Exploring Acute Kidney Injury Complexity: Comparing Two Unsupervised Cluster Analysis Methods to Identify Phenotypic Patterns in Critical Care Patients

Background

Emerging evidence of distinct Acute Kidney Injury (AKI) phenotypes offers predictive insights into patient outcomes, especially for critically ill patients at high mortality risk[1]. Patient phenotyping is essentially a clustering problem[2]. This study assessed the incidence of AKI during the first week of ICU admission and identified associated factors by performing clustering analysis on a critical care patient dataset. The goal was to elucidate different AKI profiles based on clinical presentation, contributing causes, underlying disease characteristics and outcomes.

Methods

Retrospective analysis performed on the AmsterdamUMC ICU database, containing clinical data from 23,106 admissions of 20,109 patients[3]. Patients admitted for any reason in the ICU, who developed AKI in the first week of ICU stay, were included. Inclusion criteria were: length of ICU treatment >48 hours, having more than one serum creatinine (SCr) measurement during ICU stay, and AKI diagnosis in the first week of ICU, as defined by Kidney Disease: Improving Global Outcomes (KDIGO) Guidelines for AKI[4]. Exclusion criteria were: SCr level >400 µmol/L before admission, admission for nephrectomy or kidney transplant, previous end-stage renal disease, patients without more than one SCr measurement before Renal Replacement Therapy (RRT) starting, pregnancy. Data was collected on demographic features, laboratory data, ICU specific parameters and measurements (including fluid therapy, vasoactive drugs, antibiotics, mechanical ventilation, exposure to nephrotoxic drugs, ICU length of stay). Data quality was reviewed, and records with errors and outliers were removed. After scaling, autoencoders were used to reduce dimensionality, and an internal layer was used to perform K-means clustering. The optimal number of clusters was determined by silhouette analysis and dendrogram plot evaluation. Python 3, along with the Matplotlib+Seaborn, scikit-learn and Keras+Tensorflow modules, was employed for computing, analyzing, and visualizing data.

Results

A total number of 2395 admissions of patients with AKI were found. Patients were classified by their worst KDIGO staging. Different clustering methods were performed to allow exploration of the most plausible clinical phenotypes. K-means clustering with four clusters was selected. Autoencoder and Variational Autoencoder methods seemed to differentiate

four different clusters, respectively shown on Figure 1 and Figure 2, which resulted in four different AKI phenotypes. First phenotype is characterized by a low burden of AKI, with little to no incidence of RRT. Second phenotype is associated with planned cardiovascular surgery and coronary heart disease. Third phenotype is linked to a higher burden of AKI, particularly due to severe shock and organ dysfunction; Variational Autoencoder method also identified higher serum bilirubin and lower platelet levels, along with more albumin infusion, possibly correlating with more severe organ dysfunction or hepatorenal syndrome. A fourth phenotype seems to be related to patients with prolonged ICU stay and extended mechanical ventilation, indicative of chronic critical illness.

Conclusion

In a clinical-surgical ICU subset, two distinct clustering methods identified four different AKI phenotypes. Additional research is needed to validate the differences among these groups.

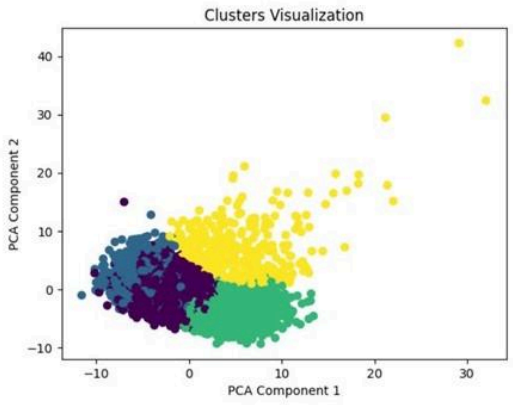

Figure 1. Autoencoder clustering results.

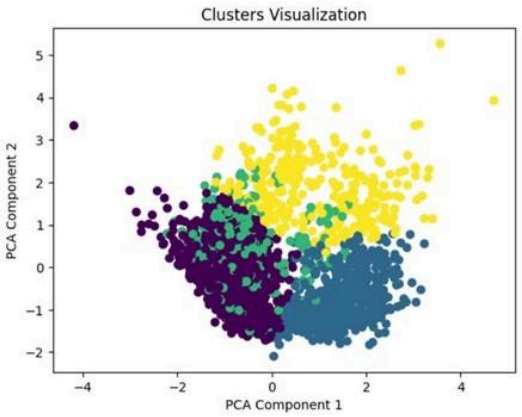

Figure 2. Variational Autoencoder clustering results.

References

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