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Comparison between machine learning methods for mortality prediction for sepsis patients with different social determinants

Hanyin Wang¹, Yikuan Li¹, Andrew Naidech² and Yuan Luo^{1*} 

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Abstract

Background: Sepsis is one of the most life-threatening circumstances for critically ill patients in the United States, while diagnosis of sepsis is challenging as a standardized criteria for sepsis identification is still under development. Disparities in social determinants of sepsis patients can interfere with the risk prediction performances using machine learning.

Methods: We analyzed a cohort of critical care patients from the Medical Information Mart for Intensive Care (MIMIC)-III database. Disparities in social determinants, including race, sex, marital status, insurance types and languages, among patients identified by six available sepsis criteria were revealed by forest plots with 95% confidence intervals. Sepsis patients were then identified by the Sepsis-3 criteria. Sixteen machine learning classifiers were trained to predict in-hospital mortality for sepsis patients on a training set constructed by random selection. The performance was measured by area under the receiver operating characteristic curve (AUC). The performance of the trained model was tested on the entire randomly conducted test set and each sub-population built based on each of the following social determinants: race, sex, marital status, insurance type, and language. The fluctuations in performances were further examined by permutation tests.

Results: We analyzed a total of 11,791 critical care patients from the MIMIC-III database. Within the population identified by each sepsis identification method, significant differences were observed among sub-populations regarding race, marital status, insurance type, and language. On the 5783 sepsis patients identified by the Sepsis-3 criteria statistically significant performance decreases for mortality prediction were observed when applying the trained machine learning model on Asian and Hispanic patients, as well as the Spanish-speaking patients. With pairwise comparison, we detected performance discrepancies in mortality prediction between Asian and White patients, Asians and patients of other races, as well as English-speaking and Spanish-speaking patients.

Conclusions: Disparities in proportions of patients identified by various sepsis criteria were detected among the different social determinant groups. The performances of mortality prediction for sepsis patients can be compromised

*Correspondence: Yuan.Luo@northwestern.edu

¹ Department of Preventive Medicine, Feinberg School of Medicine, Northwestern University, Chicago, IL, USA
Full list of author information is available at the end of the article



when applying a universally trained model for each subpopulation. To achieve accurate diagnosis, a versatile diagnostic system for sepsis is needed to overcome the social determinant disparities of patients.

Keywords: Sepsis, Machine learning, Social determinants, Disparity, Mortality prediction

Background

Sepsis, one of the most life-threatening circumstances for critically ill patients in the United States, is the culmination of complex interactions between the infecting microorganism and the host immune, inflammatory, and coagulation responses [1, 2]. Each year, more than 1.7 million adults in the United States develop sepsis, and approximately 270,000 die because of sepsis. The prevalence of sepsis is around one-third among hospitalized patients [3]. With a few identification methods currently available, a standardized criteria is still under development [4].

Disparities in critical care can be induced by multi-factored causes [5–8]. Biases are observed in healthcare for patients from different social status groups [9, 10]. With more data-driven and artificial intelligence (AI) involved in healthcare, disparities among sub-populations are more frequently observed and attracted more attention [11–15]. Machine learning applications for risk prediction in healthcare are becoming more powerful with the development of electronic health records (EHRs) [16–20]. Risk predictions for sepsis patients using machine learning techniques have been studied [21–24]. However, the discussions over how the disparities and biases interact with risk prediction models for sepsis patients remain undefined. In this study, we revealed the disparities in the proportions of sepsis in subpopulations of social determinants groups from a cohort of patients admitted for critical care services and examined the fluctuations in the performances of mortality prediction for subpopulations of sepsis patients when using machine learning classifiers.

Methods

Data

Medical Information Mart in Intensive Care (MIMIC)-III v1.4 is an open-sourced large scale database of critical care patients with enriched features [25]. From a total of 23,620 intensive care unit (ICU) admission records, 11,791 patients with their initial admission records were identified and utilized in this study. Selection criteria were applied to filter out nonadults, patients with suspected infection more than 24 h before the ICU admission or more than 24 h after the ICU admission, patients with missing data, and patients admitted for cardiothoracic surgery services. The data selection algorithms were elaborated in a previous study [4].

Social determinants

Five social determinants were studied, including race, sex, insurance type, marital status, and language. Race of all subjects was re-leveled into five categories, Asian, Black or African American, Hispanic or Latino, White and other, where the “other” category covers American Indian and Alaska Native, Native Hawaiian or other Pacific Islander, multi-race, unspecified race, and other races not mentioned above. Dichotomous sex, female and male, was considered. Insurance types were taken directly from the MIMIC-III database, which includes government, Medicaid, Medicare, private, and self-pay. Marital status was re-factorized into the following categories: significant other, single, separated, widowed, and unknown, where the “significant other” category covers the situations if life partner or married was indicated in the MIMIC-III database, the “separated” category covers the circumstances if divorced or separated was displayed in the database, the “unknown” category covers the situation if unknown (default) was indicated in the database and was coded for those patients did not specify the marital status. Languages were re-grouped into English, Spanish and other, where the “other” category covers any languages documented in the database other than the two stated.

Disparities in social determinants across various sepsis criteria

We compared the disparities between each sub-category of social determinants in the sepsis population detected by the six identification methods for sepsis: (1) explicit criteria: two codes explicitly mentioning sepsis (995.92 and 785.52 for severe sepsis and septic shock, respectively) defined by International Classification of Diseases, 9th version (ICD-9); (2) Angus methodology [26]; (3) Martin methodology [27]; (4) criteria presented by Centers for Medicare & Medicaid Services (CMS) [28]; (5) the complete surveillance criteria presented by Center of Disease Control and Prevention (CDC) [29]; (6) Sepsis-3 [30]. Forest plots were generated for the proportion of each subpopulation that was identified as sepsis by each method. For example, a proportion of 0.274 for Asian and “Angus” represents 27.4% of the Asians in the dataset were identified as sepsis by the Angus criteria. A 95% confidence interval was constructed by bootstrapping (1000 simulations) and shown in the forest plots for each proportion.

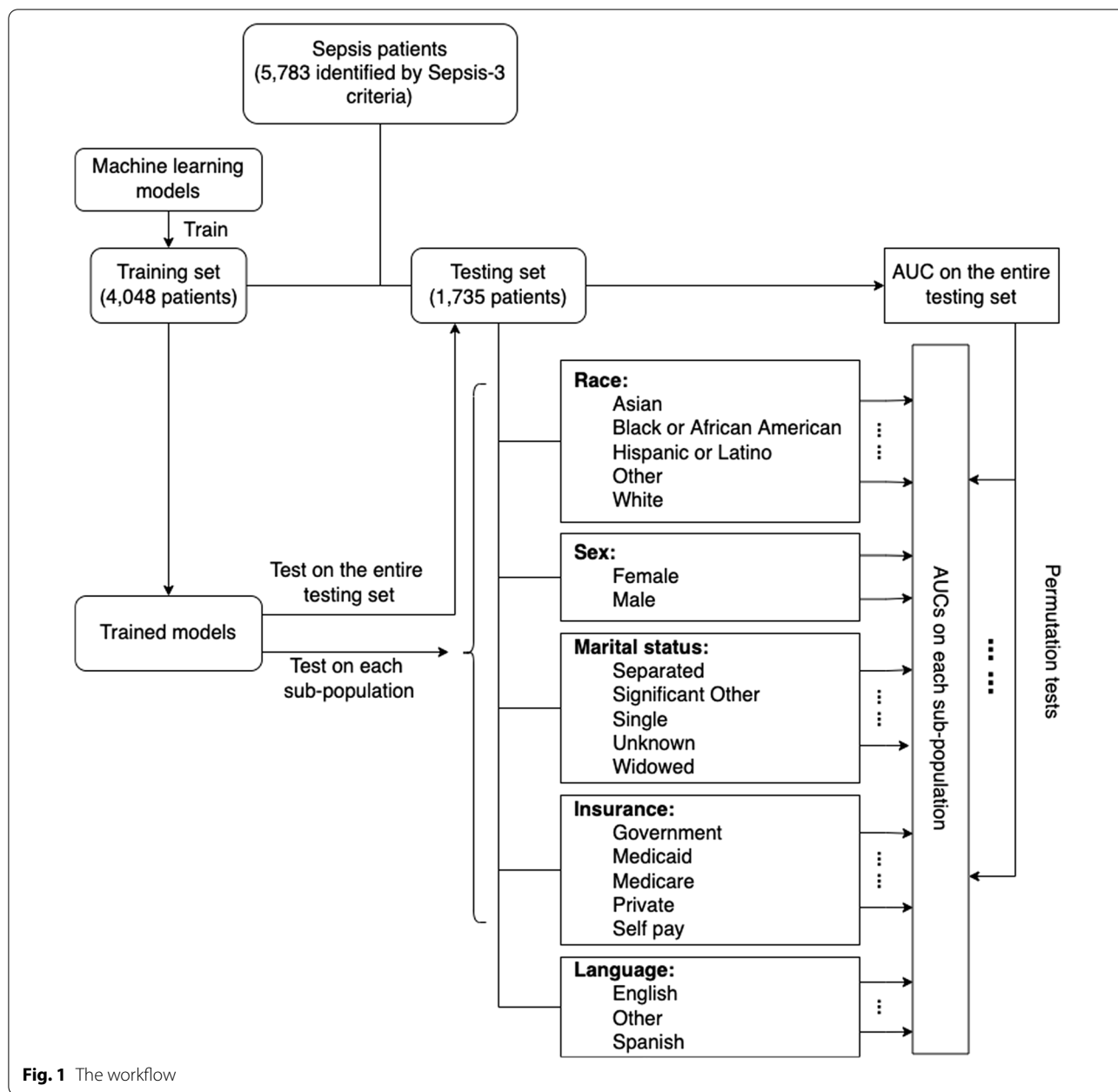
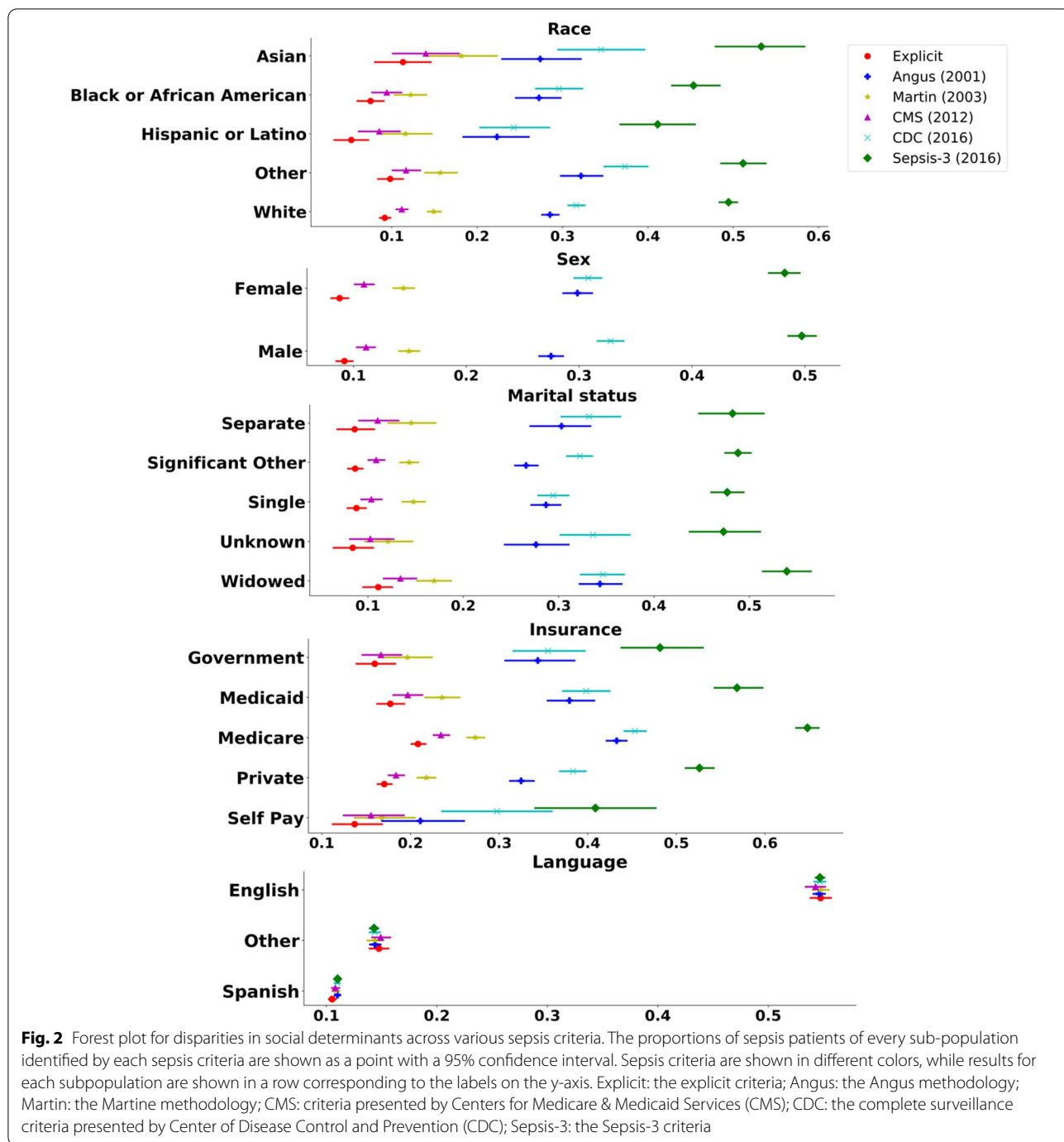


Fig. 1 The workflow

Mortality prediction for sepsis patients using machine learning

We built machine learning classifiers to predict mortality for sepsis patients. The sepsis patient population was constructed using the Sepsis-3 identification method since it is the latest and most conservative among the six methods being discussed [4]. The entire cohort of patients was split into training and testing sets to a proportion of 7:3. Sixteen machine learning configurations were built and trained to predict in-hospital mortality for the sepsis patients, that include

Ridge classifier, perceptron, passive-aggressive classifier, k-nearest neighbors (kNN), random forest, support vector machine with linear kernel (linearSVC) and L1 or L2 regularization, support vector machine with linear kernel and L2 regularization, stochastic gradient descent (SGD) classifier with L1, L2, or elastic net regularization, multinomial naïve Bayes, Bernoulli naïve Bayes, logistic regression, support vector machine (SVM) with rbf, polynomial, or sigmoid kernel. Sequential organ failure assessment (SOFA) score [31] during the first 24 h of admission, systemic inflammatory



response syndrome (SIRS) score [32] during the first 24 h of admission, and age were employed as features. Before training the machine learning configurations, each feature was scaled to 0 to 1 to avoid the impact of different magnitudes. Five-fold cross-validation was employed to find the optimal hyper-parameters for each machine learning configuration. The best-suited thresholds for each classifier were set according to

Youden’s J statistics. The performances of the machine learning configurations were measured by the area under the receiver operating characteristic curve (AUC).

Table 1 Statistics of 5783 sepsis patients

Social Determinants	Category	n	% sepsis population	In-hospital mortality	% in-hospital mortality	Training	Testing
Race	Asian	179	3.10	26	14.53	129	50
	Black or African American	501	8.66	52	10.38	348	153
	Hispanic or Latino	188	3.25	18	9.57	132	56
	Other	714	12.35	165	23.11	527	187
	White	4201	72.64	575	13.69	2912	1289
Sex	Female	2562	44.30	384	14.99	1798	764
	Male	3221	55.70	452	14.03	2250	971
Marital status	Separated	398	6.88	52	13.07	287	111
	Significant other	2559	44.25	363	14.19	1788	771
	Single	1638	28.32	174	10.62	1157	481
	Unknown	332	5.74	102	30.72	248	84
	Widowed	856	14.80	145	16.94	568	288
Insurance type	Government	166	2.87	13	7.83	115	51
	Medicaid	570	9.86	67	11.75	395	175
	Medicare	3358	58.07	560	16.68	2335	1023
	Private	1639	28.34	185	11.29	1168	471
	Self-pay	50	0.86	11	22.00	35	15
Language	English	5167	89.35	727	14.07	3631	1536
	Other	499	8.63	94	18.84	339	160
	Spanish	117	2.02	15	12.82	78	39

Categories of each social determinant are ranked alphabetically; n: number of sepsis patients in the category; % sepsis population: percentage of the number of sepsis patients in the category among the 5,783 sepsis patients; In-hospital mortality: number of patients in the category deceased in-hospital; % in-hospital mortality: percentage of patients in the category deceased in-hospital; Training: number of patients of the given category that were assigned to the training set during train-test split; Testing: number of patients of the given category that were assigned to the test set during train-test split

Table 2 Detailed performances on the entire testing set

	Accuracy	AUC	Precision	Recall	F1_binary	F1_macro	Specificity
Ridge classifier	0.6790	0.7774	0.2682	0.7052	0.3886	0.5855	0.6745
Perceptron	0.6720	0.7786	0.2634	0.7052	0.3835	0.5801	0.6664
Passive-aggressive	0.6841	0.7582	0.2733	0.7131	0.3951	0.5907	0.6792
kNN	0.7135	0.7299	0.2780	0.6135	0.3826	0.5981	0.7305
Random forest	0.7516	0.6459	0.2826	0.4661	0.3519	0.5991	0.7999
LinearSVC_L1	0.6749	0.7781	0.2654	0.7052	0.3856	0.5823	0.6698
LinearSVC_L2	0.6784	0.7777	0.2678	0.7052	0.3882	0.5850	0.6739
SGDClassifier_L1	0.6790	0.7759	0.2682	0.7052	0.3886	0.5855	0.6745
SGDClassifier_L2	0.6790	0.7749	0.2668	0.6972	0.3859	0.5843	0.6759
SGDClassifier_EN	0.6801	0.7753	0.2683	0.7012	0.3881	0.5858	0.6765
MultinomialNB	0.6392	0.7040	0.2348	0.6614	0.3466	0.5487	0.6354
BernoulliNB	0.3107	0.5724	0.1665	0.9402	0.2830	0.3096	0.2042
Logistic regression	0.6824	0.7761	0.2720	0.7131	0.3938	0.5893	0.6772
SVC_rbf	0.6847	0.7744	0.2702	0.6932	0.3888	0.5882	0.6833
SVC_poly	0.6749	0.7751	0.2654	0.7052	0.3856	0.5823	0.6698
SVC_sigmoid	0.6277	0.6873	0.2349	0.6972	0.3514	0.5451	0.6159

F1 binary: F1 score for the positive class; F1_macro: macro-averaged F1 score; Passive-aggressive: passive-aggressive classifier; kNN: k-Nearest Neighbors; LinearSVC_L1 or _L2: support vector machine with linear kernel coupled with L1 or L2 regularization; SGDClassifier_L1 or _L2 or _EN: stochastic gradient descent with L1 or L2 or Elastic Net regularization; MultinomialNB: Multinomial naïve Bayes; BernoulliNB: Bernoulli naïve Bayes; SVC_rbf or _poly or _sigmoid: support vector machine with rbf kernel or polynomial kernel or sigmoid kernel

Table 3 Observed differences between the testing results and each race with *p* values from permutation tests

	Asian		Black or African American		Hispanic or Latino		Other		White	
	Observed difference	<i>p_val</i>	Observed difference	<i>p_val</i>	Observed difference	<i>p_val</i>	Observed difference	<i>p_val</i>	Observed difference	<i>p_val</i>
Ridge classifier	- 0.2812	0.009	- 0.0241	0.366	- 0.2208	0.038	0.0011	0.528	0.0175	0.286
Perceptron	- 0.2748	0.007	0.0078	0.448	- 0.2453	0.025	- 0.0026	0.502	0.0158	0.312
Passive-aggressive	- 0.3188	0.003	- 0.0075	0.464	- 0.1749	0.083	0.0159	0.381	0.0111	0.370
KNN	- 0.1314	0.141	- 0.0628	0.219	- 0.1865	0.069	- 0.0144	0.372	0.0214	0.245
Random forest	- 0.0834	0.207	- 0.0939	0.046	- 0.1226	0.112	0.0536	0.120	0.0056	0.429
LinearSVC_L1	- 0.2819	0.012	- 0.0172	0.410	- 0.2247	0.039	0.0003	0.481	0.0173	0.285
LinearSVC_L2	- 0.2815	0.009	- 0.0221	0.385	- 0.2211	0.045	0.0005	0.490	0.0175	0.294
SGDClassifier_L1	- 0.2872	0.008	- 0.0041	0.482	- 0.2159	0.044	0.0036	0.478	0.0184	0.266
SGDClassifier_L2	- 0.2900	0.008	- 0.0087	0.455	- 0.2182	0.039	0.0044	0.469	0.0191	0.263
SGDClassifier_EN	- 0.2905	0.010	- 0.0046	0.461	- 0.2186	0.058	0.0050	0.497	0.0181	0.300
MultinomialNB	- 0.2797	0.010	0.0671	0.182	- 0.2373	0.033	0.0051	0.484	0.0051	0.416
BernoulliNB	- 0.1974	0.025	- 0.0034	0.483	0.0476	0.331	0.0173	0.368	0.0012	0.490
Logistic regression	- 0.2875	0.010	- 0.0257	0.377	- 0.2061	0.054	0.0043	0.495	0.0174	0.273
SVC_rbf	- 0.3085	0.005	0.0042	0.480	- 0.2311	0.031	- 0.0176	0.383	0.0175	0.275
SVC_poly	- 0.2978	0.006	0.0027	0.483	- 0.2751	0.017	0.0087	0.431	0.0154	0.287
SVC_sigmoid	- 0.1343	0.144	- 0.0941	0.083	- 0.0606	0.332	- 0.0099	0.455	0.0208	0.247

Observed difference: observed difference in AUC when compared with the performance on the entire testing set; *p_val*: *p* value, *p* values less than or equal to 0.05 were highlighted; Passive-aggressive: passive-aggressive classifier; KNN: k-Nearest Neighbors; LinearSVC_L1 or _L2: support vector machine with linear kernel coupled with L1 or L2 regularization; SGDClassifier_L1 or _L2: stochastic gradient descent with L1 or L2 regularization; MultinomialNB: Multinomial naïve Bayes; BernoulliNB: Bernoulli naïve Bayes; SVC_rbf or _poly or _sigmoid: support vector machine with rbf kernel or polynomial kernel or sigmoid kernel

Table 4 Observed differences between the testing results and each language with *p* values from permutation tests

	English		Other		Spanish	
	Observed difference	<i>p_val</i>	Observed difference	<i>p_val</i>	Observed difference	<i>p_val</i>
Ridge classifier	0.0154	0.279	− 0.0760	0.107	− 0.3422	0.012
Perceptron	0.0182	0.252	− 0.0916	0.053	− 0.3551	0.004
Passive-aggressive	0.0122	0.301	− 0.0555	0.172	− 0.2288	0.053
kNN	0.0166	0.263	− 0.0768	0.102	− 0.3063	0.017
Random forest	0.0037	0.409	− 0.0057	0.489	− 0.2342	0.002
LinearSVC_L1	0.0160	0.299	− 0.0772	0.102	− 0.3428	0.003
LinearSVC_L2	0.0156	0.297	− 0.0763	0.121	− 0.3424	0.007
SGDClassifier_L1	0.0184	0.246	− 0.0783	0.093	− 0.3347	0.008
SGDClassifier_L2	0.0187	0.269	− 0.0752	0.107	− 0.3396	0.004
SGDClassifier_EN	0.0181	0.259	− 0.0760	0.105	− 0.3283	0.006
MultinomialNB	0.0221	0.224	− 0.1210	0.021	− 0.2746	0.031
BernoulliNB	0.0076	0.389	− 0.0621	0.082	0.0306	0.422
Logistic regression	0.0145	0.293	− 0.0703	0.125	− 0.3173	0.014
SVC_rbf	0.0159	0.306	− 0.0825	0.080	− 0.3332	0.012
SVC_poly	0.0176	0.275	− 0.0860	0.079	− 0.3633	0.002
SVC_sigmoid	− 0.0030	0.454	0.0341	0.288	− 0.1814	0.089

Observe difference: observed difference in AUC when compared with the performance on the entire testing set; *p_val*: *p*-value, *p* values less than or equal to 0.05 were highlighted; Passive-aggressive: passive-aggressive classifier; kNN: k-Nearest Neighbors; LinearSVC_L1 or _L2: support vector machine with linear kernel coupled with L1 or L2 regularization; SGDClassifier_L1 or _L2 or _EN: stochastic gradient descent with L1 or L2 or Elastic Net regularization; MultinomialNB: Multinomial naïve Bayes; BernoulliNB: Bernoulli naïve Bayes; SVC_rbf or _poly or _sigmoid: support vector machine with rbf kernel or polynomial kernel or sigmoid kernel

Statistical analysis for disparities in performances on sub-populations of social determinants

The training procedures were carried out on the entire training set, after which trained configurations and evaluation metrics on the entire cohort were saved. In the next step, we tested the performance on every sub-population of each of the five social determinants. To detect the disparities in performances, we compared the AUCs on the entire cohort with those on the subpopulations by permutation tests (1000 times). A one-tailed permutation test was employed to determine if the decrease or increase of the performance is significant statistically when testing on sub-groups of patients. To further illustrate the disparities, we conducted pairwise permutation tests (1000 times) among each pair of the sub-populations. A two-tailed permutation test was used to show if there are significant disparities in performances among each pair. The entire workflow can be found in Fig. 1.

The analysis was conducted using Python 3.6.8. Machine learning classifiers, cross-validation, and evaluation metrics were conducted using Sci-kit Learn 0.23.2.

Results

Disparities in social determinants across various sepsis criteria

Forest plots for the disparities in social determinants across various sepsis criteria are shown in Fig. 2.

Proportions of sepsis patients identified by different methods showed significant discrepancies, with the Sepsis-3 criteria as the most conservative one. Within the population identified by the same sepsis identification method, significant differences were observed among sub-populations regarding race, marital status, insurance type, and language. Numeric values of the proportions and 95% confidence interval can be found in the Table S1 in the Additional file 1.

Mortality prediction for sepsis patients using machine learning

In total, 5783 patients were identified as sepsis by the Sepsis-3 criteria. Statistics of this cohort of sepsis patients are shown in Table 1. The detailed testing performances on the entire testing set are shown in Table 2.

We compared the performances (AUC) for each of the sixteen classifiers on the entire testing set and every sub-population by permutations tests. Significant results at a confidence level of 0.05 were found for race and languages. The observed differences and the corresponding *p*-values yielded from the permutation tests are shown in Tables 3 and 4. Among all the racial groups, we observed significant decreases in the performances of most of the classifiers for Asian and Hispanic patients (Table 3). Interestingly, significant performance drops were observed when applying the classifiers for

Table 5 Pairwise comparisons among different racial groups

	Asian v.s. Black or African American		Asian v.s. Hispanic or Latino		Asian v.s. Other		Asian v.s. White		Black or African American v.s. Hispanic or Latino	
	Observed difference	p_val	Observed difference	p_val	Observed difference	p_val	Observed difference	p_val	Observed difference	p_val
Ridge classifier	0.2572	0.074	0.0605	0.738	0.2824	0.033	0.2988	0.018	-0.1967	0.189
Perceptron	0.2827	0.042	0.0295	0.883	0.2722	0.051	0.2906	0.021	-0.2531	0.081
Passive-aggressive	0.3114	0.045	0.1439	0.432	0.3348	0.018	0.3299	0.008	-0.1674	0.238
kNN	0.0686	0.647	-0.0552	0.763	0.1170	0.380	0.1528	0.224	-0.1238	0.413
Random forest	-0.0104	0.916	-0.0392	0.715	0.1370	0.211	0.0890	0.372	-0.0287	0.781
LinearSVC_L1	0.2647	0.075	0.0571	0.756	0.2822	0.043	0.2991	0.020	-0.2076	0.156
LinearSVC_L2	0.2594	0.084	0.0605	0.752	0.2820	0.042	0.2990	0.019	-0.1990	0.179
SGDclassifier_L1	0.2832	0.052	0.0714	0.668	0.2908	0.036	0.3057	0.022	-0.2118	0.136
SGDclassifier_L2	0.2813	0.050	0.0718	0.692	0.2944	0.019	0.3091	0.015	-0.2095	0.151
SGDclassifier_EN	0.2858	0.058	0.0718	0.706	0.2954	0.035	0.3086	0.015	-0.2140	0.142
MultinomialNB	0.3468	0.013	0.0424	0.800	0.2848	0.035	0.2848	0.029	-0.3044	0.032
BernoulliNB	0.1940	0.043	0.2450	0.068	0.2147	0.015	0.1986	0.021	0.0510	0.609
Logistic regression	0.2617	0.082	0.0814	0.620	0.2918	0.037	0.3049	0.019	-0.1804	0.198
SVC_rbf	0.3127	0.025	0.0774	0.653	0.2909	0.030	0.3259	0.013	-0.2352	0.093
SVC_poly	0.3005	0.024	0.0227	0.889	0.3066	0.025	0.3132	0.016	-0.2778	0.056
SVC_sigmoid	0.0402	0.780	0.0736	0.666	0.1244	0.375	0.1551	0.235	0.0334	0.796
	Black or African American v.s. Other		Black or African American v.s. White		Hispanic or Latino v.s. Other		Hispanic or Latino v.s. White		Other v.s. White	
	Observed difference	p_val	Observed difference	p_val	Observed difference	p_val	Observed difference	p_val	Observed difference	p_val
Ridge classifier	0.0252	0.781	0.0416	0.557	0.2219	0.103	0.2383	0.055	0.0164	0.783
Perceptron	-0.0104	0.930	0.0080	0.926	0.2427	0.076	0.2611	0.032	0.0184	0.747
Passive-aggressive	0.0234	0.764	0.0186	0.791	0.1908	0.167	0.1860	0.134	-0.0048	0.931
kNN	0.0484	0.564	0.0841	0.225	0.1721	0.189	0.2079	0.081	0.0358	0.537
Random forest	0.1474	0.029	0.0994	0.089	0.1762	0.101	0.1282	0.182	-0.0480	0.278
LinearSVC_L1	0.0175	0.832	0.0344	0.629	0.2251	0.106	0.2420	0.065	0.0170	0.764
LinearSVC_L2	0.0226	0.792	0.0396	0.585	0.2216	0.088	0.2386	0.065	0.0170	0.756
SGDclassifier_L1	0.0076	0.931	0.0225	0.753	0.2194	0.108	0.2343	0.075	0.0149	0.794
SGDclassifier_L2	0.0131	0.882	0.0278	0.699	0.2226	0.080	0.2373	0.059	0.0147	0.786
SGDclassifier_EN	0.0096	0.932	0.0228	0.765	0.2236	0.088	0.2368	0.070	0.0132	0.830
MultinomialNB	-0.0620	0.491	-0.0620	0.425	0.2423	0.073	0.2424	0.053	0.0001	1.000
BernoulliNB	0.0207	0.702	0.0046	0.935	-0.0303	0.764	-0.0464	0.607	-0.0161	0.650
Logistic regression	0.0301	0.705	0.0432	0.579	0.2104	0.130	0.2235	0.083	0.0131	0.827
SVC_rbf	-0.0218	0.799	0.0133	0.860	0.2135	0.110	0.2485	0.047	0.0350	0.527

Table 5 (continued)

	Black or African American v.s. Other		Black or African American v.s. White		Hispanic or Latino v.s. Other		Hispanic or Latino v.s. White		Other v.s. White	
	Observed difference	p_val	Observed difference	p_val	Observed difference	p_val	Observed difference	p_val	Observed difference	p_val
SVC_poly	0.0060	0.930	0.0127	0.848	0.2838	0.027	0.2905	0.0066	0.019	0.904
SVC_sigmoid	0.0841	0.286	0.1149	0.110	0.0507	0.727	0.0814	0.0307	0.544	0.584

Observe difference: observed difference in AUC when comparing the performance between the sub-populations; p_val: p-value, p values less than or equal to 0.05 were highlighted; Passive-aggressive: passive-aggressive classifier; KNN: k-Nearest Neighbors; LinearSVC_L1 or _L2: support vector machine with linear kernel coupled with L1 or L2 regularization; SGDClassifier_L1 or _L2 or _EN: stochastic gradient descent with L1 or L2 or Elastic Net regularization; MultinomialNB: Multinomial naive Bayes; SVC_rbf or _poly or _sigmoid: support vector machine with rbf kernel or polynomial kernel or sigmoid kernel

Table 6 Pairwise comparisons among different language groups

	English v.s. Other		English v.s. Spanish		Other v.s. Spanish	
	Observed difference	<i>p_val</i>	Observed difference	<i>p_val</i>	Observed difference	<i>p_val</i>
Ridge classifier	− 0.0915	0.135	− 0.3576	0.008	− 0.2661	0.081
Perceptron	− 0.1098	0.070	− 0.3733	0.005	− 0.2635	0.095
Passive-aggressive	− 0.0677	0.266	− 0.2410	0.087	− 0.1733	0.281
kNN	− 0.0934	0.159	− 0.3230	0.021	− 0.2295	0.121
Random forest	− 0.0094	0.833	− 0.2379	0.023	− 0.2285	0.064
LinearSVC_L1	− 0.0931	0.132	− 0.3587	0.007	− 0.2656	0.097
LinearSVC_L2	− 0.0919	0.135	− 0.3580	0.008	− 0.2661	0.095
SGDClassifier_L1	− 0.0967	0.113	− 0.3531	0.015	− 0.2564	0.097
SGDClassifier_L2	− 0.0939	0.143	− 0.3583	0.009	− 0.2643	0.078
SGDClassifier_EN	− 0.0940	0.136	− 0.3463	0.009	− 0.2523	0.093
MultinomialNB	− 0.1432	0.017	− 0.2967	0.034	− 0.1535	0.295
BernoulliNB	− 0.0697	0.091	0.0230	0.818	0.0927	0.397
Logistic regression	− 0.0849	0.174	− 0.3318	0.025	− 0.2469	0.093
SVC_rbf	− 0.0984	0.112	− 0.3491	0.013	− 0.2507	0.104
SVC_poly	− 0.1035	0.100	− 0.3809	0.009	− 0.2773	0.072
SVC_sigmoid	0.0372	0.544	− 0.1784	0.203	− 0.2155	0.151

Observe difference: observed difference in AUC when comparing the performance between the sub-populations; *p_val*: p-value, p-values less than or equal to 0.05 were highlighted; Passive-aggressive: passive-aggressive classifier; kNN: k-Nearest Neighbors; LinearSVC_L1 or _L2: support vector machine with linear kernel coupled with L1 or L2 regularization; SGDClassifier_L1 or _L2 or _EN: stochastic gradient descent with L1 or L2 or Elastic Net regularization; MultinomialNB: Multinomial naïve Bayes; BernoulliNB: Bernoulli naïve Bayes; SVC_rbf or _poly or _sigmoid: support vector machine with rbf kernel or polynomial kernel or sigmoid kernel

the group of patients that speak Spanish (Table 4). We put the results of the social determinants associated with very few to no significant findings in the Table S2-S4 in the Additional file 1. For a further illustration of the disparities, we showed the pairwise comparison results in Tables 5 and 6. Among all the pairs of the racial groups, discrepancies were observed between Asian and White, as well as Asian and other races in most of the classifiers. Significant differences were also observed between Asian and Black sepsis patients in a few classifiers. The disparities between patients speaking various languages were majorly detected between the English-speaking patients and the Spanish-speaking patients. The pairwise comparison results with very few to no significant findings in the Table S5-S7 in the Additional file 1.

Discussion

Currently, the “gold standard” for sepsis diagnosis is still absent. Among those available criteria, we observed different sensitivities in identifying patients. Meanwhile, we observed disparities in the proportions of population identified by each criteria across various social determinant groups. This brings us the concern that a universal diagnostic system might not work equally on each sub-population. By systematically examining the discrepancies, we hope to provide evidence for a more versatile detection system that takes the disparities in social determinants into consideration. In this study, we

have excluded patients with missing data and performed complete case analysis. In future study, we plan to apply advanced missing data imputation techniques [33–35] to relax this exclusion criteria and investigate the potential links between missing data and social determinants of health.

The discrepancies among subpopulations of social determinants groups hinder the performance of a machine learning model trained on the entire population. In a previous study, racial disparities [36] and region disparities [37] in sepsis-related mortality were revealed by retrospective studies. Prediction of mortality using machine learning has been well-discussed during recent years. However, more effort was devoted to improving the overall performances on the entire given population. While what was being less discussed was the fairness of applying trained machine learning algorithms on various groups of patients. It is by nature that patients are of various social status and it is essential not to underestimate such discrepancies. In this current study, we tested the performance fluctuations when applying the same trained model on patients from each social determinant groups and revealed statistically significant shifts in the performance. Even though the overall performance of a given classifier is descent, it should be kept in mind that there are still sub-populations not benefitting from the model as others. On the one hand, we hope such evidence provides a perspective on the impacts of social determinants

for not only the medical society that is working diligently towards a fairer diagnostic method but also the artificial intelligence researchers trying to improve the predictive algorithms one more step towards clinically ready. Additionally, in future studies, we would take the interaction between features into consideration for a more thorough perspective.

Conclusions

Disparities in social determinants were observed in the groups of sepsis patients identified by various currently available diagnostic criteria. The performance of risk prediction tasks for sepsis patients can be compromised when applying a universally trained model for each sub-population. To achieve more accurate identification, a more versatile diagnostic system for sepsis is in need to overcome the social determinant disparities of patients.

Abbreviations

MIMIC-III: Medical Information Mart for Intensive Care-III; AUC: Area under the receiver operating characteristic curve; AI: Artificial intelligence; EHR: Electronic health record; ICU: Intensive care unit; ICD-9: International Classification of Diseases, 9th version; CMS: Centers for Medicare & Medicaid Services; CDC: Center of Disease Control and Prevention; kNN: K-nearest neighbors; linearSVC: Support vector machine with linear kernel; SGD: Stochastic gradient descent; EN: Elastic net; NB: Naive Bayes; SVC: Support vector machine; SOFA: Sequential organ failure assessment; SIRS: Systemic inflammatory response syndrome.

Supplementary Information

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Additional file 1. Supplementary tables for proportions of subpopulations, observed differences for sex, marital status, and insurance type groups, and pairwise comparisons among sex, marital status, and insurance type groups.

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Author contributions

YLuo, AN, and HW conceptualized the study. HW carried out all the data analysis, tables, and figures, and was a major contributor in writing the manuscript. YLi contributed to the optimization of the data visualizations. All authors contributed to the design of the research and to editing the original and the final manuscripts. All authors read and approved the final manuscript.

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Availability of data and materials

The datasets supporting the conclusions of this article are available in the freely accessible database MIMIC-III through PhysioNet (<https://physionet.org/content/mimiciii-demo/1.4/>).

Declarations

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Consent for publication

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Competing interests

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Author details

¹Department of Preventive Medicine, Feinberg School of Medicine, Northwestern University, Chicago, IL, USA. ²Department of Neurology, Feinberg School of Medicine, Northwestern University, Chicago, IL, USA.

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References

- Hotchkiss RS, Karl IE. The pathophysiology and treatment of sepsis. *N Engl J Med*. 2003;348(2):138–50.
- Russell JA. Management of sepsis. *N Engl J Med*. 2006;355(16):1699–713.
- Novosad SA, Sapiano MR, Grigg C, Lake J, Robyn M, Dumyati G, Felsen C, Blog D, Dufort E, Zansky S. Vital signs: epidemiology of sepsis: prevalence of health care factors and opportunities for prevention. *Morb Mortal Wkly Rep*. 2016;65(33):864–9.
- Johnson AE, Aboab J, Raffa JD, Pollard TJ, Deliberato RO, Celi LA, Stone DJ. A comparative analysis of sepsis identification methods in an electronic database. *Crit Care Med*. 2018;46(4):494.
- Kent JA, Patel V, Varela NA. Gender disparities in health care. *Mount Sinai J Med: J Transl Personal Med*. 2012;79(5):555–9.
- Orlovic M, Smith K, Mossialos E. Racial and ethnic differences in end-of-life care in the United States: Evidence from the Health and Retirement Study (HRS). *SSM-Popul Health*. 2019;7: 100331.
- Quindemil K, Nagl-Cupal M, Anderson KH, Mayer H. Migrant and minority family members in the intensive care unit. A review of the literature. *HeilberufeSCIENCE*. 2013;4(4):128–35.
- Soto GJ, Martin GS, Gong MN. Healthcare disparities in critical illness. *Crit Care Med*. 2013;41(12):2784.
- Obermeyer Z, Powers B, Vogeli C, Mullainathan S. Dissecting racial bias in an algorithm used to manage the health of populations. *Science*. 2019;366(6464):447–53.
- Wiens J, Price WN, Sjoding MW. Diagnosing bias in data-driven algorithms for healthcare. *Nat Med*. 2020;26(1):25–6.
- Ahmad MA, Patel A, Eckert C, Kumar V, Teredesai A. Fairness in machine learning for healthcare. In: *Proceedings of the 26th ACM SIGKDD International Conference on Knowledge Discovery & Data Mining: 2020*; 2020: 3529–3530.
- Chen IY, Szolovits P, Ghassemi M. Can AI help reduce disparities in general medical and mental health care? *AMA J Ethics*. 2019;21(2):167–79.
- Grote T, Berens P. On the ethics of algorithmic decision-making in healthcare. *J Med Ethics*. 2020;46(3):205–11.
- Wang H, Li Y, Ning H, Wilkins J, Lloyd-Jones D, Luo Y. Using machine learning to integrate sociobehavioral factors in predicting cardiovascular-related mortality risk. *Stud Health Technol Inform*. 2019;264:433–7.
- Bhavani SV, Luo Y, Miller WD, Sanchez-Pinto LN, Han X, Mao C, Sandıkcı B, Peek ME, Coopersmith CM, Michelson KN. Simulation of ventilator

- allocation in critically ill patients with COVID-19. *Am J Respir Crit Care Med.* 2021;204(10):1224–7.
16. Ahmad MA, Eckert C, Teredesai A. Interpretable machine learning in healthcare. In: *Proceedings of the 2018 ACM international conference on bioinformatics, computational biology, and health informatics: 2018*; 2018: 559–560.
 17. Callahan A, Shah NH. Machine learning in healthcare. In: *Key advances in clinical informatics.* Elsevier; 2017: 279–291.
 18. Chen M, Hao Y, Hwang K, Wang L, Wang L. Disease prediction by machine learning over big data from healthcare communities. *IEEE Access.* 2017;5:8869–79.
 19. Luo Y, Xin Y, Joshi R, Celi L, Szolovits P. Predicting ICU mortality risk by grouping temporal trends from a multivariate panel of physiologic measurements. In: *Proceedings of the 30th AAAI Conference on Artificial Intelligence: 2016*; 2016: 42–50.
 20. Sanchez-Pinto N, Stroup E, Pendergrast T, Pinto N, Luo Y. Derivation and validation of novel phenotypes of multiple organ dysfunction syndrome in critically ill children. *JAMA Netw Open.* 2020;3(8):e209271–e209271.
 21. Scott H, Colborn K. Machine learning for predicting sepsis in-hospital mortality: an important start. *Acad Emerg Med.* 2016;23(11):1307–1307.
 22. Taylor RA, Pare JR, Venkatesh AK, Mowafi H, Melnick ER, Fleischman W, Hall MK. Prediction of in-hospital mortality in emergency department patients with sepsis: a local big data–driven, machine learning approach. *Acad Emerg Med.* 2016;23(3):269–78.
 23. Kong G, Lin K, Hu Y. Using machine learning methods to predict in-hospital mortality of sepsis patients in the ICU. *BMC Med Inform Decis Mak.* 2020;20(1):1–10.
 24. Ding M, Luo Y. Unsupervised phenotyping of sepsis using nonnegative matrix factorization of temporal trends from a multivariate panel of physiological measurements. *BMC Med Inform Decis Mak.* 2021;21(5):1–15.
 25. Johnson AE, Pollard TJ, Shen L, Li-Wei HL, Feng M, Ghassemi M, Moody B, Szolovits P, Celi LA, Mark RG. MIMIC-III, a freely accessible critical care database. *Sci Data.* 2016;3(1):1–9.
 26. Angus DC, Linde-Zwirble WT, Lidicker J, Clermont G, Carcillo J, Pinsky MR. Epidemiology of severe sepsis in the United States: analysis of incidence, outcome, and associated costs of care. *Read Online: Crit Care Med* [Soc Crit Care Med. 2001, 29(7):1303–1310.
 27. Martin GS, Mannino DM, Eaton S, Moss M. The epidemiology of sepsis in the United States from 1979 through 2000. *N Engl J Med.* 2003;348(16):1546–54.
 28. Medicare Cf, Services M. Implementation of severe sepsis and septic shock: management bundle measure (NQF# 0500). In: *National Quality Forum: 2012*; 2012.
 29. Seymour CW, Coopersmith CM, Deutschman CS, Gesten F, Klompas M, Levy M, Martin GS, Osborn TM, Rhee C, Warren D. Application of a framework to assess the usefulness of alternative sepsis criteria. *Crit Care Med.* 2016;44(3): e122.
 30. Seymour CW, Liu VX, Iwashyna TJ, Brunkhorst FM, Rea TD, Scherag A, Rubenfeld G, Kahn JM, Shankar-Hari M, Singer M. Assessment of clinical criteria for sepsis: for the Third International Consensus Definitions for Sepsis and Septic Shock (Sepsis-3). *JAMA.* 2016;315(8):762–74.
 31. Vincent J-L, Moreno R, Takala J, Willatts S, De Mendonça A, Bruining H, Reinhart C, Suter P, Thijs LG. The SOFA (Sepsis-related Organ Failure Assessment) score to describe organ dysfunction/failure. *New York:* Springer-Verlag; 1996.
 32. Rangel-Frausto MS, Pittet D, Costigan M, Hwang T, Davis CS, Wenzel RP. The natural history of the systemic inflammatory response syndrome (SIRS): a prospective study. *JAMA.* 1995;273(2):117–23.
 33. Luo Y: Evaluating the state of the art in missing data imputation for clinical data. *Brief Bioinform.* 2022; 23(1):bbab489.
 34. Luo Y, Szolovits P, Dighe AS, Baron JM. 3D-MICE: integration of cross-sectional and longitudinal imputation for multi-analyte longitudinal clinical data. *J Am Med Inform Assoc (JAMIA).* 2017;25(6):645–53.
 35. Cao W, Wang D, Li J, Zhou H, Li L, Li Y. Brits: Bidirectional recurrent imputation for time series. *arXiv preprint arXiv:180510572* 2018.
 36. Jones JM, Fingar KR, Miller MA, Coffey R, Barrett M, Flottesmesch T, Heslin KC, Gray DT, Moy E. Racial disparities in sepsis-related in-hospital mortality: using a broad case capture method and multivariate controls for clinical and hospital variables, 2004–2013. *Crit Care Med.* 2017;45(12):e1209–17.
 37. Ogunidipe F, Kodadhala V, Ogunidipe T, Mehari A, Gillum R. Disparities in sepsis mortality by region, urbanization, and race in the USA: a multiple cause of death analysis. *J Racial Ethn Health Disparities.* 2019;6(3):546–51.

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