Import - Lithic analysis from three sites: Balver Höhle, Buhlen & Ramioul

Lisa Schunk

2021-01-28

# Goal of the script

This script reads the three xlsx files (database techno-typological analysis) and formats the data for a statistical analysis.  
The script will:

1. Read in the original xlsx files
2. Change and sort the data in order to do stats
3. Save the data as a new single xlsx file and R object

dir\_in <- "analysis/all\_sites/raw\_data/"  
dir\_out <- "analysis/all\_sites/derived\_data/"

Raw data must be located in “analysis/all\_sites/raw\_data/”.  
Formatted data will be saved in “analysis/all\_sites/derived\_data/”. The knit directory for this script is the project directory.

# Load packages

library(openxlsx)  
library(readxl)  
library(R.utils)  
library(tools)  
library(data.table)  
library(chron)  
library(dplyr)

# Get name, path and information of the files

data\_files <- list.files(dir\_in, pattern = "\\.xlsx$", full.names = TRUE)  
md5\_in <- md5sum(data\_files)  
info\_in <- data.frame(files = basename(names(md5\_in)), checksum = md5\_in,   
 row.names = NULL)

The checksum (MD5 hashes) of the imported files are:

files checksum  
1 Balve\_lithic\_analysis.xlsx b666e57574b699fcb078f22f89685bce  
2 Buhlen\_lithic\_analysis.xlsx 15d87c7bcb73685534495b53e896d4c5  
3 Ramioul\_lithic\_analysis.xlsx 86d5a13ef2d585b384a2946598f1bd33

# Read in original xlsx-files

imp\_data <- vector(mode = "list", length = length(data\_files))  
names(imp\_data) <- basename(data\_files)  
  
# loop for import data due to the three different CSV files   
for (i in seq\_along(data\_files)) {  
 imp\_data[[i]] <- read.xlsx(data\_files[i], sheet = 1, colNames = TRUE,  
 rowNames = FALSE, skipEmptyCols = FALSE)  
}  
str(imp\_data)

List of 3  
 $ Balve\_lithic\_analysis.xlsx :'data.frame': 347 obs. of 34 variables:  
 ..$ site : chr [1:347] "Balver\_Höhle" "Balver\_Höhle" "Balver\_Höhle" "Balver\_Höhle" ...  
 ..$ ID : chr [1:347] "HE-012" "HE-013" "HE-014" "HE-015" ...  
 ..$ raw.material : chr [1:347] "baltic\_flint" "silicified\_schist" "silicified\_schist" "silicified\_schist" ...  
 ..$ technological.class : chr [1:347] "Keilmesser" "Keilmesser" "Keilmesser" "Keilmesser" ...  
 ..$ artefact.state : chr [1:347] "complete" "semifinished\_product" "complete" "complete" ...  
 ..$ blank : chr [1:347] "core" "core" "flake" "core" ...  
 ..$ morpho.type : chr [1:347] "Bockstein" "Bockstein" "Balve" "Pradnik" ...  
 ..$ cortex : chr [1:347] "YES" "YES" "YES" "N/A" ...  
 ..$ cortex.percentage : chr [1:347] "N/A" "N/A" "N/A" NA ...  
 ..$ cortex.location : chr [1:347] "back" "back" "back" NA ...  
 ..$ morphology.back : chr [1:347] "cortex/unworked" "cortex/unworked" "cortex/unworked" "partly\_retouched" ...  
 ..$ retouch.active.edge : chr [1:347] "YES" "YES" "YES" "YES" ...  
 ..$ retouch.type.edge : chr [1:347] "bifacial" "bifacial" "bifacial" "bifacial" ...  
 ..$ tip.morphology : chr [1:347] "undeterminable" "undeterminable" "undeterminable" "undeterminable" ...  
 ..$ application.Pradnikmethod : chr [1:347] "YES" "NO" "NO" "NO" ...  
 ..$ frequency.application.Pradnikmethod: chr [1:347] "N/A" NA NA NA ...  
 ..$ type.lateral.sharpening.spall : chr [1:347] NA NA NA NA ...  
 ..$ tool.lateralisation : chr [1:347] "sin." "sin." "dex." "sin." ...  
 ..$ length : num [1:347] 72.5 142.8 52.4 48.3 58.9 ...  
 ..$ width : num [1:347] 41.6 69.7 38.2 34 30.5 ...  
 ..$ thickness : num [1:347] 17.8 24.2 20.9 11.6 19.7 ...  
 ..$ weight : num [1:347] 0.058 0.129 0.035 0.022 0.037 ...  
 ..$ perimeter.basis.back : num [1:347] 10.6 18.7 5.7 4.1 9.6 7.6 6.3 8.5 4.6 10.8 ...  
 ..$ perimeter.distal.posterior.part : chr [1:347] "1" "4" "4" " 4.6" ...  
 ..$ perimeter.active.edge : num [1:347] 6.7 11.4 4.7 4.4 4.4 6.4 5.9 5.4 5.9 5.4 ...  
 ..$ perimeter.total : num [1:347] 18.3 34.1 14.1 13.1 15.3 ...  
 ..$ thickness.back : num [1:347] 17.16 22.07 19.03 7.06 20.03 ...  
 ..$ taphonomic.visual.inspection : chr [1:347] "N/A" "N/A" "N/A" "N/A" ...  
 ..$ tool.edges.preservation : chr [1:347] "N/A" "N/A" "N/A" "N/A" ...  
 ..$ macroscopically.visible.use-wear : chr [1:347] "N/A" "N/A" "N/A" "N/A" ...  
 ..$ use-wear.analysis : chr [1:347] "N/A" "N/A" "N/A" "N/A" ...  
 ..$ 3D-scan : chr [1:347] "N/A" "N/A" "N/A" "N/A" ...  
 ..$ schistosity : chr [1:347] "N/A" "N/A" "N/A" "N/A" ...  
 ..$ orientation.schistosity : chr [1:347] NA NA NA NA ...  
 $ Buhlen\_lithic\_analysis.xlsx :'data.frame': 199 obs. of 34 variables:  
 ..$ site : chr [1:199] "Buhlen" "Buhlen" "Buhlen" "Buhlen" ...  
 ..$ ID : chr [1:199] "BU-002" "BU-003" "BU-004" "BU-005" ...  
 ..$ raw.material : chr [1:199] "silicified\_schist" "silicified\_schist" "silicified\_schist" "silicified\_schist" ...  
 ..$ technological.class : chr [1:199] "Keilmesser" "Keilmesser" "Keilmesser" "Keilmesser" ...  
 ..$ artefact.state : chr [1:199] "complete" "complete" "complete" "complete" ...  
 ..$ blank : chr [1:199] "core" "core" "core" "core" ...  
 ..$ morpho.type : chr [1:199] "Bockstein" "Buhlen" "Pradnik" "Balve" ...  
 ..$ cortex : chr [1:199] "YES" "YES" "YES" "YES" ...  
 ..$ cortex.percentage : chr [1:199] "25-50" "<25" "<25" "50-75" ...  
 ..$ cortex.location : chr [1:199] "back" "base" "back" "ventral\_and\_dorsal" ...  
 ..$ morphology.back : chr [1:199] "cortex/unworked" "cortex/partly\_retouched" "cortex/unworked" "cortex/unworked" ...  
 ..$ retouch.active.edge : chr [1:199] "YES" "YES" "YES" "YES" ...  
 ..$ retouch.type.edge : chr [1:199] "bifacial" "bifacial" "bifacial" "bifacial" ...  
 ..$ tip.morphology : chr [1:199] "rounded" "rounded" "rounded" "pointed" ...  
 ..$ application.Pradnikmethod : chr [1:199] "NO" "YES" "YES" "NO" ...  
 ..$ frequency.application.Pradnikmethod: chr [1:199] NA "one" "one" NA ...  
 ..$ type.lateral.sharpening.spall : chr [1:199] NA NA NA NA ...  
 ..$ tool.lateralisation : chr [1:199] "dex." "dex." "dex." "dex." ...  
 ..$ length : num [1:199] 48 58 56.3 69 53.7 ...  
 ..$ width : num [1:199] 35 31 38.8 46 36.2 ...  
 ..$ thickness : num [1:199] 14 18 16 14 17 18 19 31 13 12 ...  
 ..$ weight : num [1:199] 0.0259 0.0337 0.0391 0.0561 0.0367 0.0258 0.0387 0.0733 0.0224 0.0204 ...  
 ..$ perimeter.basis.back : num [1:199] 8.4 8.2 7.5 8.4 8.2 7.6 7.7 9.4 8.1 8.8 ...  
 ..$ perimeter.distal.posterior.part : num [1:199] 0 1.6 2.1 2.2 1 1.5 3.9 2.5 2.4 1 ...  
 ..$ perimeter.active.edge : num [1:199] 5.6 4.7 6.5 8.2 4.4 4.2 5.7 7 5.1 4.7 ...  
 ..$ perimeter.total : num [1:199] 0 11 0 0 0 0 0 0 0 0 ...  
 ..$ thickness.back : num [1:199] 14 11 14 12 17.3 ...  
 ..$ taphonomic.visual.inspection : chr [1:199] "Sharp\_edges\_and\_preserved\_surface" "Sharp\_edges\_and\_preserved\_surface" "Sharp\_edges\_and\_preserved\_surface" "Sharp\_edges\_and\_preserved\_surface" ...  
 ..$ tool.edges.preservation : chr [1:199] "edges\_preserved" "edges\_preserved" "edges\_preserved" "edges\_preserved" ...  
 ..$ macroscopically.visible.use-wear : chr [1:199] "NO" "NO" "NO" "NO" ...  
 ..$ use-wear.analysis : chr [1:199] "NO" "YES" "YES" "NO" ...  
 ..$ 3D-scan : chr [1:199] "YES" "YES" "YES" "YES" ...  
 ..$ schistosity : chr [1:199] "N/A" "NO" "NO" "YES" ...  
 ..$ orientation.schistosity : chr [1:199] NA NA NA "parallel\_to\_the\_active\_edge" ...  
 $ Ramioul\_lithic\_analysis.xlsx:'data.frame': 20 obs. of 34 variables:  
 ..$ site : chr [1:20] "Ramioul" "Ramioul" "Ramioul" "Ramioul" ...  
 ..$ ID : chr [1:20] "R-001" "R-002" "R-003" "R-004" ...  
 ..$ raw.material : chr [1:20] "baltic\_flint" "baltic\_flint" "baltic\_flint" "baltic\_flint" ...  
 ..$ technological.class : chr [1:20] "Keilmesser" "Keilmesser" "scraper" "scraper" ...  
 ..$ artefact.state : chr [1:20] "complete" "complete" "complete" "complete" ...  
 ..$ blank : chr [1:20] "core" "core" "core" "flake" ...  
 ..$ morpho.type : chr [1:20] "Balve" "Klausennische" NA NA ...  
 ..$ cortex : chr [1:20] "YES" "YES" "YES" "YES" ...  
 ..$ cortex.percentage : chr [1:20] "<25" "<25" "25-50" "25-50" ...  
 ..$ cortex.location : chr [1:20] "back" "back" "back" "medial\_dorsa" ...  
 ..$ morphology.back : chr [1:20] "cortex/partly\_retouched" "cortex/unworked" NA NA ...  
 ..$ retouch.active.edge : chr [1:20] "YES" "YES" "YES" "YES" ...  
 ..$ retouch.type.edge : chr [1:20] "bifacial" "semi-bifacial" "semi-bifacial" "unifacial" ...  
 ..$ tip.morphology : chr [1:20] "rounded" "rounded" "rounded" "undeterminable" ...  
 ..$ application.Pradnikmethod : chr [1:20] "YES" "YES" NA NA ...  
 ..$ frequency.application.Pradnikmethod: chr [1:20] "one" "one" NA NA ...  
 ..$ type.lateral.sharpening.spall : num [1:20] NA NA NA NA NA NA NA NA NA NA ...  
 ..$ tool.lateralisation : chr [1:20] "dex." "dex." NA NA ...  
 ..$ length : num [1:20] 50 44 51 42 54 53 76 75 99 52 ...  
 ..$ width : num [1:20] 33 27 31 24 27 31 37 43 42 35 ...  
 ..$ thickness : num [1:20] 16 21 20 9 16 16 21 23 25 14 ...  
 ..$ weight : num [1:20] 0.025 0.02 0.029 0.01 0.016 0.018 0.062 0.066 0.075 0.0017 ...  
 ..$ perimeter.basis.back : num [1:20] 6.7 6.4 6.5 0 0 5.7 9.5 7.3 0 8.2 ...  
 ..$ perimeter.distal.posterior.part : num [1:20] 3 2.5 3.1 0 0 3.1 1.9 4.4 0 2 ...  
 ..$ perimeter.active.edge : num [1:20] 5 4 4.9 0 0 4.4 6.5 7.6 0 4.5 ...  
 ..$ perimeter.total : num [1:20] 0 0 0 0 0 0 0 0 0 0 ...  
 ..$ thickness.back : num [1:20] 16 21 14 0 0 6 21 17 0 5 ...  
 ..$ taphonomic.visual.inspection : chr [1:20] "sharp\_edges\_and\_patinated\_surface" "sharp\_edges\_and\_patinated\_surface" "sharp\_edges\_and\_patinated\_surface" "sharp\_edges\_and\_patinated\_surface" ...  
 ..$ tool.edges.preservation : chr [1:20] "edges\_preserved" "edges\_preserved" "edges\_preserved" "edges\_preserved" ...  
 ..$ macroscopically.visible.use-wear : chr [1:20] "NO" "NO" "NO" "NO" ...  
 ..$ use-wear.analysis : chr [1:20] "YES" "YES" "NO" "YES" ...  
 ..$ 3D-scan : chr [1:20] "YES" "YES" "YES" "YES" ...  
 ..$ schistosity : chr [1:20] "N/A" "N/A" "N/A" "N/A" ...  
 ..$ orientation.schistosity : num [1:20] NA NA NA NA NA NA NA NA NA NA ...

# check pairwisely if the three lines of headers are identical among the datasets  
# merges the data based on the three lines of headers while they get only   
# used in the first CSV file   
comp <- all(sapply(list(names(imp\_data[[1]]), names(imp\_data[[2]])),   
 FUN = identical, names(imp\_data[[3]])))  
merged\_data <- do.call(rbind, imp\_data)  
  
str(merged\_data)

'data.frame': 566 obs. of 34 variables:  
 $ site : chr "Balver\_Höhle" "Balver\_Höhle" "Balver\_Höhle" "Balver\_Höhle" ...  
 $ ID : chr "HE-012" "HE-013" "HE-014" "HE-015" ...  
 $ raw.material : chr "baltic\_flint" "silicified\_schist" "silicified\_schist" "silicified\_schist" ...  
 $ technological.class : chr "Keilmesser" "Keilmesser" "Keilmesser" "Keilmesser" ...  
 $ artefact.state : chr "complete" "semifinished\_product" "complete" "complete" ...  
 $ blank : chr "core" "core" "flake" "core" ...  
 $ morpho.type : chr "Bockstein" "Bockstein" "Balve" "Pradnik" ...  
 $ cortex : chr "YES" "YES" "YES" "N/A" ...  
 $ cortex.percentage : chr "N/A" "N/A" "N/A" NA ...  
 $ cortex.location : chr "back" "back" "back" NA ...  
 $ morphology.back : chr "cortex/unworked" "cortex/unworked" "cortex/unworked" "partly\_retouched" ...  
 $ retouch.active.edge : chr "YES" "YES" "YES" "YES" ...  
 $ retouch.type.edge : chr "bifacial" "bifacial" "bifacial" "bifacial" ...  
 $ tip.morphology : chr "undeterminable" "undeterminable" "undeterminable" "undeterminable" ...  
 $ application.Pradnikmethod : chr "YES" "NO" "NO" "NO" ...  
 $ frequency.application.Pradnikmethod: chr "N/A" NA NA NA ...  
 $ type.lateral.sharpening.spall : chr NA NA NA NA ...  
 $ tool.lateralisation : chr "sin." "sin." "dex." "sin." ...  
 $ length : num 72.5 142.8 52.4 48.3 58.9 ...  
 $ width : num 41.6 69.7 38.2 34 30.5 ...  
 $ thickness : num 17.8 24.2 20.9 11.6 19.7 ...  
 $ weight : num 0.058 0.129 0.035 0.022 0.037 ...  
 $ perimeter.basis.back : num 10.6 18.7 5.7 4.1 9.6 7.6 6.3 8.5 4.6 10.8 ...  
 $ perimeter.distal.posterior.part : chr "1" "4" "4" " 4.6" ...  
 $ perimeter.active.edge : num 6.7 11.4 4.7 4.4 4.4 6.4 5.9 5.4 5.9 5.4 ...  
 $ perimeter.total : num 18.3 34.1 14.1 13.1 15.3 ...  
 $ thickness.back : num 17.16 22.07 19.03 7.06 20.03 ...  
 $ taphonomic.visual.inspection : chr "N/A" "N/A" "N/A" "N/A" ...  
 $ tool.edges.preservation : chr "N/A" "N/A" "N/A" "N/A" ...  
 $ macroscopically.visible.use-wear : chr "N/A" "N/A" "N/A" "N/A" ...  
 $ use-wear.analysis : chr "N/A" "N/A" "N/A" "N/A" ...  
 $ 3D-scan : chr "N/A" "N/A" "N/A" "N/A" ...  
 $ schistosity : chr "N/A" "N/A" "N/A" "N/A" ...  
 $ orientation.schistosity : chr NA NA NA NA ...

# adds indices as row names   
row.names(merged\_data) <- 1:nrow(merged\_data)

# Data analsysis - sorting

## Dimension

# keeps only columns relevant for dimensions and sorts them based on   
# their technological class  
keep\_col <- c(1:2, 4:5, 19:21)  
dimensions <- merged\_data[, keep\_col] %>% arrange(technological.class)  
  
KM\_dimensions <- dimensions[4:333, ]   
PS\_dimensions <- dimensions[493:546, ]   
LSS\_dimensions <- dimensions[334:492, ]

## Perimeter

# keeps only columns relevant for perimeter measurements and sorts them   
# based on their technological class  
keep\_col <- c(1:2, 4:5,7,23:26)  
perimeter <- merged\_data[, keep\_col] %>% arrange(technological.class)  
  
KM\_perimeter <- perimeter[4:333, ] %>% arrange(artefact.state)  
PS\_perimeter <- perimeter[493:546, ]

## Raw material

# keeps only columns relevant for raw material classification and sorts them   
# based on their technological class  
keep\_col <- c(2, 4:5, 3)  
raw\_material <- merged\_data[, keep\_col] %>% arrange(technological.class)  
  
KM\_raw\_material <- raw\_material[4:333, ] %>% arrange(artefact.state)  
PS\_raw\_material <- raw\_material[493:546, ] %>% arrange(artefact.state)  
LSS\_raw\_material <- raw\_material[334:492, ] %>% arrange(artefact.state)

## Cortex + blanks

# keeps only columns relevant for cortex and blank classification and sorts them   
# based on their technological class  
keep\_col <- c(2, 4:5, 6, 8:10)  
cortex\_blanks <- merged\_data[, keep\_col] %>% arrange(technological.class)  
  
KM\_cortex\_blanks <- cortex\_blanks[4:333, ] %>% arrange(artefact.state)  
PS\_cortex\_blanks <- cortex\_blanks[493:546, ] %>% arrange(artefact.state)

## Back

# keeps only columns relevant for back modifications and sorts them based   
# on their technological class  
keep\_col <- c(2, 4:5, 11, 27)  
back <- merged\_data[, keep\_col] %>% arrange(technological.class)  
  
KM\_back <- back[4:333, ] %>% arrange(artefact.state)   
PS\_back <- back[493:546, ] %>% arrange(artefact.state)

## Morpho type

# keeps only columns relevant for morpho type classification and sorts them   
# based on their technological class  
keep\_col <- c(2, 4:5, 7, 19:21)  
morpho.type <- merged\_data[, keep\_col] %>% arrange(technological.class)  
  
KM\_morpho.type <- morpho.type[4:333, ] %>% arrange(artefact.state)  
PS\_morpho.type <- morpho.type[493:546, ] %>% arrange(artefact.state)

## Application ‘Pradnik method’

# keeps only columns relevant for 'morpho type 'Pradnik method' classification   
# and sorts them based on their technological class  
keep\_col <- c(2, 4:5, 15:16)  
Pradnik.method <- merged\_data[, keep\_col] %>% arrange(technological.class)  
  
KM\_Pradnik.method <- Pradnik.method[4:333, ] %>% arrange(artefact.state)  
PS\_Pradnik.method <- Pradnik.method[493:546, ] %>% arrange(artefact.state)

## Lateralisation

# keeps only columns relevant for lateralisation and sorts them based on their  
# technological class  
keep\_col <- c(2, 4:5, 18)  
lateralisation <- merged\_data[, keep\_col] %>% arrange(technological.class)  
  
KM\_lateralisation <- lateralisation[4:333, ] %>% arrange(artefact.state)  
PS\_lateralisation <- lateralisation[493:546, ] %>% arrange(artefact.state)

# Type lateral sharpening spall

# keeps only columns relevant for lateral sharpening spall classification and sorts   
# them based on their technological class  
keep\_col <- c(2, 4:5, 17:18)  
lss\_type <- merged\_data[, keep\_col] %>% arrange(technological.class)  
  
LSS\_type <- lss\_type[334:492, ] %>% arrange(artefact.state)

# Save data

## Format name of output file

file\_out <- "all\_sites\_analysis"

The files will be saved as “~/all\_sites\_analysis.[ext]”.

## Write to XLSX

write.xlsx(list(data = merged\_data, dimensions = dimensions, KM\_dimensions = KM\_dimensions,   
 PS\_dimensions = PS\_dimensions, LSS\_dimensions = LSS\_dimensions, KM\_perimeter =   
 KM\_perimeter, PS\_perimeter = PS\_perimeter, KM\_raw\_material = KM\_raw\_material,  
 PS\_raw\_material = PS\_raw\_material, LSS\_raw\_material = LSS\_raw\_material,   
 KM\_cortex\_blanks = KM\_cortex\_blanks, PS\_cortex\_blanks = PS\_cortex\_blanks,   
 KM\_back = KM\_back, PS\_back = PS\_back, KM\_morpho.type = KM\_morpho.type,   
 PS\_morpho.type = PS\_morpho.type, KM\_Pradnik.method = KM\_Pradnik.method,   
 PS\_Pradnik.method = PS\_Pradnik.method, KM\_lateralisation = KM\_lateralisation,   
 PS\_lateralisation = PS\_lateralisation, LSS\_type = LSS\_type),   
 file = paste0(dir\_out, file\_out, ".xlsx"))

## Save R object

saveObject(merged\_data, file = paste0(dir\_out, file\_out, ".Rbin"))

## Show file information

file\_out <- c(paste0(dir\_out, file\_out, ".xlsx"), paste0(dir\_out, file\_out, ".Rbin"))  
md5\_out <- md5sum(file\_out)  
info\_out <- data.frame(files = basename(names(md5\_out)), checksum = md5\_out,   
 row.names = NULL)

The checksum (MD5 hashes) of the exported files are:

files checksum  
1 all\_sites\_analysis.xlsx 869c4c0ec5dfe5238380f3b8116b88bd  
2 all\_sites\_analysis.Rbin 8ea39ee09113eff29eeaebfe8b886ed3

# sessionInfo() and RStudio version

sessionInfo()

R version 4.0.2 (2020-06-22)  
Platform: x86\_64-w64-mingw32/x64 (64-bit)  
Running under: Windows 10 x64 (build 19041)  
  
Matrix products: default  
  
locale:  
[1] LC\_COLLATE=German\_Germany.1252 LC\_CTYPE=German\_Germany.1252   
[3] LC\_MONETARY=German\_Germany.1252 LC\_NUMERIC=C   
[5] LC\_TIME=German\_Germany.1252   
  
attached base packages:  
[1] tools stats graphics grDevices utils datasets methods   
[8] base   
  
other attached packages:  
[1] dplyr\_1.0.2 chron\_2.3-56 data.table\_1.13.0 R.utils\_2.10.1   
[5] R.oo\_1.24.0 R.methodsS3\_1.8.1 readxl\_1.3.1 openxlsx\_4.1.5   
  
loaded via a namespace (and not attached):  
 [1] Rcpp\_1.0.5 knitr\_1.29 magrittr\_1.5 tidyselect\_1.1.0  
 [5] R6\_2.4.1 rlang\_0.4.7 stringr\_1.4.0 xfun\_0.16   
 [9] ellipsis\_0.3.1 htmltools\_0.5.0 yaml\_2.2.1 digest\_0.6.25   
[13] tibble\_3.0.3 lifecycle\_0.2.0 crayon\_1.3.4 zip\_2.1.1   
[17] purrr\_0.3.4 vctrs\_0.3.4 glue\_1.4.2 evaluate\_0.14   
[21] rmarkdown\_2.3 stringi\_1.5.3 pillar\_1.4.6 compiler\_4.0.2   
[25] cellranger\_1.1.0 generics\_0.0.2 pkgconfig\_2.0.3

RStudio version 1.3.1073.

END OF SCRIPT