

Tick-Borne Encephalitis Virus Antibodies in Roe Deer, the Netherlands

Appendix

Supplemental Material for R Script

```
library(readr)

setwd("...")

tbe <- read_csv("tbe.csv", col_types = cols(
  Datefound = col_date(format = "%d/%m/%Y"),
  Datereceived = col_date(format = "%d/%m/%Y")
))

case <- ifelse(tbe$TBEResult == "positive", 1, 0)
noncase <- ifelse(tbe$TBEResult == "negative", 1, 0)

attach(tbe)

weight <- as.numeric(Weight)

AgeCategory1 <- factor(AgeCategory, levels = c("Juvenile," "Immature," "Mature"))
names(tbe)
```

#Effect of Year and Confounders on Cases: Binomial Logistic Regression Model

```
fit <-
glm(case~factor(Year)+factor(Gender)+AgeCategory1+factor(NutritionalCondition), family =
binomial)

summary(fit)

cbind(exp(coef(fit)), exp(confint(fit)))

fit <-
```

```
glm(case~factor(Year)+factor(Gender)+AgeCategory1+factor(NutritionalCondition),family = binomial)
```

```
summary(fit)
```

```
cbind(exp(coef(fit)),exp(confint(fit)))
```

```
fit <-
```

```
glm(case~factor(Year)+factor(Gender)+AgeCategory1,family = binomial)
```

```
summary(fit)
```

```
cbind(exp(coef(fit)),exp(confint(fit)))
```

```
fit <-
```

```
glm(case~factor(Year)+factor(Gender)+factor(NutritionalCondition),family = binomial)
```

1)

```
summary(fit)
```

```
cbind(exp(coef(fit)),exp(confint(fit)))
```

```
fit <-
```

```
glm(case~factor(Year)+AgeCategory1+factor(NutritionalCondition),family = binomial)
```

1)

```
summary(fit)
```

```
cbind(exp(coef(fit)),exp(confint(fit)))
```

```
fit <-
```

```
glm(case~factor(Year)+AgeCategory1,family = binomial)
```

```
summary(fit)
```

```
cbind(exp(coef(fit)),exp(confint(fit)))
```

```
fit <-
```

```
glm(case~factor(Year)+factor(NutritionalCondition),family = binomial)
```

```
summary(fit)
```

```
cbind(exp(coef(fit)),exp(confint(fit)))
```

```
fit <-
```

```

glm(case~factor(Year)+factor(Gender),family = binomial)
summary(fit)
cbind(exp(coef(fit)),exp(confint(fit)))
fit <- glm(case~factor(Year),family = binomial)
summary(fit0)
cbind(exp(coef(fit)),exp(confint(fit)))

```

#Probability of Geographic Expansion: Probability Distribution (haard = focus)

```

tbe17 <- subset(tbe, Year == "2017")
detach(tbe)
names(tbe17)
n.haard <- NULL
for (i in 1:100000){
x <- sample(tbe17$Haard,297)
n.haard[i] <- length(names(table(x)))
y <- as.numeric(names(table(x)))[1]
if (y == 0) n.haard[i] <- n.haard[i]-1
}
table(n.haard)/100000
0:10%*%table(n.haard)/100000
barplot(table(n.haard)/100000)

```