Finding SNPs from the genome of supercentenarians

```
#Clean the workspace

rm(list=ls())

#Import the libraries

library(vcfR)

#Read the files

file <- read.vcfR("sample_id.vcf")

dataframe <- as.data.frame(file@fix)

#Write all mutations to a csv file

all_mutations <- dataframe [which(dataframe$CHROM == "chr1"),]

write.csv(all_mutations, "sample_id chr1 all mutations.csv",
row.names=FALSE)

#Filter the dataframe for PASS variants

filterpass <- dataframe [which(dataframe$FILTER == "PASS"),]

#Filter the dataframe fr chromsome

Filtered_mutation <- filterpass[which(filterpass$CHROM == "chr1"),]

pos <- as.numeric(filtered_mutation$POS)

#Write filtered mutations to a csv file

write.csv(filtered mutation, "sample_id chr1 filtered.csv",
row.names=FALSE)
```

Sorting SNPs among centenarians and supercentenarians.

```
#Clean the workspace

rm(list=ls())

#Import the libraries

library(openxlsx)

library(readxl)

# Create an Excel file

wb <- createWorkbook()

# List of chromosomes
```

```
chromosomes <- c("chr1", "chr2", "chr3", "chr4", "chr5", "chr6",
"chr7", "chr8", "chr9", "chr10", "chr11", "chr12", "chr13", "chr14",
"chr15", "chr16", "chr17", "chr18", "chr19", "chr20", "chr21",
"chr22", "chrX", "chrY", "chrM")

# Function to process a chromosome

processChromosome <- function(chr) {

  excel <- read_excel("input.xlsx", sheet = chr)

  data <- data.frame(excel)

  unique_values <- unique(unlist(data))

  unique_values <- unique(na.omit(unique_values))

  sorted_positions <- sort(unique_values)

  presence <- sapply(data, function(column) ifelse(sorted_positions
%in% column, 1, 0))

  data_with_positions <- data.frame(positions = sorted_positions,
presence)

  data_with_positions$sum_of_values <- rowSums(data_with_positions[-
1], na.rm = TRUE)

  return(data_with_positions)

}

# Loop through chromosomes and add them to the Excel file

for (chr in chromosomes) {

  data_with_positions <- processChromosome(chr)

  addWorksheet(wb, sheetName = chr)

  writeData(wb, sheet = chr, data_with_positions)

}

# Save the Excel file

saveWorkbook(wb, "output.xlsx")
```

Finding mutations unique and common among supercentenarians.

```
rm(list=ls())

library(readxl)
```

```
library(openxlsx)


# Create an Excel file

wb <- createWorkbook()

addWorksheet(wb, "sheetname")


# List of chromosomes

chromosomes <- c("chr1", "chr2", "chr3", "chr4", "chr5", "chr6",
"chr7", "chr8", "chr9", "chr10", "chr11", "chr12", "chr13", "chr14",
"chr15", "chr16", "chr17", "chr18", "chr19", "chr20", "chr21",
"chr22", "chrX", "chrY", "chrM")


# Loop through the chromosomes and process each one

start_col <- 1

for (chr in chromosomes) {

  excel <- read_excel("input.xlsx", sheet = chr)

  data <- data.frame(excel)

  unique_values <- unique(na.omit(unlist(data)))

  sorted_positions <- sort(unique_values)

  positions <- data.frame(positions = sorted_positions)

  presence <- sapply(data, function(column) ifelse(sorted_positions
%in% column, 1, 0))

  data_with_positions <- data.frame(positions = sorted_positions,
presence)

  data_with_positions$sum_of_values <- rowSums(data_with_positions[-
1], na.rm = TRUE)


  # Filter positions with a sum (1 for unique, 3 for common
centenarians, 18 for supercentenarians and 21 for both)

  positions_with_sum_1 <-
data_with_positions$positions[data_with_positions$sum_of_values == 1]


  # Create a data frame for the chromosome
```

```
  chromosome_data <- data.frame(chr = positions_with_sum_1)


  # Write the data to the Excel workbook
  writeData(wb, sheet = "sheetname", x = chromosome_data, startCol =
start_col)
  start_col <- start_col + 1
}


# Save the Excel file
saveWorkbook(wb, "output.xlsx", overwrite = TRUE)
```