Computer-Aided Diagnosis of Heart Allograft Rejection Using Graph-Based Features

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Heart allograft rejection occurs when transplanted cardiac tissue is rejected by the recipient’s immune system, which destroys the transplanted tissue. The effect of its treatment heavily depends on the accuracy of pathologists’ diagnosis after a biopsy. The current diagnostic process is time-consuming, and prone to subjective variance. The aim of this project is to build a computer-aided diagnosis system to provide physicians a second opinion to effectively diagnose heart allograft rejection. The system is able to automatically detect regions of interest (ROI’s) containing destroyed transplanted tissue in the histopathological image. Delaunay Triangulation is employed to find the cells in high cell-density regions, and K-means clustering is performed on the cell nuclei to group them into the optimal ROI's. Finally, a Support Vector Machine (SVM) classifies the heart allograft rejection severity in each ROI. In this study, 30 graph-based features were computed based on the Voronoi diagram, Minimum Spanning Tree, and Delaunay Triangulation, which were constructed upon segmented cell nuclei in histopathological images. Using statistical analysis, 12 high-correlation graph-based features (with p-values less than 0.05) were determined. Each of the 30 features was also evaluated using the SVM classifier, and the top 12 high-accuracy features were identified. The intersecting set of high-accuracy and high-correlation features was used by the SVM to classify heart allograft rejection severity, thereby achieving a classification accuracy of 92%. The quantitative results demonstrated that a computer-aided diagnosis system based on graph-based features could potentially assist physicians in therapeutic decision-making of heart allograft rejection.

Awards Won:
Third Award of $1,000