



Application of Machine Learning for Clinical Subphenotype Identification in Sepsis

A MACHINE LEARNING-BASED, CLUSTER ANALYSIS

Question

Can machine learning algorithms be applied to identify possible sepsis subphenotypes using routinely available clinical data?

Database and population



MIMIC-IV
2008-2019

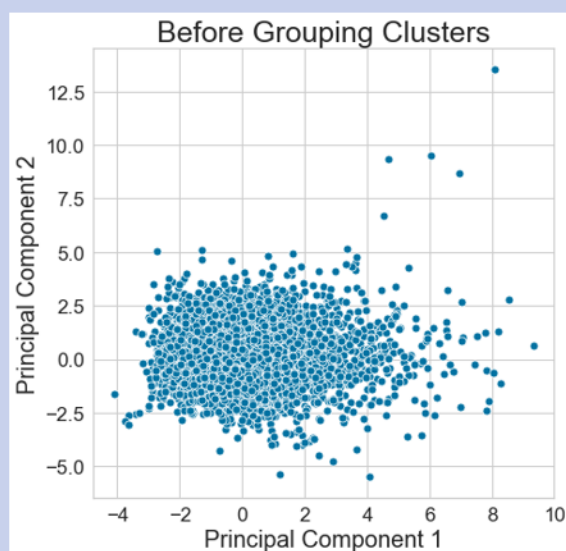


Sepsis
N = 8817

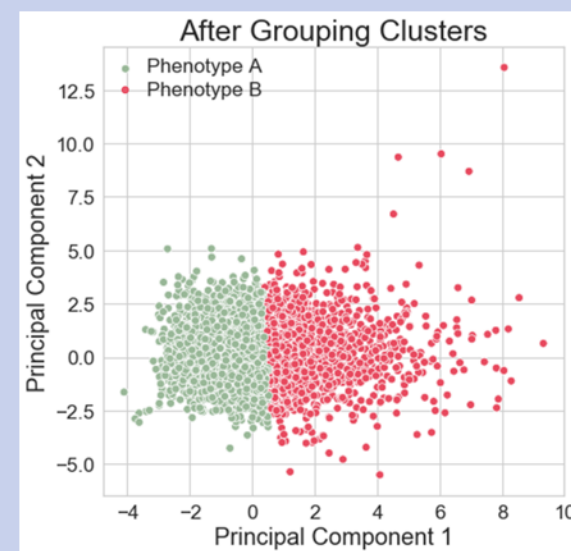


Age: 66.8 years
Female: 38.1%

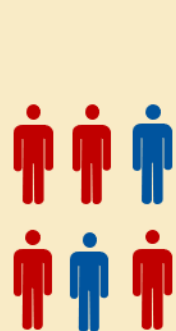
Methods



Cluster analysis



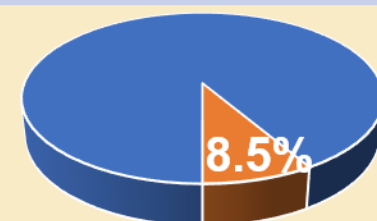
Results



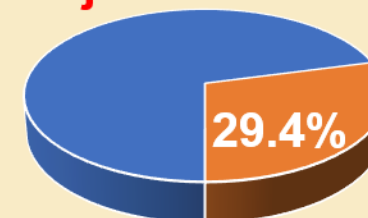
Phenotype A
(N = 7094)

Phenotype B
(N = 1723)

In-hospital mortality



Adjusted $P < 0.001$



Two sepsis subphenotypes with different clinical outcomes can be rapidly identified using the K-means clustering analysis based on routinely available clinical data. This finding may help clinicians to rapidly and easily identify subphenotype of sepsis at the bedside.

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