diabetes\_one\_18082020\_20\_39

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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.

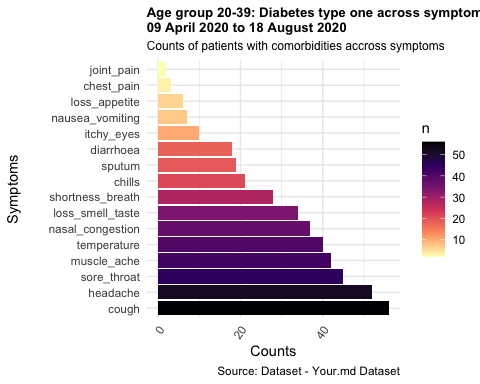
covid\_tested\_levels <- c("positive" = "showing symptoms")  
  
data\_age\_band <- data\_categ\_nosev %>%  
 dplyr::mutate(age\_band = dplyr::case\_when(  
 age == 0 | age <= 19 ~ '0-19',  
 age == 20 | age <= 39 ~ '20-39',  
 age == 40 | age <= 59 ~ '40-59',  
 age >= 60 ~ "60+")) %>%  
 dplyr::filter(number\_morbidities <= 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 == "20-39")  
  
  
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   
## 40867 120

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 20-39: 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   
## -0.0767 -0.0767 -0.0767 -0.0767 3.4203   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.82719 0.10065 -57.90 <2e-16 \*\*\*  
## chillsYes -0.01925 0.24058 -0.08 0.936   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1639.7 on 40985 degrees of freedom  
## AIC: 1643.7  
##   
## Number of Fisher Scoring iterations: 8

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   
## 0.9362347

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) | 0.0029463 | 0.0024028 | 0.0035665 | 0.9362347 |
| chillsYes | 0.9809365 | 0.5960769 | 1.5383629 | 0.9362347 |

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ cough, family = binomial, data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.0813 -0.0813 -0.0730 -0.0730 3.4432   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.9252 0.1252 -47.343 <2e-16 \*\*\*  
## coughYes 0.2149 0.1832 1.173 0.241   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1638.3 on 40985 degrees of freedom  
## AIC: 1642.3  
##   
## Number of Fisher Scoring iterations: 8

## (Intercept) coughYes   
## 0.002671342 1.239768739

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   
## 0.2408455

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) | 0.0026713 | 0.0020686 | 0.0033815 | 0.2408455 |
| coughYes | 1.2397687 | 0.8635990 | 1.7747032 | 0.2408455 |

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   
## -0.0786 -0.0786 -0.0786 -0.0786 3.4882   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.77899 0.09916 -58.277 <2e-16 \*\*\*  
## diarrhoeaYes -0.30234 0.25590 -1.181 0.237   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1638.2 on 40985 degrees of freedom  
## AIC: 1642.2  
##   
## Number of Fisher Scoring iterations: 8

# 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   
## 0.003091846 0.739084102

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   
## 0.2374166

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) | 0.0030918 | 0.0025293 | 0.0037325 | 0.2374166 |
| diarrhoeaYes | 0.7390841 | 0.4332241 | 1.1888389 | 0.2374166 |

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   
## -0.0794 -0.0794 -0.0794 -0.0733 3.4414   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.7575 0.1215 -47.404 <2e-16 \*\*\*  
## headacheYes -0.1613 0.1845 -0.875 0.382   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1638.9 on 40985 degrees of freedom  
## AIC: 1642.9  
##   
## Number of Fisher Scoring iterations: 8

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   
## 0.3818271

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) | 0.0031591 | 0.0024657 | 0.0039722 | 0.3818271 |
| headacheYes | 0.8510130 | 0.5904900 | 1.2193789 | 0.3818271 |

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   
## -0.0792 -0.0792 -0.0792 -0.0709 3.4606   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.7621 0.1080 -53.354 <2e-16 \*\*\*  
## loss\_smell\_tasteYes -0.2232 0.2028 -1.101 0.271   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1638.4 on 40985 degrees of freedom  
## AIC: 1642.4  
##   
## Number of Fisher Scoring iterations: 8

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   
## 0.2711109

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) | 0.0031444 | 0.0025250 | 0.003858 | 0.2711109 |
| loss\_smell\_tasteYes | 0.7999402 | 0.5306756 | 1.178620 | 0.2711109 |

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   
## -0.0771 -0.0771 -0.0771 -0.0757 3.4224   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.81806 0.11339 -51.310 <2e-16 \*\*\*  
## muscle\_acheYes -0.03537 0.19166 -0.185 0.854   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1639.7 on 40985 degrees of freedom  
## AIC: 1643.7  
##   
## Number of Fisher Scoring iterations: 8

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   
## 0.002973354 0.965249527

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   
## 0.8535886

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) | 0.0029734 | 0.0023606 | 0.0036842 | 0.8535886 |
| muscle\_acheYes | 0.9652495 | 0.6575638 | 1.3970694 | 0.8535886 |

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   
## -0.0824 -0.0824 -0.0824 -0.0670 3.4933   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.6828 0.1099 -51.686 <2e-16 \*\*\*  
## nasal\_congestionYes -0.4164 0.1979 -2.104 0.0354 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1635.1 on 40985 degrees of freedom  
## AIC: 1639.1  
##   
## Number of Fisher Scoring iterations: 8

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   
## 0.003404011 0.659398926

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   
## 0.03535059

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) | 0.0034040 | 0.0027223 | 0.0041914 | 0.0353506 |
| nasal\_congestionYes | 0.6593989 | 0.4425290 | 0.9638408 | 0.0353506 |

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   
## -0.0819 -0.0763 -0.0763 -0.0763 3.4180   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.8384 0.0942 -61.976 <2e-16 \*\*\*  
## nausea\_vomitingYes 0.1427 0.3901 0.366 0.714   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1639.6 on 40985 degrees of freedom  
## AIC: 1643.6  
##   
## Number of Fisher Scoring iterations: 8

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   
## 0.002913573 1.153407902

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   
## 0.7144965

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) | 0.0029136 | 0.0024082 | 0.0034853 | 0.7144965 |
| nausea\_vomitingYes | 1.1534079 | 0.4865918 | 2.2987222 | 0.7144965 |

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   
## -0.0882 -0.0739 -0.0739 -0.0739 3.4368   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.9030 0.1044 -56.548 <2e-16 \*\*\*  
## shortness\_breathYes 0.3561 0.2162 1.647 0.0996 .   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1637.2 on 40985 degrees of freedom  
## AIC: 1641.2  
##   
## Number of Fisher Scoring iterations: 8

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   
## 0.09960786

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) | 0.0027311 | 0.0022098 | 0.0033288 | 0.0996079 |
| shortness\_breathYes | 1.4276926 | 0.9181608 | 2.1503819 | 0.0996079 |

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   
## -0.0810 -0.0810 -0.0810 -0.0706 3.4626   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.7193 0.1157 -49.451 <2e-16 \*\*\*  
## sore\_throatYes -0.2730 0.1888 -1.446 0.148   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1637.6 on 40985 degrees of freedom  
## AIC: 1641.6  
##   
## Number of Fisher Scoring iterations: 8

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   
## 0.1482079

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) | 0.0032820 | 0.0025933 | 0.0040834 | 0.1482079 |
| sore\_throatYes | 0.7610991 | 0.5221192 | 1.0968801 | 0.1482079 |

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   
## -0.0768 -0.0768 -0.0768 -0.0768 3.4249   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.82457 0.09965 -58.453 <2e-16 \*\*\*  
## sputumYes -0.03742 0.25041 -0.149 0.881   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1639.7 on 40985 degrees of freedom  
## AIC: 1643.7  
##   
## Number of Fisher Scoring iterations: 8

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   
## 0.8812181

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) | 0.0029541 | 0.0024141 | 0.0035693 | 0.8812181 |
| sputumYes | 0.9632743 | 0.5720471 | 1.5354065 | 0.8812181 |

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   
## -0.0852 -0.0852 -0.0732 -0.0732 3.4424   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.9222 0.1119 -52.904 <2e-16 \*\*\*  
## temperatureYes 0.3047 0.1940 1.571 0.116   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1637.3 on 40985 degrees of freedom  
## AIC: 1641.3  
##   
## Number of Fisher Scoring iterations: 8

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   
## 0.11618

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) | 0.0026793 | 0.0021336 | 0.003311 | 0.11618 |
| temperatureYes | 1.3562409 | 0.9188298 | 1.970045 | 0.11618 |

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   
## -0.0784 -0.0784 -0.0784 -0.0784 3.5331   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.78357 0.09549 -60.57 <2e-16 \*\*\*  
## itchy\_eyesYes -0.45592 0.33044 -1.38 0.168   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1637.5 on 40985 degrees of freedom  
## AIC: 1641.5  
##   
## Number of Fisher Scoring iterations: 8

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   
## 0.167667

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) | 0.0030777 | 0.0025371 | 0.0036903 | 0.167667 |
| itchy\_eyesYes | 0.6338635 | 0.3104769 | 1.1506676 | 0.167667 |

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   
## -0.0772 -0.0772 -0.0772 -0.0772 3.5506   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.81505 0.09258 -62.809 <2e-16 \*\*\*  
## chest\_painYes -0.48635 0.58477 -0.832 0.406   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1638.9 on 40985 degrees of freedom  
## AIC: 1642.9  
##   
## 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   
## 0.4055862

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) | 0.0029823 | 0.0024734 | 0.0035568 | 0.4055862 |
| chest\_painYes | 0.6148683 | 0.1513432 | 1.6291475 | 0.4055862 |

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   
## -0.0773 -0.0773 -0.0773 -0.0773 3.5056   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.81114 0.09379 -61.96 <2e-16 \*\*\*  
## loss\_appetiteYes -0.33125 0.41917 -0.79 0.429   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1639.0 on 40985 degrees of freedom  
## AIC: 1643  
##   
## Number of Fisher Scoring iterations: 8

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   
## 0.4293707

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) | 0.0029940 | 0.0024769 | 0.0035788 | 0.4293707 |
| loss\_appetiteYes | 0.7180224 | 0.2807473 | 1.4959664 | 0.4293707 |

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   
## -0.0777 -0.0777 -0.0777 -0.0777 3.6897   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.8022 0.0922 -62.933 <2e-16 \*\*\*  
## joint\_painYes -1.0035 0.7135 -1.407 0.16   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1636.9 on 40985 degrees of freedom  
## AIC: 1640.9  
##   
## Number of Fisher Scoring iterations: 9

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   
## 0.1595494

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) | 0.0030209 | 0.0025075 | 0.0036003 | 0.1595494 |
| joint\_painYes | 0.3665841 | 0.0604859 | 1.1528429 | 0.1595494 |

## 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 ~ nasal\_congestion + shortness\_breath, data = diabetes\_type\_one\_data, family = binomial)  
  
summary(diabetes\_type\_one\_model)

##   
## Call:  
## glm(formula = diabetes\_type\_one ~ nasal\_congestion + shortness\_breath,   
## family = binomial, data = diabetes\_type\_one\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.0971 -0.0796 -0.0796 -0.0637 3.5215   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.7543 0.1190 -48.368 <2e-16 \*\*\*  
## nasal\_congestionYes -0.4441 0.1986 -2.235 0.0254 \*   
## shortness\_breathYes 0.3994 0.2170 1.840 0.0657 .   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1639.7 on 40986 degrees of freedom  
## Residual deviance: 1631.9 on 40984 degrees of freedom  
## AIC: 1637.9  
##   
## Number of Fisher Scoring iterations: 9

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) | 0.0031691 | 0.0024887 | 0.0039694 |
| nasal\_congestionYes | 0.6414297 | 0.4298938 | 0.9389227 |
| shortness\_breathYes | 1.4908741 | 0.9574256 | 2.2492425 |

# 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) 0.003169124 0.002488669 0.003969433  
## nasal\_congestionYes 0.641429731 0.429893793 0.938922746  
## shortness\_breathYes 1.490874149 0.957425574 2.249242467

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) nasal\_congestionYes shortness\_breathYes   
## 0.00000000 0.07616958 0.19718634

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) | 0.0031691 | 0.0024887 | 0.0039694 | 0.0000000 |
| nasal\_congestionYes | 0.6414297 | 0.4298938 | 0.9389227 | 0.0761696 |
| shortness\_breathYes | 1.4908741 | 0.9574256 | 2.2492425 | 0.1971863 |

vif(diabetes\_type\_one\_model)

## nasal\_congestionYes shortness\_breathYes   
## 1.007147 1.007147