BP 29: Posters: Systems biology

Time: Tuesday 14:00–16:00 Location: Poster A

BP 29.1 Tue 14:00 Poster A

Control of ventricular tachycardia under myocardial ischemic conditions and infarction — •Edda Boccia and Stefan Luther — Max Planck Institute for Dynamics and Self-Organization, Am Fassberg 17, Göttingen, Germany

Myocardial ischemia arises when blood supply of substrates doesn't meet tissue's metabolic demands. It can degenerate to acute ischemia and infarction. Ischemia is followed by profound metabolic changes: hyperkalemia (increment of extracellular potassium), hypoxia (deprivation of oxygen supply) and acidosis (increment of acidity in the blood). We present a modified version of the Luo-Rudy I model, adopted to investigate action potential propagation under ischemia and infarction. The domain is represented by a 2D virtual sheet of myocardial tissue, where heterogeneity is introduced by subdividing it in three distinct zones: a central circular ischemic area (CZ), a ring-shaped border zone (BZ, linear transition between physiological and ischemic values) and normal tissue. As a first approximation, hyperkalemia and acidosis were simulated and parameters were changed in the CZ and in the BZ at each time after the onset of ischemia. We study the interaction of propagating waves with ischemic regions and the onset of cardiac arrhythmias, including ventricular tachycardia (VT) and fibrillation (VF). We investigate pinning and unpinning of rotating waves to and from infarction zones using pulsed electric fields. We will discuss the implications of our findings for the development and optimization of low energy control of cardiac arrhythmias including Low-Energy Anti-Fibrillation Pacing (LEAP, Luther & Fenton et al., Nature 2011).

BP 29.2 Tue 14:00 Poster A

combined x-ray phase contrast tomography and scanning x-ray micro-diffraction for multi-scale investigation in regenerative medicine — •alessia cedola[1], gaetano campi[2], inna bukreeva[1], michela fratini[1], giuliana tromba[3], maddalena mastrogiacomo[4], ranieri cancedda[4], and manfred burghammer[5] — [1]ipcf-cnrc/o Physics Departement- Sapienza University- Rome-Italy. — [2]Istituto di Cristallografia- CNR, Monterotondo Rome, Italy. — [3]Sincrotrone Trieste SCpA, 34149 Basovizza (Trieste), Italy. — [4]Dipartimento di Medicina Sperimentale-Università di Genova — [5]esrf-Grenoble-France

The importance of investigating the engineered bone, which is formed when porous ceramic constructs are loaded with bone marrow stromal cells and implanted in vivo, is a key point for Regenerative Medicine. Several aspects of the mechanisms leading to the generation of the new bone,in particular the dynamics of collagen packing during mineralization, requires a deeper understanding. The hierarchical structure of bone makes the combination of X-ray micro-diffraction scanning technique (XR*D) and the X-ray phase contrast tomography (XRPCT) the most effective tool to investigate the structural features of this tissue at different length scales.In particular we use XRPCT to provide the direct 3D image of the collagen network organization and XR*D to probe the structural fluctuations of the collagen lateral spacing and orientation during the growth of mineral particles at molecular and atomic scale. Moreover, we image by XRPCT the 3D microvascular networks in different bone-engineered constructs.

BP 29.3 Tue 14:00 Poster A

Modeling of gene silencing in RNA interference — •Simon Dornseifer[1], Georg Sczakiel[1], Tobias Restle[1], and Jens Christian Claussen[2] — [1]IMM, Universität zu Lübeck, Germany — [2]Computational Systems Biology Lab, Research II, Jacobs University Bremen, Germany

RNA interference (RNAi) is a mechanism of post-transcriptional gene silencing that, since its discovery, gained high attention, and gave rise to the development of new nucleic acid-based tools. Here we propose and investigate a computational systems biology model of siRNA-mediated RNAi in human cells in order to link precise quantitative kinetic data and new molecular findings with a quantitative and time-resolved understanding of RNAi in the human system. Cell culture experiments suggest that the RNAi machinery adopts to large variations in target mRNA level, independent of siRNA or Ago2 concentrations. These experimental findings are not explained by the common literature view of RNAi, here termed dissociative mechanism, where the departing ligand (here, cleaved RNA fragments) leaves the complex in a slow step. Here, we investigate an alternatice, associative mechanism of target strand recognition by Argonaute 2 (Ago2). The associative model is compatible with the high multiple turnover rates of RNAi-based gene silencing in living cells and accounts for target mRNA concentration-dependent acceleration of the RNAi machinery. The associative model proposed here suggests that the efficacy of an siRNA or miRNA depends on the expression level of its target RNA such that high target levels allow better regulation via RNAi.

BP 29.4 Tue 14:00 Poster A

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