kidney\_18082020\_39\_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()  
## )

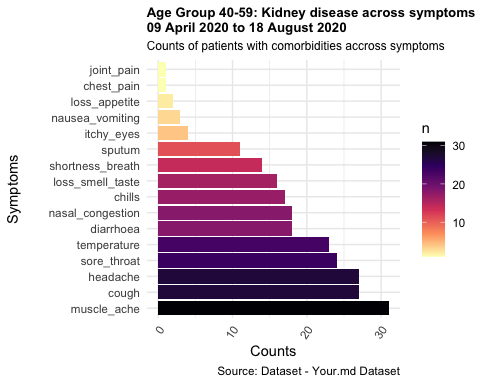
## See spec(...) for full column specifications.

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)

kidney\_disease\_data <- data\_categ\_covid %>%  
 dplyr::select(kidney\_disease, chills, cough, diarrhoea, headache, loss\_smell\_taste, muscle\_ache,   
 nasal\_congestion, nausea\_vomiting, shortness\_breath, sore\_throat, sputum, temperature, chest\_pain, joint\_pain, loss\_appetite, itchy\_eyes) %>%  
 tidyr::drop\_na()

kidney\_count <- kidney\_disease\_data %>%  
 tidyr::pivot\_longer(cols = 2:17,   
 names\_to = "symptoms",   
 values\_to = "yes\_no") %>%  
 dplyr::filter(kidney\_disease == "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: Kidney disease 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\_kidney\_sympt <-  
 ggplot2::ggplot(kidney\_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(kidney\_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\_kidney\_sympt



# Univariate analysis for kidney disease and Covid-19 symptoms

The most Covid symptoms that are associated with kidney disease are shorthness and breath and temperature.

1. Kidney disease and chills

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

##   
## Call:  
## glm(formula = kidney\_disease ~ chills, family = binomial, data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.1000 -0.0826 -0.0826 -0.0826 3.3708   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.6777 0.1493 -38.023 <2e-16 \*\*\*  
## chillsYes 0.3818 0.2853 1.338 0.181   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 815.30 on 16605 degrees of freedom  
## AIC: 819.3  
##   
## Number of Fisher Scoring iterations: 8

coef\_kidney\_disease\_chills <- coef(kidney\_disease\_chills)

kidney\_disease\_chills\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_chills), confint(kidney\_disease\_chills)))

## Waiting for profiling to be done...

P-values adjusted

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

## chillsYes   
## 0.1808924

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0034213 | 0.0025154 | 0.004523 | 0.1808924 |
| chillsYes | 1.4648912 | 0.8147860 | 2.512725 | 0.1808924 |

##   
## Call:  
## glm(formula = kidney\_disease ~ cough, family = binomial, data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.0914 -0.0914 -0.0832 -0.0832 3.3670   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.6648 0.1693 -33.456 <2e-16 \*\*\*  
## coughYes 0.1895 0.2566 0.738 0.46   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 816.44 on 16605 degrees of freedom  
## AIC: 820.44  
##   
## Number of Fisher Scoring iterations: 8

## (Intercept) coughYes   
## 0.00346569 1.20860334

kidney\_disease\_cough\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_cough), confint(kidney\_disease\_cough)))

## Waiting for profiling to be done...

P-values adjusted

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

## coughYes   
## 0.4603514

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0034657 | 0.0024394 | 0.004747 | 0.4603514 |
| coughYes | 1.2086033 | 0.7249685 | 1.993069 | 0.4603514 |

kidney\_disease\_diarrhea <- glm(kidney\_disease ~ diarrhoea, data = kidney\_disease\_data, family = binomial)  
  
summary(kidney\_disease\_diarrhea)

##   
## Call:  
## glm(formula = kidney\_disease ~ diarrhoea, family = binomial,   
## data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.1084 -0.0807 -0.0807 -0.0807 3.3849   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.7255 0.1510 -37.918 <2e-16 \*\*\*  
## diarrhoeaYes 0.5914 0.2805 2.108 0.035 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 812.92 on 16605 degrees of freedom  
## AIC: 816.92  
##   
## Number of Fisher Scoring iterations: 8

# get coef  
coef\_ob\_diarrhea <- coef(kidney\_disease\_diarrhea)  
  
# odd ratios  
odd\_ratio\_ob\_diar <- exp(coef\_ob\_diarrhea)  
  
odd\_ratio\_ob\_diar

## (Intercept) diarrhoeaYes   
## 0.003261675 1.806427613

kidney\_disease\_diarrhea\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_diarrhea), confint(kidney\_disease\_diarrhea)))

## Waiting for profiling to be done...

P-values adjusted

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

## diarrhoeaYes   
## 0.03501669

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0032617 | 0.0023894 | 0.0043249 | 0.0350167 |
| diarrhoeaYes | 1.8064276 | 1.0170113 | 3.0761600 | 0.0350167 |

kidney\_disease\_headache <- glm(kidney\_disease ~ headache, data = kidney\_disease\_data, family = binomial)  
  
summary(kidney\_disease\_headache)

##   
## Call:  
## glm(formula = kidney\_disease ~ headache, family = binomial, data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.0868 -0.0868 -0.0868 -0.0861 3.3462   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.58038 0.16935 -32.952 <2e-16 \*\*\*  
## headacheYes -0.01447 0.25662 -0.056 0.955   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 816.98 on 16605 degrees of freedom  
## AIC: 820.98  
##   
## Number of Fisher Scoring iterations: 8

OR and CI

kidney\_disease\_headache\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_headache), confint(kidney\_disease\_headache)))

## Waiting for profiling to be done...

P-values adjusted

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

## headacheYes   
## 0.9550254

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0037711 | 0.0026543 | 0.0051657 | 0.9550254 |
| headacheYes | 0.9856317 | 0.5912402 | 1.6253187 | 0.9550254 |

kidney\_disease\_loss\_smell <- glm(kidney\_disease ~ loss\_smell\_taste, data = kidney\_disease\_data, family = binomial)  
  
  
summary(kidney\_disease\_loss\_smell)

##   
## Call:  
## glm(formula = kidney\_disease ~ loss\_smell\_taste, family = binomial,   
## data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.0872 -0.0872 -0.0872 -0.0845 3.3578   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.56975 0.14772 -37.704 <2e-16 \*\*\*  
## loss\_smell\_tasteYes -0.06414 0.29076 -0.221 0.825   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 816.93 on 16605 degrees of freedom  
## AIC: 820.93  
##   
## Number of Fisher Scoring iterations: 8

OR and CI

kidney\_disease\_loss\_smell\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_loss\_smell), confint(kidney\_disease\_loss\_smell)))

## Waiting for profiling to be done...

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

## loss\_smell\_tasteYes   
## 0.8254044

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0038114 | 0.0028120 | 0.0050244 | 0.8254044 |
| loss\_smell\_tasteYes | 0.9378715 | 0.5145902 | 1.6220035 | 0.8254044 |

library(fmsb)

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

kidney\_disease\_muscle\_ache <- glm(kidney\_disease ~ muscle\_ache, data = kidney\_disease\_data, family = binomial)  
   
summary(kidney\_disease\_muscle\_ache)

##   
## Call:  
## glm(formula = kidney\_disease ~ muscle\_ache, family = binomial,   
## data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.0996 -0.0996 -0.0775 -0.0775 3.4086   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.8064 0.1799 -32.282 <2e-16 \*\*\*  
## muscle\_acheYes 0.5016 0.2545 1.971 0.0487 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 813.14 on 16605 degrees of freedom  
## AIC: 817.14  
##   
## Number of Fisher Scoring iterations: 8

coef\_ob\_muscle\_ac <- coef(kidney\_disease\_muscle\_ache)  
  
odd\_ratio\_ob\_los <- exp(coef\_ob\_muscle\_ac)  
  
odd\_ratio\_ob\_los

## (Intercept) muscle\_acheYes   
## 0.003008248 1.651442301

OR and CI

kidney\_disease\_muscle\_ache\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_muscle\_ache), confint(kidney\_disease\_muscle\_ache)))

## Waiting for profiling to be done...

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

## muscle\_acheYes   
## 0.048711

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0030082 | 0.0020687 | 0.0041974 | 0.048711 |
| muscle\_acheYes | 1.6514423 | 1.0002548 | 2.7265679 | 0.048711 |

kidney\_disease\_nasal\_cong <- glm(kidney\_disease ~ nasal\_congestion, data = kidney\_disease\_data, family = binomial)  
  
summary(kidney\_disease\_nasal\_cong)

##   
## Call:  
## glm(formula = kidney\_disease ~ nasal\_congestion, family = binomial,   
## data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.0879 -0.0879 -0.0879 -0.0834 3.3655   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.5552 0.1510 -36.778 <2e-16 \*\*\*  
## nasal\_congestionYes -0.1047 0.2803 -0.374 0.709   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 816.84 on 16605 degrees of freedom  
## AIC: 820.84  
##   
## Number of Fisher Scoring iterations: 8

coef\_ob\_nas\_cong <- coef(kidney\_disease\_nasal\_cong)  
  
odd\_ratio\_ob\_nas\_cong <- exp(coef\_ob\_nas\_cong)  
  
odd\_ratio\_ob\_nas\_cong

## (Intercept) nasal\_congestionYes   
## 0.003867452 0.900585773

OR and CI

kidney\_disease\_nasal\_cong\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_nasal\_cong), confint(kidney\_disease\_nasal\_cong)))

## Waiting for profiling to be done...

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

## nasal\_congestionYes   
## 0.7087187

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0038675 | 0.0028329 | 0.0051286 | 0.7087187 |
| nasal\_congestionYes | 0.9005858 | 0.5072199 | 1.5329211 | 0.7087187 |

kidney\_disease\_nausea\_vomitting <- glm(kidney\_disease ~ nausea\_vomiting, data = kidney\_disease\_data, family = binomial)  
  
summary(kidney\_disease\_nausea\_vomitting)

##   
## Call:  
## glm(formula = kidney\_disease ~ nausea\_vomiting, family = binomial,   
## data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.0920 -0.0862 -0.0862 -0.0862 3.3455   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.5926 0.1304 -42.88 <2e-16 \*\*\*  
## nausea\_vomitingYes 0.1302 0.5931 0.22 0.826   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 816.94 on 16605 degrees of freedom  
## AIC: 820.94  
##   
## Number of Fisher Scoring iterations: 8

coef\_ob\_naus\_vom <- coef(kidney\_disease\_nausea\_vomitting)  
  
odd\_ratio\_ob\_naus\_vom <- exp(coef\_ob\_naus\_vom)  
  
odd\_ratio\_ob\_naus\_vom

## (Intercept) nausea\_vomitingYes   
## 0.003725218 1.139069355

OR and CI

kidney\_disease\_nausea\_vomitting\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_nausea\_vomitting), confint(kidney\_disease\_nausea\_vomitting)))

## Waiting for profiling to be done...

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

## nausea\_vomitingYes   
## 0.8262239

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0037252 | 0.0028525 | 0.0047607 | 0.8262239 |
| nausea\_vomitingYes | 1.1390694 | 0.2775161 | 3.0846594 | 0.8262239 |

kidney\_disease\_short\_breath <- glm(kidney\_disease ~ shortness\_breath, data = kidney\_disease\_data, family = binomial)  
  
summary(kidney\_disease\_short\_breath)

##   
## Call:  
## glm(formula = kidney\_disease ~ shortness\_breath, family = binomial,   
## data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.1002 -0.0835 -0.0835 -0.0835 3.3651   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.6584 0.1446 -39.135 <2e-16 \*\*\*  
## shortness\_breathYes 0.3658 0.3045 1.202 0.23   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 815.64 on 16605 degrees of freedom  
## AIC: 819.64  
##   
## Number of Fisher Scoring iterations: 8

OR and CI

kidney\_disease\_short\_breath\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_short\_breath), confint(kidney\_disease\_short\_breath)))

## Waiting for profiling to be done...

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

## shortness\_breathYes   
## 0.2295535

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0034881 | 0.0025910 | 0.0045725 | 0.2295535 |
| shortness\_breathYes | 1.4416756 | 0.7646752 | 2.5468035 | 0.2295535 |

kidney\_disease\_sore\_thr <- glm(kidney\_disease ~ sore\_throat, data = kidney\_disease\_data, family = binomial)  
  
summary(kidney\_disease\_sore\_thr)

##   
## Call:  
## glm(formula = kidney\_disease ~ sore\_throat, family = binomial,   
## data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.0869 -0.0869 -0.0869 -0.0858 3.3486   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.57645 0.16253 -34.311 <2e-16 \*\*\*  
## sore\_throatYes -0.02629 0.26122 -0.101 0.92   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 816.97 on 16605 degrees of freedom  
## AIC: 820.97  
##   
## Number of Fisher Scoring iterations: 8

OR and CI

kidney\_disease\_sore\_thr\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_sore\_thr), confint(kidney\_disease\_sore\_thr)))

## Waiting for profiling to be done...

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

## sore\_throatYes   
## 0.9198443

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0037860 | 0.0027048 | 0.0051239 | 0.9198443 |
| sore\_throatYes | 0.9740562 | 0.5763939 | 1.6139014 | 0.9198443 |

kidney\_disease\_sputum <- glm(kidney\_disease ~ sputum, data = kidney\_disease\_data, family = binomial)  
  
  
summary(kidney\_disease\_sputum)

##   
## Call:  
## glm(formula = kidney\_disease ~ sputum, family = binomial, data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.0914 -0.0855 -0.0855 -0.0855 3.3504   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.6090 0.1403 -39.983 <2e-16 \*\*\*  
## sputumYes 0.1325 0.3331 0.398 0.691   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 816.83 on 16605 degrees of freedom  
## AIC: 820.83  
##   
## Number of Fisher Scoring iterations: 8

OR and CI

kidney\_disease\_sputum\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_sputum), confint(kidney\_disease\_sputum)))

## Waiting for profiling to be done...

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

## sputumYes   
## 0.6907982

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0036648 | 0.0027476 | 0.0047673 | 0.6907982 |
| sputumYes | 1.1416851 | 0.5638488 | 2.1085824 | 0.6907982 |

kidney\_disease\_temperature <- glm(kidney\_disease ~ temperature, data = kidney\_disease\_data, family = binomial)  
  
  
summary(kidney\_disease\_temperature)

##   
## Call:  
## glm(formula = kidney\_disease ~ temperature, family = binomial,   
## data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.1039 -0.1039 -0.0796 -0.0796 3.3932   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.7536 0.1604 -35.876 <2e-16 \*\*\*  
## temperatureYes 0.5352 0.2635 2.031 0.0423 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 813.08 on 16605 degrees of freedom  
## AIC: 817.08  
##   
## Number of Fisher Scoring iterations: 8

OR and CI

kidney\_disease\_temperature\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_temperature), confint(kidney\_disease\_temperature)))

## Waiting for profiling to be done...

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

## temperatureYes   
## 0.04226293

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0031712 | 0.0022762 | 0.0042756 | 0.0422629 |
| temperatureYes | 1.7077152 | 1.0043338 | 2.8379269 | 0.0422629 |

kidney\_disease\_itchy\_eyes <- glm(kidney\_disease ~ itchy\_eyes, data = kidney\_disease\_data, family = binomial)  
  
summary(kidney\_disease\_itchy\_eyes)

##   
## Call:  
## glm(formula = kidney\_disease ~ itchy\_eyes, family = binomial,   
## data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.0889 -0.0889 -0.0889 -0.0889 3.5090   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.5326 0.1316 -42.052 <2e-16 \*\*\*  
## itchy\_eyesYes -0.6218 0.5173 -1.202 0.229   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 815.25 on 16605 degrees of freedom  
## AIC: 819.25  
##   
## Number of Fisher Scoring iterations: 8

OR and CI

kidney\_disease\_itchy\_eyes\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_itchy\_eyes), confint(kidney\_disease\_itchy\_eyes)))

## Waiting for profiling to be done...

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

## itchy\_eyesYes   
## 0.2294333

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0039558 | 0.0030217 | 0.0050658 | 0.2294333 |
| itchy\_eyesYes | 0.5370009 | 0.1627067 | 1.3070066 | 0.2294333 |

kidney\_disease\_chest\_pain <- glm(kidney\_disease ~ chest\_pain, data = kidney\_disease\_data, family = binomial)  
  
summary(kidney\_disease\_chest\_pain)

##   
## Call:  
## glm(formula = kidney\_disease ~ chest\_pain, family = binomial,   
## data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.0872 -0.0872 -0.0872 -0.0872 3.5344   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.5713 0.1283 -43.431 <2e-16 \*\*\*  
## chest\_painYes -0.6728 1.0085 -0.667 0.505   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 816.43 on 16605 degrees of freedom  
## AIC: 820.43  
##   
## Number of Fisher Scoring iterations: 8

OR and CI

kidney\_disease\_chest\_pain\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_chest\_pain), confint(kidney\_disease\_chest\_pain)))

## Waiting for profiling to be done...

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

## chest\_painYes   
## 0.5046901

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0038054 | 0.0029273 | 0.0048443 | 0.5046901 |
| chest\_painYes | 0.5102662 | 0.0288488 | 2.3166351 | 0.5046901 |

kidney\_disease\_loss\_appetite <- glm(kidney\_disease ~ loss\_appetite, data = kidney\_disease\_data, family = binomial)  
  
summary(kidney\_disease\_loss\_appetite)

##   
## Call:  
## glm(formula = kidney\_disease ~ loss\_appetite, family = binomial,   
## data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.0879 -0.0879 -0.0879 -0.0879 3.5374   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.5545 0.1293 -42.942 <2e-16 \*\*\*  
## loss\_appetiteYes -0.7003 0.7190 -0.974 0.33   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 815.80 on 16605 degrees of freedom  
## AIC: 819.8  
##   
## Number of Fisher Scoring iterations: 8

OR and CI

kidney\_disease\_loss\_appetite\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_loss\_appetite), confint(kidney\_disease\_loss\_appetite)))

## Waiting for profiling to be done...

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

## loss\_appetiteYes   
## 0.3301066

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0038700 | 0.0029702 | 0.0049361 | 0.3301066 |
| loss\_appetiteYes | 0.4964462 | 0.0813297 | 1.5895392 | 0.3301066 |

kidney\_disease\_joint\_pain <- glm(kidney\_disease ~ joint\_pain, data = kidney\_disease\_data, family = binomial)  
  
  
summary(kidney\_disease\_joint\_pain)

##   
## Call:  
## glm(formula = kidney\_disease ~ joint\_pain, family = binomial,   
## data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.0877 -0.0877 -0.0877 -0.0877 3.6193   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.5599 0.1283 -43.34 <2e-16 \*\*\*  
## joint\_painYes -0.9884 1.0089 -0.98 0.327   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 815.64 on 16605 degrees of freedom  
## AIC: 819.64  
##   
## Number of Fisher Scoring iterations: 9

OR and CI

kidney\_disease\_joint\_pain\_or\_ci <- exp(cbind(OR = coef(kidney\_disease\_joint\_pain), confint(kidney\_disease\_joint\_pain)))

## Waiting for profiling to be done...

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

## joint\_painYes   
## 0.3272638

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0038493 | 0.0029611 | 0.0049003 | 0.3272638 |
| joint\_painYes | 0.3721875 | 0.0210472 | 1.6882907 | 0.3272638 |

# Multivariate analysis for Kidney disease

The selected variables for the final model are: shortness of breath, temperature.

In patients showing covid-19 symptoms/of patients with a positive covid test,when adjusting for all relevant variables, in respondents with kidney disease there was a: - 64% increase in the odds of experiencing shortness of breaht compared to those who do not have kidney disease - 33 % increase in the odds of experiencing 38.1 -39 temperature compared to those who do not have kidney disease - 305 % ?? not sure - increase in odds of experiencing 39.1-41 temperature compared to those who do not have kidney disease

kidney\_model <- glm(kidney\_disease ~ diarrhoea + muscle\_ache + temperature, data = kidney\_disease\_data, family = binomial)  
  
summary(kidney\_model)

##   
## Call:  
## glm(formula = kidney\_disease ~ diarrhoea + muscle\_ache + temperature,   
## family = binomial, data = kidney\_disease\_data)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.1311 -0.0894 -0.0852 -0.0711 3.4588   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -5.9791 0.2011 -29.727 <2e-16 \*\*\*  
## diarrhoeaYes 0.4587 0.2871 1.597 0.110   
## muscle\_acheYes 0.3625 0.2629 1.379 0.168   
## temperatureYes 0.4049 0.2706 1.496 0.135   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 816.98 on 16606 degrees of freedom  
## Residual deviance: 808.06 on 16603 degrees of freedom  
## AIC: 816.06  
##   
## Number of Fisher Scoring iterations: 8

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

## Waiting for profiling to be done...

kidney\_model\_or\_ci

## OR 2.5 % 97.5 %  
## (Intercept) 0.002531222 0.001669086 0.003679493  
## diarrhoeaYes 1.581982499 0.880145329 2.731396421  
## muscle\_acheYes 1.436949793 0.855996890 2.410441925  
## temperatureYes 1.499080405 0.870159857 2.526813070

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

## (Intercept) diarrhoeaYes muscle\_acheYes temperatureYes   
## 1.387303e-193 4.406920e-01 6.717402e-01 5.382899e-01

OR, CI and pval adjusted

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | OR | 2.5 % | 97.5 % | pvalues |
| (Intercept) | 0.0025312 | 0.0016691 | 0.0036795 | 0.0000000 |
| diarrhoeaYes | 1.5819825 | 0.8801453 | 2.7313964 | 0.4406920 |
| muscle\_acheYes | 1.4369498 | 0.8559969 | 2.4104419 | 0.6717402 |
| temperatureYes | 1.4990804 | 0.8701599 | 2.5268131 | 0.5382899 |

Multicolinearity

vif(kidney\_model)

## diarrhoeaYes muscle\_acheYes temperatureYes   
## 1.047433 1.066835 1.053912