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. Congential HeartDisease occurs in approximately 1% of all births globally and has a 48.1% infant mortality rate. Giventhat there is significant ambiguity with identification of which bio-markers and genetic factors that areassociated with CHD, there is significant need for a comprehensive and longitudinal understanding of CHD.Iinvestigated the gene interactions in congenital heart disease by using a generative tensorial reinforcementlearning network (GENTRL) to map the active kinase trends and molecular structural trends to see activationpatterns in amniotic fluid. This system was able to identify 132 novel gene interaction pathways. Based onthe genetic analysis trends I developed a conditional generative adversarial network that is able to predictthe morphological deformation and develop a 3D model. The reconstruction accuracy was evaluated at86.32%±5.84% as evaluated by the dice similarity coefficient. Based on the 3D reconstruction a Gaussianapproximation metric was used to create pseudo ECG data with 94.6% accuracy. the data suggests that thecombined genetic and morphological metric serves as a viable early-detection and diagnostic tool for CHD.

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