

tgccode

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Intro

This vignette provides examples on how to use the functions within the tgccode package

Load actual datasets

```
rm(list=ls())
library(tgccode)

df_name_and_path <- "~/Desktop/TCGA-CDR-SupplementalTableS1.xlsx"

data_tgca_tumor_stat <- run_import_data(df_name_and_path,1,"tumor_status","TUMOR FREE","WITH TUMOR")
```

Making boxplots

```
plotin(data_tgca_tumor_stat, cancer_type = c("ACC","BRCA") , metadata_col_num= "OS.time",
metadata_col ="race", metadata_levels=c("WHITE","ASIAN") )

plotin(data_tgca_tumor_stat, cancer_type = c("ACC") , metadata_col_num= "age_at_initial_pathologic_diagnosis",
metadata_col ="age_at_initial_pathologic_diagnosis", metadata_levels=c("0-10","11-20","21-30","31-40","41-50","51-60","61-70","71-80","81-90","91-100") )

plotin(data_tgca_tumor_stat, patients= data_tgca_tumor_stat$bcr_patient_barcode[grep("TCGA-B*",data_tgca_tumor_stat$bcr_patient_barcode)],
metadata_col_num= "OS.time", metadata_col ="vital_status", metadata_levels=c("Dead","Alive") )
```

Performing test statistic

```
#Within individuals with BRCA cancer type, comparing the age between stage 1 and stage 4 tumor stage
patho_age <- stat_test(data_tgca_tumor_stat, cancer_type = c("BRCA") , metadata_col_num= "age_at_initial_pathologic_diagnosis",
metadata_col ="age_at_initial_pathologic_diagnosis", metadata_levels=c("0-10","11-20","21-30","31-40","41-50","51-60","61-70","71-80","81-90","91-100") )

#Across all individuals, comparing the age between female and male
gender_age <- stat_test(data_tgca_tumor_stat, patients=data_tgca_tumor_stat$bcr_patient_barcode[grep("TCGA-B*",data_tgca_tumor_stat$bcr_patient_barcode)],
metadata_col_num= "age_at_initial_pathologic_diagnosis", metadata_col ="age_at_initial_pathologic_diagnosis", metadata_levels=c("0-10","11-20","21-30","31-40","41-50","51-60","61-70","71-80","81-90","91-100") )

#Within individuals with BRCA cancer type, comparing survival time between vital status
vita_ostime <- stat_test(data_tgca_tumor_stat, cancer_type = "BRCA", metadata_col_num= "OS.time",
metadata_col ="vital_status", metadata_levels=c("Dead","Alive") )
```