

8.7 Appendix 7

R Studio script – R Studio version 1.4.1106.

```
## Load data
df_a <- read.csv("~/analysis_df.csv", header=FALSE)
View(df_a)

## Amend headers
names(df_a) <- df_a[1,]
df_a <- df_a[-1,]
head(df_a)
summary(df_a)

## Update types
df_a$warning_status <- as.numeric(df_a$warning_status)
df_a$provider_type <- as.factor(df_a$provider_type)
df_a$provider_specialty <- as.factor(df_a$provider_specialty)
df_a$description <- as.factor(df_a$description)
df_a$context <- as.factor(df_a$context)
df_a$drug_allergy_reactions <- as.factor(df_a$drug_allergy_reactions)
df_a$age_range <- as.factor(df_a$age_range)
df_a$sex <- as.factor(df_a$sex)
str(df_a)

## Install packages
install.packages('aod')
library(aod)

## Unadjusted logistic regression, ORs, CIs and Wald test for trend
## provider_type
mylogit2 <- glm(warning_status ~ provider_type, data = df_a, family = "binomial")
summary(mylogit2)
exp(cbind(OR = coef(mylogit2), confint(mylogit2)))
wald.test(b = coef(mylogit2), Sigma = vcov(mylogit2), Terms = 1:12)

## provider_specialty
mylogit3 <- glm(warning_status ~ provider_specialty, data = df_a, family = "binomial")
summary(mylogit3)
exp(cbind(OR = coef(mylogit3), confint(mylogit3)))
wald.test(b = coef(mylogit3), Sigma = vcov(mylogit3), Terms = 1:9)

## description
mylogit5 <- glm(warning_status ~ description, data = df_a, family = "binomial")
summary(mylogit5)
exp(cbind(OR = coef(mylogit5), confint(mylogit5)))
wald.test(b = coef(mylogit5), Sigma = vcov(mylogit5), Terms = 1:9)

## context
mylogit6 <- glm(warning_status ~ context, data = df_a, family = "binomial")
summary(mylogit6)
exp(cbind(OR = coef(mylogit6), confint(mylogit6)))
wald.test(b = coef(mylogit6), Sigma = vcov(mylogit6), Terms = 1:3)

## drug_allergy_reactions
mylogit7 <- glm(warning_status ~ drug_allergy_reactions, data = df_a, family = "binomial")
summary(mylogit7)
exp(cbind(OR = coef(mylogit7), confint(mylogit7)))
wald.test(b = coef(mylogit7), Sigma = vcov(mylogit7), Terms = 1:8)

## age_range
mylogit8 <- glm(warning_status ~ age_range, data = df_a, family = "binomial")
summary(mylogit8)
exp(cbind(OR = coef(mylogit8), confint(mylogit8)))
wald.test(b = coef(mylogit8), Sigma = vcov(mylogit8), Terms = 1:9)

## sex
mylogit9 <- glm(warning_status ~ sex, data = df_a, family = "binomial")
summary(mylogit9)
```

```
exp(cbind(OR = coef(mylogit9), confint(mylogit9)))
wald.test(b = coef(mylogit9), Sigma = vcov(mylogit9), Terms = 1:2)
str(df_a)
```

```
#####
```

```
## Adjusted regression - provider_type + provider_specialty
```

```
mylogit_b <- glm(formula = warning_status ~ provider_type + provider_specialty + description + context + drug_allergy_reactions +  
age_range + sex, family = "binomial", data = df_a)
```

```
summary(mylogit_b)
```

```
## odds ratios and 95% CI
```

```
exp(cbind(OR = coef(mylogit_b), confint(mylogit_b)))
```