## 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)))