

Chair Digital Health - Personalized Medicine & The Hasso Plattner Institute for Digital Health at Mount Sinai

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Subphenotyping of COVID-19 associated AKI using deep learning

Acute kidney injury (AKI) is a sudden decrease in kidney function which happens because of damage to the kidneys and is associated with a 3-10-fold increase in mortality. However, despite many years of investment, no new therapies have been found. A primary reason for this is that all AKI is being treated as a single entity. It is becoming increasingly recognized now that most complex disease entities are not just one homogenous disease, but complex diseases have inherent subtypes in them. We have shown this previously in sepsis associated AKI that there are latent subtypes that can be discovered using the bottleneck layer of an autoencoder. (Figure 1)

Figure 2. T Distributed stochastic neighbor embedding visual representation of subphenotype 1 in blue, subphenotype 2 in orange, and subphenotype 3 in green.

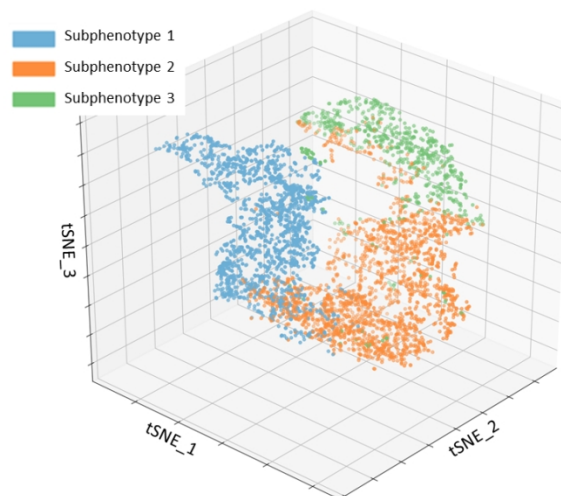


Figure 1. T Distributed stochastic neighbor embedding (t-SNE) visual representation of subphenotype 1 in blue, subphenotype 2 in orange, and subphenotype 3 in green. The t-SNE plot is a method of visualizing high-dimensional data in a low dimensional space (in this case 3-dimensions). Each dot represents a patient and displays clusters within the scaled down and dimensionally reduced space of the autoencoder embeddings.

One of the most severe complications of COVID-19 is AKI which affects approximately 50% of patients. Discovering subtypes within this large patient population and multi-dimensional dataset using deep learning techniques would have implications for risk prediction and treatment approaches

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