A Novel Computational Method for Subdividing Hepatocellular Carcinoma Patients into Uniquely Treatable Clusters

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An estimated 25 million people in the United States suffer from diseases for which there is no effective FDA-approved treatment. This issue exists for a variety of reasons; development of drugs for rare maladies is often neglected due to high costs and limited demand, lack of research in certain areas, and the many years that it takes to bring a new FDA-approved medication to market. While new drugs are being developed, patients are dying. Last year, during the previous stage of this project, a program was designed to pair disease genes with possible FDA-approved drug candidates. The program, and others like it, are limited due to their treating of all patients with a given disease as one unit, while in reality, they vary greatly. In order to remove this limitation and improve the quality of drug suggestions, a novel patient clustering algorithm was devised in this study creates a computational method of identifying existing FDA-approved treatments for individual patients of a given disease. Using anonymous data from 250 hepatocellular carcinoma (HCC) patients as a sample set, this study proposes a novel clustering system which integrates additional chemical and biological data into an unsupervised clustering system in order to provide more statistically significant groupings. The novel algorithm, called Enrichment Vector Clustering (EVC), was able to effectively generate patient subgroups, each of which had a completely distinct treatment candidate drug. This fact, in conjunction with the results of the Survival Log-Rank test applied to cluster outcomes ($p = .020$), provides evidence that EVC is more adept at generating clusters with treatment-relevant separations than existing clustering methods, and is a strong step forward towards personalized medicine.

Awards Won:

Second Award of $2,000