Classifying Breast Cancer Benign or Malignnant

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Abbreviations

FNA	Fine needle aspiration
PCA	Principal component analysis

Contents

1 Introduction

Breast cancer is a major health threat for women. In 2020 it was the most commonly diagnosed cancer with 11.7% of all newly diagnosed cancer cases being breast cancer. Furthermore it is the leading cause of cancer death in females with 685,000 deaths (15.5% of all female cancer deaths) in 2020 [1]. Early detection of breast cancer is a crucial factor in the prognosis and survival rate of the patients [2].

Fine needle aspiration (FNA) is a type of biopsy used to collect a sample of cells from a lump or mass. This sample can be viewed under a microscope and different cytological characteristics can be observed. FNA is a cost-effective, fast and complication-free technique to investigate a lump or mass [3]. But even though some of the cytological characteristics observed with FNA show a statistical significant difference between benign and malignant samples, not one single characteristic can be used to accurately separate the benign from the malignant samples [4]. If breast FNA samples are used to triage possible breast cancer patients it is of utmost importance to have a high level of certainty in determining which of the samples are malignant. It is very important not to classify a malignant sample as benign, as those patients will not go for further examination and treatment. The other way around, classifying a benign sample as malignant, is less disastrous, as the further examination of the patients will identify those samples as benign.

To distinguish the malignant from the benign samples the practice of data mining might be able to help. Data mining is a modern technique used to find patterns in large batches of data. Between January of 1989 and November 1991 Dr. William H. Wolberg from the University of Wisconsin Hospitals has collected 699 breast FNA samples. Of these samples nine cytological characteristics were scored on a scale from 1 to 10 with 1 being the closest to benign and 10 being the most to anaplastic [5]. These nine characteristics are all considered to differ significantly between benign and malignant samples [4]. In the *Breast Cancer Wisconsin (Original) Data Set* that was assembled from this data, Dr. Wolberg added the correct classification to each sample: benign or malignant [6]. This report will revolve around determining whether this data set is well suited for the purpose of data mining and cleaning it up where needed.

2 Results

The data found in the *Breast Cancer Wisconsin (Original) Data Set* is described in table 1, it can be seen that every sample, also called an instance, is comprised of one sample code number, nine cytological characteristic scores and a class label. This data set has a total of 699 instances.

Table 1: Attribute Information from the Breast Cancer Wisconsin (Original) Data Set

Column	Attribute	Unit	Description
1	Sample code number	id number	Unique number given to each sample
2	Clump Thickness	1-10	Assesses if cells are mono or multi-layered
3	Uniformity of Cell Size	1-10	Evaluate the consistency in size of the cells in the sample
4	Uniformity of Cell Shape	1-10	Evaluate the consistency in shape of the cells in the sample
5	Marginal Adhesion	1-10	Quantifies proportion of cells that stick together
6	Single Epithelial Cell Size	1-10	Measures the enlargement of epithelial cells size
7	Bare Nuclei	1-10	Proportion of nuclei surrounded by cytoplasm versus those that are not
8	Bland Chromatin	1-10	Rates the uniform texture of the nucleus in a range from fine to coarse
9	Normal Nucleoli	1-10	Determines whether the nucleoli are small and barely visible or larger, more visible, and more plentiful
10	Mitoses	1-10	Describes the level of mitotic activity
11	Class	2 or 4	Classification: 2 for benign and 4 for malignant

The cytological characteristics of breast FNAs (seen in rows 2-10) get a score from 1 to 10 by an examining physician with 1 being the closest to benign and 10 the most anaplastic.

Duplicated data

While inspecting the instances of the data set it became apparent that there were a lot of duplicated sample code numbers, even thought these are supposed to be unique. There are 100 instances that share their sample code number with at least 1 other instance and there are 46 sample code numbers that are found at least twice in the data set. In table 2 and table 3 all the instances with duplicated sample code numbers are displayed. In some cases not only the sample code number is duplicated, but every attribute of the instance is the exact same as another instance. In tables 2 and 3 the rows with the instances with sample code numbers that have an exact copy are colored red.

When inspecting these tables it can be seen that the duplicated data is sometimes in consecutive rows, but not always. It can also be seen that most of the instances with duplicated sample code numbers have the same class label, but not always. Most duplicates come in pairs, but they also come in bigger groups, up to 6 instances with the same sample code number. Since no reason can be found as to why these double sample code numbers and instances exist, it can not be verified that these samples are not from the same origin. Therefore the choice has been made to remove all but one of every duplicate sample code number to guarantee the uniqueness of every sample.

Missing data

In table 4 all the instances that have at least one missing attribute are shown. It can be seen that there are 16 instances that do not have a complete record, all of them missing the *Bare Nuclei* attribute. Since this concerns only a fraction of the total number of instances (less than $\frac{1}{40}$) and since it is undesirable that missing attributes will influence the data mining the choice has been made to delete these instances from the data set.

The order of removing data

The missing data will be removed from the data set before the instances with duplicated sample code numbers are removed. This is done so that when one of the instances with a duplicated sample code number has missing data the other instance of this sample code number can be kept in the data. If it were to be done the other way around it could happen that an instances with a duplicated sample code number with a full record would be removed and an instance with missing data kept in the data, only for the instance with the missing data to be removed in the next processing step. After these filtering steps there are 630 instances left in the data set.

Table 2: Instances with duplicate sample code number (the rows with the instances with sample code numbers that have an exact copy are colored red)

	Sample code number	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	Normal Nucleoli	Mitoses	Class
268	320675	3	3	5	2	3	10	7	1	1	Malignant
273	320675	3	3	5	2	3	10	7	1	1	Malignant
270	385103	1	1	1	1	2	1	3	1	1	Benign
576	385103	5	1	2	1	2	1	3	1	1	Benign
272	411453	5	1	1	1	2	1	3	1	1	Benign
608	411453	1	1	1	1	2	1	1	1	1	Benign
684	466906	1	1	1	1	2	1	1	1	1	Benign
685	466906	1	1	1	1	2	1	1	1	1	Benign
372	493452	1	1	3	1	2	1	1	1	1	Benign
373	493452	4	1	2	1	2	1	2	1	1	Benign
291	560680	1	1	1	1	2	1	1	1	1	Benign
375	560680	3	1	2	1	2	1	2	1	1	Benign
690	654546	1	1	1	1	2	1	1	1	8	Benign
691	654546	1	1	1	3	2	1	1	1	1	Benign
578	695091	1	1	1	1	2	1	2	1	1	Benign
692	695091	5	10	10	5	4	5	4	4	1	Malignant
315	704097	1	1	1	1	1	1	2	1	1	Benign
339	704097	1	1	1	1	1	1	2	1	1	Benign
322	733639	3	1	1	1	2	NA	3	1	1	Benign
323	733639	3	1	1	1	2	1	3	1	1	Benign
443	734111	1	1	1	3	2	3	1	1	1	Benign
444	734111	1	1	1	1	2	2	1	1	1	Benign
526	769612	3	1	1	2	2	1	1	1	1	Benign
527	769612	4	1	1	1	2	1	1	1	1	Benign
338	798429	1	1	1	1	2	1	3	1	1	Benign
528	798429	4	1	1	1	2	1	3	1	1	Benign
345	822829	7	6	4	8	10	10	9	5	3	Malignant
613	822829	8	10	10	10	6	10	10	10	10	Malignant
698	897471	4	8	6	4	3	4	10	6	1	Malignant
699	897471	4	8	8	5	4	5	10	4	1	Malignant
5	1017023	4	1	1	3	2	1	3	1	1	Benign
253	1017023	6	3	3	5	3	10	3	5	3	Benign
9	1033078	2	1	1	1	2	1	1	1	5	Benign
10	1033078	4	2	1	1	2	1	2	1	1	Benign
536	1061990	1	1	3	2	2	1	3	1	1	Benign
619	1061990	4	1	1	1	2	1	2	1	1	Benign
30	1070935	1	1	3	1	2	1	1	1	1	Benign
31	1070935	3	1	1	1	1	1	2	1	1	Benign
43	1100524	6	10	10	2	8	10	7	3	3	Malignant
254	1100524	6	10	10	2	8	10	7	3	3	Malignant
48	1105524	1	1	1	1	2	1	2	1	1	Benign
469	1105524	4	1	1	1	2	1	1	1	1	Benign
388	1114570	5	3	3	2	3	1	3	1	1	Benign
389	1114570	2	1	1	1	2	1	2	2	1	Benign
62	1115293	1	1	1	1	2	2	2	1	1	Benign
491	1115293	1	1	1	1	2	1	1	1	1	Benign
63	1116116	9	10	10	1	10	8	3	3	1	Malignant
255	1116116	9	10	10	1	10	8	3	3	1	Malignant
65	1116192	1	1	1	1	2	1	2	1	1	Benign
538	1116192	5	1	2	1	2	1	3	1	1	Benign

Table 3: Instances with duplicate sample code number (the rows with the instances with sample code numbers that have an exact copy are colored red) continued

	Sample code number	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	Normal Nucleoli	Mitoses	Class
82	1143978	4	1	1	2	2	1	2	1	1	Benign
83	1143978	5	2	1	1	2	1	3	1	1	Benign
94	1158247	1	1	1	1	2	1	2	1	1	Benign
394	1158247	1	1	1	1	1	1	1	1	1	Benign
105	1168736	10	10	10	10	10	1	8	8	8	Malignant
256	1168736	5	6	6	2	4	10	3	6	1	Malignant
109	1171710	1	1	1	1	2	1	2	3	1	Benign
110	1171710	6	5	4	4	3	9	7	8	3	Malignant
116	1173347	1	1	1	1	2	5	1	1	1	Benign
117	1173347	8	3	3	1	2	2	3	2	1	Benign
121	1174057	1	1	2	2	2	1	3	1	1	Benign
122	1174057	4	2	1	1	2	2	3	1	1	Benign
137	1182404	4	1	1	1	2	1	2	1	1	Benign
257	1182404	3	1	1	1	2	1	1	1	1	Benign
258	1182404	3	1	1	1	2	1	2	1	1	Benign
266	1182404	5	1	4	1	2	1	3	2	1	Benign
449	1182404	1	1	1	1	1	1	1	1	1	Benign
498	1182404	4	2	1	1	2	1	1	1	1	Benign
169	1198641	3	1	1	1	2	1	3	1	1	Benign
259	1198641	3	1	1	1	2	1	3	1	1	Benign
267	1198641	10	10	6	3	3	10	4	3	2	Malignant
195	1212422	3	1	1	1	2	1	3	1	1	Benign
196	1212422	4	1	1	1	2	1	3	1	1	Benign
208	1218860	1	1	1	1	1	1	3	1	1	Benign
209	1218860	1	1	1	1	1	1	3	1	1	Benign
472	1238777	6	1	1	3	2	1	1	1	1	Benign
633	1238777	1	1	1	1	2	1	1	1	1	Benign
548	1240603	2	1	1	1	1	1	1	1	1	Benign
549	1240603	3	1	1	1	1	1	1	1	1	Benign
242	1276091	3	1	1	3	1	1	3	1	1	Benign
430	1276091	2	1	1	1	2	1	2	1	1	Benign
431	1276091	1	3	1	1	2	1	2	2	1	Benign
432	1276091	5	1	1	3	4	1	3	2	1	Benign
463	1276091	6	1	1	3	2	1	1	1	1	Benign
639	1277792	4	1	1	1	2	1	1	1	1	Benign
640	1277792	5	1	1	3	2	1	1	1	1	Benign
434	1293439	3	2	2	3	2	1	1	1	1	Benign
435	1293439	6	9	7	5	5	8	4	2	1	Benign
468	1299596	6	6	6	5	4	10	7	6	2	Malignant
645	1299596	2	1	1	1	2	1	1	1	1	Benign
512	1299924	5	1	1	1	2	1	2	1	1	Benign
553	1299924	3	2	2	2	2	1	4	2	1	Benign
517	1320077	1	1	1	1	1	1	1	1	1	Benign
518	1320077	1	1	1	1	1	1	2	1	1	Benign
561	1321942	5	1	1	1	2	1	3	1	1	Benign
562	1321942	5	1	1	1	2	1	3	1	1	Benign
661	1339781	1	1	1	1	2	1	2	1	1	Benign
662	1339781	4	1	1	1	2	1	3	1	1	Benign
673	1354840	2	1	1	1	2	1	3	1	1	Benign
674	1354840	5	3	2	1	3	1	1	1	1	Benign

Table 4: Instances with missing data from the Breast Cancer Wisconsin (Original) Data Set

	Sample code number	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	Normal Nucleoli	Mitoses	Class
24	1057013	8	4	5	1	2	NA	7	3	1	Malignant
41	1096800	6	6	6	9	6	NA	7	8	1	Benign
140	1183246	1	1	1	1	1	NA	2	1	1	Benign
146	1184840	1	1	3	1	2	NA	2	1	1	Benign
159	1193683	1	1	2	1	3	NA	1	1	1	Benign
165	1197510	5	1	1	1	2	NA	3	1	1	Benign
236	1241232	3	1	4	1	2	NA	3	1	1	Benign
250	169356	3	1	1	1	2	NA	3	1	1	Benign
276	432809	3	1	3	1	2	NA	2	1	1	Benign
293	563649	8	8	8	1	2	NA	6	10	1	Malignant
295	606140	1	1	1	1	2	NA	2	1	1	Benign
298	61634	5	4	3	1	2	NA	2	3	1	Benign
316	704168	4	6	5	6	7	NA	4	9	1	Benign
322	733639	3	1	1	1	2	NA	3	1	1	Benign
412	1238464	1	1	1	1	1	NA	2	1	1	Benign
618	1057067	1	1	1	1	1	NA	1	1	1	Benign

Data distribution

Class distribution

It is important to look at the class distribution because studies have shown that the distribution of the class labels can have an effect on classifier learning, and that the natural class distribution does not always give the best classifiers [7][8]. According to [7] there are several explanations for why the minority class generally has a higher error rate than the majority class when using unbalanced data while training a classifier.

Ways to handle the unbalanced data while making a classifier include under-sampling of the majority class and over-sampling of the minority-class. Another way is to tackle this problem is to use a cost-sensitive classifier that gives a heavier weight to misclassifying the minority class. These techniques have their own advantages and drawbacks [9].

When using over- or under-sampling techniques it is important to keep in mind that this will result in a bias in the model, this bias will cause the over-sampled class to be predicted too often. This bias will improve the performance of the classifier on the over-sampled class, but the overall performance will deteriorate due to this bias. To compensate for this bias a correction has to be built into the model, one way of using a correction is shown in [7]. When using these techniques it is also important to keep in mind that class imbalance is a relative problem that does not only depend on the degree of class imbalance, but also on the complexity of the concept representing the data, the size of the training set and also on the classifier involved. When using a classifier that is not susceptible to the class imbalance problem the use of over- and under-sampling could hurt the classifier instead of helping it [8].

In figure 1 the class distribution of the Breast Cancer Wisconsin (Original) Data Set can be seen before and after filtering. It can be seen that the data before filtering as well as the data after filtering seems to be unbalanced, it has a minority and majority class. However the data does not seem to be extremely unbalanced. It can also be seen that the data after the filtering step is slightly more balanced than before filtering.

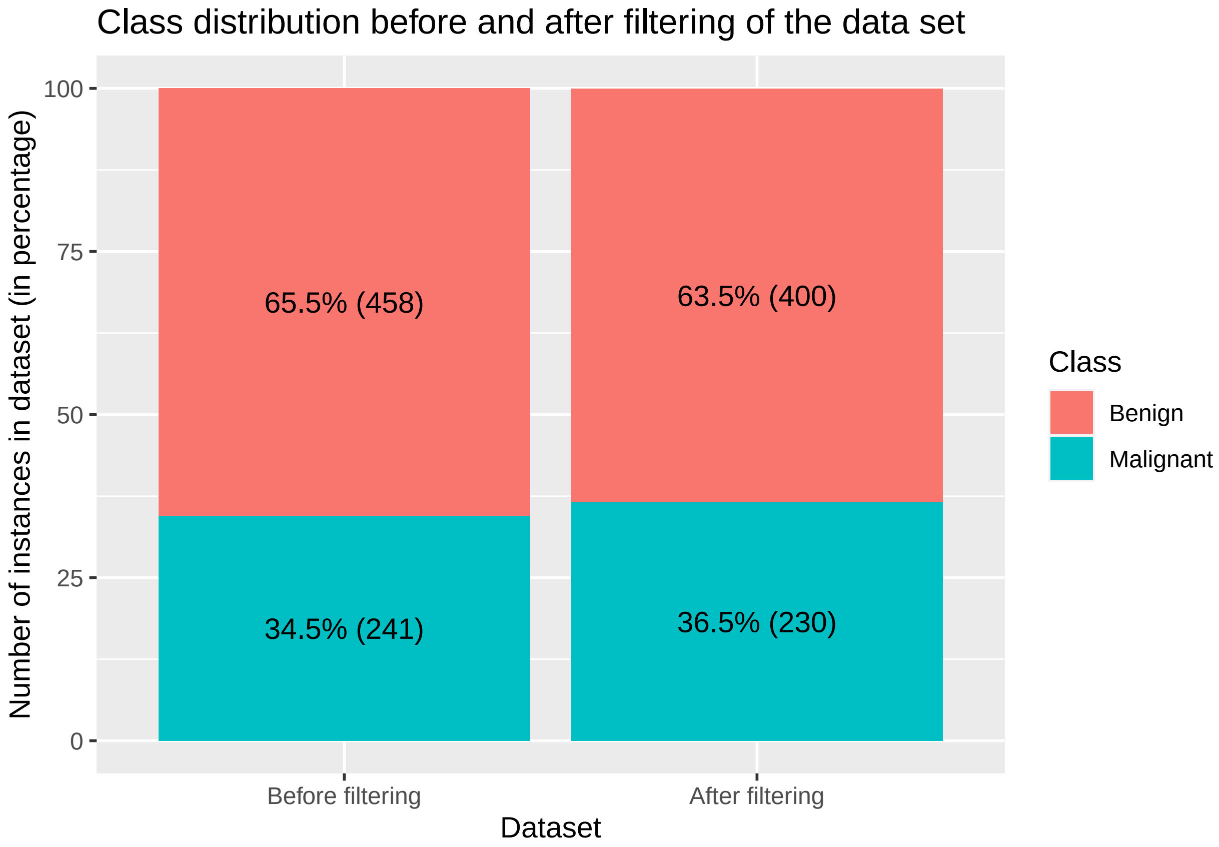


Figure 1: Distribution of the class attribute of the data before and after the filtering steps (the filtering steps are: removing rows with missing data, and than removing duplicated sample code numbers). The numbers between parentheses are the actual number of instances in the data sets.

Attribute distributions

For the attributes to be useful for building a machine learning classifier it is important that the distributions for these attribute are discriminative for the different classes. The literature already states that the nine attributes involved in the *Breast Cancer Wisconsin (Original) Data Set* are significantly different between benign and malignant cases [4]. Figure 2 shows a visual representation of the attribute distributions for benign and malignant samples, as well as the distribution for all the samples together. When looking at this figure it is important to keep in mind that the majority class (the benign instances) have a bigger influence on the overall distribution than the minority class.

All the attributes seem to be very differently distributed between the benign and malignant instances, except for the mitoses attribute. For both the benign and malignant cases the mitoses attribute most often has a score of 1. However when looking at the mitoses distribution of the malignant instances, there is a longer tail towards the higher score than the benign cases show, this might still be a significant difference.

The seemingly (big) difference in distributions for all of these attributes is a positive sign for machine learning, all of these attributes could be useful in differentiating benign and malignant samples from one another.

To verify that the difference is indeed significant for all the attributes a one-sided Mann–Whitney U test is executed for each attribute. The results of these tests and the corresponding p values can be found in table 5. The tests have the following hypotheses:

- Null hypothesis: the two samples (benign and malignant) come from the same population.

- Alternative hypothesis: observations in the malignant sample tend to be higher than observations in the benign sample (the malignant sample is shifted to the right compared to the benign sample).

With $\alpha = 0.05$ the null hypothesis is rejected for all the tests, and the alternative hypothesis is accepted. All of the differences might be significant, when looking at the estimate median of difference (that is the estimated median of the difference between all the observation from one sample and all the observations in another sample, and not the estimated difference in medians between the two samples) it is once again obvious that the difference in mitoses is quite small. The difference in all the other attributes seems quite large, especially the bare nuclei attribute. This could mean that the mitoses attribute is less useful for machine learning than the other attributes.

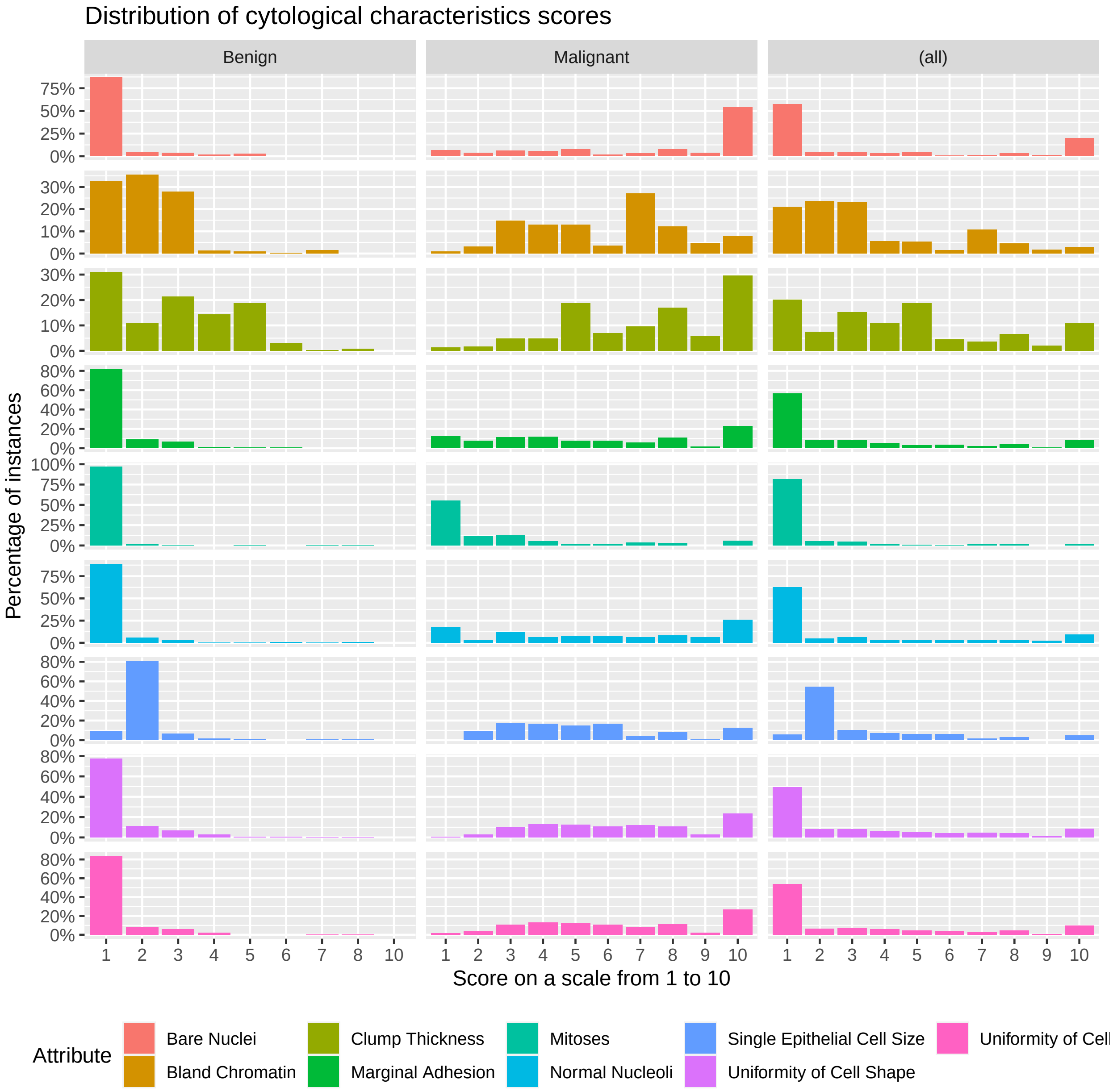
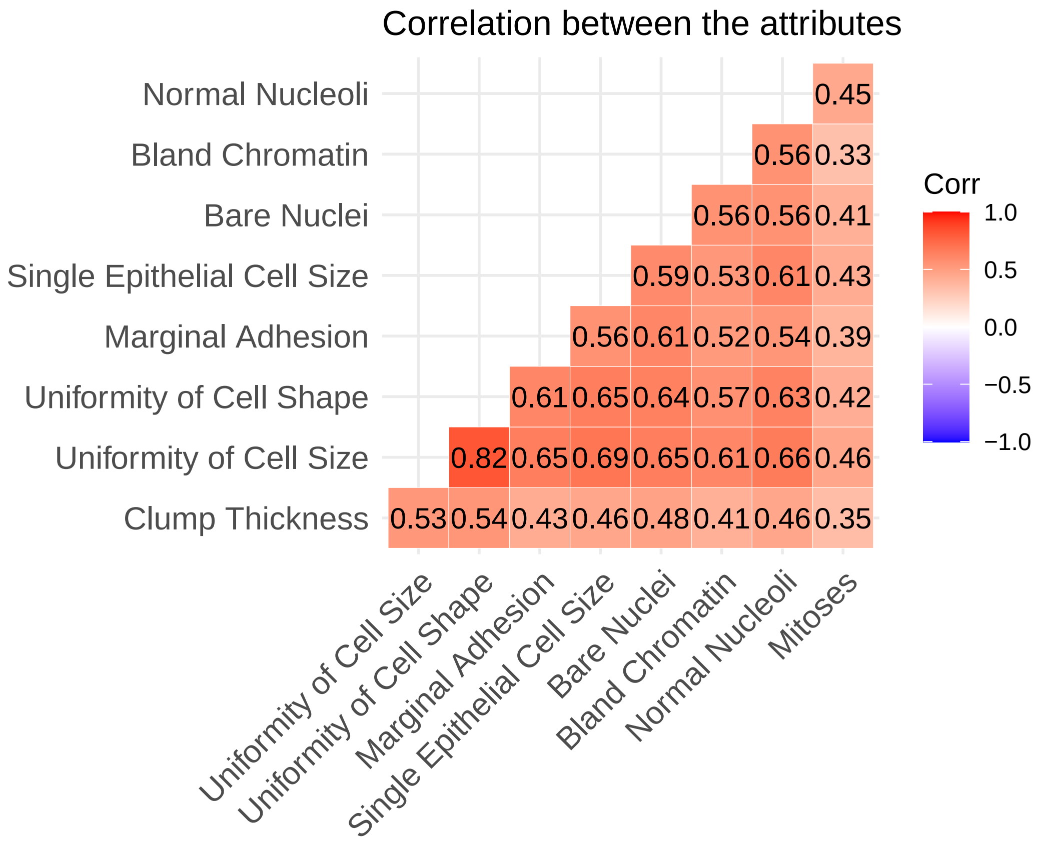


Figure 2: Distribution of data in percentage for 9 different cytological characteristics for benign instances, malignant instances and for all instances together

Table 5: Results of one-sided Mann–Whitney U test for each attribute where the null hypothesis is that the distribution of the malignant samples **is not** higher than that of the benign samples. And the alterernative hypothesis is that the distribution of the Malignant samples **is** higher than that of the benign samples. All of the p-values are well below 0.05 so we reject the null hypothesis for each attribute.

Attribute name	Estimate median of difference	P value
Clump Thickness	4.0000287732	1.736520e-68
Uniformity of Cell Size	5.0000208895	0.000000e+00
Uniformity of Cell Shape	5.0000340393	3.000000e-100
Marginal Adhesion	4.0000478861	1.197571e-77
Single Epithelial Cell Size	2.9999504915	1.339529e-84
Bare Nuclei	7.9999934047	8.290000e-98
Bland Chromatin	4.0000370221	3.375664e-79
Normal Nucleoli	4.9999897428	2.285017e-79
Mitoses	0.0000555406	1.003309e-39



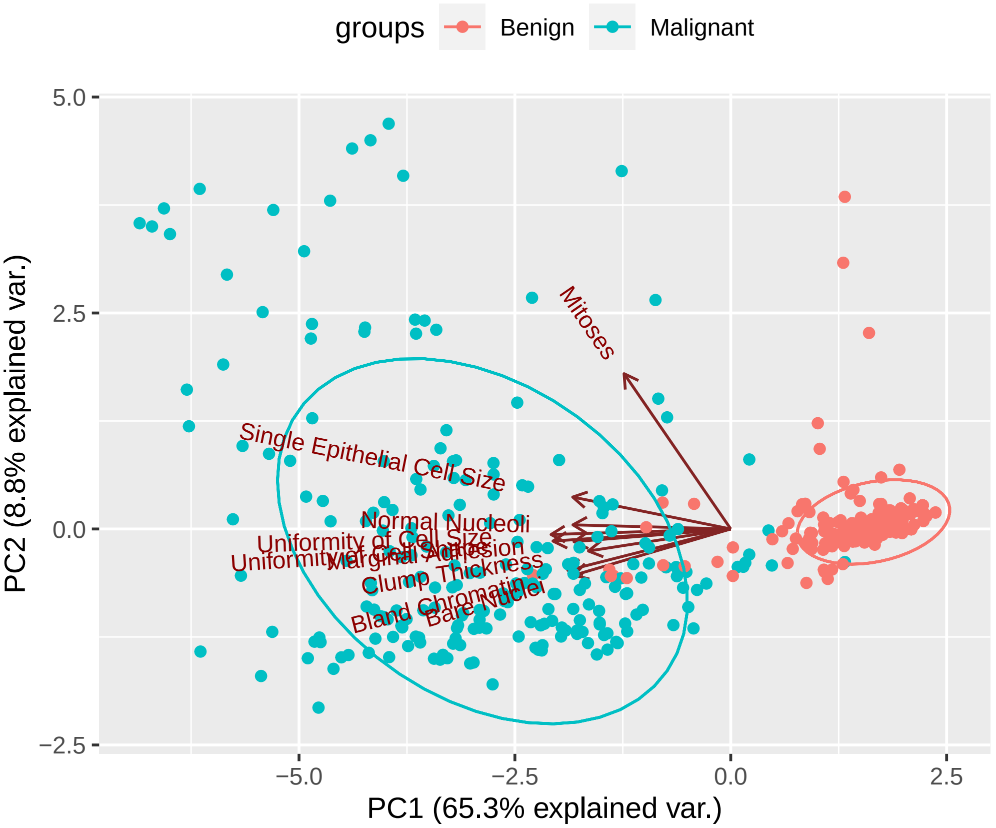


Table 6: PCA: Rotation matrix of the 9 cytological characteristics to each principal component, scaled = TRUE

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
Clump Thickness	-0.3026067	-0.1277601	0.8730402	-0.0509633	0.0200015	0.2080380	0.0594103	0.2830144	-0.0018746
Uniformity of Cell Size	-0.3821300	-0.0320382	-0.0386545	0.1856231	-0.1336961	0.2422388	-0.1310226	-0.4164032	-0.7415439
Uniformity of Cell Shape	-0.3780364	-0.0701172	0.0287437	0.1593851	-0.0888896	0.1701730	-0.0535618	-0.5990616	0.6537113
Marginal Adhesion	-0.3333947	-0.0734380	-0.3931759	-0.5003666	0.0309380	0.5636711	0.3050514	0.2529206	0.0528526
Single Epithelial Cell Size	-0.3360831	0.1847634	-0.1429394	0.3430707	-0.7025839	-0.1980931	0.1571675	0.3895393	0.0739862
Bare Nuclei	-0.3335249	-0.2678899	0.0273743	-0.5168253	-0.0492067	-0.6806530	0.1963920	-0.1930489	-0.0871259
Bland Chromatin	-0.3465219	-0.2393446	-0.1911542	0.0159296	0.2005512	-0.1029457	-0.7827851	0.3403353	0.0802731
Normal Nucleoli	-0.3355534	0.0240361	-0.1277002	0.4830818	0.6411883	-0.1749484	0.4228656	0.1273752	-0.0195346
Mitoses	-0.2268878	0.8992081	0.0828547	-0.2621999	0.1596186	-0.0873072	-0.1689347	-0.0510517	0.0093337

3 Discussion & Conclusion

4 References

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