diabetes\_one\_18082020\_40\_59

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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.

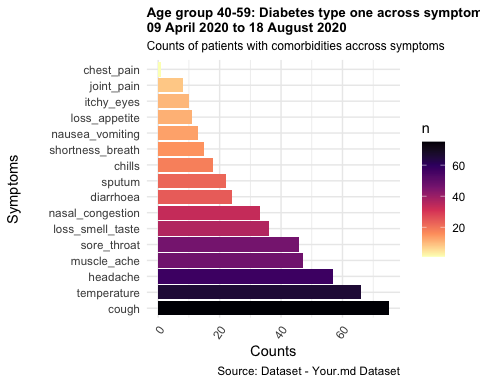
covid\_tested\_levels <- c("positive" = "showing symptoms")  
  
data\_age\_band <- data\_categ\_nosev %>%  
 dplyr::mutate(age\_band = dplyr::case\_when(  
 age == 0 | age <= 19 ~ '0-19',  
 age == 20 | age <= 39 ~ '20-39',  
 age == 40 | age <= 59 ~ '40-59',  
 age >= 60 ~ "60+")) %>%  
 dplyr::filter(number\_morbidities <= 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 == "40-59")  
  
  
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   
## 15358 1249

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   
## -0.4425 -0.4425 -0.4425 -0.1029 3.2385   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.27433 0.02993 -75.98 <2e-16 \*\*\*  
## chillsYes -2.96418 0.23808 -12.45 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 8408.6 on 16605 degrees of freedom  
## AIC: 8412.6  
##   
## Number of Fisher Scoring iterations: 7

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   
## 1.390659e-35

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) | 0.1028662 | 0.0969593 | 0.1090310 | 0 |
| chillsYes | 0.0516027 | 0.0311519 | 0.0796949 | 0 |

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ cough, family = binomial, data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.4962 -0.4962 -0.4962 -0.1527 2.9859   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.03235 0.03104 -65.48 <2e-16 \*\*\*  
## coughYes -2.41390 0.12022 -20.08 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 8085.3 on 16605 degrees of freedom  
## AIC: 8089.3  
##   
## Number of Fisher Scoring iterations: 7

## (Intercept) coughYes   
## 0.13102679 0.08946578

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   
## 1.127971e-89

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) | 0.1310268 | 0.1232342 | 0.1391799 | 0 |
| coughYes | 0.0894658 | 0.0701078 | 0.1123882 | 0 |

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   
## -0.4356 -0.4356 -0.4356 -0.1252 3.1152   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.30739 0.02996 -77.02 <2e-16 \*\*\*  
## diarrhoeaYes -2.53713 0.20709 -12.25 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 8501.9 on 16605 degrees of freedom  
## AIC: 8505.9  
##   
## Number of Fisher Scoring iterations: 7

# 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   
## 0.09952068 0.07909345

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   
## 1.657015e-34

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) | 0.0995207 | 0.0938004 | 0.1054903 | 0 |
| diarrhoeaYes | 0.0790934 | 0.0512584 | 0.1158538 | 0 |

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   
## -0.5233 -0.5233 -0.1253 -0.1253 3.1149   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -1.91919 0.03102 -61.88 <2e-16 \*\*\*  
## headacheYes -2.92431 0.13654 -21.42 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 7792.9 on 16605 degrees of freedom  
## AIC: 7796.9  
##   
## 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   
## 9.127761e-102

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) | 0.1467258 | 0.1380077 | 0.1558514 | 0 |
| headacheYes | 0.0537019 | 0.0406403 | 0.0694773 | 0 |

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   
## -0.4593 -0.4593 -0.4593 -0.1269 3.1069   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.19585 0.03027 -72.55 <2e-16 \*\*\*  
## loss\_smell\_tasteYes -2.62264 0.17005 -15.42 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 8302.6 on 16605 degrees of freedom  
## AIC: 8306.6  
##   
## Number of Fisher Scoring iterations: 7

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   
## 1.14534e-53

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) | 0.111264 | 0.1048056 | 0.1180094 | 0 |
| loss\_smell\_tasteYes | 0.072611 | 0.0510963 | 0.0997125 | 0 |

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   
## -0.4973 -0.4973 -0.4973 -0.1227 3.1284   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.02802 0.03068 -66.10 <2e-16 \*\*\*  
## muscle\_acheYes -2.85800 0.14958 -19.11 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 7984.7 on 16605 degrees of freedom  
## AIC: 7988.7  
##   
## Number of Fisher Scoring iterations: 7

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   
## 0.13159623 0.05738321

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   
## 2.240442e-81

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) | 0.1315962 | 0.1238576 | 0.1396889 | 0 |
| muscle\_acheYes | 0.0573832 | 0.0422214 | 0.0759942 | 0 |

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   
## -0.4745 -0.4745 -0.4745 -0.1130 3.1803   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.12731 0.03034 -70.12 <2e-16 \*\*\*  
## nasal\_congestionYes -2.92352 0.17721 -16.50 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 8144.6 on 16605 degrees of freedom  
## AIC: 8148.6  
##   
## Number of Fisher Scoring iterations: 7

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   
## 0.11915728 0.05374441

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   
## 3.853508e-61

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) | 0.1191573 | 0.1122259 | 0.1263992 | 0 |
| nasal\_congestionYes | 0.0537444 | 0.0372239 | 0.0747396 | 0 |

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   
## -0.4023 -0.4023 -0.4023 -0.4023 2.8285   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.47331 0.02962 -83.50 < 2e-16 \*\*\*  
## nausea\_vomitingYes -1.50853 0.28146 -5.36 8.33e-08 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 8817.2 on 16605 degrees of freedom  
## AIC: 8821.2  
##   
## 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   
## 0.0843053 0.2212360

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   
## 8.33498e-08

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) | 0.0843053 | 0.0795124 | 0.0893022 | 1e-07 |
| nausea\_vomitingYes | 0.2212360 | 0.1208806 | 0.3677028 | 1e-07 |

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   
## -0.4327 -0.4327 -0.4327 -0.4327 3.2338   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.32145 0.02983 -77.82 <2e-16 \*\*\*  
## shortness\_breathYes -2.90178 0.26047 -11.14 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 8501.4 on 16605 degrees of freedom  
## AIC: 8505.4  
##   
## 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   
## 7.955027e-29

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) | 0.0981312 | 0.0925143 | 0.1039916 | 0 |
| shortness\_breathYes | 0.0549251 | 0.0314801 | 0.0880751 | 0 |

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   
## -0.5043 -0.5043 -0.5043 -0.1189 3.1483   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -1.99808 0.03072 -65.03 <2e-16 \*\*\*  
## sore\_throatYes -2.95068 0.15110 -19.53 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 7917.2 on 16605 degrees of freedom  
## AIC: 7921.2  
##   
## Number of Fisher Scoring iterations: 7

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   
## 6.421014e-85

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) | 0.1355951 | 0.1276113 | 0.1439457 | 0 |
| sore\_throatYes | 0.0523042 | 0.0383572 | 0.0694560 | 0 |

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   
## -0.4288 -0.4288 -0.4288 -0.4288 3.0943   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.34017 0.02989 -78.29 <2e-16 \*\*\*  
## sputumYes -2.43895 0.21616 -11.28 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 8565.8 on 16605 degrees of freedom  
## AIC: 8569.8  
##   
## Number of Fisher Scoring iterations: 7

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   
## 1.594735e-29

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) | 0.0963108 | 0.0907871 | 0.1020741 | 0 |
| sputumYes | 0.0872525 | 0.0554020 | 0.1298149 | 0 |

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   
## -0.4490 -0.4490 -0.4490 -0.1765 2.8878   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.24374 0.03058 -73.38 <2e-16 \*\*\*  
## temperatureYes -1.91039 0.12773 -14.96 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 8477.3 on 16605 degrees of freedom  
## AIC: 8481.3  
##   
## 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   
## 1.406809e-50

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) | 0.1060606 | 0.0998422 | 0.1125572 | 0 |
| temperatureYes | 0.1480223 | 0.1141539 | 0.1885174 | 0 |

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   
## -0.4193 -0.4193 -0.4193 -0.4193 3.2373   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.38698 0.02969 -80.406 <2e-16 \*\*\*  
## itchy\_eyesYes -2.84787 0.31828 -8.948 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 8628.2 on 16605 degrees of freedom  
## AIC: 8632.2  
##   
## Number of Fisher Scoring iterations: 7

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...

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   
## 3.625958e-19

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) | 0.0919071 | 0.0866710 | 0.0973680 | 0 |
| itchy\_eyesYes | 0.0579678 | 0.0289427 | 0.1022017 | 0 |

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   
## -0.4018 -0.4018 -0.4018 -0.4018 3.5344   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.47599 0.02947 -84.009 < 2e-16 \*\*\*  
## chest\_painYes -3.76818 1.00078 -3.765 0.000166 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 8792.7 on 16605 degrees of freedom  
## AIC: 8796.7  
##   
## Number of Fisher Scoring iterations: 8

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   
## 0.0001663827

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) | 0.0840800 | 0.0793230 | 0.0890385 | 0.0001664 |
| chest\_painYes | 0.0230941 | 0.0013153 | 0.1020783 | 0.0001664 |

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   
## -0.4072 -0.4072 -0.4072 -0.4072 3.0173   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.44858 0.02962 -82.656 < 2e-16 \*\*\*  
## loss\_appetiteYes -2.09278 0.30456 -6.872 6.35e-12 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 8764.7 on 16605 degrees of freedom  
## AIC: 8768.7  
##   
## Number of Fisher Scoring iterations: 7

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   
## 6.350196e-12

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) | 0.0864163 | 0.0815028 | 0.0915394 | 0 |
| loss\_appetiteYes | 0.1233438 | 0.0637324 | 0.2127499 | 0 |

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   
## -0.403 -0.403 -0.403 -0.403 2.990   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.46968 0.02956 -83.539 < 2e-16 \*\*\*  
## joint\_painYes -1.98901 0.35627 -5.583 2.36e-08 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 8801.3 on 16605 degrees of freedom  
## AIC: 8805.3  
##   
## 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   
## 2.364895e-08

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) | 0.0846117 | 0.0798102 | 0.0896172 | 0 |
| joint\_painYes | 0.1368307 | 0.0622159 | 0.2567037 | 0 |

## 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 + headache + nausea\_vomiting + shortness\_breath + temperature + loss\_appetite, data = diabetes\_type\_one\_data, family = binomial)  
  
summary(diabetes\_type\_one\_model)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ cough + headache + nausea\_vomiting +   
## shortness\_breath + temperature + loss\_appetite, family = binomial,   
## data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.7307 -0.3587 -0.2045 -0.0598 4.4663   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -1.18413 0.03515 -33.684 < 2e-16 \*\*\*  
## coughYes -2.11929 0.12186 -17.390 < 2e-16 \*\*\*  
## headacheYes -2.67292 0.13769 -19.413 < 2e-16 \*\*\*  
## nausea\_vomitingYes -0.26042 0.30041 -0.867 0.386   
## shortness\_breathYes -2.47010 0.26298 -9.393 < 2e-16 \*\*\*  
## temperatureYes -1.52744 0.13084 -11.674 < 2e-16 \*\*\*  
## loss\_appetiteYes -1.62178 0.31052 -5.223 1.76e-07 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8865.1 on 16606 degrees of freedom  
## Residual deviance: 6694.9 on 16600 degrees of freedom  
## AIC: 6708.9  
##   
## Number of Fisher Scoring iterations: 8

knitr::kable(exp(cbind(OR = coef(diabetes\_type\_one\_model), confint(diabetes\_type\_one\_model))))

## Waiting for profiling to be done...

|  |  |  |  |
| --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % |
| (Intercept) | 0.3060125 | 0.2855209 | 0.3277105 |
| coughYes | 0.1201170 | 0.0938442 | 0.1514126 |
| headacheYes | 0.0690501 | 0.0521472 | 0.0895506 |
| nausea\_vomitingYes | 0.7707287 | 0.4082644 | 1.3379755 |
| shortness\_breathYes | 0.0845766 | 0.0482848 | 0.1363658 |
| temperatureYes | 0.2170912 | 0.1664861 | 0.2782742 |
| loss\_appetiteYes | 0.1975468 | 0.1011040 | 0.3455476 |

# 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) 0.30601253 0.28552087 0.32771050  
## coughYes 0.12011704 0.09384421 0.15141258  
## headacheYes 0.06905011 0.05214722 0.08955056  
## nausea\_vomitingYes 0.77072866 0.40826441 1.33797547  
## shortness\_breathYes 0.08457664 0.04828476 0.13636580  
## temperatureYes 0.21709120 0.16648614 0.27827421  
## loss\_appetiteYes 0.19754676 0.10110398 0.34554760

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 headacheYes nausea\_vomitingYes   
## 6.958421e-248 6.820335e-67 4.213509e-83 1.000000e+00   
## shortness\_breathYes temperatureYes loss\_appetiteYes   
## 4.098430e-20 1.209659e-30 1.233240e-06

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) | 0.3060125 | 0.2855209 | 0.3277105 | 0.0e+00 |
| coughYes | 0.1201170 | 0.0938442 | 0.1514126 | 0.0e+00 |
| headacheYes | 0.0690501 | 0.0521472 | 0.0895506 | 0.0e+00 |
| nausea\_vomitingYes | 0.7707287 | 0.4082644 | 1.3379755 | 1.0e+00 |
| shortness\_breathYes | 0.0845766 | 0.0482848 | 0.1363658 | 0.0e+00 |
| temperatureYes | 0.2170912 | 0.1664861 | 0.2782742 | 0.0e+00 |
| loss\_appetiteYes | 0.1975468 | 0.1011040 | 0.3455476 | 1.2e-06 |

vif(diabetes\_type\_one\_model)

## coughYes headacheYes nausea\_vomitingYes shortness\_breathYes   
## 1.000576 1.001703 1.005024 1.000654   
## temperatureYes loss\_appetiteYes   
## 1.002841 1.001877