Three stages of reproducibility of given data



**Folder Structure in each stage (** Folder Structure has been implemented in Question1\_Project\_Structure folder in the repository**)**

We create a folder named Strength\_Analysis and in that, we add subfolders data\_raw, data\_clean, results, and src.

**data\_raw** folder contains all the data files and metadata that we have collected during data collection i.e in stage 1

**data\_clean** folder contains all the data files and metadata that have been cleaned and processed in stage 2 which will be produced by clean script in this project

**results** folder contains documentation files that have been generated as a result of the analysis done by the analysis script written in the source folder

**src** foldercontains scripts that are written to process, clean, analyze, visualize the data

**Stage 1**

Strength\_Analysis

|— data\_raw

|—grip\_strength\_frailty.csv

|—readme.txt (this has metadata)

|— data\_clean

|— results

|— src

**Stage 2**

Strength\_Analysis

|— data\_raw

|—grip\_strength\_frailty.csv

|—readme.txt (this has metadata)

|— data\_clean

|—grip\_strength\_frailty.csv (this file is created by clean script in src folder)

|—readme.txt (this has metadata)

|— results

|— src

|—data\_clean.py

**Stage 3**

Strength\_Analysis

|— data\_raw

|—grip\_strength\_frailty.csv

|—readme.txt (this has metadata)

|— data\_clean

|—grip\_strength\_frailty.csv (this file is generated by data\_clean script in src folder)

|—readme.txt (this has metadata)

|— results

|—result.txt

|— src

|—clean\_data.py

|—analysis.py

By analysis of the given data with heatmap corelation, we can say there is corelation between weight and fraility

