



SENIOR DESIGN PROJECT

**AYŞE NUR ÖZER
MUĞLA SITKI KOÇMAN UNIVERSITY**

**ADVISOR:
DR. TUĞBA ÖNAL SÜZEK
MUĞLA SITKI KOÇMAN UNIVERSITY
DEPARTMENT OF COMPUTER ENGINEERING**





CONTENT



01

ABOUT PROJECT

02

AIM OF THE PROJECT

03

METHODS

04

WEB APPLICATION

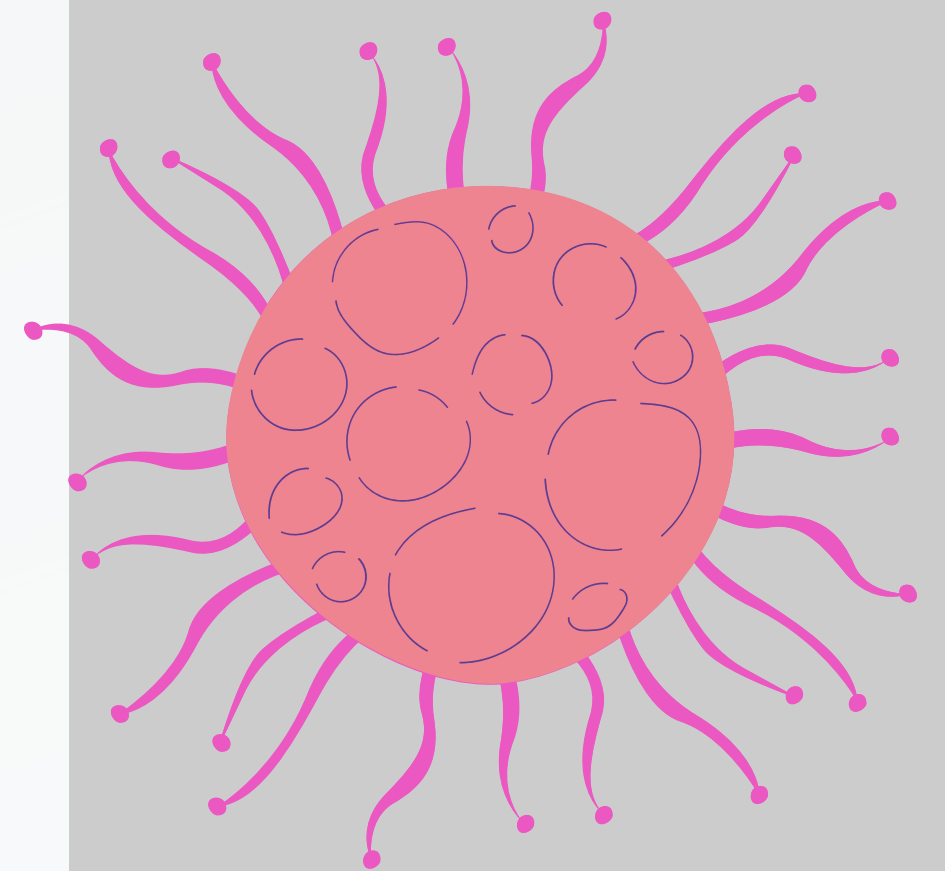
05

WORKFLOW

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.



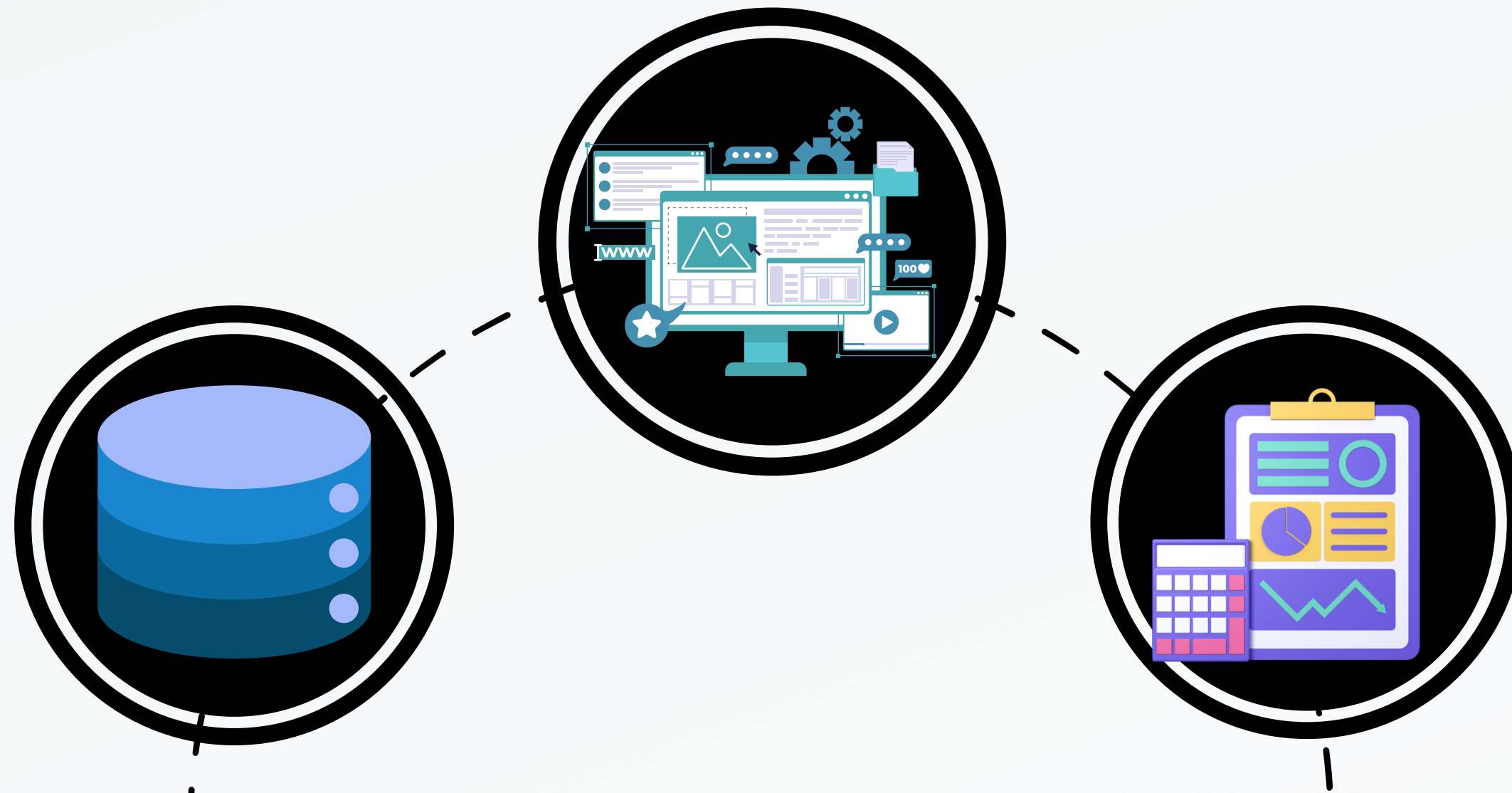
METHODS

Data Preprocessing

Creating User
Interface

User Interface
Integration

Comparison of Data
with TCGAnalyzerR



DATA PREPROCESSING

- **DPLYR**

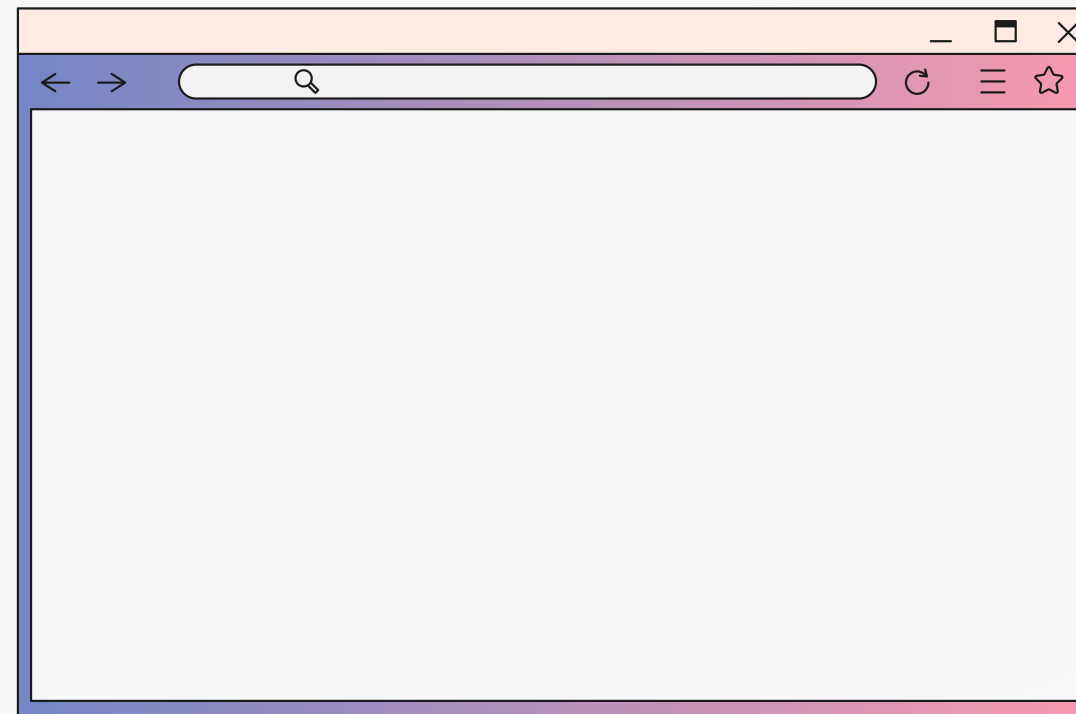
R

- **PANDAS**



CREATING USER INTERFACE

- **SHINY**





USER INTERFACE INTEGRATION

- **ADDING INTERFACE TO
TCGANALYZER**
- 

COMPARISON OF DATA WITH TCGANALYZER

- **DATACOMPY**



WEB APPLICATION

MyGenes

-

+ Add

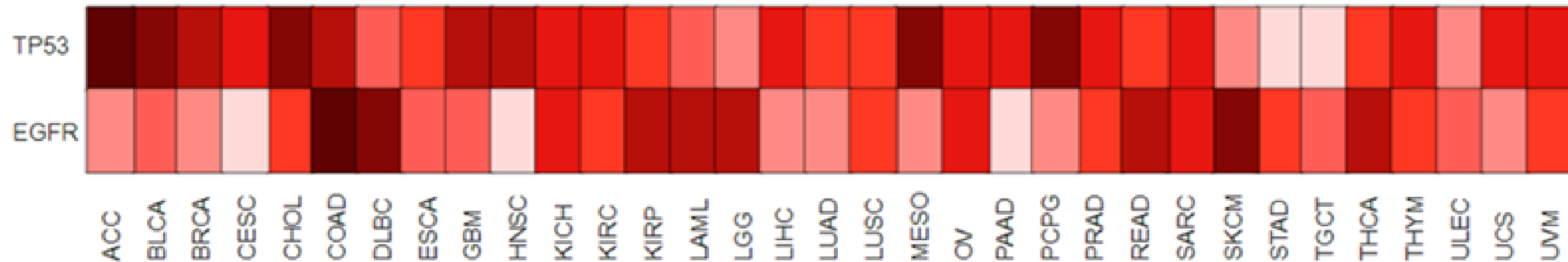
Single Nucleotid

Copy Number Var

Transcriptome

TCGAnalyzeR Pan-Cancer View

Percent of Mutated Patients HeatMap



Filter By

MSI

Immune

iclust

WEB APPLICATION

MyGenes

-

+ Add

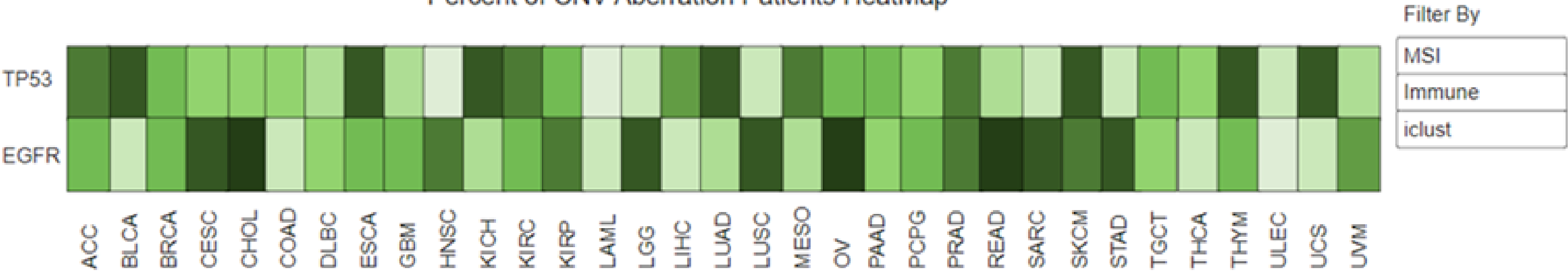
Single Nucleotid

Copy Number Var

Transcriptome

TCGAnalyzerR Pan-Cancer View

Percent of CNV Aberration Patients HeatMap



WEB APPLICATION

MyGenes

-

+ Add

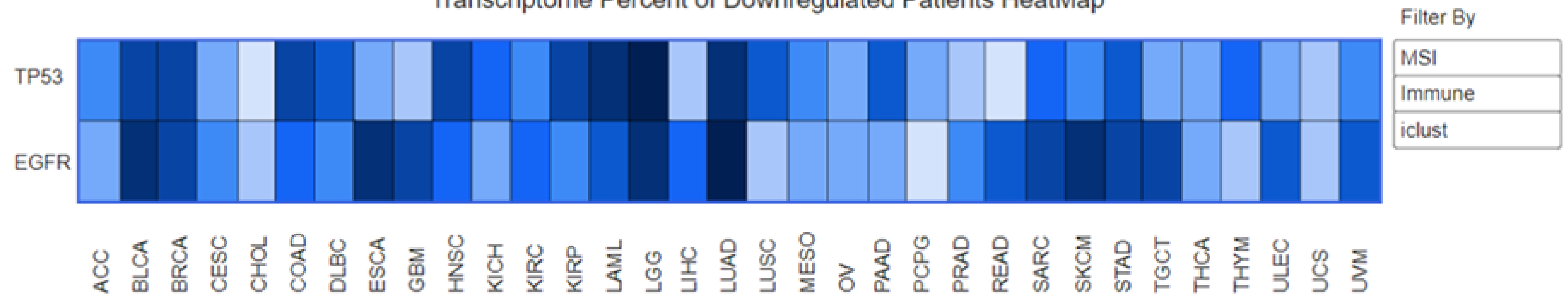
Single Nucleotid

Copy Number Var

Transcriptome

TCGAnalyzeR Pan-Cancer View

Transcriptome Percent of Downregulated Patients HeatMap



WEB APPLICATION

MyGenes

+

+ Add

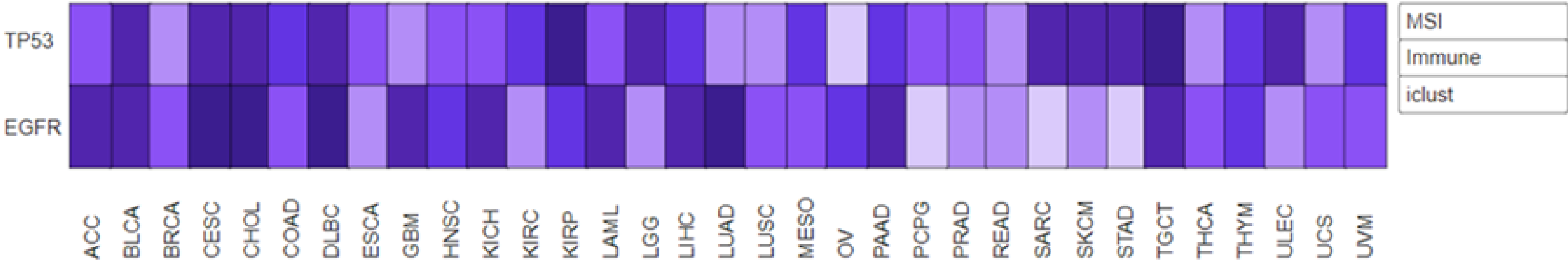
Single Nucleotid

Copy Number Var

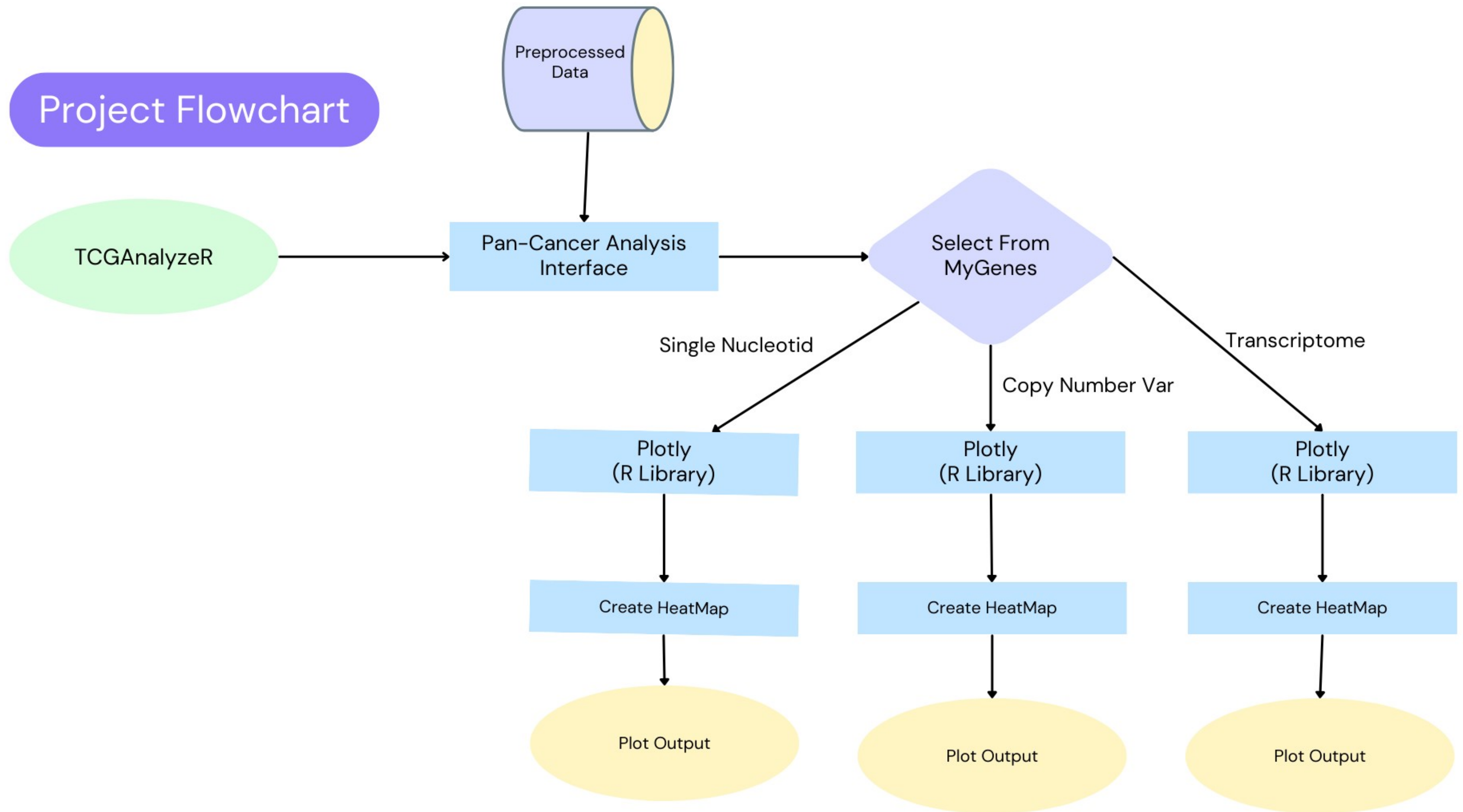
Transcriptome

TCGAnalyzeR Pan-Cancer View

Transcriptome Percent of Upregulated Patients HeatMap



Project Flowchart



THANKS

