

## Part 1: Review Questions

### General Concepts

1. What is TCGA and why is it important?

The Cancer Genome Atlas (TCGA), founded in December of 2005, is a cancer genomics program hosted by the National Cancer Institute and the National Human Genome Research Institute. The publicly available data from this project includes genomic, epigenomic, transcriptomic, and proteomic data. This data was collected from 20,000 different samples that span 33 different cancer types. TCGA helped establish the importance of cancer genomics, transformed our understanding of cancer, and even begun to change how the disease is treated in the clinic.

2. What are some strengths and weaknesses of TCGA?

TCGA has a massive data collection which was collected from 20,000 different samples that span 33 different cancer types. However, its data can sometimes be spotty because almost all of the samples are primarily untreated, without any response data and short follow up.

### Coding Skills

1. What commands are used to save a file to your GitHub repository?

Git status, git add, git commit, git push

2. What command(s) must be run in order to use a package in R?

Install.packages("the Package")

Library("the Package")

3. What command(s) must be run in order to use a *Bioconductor* package in R?

BiocManager::install("MyPackage")

4. What is boolean indexing? What are some applications of it?

Boolean indexing is using to filter data through the use of boolean vectors. We can apply Boolean indexing when subsetting data according to certain conditions.

5. Draw a mock up (just a few rows and columns) of a sample dataframe. Show an example of the following and explain what each line of code does.

a. an `ifelse()` statement

b. boolean indexing

Patient	Sex	Age
1	Men	20
2	Women	35
3	Women	15
4	Men	36

```
Sex_mask<-ifelse(dataframe@sex=="Men",T,F)
```

*Create a Boolean vector which is true for men and false for women*

```
Dataframe_men<-dataframe[sex_mask,]
```

*Apply the boolean mask to new dataframe which only has men*