

H.w1 by Daniel Safavisohi

Using Python libraries like Pandas and NumPy, I find that:

- Number of unique mutations contained in the data file is 7529.
- Number of individual samples contained in the data file is 271.
- Number of mutations for individual C1 is 4.
- Number of mutations for individual NC1 is 155.
- The average number of mutations per individual is 59.33.
- The minimum and maximum number of mutations per individual are 0 and 1757, respectively.
- Number of individuals who have a mutation in the 'BRAF' gene is 0.
- Number of individuals who have a mutation in the 'KRAS' gene depends on gene. There are 4 genes that have KRAS in their name, and the number of individuals with mutations are 2, 3, 5 and 22, respectively.
- The average number of individuals per mutation is 2.14.
- The minimum and maximum number of individuals per mutation are 1 and 24, respectively.