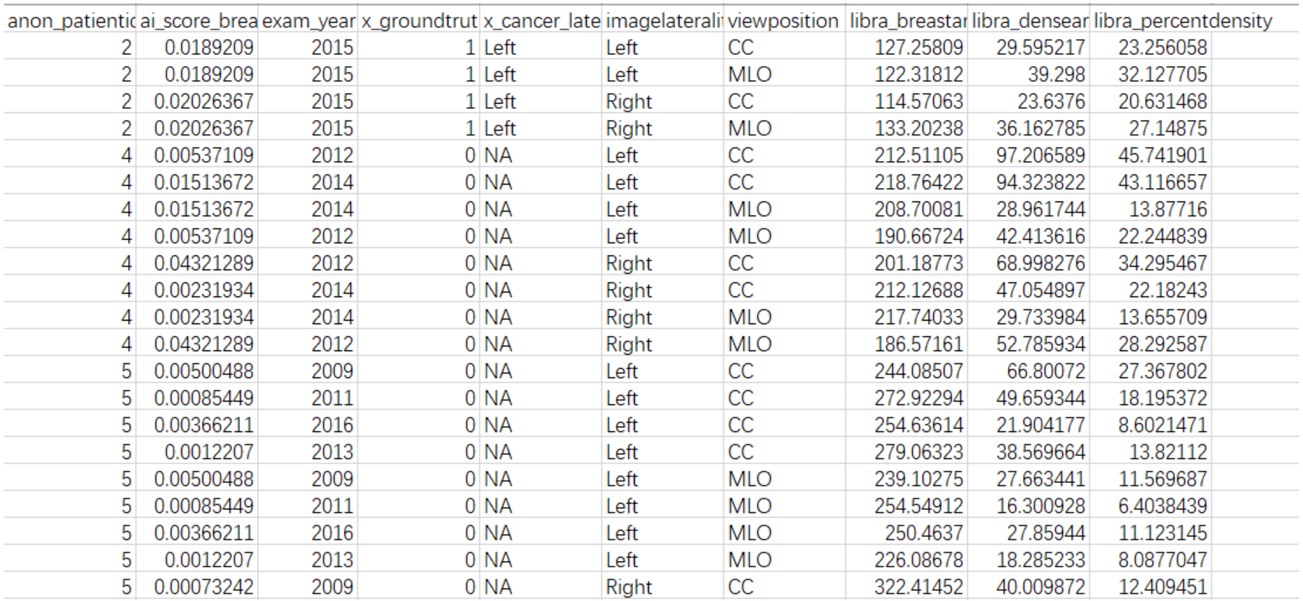
Analysis of AI scores from the mammography exam

Reporter: Rudan Xiao

Date: 11/04/2022

- Data Description and Statistical Analysis
  - Data description
  - Data distribution & correlation analysis
  - Nonparametric tests
- Evaluation Index & AI score Related Features
- Methods of Classification
- Screening for Potential Cancer
- Conclusion

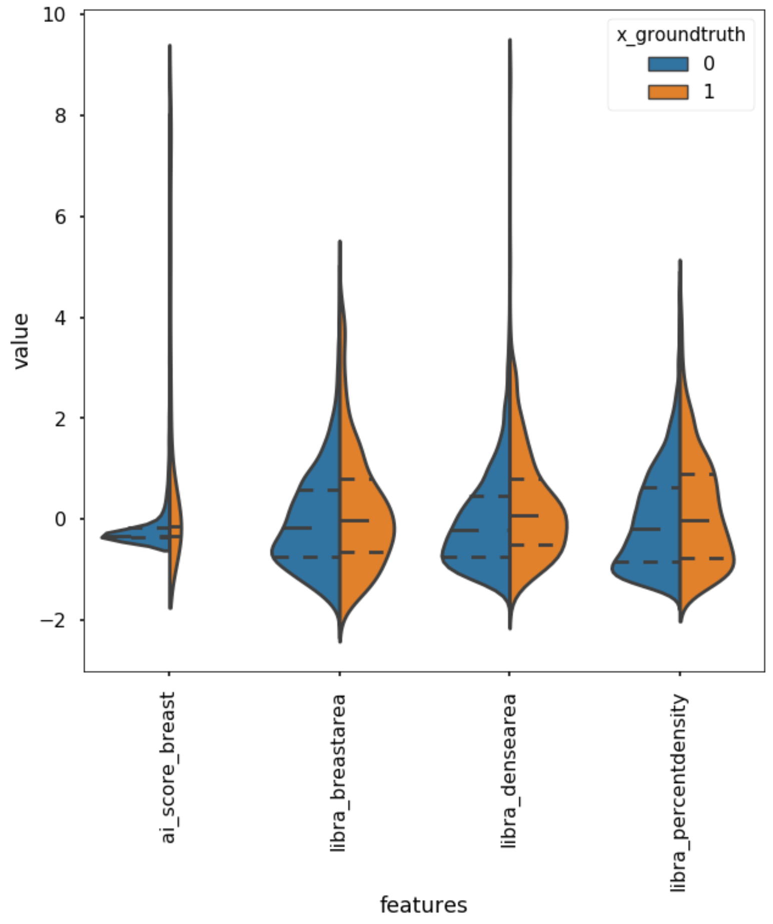


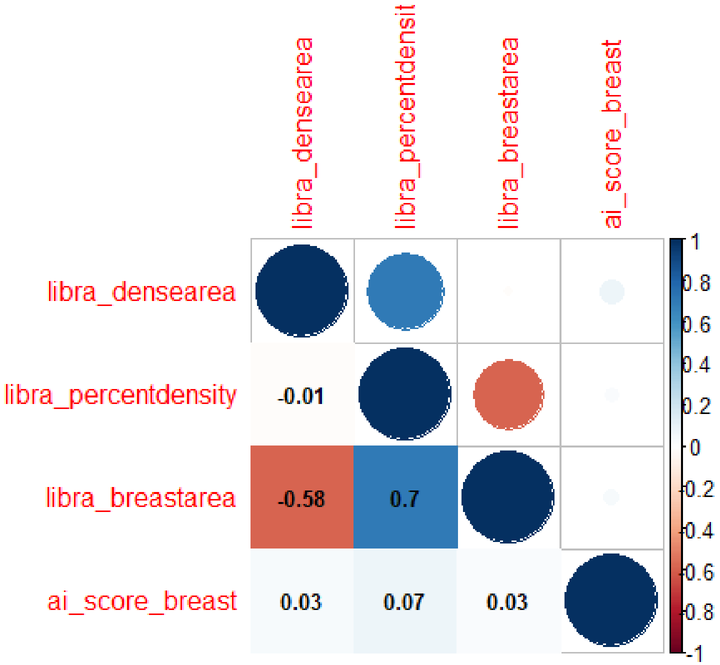
anon_patientic	ai_score_brea	exam_year	x_groundtrut	x_cancer_late	imagelaterali	viewposition	libra_breastar	libra_densear	libra_percentdensity
2	0.0189209	2015	1	Left	Left	CC	127.25809	29.595217	23.256058
2	0.0189209	2015	1	Left	Left	MLO	122.31812	39.298	32.127705
2	0.02026367	2015	1	Left	Right	CC	114.57063	23.6376	20.631468
2	0.02026367	2015	1	Left	Right	MLO	133.20238	36.162785	27.14875
4	0.00537109	2012	0	NA	Left	CC	212.51105	97.206589	45.741901
4	0.01513672	2014	0	NA	Left	CC	218.76422	94.323822	43.116657
4	0.01513672	2014	0	NA	Left	MLO	208.70081	28.961744	13.87716
4	0.00537109	2012	0	NA	Left	MLO	190.66724	42.413616	22.244839
4	0.04321289	2012	0	NA	Right	CC	201.18773	68.998276	34.295467
4	0.00231934	2014	0	NA	Right	CC	212.12688	47.054897	22.18243
4	0.00231934	2014	0	NA	Right	MLO	217.74033	29.733984	13.655709
4	0.04321289	2012	0	NA	Right	MLO	186.57161	52.785934	28.292587
5	0.00500488	2009	0	NA	Left	CC	244.08507	66.80072	27.367802
5	0.00085449	2011	0	NA	Left	CC	272.92294	49.659344	18.195372
5	0.00366211	2016	0	NA	Left	CC	254.63614	21.904177	8.6021471
5	0.0012207	2013	0	NA	Left	CC	279.06323	38.569664	13.82112
5	0.00500488	2009	0	NA	Left	MLO	239.10275	27.663441	11.569687
5	0.00085449	2011	0	NA	Left	MLO	254.54912	16.300928	6.4038439
5	0.00366211	2016	0	NA	Left	MLO	250.4637	27.85944	11.123145
5	0.0012207	2013	0	NA	Left	MLO	226.08678	18.285233	8.0877047
5	0.00073242	2009	0	NA	Right	CC	322.41452	40.009872	12.409451

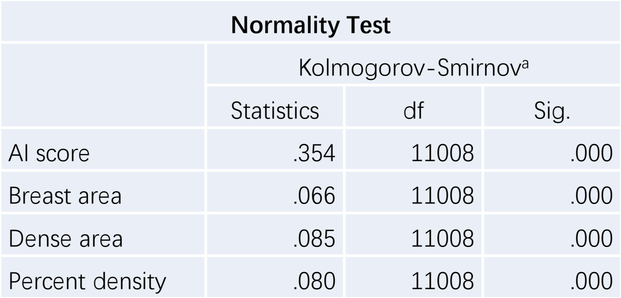
Number of samples

	cancer	healthy
patients	57	721
Ai score	632	10376
Cancer in left laterality	332 (33)	___
Cancer in right laterality	300 (24)	___

- ➢ Which AI score is most relevant to the cancer diagnosis?
- ➢ Which method works best for classifying cancer and healthy?
- ➢ Which healthy person should be recalled for the next diagnosis?





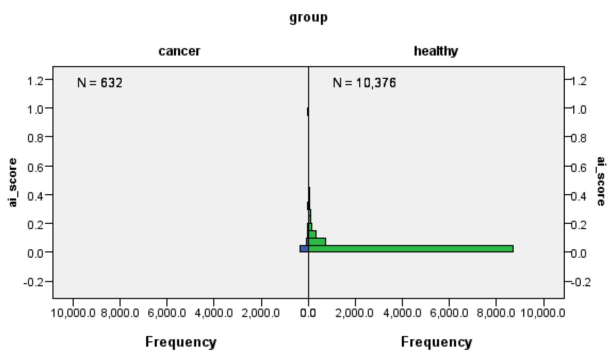


Normality Test			
	Kolmogorov-Smirnov[a]		
	Statistics	df	Sig.
AI score	.354	11008	.000
Breast area	.066	11008	.000
Dense area	.085	11008	.000
Percent density	.080	11008	.000

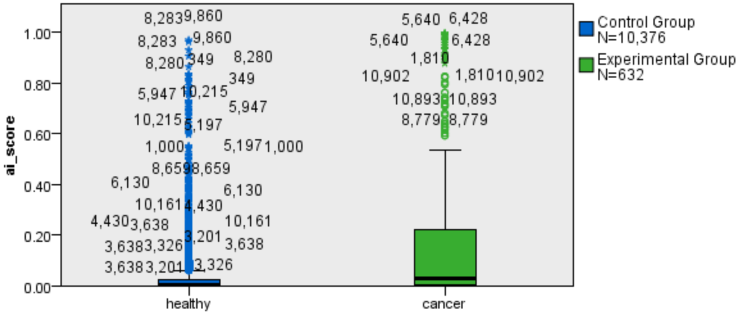
Data do **not** follow a **normal** distribution and **unbalanced**

AI score is more related with **breast area**.

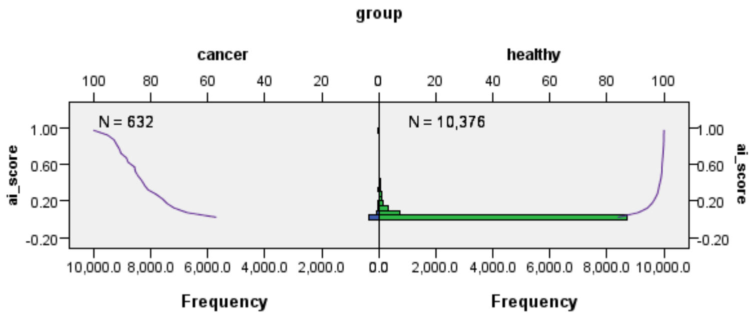
Independent-Samples Wald-Wolfowitz Runs Test

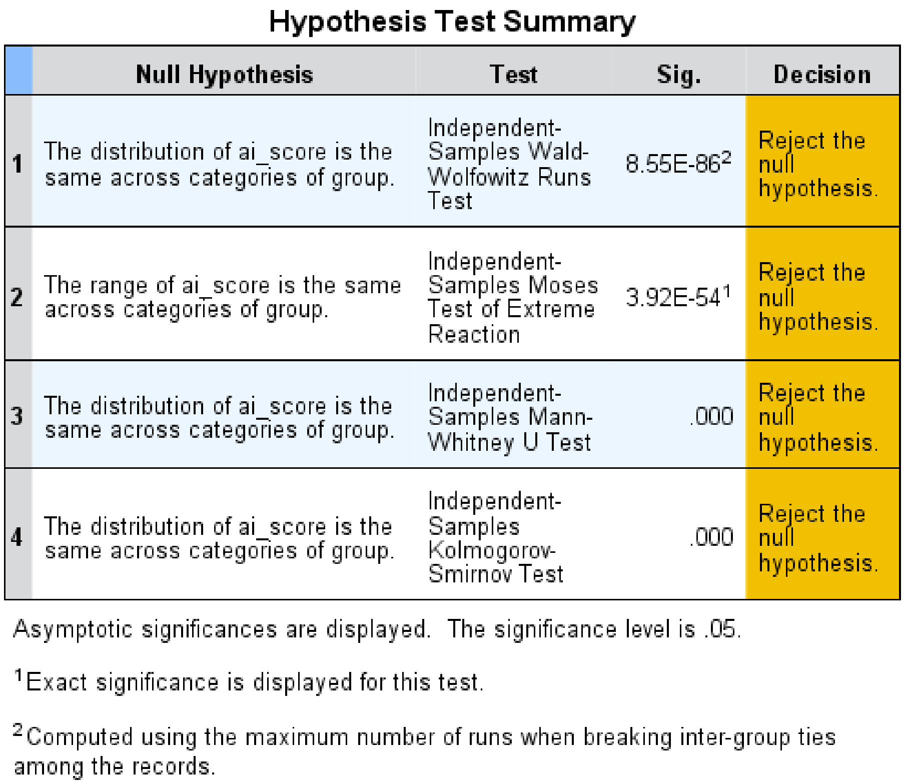


Independent-Samples Moses Test of Extreme Reaction



Independent-Samples Kolmogorov-Smirnov Test





Hypothesis Test Summary

	Null Hypothesis	Test	Sig.	Decision
1	The distribution of ai_score is the same across categories of group.	Independent-Samples Wald-Wolfowitz Runs Test	8.55E-86[2]	Reject the null hypothesis.
2	The range of ai_score is the same across categories of group.	Independent-Samples Moses Test of Extreme Reaction	3.92E-54[1]	Reject the null hypothesis.
3	The distribution of ai_score is the same across categories of group.	Independent-Samples Mann-Whitney U Test	.000	Reject the null hypothesis.
4	The distribution of ai_score is the same across categories of group.	Independent-Samples Kolmogorov-Smirnov Test	.000	Reject the null hypothesis.

Asymptotic significances are displayed. The significance level is .05.

[1] Exact significance is displayed for this test.

[2] Computed using the maximum number of runs when breaking inter-group ties among the records.

The **difference in AI-score** between **cancer** patients (ground truth is 1) and the **healthy** patients (ground truth is 0) are **significant** under all test methods.

- Data Description and Statistical Analysis
- Evaluation Index & AI score Related Features
    - Evaluation index
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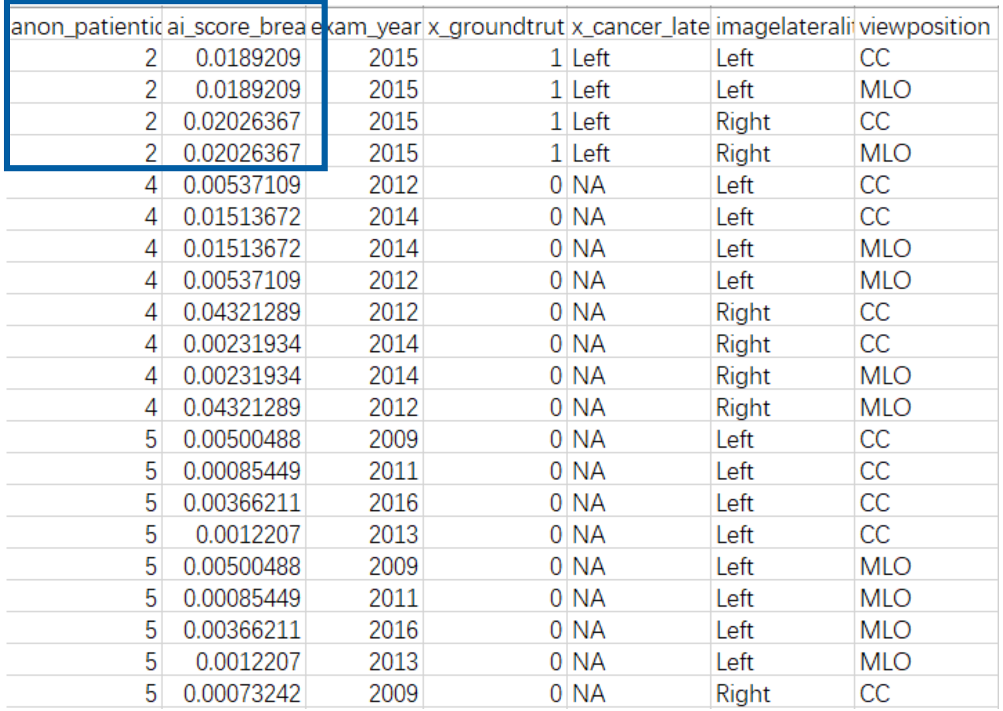
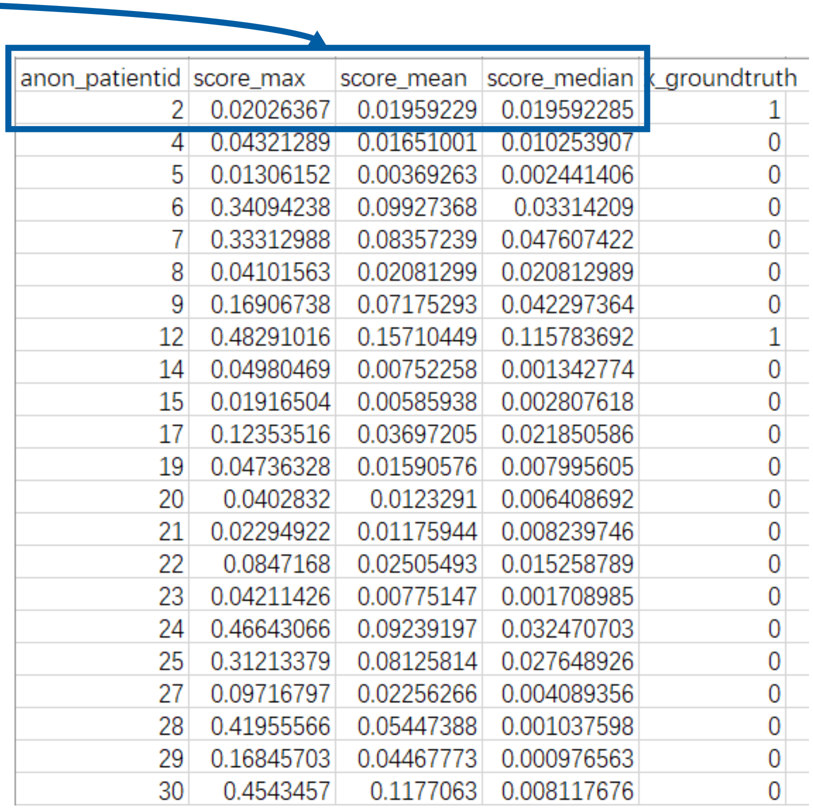
Evaluation index of classification

index	Notes	Formula
sensitivity (recall, true positive rate TPR)	the ability of a test to correctly identify patients with a disease	TP/(TP+FN)
specificity (selectivity, true negative rate (TNR))	the ability of a test to correctly identify people without the disease	TN/(TN+FP)
accuracy	Ratio of correct predictions to total predictions	(TP+TN)/(TP+TN+FP+FN)
precision (positive predictive value (PPV))	Ratio of true positives to total predicted positives	TP/(TP+FP)
f1_score	the harmonic mean of precision and sensitivity	2TP/(2TP+FP+FN)

Calculate the **max**, **mean**, and **median of AI score** by a group of patient ID

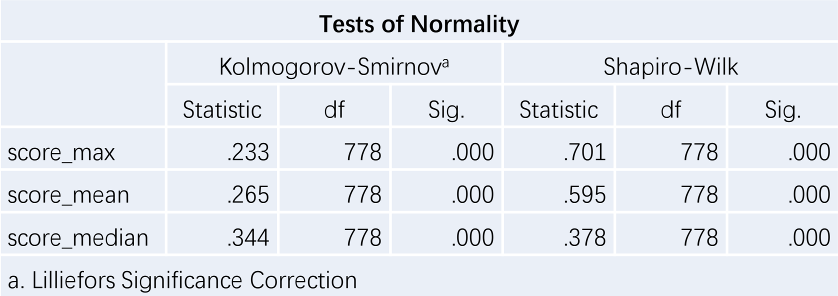


anon_patientic	ai_score_brea	exam_year	x_groundtrut	x_cancer_late	imagelaterali	viewposition
2	0.0189209	2015	1	Left	Left	CC
2	0.0189209	2015	1	Left	Left	MLO
2	0.02026367	2015	1	Left	Right	CC
2	0.02026367	2015	1	Left	Right	MLO
4	0.00537109	2012	0	NA	Left	CC
4	0.01513672	2014	0	NA	Left	CC
4	0.01513672	2014	0	NA	Left	MLO
4	0.00537109	2012	0	NA	Left	MLO
4	0.04321289	2012	0	NA	Right	CC
4	0.00231934	2014	0	NA	Right	CC
4	0.00231934	2014	0	NA	Right	MLO
4	0.04321289	2012	0	NA	Right	MLO
5	0.00500488	2009	0	NA	Left	CC
5	0.00085449	2011	0	NA	Left	CC
5	0.00366211	2016	0	NA	Left	CC
5	0.0012207	2013	0	NA	Left	CC
5	0.00500488	2009	0	NA	Left	MLO
5	0.00085449	2011	0	NA	Left	MLO
5	0.00366211	2016	0	NA	Left	MLO
5	0.0012207	2013	0	NA	Left	MLO
5	0.00073242	2009	0	NA	Right	CC



anon_patientid	score_max	score_mean	score_median	x_groundtruth
2	0.02026367	0.01959229	0.019592285	1
4	0.04321289	0.01651001	0.010253907	0
5	0.01306152	0.00369263	0.002441406	0
6	0.34094238	0.09927368	0.03314209	0
7	0.33312988	0.08357239	0.047607422	0
8	0.04101563	0.02081299	0.020812989	0
9	0.16906738	0.07175293	0.042297364	0
12	0.48291016	0.15710449	0.115783692	1
14	0.04980469	0.00752258	0.001342774	0
15	0.01916504	0.00585938	0.002807618	0
17	0.12353516	0.03697205	0.021850586	0
19	0.04736328	0.01590576	0.007995605	0
20	0.0402832	0.0123291	0.006408692	0
21	0.02294922	0.01175944	0.008239746	0
22	0.0847168	0.02505493	0.015258789	0
23	0.04211426	0.00775147	0.001708985	0
24	0.46643066	0.09239197	0.032470703	0
25	0.31213379	0.08125814	0.027648926	0
27	0.09716797	0.02256266	0.004089356	0
28	0.41955566	0.05447388	0.001037598	0
29	0.16845703	0.04467773	0.000976563	0
30	0.4543457	0.1177063	0.008117676	0

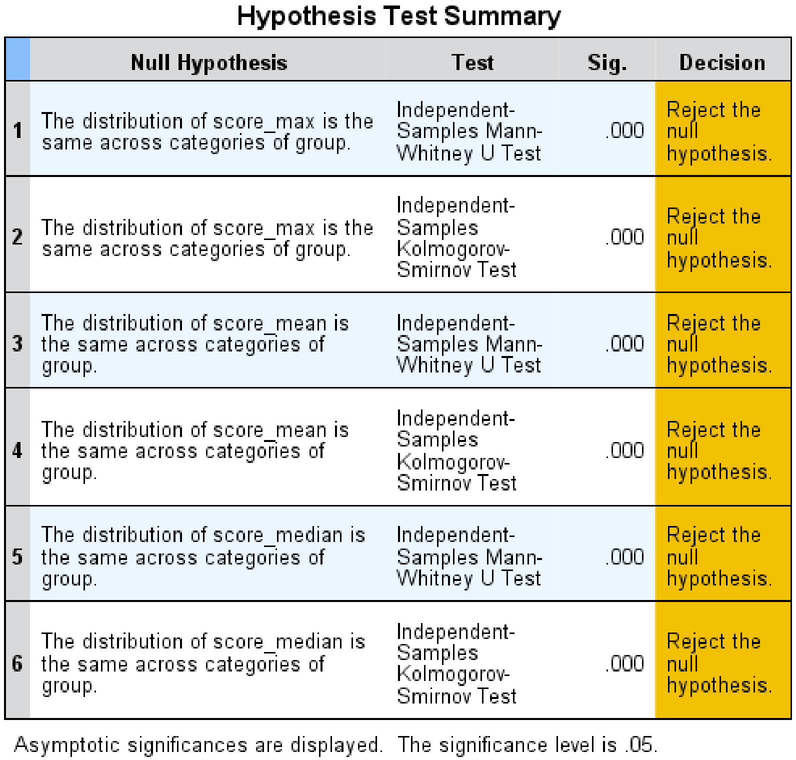
Nonparametric Tests



Tests of Normality

	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
	Statistic	df	Sig.	Statistic	df	Sig.
score_max	.233	778	.000	.701	778	.000
score_mean	.265	778	.000	.595	778	.000
score_median	.344	778	.000	.378	778	.000

a. Lilliefors Significance Correction

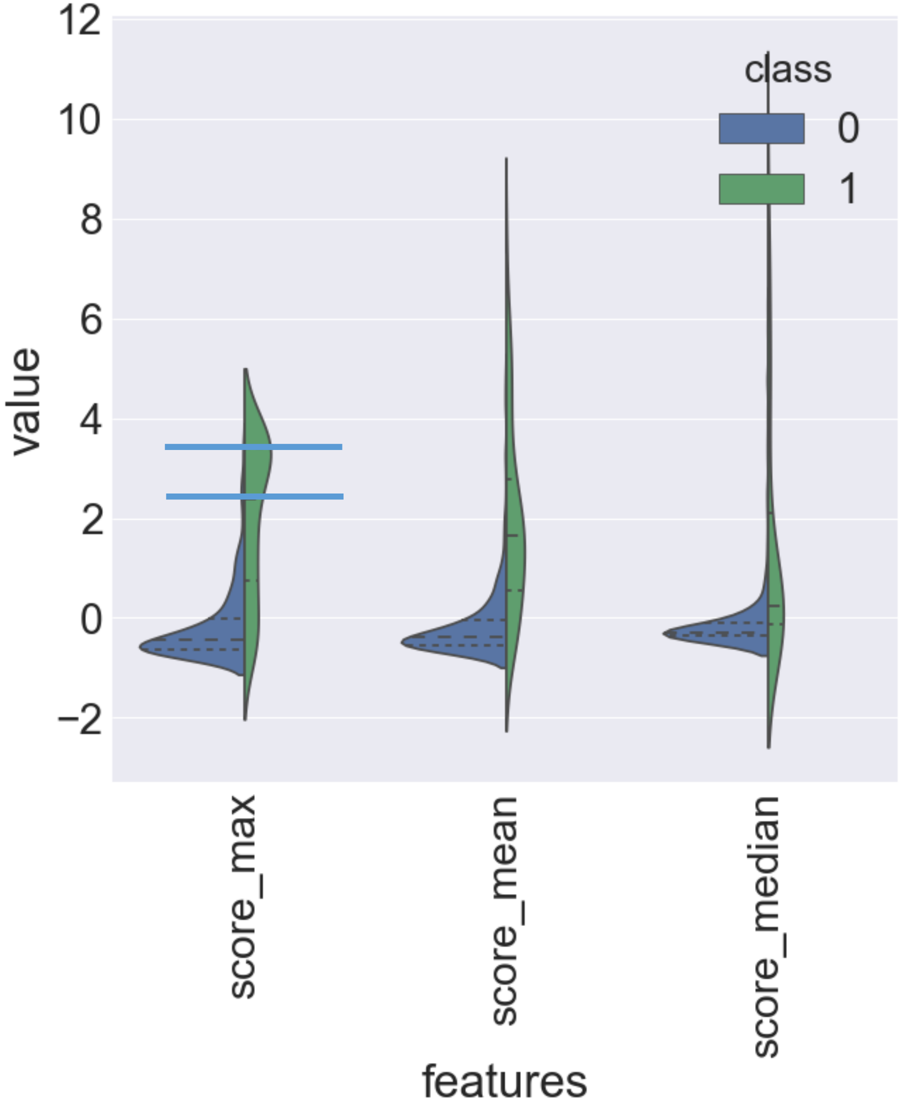


Hypothesis Test Summary

	Null Hypothesis	Test	Sig.	Decision
1	The distribution of score_max is the same across categories of group.	Independent-Samples Mann-Whitney U Test	.000	Reject the null hypothesis.
2	The distribution of score_max is the same across categories of group.	Independent-Samples Kolmogorov-Smirnov Test	.000	Reject the null hypothesis.
3	The distribution of score_mean is the same across categories of group.	Independent-Samples Mann-Whitney U Test	.000	Reject the null hypothesis.
4	The distribution of score_mean is the same across categories of group.	Independent-Samples Kolmogorov-Smirnov Test	.000	Reject the null hypothesis.
5	The distribution of score_median is the same across categories of group.	Independent-Samples Mann-Whitney U Test	.000	Reject the null hypothesis.
6	The distribution of score_median is the same across categories of group.	Independent-Samples Kolmogorov-Smirnov Test	.000	Reject the null hypothesis.

Asymptotic significances are displayed. The significance level is .05.

The **difference** in **three features (score_max, score_mean, and score_median)** between **cancer** patients (ground truth is 1) and the **healthy** patients (ground truth is 0) are **significant** under all test methods



From the **features distribution** of class 0 (healthy) and class 1 (cancer), **score_max** seems to be easier to distinguish **by quartile threshold.**

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  - Threshold
  - Traditional machine learning
  - Multi-Layer perceptron (MLP)
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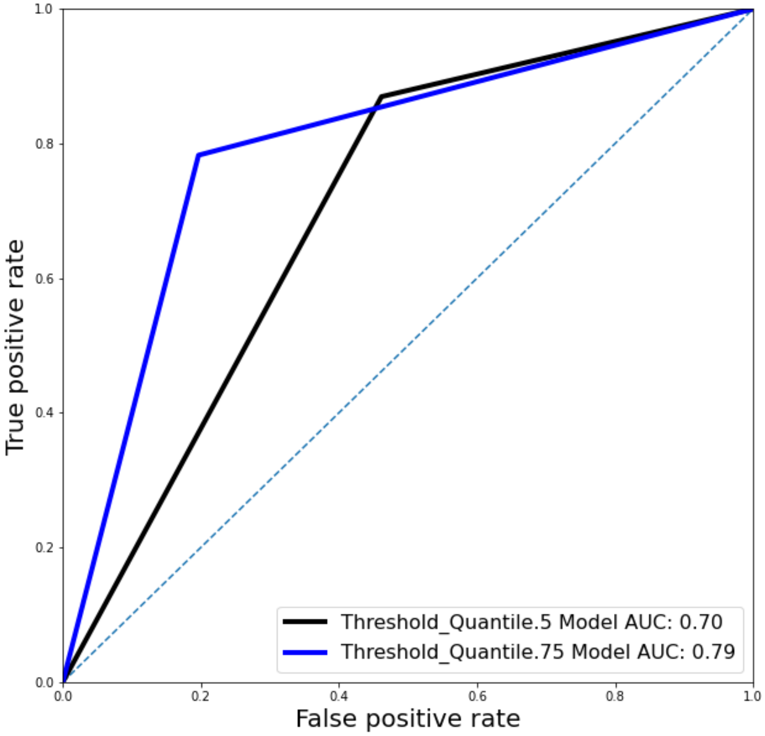
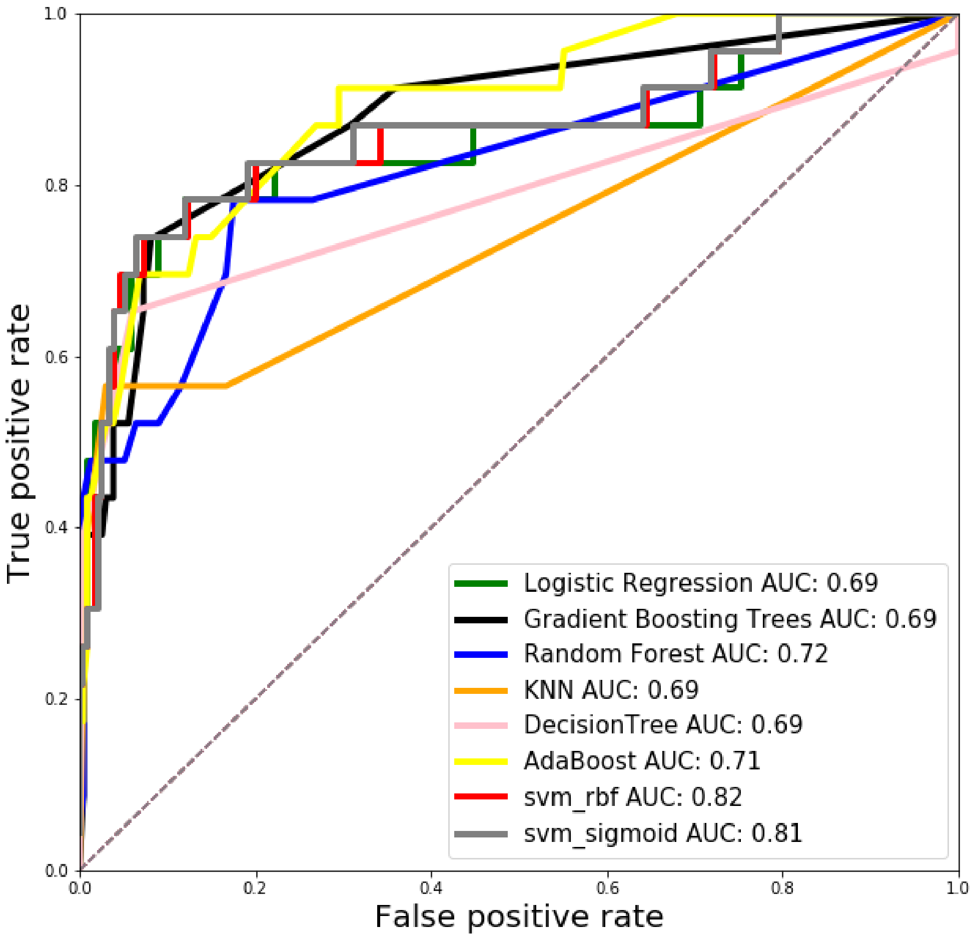


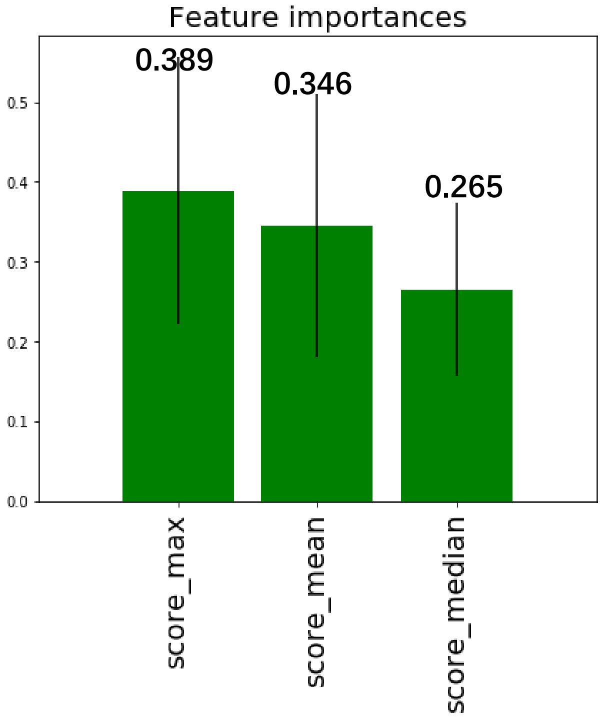
Receiver Operating Characteristic curve (ROC)

Evaluation Result

index	Threshold (Quartile=0.5)	Threshold (Quartile=0.75)
sensitivity	**0.8772**	0.7895
specificity	0.5298	**0.7920**
accuracy	0.5553	**0.7918**
precision	0.1285	**0.2308**
f1_score	0.2242	**0.3571**
AUC	0.70	**0.79**



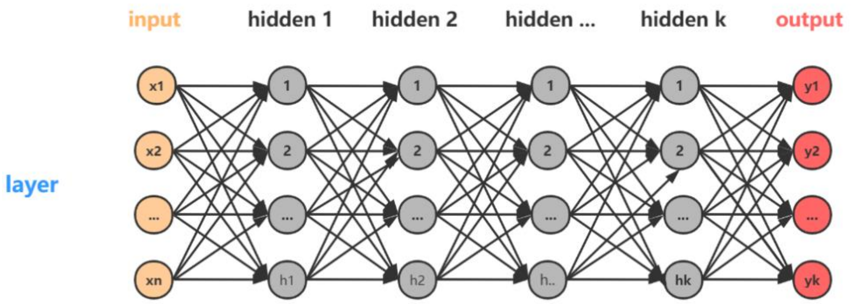
Receiver Operating Characteristic curve (ROC)



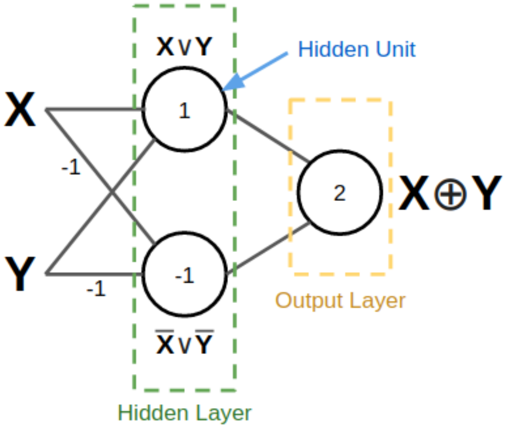
- **SVM_rbf** performs **best** among all the traditional machine learning methods of classification.
- **Score_max** performs **best** among all the features.

The evaluation result of all the traditional machine learning models

	sensitivity	specificity	accuracy	precision	f1_score	AUC
Logistic Regression	0.3478	0.9915	0.9339	0.8	0.4848	0.69
Gradient Boosting Trees	0.3913	**0.9957**	0.9416	0.9	0.5455	0.69
Random Forest	0.4348	**0.9957**	**0.9455**	**0.9091**	0.5882	0.72
KNN	0.4348	0.9786	0.93	0.6667	0.5263	0.69
DecisionTree	0.3913	**0.9957**	0.9416	0.9	0.5455	0.69
AdaBoost	0.3913	0.9915	0.9377	0.8182	0.5294	0.71
svm_rbf	**0.6957**	0.9359	0.9144	0.5161	**0.5926**	**0.82**
svm_sigmoid	0.6087	0.6087	0.93	0.6087	0.6087	0.81



MLP is a kind of **neural network**



With a **layered** structure, we can obtain the **intermediate results** and use them **as the inputs to the next layer**. We call this structure the multi-layer perceptron (MLP)

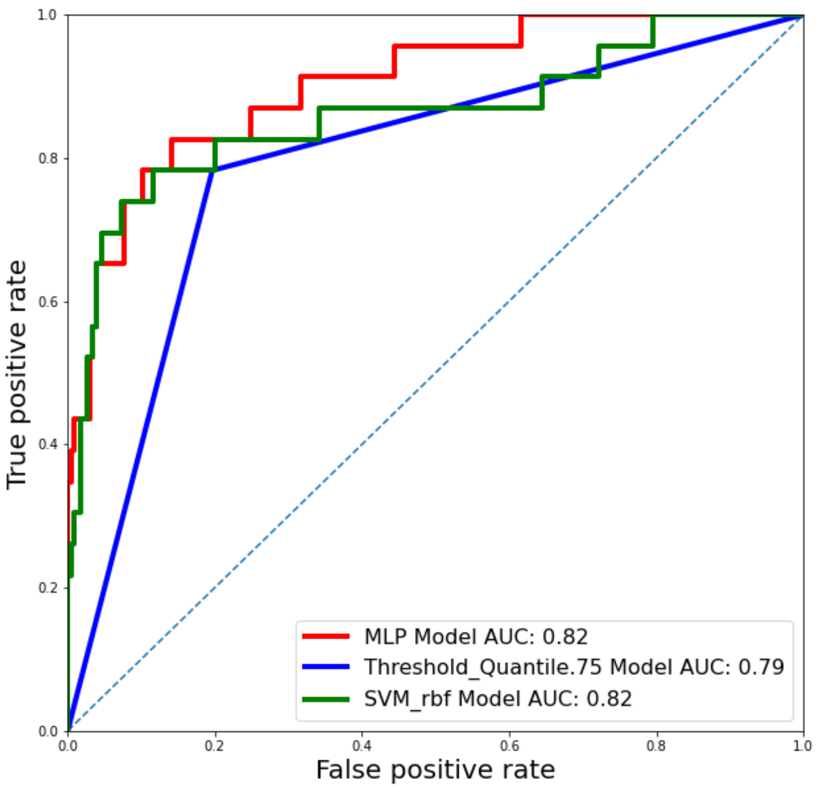
$$L(w) = \sum_{x_i \in D} -y_i(w^T x_i + b),$$

$$D = \{x_i \mid y_i(w^T x_i + b) < 0\}$$

Loss Function

Evaluation Result

index	Threshold (Quartile=0.5)
sensitivity	0.4348
specificity	0.9872
accuracy	0.9377
precision	0.7692
f1_score	0.5556
AUC	0.82



Receiver Operating Characteristic curve (ROC)

Significant test in the difference of AUC by DeLong

	P-Value (0.05)
MLP V.S. **SVM_rbf**	0.2377
Threshold V.S. **SVM_rbf**	0.1098
MLP V.S. **Threshold**	**0.0067**

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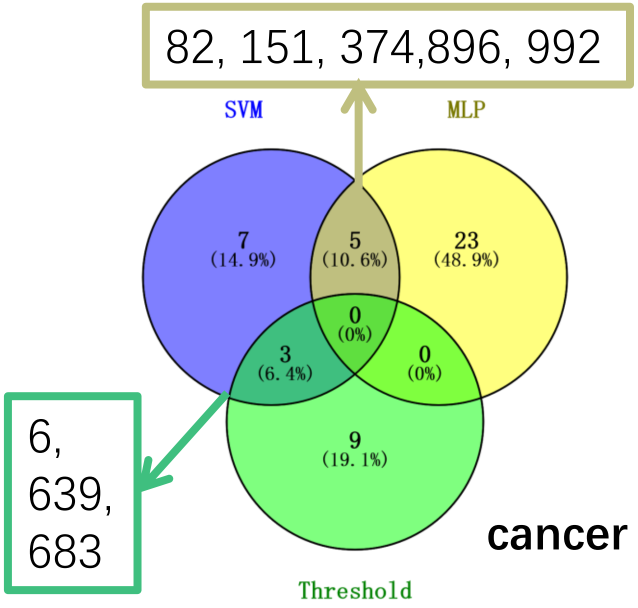
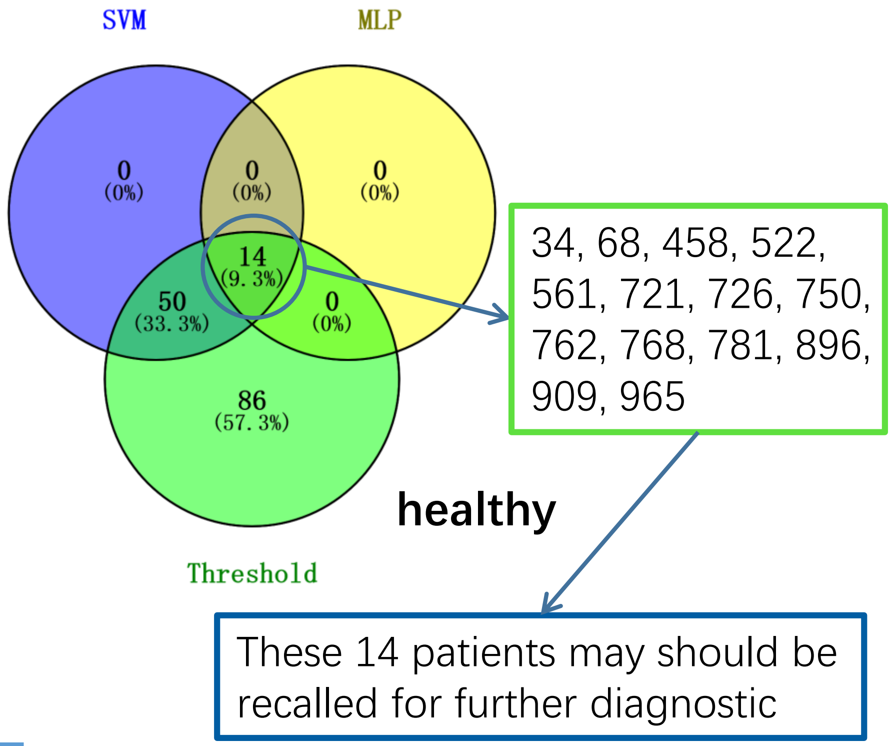


82, 151, 374,896, 992

6, 639, 683



34, 68, 458, 522, 561, 721, 726, 750, 762, 768, 781, 896, 909, 965

These 14 patients may should be recalled for further diagnostic

https://bioinfogp.cnb.csic.es/tools/venny/index.html

Number of wrong classify patients

	MLP	SVM_rbf	Threshold (Quartile=0.75)
Cancer (x_groundtruth=1)	28	15	12
Healthy (x_groundtruth=0)	14	64	150

- The three classifiers are **more consistent** in the **classification of healthy** people (possibly due to data imbalanced).
- **14** patients **misclassified** as cancer in **all three classifiers** may need to be **recalled**.

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1. **MLP** performs **best** among all **classifiers**.

2. **Traditional machine learning** models are more **explanatory** and can explain the **contribution** of each **feature**.

3. The **distribution of features** data and the **features rank** results of machine learning both show that the **score_max** has the **largest contribution**.

Thanks

- **AIR** (abnormal interpretation rate) seems to be commonly used for evaluation in **cohort studies**, combined with some clinical data.

- For the **time series analysis**, now the data seems does not include enough time information, for example, patients with groundtruth 1, what time is the **date of the first diagnosis**?

- **CC** and **MLO** have the **same AI score** value?

- Solve the problem of **unbalanced**.