```{r}
knitr::opts_knit$set(root.dir = normalizePath("/Users/sankalpm/Documents/QBIO_490_sp23/qbio_490_sankalp/analysis_data/"))

```

```{r}
if (!require("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
  BiocManager::install(version = "3.14")
if (!require("TCGAbiolinks", quietly = TRUE))
  BiocManager::install("TCGAbiolinks")
if (!require("maftools", quietly = TRUE))
  BiocManager::install("maftools")
  library(BiocManager)
  library(TCGAbiolinks)
  library(maftools)
```
```{r}
clin_query <- GDCquery(project = "TCGA-BRCA",
                       data.category = "Clinical",
                       file.type = "xml")
GDCdownload(clin_query)
clinic <- GDCprepare_clinic(clin_query,
                            clinical.info = "patient")
```
```{r}
colnames(clinic)[ colnames(clinic) == "bcr_patient_barcode" ] <-
  "Tumor_Sample_Barcode"
  maf_query <- GDCquery(
    project = "TCGA-BRCA",
    data.category = "Simple Nucleotide Variation",
    access = "open",
    data.type = "Masked Somatic Mutation",
    workflow.type = "Aliquot Ensemble Somatic Variant Merging and Masking"
  )
  GDCdownload(maf_query)
  maf <- GDCprepare(maf_query)
  maf_object <- read.maf(maf = maf,
                         clinicalData = clinic,
                         isTCGA = TRUE)
```

```{r}
rna_query <- GDCquery(project ="TCGA-BRCA",
                      data.category = "Transcriptome Profiling",
                      data.type = "Gene Expression Quantification",
                      workflow.type = "STAR - Counts")
  GDCdownload(rna_query)
  rna_se <- GDCprepare(rna_query)

```

```
In [1]: import os
        os.chdir('/Users/sankalpm/Documents/QBIO_490_sp23/qbio_490_sankalp/analysis_data')
        import cptac
        cptac.download(dataset="Brca")

Out[1]: True

In [ ]:
```