Introduction into machine learning and analysis of Breast Cancer Proteomes

Theme09 - Introduction to Machine Learning

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October 5, 2022
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Abstract

the data were used to assess how the mutations in the DNA are affecting the protein expression landscape in breast cancer. Genes in our DNA are first transcribed into RNA molecules which then are translated into proteins. Changing the information content of DNA has impact on the behavior of the proteome, which is the main functional unit of cells, taking care of cell division, DNA repair, enzymatic reactions and signaling etc. my question is: Are there different ways to categorize breast cancer based on protein expression data, with machine learning being used to classify them without using the pam50 proteins?

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List of Abbreviations

EDA	Exploratory Data Analysis
TCGA	The cancer Genome Atlas Program
CPTAC	Clinical Proteomic Tumor Analysis Consortium
DNA	Deoxyribonucleic Acid
RNA	Ribonucleic Acid

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When looking at the dimensions of the data set we can see there are allot of proteins see table 1

Row.names	Tumor	Tumor..T1.Coded	AJCC.Stage	Vital.Status	NP_958782
TCGA-A2-A0CM	T2	T_Other	Stage IIA	DECEASED	0.6834
TCGA-A2-A0D2	T2	T_Other	Stage IIB	LIVING	0.1075
TCGA-A2-A0EQ	T2	T_Other	Stage IIA	LIVING	-0.9127
TCGA-A2-A0EV	T1	T1	Stage IA	LIVING	0.453
TCGA-A2-A0EX	T3	T_Other	Stage IIB	LIVING	1.185
TCGA-A2-A0EY	T2	T_Other	Stage IIB	LIVING	1.175

```
## number of rows: 77 number of columns: 9204
```

after this first assessment of the data we started looking at the number of missing values as seen in the figures' fig 1 and 2 below

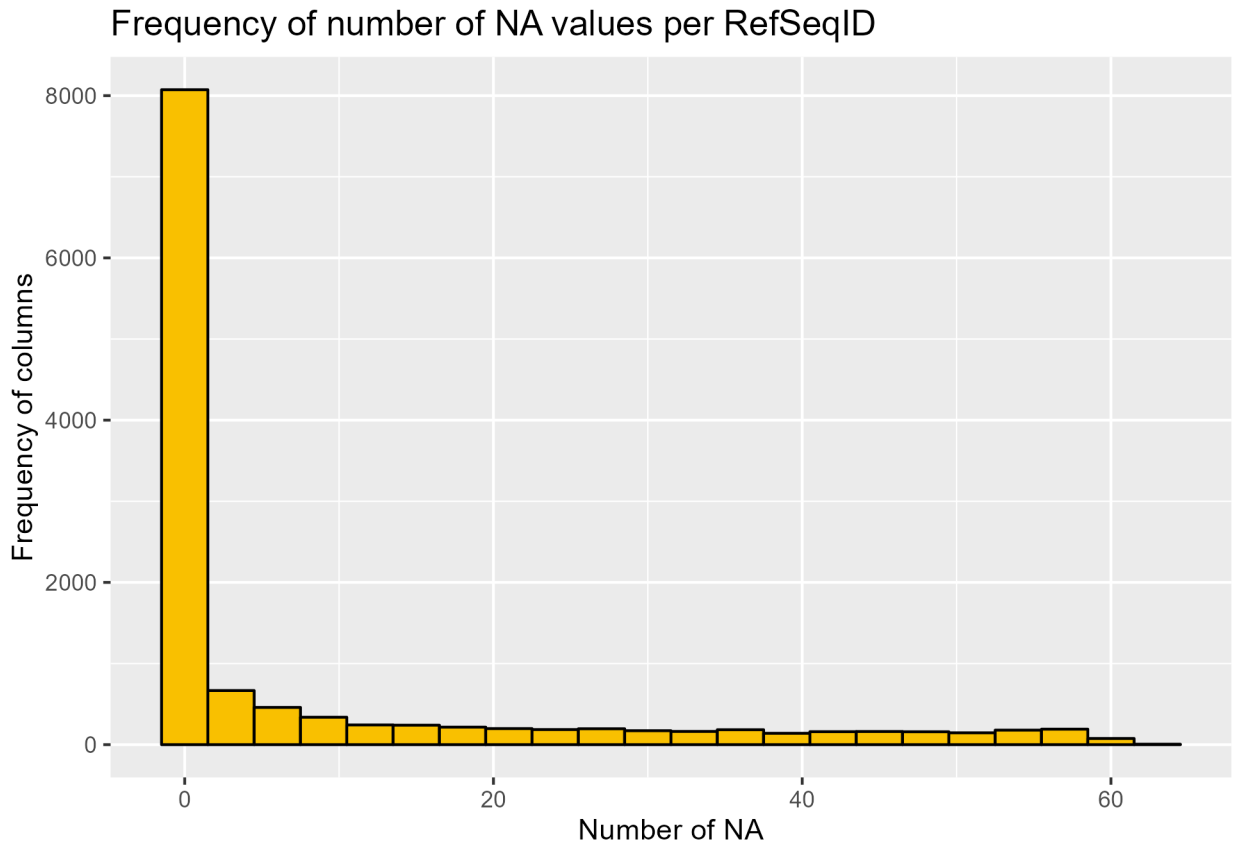

Figure 1: figure 1

as we can see in these figures 1 and 2 the distribution is very much to the left where a lot of proteins have one or only two missing values, further more there are still a couple of proteins that have a high number of missing values these are to be filtered out because this can create a false set of results when we are using

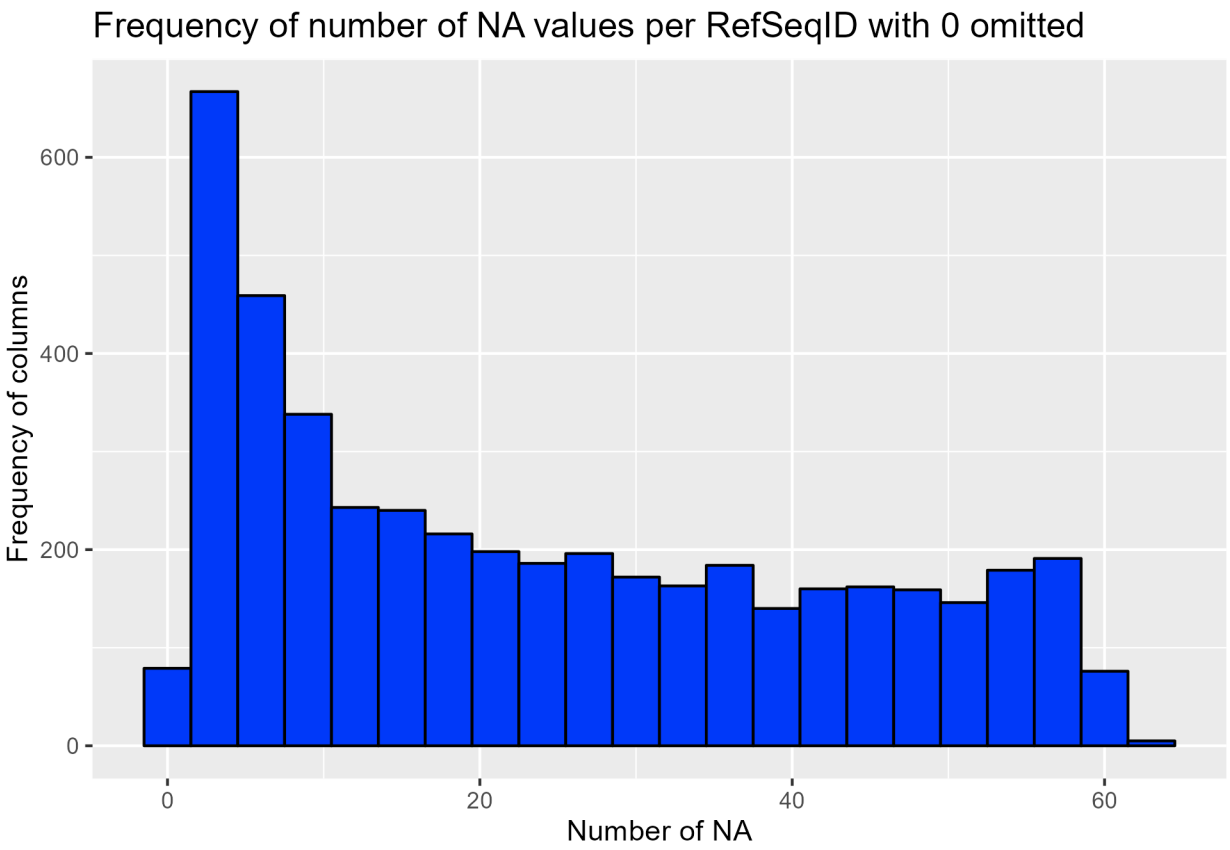

Figure 2: figure 2

them in our machine learning algoritme for clustering them o there cancer stage. so to further see how the data is we took the distribution of a couple of proteins in a multi boxplot as seen in figure 3

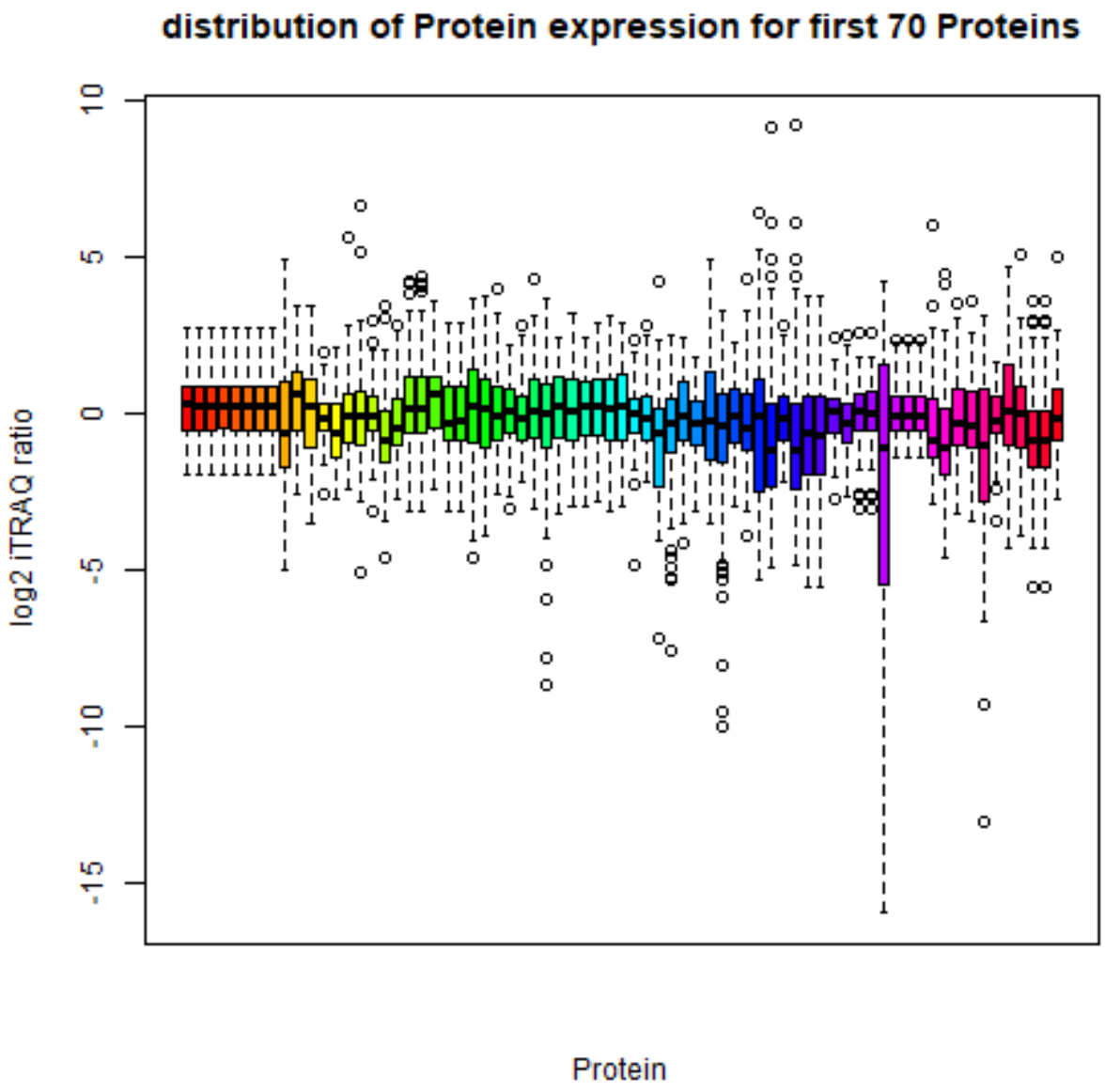

Figure 3: figure 3

in this figure 3 we can clearly see that for the first 70 protein that most have a distribution of their log2 itraq expression between 5 and -5 but there are some that have higher numbers. to further make sense of all the 12 to 9 thousand proteins in the data we calculated the standard deviation of them see figure 4

in this figure 4 we compared the normal data set and the one filterd that has had protein with more tha 10% of their values missing removed. in it we can clearly see that a lot of proteins with high deviation are removed from the data. to make a further analyse of these samples

in this figure 5 we can see how the diffrent samples are spread according to there cancer stages.

Figure 4: figure 4

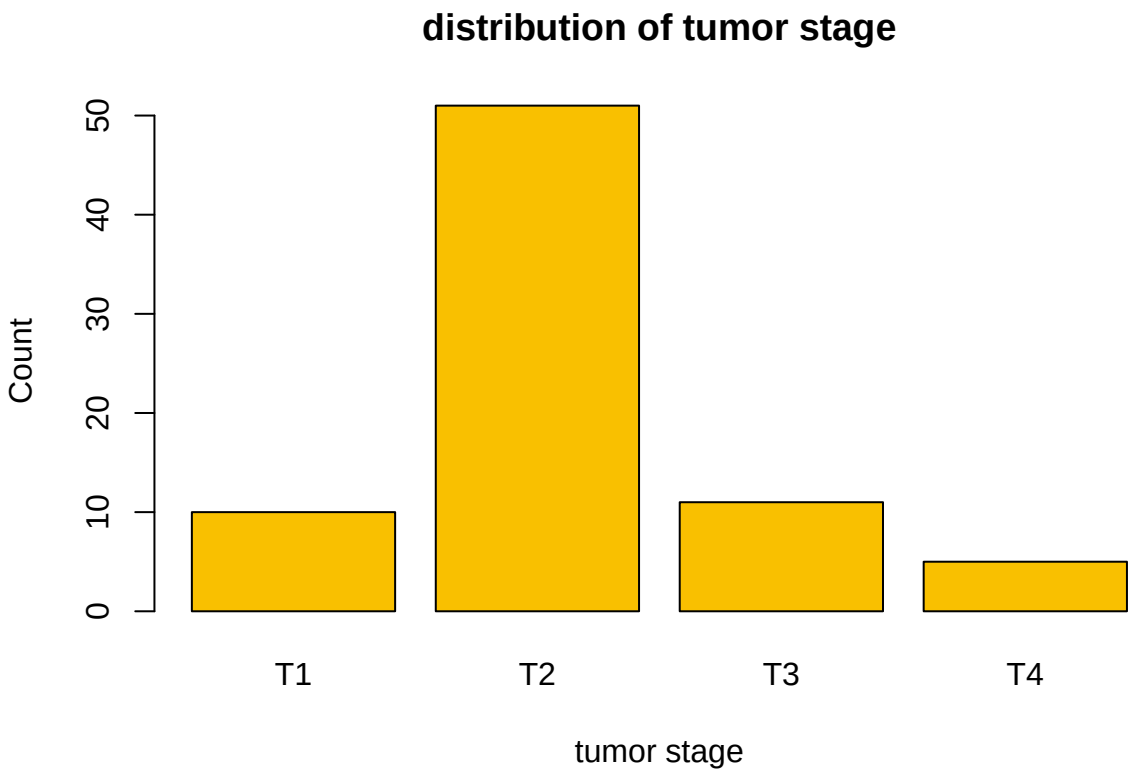

Figure 5: distribution of amount of samples per tumor stage

4 Discussion and Conclusion

in the results section we can see from the figures 1 and two that although the data set was supplied with the label as high quality there are still proteis in the data with more tha 10% of there expression values missing, this combined with the need for using the expressing data with the clinical categorical data, the sample names needed to be changed to be compared. all this wasnt something to be expecting of high quality data. also in figure 5 it is clearlyt visible that the catagorisation of the tumor stage there are allot of T2 stages in the samples than any other.

5 References

Mertins, Philipp, D R Mani, Kelly Ruggles, Michael Gillette, Karl Clauser, Pei Wang, Xianlong Wang, et al. 2016. "Proteogenomics Connects Somatic Mutations to Signaling in Breast Cancer." *Nature* 534 (May). https://doi.org/10.1038/nature18003.

6 Appendices