Category : Outcome scores

A124 - *Novel sub-phenotypes highlight heterogeneity of characteristics and guide individualized treatment in chronic critical illness*

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Introduction:

Patients who survived from the initial attack in ICU yet represent the long-term stay status with persistent organ dysfunction are recognized as chronic critical illness (CCI) and cause heavy burden on their family, healthcare system and the society. CCI patients showed great heterogeneity. Therefore, it is important to identify the subtypes in order to guide clinical practice and trials. In this study, we used multiple machine learning methods to identified CCI phenotypes and their characteristics in disease pattern and heterogenous treatment effect.

Methods:

Data from three large critical care electronic healthcare record databases and one single-center tertiary referral hospital in China were extracted and formed four observational cohorts. Multiple unsupervised clustering algorithms were employed independently for phenotypes derivation and cross validation. A Bayesian-based framework was applied for treatment effect investigation.
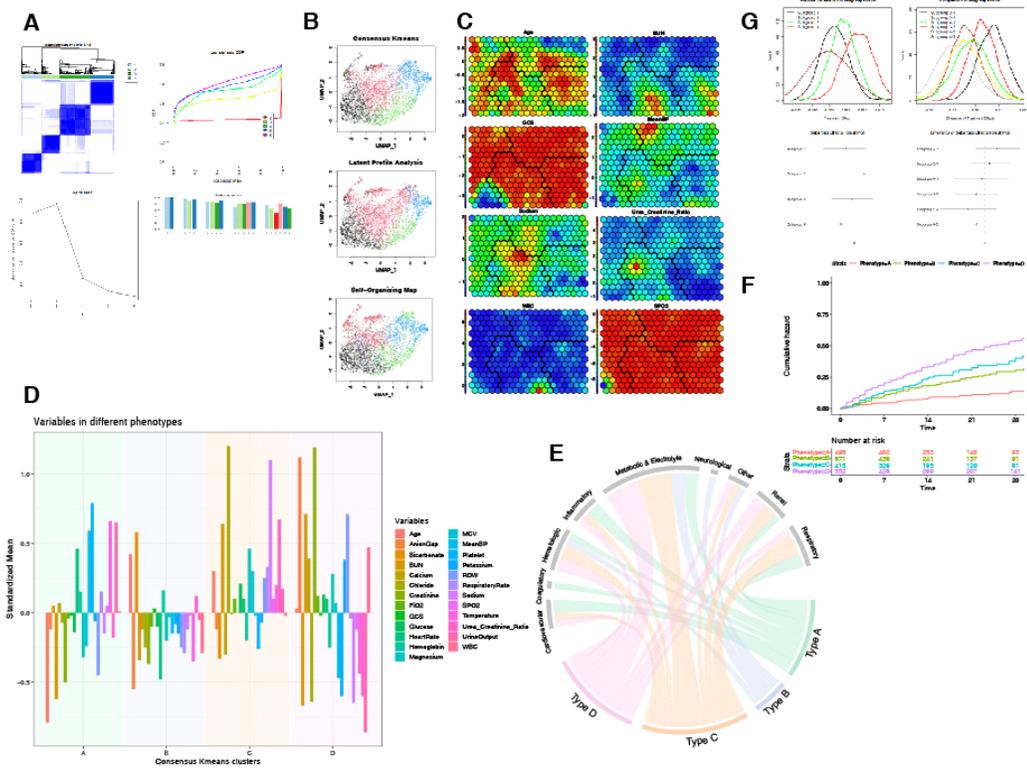
Results:

In total 6862 patients were enrolled in this study. Clustering process identified four CCI phenotypes as A (mild), B (short course), C (dehydrated and catabolic multiple organ dysfunction), and D (multiple organ failure). Each phenotype showed distinct clinical features and disease behaviors (Figure 1). Survival analysis indicated that Type D has the worst prognosis (ICU mortality: 29.9%, $p < 0.001$) and Type A has the best prognosis (ICU mortality: 13.1%, $p < 0.001$). Bayesian causal inference analysis demonstrated that there were great differences in the efficacy of various therapies in different subtypes and we proposed an optimized treatment framework in order to individually improve critical care.

Conclusion:

We identified four novel phenotypes that revealed the different patterns within CCI patients. Our findings could assist clinical practice and enlighten future researches.

Image :

A) Consensus Kmeans results showed best cluster number as 4; B) UMAP plots for comparison of three independent unsupervised clustering processes (Consensus Kmeans, Latent profile analysis, and Self-organizing map) showed similar phenotypes distribution; C) Selected representative variable property maps of SOM showed heterogeneous assignment of different subgroups; D) Standardized mean values of variables barplot in four CCI phenotypes; E) Chord plot showed four phenotypes with different pattern features on organ system level; F) Kaplan-Meier curve showed distinct cumulative hazard in subclasses; G) Bayesian hierarchical modeling revealed heterogeneity of phenotypes responses to sedation drug dose rate.