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Modelling heart rhytm variability in heart transplant patients by cellular automata on complex networks

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In patients with end-stage heart disease the heart transplantation (HTx) is associated with significant improvement in survival and in quality of life. However strong immunosuppressive drugs together with processes of aging could lead to vasculopathy and fibrosis of the donor heart. Moreover a spontaneous process of reinnervation proceeds in the myocardial tissue. All together impact on progressive alternations in the myocardial structure what influence propagation of activation wave fronts. A variety of arrhythmias – abnormal heart rhythm, may occur which adversely affect the patient long term survival.

Cellular automata modeling of signal propagation in the atrial muscle tissue is a rational compromise in resolving of physiological complexity, justified by efficiency in reproducing details of myocardial architecture. Consequently this modeling may explain key relationships between heart muscle structure and the propagation of activation wave fronts, possible reasons for the risk of arrhythmia.

Combining our proposition for stochastic network cellular automata model of the human pacemaker [1] and 2D cellular automata model of fibrosis in atria proposed in [2], we investigate which changes in myocardial structure affects propagation of cell-to-cell signals to contract in such way that we observe abnormal heart rhythm. 24-hour Holter measurement, a noninvasive and cheap ECG recording provides information on erratic rhythms of HTx patients. By modeling of structural alternates in the heart tissue we reproduce properties of some individual HTx patient heart rhythm [3].

References

1. D. Makowiec Acta Phys.Pol.B Proc.Suppl. 7(2014) 347
2. K. Christensen et al, Phys. Rev. Lett. 114 (2015) 028104
3. D. Makowiec et al, Chaos, Solitons & Fractals 90 (2016) 101

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