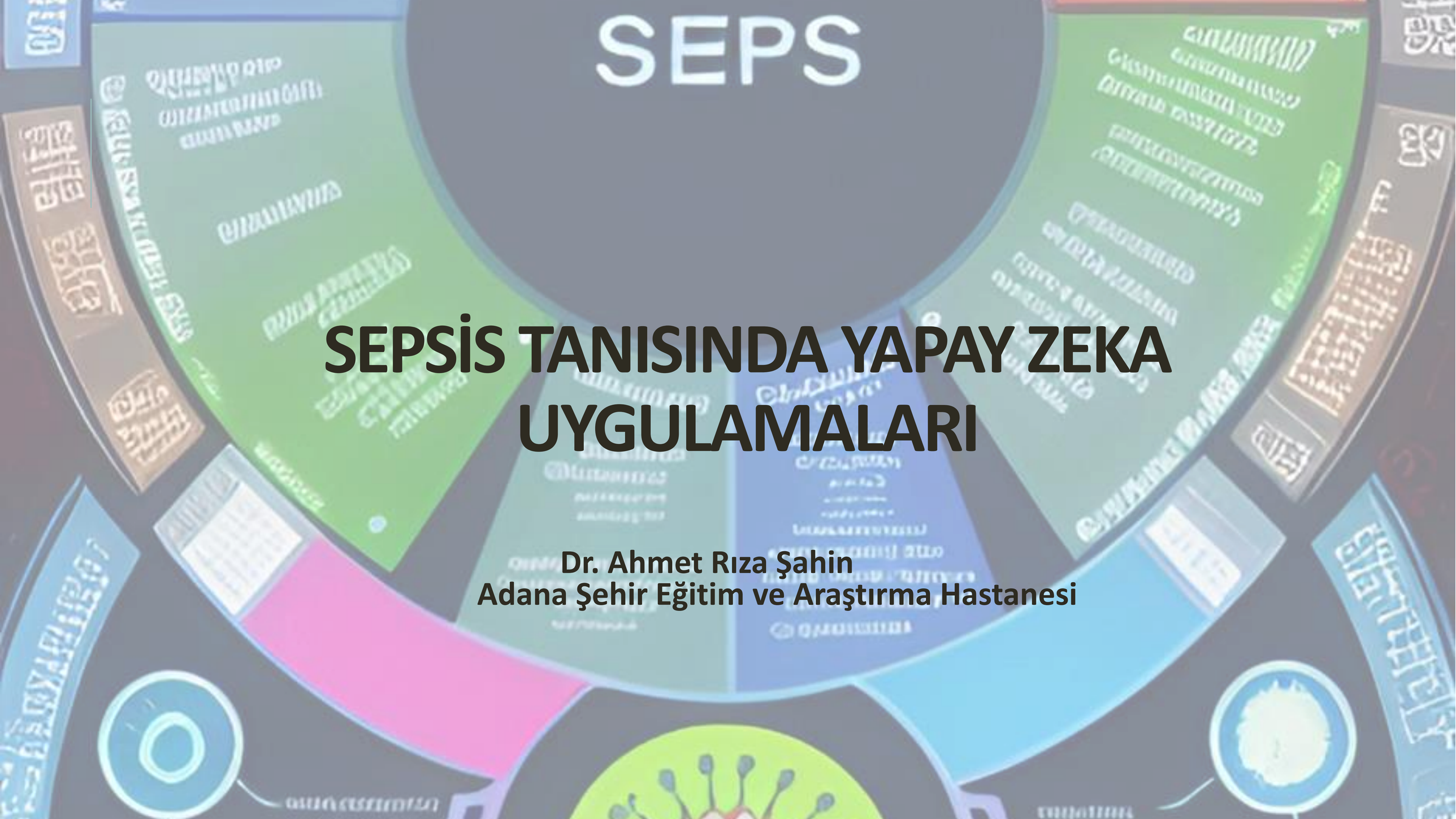
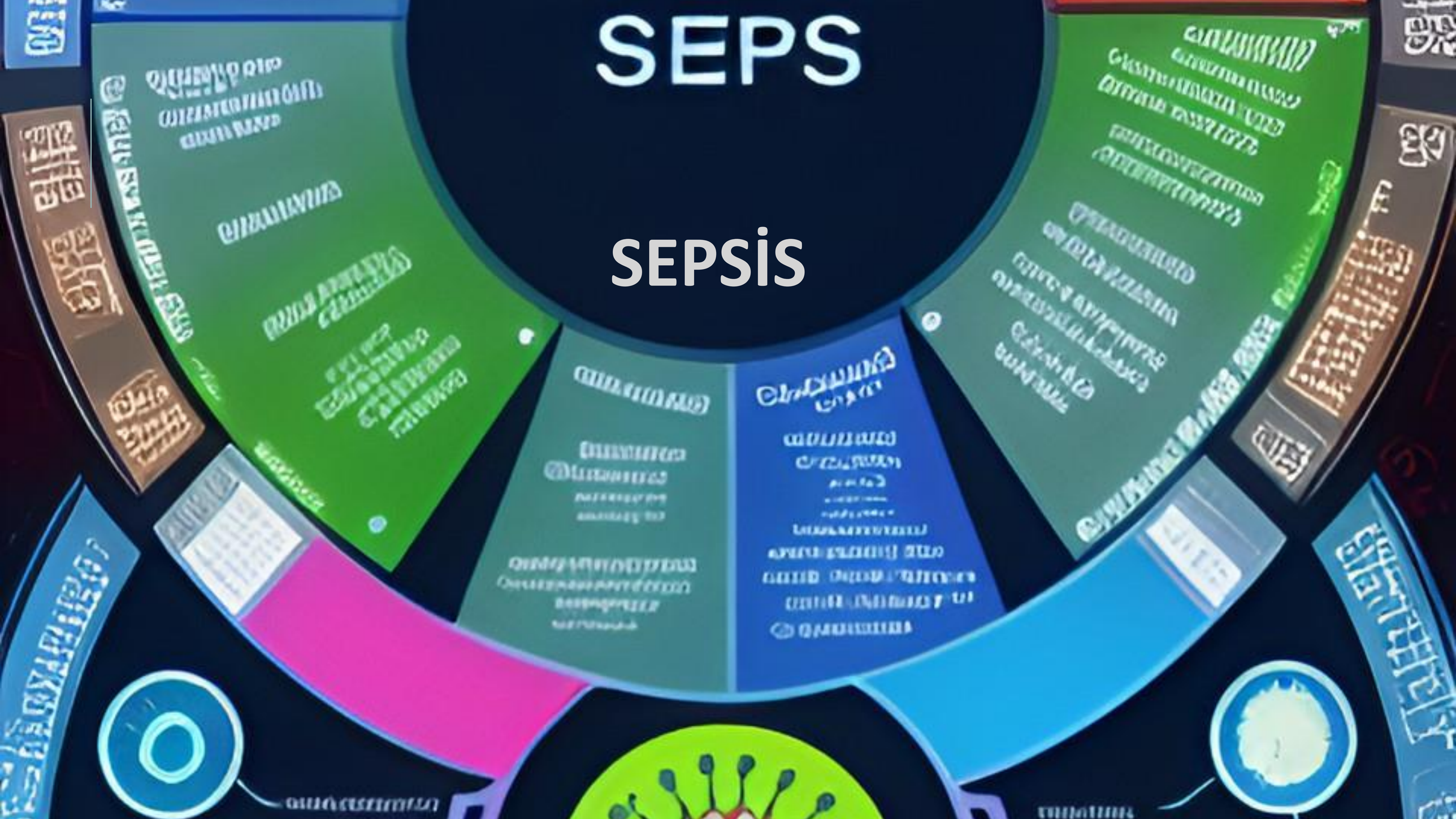


SEPSİS TANISINDA YAPAY ZEKA UYGULAMALARI

Dr. Ahmet Rıza Şahin
Adana Şehir Eğitim ve Araştırma Hastanesi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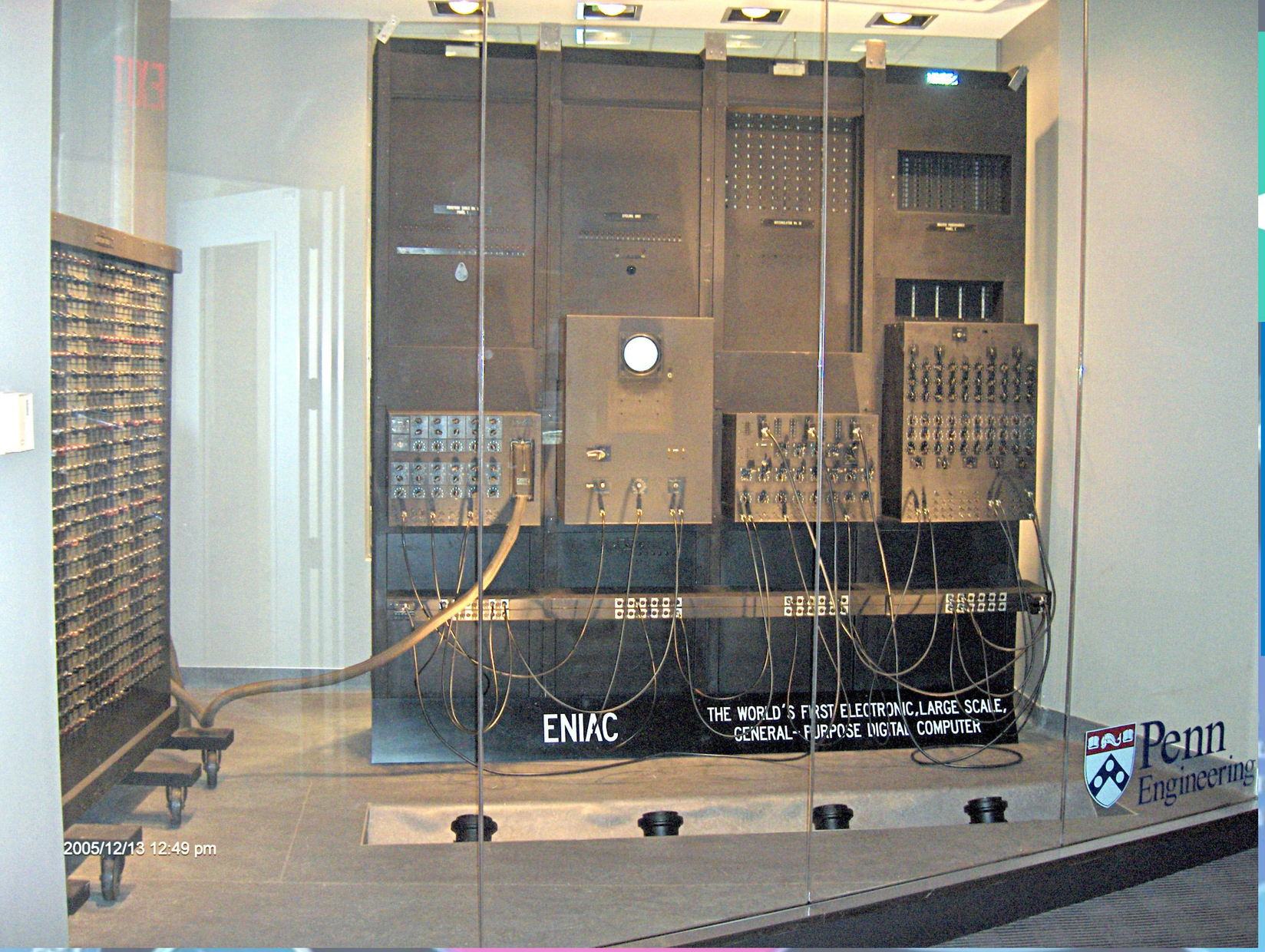


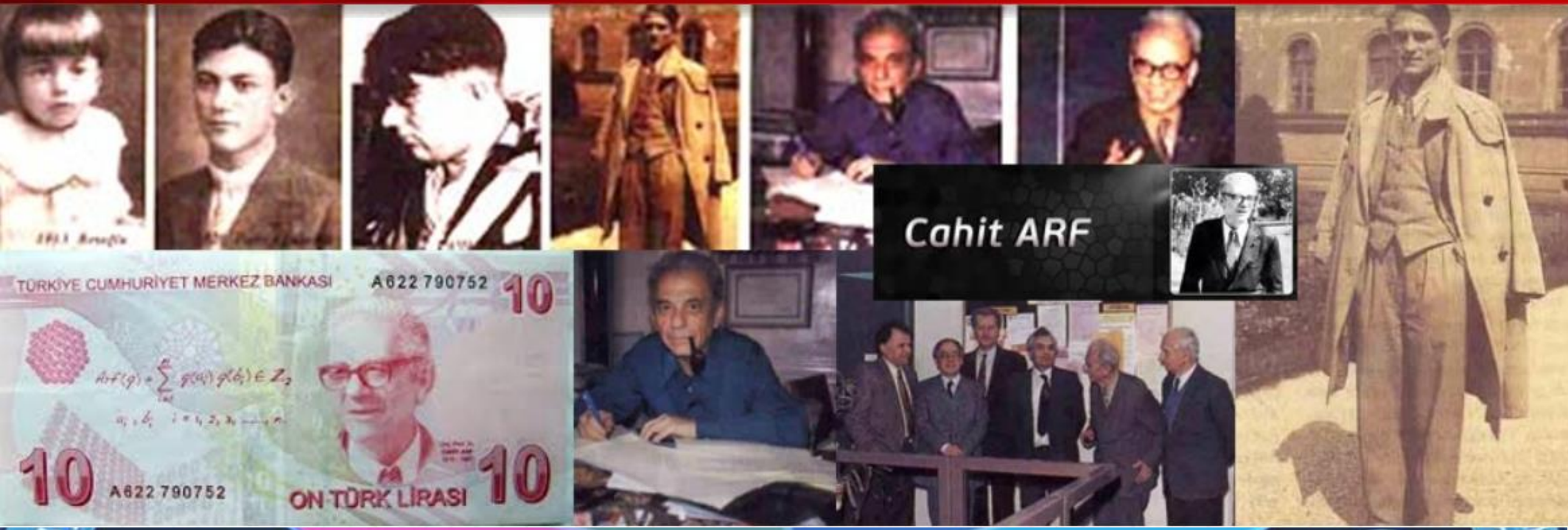
IBM Watson Health

STAT
FOR ONCOLOGY

ICCA

DeepMind Health

SEPS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RESULTS BY YEAR

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1975

1 Cite Share

Computer-based consultations in clinical therapeutics: explanation and rule acquisition capabilities of the **MYCIN** system.

Shortliffe EH, Davis R, Axline SG, Buchanan BG, Green CC, Cohen SN.

Comput Biomed Res. 1975 Aug;8(4):303-20. doi: 10.1016/0010-4809(75)90009-9.

PMID: 1157471 No abstract available.

Possible use of established cell lines for MLR locus typing.

PubMed®

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RESULTS BY YEAR

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1979

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- Abstract
- Free full text
- Full text

ARTICLE ATTRIBUTE

- Associated data

1 Cite Share

Antimicrobial selection by a computer. A blinded evaluation by infectious diseases experts.

Yu VL, Fagan LM, Wraith SM, Clancey WJ, Scott AC, Hannigan J, Blum RL, Buchanan BG, Cohen SN.

JAMA. 1979 Sep 21;242(12):1279-82.

PMID: 480542

An evaluation of a computer-based consultation system called **MYCIN** was made. Eight independent evaluators with special expertise in the management of meningitis compared **MYCIN**'s choice of antimicrobials with the choices of nine human prescribers for ten test cases o ...

2 Cite Share

Evaluating the performance of a computer-based consultant.

Yu VL, Buchanan BG, Shortliffe EH, Wraith SM, Davis R, Scott AC, Cohen SN.

Comput Programs Biomed. 1979 Jan;9(1):95-102. doi: 10.1016/0010-468x(79)90022-9.

PMID: 365439

The performance of a computer-based clinical consultation system is evaluated. The program, called **MYCIN**, is designed to function as an aid for infectious disease diagnosis and therapy selection, with an initial emphasis on bacteremias. The evaluation methodology is discus ...

Windows'u Etkinle

› Am J Hosp Pharm. 1976 Dec;33(12):1304-8.

Computerized consultation system for selection of antimicrobial therapy

S M Wraith, J S Aikins, B G Buchanan, W J Clancey, R Davis, L M Fagan, J F Hannigan, A C Scott, E H Shortliffe, W J van Melle, V L Yu, S G Axline, S N Cohen

PMID: 998649

Abstract

Mycin, a computer-based consultation system which provides to physicians antimicrobial therapy recommendations for patients with bacterial infections, is described. The consultation program arrives at therapeutic decisions using a built-in knowledge base as well as patient data entered by the physician. The system is capable of explaining its recommendations and answering questions about its reasoning process. The system's knowledge can be updated and corrected easily by infectious disease experts. At present the system is operational within a research setting; its routine use in a clinical setting will require further evaluation of its reliability and effectiveness.

SEPSİSİ TANIYAN BİR YAPAY ZEKA YAPALIM?

Veri kalitesi:

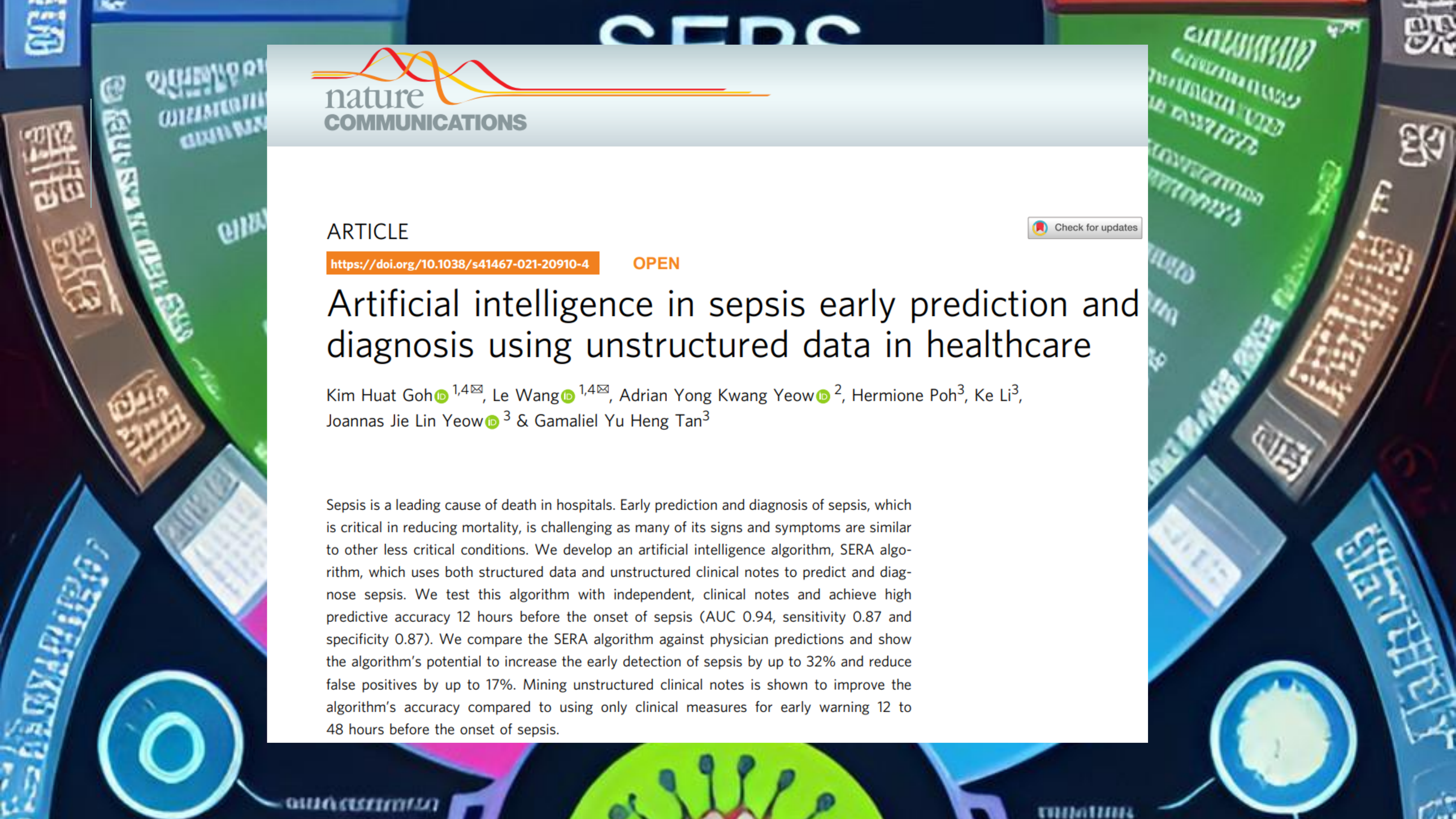
Algoritma seçimi:

Eğitim verileri:

Sepsis tanısı:

Etkinlik:

Yapay zeka modelinin doğruluğu:



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https://doi.org/10.1038/s41467-021-20910-4 OPEN

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Artificial intelligence in sepsis early prediction and diagnosis using unstructured data in healthcare

Kim Huat Goh[1,4✉], Le Wang[1,4✉], Adrian Yong Kwang Yeow[2], Hermione Poh[3], Ke Li[3], Joannas Jie Lin Yeow[3] & Gamaliel Yu Heng Tan[3]

Sepsis is a leading cause of death in hospitals. Early prediction and diagnosis of sepsis, which is critical in reducing mortality, is challenging as many of its signs and symptoms are similar to other less critical conditions. We develop an artificial intelligence algorithm, SERA algorithm, which uses both structured data and unstructured clinical notes to predict and diagnose sepsis. We test this algorithm with independent, clinical notes and achieve high predictive accuracy 12 hours before the onset of sepsis (AUC 0.94, sensitivity 0.87 and specificity 0.87). We compare the SERA algorithm against physician predictions and show the algorithm's potential to increase the early detection of sepsis by up to 32% and reduce false positives by up to 17%. Mining unstructured clinical notes is shown to improve the algorithm's accuracy compared to using only clinical measures for early warning 12 to 48 hours before the onset of sepsis.

Table 5 Topic categories.

Category	Count	Definition
Clinical status	28	Routine updates of clinical conditions as well as diagnosis (e.g., vitals) excluding lab and radio-diagnostic tests
Communication	3	Communication between staff
lab test	24	Orders and reports of lab or radio-diagnostic test results
Non-clinical status	2	Routine updates of non-clinical conditions
Social relationship	2	Information about family and social aspects of patient
Symptom	10	Clinical symptoms
Treatment	31	Treatment procedure or medication prescribed as well as the status of the treatment/ medication

The 100 topics are classified into seven different categories. The distribution of topics among categories is similar if 25, 50, 75, or 150 topics are extracted instead. Detailed results are available upon request from the corresponding authors.

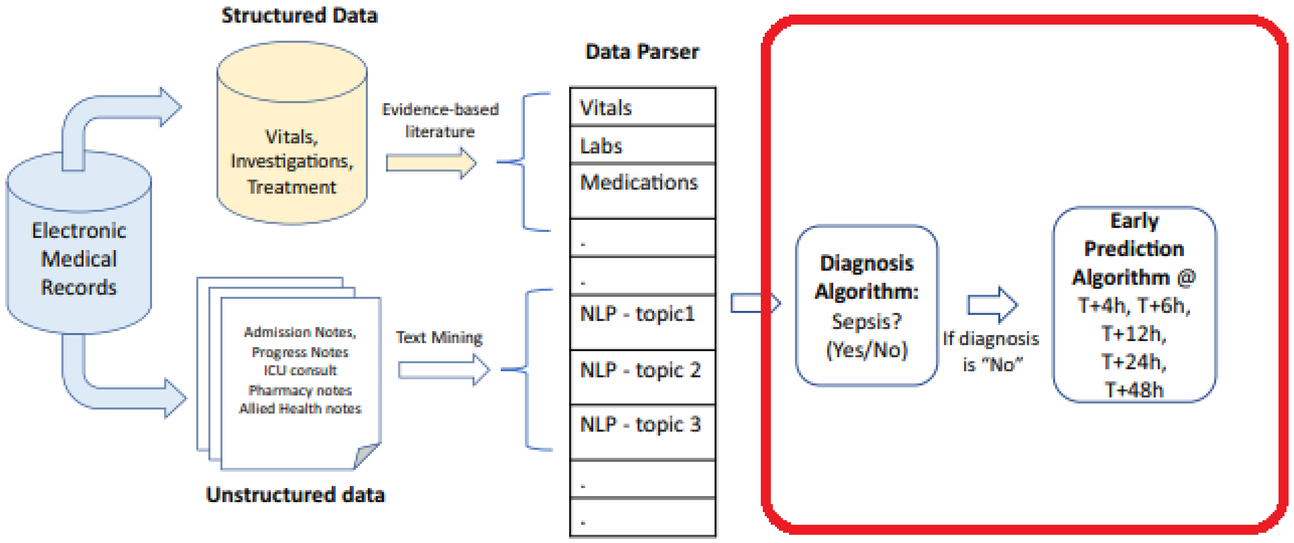


Fig. 1 Setup of SERA algorithm. The flow diagram shows the steps used to develop the SERA Algorithm. Both structured data (vitals, investigations, and treatment) and unstructured data (clinical notes) are used in the process of diagnosing and predicting sepsis.

Machine learning algorithm. Ensemble methods are machine-learning algorithms that utilize multiple classifiers to determine the predicted outcome by taking a (weighted) vote of their predictions. These methods often perform better than any single classifier[38,39]. There are several different ensemble methods, such as voting, bagging, stacking, and boosting.

In our main estimation, we use a voting ensemble. Voting is an ensemble machine learning model that combines the predictions from multiple other models (base classifiers). Here, we use two base classifiers: a stochastic gradient descent (SGD) based logistics regression and a random forest algorithm. Our combination rule is an average of probabilities, i.e., we calculate the average probability of the two base models as our voted probability.

The first base classifier, SGD, is an optimizing algorithm that seeks to minimize the error in prediction by learning iteratively from prior fitted estimates. The method iteratively draws random samples from the training sample to estimate the parameters of the model that is used to classify a patient as having sepsis or not having sepsis. It learns from each sampling iteration to determine the accuracy of the classification and adjust the parameter estimation until further improvements in prediction results are minimal.

For each iteration, the predicted parameter β is calculated, and the model is updated using the following logistic equation:

$$\beta^{\text{new}} = \beta^{\text{old}} + \text{lr}(y - \hat{y})\hat{y}(1 - \hat{y})x \quad (1)$$

where β is the optimized parameter, lr is a learning rate, $y - \hat{y}$ is the prediction error for the model in a particular iteration in the training data, $\hat{y}$ is the prediction made by the coefficients, and x is the input value. In our case, the input variables were a combination of the structured variables (as indicated in Table 1) and the topic loadings of each clinical note on the 100 topics we extracted in the text mining procedure.

The second classifier used here for voting is a random forest classifier, with the case of sepsis being the target variable. The probabilities of both classifiers are averaged out to arrive at the final probability used in our voting ensemble model.

Table 3 Statistics of diagnosis and early prediction algorithm (in low prevalence condition without SMOTE).

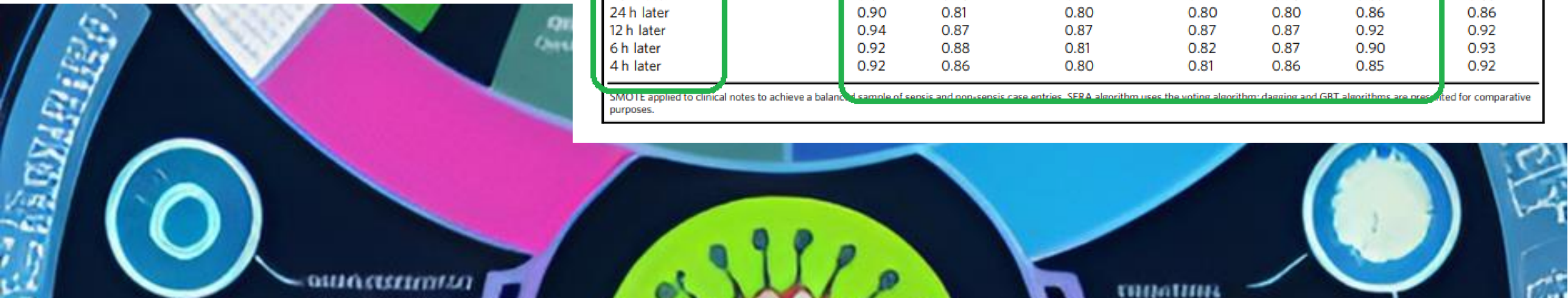
Diagnosis algorithm								
Outcome predict if the patient has sepsis At the present time	Voting Prevalence	AUC	Sensitivity	Specificity	PPV	NPV	Dagging AUC	GBT AUC
	0.177	0.94	0.89	0.87	0.59	0.97	0.92	0.94
Early prediction algorithm								
Outcome predict if patient will have sepsis	Voting Prevalence	AUC	Sensitivity	Specificity	PPV	NPV	Dagging AUC	GBT AUC
48 h later	0.012	0.87	0.76	0.76	0.04	0.99	0.82	0.85
24 h later	0.010	0.90	0.81	0.79	0.04	0.99	0.88	0.89
12 h later	0.008	0.94	0.88	0.82	0.04	0.99	0.92	0.93
6 h later	0.002	0.92	0.88	0.83	0.01	0.99	0.90	0.93
4 h later	0.001	0.92	0.89	0.87	0.01	0.99	0.92	0.94

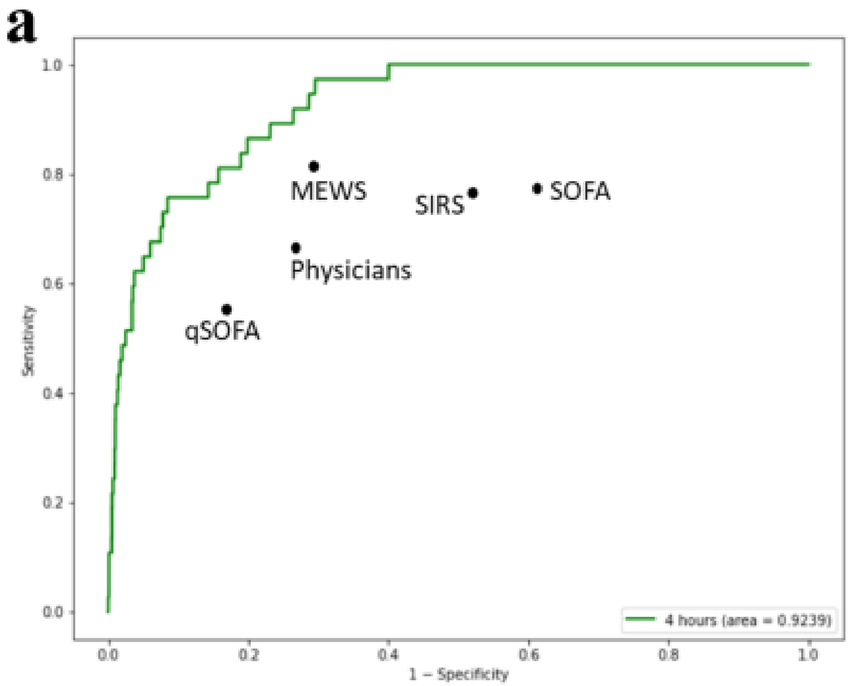
No oversampled applied. Prevalence is computed at the clinical note level. For the same number of sepsis cases, the clinical note occurrences are different for a different time window. SERA algorithm uses the voting algorithm; dagging, and GBT algorithms are presented for comparative purposes.

Table 2 Statistics of diagnosis and early prediction algorithm (SMOTE).

Diagnosis algorithm							
Outcome predict if the patient has sepsis At the present time	Voting AUC	Sensitivity	Specificity	PPV	NPV	Dagging AUC	GBT AUC
	0.94	0.89	0.87	0.85	0.90	0.92	0.94
Early prediction algorithm							
Outcome predict if patient will have sepsis	Voting AUC	Sensitivity	Specificity	PPV	NPV	Dagging AUC	GBT AUC
48 h later	0.87	0.78	0.77	0.77	0.78	0.83	0.83
24 h later	0.90	0.81	0.80	0.80	0.80	0.86	0.86
12 h later	0.94	0.87	0.87	0.87	0.87	0.92	0.92
6 h later	0.92	0.88	0.81	0.82	0.87	0.90	0.93
4 h later	0.92	0.86	0.80	0.81	0.86	0.85	0.92

SMOTE applied to clinical notes to achieve a balanced sample of sepsis and non-sepsis case entries. SERA algorithm uses the voting algorithm; dagging and GBT algorithms are presented for comparative purposes.





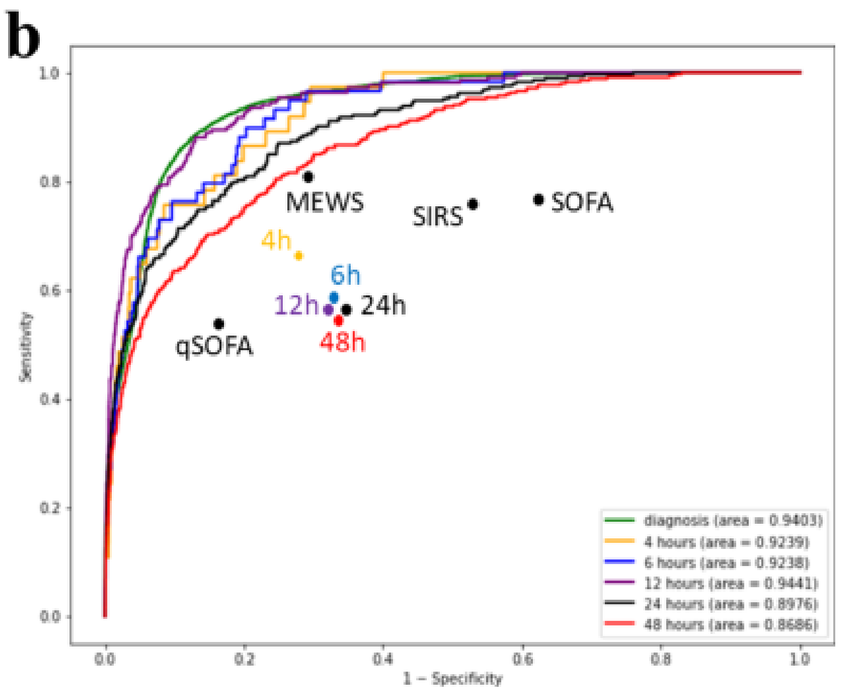
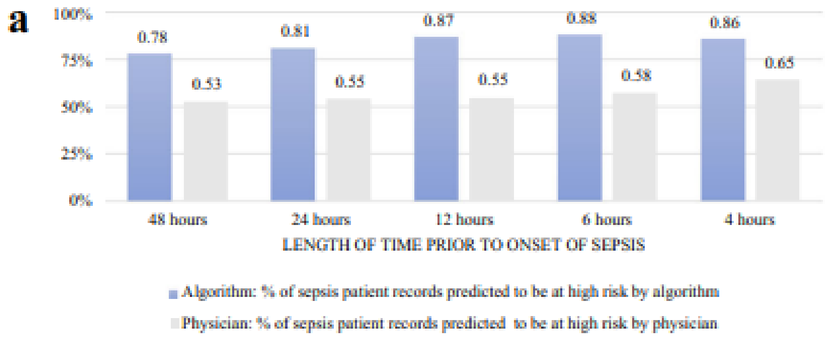
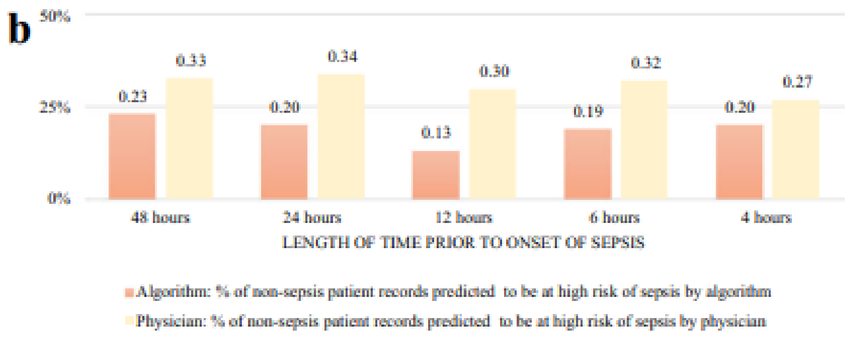


Fig. 2 ROC curves for 48, 24, 12, 6, and 4-h early prediction. a, **b** The ROCs represent the performance of early prediction algorithm at 4, 6, 12, 24, and 48 h prior to the onset of sepsis using the independent, test sample. "qSOFA", "MEWS", "SIRS", and "SOFA" represent the TPR and FPR from these methods employed by physicians in prior studies at 0–4 h prior to the onset of sepsis. "Physicians" represent TPR and FPR of patients in the independent, test sample set that were suspected by hospital's physicians to have sepsis at 4 h prior to the onset of sepsis. **b** "4 h", "6 h", "12 h", "24 h", and "48 h" represent TPR and FPR of patients in the independent, test sample set that were suspected by hospital's physicians to have sepsis at the respective time prior to the onset of sepsis.



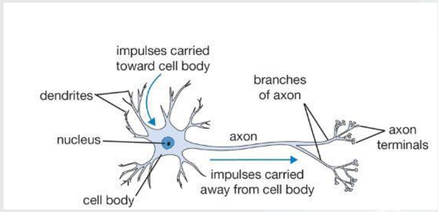


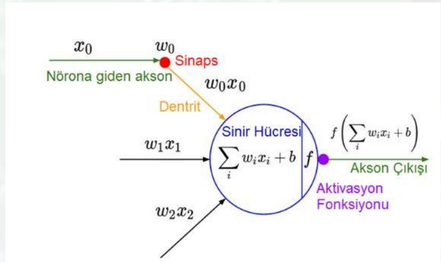
SEPS
Veri Yönetimi

- Uygulamalarda en önemli bileşen
- Yapay zeka algoritmalarında kullanılacak verilere ulaşabiliyorsa açık kaynak kodlu kaynakları tercih edilebilir.
- Veri satan şirketler mevcut.
- Hasta tanımlayıcıları (dosya numarası-hasta adı) kullanmadan doğrudan etik kurul başvurusu yaparak ve anonim hale getirerek çalışır.
- Ayrıca hibrit yöntemlerin kullanıldığı projeler var.
- Bütün veriler ISO-27001 standartlarında korunmalıdır.

SEPSİSİ TANIYAN BİR YAPAY ZEKA YAPALIM?

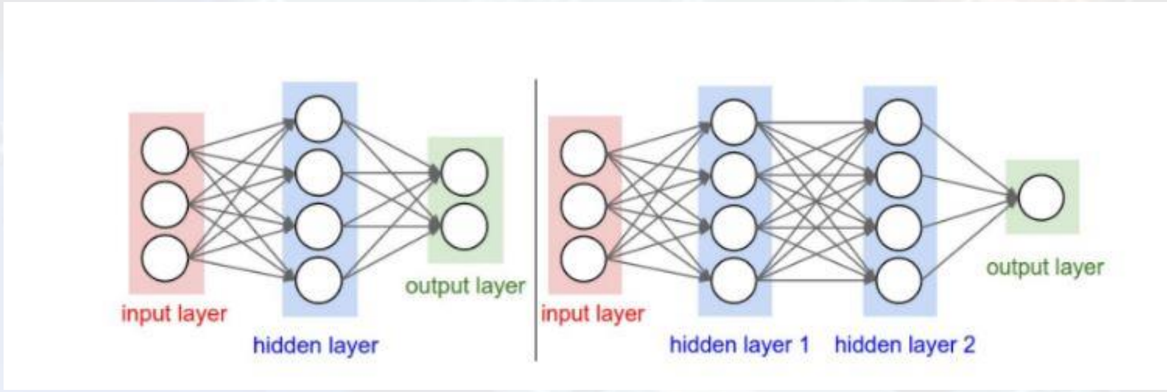
Veri kalitesi:





Algoritma seçimi:

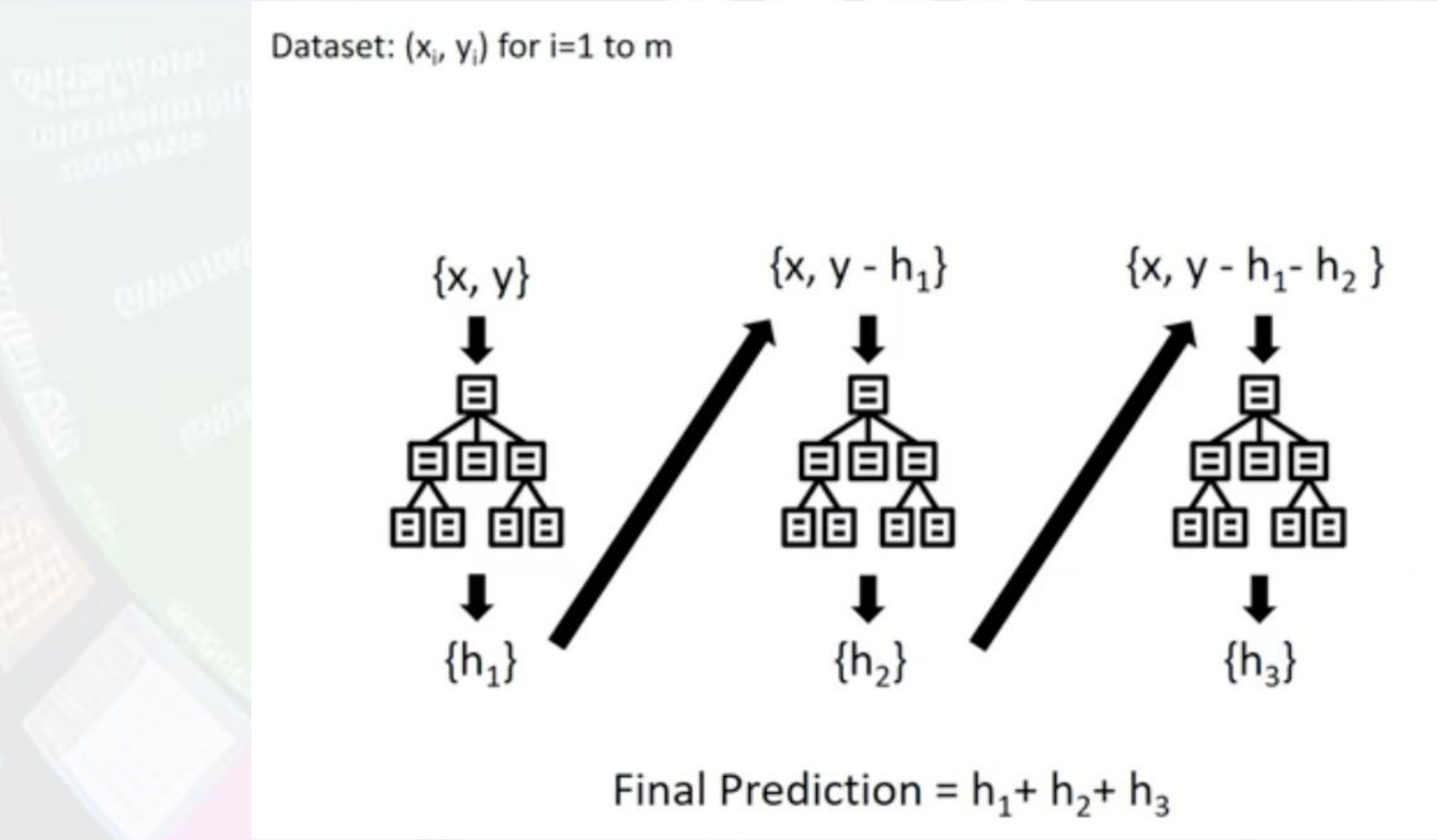
Eğitim verileri:



Sepsis tanısı:

Etkinlik:

Yapay zeka modelinin doğruluğu:



Şekil 9: Gradyen Artırma modeli. X bağımsız değişkenlerine karşılık gelen Y bağımlı değişkenlerinden oluşan bir veri setinde karar destek ağacı sonucu “h” tahminleri elde edilir ve bu tahminler her aşamada bir önceki tahmin sürecinden çıkarılarak hata “error” sonuçları ile tekrar besleme yapılır. Sonuçta ortaya çıkan tahmin her bir karar destek ağacından elde edilen tahminlerin toplamıdır.

III.PROPOSED SYSTEM

The sepsis dataset is collected from ICU patients in three different hospital systems. The training dataset consists of 20,336 subjects and 20,000 subjects. A table of measurements over time is included in each training data file. The features are described in table 1.

Features	Description
HR	Heart rate (beats per minute)
O2Sat	Pulse oximetry (%)
Temp	Temperature (Deg C)
SBP	Systolic BP (mm Hg)
MAP	Mean arterial pressure (mm Hg)
DBP	Diastolic BP (mm Hg)
HCO3	Bicarbonate (mmol/L)
FiO2	Fraction of inspired oxygen (%)
pH	N/A
AST	Aspartate transaminase (IU/L)
Alkalinephos	Alkaline phosphatase (IU/L)
Calcium	(mg/dL)
Chloride	(mmol/L)
Creatinine	(mg/dL)
Bilirubin_direct	Bilirubin direct (mg/dL)
Glucose	Serum glucose (mg/dL)
Lactate	Lactic acid (mg/dL)
Magnesium	(mmol/dL)
Phosphate	(mg/dL)
Potassium	(mmol/L)
Bilirubin_total	Total bilirubin (mg/dL)
TroponinI	Troponin I (ng/mL)
Hct	Hematocrit (%)
Hgb	Hemoglobin (g/dL)
Fibrinogen	(mg/dL)
Platelets	(count*10^3/µL)

Table 1: Sepsis Training Dataset features and its description.

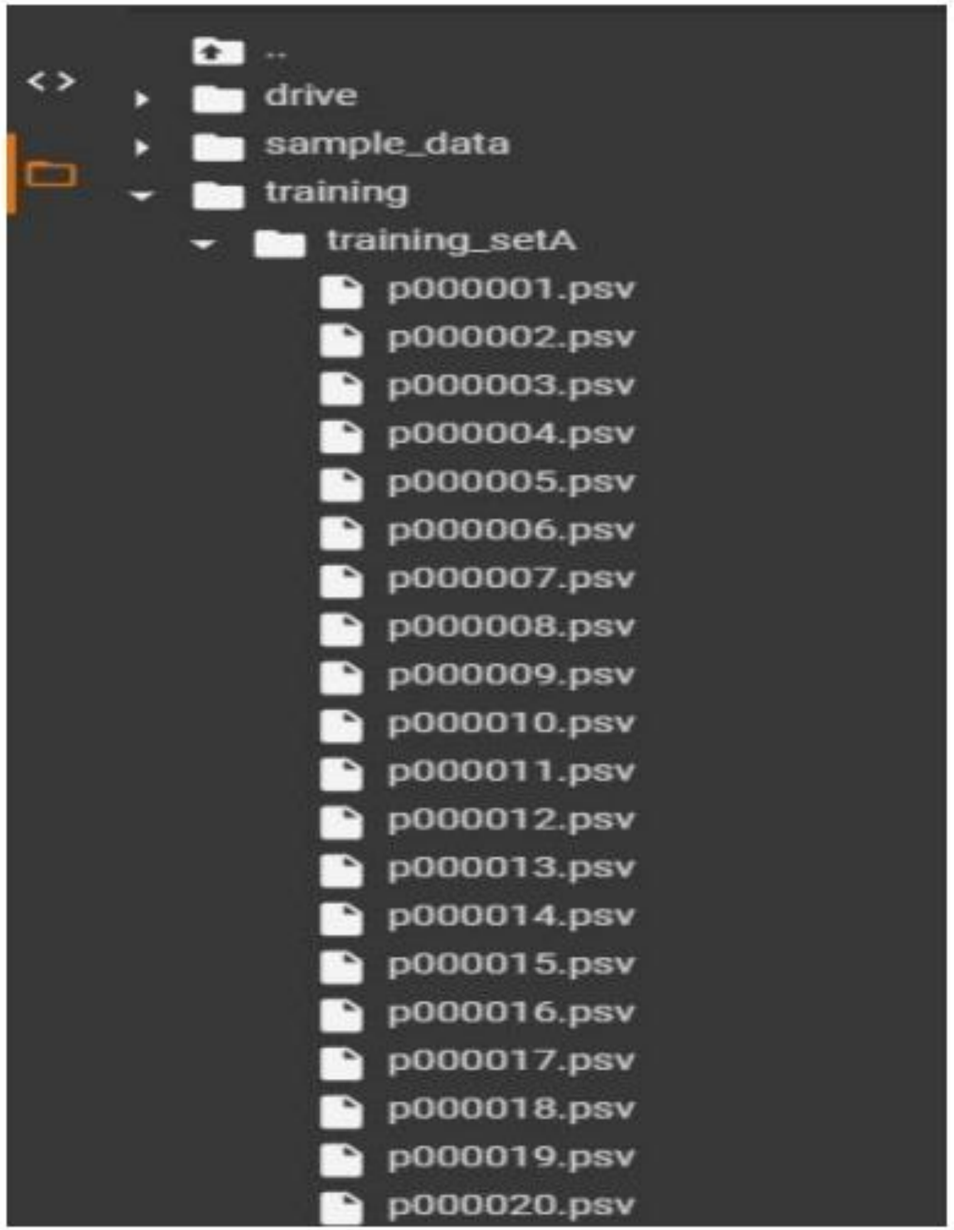
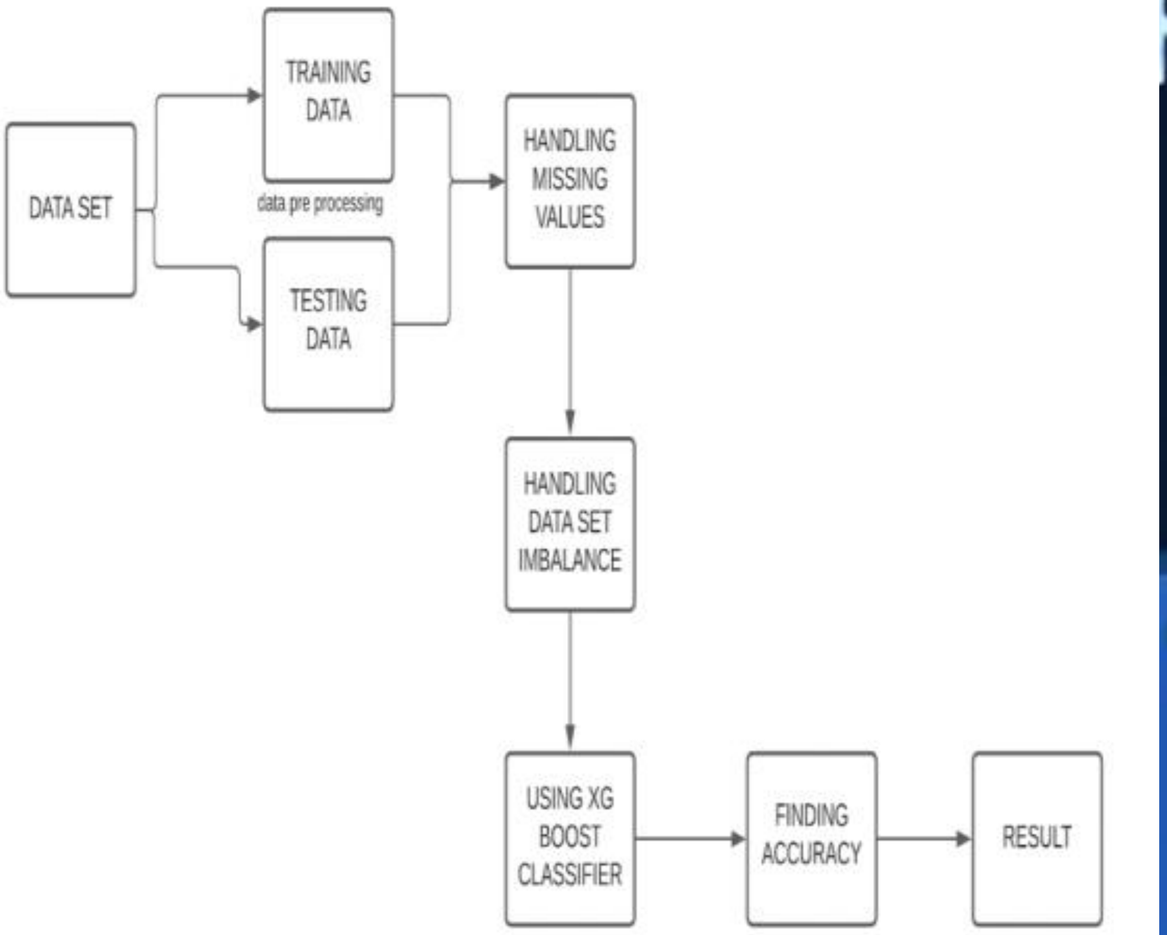


Figure 2: Data set: this is the list of training data set



Confusion matrix= [179804 7048

2374 455]

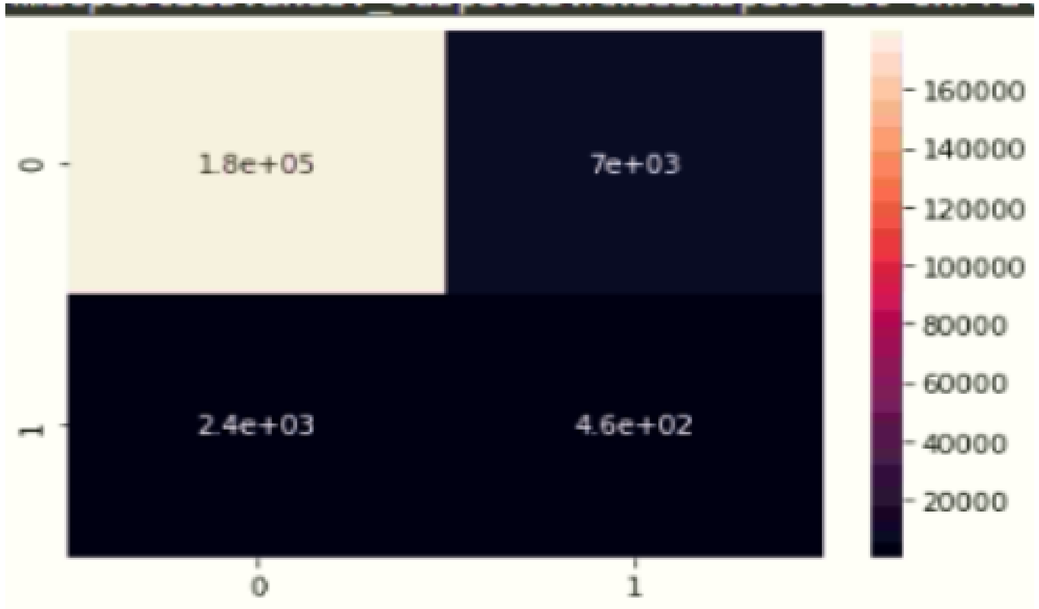


Figure 5: Confusion matrix

Doğru pozitif+doğru negatif/ doğru pozitif+yanlış pozitif+doğru negatif+yanlış negatif

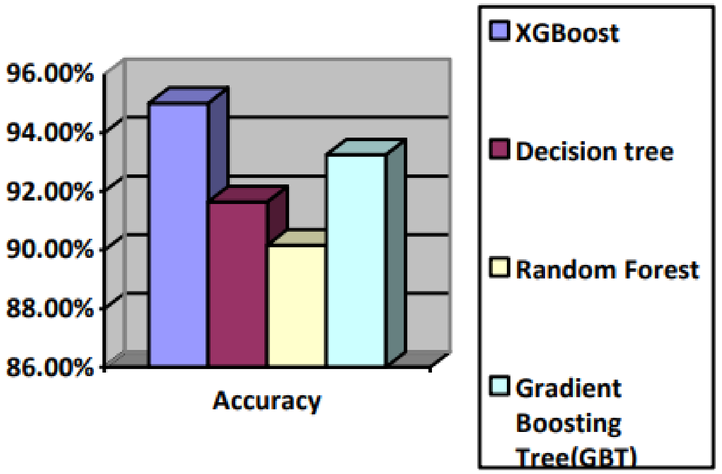


Figure 6: Comparison of accuracy of XGBoost vs other machine learning algorithms.

V. CONCLUSION

Machine Learning model XGBoost is employed to predict sepsis and the model is validated against the testing dataset which produces the accuracy of 95.01%. Decision tree, Random Forest, Gradient Boosting Tree (GBT) models are validated with accuracy of 91.65%, 90.17%, 93.25% respectively. XGBoost outperforms Decision tree, Random Forest, Gradient Boosting Tree (GBT) models. Further feature selection can be employed for better results and better model building with the under the guidance of a good health science domain expert. Using deep learning algorithms, the accuracy of sepsis prediction can be increased even more.

Table 1. Study characteristics

Study (year)	Clinical setting and data source	Sample size[a]	Cohort criteria infection definition	Task and objective
Horng et al.[47] (2017)	• ED • Beth Israel Deaconess (Boston, MA, United States) • Dec 17, 2008—Feb 17, 2013	230 936 patient visits • Infection: 32 103 P; 14% • No infection: 198 833 P; 86% Train : 147 799 P; 64% Validation: 46 187 P; 20% Test: 36 950 P; 16%	Angus Sepsis ICD-9-CM abstraction criteria[79]	Identify patients with suspected infection to demonstrate benefits of using clinical text with structured data for detecting ED patients with suspected infection.
Apostolova and Velez[48] (2017)	• ICU • MIMIC-III • 2001–2012	634 369 nursing notes • Infection presence: 186 158 N; 29% • Possible infection: 3262 N; 1% • No infection: 448 211 N; 70% Train: 70% Test: 30%	Notes describing patient taking or being prescribed antibiotics for treating infection	Identify notes with suspected or presence of infection to develop a system for detecting infection signs and symptoms in free-text nursing notes.
Culliton et al.[49] (2017)	• Inpatient care • Baystate hospitals (Springfield, MA, United States) • 2012–2016	203 000 adult inpatient admission encounters • Used 68 482 E • Severe sepsis: 1427 E; 2.1% 3-fold cross validation: only text data Model construction: 2012–2015 data Test set: 2016 data: • Used 13 603 E • Severe sepsis: 425 P; 3.1%	Modified Baystate clinical definition of severe sepsis (8 structured variables) and severe sepsis ICD codes	Predict severe sepsis 4, 8, and 24 h before the earliest time structured variables meet the severe sepsis definition to compare accuracy of predicting patients that will meet the clinical definition of sepsis when using unstructured data only, structured data only, or both types.
Delahanty et al.[51] (2019)	• ED • Tenet Healthcare Hospitals (Nashville, TN, United States) • January 1, 2016—October 31, 2017	2 759 529 patient encounters • Sepsis: 54 661 E; 2% • No Sepsis: 2 704 868 E; 98% Train: 1 839 503 E; 66.7% • Sepsis: 36 458 E; 2% • No sepsis: 1 803 045 E; 98% Test: 920 026 E; 33.3% • Sepsis: 18 203 E; 2% • No sepsis: 901 823 E; 98%	Rhee's modified Sepsis-3 definition[80]	Predict sepsis risk in patients 1, 3, 6, 12, and 24 h after the first vital sign or laboratory result is recorded in the EHR to develop a new sepsis screening tool comparable to benchmark screening tools.
Liu et al.[50] (2019)	• ICU • MIMIC-III • 2001–2012	38 645 adult patients Train: 70% P Test: 30% P Applied model to: 15 930 P with suspected infection and at least 1 physiological EHR data	Sepsis-3 definition[1]	Predict septic shock in sepsis patients before the earliest time septic shock criteria are met to demonstrate an approach using NLP features for septic shock prediction.
Amrollahi et al.[53] (2020)	• ICU • MIMIC-III • 2001–2012	40 175 adult patients • Sepsis: 2805 P; ~7% Train 80% P Test 20% P	Sepsis-3 definition[1]	Predict sepsis onset hours in advance using a deep learning approach to show a pre-trained neural language representation model can improve early sepsis detection.

(continued)

Table 1. continued

Study (year)	Clinical setting and data source	Sample size[a]	Cohort criteria infection definition	Task and objective
Hammoud et al.[54] (2020)	• ICU • MIMIC-II • 2001–2007	17 763 patients • Sepsis: 6097 P • Severe sepsis: 3962 P • Septic shock : 1469 P 5-fold cross validation	Sepsis definition based on what Henry et al[78] used	Predict early septic shock in ICU patients using a model that can be optimized based on user preference or performance metrics.
Goh et al.[52] (2021)	• ICU • Singapore government-based hospital (Singapore, Singapore) • Apr 2, 2015—Dec 31, 2017	5317 patients (114 602 notes) Train and validation: 3722 P (80 162 N) • Sepsis: 6.45% • No sepsis: 93.55% Test: 1595 P (34 440 N) • Sepsis: 5.45% • No sepsis: 94.55%	ICU admission with an ICD-10 code for sepsis, severe sepsis, or sepsis shock	Identify if a patient has sepsis at consultation time or predict sepsis 4, 6, 12, 24, and 48 h after consultation to develop an algorithm that uses structured and unstructured data to diagnose and predict sepsis.
Qin et al.[55] (2021)	• ICU • MIMIC-III • 2001–2012	49 168 patients Train: 33 434 P • Sepsis: 1353 P • No Sepsis: 32 081 P Validation: 8358 P • Sepsis: 338 P • No Sepsis: 8020 P Test: 7376 P • Sepsis: 229 P • No Sepsis: 7077 P	PhysioNet Challenge restrictive Sepsis-3 definition[81]	Predict if a patient will develop sepsis to explore how numerical and textual features can be used to build a predictive model for early sepsis prediction.

ED: emergency department; ICU: intensive care unit; ICD: International Classification of Diseases; ICD-9 CM: ICD Clinical Modification, 9th revision; ICD-10: ICD 10th revision; MIMIC-II: Multiparameter Intelligent Monitoring in Intensive Care II database; MIMIC-III: Medical Information Mart for Intensive Care dataset.

ıses were searched. Articles
recognize, diagnose, or pre-
ɔonse syndrome, sepsis, se-
ta, ML models, NLP techni-

ɔhysicians, and specialists in
mographics, vital signs, lab-
ve (AUC) comparison of ML
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measurements among the 9

: no studies used patient his-
cts reporting methods, out-
intensive care, making them

both unstructured text and

Table 4. Study outcome overview of best and worst area under the curve values

Study (year)	Hours[a]	Data types[b]		Models[d] (NLP)[e]	AUC[f]
		DVLMC	T[c]		
Horng et al.[47] (2017)	Identify	DV- - -	CC + NN	RF (BoW)	0.87
		DV- - -	–	NB	0.65
Apostolova and Velez[48] (2017)	Identify	- - - - -	NN	SVM (BoW + tf-idf)	–
		- - - - -	NN	Logistic regression + KNN + SVM (PV)	–
Culliton et al.[49] (2017)	−4	- - - - -	CN	Ridge regression (GloVe)	0.64
	−8	- - - - -	CN	Ridge regression (GloVe)	0.66
	−24	- - - - -	CN	Ridge regression (GloVe)	0.73
	−24[g]	-V- -C	CN	Ridge regression (GloVe)	0.85
		-V- -C	–	Ridge regression (GloVe)	0.80
Delahanty et al.[51] (2019)	+1	-VL- -	–	GBT	0.93
	+3	-VL- -	–	GBT	0.95
	+6	-VL- -	–	GBT	0.96
	+12	-VL- -	–	GBT	0.97
	+24	-VL- -	–	GBT	0.97
Liu et al.[50] (2019)	−7	-VLM-	CN	GRU (GloVe)	0.92
	−7.3	-VLM-	CN	GBT (BoW)	0.91
	−6	-VLM-	–	GBT	0.85
Amrollahi et al.[53] (2020)	−4[h]	-VL- -	PN + NN	LSTM (ClinicalBERT)	0.84
		- - - - -	PN + NN	LSTM (ClinicalBERT)	0.74
Hammoud et al.[54] (2020)	−30.6	DVL- -	CN	Lasso regression (BoW + tf-idf)	0.89
Goh et al.[52] (2021)	Identify	DVLM-	PN	Logistic regression + RF (LDA)	0.94
		DVLM-	PN	dag + Logistic regression (LDA)	0.92
	−4	DVLM-	–	Logistic regression + RF	0.93
		DVLM-	PN	dag + Logistic regression (LDA)	0.85
	−6	DVLM-	PN	Logistic regression + RF (LDA)	0.92
		DVLM-	PN	dag + Logistic regression (LDA)	0.89
	−12	DVLM-	PN	Logistic regression + RF (LDA)	0.94
		DVLM-	–	Logistic regression + RF	0.79
	−24	DVLM-	PN	Logistic regression + RF (LDA)	0.90
		DVLM-	–	Logistic regression + RF	0.78
	−48	DVLM-	PN	Logistic regression + RF (LDA)	0.87
		DVLM-	–	Logistic regression + RF	0.77
Qin et al.[55] (2021)	−6 to 0[i]	-VL- -	CN	GBT (ClinicalBERT-sf)	0.89[i]
		-VL- -	–	GBT (ClinicalBERT-m)	0.86[i]

YAPAY ZEKANIN BİLEŞENLERİ

- Çok sayıda alt ünitenin bir iç dolaşım ve dış dolaşım bağlantısı ile kusursuz olarak çalışması gerekir.

✓ Elektronik sağlık kayıtları
✓ Sağlık bilgi değişimi (SBD) ağlarıdır.

- Tıp terminolojileri, kapsamları ve ölçüm yöntemleri farklılık gösterebilir.
- Tıp terminolojileri en önemli gereksinim ölçütlerin, analizlerin, numunelerin ideal olarak ortak bir kodu paylaşmasıdır.

NPU:
LOINC:
SNOMED CT:
UCUM:

- Örnek vermek gerekirse Escherichia coli'i temsil eden 112283007, genişletilmiş spektrumlu beta laktamaz enzimi üretiyor ise 40980000, Kapbapenemaz enzim geni taşıyorsa 737528008 direnç özellikleri için SNOMED CT kodu ile tanımlanır.

- Sağlıkta, UCUM kodları elektronik iletişimde (Dijital hastane 7. Seviye normları tarafından tanımlanan formatlardaki mesajlar veya belgeler gibi) kullanılmak üzere tasarlanmıştır ve genellikle insan yorumuna aşina olan diğer birim dizeleri de bulunur.

YAPAY ZEKANIN BİLEŞENLERİ

Code System Concept

Code System Concept Code	86406008
Code System Concept Name	Human immunodeficiency virus infection (disorder)
Code System Preferred Concept Name	Human immunodeficiency virus infection (disorder)
Concept Status	Published
Concept Status Date	03/01/2019
Code System Name	SNOMED-CT

- Asymptomatic human immunodeficiency virus infection (disorder) {91947003 , SNOMED-CT }
- Candidiasis of mouth co-occurrent with human immunodeficiency virus infection (disorder) {713497004 , SNOMED-CT }
- Cognitive impairment co-occurrent and due to human immunodeficiency virus infection (disorder) {15928141000119107 , SNOMED-CT }
- Congenital human immunodeficiency virus infection (disorder) {52079000 , SNOMED-CT }
- Disorder of central nervous system co-occurrent with human immunodeficiency virus infection (disorder) {713571008 , SNOMED-CT }
- Disorder of eye proper co-occurrent with human immunodeficiency virus infection (disorder) {713299003 , SNOMED-CT }
- Disorder of gastrointestinal tract co-occurrent with human immunodeficiency virus infection (disorder) {713300006 , SNOMED-CT }

LOINC VERSION 2.66

LOINC CODE
69668-2

LONG COMMON NAME
HIV 1 and 2 Ab [Identifier] in Serum or Plasma by Rapid immunoassay

LOINC STATUS
Active

FULLY-SPECIFIED NAME

Component	HIV 1 & 2 Ab
Property	Prid
Time	Pt
System	Ser/Plas
Scale	Nom
Method	IA.rapid

Additional Names

Short Name	HIV 1 & 2 Ab SerPl IA.rapid
Display Name BETA	HIV 1 and 2 Ab IA.rapid Nom
Consumer Name ALPHA	HIV 1 and 2 Antibody, Blood

Most Common Healthcare Units

Valid UCUM Code	Descriptive Name	Common Synonym (non-UCUM)	Dimension (IUPAC)
%	Percent	%	1
/uL	PerMicroLiter	/uL	L-3
[iU]/L	InternationalUnitsPerLiter	IU/L	L-3[arb]
10*3/uL	ThousandsPerMicroLiter	K/uL, x10^3/mm^3	L-3
10*6/uL	MillionsPerMicroLiter	M/uL, x10^6/mm^3	L-3
fL	FemtoLiter	fL	L-3
g/dL	GramsPerDeciLiter	g/dL	L-3M
g/L	GramsPerLiter	g/L	L-3M
g/mL	GramsPerMilliLiter	g/mL	L-3M
kPa	KiloPascal	kPa	L-1MT-2
m[iU]/mL	MilliInternationalUnitsPerMilliLiter	mIU/mL	L-3[arb]
meq/L	MilliEquivalentsPerLiter	mEq/L	L-3N
mg/dL	MilliGramsPerDeciLiter	mg/dL	L-3M
mm[Hg]	MilliMetersOfMercury	mm Hg	L-1MT-2
mmol/kg	MilliMolesPerKiloGram	mmol/kg	M-1N
mmol/L	MilliMolesPerLiter	mmol/L	L-3N
mosm/kg	MilliOsmolesPerKiloGram	mOsm/kg	M-1N
ng/mL	NanoGramsPerMilliLiter	ng/mL	L-3M
nmol/L	NanoMolesPerLiter	nmol/L	L-3N
pg	PicoGrams	pg	M

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Clinical applications of artificial intelligence in sepsis: A narrative review

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ABSTRACT

Many studies have been published on a variety of clinical applications of artificial intelligence (AI) for sepsis, while there is no overview of the literature. The aim of this review is to give an overview of the literature and thereby identify knowledge gaps and prioritize areas with high priority for further research.

A literature search was conducted in PubMed from inception to February 2019. Search terms related to AI were combined with terms regarding sepsis. Articles were included when they reported an area under the receiver operator characteristics curve (AUROC) as outcome measure.

Fifteen articles on diagnosis of sepsis with AI models were included. The best performing model reached an AUROC of 0.97. There were also seven articles on prognosis, predicting mortality over time with an AUROC of up to 0.895. Finally, there were three articles on assistance of treatment of sepsis, where the use of AI was associated with the lowest mortality rates. Of the articles, twenty-two were judged to be at high risk of bias or had major concerns regarding applicability. This was mostly because predictor variables in these models, such as blood pressure, were also part of the definition of sepsis, which led to overestimation of the performance.

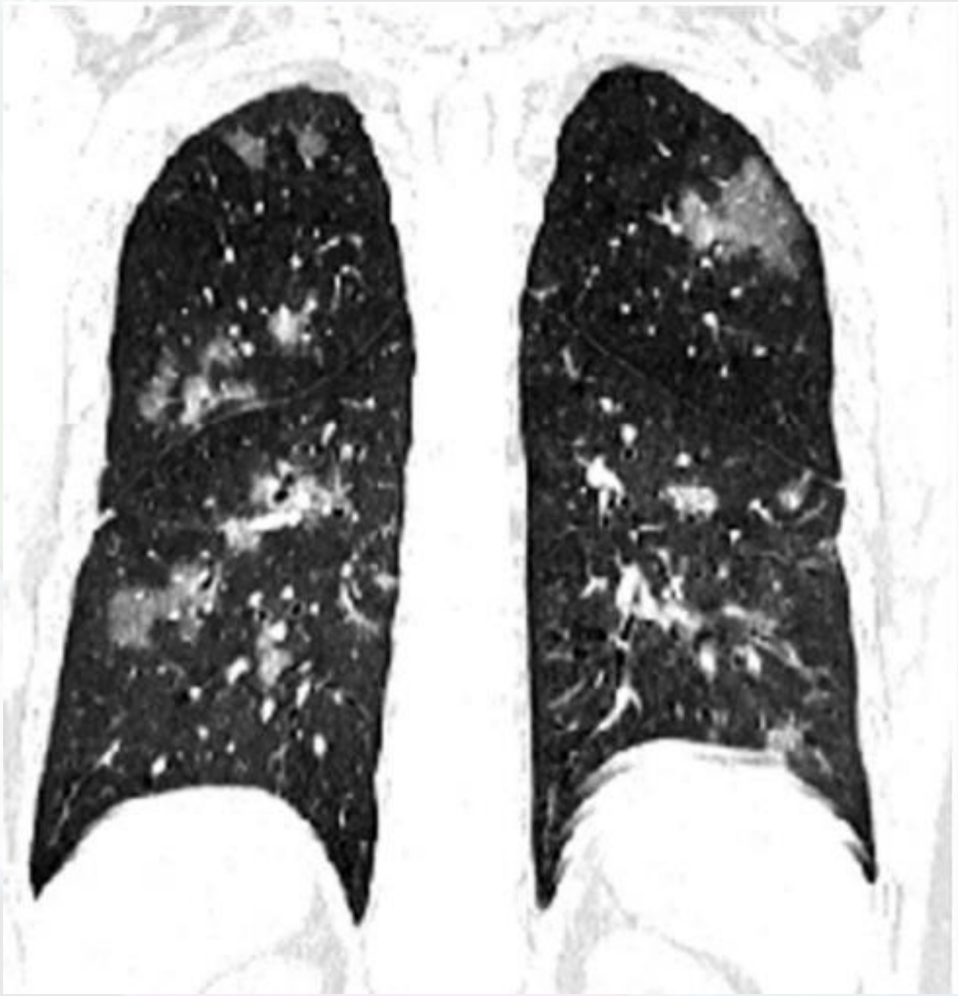
We conclude that AI models have great potential for improving early identification of patients who may benefit from administration of antibiotics. Current AI prediction models to diagnose sepsis are at major risks of bias when the diagnosis criteria are part of the predictor variables in the model. Furthermore, generalizability of these models is poor due to overfitting and a lack of standardized protocols for the construction and validation of the models. Until these problems have been resolved, a large gap remains between the creation of an AI algorithm and its implementation in clinical practice.

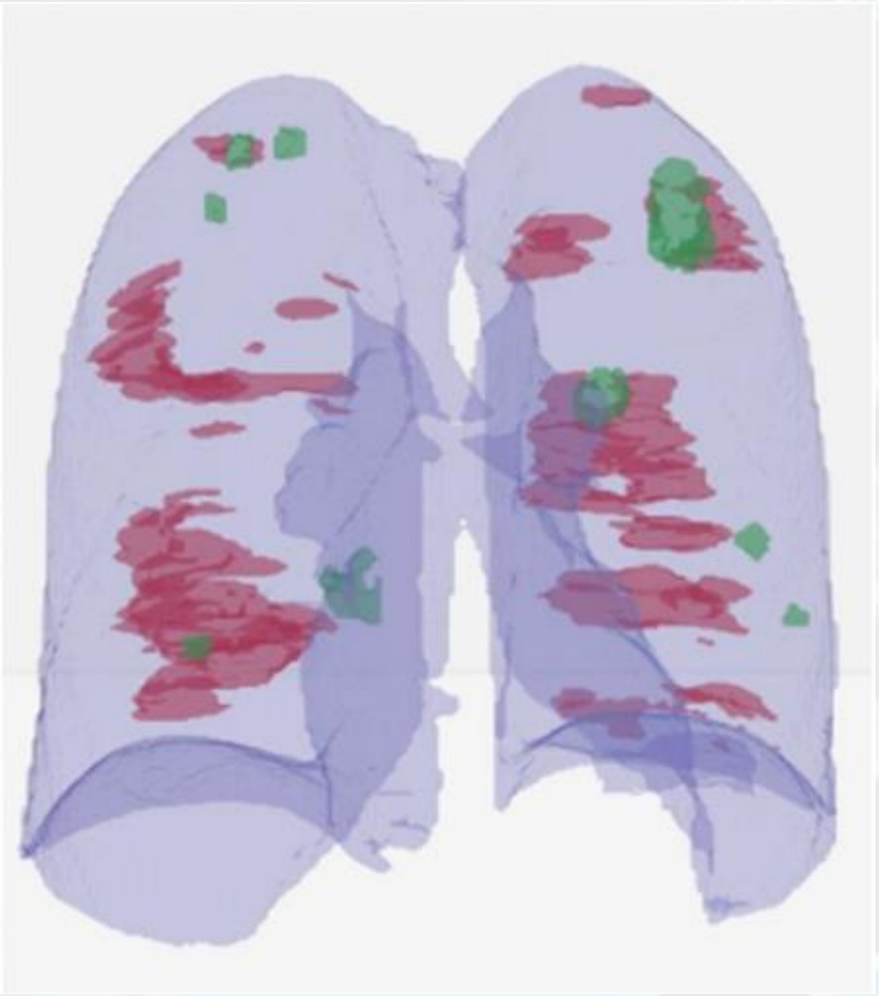
Table 1
Characteristics of the included studies.

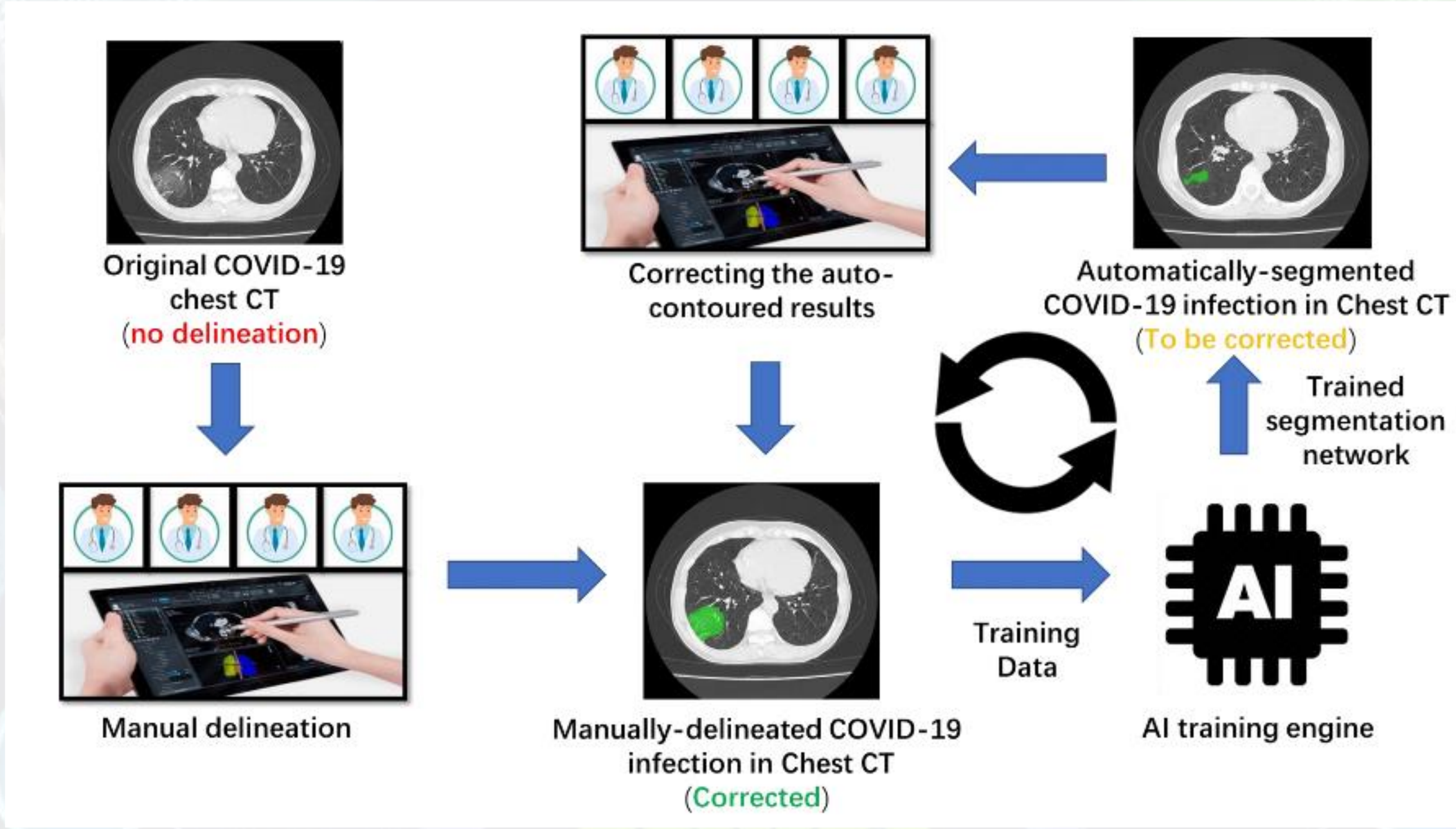
Author, year	Study design	Setting	Database (MIMIC = Medical Information Mart for Intensive Care)	No. predictor variables in model	Outcome	PROBAST-assessment (Risk of bias; concern with applicability)
Diagnosis						
Delahanty, 2019	Retrospective	Emergency Department	Hospital database (2.759.529 patient encounters)	13	AUROC: 0.93 at 1-h, AUROC 0.97 at 24-h	ROB: high, applicability: high
Desautels, 2016	Retrospective	Intensive Care	MIMIC-III	8	AUROC: 0.880 at disease onset	ROB: high, applicability: low
Kaji, 2019	Retrospective	Intensive Care	MIMIC-III	119	AUROC: 0.952 at same-day, 0.876 at next-day	ROB: high, applicability: unclear
Kam, 2017	Retrospective	Intensive Care	MIMIC-III	9	AUROC: 0.929	ROB: high, applicability: low
Mao, 2018	Retrospective	Hospital wide	Hospital database (17.467.987 patient encounters) MIMIC-III	6	AUROC: 0.92 4-h before sepsis onset.	ROB: high, applicability: low
Nemati, 2017	Retrospective	Intensive Care	Hospital database (27.527 patient encounters) MIMIC-III	65	AUROC: 0.85 4-h before sepsis	ROB: high, applicability: high
Taneja, 2017	Retrospective	Hospital wide	Hospital database (444 patient encounters)	21	AUROC: 0.81 at disease onset	ROB: high, applicability: high
Henry, 2015	Retrospective	Intensive care	MIMIC-III	26	AUROC: 0.83 28.2-h before sepsis onset.	ROB: high, applicability: high
Saqib, 2018	Retrospective	Intensive care	MIMIC-III	12	AUROC: 0.696	ROB: high, applicability: low
Shashikumar, 2017	Retrospective	Intensive Care	Hospital database (242 patient encounters)	Unclear	AUROC: 0.78 4-h before sepsis onset.	ROB: high, applicability: low
Barton, 2019	Retrospective	Hospital Wide	Hospital database (91,445 patient encounters) MIMIC-III	6	AUROC: 0.83 48-h before onset.	ROB: high, applicability: low
Pathogen prediction						
Van Steenkiste, 2018	Retrospective	Hospital wide	Hospital database (2177patient encounters)	9	AUROC: 0.99 with 72 h of data	ROB: low, applicability: low
Oonsivalai, 2018	Retrospective	Hospital wide	Hospital database (243 patient encounters)	35	AUROC: 0.80 for ceftriaxone susceptibility	ROB: high, applicability: high
Lamping, 2018	Prospective, RCT	Pediatric ICU	Hospital based (230 patient encounters)	8	AUROC: 0.78 for infectious vs. non-infectious SIRS	ROB: high, applicability: high
Ratzinger, 2018	Prospective	Hospital wide	Hospital based (466 patient encounters)	21	AUROC: 0.73 for bacteraemia.	ROB: high, applicability: low
Prognosis						
Aushev, 2018	Retrospective	Intensive care	ShockOmics	80	AUROC: 0.845 for ICU mortality	ROB: high, applicability: high
Dybowski, 1996	Retrospective	Intensive care	Hospital database (4484 patient encounters)	11	AUROC: 0.863 for in-hospital mortality	ROB: high, applicability: high
Garcia-Gallo, 2018	Retrospective	Intensive care	MIMIC-III	18	AUROC: 0.8083 for 1 year mortality	ROB: high, applicability: low
Jaimes, 2005	Retrospective	Emergency department	Hospital database (542 patient encounters)	10	AUROC: 0.8782 for 28-day mortality	ROB: low, applicability: low
Meiring, 2018	Retrospective	Intensive care	MIMIC-II MIMIC-III	25	AUROC: 0.895 for mortality at ICU discharge	ROB: low, applicability: low
Taylor, 2016	Retrospective	Emergency department	Hospital database (4676 patient encounters)	25	AUROC: 0.86 for in-hospital mortality	ROB: high, applicability: high
Ward, 2017	Retrospective	Trials/Studies	Hospital database (2514 patient encounters)	18	AUROC: 0.79 for 30-day mortality	ROB: high, applicability: high
Treatment assistance						
Komorowski, 2018	off-policy evaluation	Intensive care	MIMIC-III eICU	48	AI policy associated with lowest mortality	ROB: high, applicability: high
Merouani, 2008	Prospective, randomized	Intensive care	Hospital database (42 patient encounters)	2	Median duration of shock significantly shorter (28.5 h versus 57.5 h).	ROB: -, applicability: -
Shimbukuro, 2017	Randomized controlled trial	Intensive care	Hospital database (142 patient encounters)	8	In-hospital mortality decreased by 12.4% points	ROB: high, applicability: low

Table 3
Specific types of artificial intelligence models.

Author	Year	Type of Learning	Type of model
Delahanty	2019	Supervised	Gradient-boosted tree model
Desautels	2016	Supervised	Gradient-boosted tree model
Mao	2018	Supervised	Gradient-boosted tree model
Kam	2017	Reinforced	Long short-term memory
Kaji	2019	Reinforced	Neural Network
Nemati	2018	Supervised	Modified Weilbull-Cox proportional hazards model
Taneja	2017	Supervised	Support Vector Machine
Van Steenkiste	2018	Reinforced	Long short-term memory neural network
Oonsivalai	2018	Supervised	Random Forest Model
Dybowski	1996	Reinforced	Artificial Neural Network
Taylor	2016	Supervised	Random Forest model
Aushev	2018	Supervised	Machine Learning
Meiring	2018	Reinforced	Deep Learning Model
Jaimes	2005	Reinforced	Artificial Neural Network
Garcia-Gallo	2018	Supervised	Stochastic Gradient Boosting
Komorowski	2018	Reinforced	Markov decision process
Merouani	2008	Reinforced	Fuzzy Logic
Shimbukuro	2017	Supervised	Machine learning
Henry	2015	Supervised	Cox proportional hazards model
Ward	2017	Supervised	Causal Probabilistic Network
Lamping	2018	Supervised	Random Forest Model
Ratzinger	2018	Supervised	Random Forest Model
Saqib	2018	Supervised	Random Forest Model
Shashikumar	2017	Supervised	Elastic Net logistic classifier
Barton	2019	Supervised	Gradient-boosted tree model






Original COVID-19 chest CT (no delineation)
Correcting the auto-contoured results
Automatically-segmented COVID-19 infection in Chest CT (To be corrected)
Trained segmentation network
Manual delineation
Manually-delineated COVID-19 infection in Chest CT (Corrected)
Training Data
AI
AI training engine

HEDEFLER:

- Hastanelerde triyajda ve yatan hasta hizmetlerinde planlama ve verimlilik
  - Yoğun bakım ünitelerinde doğru planlama, empirik antimikrobiyal tedavinin başlanması
  - Mortalitenin düşürülmesi, yatış süresinin kısaltılması, Uygun maliyetli tedavi yönetimi
  - Hastanede direnç sorununa yönelik erken tedbir alınmasını sağlayabilir.
  - Personel arasında zaman kaybının önüne geçebilir.
- Daha doğru ve hızlı bir şekilde sepsis teşhisi koyma kapasitelerinin artırılması
- Yapay zekaların sepsis tanısına destek olma sürecinde doktorların karar verme sürecine entegre edilmesi de önemlidir.
- Komorbiditeler, önceki yatış , önceki nosokomiyal enfeksiyon gibi olayları dahil ederek sepsis riskinin 48 saatten daha önce tahmin edilebilmesi

KISITLILIKLAR

- Sepsis gibi acil durumlarda veri toplama süreci karmaşık ve zaman alıcı olabilir. Bu nedenle, yapay zeka algoritmaları için yeterli yapılandırılmış veri bulunamayabilir veya verilerin kalitesi yeterli olmayabilir.
- Sepsis teşhisi koymak için kullanılan yapay zeka algoritmaları, eğitim veri setindeki durumlara benzer olmayan, farklı bir hasta grubu için doğru sonuçlar vermeyebilir.
- Yapay zeka algoritmalarının kullanımı, hastaların veri gizliliği ve güvenliği, hastaların insan dışı bir teknoloji tarafından teşhis edilmesi ve tedavi edilmesi gibi etik konuları da beraberinde getirir. Bu nedenle, yapay zeka algoritmalarının kullanımıyla ilgili etik ve hukuki sorunlar dikkate alınmalıdır.

ANAHTAR NOKTALAR

- Yapay zeka tabanlı sistemler tıbbi kayıtlardan elde edilen verileri kullanarak sepsis olasılığını tahmin edebilir. Bu sistem, hastalara daha erken ve daha doğru bir teşhis konulmasına yardımcı olabilir.

- Yapay zeka algoritmaları yüksek duyarlılık ve özgüllük oranlarına ulaşabilse de doktorun klinik çalışmasını ikame etmeyi değil, tamamlayı hedefler !

- Klinisyenlerin yapay zeka bilgilerini artırmak, büyük veri işleme ve karar verme mekanizmalarının sağlıklı işleyişi için benzersiz bir fırsat sunar.

İlginiz için teşekkür ederim