

Determining Gene Interactions in Congenital Heart Disease for Development of a Comprehensive Fetal Cardiac Diagnostics Platform

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Cardiovascular malformations are the most common type of birth defects. Congenital Heart Disease occurs in approximately 1% of all births globally and has a 48.1% infant mortality rate. Given that there is significant ambiguity with identification of which biomarkers and genetic factors that are associated with CHD, there is significant need for a comprehensive and longitudinal understanding of CHD. I investigated the gene interactions in congenital heart disease by using a generative tensorial reinforcement learning network (GENTRL) to map the active kinase trends and molecular structural trends to see activation patterns in amniotic fluid. This system was able to identify 132 novel gene interaction pathways. Based on the genetic analysis trends I developed a conditional generative adversarial network that is able to predict the morphological deformation and develop a 3D model. The reconstruction accuracy was evaluated at $86.32\% \pm 5.84\%$ as evaluated by the dice similarity coefficient. Based on the 3D reconstruction a Gaussian approximation metric was used to create pseudo ECG data with 94.6% accuracy. The data suggests that the combined genetic and morphological metric serves as a viable early-detection and diagnostic tool for CHD.