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$provider_type_cat1 <- as.factor(df_a$provider_type_cat1)
df_a$provider_type_cat2 <- as.factor(df_a$provider_type_cat2)
df_a$provider_specialty_cat1 <- as.factor(df_a$provider_specialty_cat1)
df_a$provider_specialty_cat2 <- as.factor(df_a$provider_specialty_cat2)
df_a$description_cat1 <- as.factor(df_a$description_cat1)
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)
df_a$severity <- as.factor(df_a$severity)
df_a$importance_level <- as.factor(df_a$importance_level)
df_a$drug_allergy_contraindication_group <- as.factor(df_a$drug_allergy_contraindication_group)
str(df_a)

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

## Unadjusted logisic regression, ORs, CIs and Wald test for trend
## provider_type_cat1
mylogit1 <- glm(warning_status ~ provider_type_cat1, data = df_a, family = "binomial")
summary(mylogit1)
exp(cbind(OR = coef(mylogit1), confint(mylogit1)))

## provider_type_cat2
mylogit2 <- glm(warning_status ~ provider_type_cat2, 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_cat1
mylogit3 <- glm(warning_status ~ provider_specialty_cat1, 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)

## provider_specialty_cat2
mylogit4 <- glm(warning_status ~ provider_specialty_cat2, data = df_a, family = "binomial")
summary(mylogit4)
exp(cbind(OR = coef(mylogit4), confint(mylogit4)))
wald.test(b = coef(mylogit4), Sigma = vcov(mylogit4), Terms = 1:16)

## description_cat1
mylogit5 <- glm(warning_status ~ description_cat1, 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)

## severity
mylogit10 <- glm(warning_status ~ severity, data = df_a, family = "binomial")
summary(mylogit10)
exp(cbind(OR = coef(mylogit10), confint(mylogit10)))
wald.test(b = coef(mylogit10), Sigma = vcov(mylogit10), Terms = 1:3)

## importance_level
mylogit11 <- glm(warning_status ~ importance_level, data = df_a, family = "binomial")
summary(mylogit11)
exp(cbind(OR = coef(mylogit11), confint(mylogit11)))
wald.test(b = coef(mylogit11), Sigma = vcov(mylogit11), Terms = 1:3)

## drug_allergy_contraindication_group
mylogit12 <- glm(warning_status ~ drug_allergy_contraindication_group, data = df_a, family = "binomial")
summary(mylogit12)
exp(cbind(OR = coef(mylogit12), confint(mylogit12)))
wald.test(b = coef(mylogit12), Sigma = vcov(mylogit12), Terms = 1:3)
str(df_a)

#####
## Adjusted regression - provider_type_cat2 + provider_specialty_cat1
mylogit_b <- glm(formula = warning_status ~ provider_type_cat2 + provider_specialty_cat1 + description_cat1 + context +
drug_allergy_reactions + age_range + sex + severity + importance_level + drug_allergy_contraindication_group, family = "binomial", data
= df_a)
summary(mylogit_b)
## odds ratios and 95% CI
exp(cbind(OR = coef(mylogit_b), confint(mylogit_b)))
```