[group==1|group==2|group==3|group==4|group==5,]$group,ylim=c(0.5,3),ylab="O Algeria VNT titre",xlab="Groups")



**### Statistics for Figure 2 #####**

**########## O Manisa serology between groups 21 day and 7 day (including control)**

> summary(aov(data[group!=2&group!=4,]$AbOManisa~data[group!=2&group!=4,]$group))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| data[group != 2 & group != 4, ]$group | 2 | 6.352 | 3.176 | 35.29 | 2.94E-05 | \*\*\* |
| Residuals | 10 | 0.9 | 0.09 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(data[group!=2&group!=4,]$AbOManisa,data[group!=2&group!=4,]$group,pool.sd=F)

Pairwise comparisons using t tests with non-pooled SD

data: data[group != 2 & group != 4, ]$AbOManisa and data[group != 2 & group != 4, ]$group

|  |  |  |
| --- | --- | --- |
|  | 1 | 3 |
| 3 | 0.015 | - |
| 5 | 4.60E-05 | 0.015 |

P value adjustment method: holm

> summary(aov(AbOManisa~group,data[group==1|group==3,]))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| group | 1 | 1.764 | 1.764 | 15.68 | 0.00418 | \*\* |
| Residuals | 8 | 0.9 | 0.1125 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(data[group==1|group==3,]$AbOManisa,data[group==1|group==3,]$group,pool.sd=T)

Pairwise comparisons using t tests with pooled SD

data: data[group == 1 | group == 3, ]$AbOManisa and data[group == 1 | group == 3, ]$group

|  |  |
| --- | --- |
|  | 1 |
| 3 | 0.0042 |

P value adjustment method: holm

**########## O 3039 serology between groups 21 day and 7 day (including control)**

> summary(aov(data[group!=1&group!=3,]$AbO3039~data[group!=1&group!=3,]$group))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| data[group != 1 & group != 3, ]$group | 2 | 11.438 | 5.719 | 176.5 | 1.59E-08 | \*\*\* |
| Residuals | 10 | 0.324 | 0.032 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(data[group!=1&group!=3,]$AbO3039,data[group!=1&group!=3,]$group,pool.sd=F)

Pairwise comparisons using t tests with non-pooled SD

data: data[group != 1 & group != 3, ]$AbO3039 and data[group != 1 & group != 3, ]$group

|  |  |  |
| --- | --- | --- |
|  | 2 | 4 |
| 4 | 0.00099 | - |
| 5 | 5.10E-05 | 2.70E-05 |

P value adjustment method: holm

> summary(aov(AbO3039~group,data[group==2|group==4,]))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| group | 1 | 1.406 | 1.4062 | 34.72 | 0.000365 | \*\*\* |
| Residuals | 8 | 0.324 | 0.0405 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(data[group==2|group==4,]$AbO3039,data[group==2|group==4,]$group)

Pairwise comparisons using t tests with pooled SD

data: data[group == 2 | group == 4, ]$AbO3039 and data[group == 2 | group == 4, ]$group

|  |  |
| --- | --- |
|  | 2 |
| 4 | 0.00036 |

P value adjustment method: holm

**########## O Alg serology between groups 21 day and 7 day (including control)**

> summary(aov(data[group!=2&group!=4,]$AbOAlg~data[group!=2&group!=4,]$group))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| data[group != 2 & group != 4, ]$group | 2 | 7.529 | 3.765 | 29.32 | 6.56E-05 | \*\*\* |
| Residuals | 10 | 1.284 | 0.128 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(data[group!=2&group!=4,]$AbOAlg,data[group!=2&group!=4,]$group,pool.sd=F)

Pairwise comparisons using t tests with non-pooled SD

data: data[group != 2 & group != 4, ]$AbOAlg and data[group != 2 & group != 4, ]$group

|  |  |  |
| --- | --- | --- |
|  | 1 | 3 |
| 3 | 0.022 | - |
| 5 | 9.70E-07 | 0.022 |

P value adjustment method: holm

> summary(aov(AbOAlg~group,data[group==1|group==3,]))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| group | 1 | 2.162 | 2.1622 | 13.63 | 0.00611 | \*\* |
| Residuals | 8 | 1.269 | 0.1586 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(data[group==1|group==3,]$AbOAlg,data[group==1|group==3,]$group,pool.sd=T)

Pairwise comparisons using t tests with pooled SD

data: data[group == 1 | group == 3, ]$AbOAlg and data[group == 1 | group == 3, ]$group

|  |  |
| --- | --- |
| 1 |  |
| 3 | 0.0061 |

P value adjustment method: holm

**########## O Algeria serology in O Combo groups**

> summary(aov(data[group!=1&group!=3,]$AbOAlg~data[group!=1&group!=3,]$group))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| data[group != 1 & group != 3, ]$group | 2 | 7.701 | 3.85 | 24.22 | 0.00015 | \*\*\* |
| Residuals | 10 | 1.59 | 0.159 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(data[group!=1&group!=3,]$AbOAlg,data[group!=1&group!=3,]$group,pool.sd=F)

Pairwise comparisons using t tests with non-pooled SD

data: data[group != 1 & group != 3, ]$AbOAlg and data[group != 1 & group != 3, ]$group

|  |  |  |
| --- | --- | --- |
|  | 2 | 4 |
| 4 | 0.06382 | - |
| 5 | 0.00011 | 0.00807 |

P value adjustment method: holm

**########## O Algeria serology in O3039 groups**

> summary(aov(data[group!=2&group!=4,]$AbOAlg~data[group!=2&group!=4,]$group))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| data[group != 2 & group != 4, ]$group | 2 | 7.529 | 3.765 | 29.32 | 6.56E-05 | \*\*\* |
| Residuals | 10 | 1.284 | 0.128 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(data[group!=2&group!=4,]$AbOAlg,data[group!=2&group!=4,]$group,pool.sd=F)

Pairwise comparisons using t tests with non-pooled SD

data: data[group != 2 & group != 4, ]$AbOAlg and data[group != 2 & group != 4, ]$group

|  |  |  |
| --- | --- | --- |
|  | 1 | 3 |
| 3 | 0.022 | - |
| 5 | 9.70E-07 | 0.022 |

P value adjustment method: holm

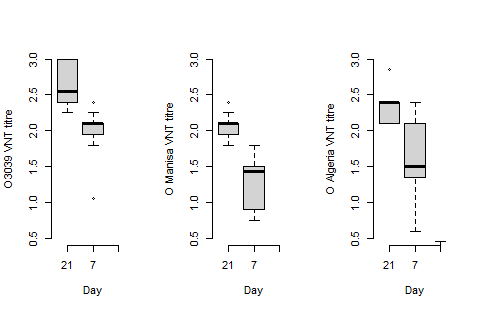
**###############Figure 3**

> par(bty='n',mfrow=c(1,3))

> boxplot(AbO3039~day, ylim=c(0.5,3),ylab="O3039 VNT titre",xlab="Day")

> boxplot(AbOManisa~day, ylim=c(0.5,3),ylab="O Manisa VNT titre",xlab="Day")

> boxplot(AbOAlg~day, ylim=c(0.5,3),ylab="O Algeria VNT titre",xlab="Day")



**###### Statistics for Figure 3 #####**

**######### O Algeria titers**

> tapply(AbOAlg,paste(group,day,vaccine),mean)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| 1 21 Combo | 2 21 O3039 | 3 7 Combo | 4 7 O3039 | 5 control Control |
| 2.34 | 2.37 | 1.41 | 1.74 | 0.35 |

> summary(aov(AbOAlg~group))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| group | 4 | 10.121 | 2.5301 | 15.93 | 9.79E-06 | \*\*\* |
| Residuals | 18 | 2.859 | 0.1588 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(AbOAlg,group)

Pairwise comparisons using t tests with pooled SD

data: AbOAlg and group

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | 1 | 2 | 3 | 4 |
| 2 | 0.9066 | - | - | - |
| 3 | 0.0101 | 0.009 | - | - |
| 4 | 0.0893 | 0.0893 | 0.4139 | - |
| 5 | 1.90E-05 | 1.70E-05 | 0.0101 | 0.0012 |

P value adjustment method: holm

> tapply(AbOAlg,vaccine,mean)

|  |  |  |
| --- | --- | --- |
| Combo | O3039 | Control |
| 1.875 | 2.055 | 0.35 |

> summary(aov(AbOAlg~vaccine))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| vaccine | 2 | 6.966 | 3.483 | 11.58 | 0.00046 | \*\*\* |
| Residuals | 20 | 6.014 | 0.301 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(AbOAlg,vaccine)

Pairwise comparisons using t tests with pooled SD

data: AbOAlg and vaccine

|  |  |  |
| --- | --- | --- |
|  | Combo | Control |
| O3039 | 0.47145 | 0.00039 |
| Control | 0.00083 | - |

P value adjustment method: holm

> summary(aov(AbOAlg~vaccine+day,data[vaccine!="control",]))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| vaccine | 2 | 6.966 | 3.483 | 22.27 | 1.04E-05 | \*\*\* |
| day | 1 | 3.042 | 3.042 | 19.45 | 0.000301 | \*\*\* |
| Residuals | 19 | 2.972 | 0.156 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(aov(AbOAlg~day))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| day | 2 | 9.846 | 4.923 | 31.42 | 6.73E-07 | \*\*\* |
| Residuals | 20 | 3.133 | 0.157 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(AbOAlg,day)

Pairwise comparisons using t tests with pooled SD

data: AbOAlg and day

|  |  |  |
| --- | --- | --- |
|  | 21 | 7 |
| 7 | 0.00027 | - |
| control | 6.30E-07 | 0.00027 |

P value adjustment method: holm

**######### O3039 titers**

> tapply(AbO3039,paste(group,day,vaccine),mean)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| 1 21 Combo | 2 21 O3039 | 3 7 Combo | 4 7 O3039 | 5 control Control |
| 2.49 | 2.76 | 1.95 | 2.01 | 0.3 |

> summary(aov(AbO3039~group))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| group | 4 | 12.732 | 3.183 | 31.99 | 5.86E-08 | \*\*\* |
| Residuals | 18 | 1.791 | 0.099 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(AbO3039,group)

Pairwise comparisons using t tests with pooled SD

data: AbO3039 and group

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | 1 | 2 | 3 | 4 |
| 2 | 0.3854 | - | - | - |
| 3 | 0.0578 | 0.0044 | - | - |
| 4 | 0.0813 | 0.0072 | 0.767 | - |
| 5 | 1.70E-07 | 3.20E-08 | 8.00E-06 | 5.60E-06 |

P value adjustment method: holm

> tapply(AbO3039,vaccine,mean)

|  |  |  |
| --- | --- | --- |
| Combo | O3039 | Control |
| 2.22 | 2.39 | 0.30 |

> summary(aov(AbO3039~vaccine))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| vaccine | 2 | 10.597 | 5.299 | 26.99 | 2.09E-06 | \*\*\* |
| Residuals | 20 | 3.926 | 0.196 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(AbO3039,vaccine)

Pairwise comparisons using t tests with pooled SD

data: AbO3039 and vaccine

|  |  |  |
| --- | --- | --- |
|  | Combo | Control |
| O3039 | 0.41 | 1.90E-06 |
| Control | 4.10E-06 | - |

P value adjustment method: holm

> summary(aov(AbO3039~vaccine+day,data[vaccine!="control",]))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| vaccine | 2 | 10.597 | 5.299 | 54.53 | 1.34E-08 | \*\*\* |
| day | 1 | 2.08 | 2.08 | 21.41 | 0.00018 | \*\*\* |
| Residuals | 19 | 1.846 | 0.097 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(aov(AbO3039~day))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| day | 2 | 12.541 | 6.271 | 63.27 | 2.24E-09 | \*\*\* |
| Residuals | 20 | 1.982 | 0.099 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(AbO3039,day)

Pairwise comparisons using t tests with pooled SD

data: AbO3039 and day

|  |  |  |
| --- | --- | --- |
|  | 21 | 7 |
| 7 | 0.00018 | - |
| control | 1.30E-09 | 1.90E-07 |

P value adjustment method: holm

**############ O Manisa titers**

> tapply(AbOManisa,paste(group,day,vaccine),mean)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| 1 21 Combo | 2 21 O3039 | 3 7 Combo | 4 7 O3039 | 5 control Control |
| 2.13 | 2.01 | 1.29 | 1.29 | 0.30 |

> summary(aov(AbOManisa~group))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| group | 4 | 8.046 | 2.011 | 21.63 | 1.13E-06 | \*\*\* |
| Residuals | 18 | 1.674 | 0.093 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(AbOManisa,group)

Pairwise comparisons using t tests with pooled SD

data: AbOManisa and group

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | 1 | 2 | 3 | 4 |
| 2 | 1 | - | - | - |
| 3 | 0.0025 | 0.0061 | - | - |
| 4 | 0.0025 | 0.0061 | 1 | - |
| 5 | 1.70E-06 | 3.90E-06 | 0.0025 | 0.0025 |

P value adjustment method: holm

> tapply(AbOManisa,vaccine,mean)

|  |  |  |
| --- | --- | --- |
| Combo | O3039 | Control |
| 1.71 | 1.65 | 0.30 |

> summary(aov(AbOManisa~vaccine))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| vaccine | 2 | 4.986 | 2.493 | 10.53 | 0.00075 | \*\*\* |
| Residuals | 20 | 4.734 | 0.2367 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(AbOManisa,vaccine)

Pairwise comparisons using t tests with pooled SD

data: AbOManisa and vaccine

|  |  |  |
| --- | --- | --- |
|  | Combo | Control |
| O3039 | 0.78556 | 0.00085 |
| Control | 0.00082 | - |

P value adjustment method: holm

> summary(aov(AbOManisa~vaccine+day,data[vaccine!="control",]))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| vaccine | 2 | 4.986 | 2.493 | 28 | 2.17E-06 | \*\*\* |
| day | 1 | 3.042 | 3.042 | 34.16 | 1.25E-05 | \*\*\* |
| Residuals | 19 | 1.692 | 0.0891 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(aov(AbOManisa~day))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| day | 2 | 8.01 | 4.005 | 46.84 | 2.84E-08 | \*\*\* |
| Residuals | 20 | 1.71 | 0.086 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(AbOManisa,day)

Pairwise comparisons using t tests with pooled SD

data: AbOManisa and day

|  |  |  |
| --- | --- | --- |
|  | 21 | 7 |
| 7 | 1.60E-05 | - |
| control | 3.80E-08 | 4.90E-05 |

P value adjustment method: holm

**###############Linear Models Ab O3039 #############**

> q0<-lm(AbO3039~1,data[vaccine!="control",])

> q1<-lm(AbO3039~day,data[vaccine!="control",])

> q2<-lm(AbO3039~vaccine,data[vaccine!="control",])

> AIC(q0,q1,q2)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| q0 | 2 | 58.69709 |
| q1 | 4 | 16.89215 |
| q2 | 4 | 32.61156 |

> q3<-lm(AbO3039~day+vaccine,data[vaccine!="control",])

> AIC(q1,q3)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| q1 | 4 | 16.89215 |
| q3 | 5 | 17.25585 |

> q4<-lm(AbO3039~day+vaccine+day:vaccine,data[vaccine!="control",])

> AIC(q1,q4)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| q1 | 4 | 16.89215 |
| q4 | 6 | 18.55861 |

> summary(q1)

Call:

lm(formula = AbO3039 ~ day, data = data[vaccine != "control", ])

Residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -0.930 | -0.203 | 0.000 | 0.120 | 0.420 |

Coefficients:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Estimate | Std. Error | t value | Pr(>|t|) |  |
| (Intercept) | 2.625 | 0.09956 | 26.367 | < 2e-16 | \*\*\* |
| day7 | -0.645 | 0.14079 | -4.581 | 0.000181 | \*\*\* |
| daycontrol | -2.325 | 0.20724 | -11.219 | 4.42E-10 | \*\*\* |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.3148 on 20 degrees of freedom

Multiple R-squared: 0.8635, Adjusted R-squared: 0.8499

F-statistic: 63.27 on 2 and 20 DF, p-value: 2.244e-09

**###############Linear Models Ab OManisa**

> q0<-lm(AbOManisa~1,data[vaccine!="control",])

> q1<-lm(AbOManisa~day,data[vaccine!="control",])

> q2<-lm(AbOManisa~vaccine,data[vaccine!="control",])

> AIC(q0,q1,q2)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| q0 | 2 | 49.46107 |
| q1 | 4 | 13.49415 |
| q2 | 4 | 36.91453 |

> q3<-lm(AbOManisa~day+vaccine,data[vaccine!="control",])

> AIC(q1,q3)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| q1 | 4 | 13.49415 |
| q3 | 5 | 15.25076 |

> q4<-lm(AbOManisa~day+vaccine+day:vaccine,data[vaccine!="control",])

> AIC(q1,q4)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| q1 | 4 | 13.49415 |
| q4 | 6 | 17.00477 |

> summary(q1)

Call:

lm(formula = AbOManisa ~ day, data = data[vaccine != "control", ])

Residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -0.54 | -0.12 | 0.03 | 0.20 | 0.51 |

Coefficients:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Estimate | Std. Error | t value | Pr(>|t|) |  |
| (Intercept) | 2.07 | 0.09247 | 22.387 | 1.24E-15 | \*\*\* |
| day7 | -0.78 | 0.13077 | -5.965 | 7.83E-06 | \*\*\* |
| daycontrol | -1.77 | 0.19248 | -9.196 | 1.27E-08 | \*\*\* |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.2924 on 20 degrees of freedom

Multiple R-squared: 0.8241, Adjusted R-squared: 0.8065

F-statistic: 46.84 on 2 and 20 DF, p-value: 2.84e-08

**###############Linear Models Ab O Algeria**

> > q0<-lm(AbOAlg~1,data[vaccine!="control",])

> q1<-lm(AbOAlg~day,data[vaccine!="control",])

> q2<-lm(AbOAlg~vaccine,data[vaccine!="control",])

> AIC(q0,q1,q2)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| q0 | 2 | 56.11246 |
| q1 | 4 | 27.42427 |
| q2 | 4 | 42.41697 |

> q3<-lm(AbOAlg~day+vaccine,data[vaccine!="control",])

> AIC(q1,q3)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| q1 | 4 | 27.42427 |
| q3 | 5 | 28.20334 |

> q4<-lm(AbOAlg~day+vaccine+day:vaccine,data[vaccine!="control",])

> AIC(q1,q4)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| q1 | 4 | 27.42427 |
| q4 | 6 | 29.31566 |

> summary(q1)

Call:

lm(formula = AbOAlg ~ day, data = data[vaccine != "control", ])

Residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -0.975 | -0.225 | 0.045 | 0.0875 | 0.825 |

Coefficients:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Estimate | Std. Error | t value | Pr(>|t|) |  |
| (Intercept) | 2.355 | 0.1252 | 18.814 | 3.46E-14 | \*\*\* |
| day7 | -0.78 | 0.177 | -4.406 | 0.000272 | \*\*\* |
| daycontrol | -2.005 | 0.2606 | -7.695 | 2.11E-07 | \*\*\* |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.3958 on 20 degrees of freedom

Multiple R-squared: 0.7586, Adjusted R-squared: 0.7344

F-statistic: 31.42 on 2 and 20 DF, p-value: 6.725e-07

**############ NOW WITHOUT CONTROLS ######################**

**######### Comparison of r1 values ############**

> data<-data[data$group!=5,]

> attach(droplevels(data))

> table(paste(vaccine,day),group)

> exp(tapply(log(r1O3039),paste(vaccine,day),mean))

Combo 21 Combo 7 O3039 21 O3039 7

0.7079458 0.2884032 0.4073803 0.5370318

> exp(tapply(log(r1O3039),paste(vaccine,day),min))

Combo 21 Combo 7 O3039 21 O3039 7

0.1258925 0.1258925 0.1258925 0.1778279

> exp(tapply(log(r1O3039),paste(vaccine,day),max))

Combo 21 Combo 7 O3039 21 O3039 7

1.4125375 0.5011872 1.0000000 1.9952623

> m0<-lm(AbO3039~1)

> m1<-lm(AbO3039~vaccine)

> m2<-lm(AbO3039~day)

> AIC(m0,m1,m2)#m2 has low AIC

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| m0 | 2 | 28.87825 |
| m1 | 3 | 30.19659 |
| m2 | 3 | 16.52755 |

> anova(m0,m1)

Analysis of Variance Table

Model 1: AbO3039 ~ 1

Model 2: AbO3039 ~ vaccine

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Res.Df | RSS | Df | Sum of Sq | F | Pr(>F) |
| 1 | 19 | 4.0624 |  |  |  |  |
| 2 | 18 | 3.9262 | 1 | 0.13612 | 0.62410 | 0.43980 |

> summary(aov(AbO3039~vaccine))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| vaccine | 1 | 0.136 | 0.1361 | 0.624 | 0.44 |
| Residuals | 18 | 3.926 | 0.2181 |  |  |

#pairwise.t.test(AbO3039,vaccine); No difference in type of vaccine

> anova(m0,m2)

Analysis of Variance Table

Model 1: AbO3039 ~ 1

Model 2: AbO3039 ~ day

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Res.Df | RSS | Df | Sum of Sq | F | Pr(>F) |  |
| 1 | 19 | 4.0624 |  |  |  |  |  |
| 2 | 18 | 1.9823 | 1 | 2.08010 | 18.889 | 0.0003892 | \*\*\* |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(aov(AbO3039~day))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| vaccine | 1 | 2.080 | 2.0801 | 18.89 | 0.000389 | \*\*\* |
| Residuals | 18 | 1.982 | 0.1101 |  |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(AbO3039,day)

Pairwise comparisons using t tests with pooled SD

data: AbO3039 and day

|  |  |
| --- | --- |
|  | 21 |
| 7 | 0.00039 |

P value adjustment method: holm

> m3<-lm(AbO3039~day+vaccine)

> AIC(m2,m3)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| m2 | 3 | 16.52755 |
| m3 | 4 | 17.10467 |

> anova(m2,m3)

Analysis of Variance Table

Model 1: AbO3039 ~ day

Model 2: AbO3039 ~ day + vaccine

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Res.Df | RSS | Df | Sum of Sq | F | Pr(>F) |
| 1 | 18 | 1.9823 |  |  |  |  |
| 2 | 17 | 1.8461 | 1 | 0.13612 | 1.254 | 0.2785 |

> data<-data[data$group!=5,]

> attach(droplevels(data))

> table(paste(vaccine,day),group)

> exp(tapply(log(r1Oman),paste(vaccine,day),mean))

Combo 21 Combo 7 O3039 21 O3039 7

1.621810 1.318257 NA NA

> exp(tapply(log(r1Oman),paste(vaccine,day),min))

Combo 21 Combo 7 O3039 21 O3039 7

0.5011872 0.7079458 NA NA

> exp(tapply(log(r1Oman),paste(vaccine,day),max))

Combo 21 Combo 7 O3039 21 O3039 7

2.818383 3.981072 NA NA

> m0<-lm(AbOManisa~1)

> m1<-lm(AbOManisa~vaccine)

> m2<-lm(AbOManisa~day)

> AIC(m0,m1,m2)#m2 has low AIC

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| m0 | 2 | 32.01421 |
| m1 | 3 | 33.93831 |
| m2 | 3 | 13.57276 |

> anova(m0,m1)

Analysis of Variance Table

Model 1: AbOManisa ~ 1

Model 2: AbOManisa ~ vaccine

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Res.Df | RSS | Df | Sum of Sq | F | Pr(>F) |
| 1 | 19 | 4.752 |  |  |  |  |
| 2 | 18 | 4.734 | 1 | 0.018 | 0.0684 | 0.7966 |

> summary(aov(AbOManisa~vaccine))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| vaccine | 1 | 0.018 | 0.018 | 0.068 | 0.797 |
| Residuals | 18 | 4.734 | 0.263 |  |  |

#pairwise.t.test(AbOManisa,vaccine); No difference in type of vaccine

> anova(m0,m2)

Analysis of Variance Table

Model 1: AbOManisa ~ 1

Model 2: AbOManisa ~ day

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Res.Df | RSS | Df | Sum of Sq | F | Pr(>F) |  |
| 1 | 19 | 4.752 |  |  |  |  |  |
| 2 | 18 | 1.710 | 1 | 3.042 | 32.021 | 2.28E-05 | \*\*\* |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(aov(AbOManisa~day))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| day | 1 | 3.042 | 3.042 | 32.02 | 2.28E-05 | \*\*\* |
| Residuals | 18 | 1.710 | 0.095 |  |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(AbOManisa,day)

Pairwise comparisons using t tests with pooled SD

data: AbOManisa and day

|  |  |
| --- | --- |
|  | 21 |
| 7 | 2.28E-05 |

P value adjustment method: holm

> m3<-lm(AbOManisa~day+vaccine)

> AIC(m2,m3)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| m2 | 3 | 13.57276 |
| m3 | 4 | 15.36112 |

> anova(m2,m3)

Analysis of Variance Table

Model 1: AbOManisa ~ day

Model 2: AbOManisa ~ day + vaccine

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Res.Df | RSS | Df | Sum of Sq | F | Pr(>F) |
| 1 | 18.00 | 1.71 |  |  |  |  |
| 2 | 17 | 1.692 | 1 | 0.018 | 0.1809 | 0.676 |

##########

> table(paste(vaccine,day),group)

> m0<-lm(AbOAlg~1)

> m1<-lm(AbOAlg~vaccine)

> m2<-lm(AbOAlg~day)

> m3<-lm(AbOAlg~prot1)

> AIC(m0,m1,m2)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| m0 | 2 | 37.20605 |
| m1 | 3 | 38.67308 |
| m2 | 3 | 25.58994 |

> anova(m0,m1)

Analysis of Variance Table

Model 1: AbOAlg ~ 1

Model 2: AbOAlg ~ vaccine

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Res.Df | RSS | Df | Sum of Sq | F | Pr(>F) |
| 1 | 19 | 6.1605 |  |  |  |  |
| 2 | 18 | 5.9985 | 1 | 0.162 | 0.4861 | 0.4946 |

> anova(m0,m2)

Analysis of Variance Table

Model 1: AbOAlg ~ 1

Model 2: AbOAlg ~ day

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Res.Df | RSS | Df | Sum of Sq | F | Pr(>F) |  |
| 1 | 19 | 6.1605 |  |  |  |  |  |
| 2 | 18 | 3.1185 | 1 | 3.042 | 17.558 | 0.00055 | \*\*\* |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(aov(AbOAlg~day))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| day | 1 | 3.042 | 3.0420 | 17.56 | 0.00055 | \*\*\* |
| Residuals | 18 | 3.119 | 0.1732 |  |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> anova(m0,m3)

Analysis of Variance Table

Model 1: AbOAlg ~ 1

Model 2: AbOAlg ~ prot1

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Res.Df | RSS | Df | Sum of Sq | F | Pr(>F) |  |
| 1 | 19 | 6.1605 |  |  |  |  |  |
| 2 | 18 | 4.8256 | 1 | 1.3349 | 4.9794 | 0.03861 | \* |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> m4<-lm(AbOAlg~prot1+vaccine)

> m5<-lm(AbOAlg~prot1+day)

> m6<-lm(AbOAlg~vaccine+day)

> AIC(m1,m2,m3,m4,m5,m6)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| m1 | 3 | 38.67308 |
| m2 | 3 | 25.58994 |
| m3 | 3 | 34.32155 |
| m4 | 4 | 34.92804 |
| m5 | 4 | 26.14770 |
| m6 | 4 | 26.52302 |

> m7<-lm(AbOAlg~prot1+vaccine+day)

> m8<-lm(AbOAlg~vaccine+day+vaccine:day)

> AIC(m6,m7,m8)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| m6 | 4 | 26.52302 |
| m7 | 5 | 26.49214 |
| m8 | 5 | 27.74713 |

> anova(m6,m7)

Analysis of Variance Table

Model 1: AbOAlg ~ vaccine + day

Model 2: AbOAlg ~ prot1 + vaccine + day

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Res.Df | RSS | Df | Sum of Sq | F | Pr(>F) |
| 1 | 17 | 2.9565 |  |  |  |  |
| 2 | 16 | 2.6710 | 1 | 0.28548 | 1.7101 | 0.2095 |

> anova(m3,m4)

Analysis of Variance Table

Model 1: AbOAlg ~ prot1

Model 2: AbOAlg ~ prot1 + vaccine

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Res.Df | RSS | Df | Sum of Sq | F | Pr(>F) |
| 1 | 18 | 4.8256 |  |  |  |  |
| 2 | 17 | 4.5008 | 1 | 0.32478 | 1.2267 | 0.2835 |

> anova(m2,m6)

Analysis of Variance Table

Model 1: AbOAlg ~ day

Model 2: AbOAlg ~ vaccine + day

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Res.Df | RSS | Df | Sum of Sq | F | Pr(>F) |
| 1 | 18 | 3.12 |  |  |  |  |
| 2 | 17 | 3 | 1 | 0.16 | 0.9315 | 0.348 |

> summary(m3)

Call:

lm(formula = AbOAlg ~ prot1)

Residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -1.47353 | -0.06838 | 0.02647 | 0.32647 | 0.77647 |

Coefficients:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Estimate | Std. Error | t value | Pr(>|t|) |  |
| (Intercept) | 1.3500 | 0.2989 | 4.516 | 0.000267 | \*\*\* |
| prot1 | 0.7235 | 0.3242 | 2.231 | 0.038605 | \* |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.5178 on 18 degrees of freedom

Multiple R-squared: 0.2167, Adjusted R-squared: 0.1732

F-statistic: 4.979 on 1 and 18 DF, p-value: 0.03861

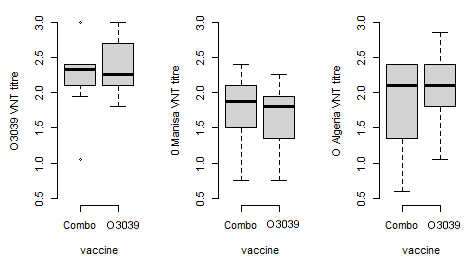
**######## Figure 4 ########**

> par(bty='n',mfrow=c(1,3))

> boxplot(AbO3039~vaccine, ylim=c(0.5,3), ylab="O3039 VNT titre",xlab="vaccine")

> boxplot(AbOManisa~vaccine, ylim=c(0.5,3), ylab="0 Manisa VNT titre",xlab="vaccine")

> boxplot(AbOAlg~vaccine, ylim=c(0.5,3), ylab="O Algeria VNT titre",xlab="vaccine")



**####### Statistics for Figure 4 ###########**

> summary(aov(AbOAlg~vaccine))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| vaccine | 1 | 0.162 | 0.162 | 0.486 | 0.495 |
| Residuals | 18 | 5.998 | 0.3332 |  |  |

> summary(aov(data[prot1==1,]$AbOAlg~data[prot1==1,]$vaccine))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| data[prot1 == 1, ]$vaccine | 1 | 0.576 | 0.5759 | 2.123 | 0.166 |
| Residuals | 15 | 4.07 | 0.2713 |  |  |

> summary(aov(data[prot1==1,]$AbOAlg~data[prot1==1,]$day))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| data[prot1 == 1, ]$day | 1 | 1.924 | 1.9241 | 10.61 | 0.00531 | \*\* |
| Residuals | 15 | 2.721 | 0.1814 |  |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(aov(AbOAlg~vaccine+day))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| vaccine | 1 | 0.162 | 0.162 | 0.932 | 0.348002 |  |
| day | 1 | 3.042 | 3.042 | 17.492 | 0.000625 | \*\*\* |
| Residuals | 17 | 2.957 | 0.1739 |  |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(aov(data[prot1==1,]$AbOAlg~data[prot1==1,]$vaccine+data[prot1==1,]$day))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| data[prot1 == 1, ]$vaccine | 1 | 0.5759 | 0.5759 | 3.533 | 0.08114 |  |
| data[prot1 == 1, ]$day | 1 | 1.7875 | 1.7875 | 10.965 | 0.00514 | \*\* |
| Residuals | 14 | 2.2822 | 0.163 |  |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(aov(AbOAlg~paste(vaccine,day)))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| paste(vaccine, day) | 3 | 3.316 | 1.1055 | 6.219 | 0.00528 | \*\* |
| Residuals | 16 | 2.844 | 0.1777 |  |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

**############# Ab PROTECTION RELATION ###############**

> m0<-glm(prot1~1,family='binomial')

> m1<-glm(prot1~AbOAlg,family='binomial')

> m2<-glm(prot1~group,family='binomial')

> m3<-glm(prot1~day,family='binomial')

> m4<-glm(prot1~vaccine,family='binomial')

> AIC(m0,m1,m2,m3,m4)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| m0 | 1 | 18.9084 |
| m1 | 2 | 16.8716 |
| m2 | 4 | 19.7341 |
| m3 | 2 | 16.2173 |
| m4 | 2 | 20.5097 |

> anova(m0,m1,test='Chisq')

Analysis of Deviance Table

Model 1: prot1 ~ 1

Model 2: prot1 ~ AbOAlg

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Resid. Df | Resid. Dev | Df | Deviance | Pr(>Chi) |  |
| 1 | 19 | 16.908 |  |  |  |  |
| 2 | 18 | 12.872 | 1 | 4.0367 | 0.04452 | \* |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> m5<-glm(prot1~AbOAlg+group,family='binomial')

> m6<-glm(prot1~AbOAlg+day,family='binomial')

> m7<-glm(prot1~AbOAlg+vaccine,family='binomial')

> AIC(m1,m5,m6,m7)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| m1 | 2 | 16.8716 |
| m5 | 5 | 20.2138 |
| m6 | 3 | 17.3856 |
| m7 | 3 | 17.5166 |

> summary(m1)

Call:

glm(formula = prot1 ~ AbOAlg, family = "binomial")

Deviance Residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -1.8619 | 0.2737 | 0.2737 | 0.3832 | 1.5659 |

Coefficients:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Estimate | Std. Error | z value | Pr(>|z|) |
| (Intercept) | -2.26 | 2.155 | -1.049 | 0.2943 |
| AbOAlg | 2.302 | 1.309 | 1.759 | 0.0785 |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 16.908 on 19 degrees of freedom

Residual deviance: 12.872 on 18 degrees of freedom

AIC: 16.872

Number of Fisher Scoring iterations: 5

**########## PA50 values ###########**

> p=0.5 #probability of protection

> (log(p/(1-p))-coef(m1)[1])/coef(m1)[2]

(Intercept) = 0.9816138

> p=0.95 #probability of protection

> (log(p/(1-p))-coef(m1)[1])/coef(m1)[2]

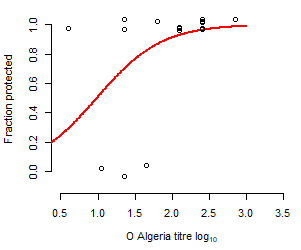
(Intercept) = 2.260536

> par(bty='n')

> plot(c(log10(1/2),log10(1024)),c(-0.1,1.1),type="n",axes=F,xlab=expression(paste("O Algeria titre log"[10])), xlim = c(0.5,3.5), ylab = "Fraction protected");axis(1);axis(2)

> lines(rep(0:300,1)/100, predict.glm(m1, data.frame(AbOAlg=rep(0:300,1)/100), type="response"),col="red",lty=1,lwd=2)

> points(AbOAlg,jitter(prot1,factor=0.2))



**####### body temperature #######**

> body<-read.csv("bodytemp.csv",sep=';')

> attach(body)

> summary(body)

> f0<-lmer(temp~1+(1|animal))

> f1<-lmer(temp~group+(1|animal))

> f2<-lmer(temp~factor(dpi)+(1|animal))

> f3<-lmer(temp~prot+(1|animal))

> AIC(f0,f1,f2,f3)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| f0 | 3 | 947.4081 |
| f1 | 7 | 966.3614 |
| f2 | 36 | 476.3922 |
| f3 | 4 | 948.8909 |

> f4<-lmer(temp~factor(dpi)+group+(1|animal))

> f5<-lmer(temp~factor(dpi)+prot+(1|animal))

> AIC(f2,f4,f5)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| f2 | 36 | 476.3922 |
| f4 | 40 | 495.3455 |
| f5 | 37 | 477.8750 |

> summary(f2)

Linear mixed model fit by REML ['lmerMod']

Formula: temp ~ factor(dpi) + (1 | animal)

REML criterion at convergence: 404.4

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -5.079 | -0.3955 | 0.0407 | 0.415 | 5.7126 |

Random effects:

Number of obs: 782, groups: animal, 23

|  |  |  |  |
| --- | --- | --- | --- |
| Groups | Name | Variance | Std.Dev. |
| animal | (Intercept) | 0.009398 | 0.09694 |
| Residual |  | 0.083230 | 0.28850 |

Fixed effects:

|  |  |  |  |
| --- | --- | --- | --- |
|  | Estimate | Std. Error | t value |
| (Intercept) | 3.89E+01 | 6.35E-02 | 612.904 |
| factor(dpi)1 | 1.17E+00 | 8.51E-02 | 13.748 |
| factor(dpi)2 | 1.27E+00 | 8.51E-02 | 14.974 |
| factor(dpi)3 | 6.83E-01 | 8.51E-02 | 8.024 |
| factor(dpi)4 | 3.70E-01 | 8.51E-02 | 4.344 |
| factor(dpi)5 | -7.39E-02 | 8.51E-02 | -0.869 |
| factor(dpi)6 | -1.26E-01 | 8.51E-02 | -1.482 |
| factor(dpi)7 | -1.00E-01 | 8.51E-02 | -1.175 |
| factor(dpi)8 | 8.70E-03 | 8.51E-02 | 0.102 |
| factor(dpi)9 | -5.22E-02 | 8.51E-02 | -0.613 |
| factor(dpi)10 | -2.61E-02 | 8.51E-02 | -0.307 |
| factor(dpi)11 | -9.57E-02 | 8.51E-02 | -1.124 |
| factor(dpi)12 | -7.83E-02 | 8.51E-02 | -0.920 |
| factor(dpi)13 | 8.44E-13 | 8.51E-02 | 0.000 |
| factor(dpi)14 | -8.70E-03 | 8.51E-02 | -0.102 |
| factor(dpi)15 | 8.59E-13 | 8.51E-02 | 0.000 |
| factor(dpi)16 | 7.83E-02 | 8.51E-02 | 0.920 |
| factor(dpi)17 | -4.78E-02 | 8.51E-02 | -0.562 |
| factor(dpi)18 | -6.96E-02 | 8.51E-02 | -0.818 |
| factor(dpi)19 | -1.26E-01 | 8.51E-02 | -1.482 |
| factor(dpi)20 | -9.13E-02 | 8.51E-02 | -1.073 |
| factor(dpi)21 | -3.91E-02 | 8.51E-02 | -0.460 |
| factor(dpi)22 | -3.04E-02 | 8.51E-02 | -0.358 |
| factor(dpi)23 | -2.17E-02 | 8.51E-02 | -0.256 |
| factor(dpi)24 | -1.74E-02 | 8.51E-02 | -0.204 |
| factor(dpi)25 | -4.78E-02 | 8.51E-02 | -0.562 |
| factor(dpi)26 | -8.70E-02 | 8.51E-02 | -1.022 |
| factor(dpi)27 | -1.44E-01 | 8.51E-02 | -1.687 |
| factor(dpi)28 | 2.17E-02 | 8.51E-02 | 0.256 |
| factor(dpi)29 | -8.70E-02 | 8.51E-02 | -1.022 |
| factor(dpi)30 | -7.39E-02 | 8.51E-02 | -0.869 |
| factor(dpi)31 | 5.65E-02 | 8.51E-02 | 0.664 |
| factor(dpi)32 | -6.96E-02 | 8.51E-02 | -0.818 |
| factor(dpi)33 | -1.30E-01 | 8.51E-02 | -1.533 |

Correlation matrix not shown by default, as p = 34 > 12.

Use print(x, correlation=TRUE) or vcov(x) if you need it

> for (i in 2:15){

+ f0<-lmer(temp~1+(1|animal),body[dpi<i,])

+ f1<-lmer(temp~group+(1|animal),body[dpi<i,])

+ f2<-lmer(temp~factor(dpi)+(1|animal),body[dpi<i,])

+ f3<-lmer(temp~factor(dpi)+group+(1|animal),body[dpi<i,])

+ print(i)

+ print(AIC(f0,f1,f2,f3)) }

boundary (singular) fit: see? is Singular

boundary (singular) fit: see? is Singular

boundary (singular) fit: see? is Singular

[1] 2

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| f0 | 3 | 120.07876 |
| f1 | 7 | 126.15642 |
| f2 | 4 | 91.16423 |
| f3 | 8 | 96.65586 |

boundary (singular) fit: see? is Singular

boundary (singular) fit: see? is Singular

[1] 3

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| f0 | 3 | 182.25030 |
| f1 | 7 | 187.17900 |
| f2 | 5 | 146.08060 |
| f3 | 9 | 149.69970 |

boundary (singular) fit: see? is Singular

[1] 4

|  |  |  |
| --- | --- | --- |
| f0 | 3 | 230.00020 |
| f1 | 7 | 232.15120 |
| f2 | 6 | 188.15440 |
| f3 | 10 | 190.22030 |

[1] 5

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| f0 | 3 | 278.70060 |
| f1 | 7 | 279.85200 |
| f2 | 7 | 228.93650 |
| f3 | 11 | 230.08790 |

boundary (singular) fit: see? is Singular

[1] 6

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| f0 | 3 | 334.35490 |
| f1 | 7 | 335.55210 |
| f2 | 8 | 260.76850 |
| f3 | 12 | 261.92160 |

boundary (singular) fit: see? is Singular

[1] 7

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| f0 | 3 | 383.77290 |
| f1 | 7 | 387.45840 |
| f2 | 9 | 287.34250 |
| f3 | 13 | 290.85250 |

boundary (singular) fit: see? is Singular

[1] 8

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| f0 | 3 | 427.19550 |
| f1 | 7 | 432.62610 |
| f2 | 10 | 309.84600 |
| f3 | 14 | 315.13510 |

boundary (singular) fit: see? is Singular

[1] 9

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| f0 | 3 | 463.94030 |
| f1 | 7 | 470.98280 |
| f2 | 11 | 331.38000 |
| f3 | 15 | 338.38030 |

boundary (singular) fit: see? is Singular

[1] 10

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| f0 | 3 | 499.34070 |
| f1 | 7 | 506.30530 |
| f2 | 12 | 348.50320 |
| f3 | 16 | 355.41730 |

boundary (singular) fit: see? is Singular

[1] 11

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| f0 | 3 | 532.43040 |
| f1 | 7 | 539.84640 |
| f2 | 13 | 367.52820 |
| f3 | 17 | 374.84470 |

boundary (singular) fit: see? is Singular

[1] 12

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| f0 | 3 | 564.35220 |
| f1 | 7 | 573.29890 |
| f2 | 14 | 382.03290 |
| f3 | 18 | 390.89560 |

boundary (singular) fit: see? is Singular

[1] 13

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| f0 | 3 | 594.07660 |
| f1 | 7 | 603.87160 |
| f2 | 15 | 394.36310 |
| f3 | 19 | 404.13700 |

[1] 14

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| f0 | 3 | 619.97490 |
| f1 | 7 | 630.79520 |
| f2 | 16 | 405.88200 |
| f3 | 20 | 416.70230 |

[1] 15

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| f0 | 3 | 647.16500 |
| f1 | 7 | 658.25870 |
| f2 | 17 | 423.36470 |
| f3 | 21 | 434.45840 |

> summary(f2)

Linear mixed model fit by REML ['lmerMod']

Formula: temp ~ factor(dpi) + (1 | animal)

Data: body[dpi < i, ]

REML criterion at convergence: 389.4

Scaled residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -3.6341 | -0.4303 | 0.0747 | 0.3981 | 3.8521 |

Random effects:

|  |  |  |
| --- | --- | --- |
| Groups Name | Variance | Std.Dev. |
| animal (Intercept) | 0.02027 | 0.1424 |
| Residual | 0.15362 | 0.3919 |

Number of obs: 345, groups: animal, 23

Fixed effects:

|  |  |  |  |
| --- | --- | --- | --- |
|  | Estimate | Std. Error | t value |
| (Intercept) | 3.89E+01 | 8.70E-02 | 447.334 |
| factor(dpi)1 | 1.17E+00 | 1.16E-01 | 10.119 |
| factor(dpi)2 | 1.27E+00 | 1.16E-01 | 11.022 |
| factor(dpi)3 | 6.83E-01 | 1.16E-01 | 5.906 |
| factor(dpi)4 | 3.70E-01 | 1.16E-01 | 3.198 |
| factor(dpi)5 | -7.39E-02 | 1.16E-01 | -0.640 |
| factor(dpi)6 | -1.26E-01 | 1.16E-01 | -1.091 |
| factor(dpi)7 | -1.00E-01 | 1.16E-01 | -0.865 |
| factor(dpi)8 | 8.70E-03 | 1.16E-01 | 0.075 |
| factor(dpi)9 | -5.22E-02 | 1.16E-01 | -0.451 |
| factor(dpi)10 | -2.61E-02 | 1.16E-01 | -0.226 |
| factor(dpi)11 | -9.57E-02 | 1.16E-01 | -0.828 |
| factor(dpi)12 | -7.83E-02 | 1.16E-01 | -0.677 |
| factor(dpi)13 | 6.05E-13 | 1.16E-01 | 0.000 |
| factor(dpi)14 | -8.70E-03 | 1.16E-01 | -0.075 |

Correlation matrix not shown by default, as p = 15 > 12.

Use print(x, correlation=TRUE) or vcov(x) if you need it

> print(f2, correlation=TRUE)

Linear mixed model fit by REML ['lmerMod']

Formula: temp ~ factor(dpi) + (1 | animal)

Data: body[dpi < i, ]

REML criterion at convergence: 389.3647

Random effects:

|  |  |
| --- | --- |
| Groups Name | Std.Dev. |
| animal (Intercept) | 0.1424 |
| Residual | 0.3919 |

Number of obs: 345, groups: animal, 23

Use print(x, correlation=TRUE) or vcov(x) if you need it

> detach(body)

**######## comparison of antibody titres between vaccine groups and controls #####**

> dat<-read.csv("Labresultaten LVZ194.csv",sep=';')

> dat$animal<-factor(dat$animal)

> dat$dpv<-factor(dat$dpv)

> dat$VNT<-ifelse(dat$VNT==0,0.3,dat$VNT)

> dat$VNtype<-factor(dat$VNtype)

> dat$VNtype<-relevel(dat$VNtype,ref="OAlg")

> dat$vactype<-factor(dat$vactype)

> dat<-dat[dat$vactype!="UVC",]

> droplevels(dat)

> summary(dat)

> attach(dat)

> tapply(VNT,VNtype,summary)

> tapply(VNT,paste(VNtype,vactype,dpv),summary)

> attach(dat[dat$vactype!="contr",])

**##### linear models #########**

> m0<-lm(VNT~1)

> m1<-lm(VNT~VNtype)

> m2<-lm(VNT~vactype)

> m3<-lm(VNT~dpv)

> AIC(m0,m1,m2,m3)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| m0 | 2 | 104.83176 |
| m1 | 4 | 94.99438 |
| m2 | 5 | 76.27451 |
| m3 | 3 | 73.13838 |

> summary(m3)

Call:

lm(formula = VNT ~ dpv)

Residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -1.015 | -0.2537 | 0.0500 | 0.3387 | 0.7850 |

Coefficients:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Estimate | Std. Error | t value | Pr(>|t|) |  |
| (Intercept) | 1.615000 | 0.07862 | 20.54 | < 2e-16 | \*\*\* |
| dpv21 | 0.735000 | 0.11119 | 6.61 | 1.32E-08 | \*\*\* |

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.4306 on 58 degrees of freedom

Multiple R-squared: 0.4297, Adjusted R-squared: 0.4198

F-statistic: 43.7 on 1 and 58 DF, p-value: 1.319e-08

> m4<-lm(VNT~dpv+VNtype)

> m5<-lm(VNT~dpv+vactype)

> AIC(m3,m4,m5)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| m3 | 3 | 73.13838 |
| m4 | 5 | 50.2549 |
| m5 | 5 | 76.27451 |

> m6<-lm(VNT~dpv+VNtype+VNtype:dpv)

> m7<-lm(VNT~dpv+VNtype+vactype)

> m8<-lm(VNT~dpv+VNtype+vactype+VNtype:vactype)

> m9<-lm(VNT~dpv+VNtype+vactype+dpv:vactype)

> m10<-lm(VNT~dpv+VNtype+vactype+dpv:VNtype)

> AIC(m4,m6,m7,m8,m9,m10)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| m4 | 5 | 50.2549 |
| m6 | 7 | 53.72209 |
| m7 | 7 | 52.89715 |
| m8 | 13 | 61.13058 |
| m9 | 7 | 52.89715 |
| m10 | 9 | 56.35209 |

> summary(m4)

Call:

lm(formula = VNT ~ dpv + VNtype)

Residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -0.9975 | -0.2475 | 0.0525 | 0.1875 | 0.8025 |

Coefficients:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Estimate | Std. Error | t value | Pr(>|t|) |  |
| (Intercept) | 1.5975 | 0.09045 | 17.663 | < 2e-16 | \*\*\* |
| dpv21 | 0.735 | 0.09045 | 8.126 | 4.79E-11 | \*\*\* |
| VNtypeO3039 | 0.3375 | 0.11077 | 3.047 | 0.00352 | \*\* |
| VNtypeOManisa | -0.2850 | 0.11077 | 2.573 | 0.01276 | \* |

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.3503 on 56 degrees of freedom

Multiple R-squared: 0.6356, Adjusted R-squared: 0.6161

F-statistic: 32.56 on 3 and 56 DF, p-value: 2.573e-12

###### linear mixed model #########

> n0<-lmer(VNT~1+(1|animal))

> n1<-lmer(VNT~VNtype+(1|animal))

> n2<-lmer(VNT~vactype+(1|animal))

> n3<-lmer(VNT~dpv+(1|animal))

> AIC(n0,n1,n2,n3)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| n0 | 3 | 99.42130 |
| n1 | 5 | 78.19286 |
| n2 | 6 | 88.33477 |
| n3 | 4 | 81.58129 |

> summary(n1)

Linear mixed model fit by REML ['lmerMod']

Formula: VNT ~ VNtype + (1 | animal)

REML criterion at convergence: 68.2

Scaled residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -1.7625 | -0.6702 | 0.1232 | 0.6607 | 1.8759 |

Random effects:

|  |  |  |
| --- | --- | --- |
| Groups Name | Variance | Std.Dev. |
| animal (Intercept) | 0.17704 | 0.4208 |
| Residual | 0.08568 | 0.2927 |

Number of obs: 60, groups: animal, 20

Fixed effects:

|  |  |  |  |
| --- | --- | --- | --- |
|  | Estimate | Std. Error | t value |
| (Intercept) | 1.965 | 0.11461 | 17.145 |
| VNtype O3039 | 0.3375 | 0.09256 | 3.646 |
| VNtype OManisa | -0.285 | 0.09256 | -3.079 |

Correlation of Fixed Effects:

|  |  |  |
| --- | --- | --- |
|  | (Intr) | VN3039 |
| VNtype O3039 | -0.404 |  |
| VNtype OManisa | -0.404 | 0.500 |

> n4<-lmer(VNT~VNtype+vactype+(1|animal))

> n5<-lmer(VNT~VNtype+dpv+(1|animal))

> n6<-lmer(VNT~VNtype+vactype+VNtype:vactype+(1|animal))

> n7<-lmer(VNT~VNtype+dpv+VNtype:dpv+(1|animal))

> n8<-lmer(VNT~VNtype+dpv+vactype+(1|animal))

fixed-effect model matrix is rank deficient so dropping 1 column / coefficient

> AIC(n1,n4,n5,n6,n7,n8)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| n1 | 5 | 78.19286 |
| n4 | 8 | 67.10633 |
| n5 | 6 | 60.35285 |
| n6 | 14 | 81.61643 |
| n7 | 8 | 66.98002 |
| n8 | 8 | 67.10633 |

> summary(m5)

Linear mixed model fit by REML ['lmerMod']

Formula: VNT ~ VNtype + dpv + (1 | animal)

REML criterion at convergence: 48.4

Scaled residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -1.81108 | -0.7265 | 0.09234 | 0.53132 | 2.28123 |

Random effects:

|  |  |  |
| --- | --- | --- |
| Groups Name | Variance | Std.Dev. |
| animal (Intercept) | 0.0384 | 0.196 |
| Residual | 0.08568 | 0.2927 |

Number of obs: 60, groups: animal, 20

Fixed effects:

|  |  |  |  |
| --- | --- | --- | --- |
|  | Estimate | Std. Error | t value |
| (Intercept) | 1.5975 | 0.09773 | 16.346 |
| VNtype O3039 | 0.3375 | 0.09256 | 3.646 |
| VNtype OManisa | -0.285 | 0.09256 | -3.079 |
| dpv21 | 0.735 | 0.11572 | 6.351 |

Correlation of Fixed Effects:

|  |  |  |  |
| --- | --- | --- | --- |
|  | (Intr) | VNO3039 | VNOManisa |
| VNtype O3039 | -0.474 |  |  |
| VNtype OManisa | -0.474 | 0.500 |  |
| dpv21 | -0.592 | 0.000 | 0.000 |

> detach(dat)

**######## post challenge antibody response ###########**

> data<-read.csv("VNT after challenge.csv",sep=';')

> data$vnt<-ifelse(data$vnt=="<0.3",0,as.numeric(as.character(data$vnt)))

Warning message:

In ifelse(data$vnt == "<0.3", 0, as.numeric(as.character(data$vnt))) :

NAs introduced by coercion

> summary(data)

> attach(data)

> tapply(vnt,animal,length)

> k0<-lmer(vnt~1+(1|animal))

> k1<-lmer(vnt~VNtype+(1|animal))

> k2<-lmer(vnt~vactype+(1|animal))

> k3<-lmer(vnt~prot+(1|animal))

> k4<-lmer(vnt~factor(dpc)+(1|animal))

> AIC(k0,k1,k2,k3,k4)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| k0 | 3 | 2618.974 |
| k1 | 5 | 2618.870 |
| k2 | 7 | 2588.195 |
| k3 | 4 | 2611.739 |
| k4 | 17 | 1348.076 |

> k5<-lmer(vnt~factor(dpc)+VNtype+(1|animal))

> k6<-lmer(vnt~factor(dpc)+vactype+(1|animal))

> k7<-lmer(vnt~factor(dpc)+prot+(1|animal))

> AIC(k4,k5,k6,k7)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| k4 | 17 | 1348.076 |
| k5 | 19 | 1317.413 |
| k6 | 21 | 1317.297 |
| k7 | 18 | 1340.841 |

> summary(k6)

Linear mixed model fit by REML ['lmerMod']

Formula: vnt ~ factor(dpc) + vactype + (1 | animal)

REML criterion at convergence: 1275.3

Scaled residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -4.016 | -0.524 | 0.093 | 0.606 | 3.15 |

Random effects:

|  |  |  |
| --- | --- | --- |
| Groups Name | Variance | Std.Dev. |
| animal (Intercept) | 0.03201 | 0.1789 |
| Residual | 0.18209 | 0.4267 |

Number of obs: 1035, groups: animal, 23

Fixed effects:

|  |  |  |  |
| --- | --- | --- | --- |
|  | Estimate | Std. Error | t value |
| (Intercept) | 2.16981 | 0.09836 | 22.060 |
| factor(dpc)1 | 0.18913 | 0.07265 | 2.603 |
| factor(dpc)2 | 0.27391 | 0.07265 | 3.770 |
| factor(dpc)3 | 0.37609 | 0.07265 | 5.177 |
| factor(dpc)4 | 0.73043 | 0.07265 | 10.054 |
| factor(dpc)5 | 1.09855 | 0.07265 | 15.121 |
| factor(dpc)6 | 1.37609 | 0.07265 | 18.941 |
| factor(dpc)7 | 1.78913 | 0.07265 | 24.627 |
| factor(dpc)11 | 1.86304 | 0.07265 | 25.644 |
| factor(dpc)14 | 1.9413 | 0.07265 | 26.721 |
| factor(dpc)18 | 1.8913 | 0.07265 | 26.033 |
| factor(dpc)21 | 1.8087 | 0.07265 | 24.896 |
| factor(dpc)25 | 1.81522 | 0.07265 | 24.986 |
| factor(dpc)28 | 1.77174 | 0.07265 | 24.387 |
| factor(dpc)31 | 1.72826 | 0.07265 | 23.789 |
| vactype Comb-7 | -0.53733 | 0.1201 | -4.474 |
| vactype Control | -1.49333 | 0.13868 | -10.768 |
| vactype O3039-21 | 0.02622 | 0.1201 | 0.218 |
| vactype O3039-7 | -0.574 | 0.1201 | -4.779 |

Correlation matrix not shown by default, as p = 19 > 12.

Use print(x, correlation=TRUE) or vcov(x) if you need it

> k8<-lmer(vnt~factor(dpc)+VNtype+factor(dpc):VNtype+(1|animal))

> k9<-lmer(vnt~factor(dpc)+vactype+factor(dpc):vactype+(1|animal))

> AIC(k4,k5,k6,k8,k9)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| k4 | 17 | 1348.076 |
| k5 | 19 | 1317.413 |
| k6 | 21 | 1317.297 |
| k8 | 47 | 1370.773 |
| k9 | 77 | 1092.748 |

> summary(k9)

Linear mixed model fit by REML ['lmerMod']

Formula: vnt ~ factor(dpc) + vactype + factor(dpc):vactype + (1 | animal)

REML criterion at convergence: 938.7

Scaled residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -4.8217 | -0.5804 | 0.0193 | 0.5795 | 2.8684 |

Random effects:

|  |  |  |
| --- | --- | --- |
| Groups Name | Variance | Std.Dev. |
| animal (Intercept) | 0.03337 | 0.1827 |
| Residual | 0.12096 | 0.3478 |

Number of obs: 1035, groups: animal, 23

Fixed effects:

|  |  |  |  |
| --- | --- | --- | --- |
|  | Estimate | Std. Error | t value |
| (Intercept) | 2.32E+00 | 1.21E-01 | 19.110 |
| factor(dpc)1 | 1.20E-01 | 1.27E-01 | 0.945 |
| factor(dpc)2 | 1.50E-01 | 1.27E-01 | 1.181 |
| factor(dpc)3 | 2.10E-01 | 1.27E-01 | 1.654 |
| factor(dpc)4 | 2.30E-01 | 1.27E-01 | 1.811 |
| factor(dpc)5 | 6.20E-01 | 1.27E-01 | 4.882 |
| factor(dpc)6 | 9.20E-01 | 1.27E-01 | 7.244 |
| factor(dpc)7 | 1.50E+00 | 1.27E-01 | 11.811 |
| factor(dpc)11 | 1.90E+00 | 1.27E-01 | 14.961 |
| factor(dpc)14 | 1.91E+00 | 1.27E-01 | 15.040 |
| factor(dpc)18 | 1.79E+00 | 1.27E-01 | 14.095 |
| factor(dpc)21 | 1.78E+00 | 1.27E-01 | 14.016 |
| factor(dpc)25 | 1.76E+00 | 1.27E-01 | 13.859 |
| factor(dpc)28 | 1.78E+00 | 1.27E-01 | 14.016 |
| factor(dpc)31 | 1.73E+00 | 1.27E-01 | 13.622 |
| vactype Comb-7 | -7.70E-01 | 1.72E-01 | -4.485 |
| vactype Control | -2.20E+00 | 1.98E-01 | -11.114 |
| vactype O3039-21 | 6.00E-02 | 1.72E-01 | 0.349 |
| vactype O3039-7 | -6.40E-01 | 1.72E-01 | -3.728 |
| factor(dpc)1:vactype Comb-7 | 3.00E-01 | 1.80E-01 | 1.670 |
| factor(dpc)2:vactype Comb-7 | 4.30E-01 | 1.80E-01 | 2.394 |
| factor(dpc)3:vactype Comb-7 | 5.20E-01 | 1.80E-01 | 2.895 |
| factor(dpc)4:vactype Comb-7 | 9.90E-01 | 1.80E-01 | 5.512 |
| factor(dpc)5:vactype Comb-7 | 7.30E-01 | 1.80E-01 | 4.065 |
| factor(dpc)6:vactype Comb-7 | 5.70E-01 | 1.80E-01 | 3.174 |
| factor(dpc)7:vactype Comb-7 | 3.80E-01 | 1.80E-01 | 2.116 |
| factor(dpc)11:vactype Comb-7 | -1.10E-01 | 1.80E-01 | -0.612 |
| factor(dpc)14:vactype Comb-7 | -8.00E-02 | 1.80E-01 | -0.445 |
| factor(dpc)18:vactype Comb-7 | 3.00E-02 | 1.80E-01 | 0.167 |
| factor(dpc)21:vactype Comb-7 | -4.00E-02 | 1.80E-01 | -0.223 |
| factor(dpc)25:vactype Comb-7 | -1.00E-02 | 1.80E-01 | -0.056 |
| factor(dpc)28:vactype Comb-7 | -9.00E-02 | 1.80E-01 | -0.501 |
| factor(dpc)31:vactype Comb-7 | -1.30E-01 | 1.80E-01 | -0.724 |
| factor(dpc)1:vactype Control | -1.37E-01 | 2.07E-01 | -0.659 |
| factor(dpc)2:vactype Control | -5.00E-02 | 2.07E-01 | -0.241 |
| factor(dpc)3:vactype Control | -4.33E-02 | 2.07E-01 | -0.209 |
| factor(dpc)4:vactype Control | 7.20E-01 | 2.07E-01 | 3.472 |
| factor(dpc)5:vactype Control | 1.56E+00 | 2.07E-01 | 7.538 |
| factor(dpc)6:vactype Control | 1.65E+00 | 2.07E-01 | 7.940 |
| factor(dpc)7:vactype Control | 1.15E+00 | 2.07E-01 | 5.545 |
| factor(dpc)11:vactype Control | 8.33E-01 | 2.07E-01 | 4.018 |
| factor(dpc)14:vactype Control | 9.07E-01 | 2.07E-01 | 4.372 |
| factor(dpc)18:vactype Control | 1.01E+00 | 2.07E-01 | 4.870 |
| factor(dpc)21:vactype Control | 8.87E-01 | 2.07E-01 | 4.275 |
| factor(dpc)25:vactype Control | 8.23E-01 | 2.07E-01 | 3.970 |
| factor(dpc)28:vactype Control | 6.20E-01 | 2.07E-01 | 2.990 |
| factor(dpc)31:vactype Control | 7.20E-01 | 2.07E-01 | 3.472 |
| factor(dpc)1:vactype O3039-21 | -1.20E-01 | 1.80E-01 | -0.668 |
| factor(dpc)2:vactype O3039-21 | -1.10E-01 | 1.80E-01 | -0.612 |
| factor(dpc)3:vactype O3039-21 | -1.00E-01 | 1.80E-01 | -0.557 |
| factor(dpc)4:vactype O3039-21 | -5.00E-02 | 1.80E-01 | -0.278 |
| factor(dpc)5:vactype O3039-21 | -7.67E-02 | 1.80E-01 | -0.427 |
| factor(dpc)6:vactype O3039-21 | 5.00E-02 | 1.80E-01 | 0.278 |
| factor(dpc)7:vactype O3039-21 | 2.40E-01 | 1.80E-01 | 1.336 |
| factor(dpc)11:vactype O3039-21 | -2.60E-01 | 1.80E-01 | -1.448 |
| factor(dpc)14:vactype O3039-21 | -1.00E-01 | 1.80E-01 | -0.557 |
| factor(dpc)18:vactype O3039-21 | -3.00E-02 | 1.80E-01 | -0.167 |
| factor(dpc)21:vactype O3039-21 | -9.00E-02 | 1.80E-01 | -0.501 |
| factor(dpc)25:vactype O3039-21 | 9.00E-02 | 1.80E-01 | 0.501 |
| factor(dpc)28:vactype O3039-21 | -7.21E-13 | 1.80E-01 | 0.000 |
| factor(dpc)31:vactype O3039-21 | 5.00E-02 | 1.80E-01 | 0.278 |
| factor(dpc)1:vactype O3039-7 | 2.20E-01 | 1.80E-01 | 1.225 |
| factor(dpc)2:vactype O3039-7 | 2.80E-01 | 1.80E-01 | 1.559 |
| factor(dpc)3:vactype O3039-7 | 3.70E-01 | 1.80E-01 | 2.060 |
| factor(dpc)4:vactype O3039-7 | 9.30E-01 | 1.80E-01 | 5.178 |
| factor(dpc)5:vactype O3039-7 | 6.10E-01 | 1.80E-01 | 3.396 |
| factor(dpc)6:vactype O3039-7 | 4.90E-01 | 1.80E-01 | 2.728 |
| factor(dpc)7:vactype O3039-7 | 2.00E-02 | 1.80E-01 | 0.111 |
| factor(dpc)11:vactype O3039-7 | -3.00E-01 | 1.80E-01 | -1.670 |
| factor(dpc)14:vactype O3039-7 | -2.20E-01 | 1.80E-01 | -1.225 |
| factor(dpc)18:vactype O3039-7 | -1.40E-01 | 1.80E-01 | -0.780 |
| factor(dpc)21:vactype O3039-7 | -2.70E-01 | 1.80E-01 | -1.503 |
| factor(dpc)25:vactype O3039-7 | -3.20E-01 | 1.80E-01 | -1.782 |
| factor(dpc)28:vactype O3039-7 | -3.20E-01 | 1.80E-01 | -1.782 |
| factor(dpc)31:vactype O3039-7 | -3.60E-01 | 1.80E-01 | -2.004 |

Correlation matrix not shown by default, as p = 75 > 12.

Use print(x, correlation=TRUE) or vcov(x) if you need it

> k10<-lmer(vnt~factor(dpc)+vactype+factor(dpc):vactype+VNtype+(1|animal))

> AIC(k9,k10)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| k9 | 77 | 1092.748 |
| k10 | 79 | 1039.240 |

> summary(k10)

Linear mixed model fit by REML ['lmerMod']

Formula: vnt ~ factor(dpc) + vactype + factor(dpc):vactype + VNtype + (1 | animal)

REML criterion at convergence: 881.2

Scaled residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -5.0949 | -0.5652 | 0.0282 | 0.5511 | 2.7938 |

Random effects:

|  |  |  |
| --- | --- | --- |
| Groups Name | Variance | Std.Dev. |
| animal (Intercept) | 3.36E-02 | 1.83E-01 |
| Residual | 0.11268 | 0.3357 |

Number of obs: 1035, groups: animal, 23

Fixed effects:

|  |  |  |  |
| --- | --- | --- | --- |
|  | Estimate | Std. Error | t value |
| (Intercept) | 2.35E+00 | 1.20E-01 | 19.581 |
| factor(dpc)1 | 1.20E-01 | 1.23E-01 | 0.979 |
| factor(dpc)2 | 1.50E-01 | 1.23E-01 | 1.224 |
| factor(dpc)3 | 2.10E-01 | 1.23E-01 | 1.713 |
| factor(dpc)4 | 2.30E-01 | 1.23E-01 | 1.876 |
| factor(dpc)5 | 6.20E-01 | 1.23E-01 | 5.058 |
| factor(dpc)6 | 9.20E-01 | 1.23E-01 | 7.506 |
| factor(dpc)7 | 1.50E+00 | 1.23E-01 | 12.238 |
| factor(dpc)11 | 1.90E+00 | 1.23E-01 | 15.501 |
| factor(dpc)14 | 1.91E+00 | 1.23E-01 | 15.582 |
| factor(dpc)18 | 1.79E+00 | 1.23E-01 | 14.603 |
| factor(dpc)21 | 1.78E+00 | 1.23E-01 | 14.522 |
| factor(dpc)25 | 1.76E+00 | 1.23E-01 | 14.359 |
| factor(dpc)28 | 1.78E+00 | 1.23E-01 | 14.522 |
| factor(dpc)31 | 1.73E+00 | 1.23E-01 | 14.114 |
| vactype Comb-7 | -7.70E-01 | 1.69E-01 | -4.565 |
| vactype Control - | 2.20E+00 | 1.95E-01 | -11.314 |
| vactype O3039-21 | 6.00E-02 | 1.69E-01 | 0.356 |
| vactype O3039-7 | -6.40E-01 | 1.69E-01 | -3.795 |
| VNtype OAlg - | 1.54E-01 | 2.56E-02 | -6.005 |
| VNtype OManisa | 5.45E-02 | 2.56E-02 | 2.132 |
| factor(dpc)1:vactype Comb-7 | 3.00E-01 | 1.73E-01 | 1.731 |
| factor(dpc)2:vactype Comb-7 | 4.30E-01 | 1.73E-01 | 2.481 |
| factor(dpc)3:vactype Comb-7 | 5.20E-01 | 1.73E-01 | 3.000 |
| factor(dpc)4:vactype Comb-7 | 9.90E-01 | 1.73E-01 | 5.711 |
| factor(dpc)5:vactype Comb-7 | 7.30E-01 | 1.73E-01 | 4.211 |
| factor(dpc)6:vactype Comb-7 | 5.70E-01 | 1.73E-01 | 3.288 |
| factor(dpc)7:vactype Comb-7 | 3.80E-01 | 1.73E-01 | 2.192 |
| factor(dpc)11:vactype Comb-7 | -1.10E-01 | 1.73E-01 | -0.635 |
| factor(dpc)14:vactype Comb-7 | -8.00E-02 | 1.73E-01 | -0.462 |
| factor(dpc)18:vactype Comb-7 | 3.00E-02 | 1.73E-01 | 0.173 |
| factor(dpc)21:vactype Comb-7 | -4.00E-02 | 1.73E-01 | -0.231 |
| factor(dpc)25:vactype Comb-7 | -1.00E-02 | 1.73E-01 | -0.058 |
| factor(dpc)28:vactype Comb-7 | -9.00E-02 | 1.73E-01 | -0.519 |
| factor(dpc)31:vactype Comb-7 | -1.30E-01 | 1.73E-01 | -0.750 |
| factor(dpc)1:vactype Control | -1.37E-01 | 2.00E-01 | -0.683 |
| factor(dpc)2:vactype Control | -5.00E-02 | 2.00E-01 | -0.250 |
| factor(dpc)3:vactype Control | -4.33E-02 | 2.00E-01 | -0.216 |
| factor(dpc)4:vactype Control | 7.20E-01 | 2.00E-01 | 3.597 |
| factor(dpc)5:vactype Control | 1.56E+00 | 2.00E-01 | 7.810 |
| factor(dpc)6:vactype Control | 1.65E+00 | 2.00E-01 | 8.227 |
| factor(dpc)7:vactype Control | 1.15E+00 | 2.00E-01 | 5.745 |
| factor(dpc)11:vactype Control | 8.33E-01 | 2.00E-01 | 4.163 |
| factor(dpc)14:vactype Control | 9.07E-01 | 2.00E-01 | 4.530 |
| factor(dpc)18:vactype Control | 1.01E+00 | 2.00E-01 | 5.046 |
| factor(dpc)21:vactype Control | 8.87E-01 | 2.00E-01 | 4.430 |
| factor(dpc)25:vactype Control | 8.23E-01 | 2.00E-01 | 4.113 |
| factor(dpc)28:vactype Control | 6.20E-01 | 2.00E-01 | 3.097 |
| factor(dpc)31:vactype Control | 7.20E-01 | 2.00E-01 | 3.597 |
| factor(dpc)1:vactype O3039-21 | -1.20E-01 | 1.73E-01 | -0.692 |
| factor(dpc)2:vactype O3039-21 | -1.10E-01 | 1.73E-01 | -0.635 |
| factor(dpc)3:vactype O3039-21 | -1.00E-01 | 1.73E-01 | -0.577 |
| factor(dpc)4:vactype O3039-21 | -5.00E-02 | 1.73E-01 | -0.288 |
| factor(dpc)5:vactype O3039-21 | -7.67E-02 | 1.73E-01 | -0.442 |
| factor(dpc)6:vactype O3039-21 | 5.00E-02 | 1.73E-01 | 0.288 |
| factor(dpc)7:vactype O3039-21 | 2.40E-01 | 1.73E-01 | 1.385 |
| factor(dpc)11:vactype O3039-21 | -2.60E-01 | 1.73E-01 | -1.500 |
| factor(dpc)14:vactype O3039-21 | -1.00E-01 | 1.73E-01 | -0.577 |
| factor(dpc)18:vactype O3039-21 | -3.00E-02 | 1.73E-01 | -0.173 |
| factor(dpc)21:vactype O3039-21 | -9.00E-02 | 1.73E-01 | -0.519 |
| factor(dpc)25:vactype O3039-21 | 9.00E-02 | 1.73E-01 | 0.519 |
| factor(dpc)28:vactype O3039-21 | -7.85E-13 | 1.73E-01 | 0.000 |
| factor(dpc)31:vactype O3039-21 | 5.00E-02 | 1.73E-01 | 0.288 |
| factor(dpc)1:vactype O3039-7 | 2.20E-01 | 1.73E-01 | 1.269 |
| factor(dpc)2:vactype O3039-7 | 2.80E-01 | 1.73E-01 | 1.615 |
| factor(dpc)3:vactype O3039-7 | 3.70E-01 | 1.73E-01 | 2.134 |
| factor(dpc)4:vactype O3039-7 | 9.30E-01 | 1.73E-01 | 5.365 |
| factor(dpc)5:vactype O3039-7 | 6.10E-01 | 1.73E-01 | 3.519 |
| factor(dpc)6:vactype O3039-7 | 4.90E-01 | 1.73E-01 | 2.827 |
| factor(dpc)7:vactype O3039-7 | 2.00E-02 | 1.73E-01 | 0.115 |
| factor(dpc)11:vactype O3039-7 | -3.00E-01 | 1.73E-01 | -1.731 |
| factor(dpc)14:vactype O3039-7 | -2.20E-01 | 1.73E-01 | -1.269 |
| factor(dpc)18:vactype O3039-7 | -1.40E-01 | 1.73E-01 | -0.808 |
| factor(dpc)21:vactype O3039-7 | -2.70E-01 | 1.73E-01 | -1.558 |
| factor(dpc)25:vactype O3039-7 | -3.20E-01 | 1.73E-01 | -1.846 |
| factor(dpc)28:vactype O3039-7 | -3.20E-01 | 1.73E-01 | -1.846 |
| factor(dpc)31:vactype O3039-7 | -3.60E-01 | 1.73E-01 | -2.077 |

Correlation matrix not shown by default, as p = 77 > 12.

Use print(x, correlation=TRUE) or vcov(x) if you need it

> k11<-lmer(vnt~factor(dpc)+vactype+factor(dpc):vactype+VNtype+factor(dpc):VNtype+(1|animal))

> k12<-lmer(vnt~factor(dpc)+vactype+factor(dpc):vactype+VNtype+vactype:VNtype+(1|animal))

> AIC(k10,k11,k12)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| k10 | 79 | 1039.2397 |
| k11 | 107 | 1066.0652 |
| k12 | 87 | 833.8429 |

> summary(k12)

Linear mixed model fit by REML ['lmerMod']

Formula: vnt ~ factor(dpc) + vactype + factor(dpc):vactype + VNtype + vactype:VNtype + (1 | animal)

REML criterion at convergence: 659.8

Scaled residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -5.5727 | -0.5326 | 0.0089 | 0.5549 | 2.7034 |

Random effects:

Groups Name Variance Std.Dev.

animal (Intercept) 0.03413 0.1847

Residual 0.08689 0.2948

Number of obs: 1035, groups: animal, 23

Fixed effects:

|  |  |  |  |
| --- | --- | --- | --- |
|  | Estimate | Std. Error | t value |
| (Intercept) | 2.23E+00 | 1.16E-01 | 19.242 |
| factor(dpc)1 | 1.20E-01 | 1.08E-01 | 1.115 |
| factor(dpc)2 | 1.50E-01 | 1.08E-01 | 1.394 |
| factor(dpc)3 | 2.10E-01 | 1.08E-01 | 1.951 |
| factor(dpc)4 | 2.30E-01 | 1.08E-01 | 2.137 |
| factor(dpc)5 | 6.20E-01 | 1.08E-01 | 5.760 |
| factor(dpc)6 | 9.20E-01 | 1.08E-01 | 8.547 |
| factor(dpc)7 | 1.50E+00 | 1.08E-01 | 13.936 |
| factor(dpc)11 | 1.90E+00 | 1.08E-01 | 17.652 |
| factor(dpc)14 | 1.91E+00 | 1.08E-01 | 17.745 |
| factor(dpc)18 | 1.79E+00 | 1.08E-01 | 16.630 |
| factor(dpc)21 | 1.78E+00 | 1.08E-01 | 16.537 |
| factor(dpc)25 | 1.76E+00 | 1.08E-01 | 16.351 |
| factor(dpc)28 | 1.78E+00 | 1.08E-01 | 16.537 |
| factor(dpc)31 | 1.73E+00 | 1.08E-01 | 16.073 |
| vactype Comb-7 | -4.43E-01 | 1.64E-01 | -2.705 |
| vactype Control | -2.41E+00 | 1.89E-01 | -12.771 |
| vactype O3039-21 | 1.18E-01 | 1.64E-01 | 0.720 |
| vactype O3039-7 | -3.18E-01 | 1.64E-01 | -1.943 |
| VNtype OAlg | 1.80E-01 | 4.81E-02 | 3.739 |
| VNtype OManisa | 1.00E-01 | 4.81E-02 | 2.077 |
| factor(dpc)1:vactype Comb-7 | 3.00E-01 | 1.52E-01 | 1.971 |
| factor(dpc)2:vactype Comb-7 | 4.30E-01 | 1.52E-01 | 2.825 |
| factor(dpc)3:vactype Comb-7 | 5.20E-01 | 1.52E-01 | 3.416 |
| factor(dpc)4:vactype Comb-7 | 9.90E-01 | 1.52E-01 | 6.504 |
| factor(dpc)5:vactype Comb-7 | 7.30E-01 | 1.52E-01 | 4.796 |
| factor(dpc)6:vactype Comb-7 | 5.70E-01 | 1.52E-01 | 3.745 |
| factor(dpc)7:vactype Comb-7 | 3.80E-01 | 1.52E-01 | 2.496 |
| factor(dpc)11:vactype Comb-7 | -1.10E-01 | 1.52E-01 | -0.723 |
| factor(dpc)14:vactype Comb-7 | -8.00E-02 | 1.52E-01 | -0.526 |
| factor(dpc)18:vactype Comb-7 | 3.00E-02 | 1.52E-01 | 0.197 |
| factor(dpc)21:vactype Comb-7 | -4.00E-02 | 1.52E-01 | -0.263 |
| factor(dpc)25:vactype Comb-7 | -1.00E-02 | 1.52E-01 | -0.066 |
| factor(dpc)28:vactype Comb-7 | -9.00E-02 | 1.52E-01 | -0.591 |
| factor(dpc)31:vactype Comb-7 | -1.30E-01 | 1.52E-01 | -0.854 |
| factor(dpc)1:vactype Control | -1.37E-01 | 1.76E-01 | -0.778 |
| factor(dpc)2:vactype Control | -5.00E-02 | 1.76E-01 | -0.284 |
| factor(dpc)3:vactype Control | -4.33E-02 | 1.76E-01 | -0.247 |
| factor(dpc)4:vactype Control | 7.20E-01 | 1.76E-01 | 4.096 |
| factor(dpc)5:vactype Control | 1.56E+00 | 1.76E-01 | 8.894 |
| factor(dpc)6:vactype Control | 1.65E+00 | 1.76E-01 | 9.368 |
| factor(dpc)7:vactype Control | 1.15E+00 | 1.76E-01 | 6.543 |
| factor(dpc)11:vactype Control | 8.33E-01 | 1.76E-01 | 4.741 |
| factor(dpc)14:vactype Control | 9.07E-01 | 1.76E-01 | 5.158 |
| factor(dpc)18:vactype Control | 1.01E+00 | 1.76E-01 | 5.746 |
| factor(dpc)21:vactype Control | 8.87E-01 | 1.76E-01 | 5.044 |
| factor(dpc)25:vactype Control | 8.23E-01 | 1.76E-01 | 4.684 |
| factor(dpc)28:vactype Control | 6.20E-01 | 1.76E-01 | 3.527 |
| factor(dpc)31:vactype Control | 7.20E-01 | 1.76E-01 | 4.096 |
| factor(dpc)1:vactype O3039-21 | -1.20E-01 | 1.52E-01 | -0.788 |
| factor(dpc)2:vactype O3039-21 | -1.10E-01 | 1.52E-01 | -0.723 |
| factor(dpc)3:vactype O3039-21 | -1.00E-01 | 1.52E-01 | -0.657 |
| factor(dpc)4:vactype O3039-21 | -5.00E-02 | 1.52E-01 | -0.328 |
| factor(dpc)5:vactype O3039-21 | -7.67E-02 | 1.52E-01 | -0.504 |
| factor(dpc)6:vactype O3039-21 | 5.00E-02 | 1.52E-01 | 0.328 |
| factor(dpc)7:vactype O3039-21 | 2.40E-01 | 1.52E-01 | 1.577 |
| factor(dpc)11:vactype O3039-21 | -2.60E-01 | 1.52E-01 | -1.708 |
| factor(dpc)14:vactype O3039-21 | -1.00E-01 | 1.52E-01 | -0.657 |
| factor(dpc)18:vactype O3039-21 | -3.00E-02 | 1.52E-01 | -0.197 |
| factor(dpc)21:vactype O3039-21 | -9.00E-02 | 1.52E-01 | -0.591 |
| factor(dpc)25:vactype O3039-21 | 9.00E-02 | 1.52E-01 | 0.591 |
| factor(dpc)28:vactype O3039-21 | -5.87E-13 | 1.52E-01 | 0.000 |
| factor(dpc)31:vactype O3039-21 | 5.00E-02 | 1.52E-01 | 0.328 |
| factor(dpc)1:vactype O3039-7 | 2.20E-01 | 1.52E-01 | 1.445 |
| factor(dpc)2:vactype O3039-7 | 2.80E-01 | 1.52E-01 | 1.839 |
| factor(dpc)3:vactype O3039-7 | 3.70E-01 | 1.52E-01 | 2.431 |
| factor(dpc)4:vactype O3039-7 | 9.30E-01 | 1.52E-01 | 6.110 |
| factor(dpc)5:vactype O3039-7 | 6.10E-01 | 1.52E-01 | 4.007 |
| factor(dpc)6:vactype O3039-7 | 4.90E-01 | 1.52E-01 | 3.219 |
| factor(dpc)7:vactype O3039-7 | 2.00E-02 | 1.52E-01 | 0.131 |
| factor(dpc)11:vactype O3039-7 | -3.00E-01 | 1.52E-01 | -1.971 |
| factor(dpc)14:vactype O3039-7 | -2.20E-01 | 1.52E-01 | -1.445 |
| factor(dpc)18:vactype O3039-7 | -1.40E-01 | 1.52E-01 | -0.920 |
| factor(dpc)21:vactype O3039-7 | -2.70E-01 | 1.52E-01 | -1.774 |
| factor(dpc)25:vactype O3039-7 | -3.20E-01 | 1.52E-01 | -2.102 |
| factor(dpc)28:vactype O3039-7 | -3.20E-01 | 1.52E-01 | -2.102 |
| factor(dpc)31:vactype O3039-7 | -3.60E-01 | 1.52E-01 | -2.365 |
| vactype Comb-7:VNtype OAlg | -7.12E-01 | 6.81E-02 | -10.459 |
| vactype Control:VNtype OAlg | 5.00E-02 | 7.86E-02 | 0.636 |
| vactype O3039-21:VNtype OAlg | -1.76E-01 | 6.81E-02 | -2.585 |
| vactype O3039-7:VNtype OAlg | -6.76E-01 | 6.81E-02 | -9.930 |
| vactype Comb-7:VNtype OManisa | -2.70E-01 | 6.81E-02 | -3.966 |
| vactype Control:VNtype OManisa | 5.80E-01 | 7.86E-02 | 7.379 |
| vactype O3039-21:VNtype OManisa | 2.67E-03 | 6.81E-02 | 0.039 |
| vactype O3039-7:VNtype OManisa | -2.90E-01 | 6.81E-02 | -4.260 |

Correlation matrix not shown by default, as p = 85 > 12.

Use print(x, correlation=TRUE) or vcov(x) if you need it

**######### NSP antibodies ###########**

**############ NSP response between groups ##########**

> data<-read.csv('LVZ194.csv',sep=';')

> table(paste(vaccine,day),group)

> tapply(nsp0,group,summary)

> summary(aov(nsp0~group))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| group | 4 | 408.3 | 102.08 | 1.353 | 0.289 |
| Residuals | 18 | 1358.4 | 75.47 | ---- |  |

> tapply(nsp5,group,summary)

> summary(aov(nsp5~group))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| group | 4 | 6.41E+02 | 160.34 | 2.138 | 0.118 |
| Residuals | 18 | 1349.7 | 74.98 |  |  |

> tapply(nsp11,group,summary)

> summary(aov(nsp11~group))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| group | 4 | 4.12E+02 | 102.9 | 3.397 | 0.0309 | \* |
| Residuals | 18 | 545.4 | 30.3 | ---- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(nsp11,group) # No pairwise difference

Pairwise comparisons using t tests with pooled SD

data: nsp11 and group

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | 1 | 2 | 3 | 4 |
| 2 | 1.000 | - | - | - |
| 3 | 0.578 | 0.998 | - | - |
| 4 | 0.998 | 0.494 | 0.053 | - |
| 5 | 0.998 | 0.578 | 0.100 | 1.000 |

P value adjustment method: holm

> tapply(nsp14,group,summary)

> summary(aov(nsp14~group))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| group | 4 | 544 | 136 | 4.583 | 0.00997 | \*\* |
| Residuals | 18 | 534.2 | 29.68 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(nsp14,group)

Pairwise comparisons using t tests with pooled SD

data: nsp14 and group

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | 1 | 2 | 3 | 4 |
| 2 | 1.000 | - | - | - |
| 3 | 0.109 | 0.527 | - | - |
| 4 | 1.000 | 0.482 | 0.016 | - |
| 5 | 1.000 | 0.527 | 0.033 | 1.000 |

P value adjustment method: holm

> tapply(nsp21,group,summary)

> summary(aov(nsp21~group))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| group | 4 | 343.7 | 85.94 | 4.597 | 0.00984 | \*\* |
| Residuals | 18 | 336.5 | 18.7 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(nsp21,group) # No pairwise difference

Pairwise comparisons using t tests with pooled SD

data: nsp21 and group

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | 1 | 2 | 3 | 4 |
| 2 | 0.673 | - | - | - |
| 3 | 0.602 | 1.000 | - | - |
| 4 | 0.673 | 0.066 | 0.051 | - |
| 5 | 0.673 | 0.076 | 0.066 | 1.000 |

P value adjustment method: holm

> tapply(nsp28,group,summary)

> summary(aov(nsp28~group))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| group | 4 | 200.6 | 50.14 | 6.128 | 0.00271 | \*\* |
| Residuals | 18 | 147.3 | 8.18 | --- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(nsp28,group)

Pairwise comparisons using t tests with pooled SD

data: nsp28 and group

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | 1 | 2 | 3 | 4 |
| 2 | 0.213 | - | - | - |
| 3 | 0.688 | 0.628 | - | - |
| 4 | 0.576 | 0.012 | 0.156 | - |
| 5 | 0.213 | 0.006 | 0.058 | 0.688 |

P value adjustment method: holm

> tapply(nsp33,group,summary)

> summary(aov(nsp33~group))

Df Sum Sq Mean Sq F value Pr(>F)

group 4 112.17 28.041 6.474 0.00207 \*\*

Residuals 18 77.96 4.331

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(nsp33,group)

Pairwise comparisons using t tests with pooled SD

data: nsp33 and group

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | 1 | 2 | 3 | 4 |
| 2 | 0.0938 | - | - | - |
| 3 | 0.8397 | 0.0689 | - | - |
| 4 | 0.7592 | 0.0060 | 0.7867 | - |
| 5 | 0.2972 | 0.0029 | 0.3489 | 0.7867 |

P value adjustment method: holm

**> ############ NSP response between vaccines ##########**

> tapply(nsp0,vaccine,summary)

> summary(aov(nsp0~vaccine))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| vaccine | 2 | 55.700 | 27.84 | 0.325 | 0.726 |
| Residuals | 20 | 1711.000 | 85.55 |  |  |

> tapply(nsp5,vaccine,summary)

> summary(aov(nsp5~vaccine))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| vaccine | 2 | 121.7 | 60.87 | 0.651 | 0.532 |
| Residuals | 20 | 1869.3 | 93.47 |  |  |

> tapply(nsp11,vaccine,summary)

> summary(aov(nsp11~vaccine))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| vaccine | 2 | 189 | 94.5 | 2.46 | 0.111 |
| Residuals | 20 | 768.1 | 38.41 |  |  |

> tapply(nsp14,vaccine,summary)

> summary(aov(nsp14~vaccine))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| vaccine | 2 | 210.7 | 105.36 | 2.429 | 0.114 |
| Residuals | 20 | 867.5 | 43.37 |  |  |

> tapply(nsp21,vaccine,summary)

> summary(aov(nsp21~vaccine))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| vaccine | 2 | 116.6 | 58.28 | 2.068 | 0.153 |
| Residuals | 20 | 563.7 | 28.18 |  |  |

> tapply(nsp28,vaccine,summary)

> summary(aov(nsp28~vaccine))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| vaccine | 2 | 74.63 | 37.31 | 2.731 | 0.894 |
| Residuals | 20 | 273.23 | 13.66 | --- |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> tapply(nsp33,vaccine,summary)

> summary(aov(nsp33~vaccine))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| vaccine | 2 | 39 | 19.501 | 2.581 | 0.101 |
| Residuals | 20 | 151.1 | 7.556 |  |  |

**> ############ NSP response between day of challenge ##########**

> tapply(nsp0,day,summary)

> summary(aov(nsp0~day))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| day | 2 | 362.1 | 181.06 | 2.578 | 0.101 |
| Residuals | 20 | 1404.6 | 70.23 |  |  |

> tapply(nsp5,day,summary)

> summary(aov(nsp5~day))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| day | 2 | 526.6 | 263.31 | 3.596 | 0.0463 | \* |
| Residuals | 20 | 1464.5 | 73.22 | ---- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(nsp5,day) # No pairwise difference

Pairwise comparisons using t tests with pooled SD

data: nsp5 and day

|  |  |  |
| --- | --- | --- |
|  | 21 | 7 |
| 7 | 0.07 | - |
| Control | 0.87 | 0.16 |

P value adjustment method: holm

> tapply(nsp11,day,summary)

> summary(aov(nsp11~day))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| day | 2 | 94 | 46.99 | 1.089 | 0.356 |
| Residuals | 20 | 863.1 | 43.16 |  |  |

> tapply(nsp14,day,summary)

> summary(aov(nsp14~day))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| day | 2.00 | 109.70 | 54.83 | 1.13 | 0.342 |
| Residuals | 20.00 | 968.50 | 48.43 |  |  |

> pairwise.t.test(nsp14,day)

Pairwise comparisons using t tests with pooled SD

data: nsp14 and day

|  |  |  |
| --- | --- | --- |
|  | 21 | 7 |
| 7 | 0.66 | - |
| control | 0.49 | 0.45 |

P value adjustment method: holm

> tapply(nsp21,day,summary)

> summary(aov(nsp21~day))

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| day | 2.00 | 107.50 | 53.76 | 1.88 | 0.179 |
| Residuals | 20.00 | 572.70 | 28.64 |  |  |

> pairwise.t.test(nsp21,day)

Pairwise comparisons using t tests with pooled SD

data: nsp21 and day

|  |  |  |
| --- | --- | --- |
|  | 21 | 7 |
| 7 | 0.47 | - |
| control | 0.20 | 0.33 |

P value adjustment method: holm

> tapply(nsp28,day,summary)

> summary(aov(nsp28~day))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| day | 2 | 107.2 | 53.59 | 4.453 | 0.0252 | \* |
| Residuals | 20 | 240.7 | 12.03 | ---- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(nsp28,day)

Pairwise comparisons using t tests with pooled SD

data: nsp28 and day

|  |  |  |
| --- | --- | --- |
|  | 21 | 7 |
| 7 | 0.181 | - |
| control | 0.027 | 0.181 |

P value adjustment method: holm

> tapply(nsp33,day,summary)

> summary(aov(nsp33~day))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |  |
| day | 2 | 73.79 | 36.9 | 6.343 | 0.00736 | \*\* |
| Residuals | 20 | 116.33 | 5.82 | ---- |  |  |

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> pairwise.t.test(nsp33,day)

Pairwise comparisons using t tests with pooled SD

data: nsp33 and day

|  |  |  |
| --- | --- | --- |
|  | 21 | 7 |
| 7 | 0.032 | - |
| control | 0.015 | 0.187 |

P value adjustment method: holm

**########## linear and linear mixed models for NSP antibodies ##############**

> ns<-read.csv("nsp.csv",sep=';')

> ns$vac<-factor(substr(ns$vactype,1,4))

> attach(ns)

> summary(ns)

> tapply(percinh,animal,length)

> h0<-lmer(percinh~(1|animal))

boundary (singular) fit: see ?isSingular

> h1<-lmer(percinh~factor(dpv)+(1|animal))

boundary (singular) fit: see ?isSingular

> h2<-lmer(percinh~vactype+(1|animal))

boundary (singular) fit: see ?isSingular

> h2a<-lmer(percinh~vac+(1|animal))

boundary (singular) fit: see ?isSingular

> h3<-lmer(percinh~prot+(1|animal))

boundary (singular) fit: see ?isSingular

> h4<-lmer(percinh~factor(dpc)+(1|animal))

> AIC(h0,h1,h2,h2a,h3,h4)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| h0 | 3 | 1491.296 |
| h1 | 5 | 1484.43 |
| h2 | 7 | 1475.986 |
| h2a | 5 | 1484.822 |
| h3 | 4 | 1487.966 |
| h4 | 9 | 1025.289 |

> summary(h4) #I do not understand the singularity we have 7 observations per animal. but we ignore it as model h4 does not give this warning

Linear mixed model fit by REML ['lmerMod']

Formula: percinh ~ factor(dpc) + (1 | animal)

REML criterion at convergence: 1007.3

Scaled residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -3.00231 | -0.54037 | 0.04811 | 0.53723 | 2.8935 |

Random effects:

|  |  |  |  |
| --- | --- | --- | --- |
| Groups | Name | Variance | Std.Dev. |
| animal | (Intercept) | 18.01 | 4.244 |
| Residual |  | 27.52 | 5.246 |

Number of obs: 161, groups: animal, 23

Fixed effects:

|  |  |  |  |
| --- | --- | --- | --- |
|  | Estimate | Std. Error | t value |
| (Intercept) | 33.364 | 1.407 | 23.714 |
| factor(dpc)5 | 7.407 | 1.547 | 4.789 |
| factor(dpc)11 | 54.06 | 1.547 | 34.949 |
| factor(dpc)14 | 55.002 | 1.547 | 35.558 |
| factor(dpc)21 | 54.674 | 1.547 | 35.345 |
| factor(dpc)28 | 56.854 | 1.547 | 36.755 |
| factor(dpc)33 | 59.007 | 1.547 | 38.147 |

Correlation of Fixed Effects:

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | (Intr) | fct()5 | fc()11 | fc()14 | fc()21 | fc()28 |
| factr(dpc)5 | -0.55 |  |  |  |  |  |
| fctr(dpc)11 | -0.55 | 0.50 |  |  |  |  |
| fctr(dpc)14 | -0.55 | 0.50 | 0.50 |  |  |  |
| fctr(dpc)21 | -0.55 | 0.50 | 0.50 | 0.50 |  |  |
| fctr(dpc)28 | -0.55 | 0.50 | 0.50 | 0.50 | 0.50 |  |
| fctr(dpc)33 | -0.55 | 0.50 | 0.50 | 0.50 | 0.50 | 0.50 |

> h5<-lmer(percinh~factor(dpc)+factor(dpv)+(1|animal))

> h6<-lmer(percinh~factor(dpc)+vactype+(1|animal))

> h6a<-lmer(percinh~factor(dpc)+vac+(1|animal))

> h7<-lmer(percinh~factor(dpc)+prot+(1|animal))

> AIC(h4,h5,h6,h6a,h7)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| h4 | 9 | 1025.289 |
| h5 | 11 | 1018.709 |
| h6 | 13 | 1006.9 |
| h6a | 11 | 1020.319 |
| h7 | 10 | 1021.786 |

> summary(h6)

Linear mixed model fit by REML ['lmerMod']

Formula: percinh ~ factor(dpc) + vactype + (1 | animal)

REML criterion at convergence: 980.9

Scaled residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -3.01572 | -0.52373 | 0.04974 | 0.50303 | 2.88008 |

Random effects:

|  |  |  |  |
| --- | --- | --- | --- |
| Groups | Name | Variance | Std.Dev. |
| animal | (Intercept) | 10.87 | 3.297 |
| Residual |  | 27.52 | 5.246 |

Number of obs: 161, groups: animal, 23

Fixed effects:

|  |  |  |  |
| --- | --- | --- | --- |
|  | Estimate | Std. Error | t value |
| (Intercept) | 32.826 | 1.997 | 16.442 |
| factor(dpc)5 | 7.407 | 1.547 | 4.789 |
| factor(dpc)11 | 54.06 | 1.547 | 34.949 |
| factor(dpc)14 | 55.002 | 1.547 | 35.558 |
| factor(dpc)21 | 54.674 | 1.547 | 35.345 |
| factor(dpc)28 | 56.854 | 1.547 | 36.755 |
| factor(dpc)33 | 59.007 | 1.547 | 38.147 |
| vactypecomb7 | -1.629 | 2.433 | -0.669 |
| vactypecontr | 2.662 | 2.81 | 0.947 |
| vactypeO303921 | -2.904 | 2.433 | -1.193 |
| vactypeO30397 | 5.408 | 2.433 | 2.222 |

Correlation of Fixed Effects:

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | (Intr) | fct()5 | fc()11 | fc()14 | fc()21 | fc()28 | fc()33 | vctyp7 | vctypc | vO303921 |
| factr(dpc)5 | -0.387 |  |  |  |  |  |  |  |  |  |
| fctr(dpc)11 | -0.387 | 0.500 |  |  |  |  |  |  |  |  |
| fctr(dpc)14 | -0.387 | 0.500 | 0.500 |  |  |  |  |  |  |  |
| fctr(dpc)21 | -0.387 | 0.500 | 0.500 | 0.500 |  |  |  |  |  |  |
| fctr(dpc)28 | -0.387 | 0.500 | 0.500 | 0.500 | 0.500 |  |  |  |  |  |
| fctr(dpc)33 | -0.387 | 0.500 | 0.500 | 0.500 | 0.500 | 0.500 |  |  |  |  |
| vactypecmb7 | -0.609 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |  |  |  |
| vactypecntr | -0.528 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.433 |  |  |
| vctyO303921 | -0.609 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.500 | 0.433 |  |
| vctypO30397 | -0.609 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.500 | 0.433 | 0.500 |

> h8<-lmer(percinh~factor(dpc)+vactype+factor(dpv)+(1|animal)) #nonsense I know dpv is part of vactype

fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients

> h9<-lmer(percinh~factor(dpc)+vactype+vactype:factor(dpc)+(1|animal))

> h10<-lmer(percinh~factor(dpc)+vactype+prot+(1|animal))

> h11<-lmer(percinh~factor(dpc)+vactype+vac+(1|animal)) #nonsense I know vac is part of vactype

fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients

> AIC(h6,h8,h9,h10,h11)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| h6 | 13 | 1006.9004 |
| h8 | 13 | 1006.9004 |
| h9 | 37 | 906.5031 |
| h10 | 14 | 1005.0319 |
| h11 | 13 | 1006.9004 |

> h11<-lmer(percinh~factor(dpc)+vactype+vactype:factor(dpc)+factor(dpv)+(1|animal))

fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients

> h12<-lmer(percinh~factor(dpc)+vactype+vactype:factor(dpc)+prot+(1|animal))

> h13<-lmer(percinh~factor(dpc)+vactype+vactype:factor(dpc)+vac+(1|animal))

fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients

> AIC(h9,h11,h12,h13)

|  |  |  |
| --- | --- | --- |
|  | df | AIC |
| h9 | 37 | 906.5031 |
| h11 | 37 | 906.5031 |
| h12 | 38 | 904.6345 |
| h13 | 37 | 906.5031 |

> summary(h12) #difference in AIC less than 2 so not truly significant t-value also low.

Linear mixed model fit by REML ['lmerMod']

Formula: percinh ~ factor(dpc) + vactype + vactype:factor(dpc) + prot + (1 | animal)

REML criterion at convergence: 828.6

Scaled residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -2.42664 | -0.43492 | 0.02643 | 0.39563 | 2.32534 |

Random effects:

|  |  |  |  |
| --- | --- | --- | --- |
| Groups | Name | Variance | Std.Dev. |
| animal | (Intercept) | 12.39 | 3.52 |
| Residual |  | 23 | 4.796 |

Number of obs: 161, groups: animal, 23

Fixed effects:

|  |  |  |  |
| --- | --- | --- | --- |
|  | Estimate | Std. Error | t value |
| (Intercept) | 30.77792 | 3.86199 | 7.969 |
| factor(dpc)5 | 6.68253 | 3.03327 | 2.203 |
| factor(dpc)11 | 56.95039 | 3.03327 | 18.775 |
| factor(dpc)14 | 59.21074 | 3.03327 | 19.520 |
| factor(dpc)21 | 57.81267 | 3.03327 | 19.060 |
| factor(dpc)28 | 59.58922 | 3.03327 | 19.645 |
| factor(dpc)33 | 61.58045 | 3.03327 | 20.302 |
| vactypecomb7 | 5.15046 | 3.80387 | 1.354 |
| vactypecontr | -1.13330 | 5.16832 | -0.219 |
| vactypeO303921 | -1.50405 | 3.76244 | -0.400 |
| vactypeO30397 | 9.16337 | 3.92554 | 2.334 |
| prot | -0.06873 | 2.79947 | -0.025 |
| factor(dpc)5:vactypecomb7 | 0.32366 | 4.28969 | 0.075 |
| factor(dpc)11:vactypecomb7 | -11.56549 | 4.28969 | -2.696 |
| factor(dpc)14:vactypecomb7 | -14.58997 | 4.28969 | -3.401 |
| factor(dpc)21:vactypecomb7 | -9.90166 | 4.28969 | -2.308 |
| factor(dpc)28:vactypecomb7 | -6.92225 | 4.28969 | -1.614 |
| factor(dpc)33:vactypecomb7 | -4.89406 | 4.28969 | -1.141 |
| factor(dpc)5:vactypecontr | -0.48700 | 4.95331 | -0.098 |
| factor(dpc)11:vactypecontr | 6.03826 | 4.95331 | 1.219 |
| factor(dpc)14:vactypecontr | 4.89898 | 4.95331 | 0.989 |
| factor(dpc)21:vactypecontr | 5.74188 | 4.95331 | 1.159 |
| factor(dpc)28:vactypecontr | 5.62888 | 4.95331 | 1.136 |
| factor(dpc)33:vactypecontr | 4.26504 | 4.95331 | 0.861 |
| factor(dpc)5:vactypeO303921 | 0.33317 | 4.28969 | 0.078 |
| factor(dpc)11:vactypeO303921 | -0.79749 | 4.28969 | -0.186 |
| factor(dpc)14:vactypeO303921 | -1.84073 | 4.28969 | -0.429 |
| factor(dpc)21:vactypeO303921 | -2.78002 | 4.28969 | -0.648 |
| factor(dpc)28:vactypeO303921 | -2.60884 | 4.28969 | -0.608 |
| factor(dpc)33:vactypeO303921 | -2.10534 | 4.28969 | -0.491 |
| factor(dpc)5:vactypeO30397 | 2.97001 | 4.28969 | 0.692 |
| factor(dpc)11:vactypeO30397 | -4.55577 | 4.28969 | -1.062 |
| factor(dpc)14:vactypeO30397 | -5.86707 | 4.28969 | -1.368 |
| factor(dpc)21:vactypeO30397 | -5.20289 | 4.28969 | -1.213 |
| factor(dpc)28:vactypeO30397 | -6.42695 | 4.28969 | -1.498 |
| factor(dpc)33:vactypeO30397 | -7.39724 | 4.28969 | -1.724 |

Correlation matrix not shown by default, as p = 36 > 12.

Use print(x, correlation=TRUE) or vcov(x) if you need it

> summary(h9) #The model indicates a lower percinh in comb7 than in comb21 especially on day 11, 14 and 21

Linear mixed model fit by REML ['lmerMod']

Formula: percinh ~ factor(dpc) + vactype + vactype:factor(dpc) + (1 | animal)

REML criterion at convergence: 832.5

Scaled residuals:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Min | 1Q | Median | 3Q | Max |
| -2.43159 | -0.44916 | 0.02033 | 0.39049 | 2.33132 |

Random effects:

|  |  |  |  |
| --- | --- | --- | --- |
| Groups | Name | Variance | Std.Dev. |
| animal | (Intercept) | 11.52 | 3.394 |
| Residual |  | 23.00 | 4.796 |

Number of obs: 161, groups: animal, 23

Fixed effects:

|  |  |  |  |
| --- | --- | --- | --- |
|  | Estimate | Std. Error | t value |
| (Intercept) | 30.7092 | 2.6275 | 11.687 |
| factor(dpc)5 | 6.6825 | 3.0333 | 2.203 |
| factor(dpc)11 | 56.9504 | 3.0333 | 18.775 |
| factor(dpc)14 | 59.2107 | 3.0333 | 19.52 |
| factor(dpc)21 | 57.8127 | 3.0333 | 19.06 |
| factor(dpc)28 | 59.5892 | 3.0333 | 19.645 |
| factor(dpc)33 | 61.5805 | 3.0333 | 20.302 |
| vactypecomb7 | 5.1642 | 3.7159 | 1.39 |
| vactypecontr | -1.0646 | 4.2907 | -0.248 |
| vactypeO303921 | -1.5040 | 3.7159 | -0.405 |
| vactypeO30397 | 9.1909 | 3.7159 | 2.473 |
| factor(dpc)5:vactypecomb7 | 0.3237 | 4.2897 | 0.075 |
| factor(dpc)11:vactypecomb7 | -11.5655 | 4.2897 | -2.696 |
| factor(dpc)14:vactypecomb7 | -14.5900 | 4.2897 | -3.401 |
| factor(dpc)21:vactypecomb7 | -9.9017 | 4.2897 | -2.308 |
| factor(dpc)28:vactypecomb7 | -6.9222 | 4.2897 | -1.614 |
| factor(dpc)33:vactypecomb7 | -4.8941 | 4.2897 | -1.141 |
| factor(dpc)5:vactypecontr | -0.4870 | 4.9533 | -0.098 |
| factor(dpc)11:vactypecontr | 6.0383 | 4.9533 | 1.219 |
| factor(dpc)14:vactypecontr | 4.8990 | 4.9533 | 0.989 |
| factor(dpc)21:vactypecontr | 5.7419 | 4.9533 | 1.159 |
| factor(dpc)28:vactypecontr | 5.6289 | 4.9533 | 1.136 |
| factor(dpc)33:vactypecontr | 4.2650 | 4.9533 | 0.861 |
| factor(dpc)5:vactypeO303921 | 0.3332 | 4.2897 | 0.078 |
| factor(dpc)11:vactypeO303921 | -0.7975 | 4.2897 | -0.186 |
| factor(dpc)14:vactypeO303921 | -1.8407 | 4.2897 | -0.429 |
| factor(dpc)21:vactypeO303921 | -2.7800 | 4.2897 | -0.648 |
| factor(dpc)28:vactypeO303921 | -2.6088 | 4.2897 | -0.608 |
| factor(dpc)33:vactypeO303921 | -2.1053 | 4.2897 | -0.491 |
| factor(dpc)5:vactypeO30397 | 2.9700 | 4.2897 | 0.692 |
| factor(dpc)11:vactypeO30397 | -4.5558 | 4.2897 | -1.062 |
| factor(dpc)14:vactypeO30397 | -5.8671 | 4.2897 | -1.368 |
| factor(dpc)21:vactypeO30397 | -5.2029 | 4.2897 | -1.213 |
| factor(dpc)28:vactypeO30397 | -6.4269 | 4.2897 | -1.498 |
| factor(dpc)33:vactypeO30397 | -7.3972 | 4.2897 | -1.724 |

Correlation matrix not shown by default, as p = 35 > 12.

Use print(x, correlation=TRUE) or vcov(x) if you need it

> detach(ns)