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SEMINAR NASIONAL TEKNIK ELEKTRO, SISTEM INFORMASI DAN TEKNIK INFORMATIKA

Machine Learning-based Models for Disease Prediction

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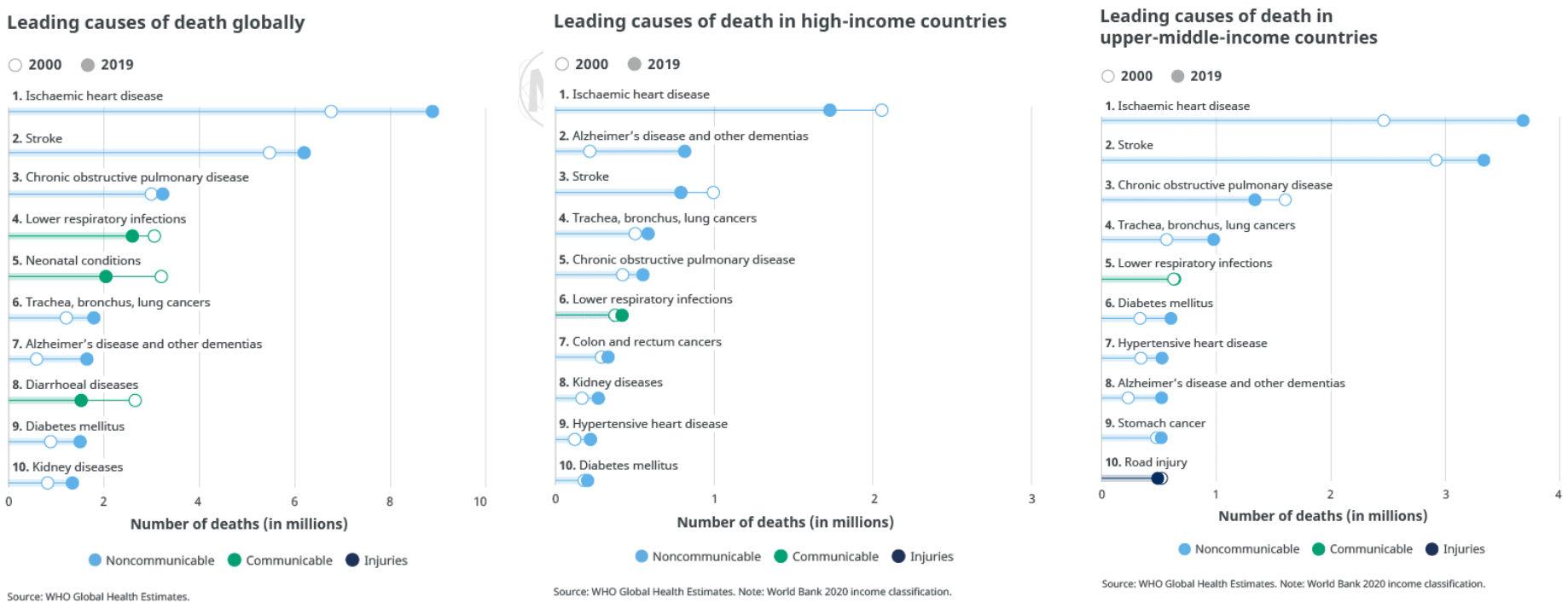
Introduction

Introduction

- According to World Health Organization report [1], in 2019, the top 10 causes of death accounted for 55% of the 55.4 million deaths worldwide.
- These top 10 serious diseases take an 'immense and increasing toll on lives' [1].



(a) (b) (c)

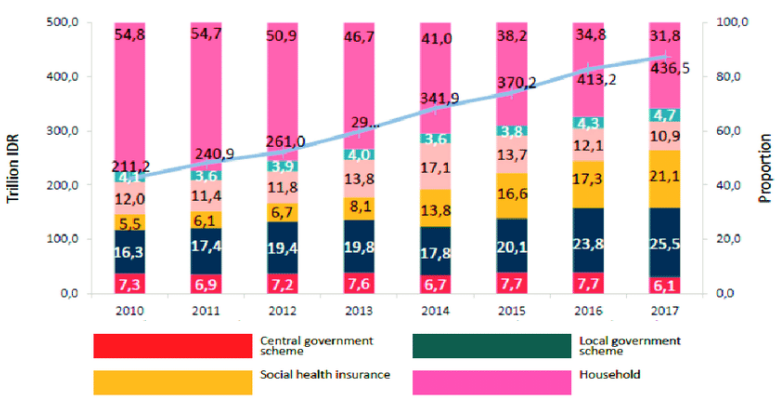
Fig 1. Worldwide leading cause death (a), in high-income countries (b), in upper-middle-income (c) [1]

Adopted from "Introduction to machine learning by Delta Analytics"

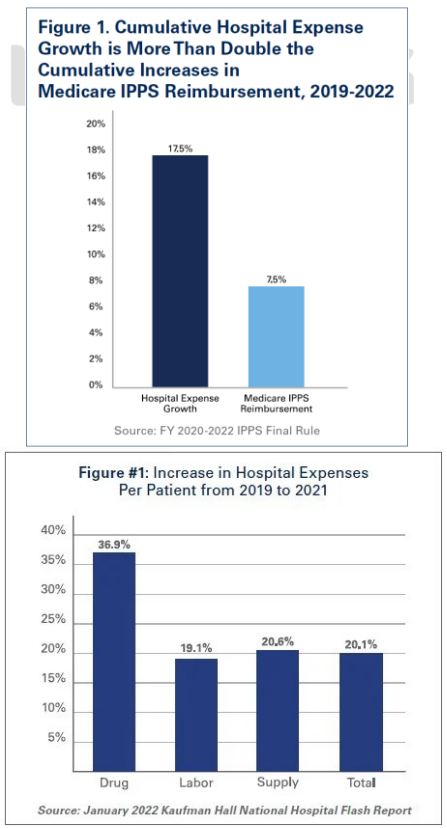
Introduction

- As the number of deaths due to chronic diseases rose annually, the cost of medical diagnosis, tests, and treatment also followed rising [2, 3] .

- Several methods and strategies should be developed as a solution to help individuals more easily and cost effectively check their health status, thus could help early detect the diseases and prevent from the occurrence of the worst-case scenario.



(a)



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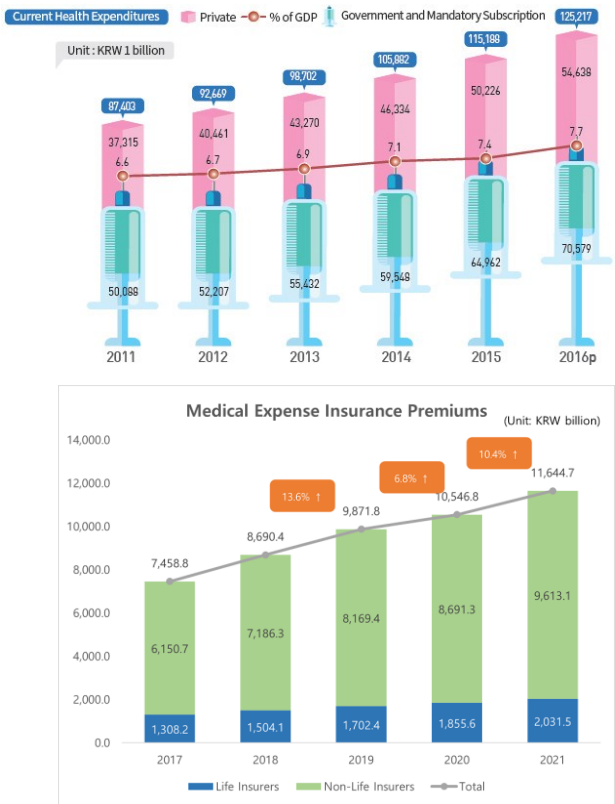

(c)

Fig 2. Total Health Expenditure of Indonesia (a), USA (b), Korea (c). [4, 5, 6, 7]

Adopted from "Introduction to machine learning by Delta Analytics"

Introduction

- One of the solutions that could be used to early detect the disease is machine learning-based prediction models development and utilization.
- Recent studies have utilized machine learning algorithms as decision-making tools to diagnose various diseases at an early stage, so that preventive action can be taken by individuals.
- The machine learning algorithms have showed high performance on predicting the diabetes [3, 8, 9, 10, 11], heart disease [12, 13, 14, 15], lung cancer [16, 17], and other diseases based on current conditions of individuals.

Disease	Author	Algorithm	Dataset	Accuracy (%)
Diabetes	Fitriyani et. al [3]	Forward Logistic Regression and MLP	NAGALA	92.11
	Patil et. al [8]	Decision Tree C4.5	The Pima Indians	92.38
	Wu et. al [9]	K-Mean and Logistic Regression	The Pima Indians	93.50
	Ijaz et. al [10]	DBSCAN+SMOTE+Random Forest	Dr John Schorling	92.55
	Fitriyani et. al [11]	iForest+SMOTETomek+Ensemble Learning	Dr John Schorling	100.00
Heart Disease	Bhatt et. al [12]	GridSearchCV+MLP	CVD (Kaggle)	87.28
	Fitriyani et. al [13]	DBSCAN+SMOTE-ENN+XGBOOST	Statlog Cleveland	95.90 98.40
	Ali et. al [14]	Stacked SVMs	Cleveland	92.22
	Gupta et. al [15]	FAMD + Random Forest	Cleveland	93.44
Lung Cancer	Dritsas and Trigka [16]	SMOTE + Rotation Forest	Lung Cancer (Kaggle)	97.10
	Alam et. al [17]	Watershed Transform + GLCM + SVM	Lung Cancer (UCI ML Rep)	97.00

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02

Machine Learning

Machine Learning

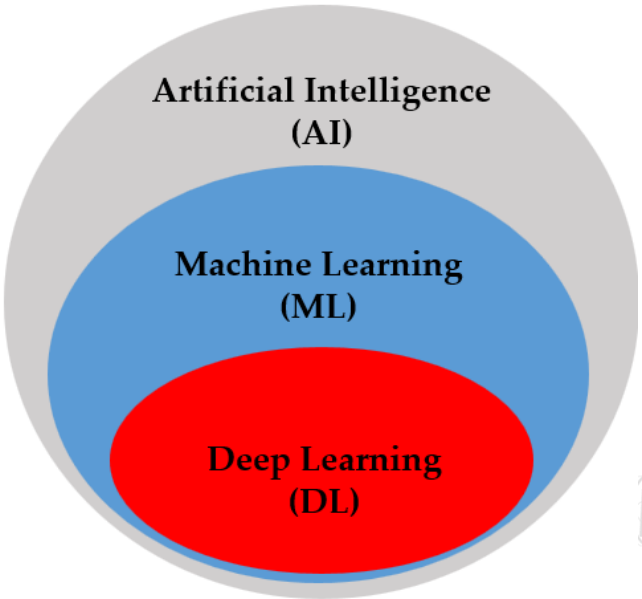

Fig 3. Hierarchy of AI, ML, and DL

ML is a subset of AI, which uses algorithms that learn from data to make predictions

Like a human would, the ML algorithm learns from historical data or past experiences and is thus able to make predictions about the future.

Fig 4. Machine learning concept

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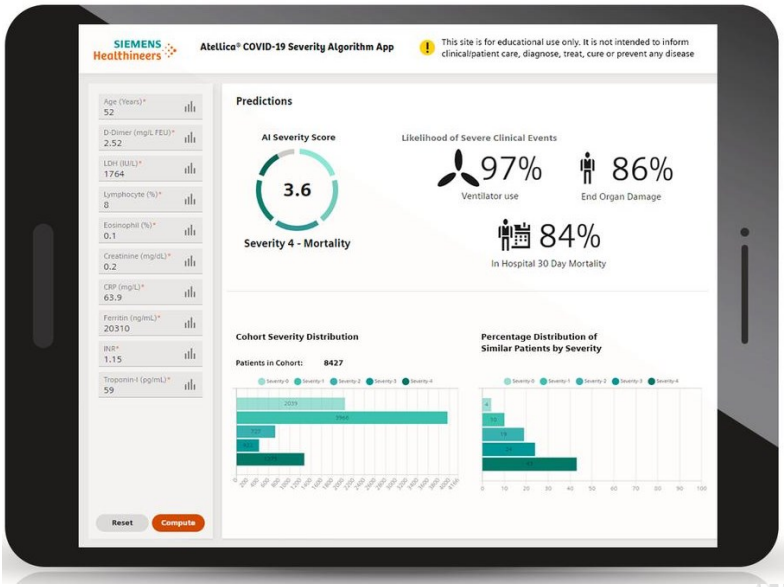
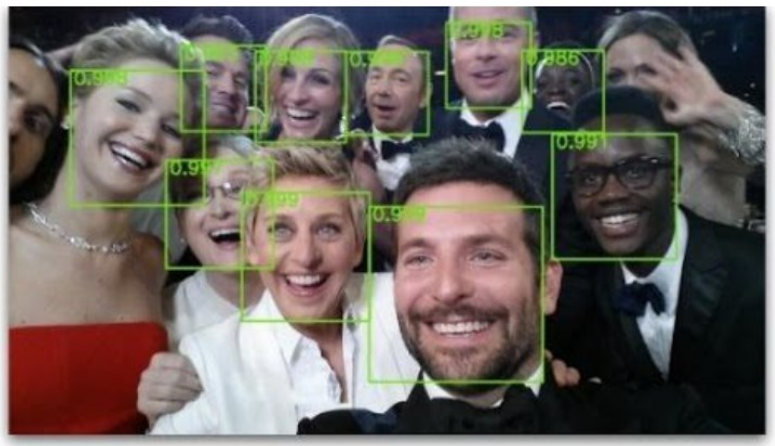
Machine Learning

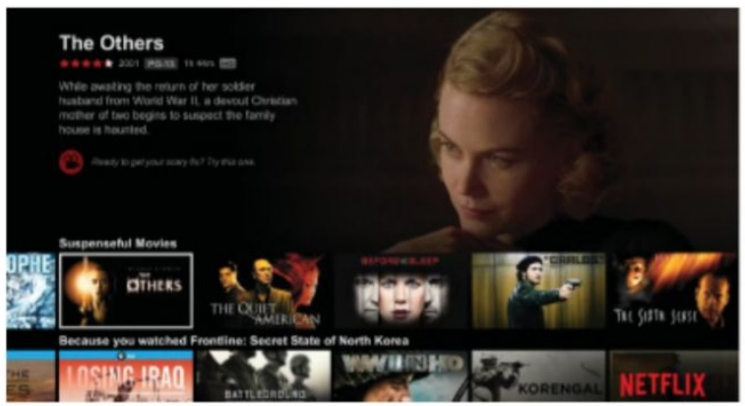
Machine learning is a powerful tool; it can…



Identify potential disease progression and predict disease



Recognize your face in a photo.



Recommend movies you will like.

Predict potential bank customer

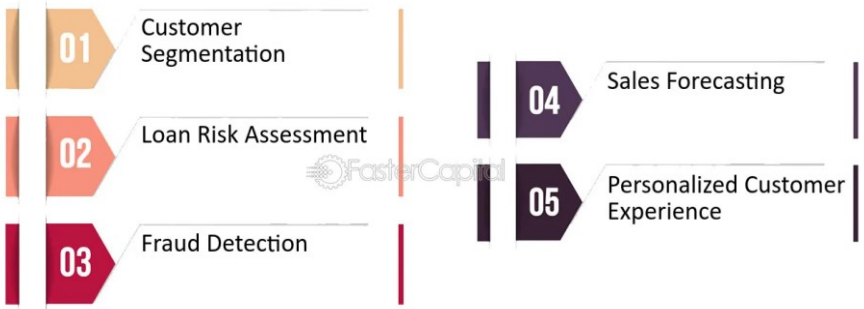


Fig 5. Real-case application of machine learning-based model in healthcare or medical

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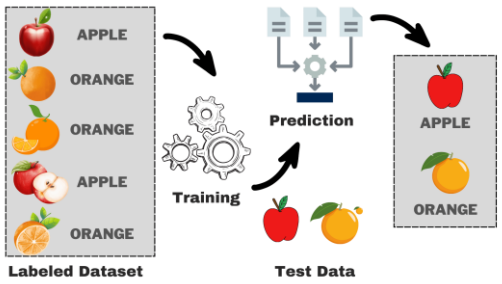
Machine Learning

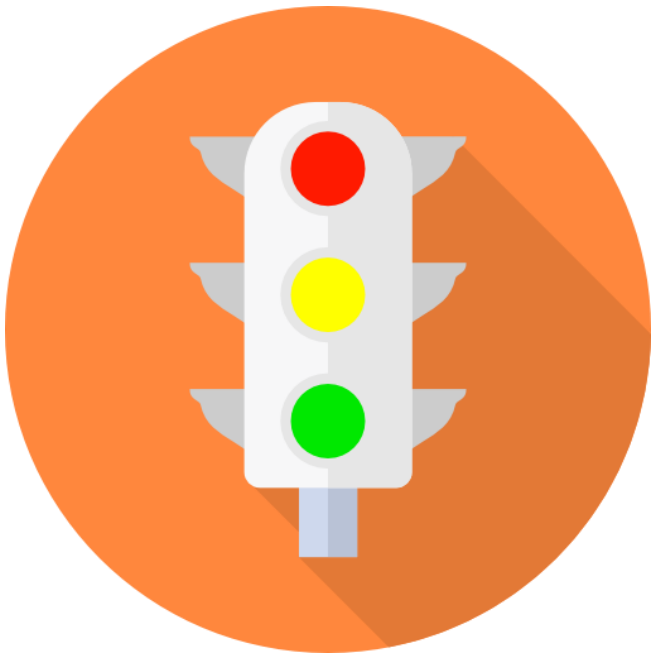
Types of Machine Learning Algorithms



ML Algorithm

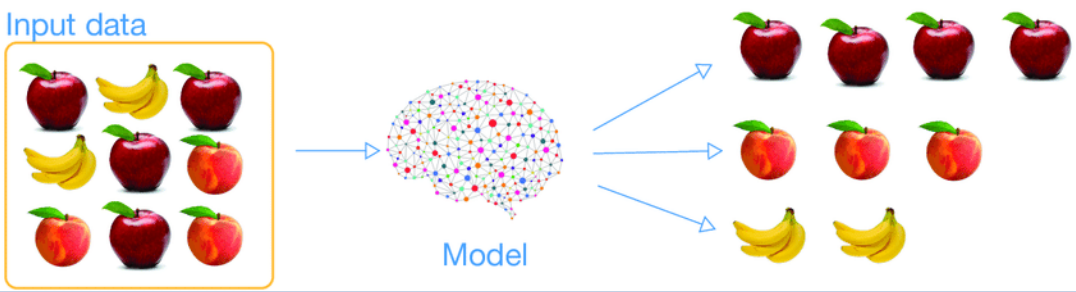
Labelled Data
(we have Y in our data)

Supervised learning



No Labelled Data
(we don't have Y in our data)

Unsupervised learning



clustering

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Machine Learning

Supervised learning task

The task function depends on the type of data the individual wants to predict. Supervised learning problems fall into two main categories: regression and classification.

The Task

Regression

Continuous variable

A regression problem is when we are trying to **predict a numerical value**, such as “stock price” or “blood sugar”

Classification

Categorical variable

A classification problem is when we are trying to **predict whether something belongs to a category**, such as “red” or “blue” or “disease” and “no disease”

We are here!

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Machine Learning

Supervised Machine Learning

- Logistic Regression
- Decision Tree
- K-Nearest Neighbor (KNN)
- Support Vector Machine (SVM)
- Neural Network : Multilayer Perceptron (MLP)
- Naïve Bayes
- Random Forest
- AdaBoost
- Extreme Gradient Boosting (XGB)
- LightGBM
- CatBoost

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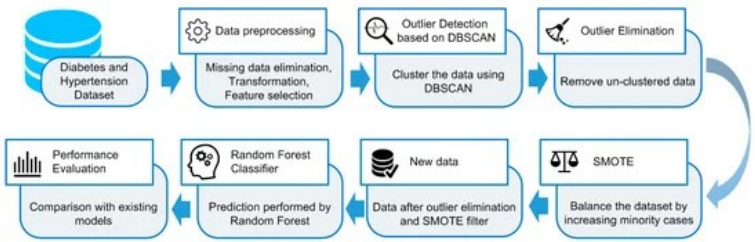
03

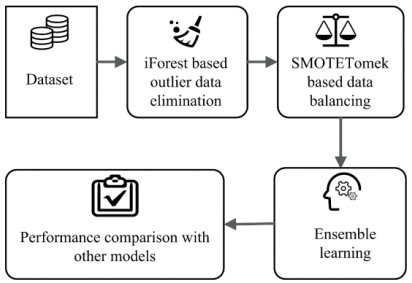
Machine Learning-based Disease Prediction Models

Development of machine learning-based disease prediction model

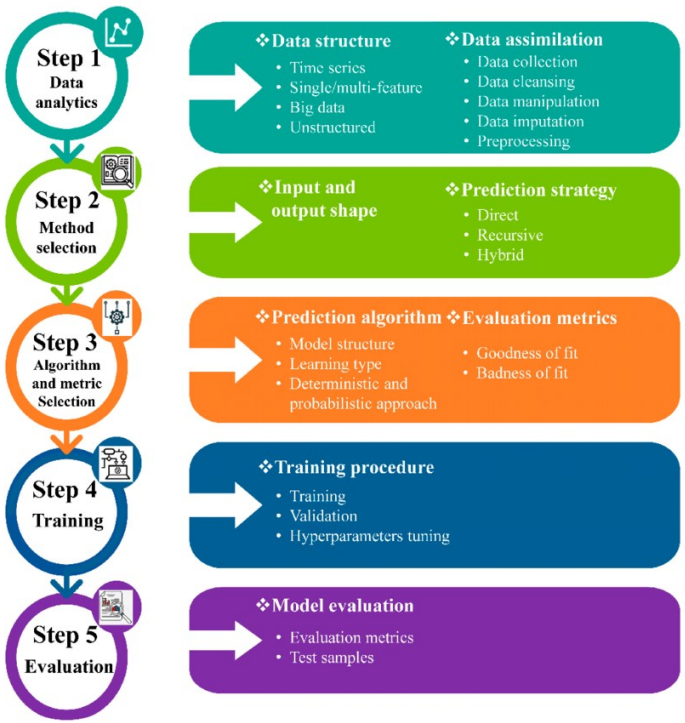
1. Data Collection
2. Data Preparation
3. Choose the Model/Algorithm
4. Training the Model
5. Evaluate the Model



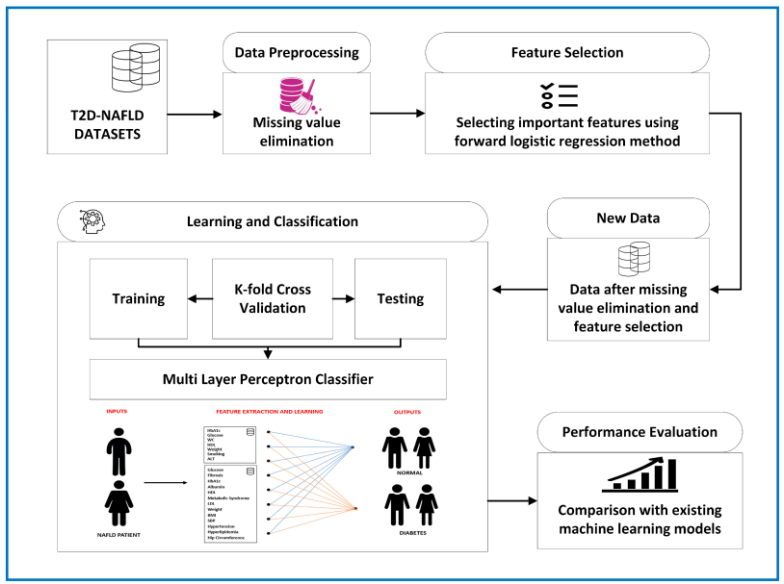
(b) [11]



(c) [12]



(d) [21]



(a) [3]

Fig 6. Machine learning-based model deployed in real-case health applications

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Development of machine learning-based disease prediction model

1. Data Collection

There are two main categories of data [22]:

Primary Data

- Primary data is newly collected data;
- It can be gathered directly from people's responses (surveys), or from their biometrics (blood pressure, weight, blood tests, etc.).
- The data is collected for other (medical) purposes by extracting the data from medical records.

Secondary Data

- Secondary data is data that already exists;
- It has already been published or complied.
- There are extant local, regional, national and international databases such as Public Health Data, government statistics, and WHO data. Public health data sources : UCI ML Repository, Kaggle, data.world, KHNES, NHIS, etc.

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Development of machine learning-based disease prediction model

1. Data Collection

Public health dataset example:

Age	Gender(I	Body Ma	Obesity	Hyperter	Hyperlip	Metaboli	Smoking_SI	AST	ALT	ALP	GGT	Total Ch	Triglycei	HDL	LDL	Glucose	Steatosis	Activity	Fibrosis	NAS sco	NAS sco	Fibrosis	Significa	Advance	Cirrhosis	Diagnosi	Type of Disease (Mild illness	Class
60	1	35.56	1	1	1	0	2	27	49	62	19	170	69	61	95	119	2	2	1	4	1	1	0	0	0	1	2	0
53	2	34.95	1	1	1	1	2	51	74	117	53	190	146	58	103	93	2	2	3	4	1	1	1	1	0	1	2	1
33	2	31.02	1	0	1	1	2	31	72	89	49	199	304	36	102	90	2	2	1	4	1	1	0	0	0	1	2	1
23	2	25.91	0	0	0	0	2	32	51	167	34	211	164	34	144	89	2	2	0	4	1	0	0	0	0	1	2	0
36	2	30.06	1	0	0	0	2	38	96	381	484	187	413	32	114	96	2	2	0	4	1	0	0	0	0	1	2	0
54	1	24.65	0	0	0	1	1	29	47	99	30	224	177	59	144	95	2	2	1	4	1	1	0	0	0	1	2	0
50	1	34.38	1	0	1	0	1	37	55	187	36	181	97	56	106	97	2	2	2	4	1	1	1	0	0	1	2	0
32	2	26.09	0	0	0	0	2	23	31	100	23	141	72	40	87	119	2	2	1	4	1	1	0	0	0	1	2	1
18	2	35.49	1	0	0	0	1	88	206	135	92	211	89	56	137	80	2	2	0	4	1	0	0	0	0	1	2	0
32	2	36.65	1	0	0	1	1	66	66	191	28	163	115	41	114	87	2	2	0	4	1	0	0	0	0	2	2	0
43	2	34.09	1	0	1	0	2	25	39	67	29	211	358	43	132	96	2	2	0	4	1	0	0	0	0	1	2	0
28	2	24.02	0	0	1	0	1	51	121	49	42	219	121	46	149	84	2	2	0	4	1	0	0	0	0	1	2	0
60	1	34.48	1	1	0	1	1	47	59	92	57	125	125	74	143	100	2	2	0	4	1	0	0	0	0	1	2	1
28	2	24.99	0	0	1	0	2	64	96	85	47	124	307	19	44	87	2	2	3	4	1	1	1	1	0	1	2	0
51	2	35.4	1	1	1	1	1	41	63	56	27	270	204	46	183	105	2	2	0	4	1	0	0	0	0	1	2	0
43	2	27.4	0	0	0	0	1	24	26	81	37	228	128	59	161	106	2	2	0	4	1	0	0	0	0	1	2	0
52	1	37.3	1	0	0	0	1	58	56	89	27	152	212	58	81	97	2	2	2	4	1	1	1	0	0	1	2	0
55	2	36.65	1	0	1	1	3	37	67	61	39	235	304	42	132	102	2	2	3	4	1	1	1	1	0	1	2	0
43	2	27.4	0	0	0	0	1	24	26	81	37	228	128	59	161	106	2	2	0	4	1	0	0	0	0	1	2	0
55	2	27.92	0	1	1	1	3	20	19	96	34	183	396	28	76	141	2	2	3	4	1	1	1	1	0	1	2	1
33	2	31.64	1	0	1	1	3	25	43	99	28	227	434	34	131	83	2	2	0	4	1	0	0	0	0	1	2	0
42	2	33.91	1	0	1	1	2	39	84	166	178	178	380	30	72	89	2	2	2	4	1	1	1	0	0	1	2	0
39	1	32.1	1	0	1	1	1	18	12	60	9	182	210	35	105	110	2	2	0	4	1	0	0	0	0	1	2	0
38	2	32	1	0	1	0	1	41	63	103	104	210	132	48	136	100	2	2	1	4	1	1	0	0	0	1	2	0
35	2	37.8	1	0	1	1	1	16	26	53	19	226	170	40	152	99	2	2	1	4	1	1	0	0	0	1	2	0
44	2	27.85	0	0	1	1	2	68	134	56	64	237	296	47	130	102	2	2	0	4	1	0	0	0	0	1	2	0
47	1	42.04	1	0	0	1	2	19	21	105	46	226	323	39	122	129	2	2	0	4	1	0	0	0	0	2	2	1

.....

563	63	2	28.61	0	1	1	1	2	36	55	48	65	283	215	40	200	115	1	4	1	6	0	1	0	0	0	1	2	0
564	44	1	40.3	1	0	1	1	1	30	39	77	29	183	106	60	110	133	1	4	3	6	0	1	1	1	0	1	2	1
565	44	1	40.35	1	0	1	1	1	30	39	77	29	183	106	60	110	133	1	4	3	6	0	1	1	1	0	1	2	1
566	64	2	29.74	0	1	1	1	3	20	20	65	176	170	262	49	58	112	1	4	3	6	0	1	1	1	0	1	2	1

565 rows × 29 columns

Development of machine learning-based disease prediction model

2. Data Preparation

- Data preparation in machine learning is the process of cleaning, transforming, and organizing raw data into a format that machine learning algorithms can understand.
- Processing the data into good quality data [22] due to lack quality of data.

Missing value elimination	Microsoft Excel, Python, etc.
Duplicate data elimination	Microsoft Excel, Python, etc.
Noise or outlier elimination	Isolation Forest, DBSCAN, Local Outlier Factor, standard deviation, interquartile range

- Processing the data due to the high quantity of data (size or dimension) that could affect the performance of the model.

Imbalance class distribution (high difference number of '+' and '–' class)	Too large data (number of features or dimension)
Over sampling Technique : SMOTE, ADSYN, Random Over Sampling (ROS) **Under sampling Technique :** Tomek Link, Random Under Sampling, NearMiss **Hybrid Technique :** SMOTE-ENN, SMOTE-Tomek	**Feature selection :** Information Gain, Chi Square Test, Fisher Score, Correlation Coefficient, Forward Selection, Backward Selection, Recursive Feature Elimination, Tree-based (RF, XGB) **Feature Extraction :** Principal Component Analysis

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Development of machine learning-based disease prediction model

2. Data Preparation

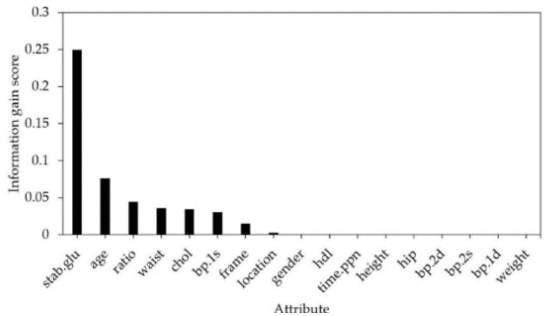

Fig 7. Feature selection based on Information Gain [11]

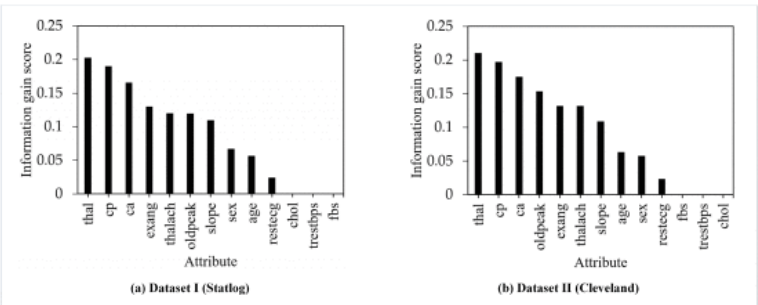

Fig 10. Feature selection based on Information Gain [13]

Dataset	*MinPts*	*eps*	# Outlier Data
Dataset I (Statlog)	5	9	3
Dataset II (Cleveland)	5	8	6

Fig 10. Outlier elimination based on DBSCAN [13]

Dataset	Before SMOTE-ENN		After SMOTE-ENN	
	Minority class (%)	Majority class (%)	Minority class (%)	Majority class (%)
I	44.19	55.81	50.79	49.21
II	46.05	53.95	49.5	50.5

Fig 11. Data balancing based on SMOTE-ENN[13]

Dataset	*MaxSample*	*NumTree*	Number of Outliers	Number of subjects before outlier removal	Number of subjects after outlier removal
I	41	100	94	403	309
II	18	100	36	175	139
III	23	100	38	224	186
IV	40	100	156	398	242

Fig 8. Outlier elimination based on Isolation Forest [11]

Dataset	Before SMOTETomek		After SMOTETomek	
	Minority (%)	Majority (%)	Minority (%)	Majority (%)
I	15 (4.85%)	294 (95.15%)	293 (50%)	293 (50%)
II	31 (22.30%)	108 (77.70%)	99 (50%)	99 (50%)
III	73 (39.25%)	113 (60.75%)	94 (50%)	94 (50%)
IV	51 (21.07%)	191 (78.93%)	191 (50%)	191 (50%)

Fig 9. Data balancing based on SMOTETomek [11]

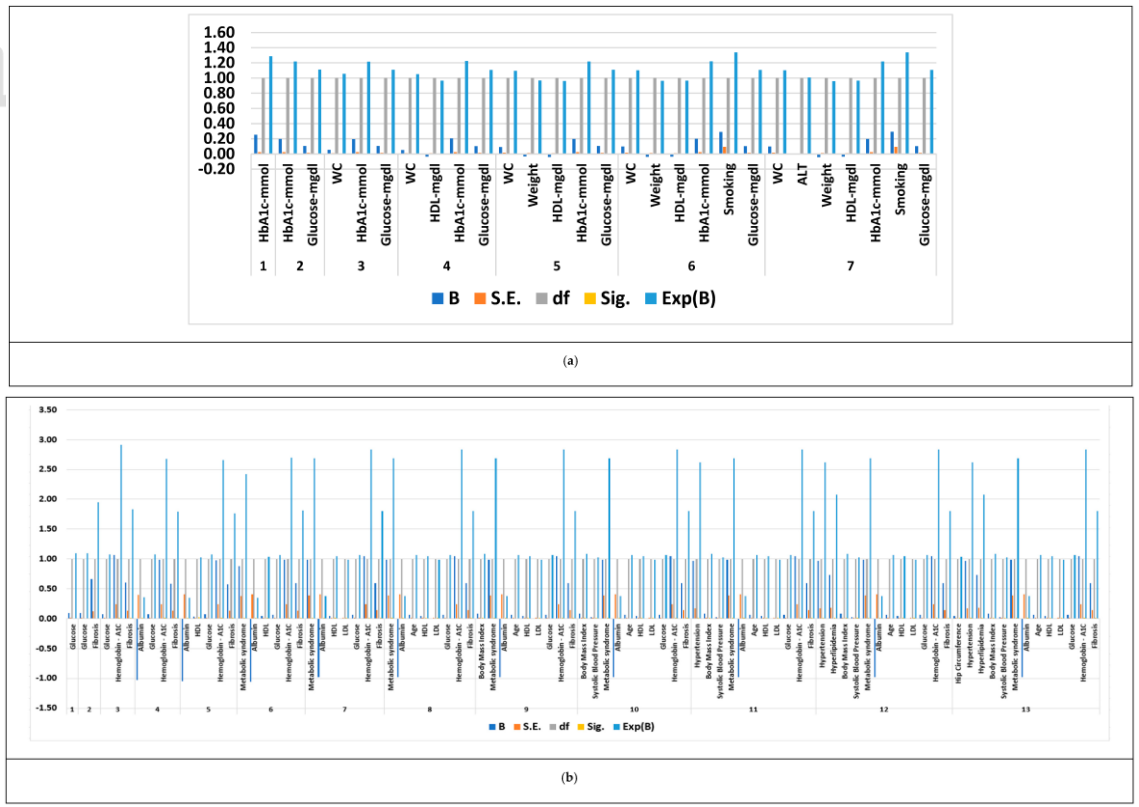

Fig 12. Feature selection based on Forward LR [3]

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Development of machine learning-based disease prediction model

3. Choose the Model/Algorithm

- In machine learning, choosing the right model is one of the most important steps in building a successful predictive model.
- Choosing the wrong model can lead to poor performance, wasted time and resources, and inaccurate results.

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Development of machine learning-based disease prediction model

3. Choose the Model/Algorithm

- Steps to choose the right machine learning model:

- **Define the problem** : the researcher needs to understand what kind of problem he/she is dealing with. Is it a classification problem or a regression problem? is he/she trying to predict a categorical or continuous outcome?

- **Consider the data** : the researcher should know the *feature types* (numerical or categorical, text or image), different models may be better suited for different feature types. *Feature importance:* are all features equally important, or are some more important than others? If some features are more important, and want to use a model that can perform feature selection or feature weighting, such as random forests [23]. *Data size*: how much data does the researcher have? If the dataset is small, simpler models may be more appropriate to avoid overfitting [23]. If dataset is large, more complex models may be able to capture the patterns. *Data distribution*: Is the data distribution balanced or imbalanced?

- **Evaluate different models or conducting model comparison:** each type of model has its own strengths and weaknesses, and it's important to evaluate each one carefully to determine which is best suited for the researcher's problem.

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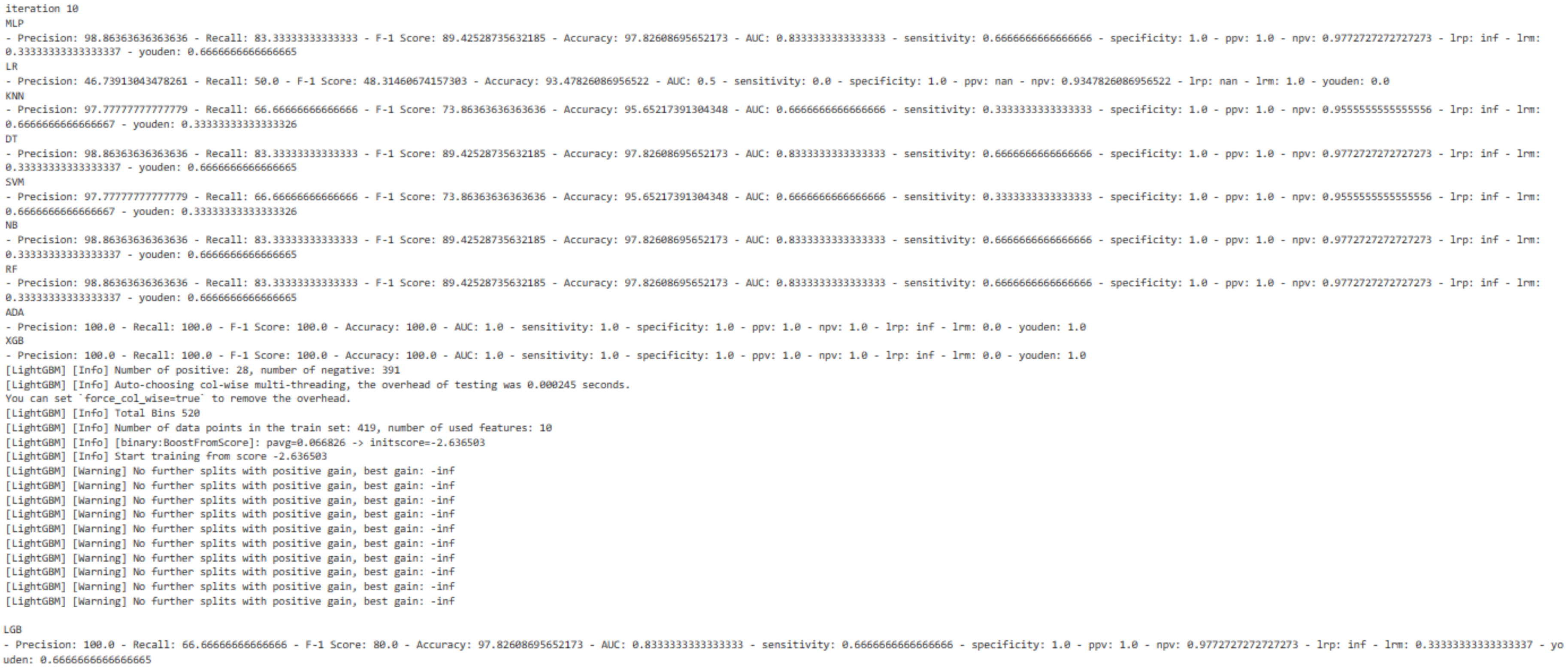
Development of machine learning-based disease prediction model

4. Training the Model

- Model training is the stage where the ML algorithm is trained by feeding datasets.
- Model training in machine language is the process of feeding an ML algorithm with data to help identify and demonstrate correlation between the input data and outcomes.



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iteration 10
MLP
- Precision: 98.86363636363636 - Recall: 83.33333333333333 - F-1 Score: 89.42528735632185 - Accuracy: 97.82608695652173 - AUC: 0.8333333333333333 - sensitivity: 0.6666666666666666 - specificity: 1.0 - ppv: 1.0 - npv: 0.9772727272727273 - lrp: inf - lrm:
0.33333333333333337 - youden: 0.6666666666666665
LR
- Precision: 46.73913043478261 - Recall: 50.0 - F-1 Score: 48.31460674157303 - Accuracy: 93.47826086956522 - AUC: 0.5 - sensitivity: 0.0 - specificity: 1.0 - ppv: nan - npv: 0.9347826086956522 - lrp: nan - lrm: 1.0 - youden: 0.0
KNN
- Precision: 97.77777777777779 - Recall: 66.66666666666666 - F-1 Score: 73.86363636363636 - Accuracy: 95.65217391304348 - AUC: 0.6666666666666666 - sensitivity: 0.3333333333333333 - specificity: 1.0 - ppv: 1.0 - npv: 0.9555555555555556 - lrp: inf - lrm:
0.6666666666666667 - youden: 0.33333333333333326
DT
- Precision: 98.86363636363636 - Recall: 83.33333333333333 - F-1 Score: 89.42528735632185 - Accuracy: 97.82608695652173 - AUC: 0.8333333333333333 - sensitivity: 0.6666666666666666 - specificity: 1.0 - ppv: 1.0 - npv: 0.9772727272727273 - lrp: inf - lrm:
0.33333333333333337 - youden: 0.6666666666666665
SVM
- Precision: 97.77777777777779 - Recall: 66.66666666666666 - F-1 Score: 73.86363636363636 - Accuracy: 95.65217391304348 - AUC: 0.6666666666666666 - sensitivity: 0.3333333333333333 - specificity: 1.0 - ppv: 1.0 - npv: 0.9555555555555556 - lrp: inf - lrm:
0.6666666666666667 - youden: 0.33333333333333326
NB
- Precision: 98.86363636363636 - Recall: 83.33333333333333 - F-1 Score: 89.42528735632185 - Accuracy: 97.82608695652173 - AUC: 0.8333333333333333 - sensitivity: 0.6666666666666666 - specificity: 1.0 - ppv: 1.0 - npv: 0.9772727272727273 - lrp: inf - lrm:
0.33333333333333337 - youden: 0.6666666666666665
RF
- Precision: 98.86363636363636 - Recall: 83.33333333333333 - F-1 Score: 89.42528735632185 - Accuracy: 97.82608695652173 - AUC: 0.8333333333333333 - sensitivity: 0.6666666666666666 - specificity: 1.0 - ppv: 1.0 - npv: 0.9772727272727273 - lrp: inf - lrm:
0.33333333333333337 - youden: 0.6666666666666665
ADA
- Precision: 100.0 - Recall: 100.0 - F-1 Score: 100.0 - Accuracy: 100.0 - AUC: 1.0 - sensitivity: 1.0 - specificity: 1.0 - ppv: 1.0 - npv: 1.0 - lrp: inf - lrm: 0.0 - youden: 1.0
XGB
- Precision: 100.0 - Recall: 100.0 - F-1 Score: 100.0 - Accuracy: 100.0 - AUC: 1.0 - sensitivity: 1.0 - specificity: 1.0 - ppv: 1.0 - npv: 1.0 - lrp: inf - lrm: 0.0 - youden: 1.0
[LightGBM] [Info] Number of positive: 28, number of negative: 391
[LightGBM] [Info] Auto-choosing col-wise multi-threading, the overhead of testing was 0.000245 seconds.
You can set `force_col_wise=true` to remove the overhead.
[LightGBM] [Info] Total Bins 520
[LightGBM] [Info] Number of data points in the train set: 419, number of used features: 10
[LightGBM] [Info] [binary:BoostFromScore]: pavg=0.066826 -> initscore=-2.636503
[LightGBM] [Info] Start training from score -2.636503
[LightGBM] [Warning] No further splits with positive gain, best gain: -inf
[LightGBM] [Warning] No further splits with positive gain, best gain: -inf
[LightGBM] [Warning] No further splits with positive gain, best gain: -inf
[LightGBM] [Warning] No further splits with positive gain, best gain: -inf
[LightGBM] [Warning] No further splits with positive gain, best gain: -inf
[LightGBM] [Warning] No further splits with positive gain, best gain: -inf
[LightGBM] [Warning] No further splits with positive gain, best gain: -inf
[LightGBM] [Warning] No further splits with positive gain, best gain: -inf
[LightGBM] [Warning] No further splits with positive gain, best gain: -inf
[LightGBM] [Warning] No further splits with positive gain, best gain: -inf

LGB
- Precision: 100.0 - Recall: 66.66666666666666 - F-1 Score: 80.0 - Accuracy: 97.82608695652173 - AUC: 0.8333333333333333 - sensitivity: 0.6666666666666666 - specificity: 1.0 - ppv: 1.0 - npv: 0.9772727272727273 - lrp: inf - lrm: 0.33333333333333337 - yo
uden: 0.6666666666666665
```

Fig 13. Model training

Adapted from “Machine learning deep dive by Delta Analytics

Development of machine learning-based disease prediction model

5. Evaluating the Model

- The model evaluation is a step where the performance of the model is tested on previously unseen data.
- The unseen data used is the testing set that is split from the master dataset before model selection.
- The performance of the model is evaluated used numerous evaluation metrics in machine learning such as accuracy, precision or positive predictive value (ppv), recall or sensitivity or true positive rate (tpr), negative predictive value (npv), f1 score, specificity, area under the curve (AUC), etc.

MLP	LR	KNN	DT	SVM
Final Acc: 96.559	Final Acc: 94.408	Final Acc: 93.978	Final Acc: 96.785	Final Acc: 96.341
Final Prec: 93.234	Final Prec: 67.185	Final Prec: 61.975	Final Prec: 88.800	Final Prec: 93.125
Final Spec: 74.583	Final Spec: 58.333	Final Spec: 55.000	Final Spec: 88.247	Final Spec: 72.917
Final Rec: 74.583	Final Rec: 58.333	Final Rec: 55.000	Final Rec: 88.247	Final Rec: 72.917
Final F1: 80.097	Final F1: 60.048	Final F1: 55.938	Final F1: 86.591	Final F1: 78.541
Final AUC: 0.746	Final AUC: 0.583	Final AUC: 0.550	Final AUC: 0.882	Final AUC: 0.729

NB	RF	ADA	XGB	LightGBM
Final Acc: 87.405	Final Acc: 96.989	Final Acc: 96.998	Final Acc: 97.428	Final Acc: 96.984
Final Prec: 83.009	Final Prec: 93.964	Final Prec: 90.437	Final Prec: 87.000	Final Prec: 91.667
Final Spec: 83.239	Final Spec: 83.704	Final Spec: 86.810	Final Spec: 90.144	Final Spec: 82.154
Final Rec: 83.239	Final Rec: 83.704	Final Rec: 86.810	Final Rec: 81.667	Final Rec: 65.000
Final F1: 78.524	Final F1: 86.400	Final F1: 87.186	Final F1: 79.810	Final F1: 71.476
Final AUC: 0.832	Final AUC: 0.837	Final AUC: 0.868	Final AUC: 0.901	Final AUC: 0.822

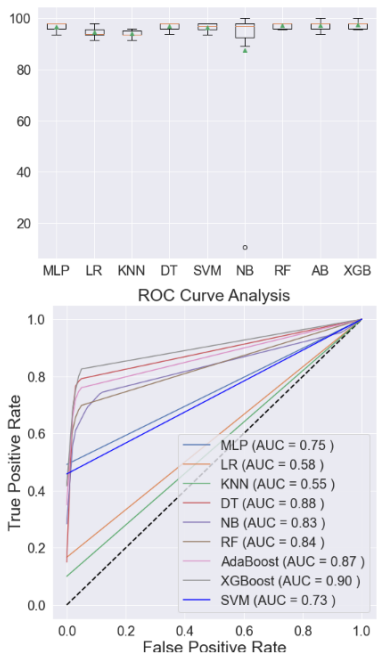


Fig 14. Model Performance

Adapted from "Machine learning deep dive by Delta Analytics"

Development of machine learning-based disease prediction model

5. Evaluating the Model

Model	Performance evaluation							
	acc (%)	*pre* (%)	*rec/sen/TPR* (%)	*f* (%)	*MCC*	*FPR* (%)	*FNR* (%)	*TNR* (%)
NB	84.07 ± 4.70	84.36 ± 7.85	80.00 ± 9.28	81.61 ± 5.46	0.68 ± 0.10	12.67 ± 7.57	20.00 ± 9.28	87.33 ± 7.57
LR	84.81 ± 4.21	85.49 ± 7.38	80.83 ± 11.81	82.21 ± 5.71	0.70 ± 0.08	12.00 ± 7.18	19.17 ± 11.81	88.00 ± 7.18
MLP	85.56 ± 4.21	86.12 ± 6.52	81.67 ± 12.25	82.99 ± 6.03	0.67 ± 0.12	11.33 ± 6.00	18.33 ± 12.25	88.67 ± 6.00
SVM	69.63 ± 7.37	72.90 ± 11.29	50.83 ± 10.83	59.52 ± 10.17	0.38 ± 0.16	15.33 ± 7.33	49.17 ± 10.83	84.67 ± 7.33
DT	74.81 ± 8.57	74.28 ± 13.61	70.83 ± 12.50	71.39 ± 9.27	0.49 ± 0.17	3.33 ± 12.74	28.33 ± 11.90	76.67 ± 12.74
RF	82.96 ± 8.15	85.15 ± 10.71	75.83 ± 12.05	79.64 ± 9.70	0.68 ± 0.14	12.00 ± 8.33	23.33 ± 11.06	88.00 ± 8.33
Proposed HDPM	**95.90 ± 5.55**	**97.14 ± 5.71**	**94.67 ± 11.08**	**95.35 ± 6.52**	**0.92 ± 0.10**	4.52 ± 6.94	3.33 ± 6.67	95.48 ± 6.94

Note: *acc* = accuracy, *pre* = Precision, *rec/sen/TPR* = recall/ sensitivity/ true positive rate, *f* = f-measure, *MCC* = Matthews correlation coefficient, FPR = false positive rate, FNR = false negative rate, TNR = true negative rate.

(a)

Model	Performance evaluation							
	acc (%)	*pre* (%)	*rec/sen/TPR* (%)	*f* (%)	*MCC*	*FPR* (%)	*FNR* (%)	*TNR* (%)
NB	83.17 ± 7.64	84.18 ± 9.75	78.79 ± 8.29	81.25 ± 8.29	0.66 ± 0.15	13.12 ± 8.59	21.21 ± 8.29	86.88 ± 8.59
LR	84.85 ± 6.91	86.12 ± 7.85	80.22 ± 9.30	82.90 ± 7.80	0.70 ± 0.14	11.25 ± 6.73	19.78 ± 9.30	88.75 ± 6.73
MLP	84.15 ± 7.76	85.01 ± 9.74	80.22 ± 9.83	82.28 ± 8.66	0.68 ± 0.12	14.37 ± 9.29	18.41 ± 9.22	85.62 ± 9.29
SVM	71.06 ± 6.16	74.65 ± 9.51	59.23 ± 14.88	64.53 ± 9.43	0.43 ± 0.12	18.75 ± 10.46	40.77 ± 14.88	81.25 ± 10.46
DT	76.09 ± 4.86	74.21 ± 7.29	75.16 ± 8.00	74.31 ± 5.18	0.52 ± 0.09	24.38 ± 8.12	27.80 ± 7.31	75.62 ± 8.12
RF	82.14 ± 6.84	83.69 ± 8.63	76.54 ± 10.09	79.63 ± 8.36	0.66 ± 0.13	12.50 ± 8.39	22.03 ± 10.27	87.50 ± 8.39
Proposed HDPM	**98.40 ± 3.21**	**98.57 ± 4.29**	**98.33 ± 5.00**	**98.32 ± 3.37**	**0.97 ± 0.06**	1.67 ± 5.00	0.00 ± 0.00	98.33 ± 5.00

(b)

Fig 15. Performance of the machine learning models for predicting heart disease in combination with the Information Gain-based feature selection, DBSCAN-based outlier removal, SMOTE-ENN-based data balancing methods in Cleveland (a) and Statlog (b) datasets [13]

Classification model	Performance metric				
	p (%)	*r* (%)	*f* (%)	*acc* (%)	AUC
MLP	52.59	48.57	45.08	84.9	0.85
SVM	88.235	41.096	56.075	81.9	0.62
DT	36.37	42.68	32.18	69.69	0.59
LR	52.5	47.14	43.77	84.9	0.91
K-means + LR [16]	91.6	96.4	-	90.7	0.957
DBSCAN + SMOTE + RF [40]	91.497	93.403	92.440	92.555	-
Proposed DPM	94.49	98.62	96.32	96.74	0.99

(a)

Classification model	Performance metric				
	p (%)	*r* (%)	*f* (%)	*acc* (%)	AUC
MLP	73.23	97.56	83.56	72.02	0.5
SVM	73.04	99.17	84.1	72.58	0.45
DT	71.35	69.42	70.13	56.96	0.46
LR	73.67	95.06	82.77	71.33	0.58
CART [19]	-	58.38	-	-	0.68
DBSCAN + SMOTE + RF [40]	78.788	70.270	74.286	76.419	-
Proposed DPM	93.57	84.89	88.8	85.73	0.87

(b)

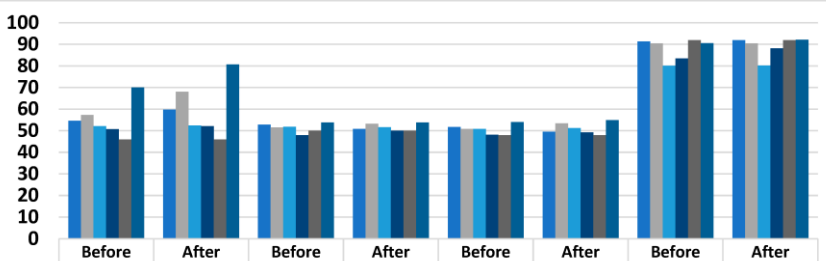
Classification model	Performance metric				
	p (%)	*r* (%)	*f* (%)	*acc* (%)	AUC
MLP	57.31	69.81	57	54.92	0.53
SVM	56.38	85.26	67.77	53.48	0.44
DT	57.33	54.1	54.69	49.96	0.49
LR	61.53	82.76	69.52	59.41	0.62
CART [19]	-	45.65	-	-	0.566
Proposed DPM	75.6	81.78	77.12	75.78	0.76

(c)

Classification model	Performance metric				
	p (%)	*r* (%)	*f* (%)	*acc* (%)	AUC
MLP	67.78	70.49	67.02	80.84	0.89
SVM	64.49	57.69	56.66	75.85	0.77
DT	61.48	56.43	56.13	72.48	0.75
LR	67.98	77.14	69.67	81.57	0.89
DBSCAN + SMOTE + RF [40]	83.665	84.677	84.168	83.644	-
Proposed DPM	100	100	100	100	1

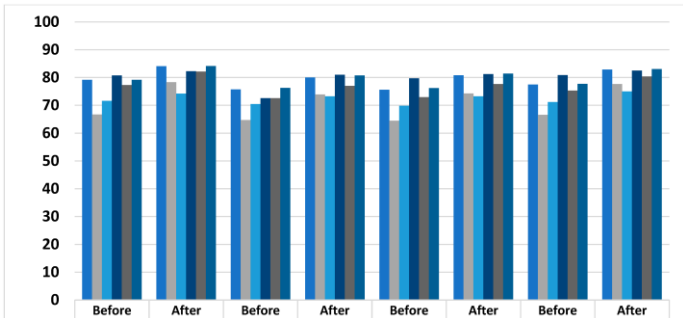
(d)

Fig 16. Performance of the machine learning models for predicting T2D and hypertension in combination with the Information Gain-based feature selection, iForest-based outlier removal, SMOTETomek-based data balancing methods [11] in Dr John Schorling (a), Golino et al male hypertension (b), Golino et al female prehypertension (c), and Dr. P. Soundarapandian, M.D., D.M CKD datasets [11]



	Before	After	Before	After	Before	After	Before	After
	Precision (%)		Recall (%)		F1 (%)		Accuracy (%)	
LR	54.62	59.74	52.81	50.81	51.72	49.51	91.34	91.85
KNN	57.26	68.01	51.46	53.13	50.83	53.39	90.43	90.43
DT	52.06	52.42	51.77	51.64	50.83	51.17	80.04	80.12
XGB	50.73	52.04	47.92	50.02	48.08	49.20	83.48	88.12
SVM	45.93	45.93	50.00	50.00	47.88	47.88	91.85	91.85
MLP	69.99	80.69	53.75	53.78	53.97	54.84	90.46	92.11

(a)



	Before	After	Before	After	Before	After	Before	After
	Precision (%)		Recall (%)		F1 (%)		Accuracy (%)	
LR	79.13	84.06	75.68	80.01	75.56	80.80	77.47	82.87
KNN	66.68	78.30	64.68	73.91	64.45	74.27	66.59	77.66
DT	71.57	74.22	70.45	73.26	69.81	73.23	71.19	74.96
XGB	80.73	82.25	72.54	80.97	79.71	81.22	80.88	82.48
SVM	77.28	82.12	72.58	76.98	72.92	77.64	75.31	80.35
MLP	79.19	84.12	76.23	80.74	76.20	81.37	77.71	83.05

(b)

Fig 17. Performance of the machine learning models for predicting T2D in patient with NAFLD in combination with forward logistic regression in NAGALA (a) and NAFLD (b) datasets [3]

Important

What should be concerned when evaluating the disease prediction model's performance?

- In order to evaluate the classification model's performance, a summarized table called the confusion matrix is used.
- The confusion matrix consists of four categories:

1. **True Negative (TN)** represents the number of samples correctly classified or predicted as belonging to the negative class. For example, the actual class is negative (0), and the predicted class is also negative (0).
2. **True Positive (TP)** represents the number of samples correctly classified or predicted as belonging to the positive class. For example, the actual class is positive (1), and the predicted class is also positive (1).
3. **False Negative (FN)** represents the number of samples incorrectly predicted as the negative class. For example, the actual class is positive (1), but the predicted class is negative (0).
4. **False Positive (FP)** represents the number of samples incorrectly predicted as the positive class. For example, the actual class is negative (0), but the predicted class is positive (1).

		MODEL'S PREDICTED VALUE	
		0	1
ACTUAL VALUE	0	True negative (TN)	False positive (FP)
	1	False negative (FN)	True positive (TP)

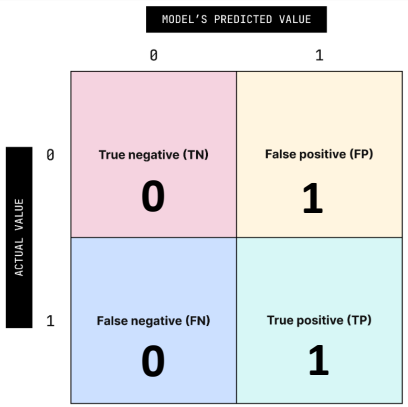
- According to Hicks et al [24], the most commonly used for evaluating the performance of the ML-based disease prediction model are accuracy, recall or sensitivity or true positive rate (tpr), precision or positive predictive value (ppv), negative predictive value (npv), f1 score, Matthew's correlation coefficient (MCC), and threat score (TS).

Adapted from "Machine learning deep dive by Delta Analytics"

Performance Evaluation

confusion matrix

y6 (predict) = y'	y target (actual) = y
1	1
1	0
1	1
1	0
1	0
1	0
1	0
1	1
1	0
1	1



- **Accuracy :** percentage of correctly classified samples over the total number of samples. Accuracy measures the overall correctness of the model's predictions.

$$\text{Accuracy} = \frac{TN+TP}{TN+TP+FP+FN}$$

$$\text{Testing Accuracy} = \frac{0+1}{0+1+1+0} = 0.5 = 50\ \%$$

- **Recall/Sensitivity/TPR :** the ratio between correctly classified positive samples and all samples assigned to the positive class [23]. When it's actually yes, how often does it predict yes?

$$\text{Recall} = \frac{TP}{Actual\ Yes\ (1)} = \frac{TP}{TP+FN}$$

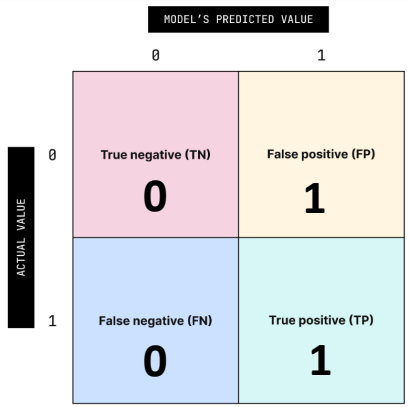
$$\text{Testing Recall} = \frac{1}{1+0} = 1 = 100\ \%$$

Adapted from "Machine learning deep dive by Delta Analytics"

Performance Evaluation

confusion matrix

y6 (predict) = y'	y target (actual) = y
1	1
1	0
1	1
1	0
1	0
1	0
1	0
1	1
1	0
1	1



- **Precision/Positive Predictive Value (PPV) :** the ratio between correctly classified samples and all samples assigned to that class. When it predicts yes, how often is it correct?

$$\text{Precision} = \frac{TP}{Predicted\ Yes\ (1)} = \frac{TP}{TP+FP}$$

$$\text{Testing Precision} = \frac{1}{1+1} = 0.5 = 50\ \%$$

- **Negative Predictive Value (NPV) :** the ratio between correctly classified negative samples and all samples classified as negative. When it predicts no, how often is it correct?

$$\text{NVP} = \frac{TN}{Predicted\ No(0)} = \frac{TN}{TN+FN}$$

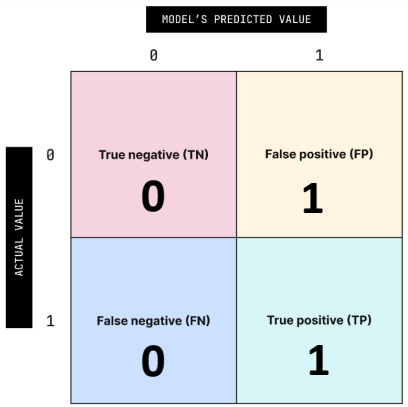
$$\text{Testing NPV} = \frac{0}{0+0} = \frac{0}{0} = 0 = 0\ \%$$

Adapted from "Machine learning deep dive by Delta Analytics"

Performance Evaluation

confusion matrix

y6 (predict) = y'	y target (actual) = y
1	1
1	0
1	1
1	0
1	0
1	0
1	0
1	1
1	0
1	1



- **F1 score :** represents the harmonic mean or weighted average of precision and recall. A large F1 score of 1 indicates excellent precision and recall, while a low score indicates poor model performance.

$$\text{F1 score} = \frac{2\ x\ precision\ x\ recall}{precision + recall}$$

$$\text{Testing F1} = \frac{2\ x\ 0.5\ x\ 1}{0.5+1} = \frac{1}{1.5} = 0.6667 = 66.67\ \%$$

- **Specificity/True Negative Rate :** how often the model predicts a negative for a value that is actually negative.

$$\text{Specificity} = \frac{TN}{Actual\ No(0)} = \frac{TN}{TN+FP}$$

$$\text{Testing Specificity} = \frac{0}{0+1} = 0 = 0\ \%$$

Adapted from "Machine learning deep dive by Delta Analytics"

04

Machine Learning-based Model for Disease Prediction Applications

Machine Learning-based Model for Disease Prediction Applications

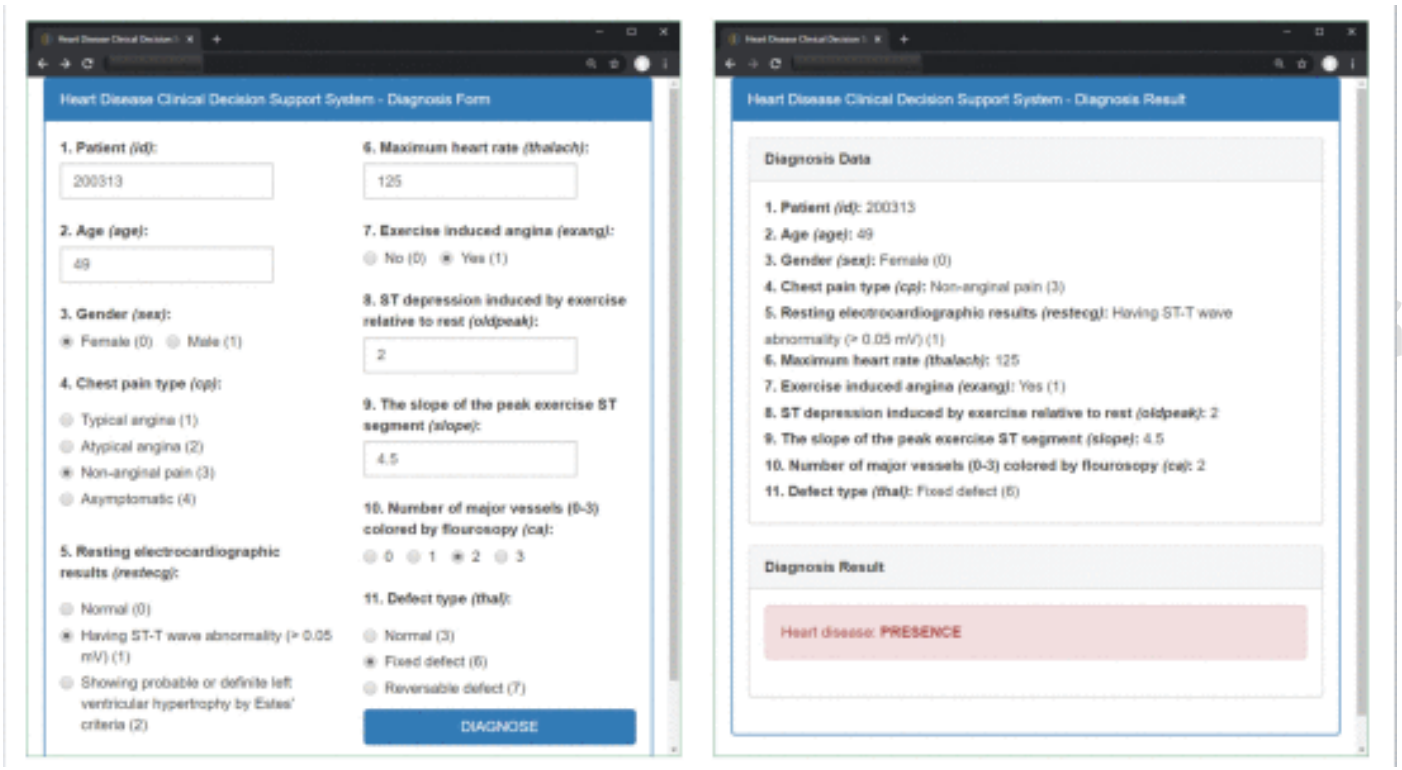


Fig 20. Web-based heart disease clinical support system [3]

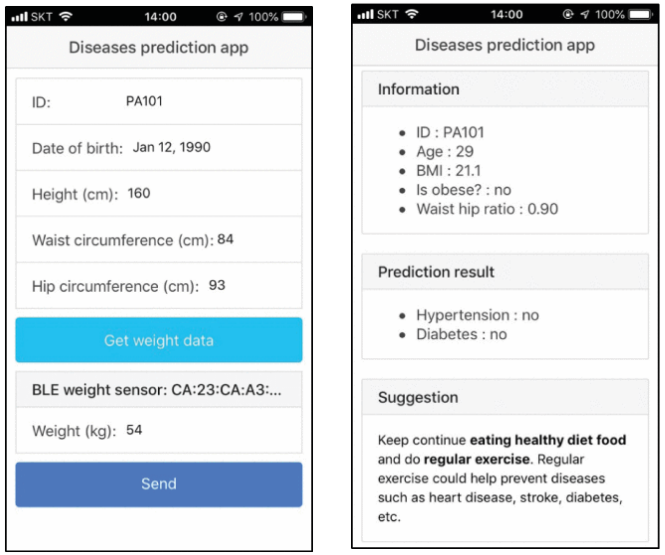


Fig 19. Web-based disease prediction application [11]

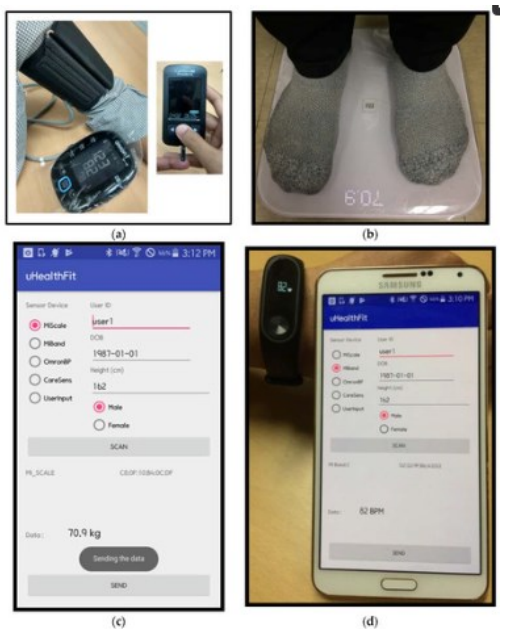
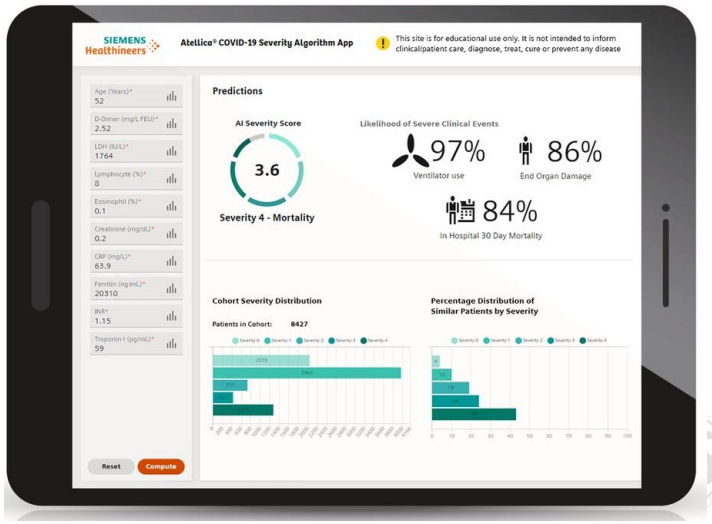


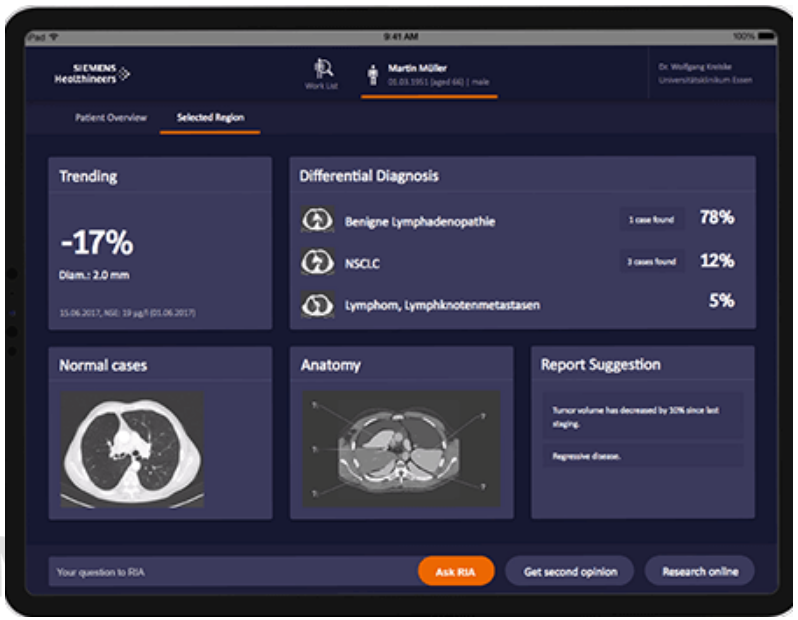
Fig 21. Personalize healthcare monitoring system [25]

Adopted from "Introduction to machine learning by Delta Analytics"

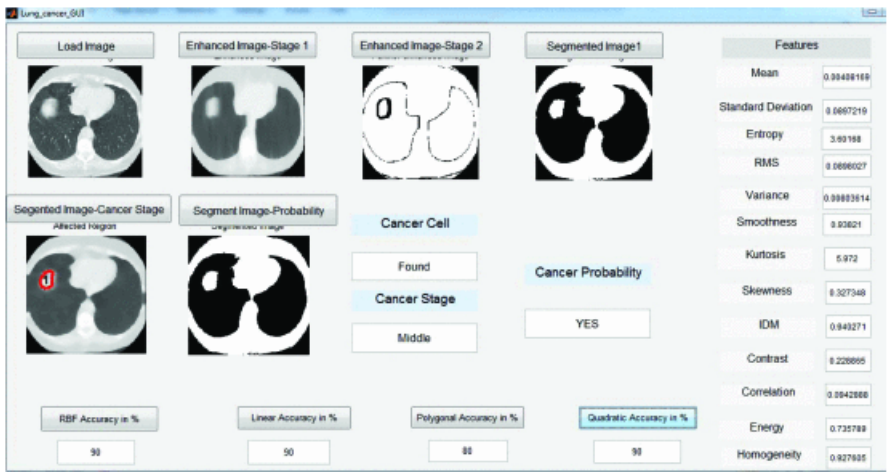
Machine Learning-based Model for Disease Prediction Applications

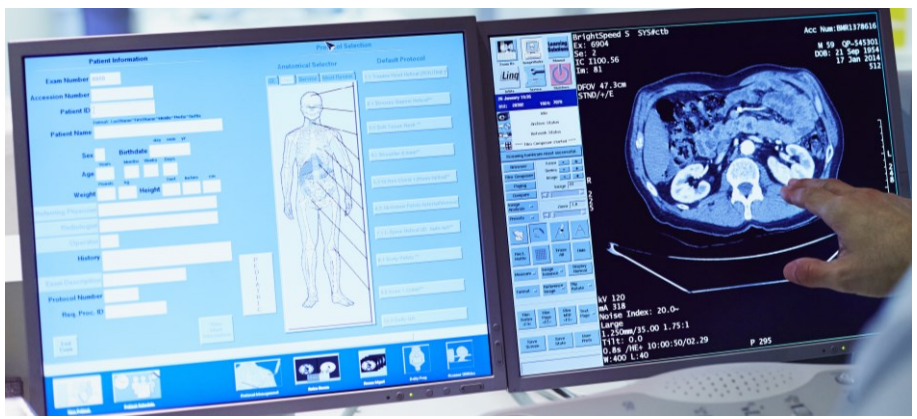


(a) Siemens Healthineers - Prediction and early identification of disease: identify potential disease progression in COVID-19 patient [18]



(b) Siemens Healthineers - Prediction and early identification of lung disease [19]





(c) and (d) Health system – detection and prediction lung cancer utilized by medical institutions [17, 20]

Fig 22. Real-case application of machine learning-based model in healthcare or medical

Adopted from "Introduction to machine learning by Delta Analytics"

05

Conclusion

05 Conclusion

- Machine learning is a powerful tool that can be utilized as one of the alternatives to early detection of the disease.
- By utilizing ML as a disease prediction tool, it could help individuals know their current health status, thus preventing the occurrence of the worst-case scenario.
- Not only in the healthcare or medical domain, but machine learning has also been widely utilized in many other domains.

06 References

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Thank you for your attention!
Any questions?

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