

PAN CANCER USER INTERFACE WITH TCG ANALYZER

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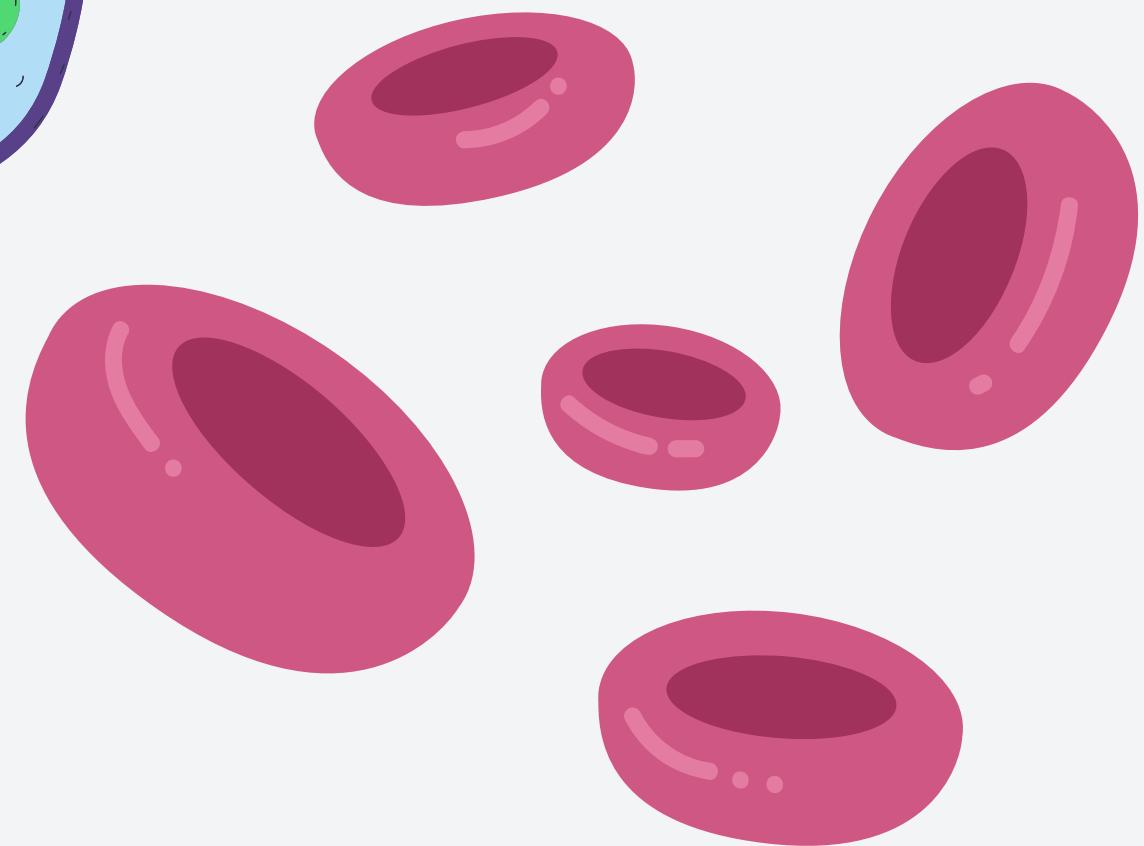
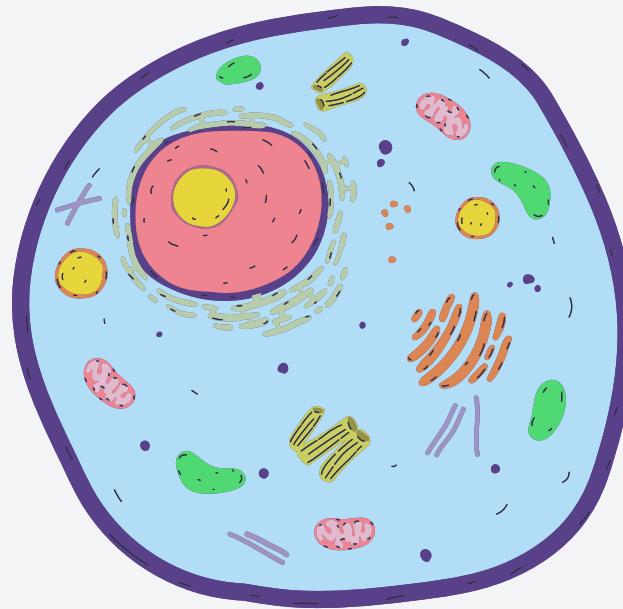
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WHAT IS CANCER

Cancer is a disease in which some of the body's cells grow uncontrollably and spread to other parts of the body.



Cancer is the second-leading cause of death worldwide.

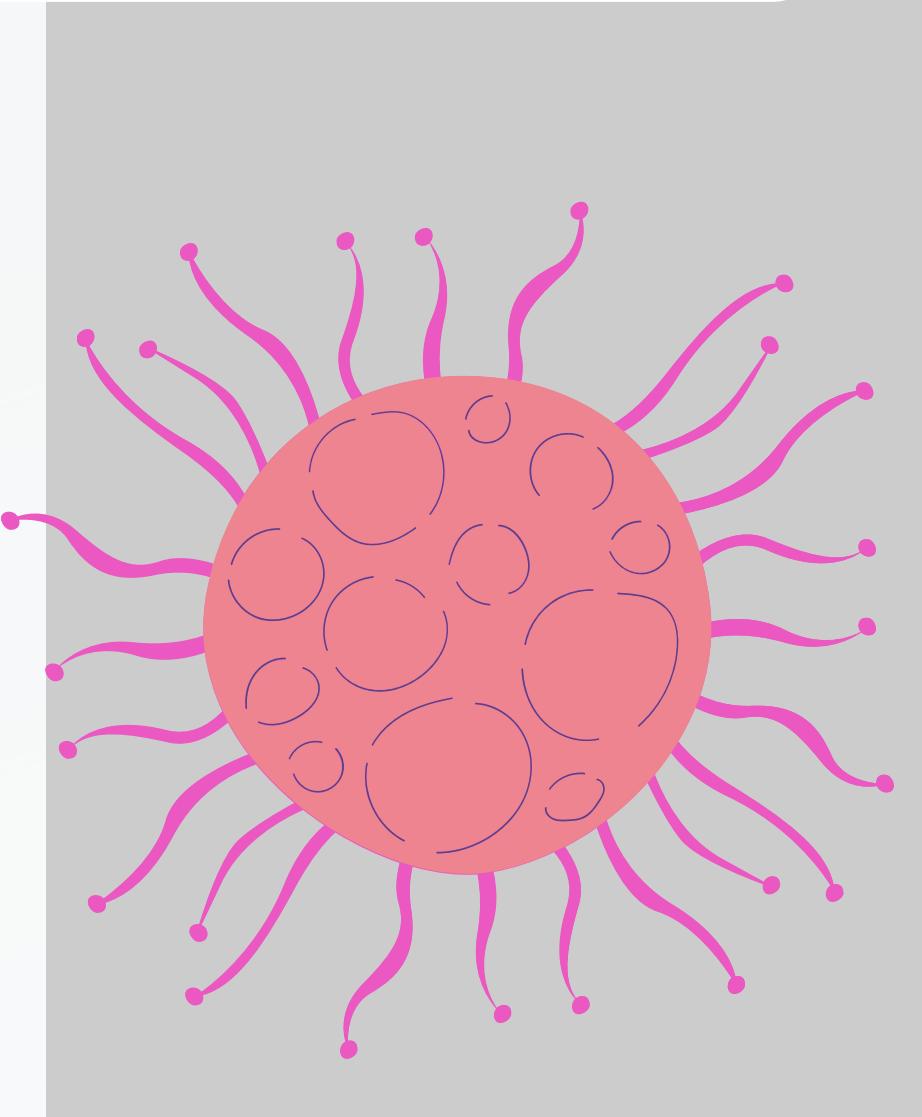


**For this reason, it is very important for us to find
innovative approaches to cancer treatments.**

ABOUT PROJECT

In this project, a pan-cancer interface will be created using the shiny library.

TCGA data will be used when creating the interface.



AIM OF THE PROJECT



The main aim of the project is to facilitate the determination of treatment methods using the developed pan-cancer interface.

We wanted to develop a project that would be beneficial to people's health thanks to our ability to quickly process big data with developing technology.



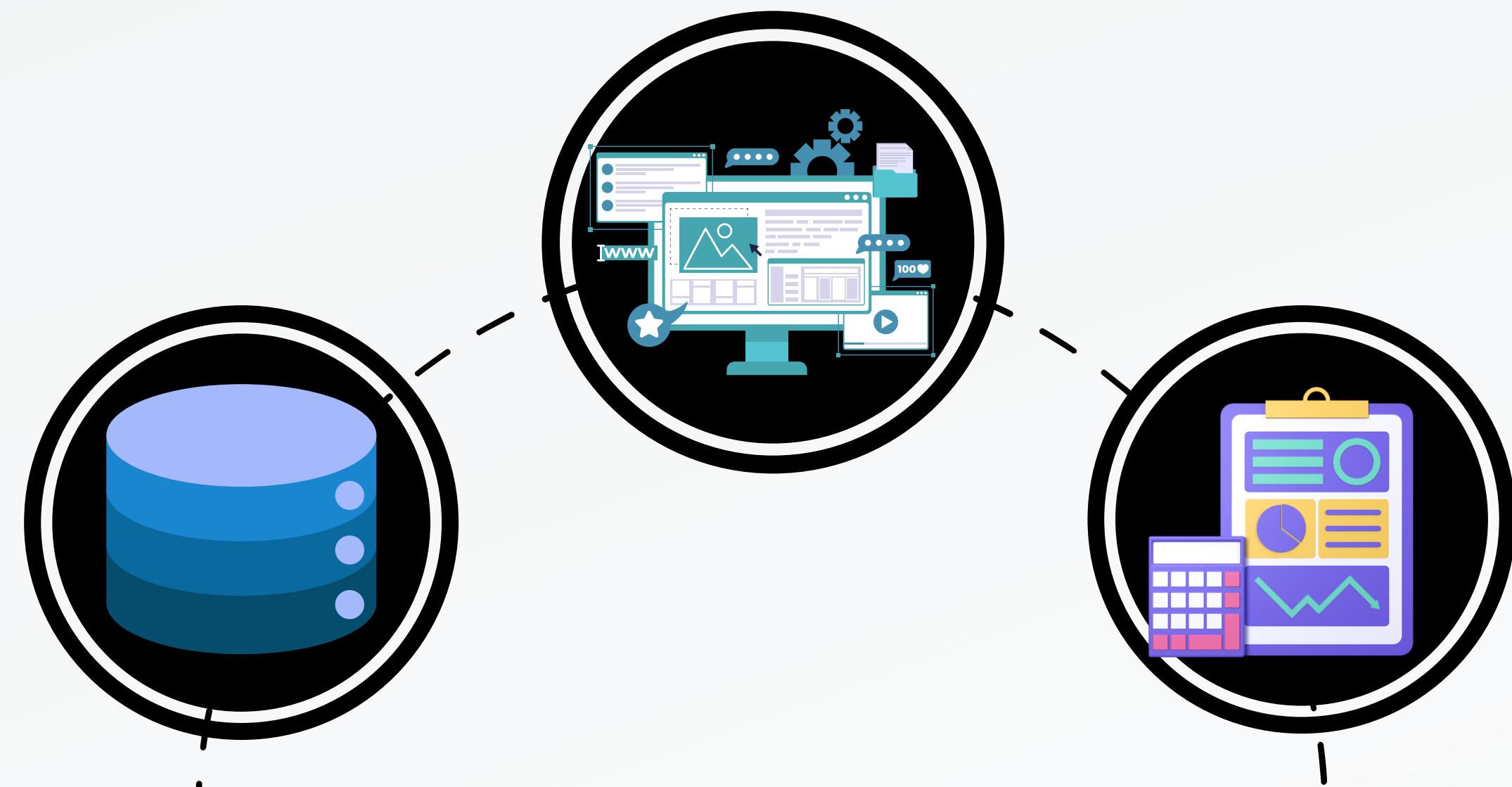
FIRST SEMESTER

TCGAnalyzer
Server

TUBITAK 2209-A

Created Prototype
UI

Examine Data

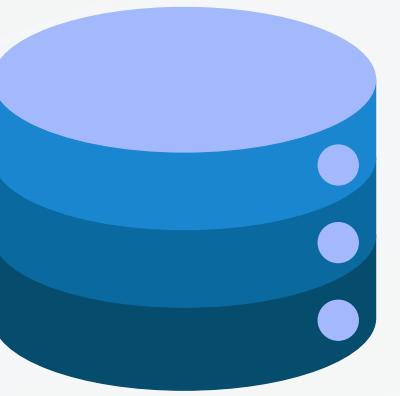




DATA

The data was pulled from TCGA

- and it contains gene mutations of patients belonging to 33 types of cancer.

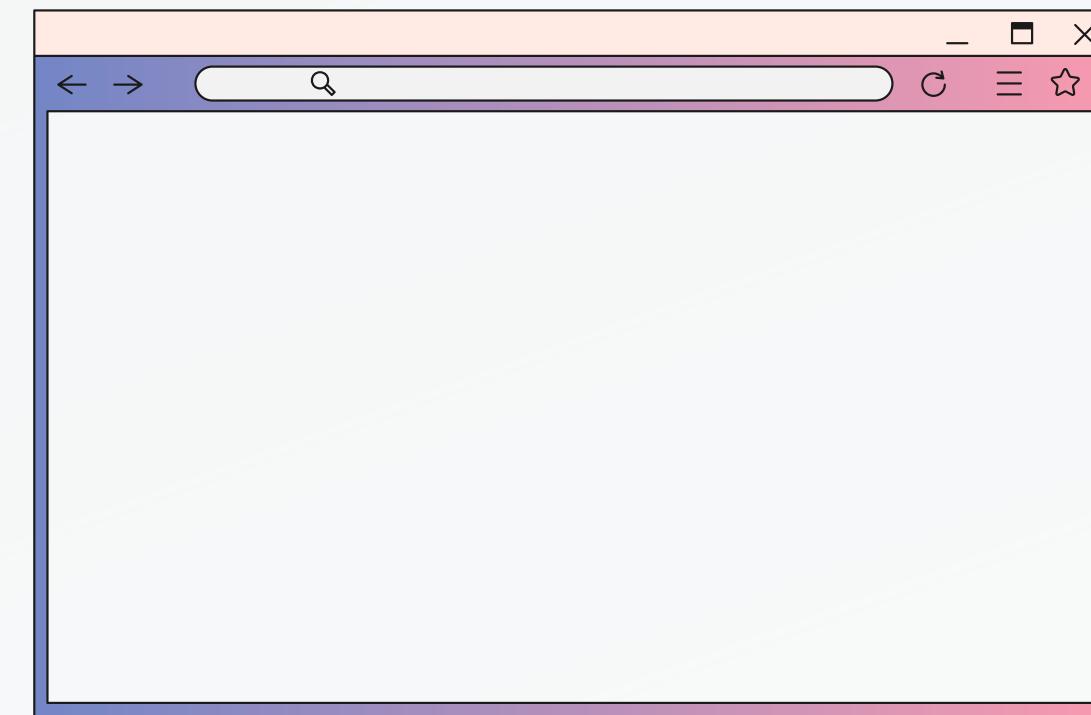


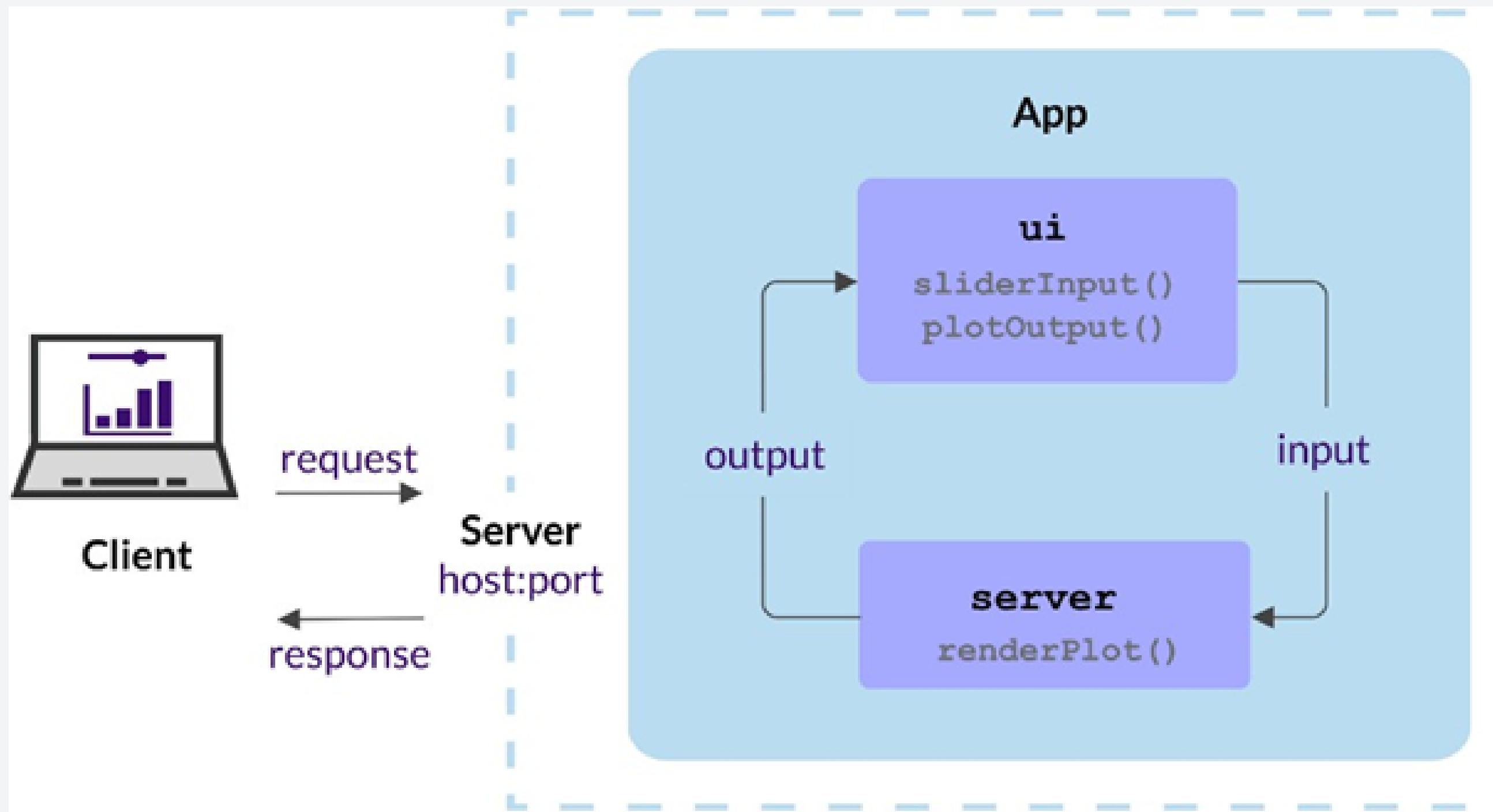
DATA PREPROCESSING

-
- DPLYR
 - R
 - MAFTOOLS

CREATING USER INTERFACE

- SHINY
PHEATMAP





WEB APPLICATION

TCGAnalyzeR Pan-Cancer View

Gene Type

Single Nucleotide

MyGenes

JAK2 LCT

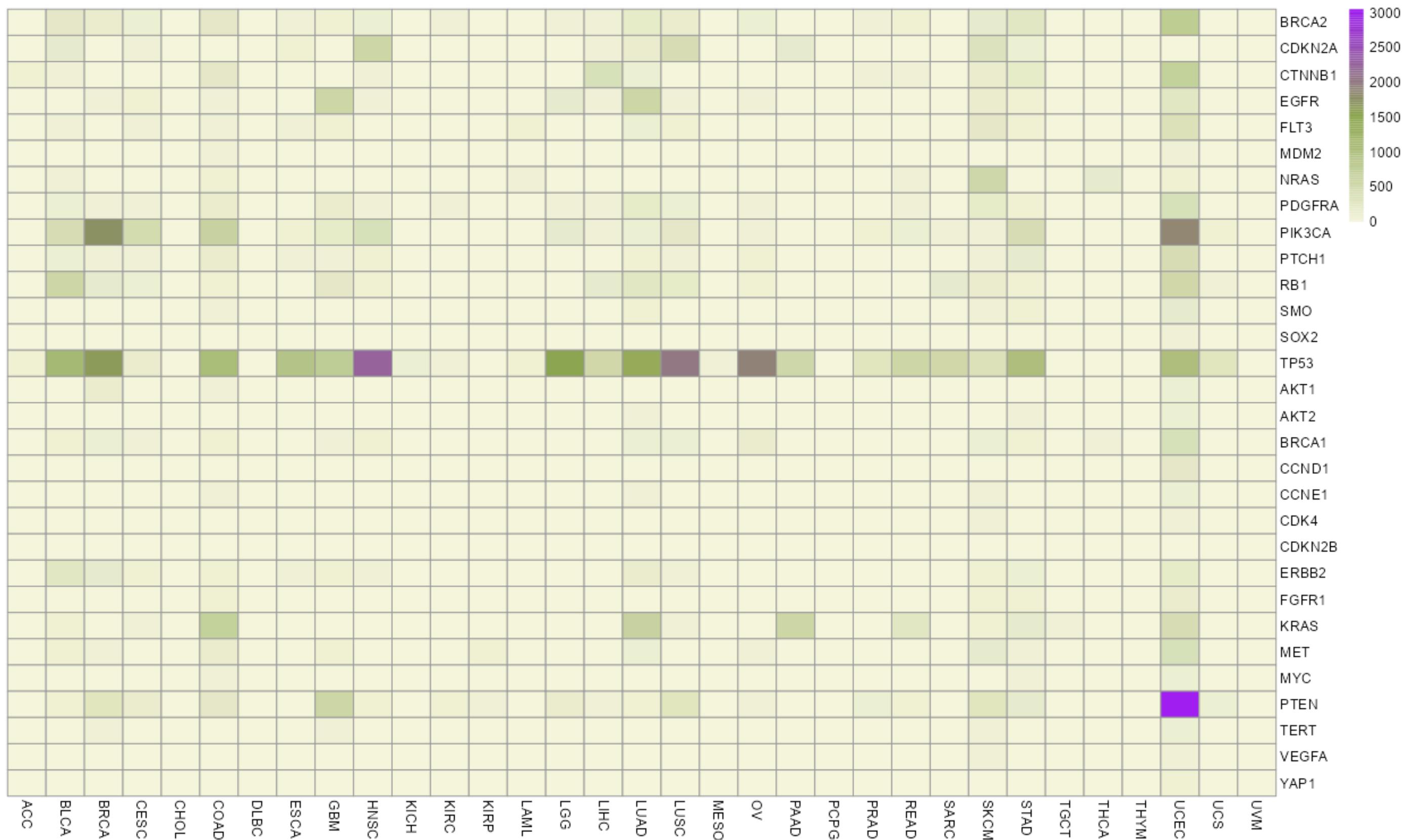
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Filter By

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WEB APPLICATION

Mutation Number of Copy Number Variations Gene Regulation Heatmap



TCGAnalyzeR Pan-Cancer View

Gene Type

Single Nucleotide ▾

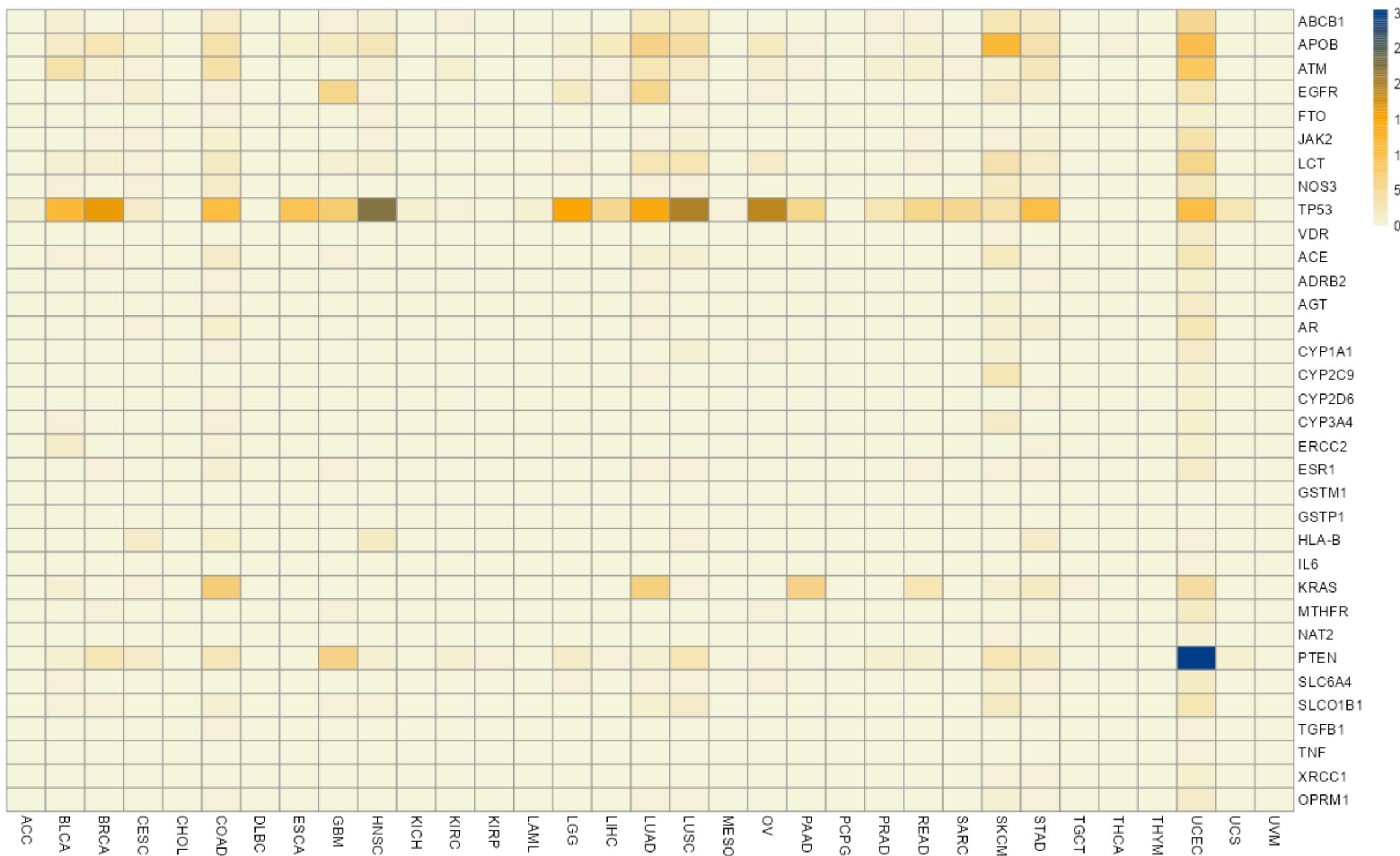
MyGenes

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Mutation Number of Single Nucleotide Gene Regulation Heatmap



CONCLUSION



Our pan-cancer analysis module integrated into TCGAnalyzeR offers a user-friendly interface for exploring genetic mutations across 33 cancer types.

CONCLUSION



This tool aims to facilitate targeted therapies and improve patient outcomes through enhanced data accessibility and analysis.



THANKS

