diabetes\_one\_60plys

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data\_categ\_nosev <- readr::read\_csv("/Users/gabrielburcea/rprojects/data/your.md/cleaned\_data\_18\_08\_2020\_fully\_cleaned\_uniq\_comorb.csv")

## Parsed with column specification:  
## cols(  
## .default = col\_character(),  
## age = col\_double(),  
## date\_completed = col\_date(format = ""),  
## how\_unwell = col\_double(),  
## number\_morbidities = col\_double(),  
## Age = col\_double()  
## )

## See spec(...) for full column specifications.

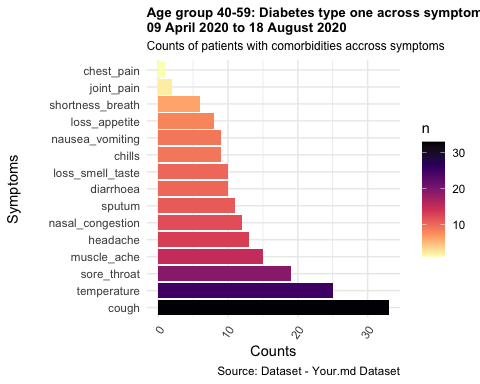
covid\_tested\_levels <- c("positive" = "showing symptoms")  
  
data\_age\_band <- data\_categ\_nosev %>%  
 dplyr::mutate(age\_band = dplyr::case\_when(  
 age == 0 | age <= 19 ~ '0-19',  
 age == 20 | age <= 39 ~ '20-39',  
 age == 40 | age <= 59 ~ '40-59',  
 age >= 60 ~ "60+")) %>%  
 dplyr::filter(number\_morbidities <= 1) %>%  
 dplyr::mutate(covid\_tested = forcats::fct\_recode(covid\_tested, !!!covid\_tested\_levels))  
  
  
data\_covid\_only <- data\_age\_band %>%  
#dplyr::filter(number\_morbidities <= 1) %>% # added this line on the 09/09/2020 as I want to check the analysis - do I get a different output, See report delivered ... compare this with the previous report generated on the date ....  
 dplyr::select(id, age, gender, covid\_tested, chills, cough, diarrhoea, fatigue, headache, loss\_smell\_taste, muscle\_ache,  
 nasal\_congestion, nausea\_vomiting, shortness\_breath, sore\_throat, sputum, temperature, loss\_appetite, chest\_pain, itchy\_eyes, joint\_pain,   
 asthma, diabetes\_type\_one, diabetes\_type\_two, obesity, hypertension, heart\_disease, lung\_condition, liver\_disease, kidney\_disease, age\_band, number\_morbidities)%>%   
 dplyr::filter(covid\_tested != "negative") %>%  
 tidyr::drop\_na()  
  
  
data\_age <- data\_covid\_only %>%   
 dplyr::filter(age\_band == "60+")  
  
  
data\_categ\_covid <- data\_age %>%  
 #dplyr::filter(number\_morbidities <= 1) %>% # added this line on the 09/09/2020 as I want to check the analysis - do I get a different output, See report delivered ... compare this with the previous report generated on the date ....  
 dplyr::select(id, age, gender, covid\_tested, chills, cough, diarrhoea, fatigue, headache, loss\_smell\_taste, muscle\_ache,   
 nasal\_congestion, nausea\_vomiting, shortness\_breath, sore\_throat, sputum, temperature, loss\_appetite, chest\_pain, itchy\_eyes, joint\_pain,   
 asthma, diabetes\_type\_one, diabetes\_type\_two, obesity, hypertension, heart\_disease, lung\_condition, liver\_disease, kidney\_disease) %>%  
 dplyr::filter(covid\_tested != "negative") %>%  
 tidyr::drop\_na()

data\_categ\_covid$country <- NULL  
data\_categ\_covid$location <- NULL  
data\_categ\_covid$date\_completed <- NULL  
data\_categ\_covid$covid\_tested <- NULL   
data\_categ\_covid$age\_band <- NULL  
data\_categ\_covid$status\_cv <- NULL  
data\_categ\_covid$sneezing <- NULL  
  
  
###########################################################################################  
### Transforming variables in factor format ###############################################  
#data\_categ\_covid$country <- as.factor(data\_categ\_covid$country)  
data\_categ\_covid$chills <- as.factor(data\_categ\_covid$chills)  
data\_categ\_covid$cough <- as.factor(data\_categ\_covid$cough)  
data\_categ\_covid$gender <- as.factor(data\_categ\_covid$gender)  
#data\_categ\_covid$covid\_tested <- as.factor(data\_categ\_covid$covid\_tested)  
data\_categ\_covid$diarrhoea <- as.factor(data\_categ\_covid$diarrhoea)  
data\_categ\_covid$fatigue <- as.factor(data\_categ\_covid$fatigue)  
data\_categ\_covid$headache <- as.factor(data\_categ\_covid$headache)  
data\_categ\_covid$loss\_smell\_taste <- as.factor(data\_categ\_covid$loss\_smell\_taste)  
data\_categ\_covid$muscle\_ache <- as.factor(data\_categ\_covid$muscle\_ache)  
data\_categ\_covid$nasal\_congestion <- as.factor(data\_categ\_covid$nasal\_congestion)  
data\_categ\_covid$nausea\_vomiting <- as.factor(data\_categ\_covid$nausea\_vomiting)  
#data\_categ\_covid$self\_diagnosis <- as.factor(data\_categ\_covid$self\_diagnosis)  
data\_categ\_covid$shortness\_breath <- as.factor(data\_categ\_covid$shortness\_breath)  
data\_categ\_covid$sore\_throat <- as.factor(data\_categ\_covid$sore\_throat)  
data\_categ\_covid$sputum <- as.factor(data\_categ\_covid$sputum)  
data\_categ\_covid$temperature <- as.factor(data\_categ\_covid$temperature)  
data\_categ\_covid$loss\_appetite <- as.factor(data\_categ\_covid$loss\_appetite)  
data\_categ\_covid$chest\_pain <- as.factor(data\_categ\_covid$chest\_pain)  
data\_categ\_covid$itchy\_eyes <- as.factor(data\_categ\_covid$itchy\_eyes)  
data\_categ\_covid$joint\_pain <- as.factor(data\_categ\_covid$joint\_pain)  
  
  
### Transforming variables in numerical format #########################################################  
data\_categ\_covid$asthma <- as.factor(data\_categ\_covid$asthma)  
data\_categ\_covid$diabetes\_type\_two <- as.factor(data\_categ\_covid$diabetes\_type\_two)  
data\_categ\_covid$obesity <- as.factor(data\_categ\_covid$obesity)  
data\_categ\_covid$hypertension <- as.factor(data\_categ\_covid$hypertension)  
data\_categ\_covid$heart\_disease <- as.factor(data\_categ\_covid$heart\_disease)  
data\_categ\_covid$kidney\_disease <- as.factor(data\_categ\_covid$kidney\_disease)  
data\_categ\_covid$lung\_condition <- as.factor(data\_categ\_covid$lung\_condition)  
data\_categ\_covid$liver\_disease <- as.factor(data\_categ\_covid$liver\_disease)  
data\_categ\_covid$diabetes\_type\_one <- as.factor(data\_categ\_covid$diabetes\_type\_one)  
#data\_categ\_covid$covid\_tested <- as.factor(data\_categ\_nose)

diabetes\_type\_one\_data <- data\_categ\_covid %>%  
 dplyr::select(diabetes\_type\_one, chills, cough, diarrhoea, headache, loss\_smell\_taste, muscle\_ache,   
 nasal\_congestion, nausea\_vomiting, shortness\_breath, sore\_throat, sputum, temperature, joint\_pain, itchy\_eyes, chest\_pain, loss\_appetite)  
  
  
diab\_t <- table(diabetes\_type\_one\_data$diabetes\_type\_one)  
  
diab\_t

##   
## No Yes   
## 1987 50

diabetes\_count <- diabetes\_type\_one\_data %>%  
 tidyr::pivot\_longer(cols = 2:17,   
 names\_to = "symptoms",   
 values\_to = "yes\_no") %>%  
 dplyr::filter(diabetes\_type\_one == "Yes" & yes\_no == "Yes") %>%  
 dplyr::group\_by(symptoms) %>%  
 dplyr::tally() %>%  
 dplyr::mutate(Percentage = n/sum(n)) %>%  
 dplyr::arrange(desc(n))  
  
start\_date = as.Date("2020-04-09", tz = "Europe/London")  
end\_date = as.Date("2020-08-18")  
title\_stub <- "Age group 40-59: Diabetes type one across symptoms\n"  
start\_date\_title <- format(as.Date(start\_date), format = "%d %B %Y")  
end\_date\_title <- format(as.Date(end\_date), format = "%d %B %Y")  
chart\_title <- paste0(title\_stub, start\_date\_title, " to ", end\_date\_title)  
  
plot\_diabetes\_sympt <-  
 ggplot2::ggplot(diabetes\_count, ggplot2::aes(x = reorder(symptoms, - Percentage), y = n, fill = n)) +  
 ggplot2::coord\_flip() +  
 ggplot2::geom\_bar(stat = "identity", position = "dodge") +  
 ggplot2::scale\_fill\_viridis\_c(option = "magma", direction = -1) +  
 ggplot2::scale\_x\_discrete(limits = unique(diabetes\_count$symptoms)) +  
 #ggplot2::theme(legend.position = "bottom") +  
 #ggplot2::guides(fill = ggplot2::guide\_legend(nrow = 3)) +  
 ggplot2::theme\_minimal() +  
 ggplot2::labs( title = chart\_title,  
 subtitle = "Counts of patients with comorbidities accross symptoms",  
 y = "Counts",  
 x = "Symptoms",  
 caption = "Source: Dataset - Your.md Dataset") +  
 ggplot2::theme(  
 axis.title.y = ggplot2::element\_text(margin = ggplot2::margin(  
 t = 0,  
 r = 21,  
 b = 0,  
 l = 0  
 )),  
 plot.title = ggplot2::element\_text(size = 10, face = "bold"),  
 plot.subtitle = ggplot2::element\_text(size = 9),  
 axis.text.x = ggplot2::element\_text(angle = 55, hjust = 1)  
 )  
  
plot\_diabetes\_sympt



## Univariate analysis for diabetes type one

The univariate analysis real that symptoms such as headaches, nasal congestion, sore throat, temperature (39.1-41) are associated with diabetes type one.

diabetes\_type\_one\_data$diabetes\_type\_one <- as.factor(diabetes\_type\_one\_data$diabetes\_type\_one)  
diabetes\_type\_one\_chills <- glm(diabetes\_type\_one ~ chills, data = diabetes\_type\_one\_data, family = binomial)  
  
summary(diabetes\_type\_one\_chills)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ chills, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.2332 -0.2332 -0.2332 -0.1889 2.8409   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.5909 0.1583 -22.683 <2e-16 \*\*\*  
## chillsYes -0.4264 0.3717 -1.147 0.251   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 468.05 on 2035 degrees of freedom  
## AIC: 472.05  
##   
## Number of Fisher Scoring iterations: 6

coef\_diabetes\_type\_one\_chills <- coef(diabetes\_type\_one\_chills)

diabetes\_type\_one\_chills\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_chills), confint(diabetes\_type\_one\_chills)))

## Waiting for profiling to be done...

P-values adjusted

diabetes\_type\_one\_chills\_pval <- summary(diabetes\_type\_one\_chills)$coefficients[,4]  
  
diabetes\_type\_one\_chills\_pval <- diabetes\_type\_one\_chills\_pval[-1]  
  
diabetes\_type\_one\_chills\_padj <- p.adjust(diabetes\_type\_one\_chills\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_chills\_padj

## chillsYes   
## 0.2512375

OR, CI and pval adjusted

diabetes\_type\_one\_chills\_or\_ci\_pval <- cbind(diabetes\_type\_one\_chills\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_chills\_padj))  
  
knitr::kable(diabetes\_type\_one\_chills\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0275723 | 0.0198955 | 0.0370655 | 0.2512375 |
| chillsYes | 0.6528293 | 0.2955060 | 1.2914403 | 0.2512375 |

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ cough, family = binomial, data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.2545 -0.2545 -0.1851 -0.1851 2.8550   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -4.0584 0.2446 -16.594 <2e-16 \*\*\*  
## coughYes 0.6442 0.3019 2.134 0.0328 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 464.69 on 2035 degrees of freedom  
## AIC: 468.69  
##   
## Number of Fisher Scoring iterations: 6

## (Intercept) coughYes   
## 0.01727642 1.90440430

diabetes\_type\_one\_cough\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_cough), confint(diabetes\_type\_one\_cough)))

## Waiting for profiling to be done...

P-values adjusted

diabetes\_type\_one\_cough\_pval <- summary(diabetes\_type\_one\_cough)$coefficients[,4]  
  
diabetes\_type\_one\_cough\_pval <- diabetes\_type\_one\_cough\_pval[-1]  
  
diabetes\_type\_one\_cough\_padj <- p.adjust(diabetes\_type\_one\_cough\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_cough\_padj

## coughYes   
## 0.03284117

OR, CI and pval adjusted

diabetes\_type\_one\_cough\_or\_ci\_pval <- cbind(diabetes\_type\_one\_cough\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_cough\_padj))  
  
knitr::kable(diabetes\_type\_one\_cough\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0172764 | 0.0102741 | 0.0269654 | 0.0328412 |
| coughYes | 1.9044043 | 1.0685329 | 3.5187965 | 0.0328412 |

diabetes\_type\_one\_diarrhea <- glm(diabetes\_type\_one ~ diarrhoea, data = diabetes\_type\_one\_data, family = binomial)  
  
summary(diabetes\_type\_one\_diarrhea)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ diarrhoea, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.2256 -0.2223 -0.2223 -0.2223 2.7250   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.68825 0.16008 -23.040 <2e-16 \*\*\*  
## diarrhoeaYes 0.02983 0.35805 0.083 0.934   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 469.48 on 2035 degrees of freedom  
## AIC: 473.48  
##   
## Number of Fisher Scoring iterations: 6

# get coef  
coef\_ob\_diarrhea <- coef(diabetes\_type\_one\_diarrhea)  
  
# odd ratios  
odd\_ratio\_ob\_diar <- exp(coef\_ob\_diarrhea)  
  
odd\_ratio\_ob\_diar

## (Intercept) diarrhoeaYes   
## 0.02501563 1.03028351

diabetes\_type\_one\_diarrhea\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_diarrhea), confint(diabetes\_type\_one\_diarrhea)))

## Waiting for profiling to be done...

P-values adjusted

diabetes\_type\_one\_diarrhea\_pval <- summary(diabetes\_type\_one\_diarrhea)$coefficients[,4]  
  
diabetes\_type\_one\_diarrhea\_pval <- diabetes\_type\_one\_diarrhea\_pval[-1]  
  
diabetes\_type\_one\_diarrhea\_padj <- p.adjust(diabetes\_type\_one\_diarrhea\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_diarrhea\_padj

## diarrhoeaYes   
## 0.9335943

OR, CI and pval adjusted

diabetes\_type\_one\_diarrhea\_or\_ci\_pval <- cbind(diabetes\_type\_one\_diarrhea\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_diarrhea\_padj))  
  
knitr::kable(diabetes\_type\_one\_diarrhea\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0250156 | 0.0179802 | 0.033732 | 0.9335943 |
| diarrhoeaYes | 1.0302835 | 0.4833297 | 1.997480 | 0.9335943 |

diabetes\_type\_one\_headache <- glm(diabetes\_type\_one ~ headache, data = diabetes\_type\_one\_data, family = binomial)  
  
summary(diabetes\_type\_one\_headache)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ headache, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.2505 -0.2505 -0.2505 -0.1767 2.8870   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.4461 0.1670 -20.636 <2e-16 \*\*\*  
## headacheYes -0.7055 0.3256 -2.167 0.0303 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 464.33 on 2035 degrees of freedom  
## AIC: 468.33  
##   
## Number of Fisher Scoring iterations: 7

OR and CI

diabetes\_type\_one\_headache\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_headache), confint(diabetes\_type\_one\_headache)))

## Waiting for profiling to be done...

P-values adjusted

diabetes\_type\_one\_headache\_pval <- summary(diabetes\_type\_one\_headache)$coefficients[,4]  
  
diabetes\_type\_one\_headache\_pval <- diabetes\_type\_one\_headache\_pval[-1]  
  
diabetes\_type\_one\_headache\_padj <- p.adjust(diabetes\_type\_one\_headache\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_headache\_padj

## headacheYes   
## 0.03025153

OR, CI and pval adjusted

diabetes\_type\_one\_headache\_or\_ci\_pval <- cbind(diabetes\_type\_one\_headache\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_headache\_padj))  
  
knitr::kable(diabetes\_type\_one\_headache\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0318691 | 0.0225691 | 0.0435146 | 0.0302515 |
| headacheYes | 0.4938486 | 0.2513390 | 0.9108149 | 0.0302515 |

diabetes\_type\_one\_loss\_smell <- glm(diabetes\_type\_one ~ loss\_smell\_taste, data = diabetes\_type\_one\_data, family = binomial)  
  
  
summary(diabetes\_type\_one\_loss\_smell)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ loss\_smell\_taste, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.2280 -0.2280 -0.2280 -0.2056 2.7810   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.6369 0.1602 -22.705 <2e-16 \*\*\*  
## loss\_smell\_tasteYes -0.2090 0.3575 -0.585 0.559   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 469.13 on 2035 degrees of freedom  
## AIC: 473.13  
##   
## Number of Fisher Scoring iterations: 6

OR and CI

diabetes\_type\_one\_loss\_smell\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_loss\_smell), confint(diabetes\_type\_one\_loss\_smell)))

## Waiting for profiling to be done...

diabetes\_type\_one\_loss\_smell\_pval <- summary(diabetes\_type\_one\_loss\_smell)$coefficients[,4]  
  
diabetes\_type\_one\_loss\_smell\_pval <- diabetes\_type\_one\_loss\_smell\_pval[-1]  
  
diabetes\_type\_one\_loss\_smell\_padj <- p.adjust(diabetes\_type\_one\_loss\_smell\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_loss\_smell\_padj

## loss\_smell\_tasteYes   
## 0.5588591

OR, CI and pval adjusted

diabetes\_type\_one\_loss\_smell\_or\_ci\_pval <- cbind(diabetes\_type\_one\_loss\_smell\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_loss\_smell\_padj))  
  
knitr::kable(diabetes\_type\_one\_loss\_smell\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0263331 | 0.0189237 | 0.0355165 | 0.5588591 |
| loss\_smell\_tasteYes | 0.8114316 | 0.3810216 | 1.5711959 | 0.5588591 |

library(fmsb)

## Registered S3 methods overwritten by 'fmsb':  
## method from  
## print.roc huge  
## plot.roc huge

diabetes\_type\_one\_muscle\_ache <- glm(diabetes\_type\_one ~ muscle\_ache, data = diabetes\_type\_one\_data, family = binomial)  
   
summary(diabetes\_type\_one\_muscle\_ache)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ muscle\_ache, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.2423 -0.2423 -0.2423 -0.1913 2.8319   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.5137 0.1715 -20.484 <2e-16 \*\*\*  
## muscle\_acheYes -0.4778 0.3119 -1.532 0.126   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 467.01 on 2035 degrees of freedom  
## AIC: 471.01  
##   
## Number of Fisher Scoring iterations: 6

coef\_ob\_muscle\_ac <- coef(diabetes\_type\_one\_muscle\_ache)  
  
odd\_ratio\_ob\_los <- exp(coef\_ob\_muscle\_ac)  
  
odd\_ratio\_ob\_los

## (Intercept) muscle\_acheYes   
## 0.02978723 0.62016188

OR and CI

diabetes\_type\_one\_muscle\_ache\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_muscle\_ache), confint(diabetes\_type\_one\_muscle\_ache)))

## Waiting for profiling to be done...

diabetes\_type\_one\_muscle\_ache\_pval <- summary(diabetes\_type\_one\_muscle\_ache)$coefficients[,4]  
  
diabetes\_type\_one\_muscle\_ache\_pval <- diabetes\_type\_one\_muscle\_ache\_pval[-1]  
  
diabetes\_type\_one\_muscle\_ache\_padj <- p.adjust(diabetes\_type\_one\_muscle\_ache\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_muscle\_ache\_padj

## muscle\_acheYes   
## 0.1256108

OR, CI and pval adjusted

diabetes\_type\_one\_muscle\_ache\_or\_ci\_pval <- cbind(diabetes\_type\_one\_muscle\_ache\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_muscle\_ache\_padj))  
  
knitr::kable(diabetes\_type\_one\_muscle\_ache\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0297872 | 0.0208856 | 0.0409971 | 0.1256108 |
| muscle\_acheYes | 0.6201619 | 0.3269125 | 1.1211021 | 0.1256108 |

diabetes\_type\_one\_nasal\_cong <- glm(diabetes\_type\_one ~ nasal\_congestion, data = diabetes\_type\_one\_data, family = binomial)  
  
summary(diabetes\_type\_one\_nasal\_cong)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ nasal\_congestion, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.2296 -0.2296 -0.2296 -0.2052 2.7825   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.6229 0.1644 -22.041 <2e-16 \*\*\*  
## nasal\_congestionYes -0.2272 0.3348 -0.679 0.497   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 469.01 on 2035 degrees of freedom  
## AIC: 473.01  
##   
## Number of Fisher Scoring iterations: 6

coef\_ob\_nas\_cong <- coef(diabetes\_type\_one\_nasal\_cong)  
  
odd\_ratio\_ob\_nas\_cong <- exp(coef\_ob\_nas\_cong)  
  
odd\_ratio\_ob\_nas\_cong

## (Intercept) nasal\_congestionYes   
## 0.02670415 0.79675252

OR and CI

diabetes\_type\_one\_nasal\_cong\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_nasal\_cong), confint(diabetes\_type\_one\_nasal\_cong)))

## Waiting for profiling to be done...

diabetes\_type\_one\_nasal\_cong\_pval <- summary(diabetes\_type\_one\_nasal\_cong)$coefficients[,4]  
  
diabetes\_type\_one\_nasal\_cong\_pval <- diabetes\_type\_one\_nasal\_cong\_pval[-1]  
  
diabetes\_type\_one\_nasal\_cong\_padj <- p.adjust(diabetes\_type\_one\_nasal\_cong\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_nasal\_cong\_padj

## nasal\_congestionYes   
## 0.4974107

OR, CI and pval adjusted

diabetes\_type\_one\_nasal\_cong\_or\_ci\_pval <- cbind(diabetes\_type\_one\_nasal\_cong\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_nasal\_cong\_padj))  
  
knitr::kable(diabetes\_type\_one\_nasal\_cong\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0267041 | 0.0190165 | 0.0362867 | 0.4974107 |
| nasal\_congestionYes | 0.7967525 | 0.3962388 | 1.4905177 | 0.4974107 |

diabetes\_type\_one\_nausea\_vomitting <- glm(diabetes\_type\_one ~ nausea\_vomiting, data = diabetes\_type\_one\_data, family = binomial)  
  
summary(diabetes\_type\_one\_nausea\_vomitting)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ nausea\_vomiting, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.3392 -0.2102 -0.2102 -0.2102 2.7653   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.8012 0.1579 -24.073 < 2e-16 \*\*\*  
## nausea\_vomitingYes 0.9746 0.3777 2.581 0.00986 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 464.01 on 2035 degrees of freedom  
## AIC: 468.01  
##   
## Number of Fisher Scoring iterations: 6

coef\_ob\_naus\_vom <- coef(diabetes\_type\_one\_nausea\_vomitting)  
  
odd\_ratio\_ob\_naus\_vom <- exp(coef\_ob\_naus\_vom)  
  
odd\_ratio\_ob\_naus\_vom

## (Intercept) nausea\_vomitingYes   
## 0.02234332 2.65003209

OR and CI

diabetes\_type\_one\_nausea\_vomitting\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_nausea\_vomitting), confint(diabetes\_type\_one\_nausea\_vomitting)))

## Waiting for profiling to be done...

diabetes\_type\_one\_nausea\_vomitting\_pval <- summary(diabetes\_type\_one\_nausea\_vomitting)$coefficients[,4]  
  
diabetes\_type\_one\_nausea\_vomitting\_pval <- diabetes\_type\_one\_nausea\_vomitting\_pval[-1]  
  
diabetes\_type\_one\_nausea\_vomitting\_padj <- p.adjust(diabetes\_type\_one\_nausea\_vomitting\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_nausea\_vomitting\_padj

## nausea\_vomitingYes   
## 0.009863338

OR, CI and pval adjusted

diabetes\_type\_one\_nausea\_vomitting\_or\_ci\_pval <- cbind(diabetes\_type\_one\_nausea\_vomitting\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_nausea\_vomitting\_padj))  
  
knitr::kable(diabetes\_type\_one\_nausea\_vomitting\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0223433 | 0.0161339 | 0.030010 | 0.0098633 |
| nausea\_vomitingYes | 2.6500321 | 1.1879787 | 5.312954 | 0.0098633 |

diabetes\_type\_one\_short\_breath <- glm(diabetes\_type\_one ~ shortness\_breath, data = diabetes\_type\_one\_data, family = binomial)  
  
summary(diabetes\_type\_one\_short\_breath)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ shortness\_breath, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.2365 -0.2365 -0.2365 -0.2365 2.9324   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.5625 0.1529 -23.30 <2e-16 \*\*\*  
## shortness\_breathYes -0.7234 0.4386 -1.65 0.099 .   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 466.25 on 2035 degrees of freedom  
## AIC: 470.25  
##   
## Number of Fisher Scoring iterations: 7

OR and CI

diabetes\_type\_one\_short\_breath\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_short\_breath), confint(diabetes\_type\_one\_short\_breath)))

## Waiting for profiling to be done...

diabetes\_type\_one\_short\_breath\_pval <- summary(diabetes\_type\_one\_short\_breath)$coefficients[,4]  
  
diabetes\_type\_one\_short\_breath\_pval <- diabetes\_type\_one\_short\_breath\_pval[-1]  
  
diabetes\_type\_one\_short\_breath\_padj <- p.adjust(diabetes\_type\_one\_short\_breath\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_short\_breath\_padj

## shortness\_breathYes   
## 0.09903697

OR, CI and pval adjusted

diabetes\_type\_one\_short\_breath\_or\_ci\_pval <- cbind(diabetes\_type\_one\_short\_breath\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_short\_breath\_padj))  
  
knitr::kable(diabetes\_type\_one\_short\_breath\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0283688 | 0.0207129 | 0.0377689 | 0.099037 |
| shortness\_breathYes | 0.4850917 | 0.1843780 | 1.0609267 | 0.099037 |

diabetes\_type\_one\_sore\_thr <- glm(diabetes\_type\_one ~ sore\_throat, data = diabetes\_type\_one\_data, family = binomial)  
  
summary(diabetes\_type\_one\_sore\_thr)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ sore\_throat, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.2255 -0.2255 -0.2214 -0.2214 2.7279   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.69611 0.18182 -20.329 <2e-16 \*\*\*  
## sore\_throatYes 0.03661 0.29503 0.124 0.901   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 469.47 on 2035 degrees of freedom  
## AIC: 473.47  
##   
## Number of Fisher Scoring iterations: 6

OR and CI

diabetes\_type\_one\_sore\_thr\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_sore\_thr), confint(diabetes\_type\_one\_sore\_thr)))

## Waiting for profiling to be done...

diabetes\_type\_one\_sore\_thr\_pval <- summary(diabetes\_type\_one\_sore\_thr)$coefficients[,4]  
  
diabetes\_type\_one\_sore\_thr\_pval <- diabetes\_type\_one\_sore\_thr\_pval[-1]  
  
diabetes\_type\_one\_sore\_thr\_padj <- p.adjust(diabetes\_type\_one\_sore\_thr\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_sore\_thr\_padj

## sore\_throatYes   
## 0.9012546

OR, CI and pval adjusted

diabetes\_type\_one\_sore\_thr\_or\_ci\_pval <- cbind(diabetes\_type\_one\_sore\_thr\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_sore\_thr\_padj))  
  
knitr::kable(diabetes\_type\_one\_sore\_thr\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0248199 | 0.0170107 | 0.0347794 | 0.9012546 |
| sore\_throatYes | 1.0372847 | 0.5721613 | 1.8328444 | 0.9012546 |

diabetes\_type\_one\_sputum <- glm(diabetes\_type\_one ~ sputum, data = diabetes\_type\_one\_data, family = binomial)  
  
  
summary(diabetes\_type\_one\_sputum)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ sputum, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.2266 -0.2266 -0.2266 -0.2114 2.7614   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.6497 0.1622 -22.502 <2e-16 \*\*\*  
## sputumYes -0.1407 0.3453 -0.407 0.684   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 469.31 on 2035 degrees of freedom  
## AIC: 473.31  
##   
## Number of Fisher Scoring iterations: 6

OR and CI

diabetes\_type\_one\_sputum\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_sputum), confint(diabetes\_type\_one\_sputum)))

## Waiting for profiling to be done...

diabetes\_type\_one\_sputum\_pval <- summary(diabetes\_type\_one\_sputum)$coefficients[,4]  
  
diabetes\_type\_one\_sputum\_pval <- diabetes\_type\_one\_sputum\_pval[-1]  
  
diabetes\_type\_one\_sputum\_padj <- p.adjust(diabetes\_type\_one\_sputum\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_sputum\_padj

## sputumYes   
## 0.6836804

OR, CI and pval adjusted

diabetes\_type\_one\_sputum\_or\_ci\_pval <- cbind(diabetes\_type\_one\_sputum\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_sputum\_padj))  
  
knitr::kable(diabetes\_type\_one\_sputum\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0260000 | 0.0186025 | 0.0351927 | 0.6836804 |
| sputumYes | 0.8687411 | 0.4207386 | 1.6514916 | 0.6836804 |

diabetes\_type\_one\_temperature <- glm(diabetes\_type\_one ~ temperature, data = diabetes\_type\_one\_data, family = binomial)  
  
  
summary(diabetes\_type\_one\_temperature)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ temperature, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.2741 -0.2741 -0.1927 -0.1927 2.8269   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.9771 0.2018 -19.704 <2e-16 \*\*\*  
## temperatureYes 0.7144 0.2868 2.491 0.0128 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 463.40 on 2035 degrees of freedom  
## AIC: 467.4  
##   
## Number of Fisher Scoring iterations: 6

OR and CI

diabetes\_type\_one\_temperature\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_temperature), confint(diabetes\_type\_one\_temperature)))

## Waiting for profiling to be done...

diabetes\_type\_one\_temperature\_pval <- summary(diabetes\_type\_one\_temperature)$coefficients[,4]  
  
diabetes\_type\_one\_temperature\_pval <- diabetes\_type\_one\_temperature\_pval[-1]  
  
diabetes\_type\_one\_temperature\_padj <- p.adjust(diabetes\_type\_one\_temperature\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_temperature\_padj

## temperatureYes   
## 0.01275546

OR, CI and pval adjusted

diabetes\_type\_one\_temperature\_or\_ci\_pval <- cbind(diabetes\_type\_one\_temperature\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_temperature\_padj))  
  
knitr::kable(diabetes\_type\_one\_temperature\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0187406 | 0.0122817 | 0.0271885 | 0.0127555 |
| temperatureYes | 2.0428790 | 1.1603673 | 3.5966773 | 0.0127555 |

diabetes\_type\_one\_itchy\_eyes <- glm(diabetes\_type\_one ~ itchy\_eyes, data = diabetes\_type\_one\_data, family = binomial)  
  
summary(diabetes\_type\_one\_itchy\_eyes)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ itchy\_eyes, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.2311 -0.2311 -0.2311 -0.2311 2.6969   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.6098 0.1433 -25.187 <2e-16 \*\*\*  
## itchy\_eyesYes -14.9562 553.2430 -0.027 0.978   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 462.32 on 2035 degrees of freedom  
## AIC: 466.32  
##   
## Number of Fisher Scoring iterations: 17

OR and CI

diabetes\_type\_one\_itchy\_eyes\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_itchy\_eyes), confint(diabetes\_type\_one\_itchy\_eyes)))

## Waiting for profiling to be done...

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred  
  
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred  
  
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred  
  
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred  
  
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred  
  
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred  
  
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred  
  
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred  
  
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred  
  
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred  
  
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

diabetes\_type\_one\_itchy\_eyes\_pval <- summary(diabetes\_type\_one\_itchy\_eyes)$coefficients[,4]  
  
diabetes\_type\_one\_itchy\_eyes\_pval <- diabetes\_type\_one\_itchy\_eyes\_pval[-1]  
  
diabetes\_type\_one\_itchy\_eyes\_padj <- p.adjust(diabetes\_type\_one\_itchy\_eyes\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_itchy\_eyes\_padj

## itchy\_eyesYes   
## 0.9784328

OR, CI and pval adjusted

diabetes\_type\_one\_itchy\_eyes\_or\_ci\_pval <- cbind(diabetes\_type\_one\_itchy\_eyes\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_itchy\_eyes\_padj))  
  
knitr::kable(diabetes\_type\_one\_itchy\_eyes\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0270563 | 0.0201646 | 0.0354081 | 0.9784328 |
| itchy\_eyesYes | 0.0000003 | 0.0000000 | 8741.6906287 | 0.9784328 |

diabetes\_type\_one\_chest\_pain <- glm(diabetes\_type\_one ~ chest\_pain, data = diabetes\_type\_one\_data, family = binomial)  
  
summary(diabetes\_type\_one\_chest\_pain)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ chest\_pain, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.2233 -0.2233 -0.2233 -0.2233 2.7749   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.6791 0.1446 -25.435 <2e-16 \*\*\*  
## chest\_painYes -0.1495 1.0211 -0.146 0.884   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 469.46 on 2035 degrees of freedom  
## AIC: 473.46  
##   
## Number of Fisher Scoring iterations: 6

OR and CI

diabetes\_type\_one\_chest\_pain\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_chest\_pain), confint(diabetes\_type\_one\_chest\_pain)))

## Waiting for profiling to be done...

diabetes\_type\_one\_chest\_pain\_pval <- summary(diabetes\_type\_one\_chest\_pain)$coefficients[,4]  
  
diabetes\_type\_one\_chest\_pain\_pval <- diabetes\_type\_one\_chest\_pain\_pval[-1]  
  
diabetes\_type\_one\_chest\_pain\_padj <- p.adjust(diabetes\_type\_one\_chest\_pain\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_chest\_pain\_padj

## chest\_painYes   
## 0.8835913

OR, CI and pval adjusted

diabetes\_type\_one\_chest\_pain\_or\_ci\_pval <- cbind(diabetes\_type\_one\_chest\_pain\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_chest\_pain\_padj))  
  
knitr::kable(diabetes\_type\_one\_chest\_pain\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0252447 | 0.0187601 | 0.0331148 | 0.8835913 |
| chest\_painYes | 0.8611358 | 0.0481357 | 4.0705661 | 0.8835913 |

diabetes\_type\_one\_loss\_appetite <- glm(diabetes\_type\_one ~ loss\_appetite, data = diabetes\_type\_one\_data, family = binomial)  
  
summary(diabetes\_type\_one\_loss\_appetite)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ loss\_appetite, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.3234 -0.2126 -0.2126 -0.2126 2.7573   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.7788 0.1561 -24.215 <2e-16 \*\*\*  
## loss\_appetiteYes 0.8543 0.3950 2.162 0.0306 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 465.58 on 2035 degrees of freedom  
## AIC: 469.58  
##   
## Number of Fisher Scoring iterations: 6

OR and CI

diabetes\_type\_one\_loss\_appetite\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_loss\_appetite), confint(diabetes\_type\_one\_loss\_appetite)))

## Waiting for profiling to be done...

diabetes\_type\_one\_loss\_appetite\_pval <- summary(diabetes\_type\_one\_loss\_appetite)$coefficients[,4]  
  
diabetes\_type\_one\_loss\_appetite\_pval <- diabetes\_type\_one\_loss\_appetite\_pval[-1]  
  
diabetes\_type\_one\_loss\_appetite\_padj <- p.adjust(diabetes\_type\_one\_loss\_appetite\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_loss\_appetite\_padj

## loss\_appetiteYes   
## 0.03058639

OR, CI and pval adjusted

diabetes\_type\_one\_loss\_appetite\_or\_ci\_pval <- cbind(diabetes\_type\_one\_loss\_appetite\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_loss\_appetite\_padj))  
  
knitr::kable(diabetes\_type\_one\_loss\_appetite\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0228509 | 0.0165671 | 0.0305911 | 0.0305864 |
| loss\_appetiteYes | 2.3496325 | 1.0070955 | 4.8366036 | 0.0305864 |

diabetes\_type\_one\_joint\_pain <- glm(diabetes\_type\_one ~ joint\_pain, data = diabetes\_type\_one\_data, family = binomial)  
  
  
summary(diabetes\_type\_one\_joint\_pain)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ joint\_pain, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.2481 -0.2221 -0.2221 -0.2221 2.7258   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -3.6904 0.1461 -25.255 <2e-16 \*\*\*  
## joint\_painYes 0.2247 0.7328 0.307 0.759   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 469.40 on 2035 degrees of freedom  
## AIC: 473.4  
##   
## Number of Fisher Scoring iterations: 6

OR and CI

diabetes\_type\_one\_joint\_pain\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_joint\_pain), confint(diabetes\_type\_one\_joint\_pain)))

## Waiting for profiling to be done...

diabetes\_type\_one\_joint\_pain\_pval <- summary(diabetes\_type\_one\_joint\_pain)$coefficients[,4]  
  
diabetes\_type\_one\_joint\_pain\_pval <- diabetes\_type\_one\_joint\_pain\_pval[-1]  
  
diabetes\_type\_one\_joint\_pain\_padj <- p.adjust(diabetes\_type\_one\_joint\_pain\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_joint\_pain\_padj

## joint\_painYes   
## 0.7591141

OR, CI and pval adjusted

diabetes\_type\_one\_joint\_pain\_or\_ci\_pval <- cbind(diabetes\_type\_one\_joint\_pain\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_joint\_pain\_padj))  
  
knitr::kable(diabetes\_type\_one\_joint\_pain\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.024961 | 0.0184902 | 0.0328294 | 0.7591141 |
| joint\_painYes | 1.251953 | 0.2018627 | 4.1649668 | 0.7591141 |

## Multivariate analysis for diabetest type one

When adding all variables that showed an association with the heart disease model, the model shows something different.

When adjusting for all variables, patients showing covid-19 symptoms/of patients with positive covid test, the results show strong evidence for an association between variables such as headaches and temperature(39.1-41) (p ≤ 0.01) in patients with diabetes type one.  
When adjusting for all variables,in patients showing covid-19 symptpms/of patients with positive covid test, in respondent with diabetes type one there was: - 54 % decrease in odds of experiencing headaches compared to those who do not suffer of diabetes type one - 406 % increase in temperature compared to those who do not suffer of heart disease

diabetes\_type\_one\_model <- glm(diabetes\_type\_one ~ cough + nausea\_vomiting + temperature + loss\_appetite, data = diabetes\_type\_one\_data, family = binomial)  
  
summary(diabetes\_type\_one\_model)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ cough + nausea\_vomiting + temperature +   
## loss\_appetite, family = binomial, data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.5468 -0.2314 -0.2069 -0.1568 2.9679   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -4.3919 0.2792 -15.729 <2e-16 \*\*\*  
## coughYes 0.5586 0.3054 1.829 0.0674 .   
## nausea\_vomitingYes 0.7845 0.3851 2.037 0.0416 \*   
## temperatureYes 0.5016 0.2972 1.688 0.0914 .   
## loss\_appetiteYes 0.7226 0.4023 1.796 0.0725 .   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 469.48 on 2036 degrees of freedom  
## Residual deviance: 453.34 on 2032 degrees of freedom  
## AIC: 463.34  
##   
## Number of Fisher Scoring iterations: 7

# odds ratio and 95% CL  
  
diabetes\_type\_one\_model\_or\_ci <- exp(cbind(OR = coef(diabetes\_type\_one\_model), confint(diabetes\_type\_one\_model)))

## Waiting for profiling to be done...

diabetes\_type\_one\_model\_or\_ci

## OR 2.5 % 97.5 %  
## (Intercept) 0.01237729 0.006882369 0.02066075  
## coughYes 1.74818899 0.973648074 3.25042278  
## nausea\_vomitingYes 2.19136718 0.970063723 4.46378827  
## temperatureYes 1.65140787 0.918413381 2.96285997  
## loss\_appetiteYes 2.05968913 0.872196070 4.30782631

diabetes\_type\_one\_model\_pval <- summary(diabetes\_type\_one\_model)$coefficients[,4]  
  
  
  
diabetes\_type\_one\_model\_padj <- p.adjust(diabetes\_type\_one\_model\_pval, method = "bonferroni")  
  
diabetes\_type\_one\_model\_padj

## (Intercept) coughYes nausea\_vomitingYes temperatureYes   
## 4.820585e-55 3.370732e-01 2.080638e-01 4.570456e-01   
## loss\_appetiteYes   
## 3.625120e-01

OR, CI and pval adjusted

diabetes\_type\_one\_model\_or\_ci\_pval <- cbind(diabetes\_type\_one\_model\_or\_ci, data.frame(pvalues = diabetes\_type\_one\_model\_padj))  
  
knitr::kable(diabetes\_type\_one\_model\_or\_ci\_pval)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0123773 | 0.0068824 | 0.0206607 | 0.0000000 |
| coughYes | 1.7481890 | 0.9736481 | 3.2504228 | 0.3370732 |
| nausea\_vomitingYes | 2.1913672 | 0.9700637 | 4.4637883 | 0.2080638 |
| temperatureYes | 1.6514079 | 0.9184134 | 2.9628600 | 0.4570456 |
| loss\_appetiteYes | 2.0596891 | 0.8721961 | 4.3078263 | 0.3625120 |

vif(diabetes\_type\_one\_model)

## coughYes nausea\_vomitingYes temperatureYes loss\_appetiteYes   
## 1.016723 1.029336 1.065759 1.024767