SCIENTIFIC SEMINAR

Antonio del Sol

CIC bioGUNE-Computational Biology Lab
Luxembourg Centre for Systems Biomedicine
of the University of Luxembourg

Multi-scale computational modeling in stem cell research and disease modeling

The generation of large amounts of OMICs data is increasingly enabling not only the processing and analyzing of large data sets, but also the development of computational models. In this regard, I will discuss how single cell technologies provide the right framework for computational modeling at different scales of biological organization, including cellular, tissue and organ level, in order to address challenges in stem cell research and disease modeling. Among these challenges, our research focuses on generating specific cell subtypes with high efficiency and fidelity for cell therapy, improving the regenerative capacity of stem cells in old tissues, and modulating the dysregulated inflammatory response associated to disease or ageing. In particular, our computational models have enabled the experimental conversion of human hindbrain neuroepithelial cells into midbrain dopaminergic neuron progenitors, predicted signalling molecules promoting quiescence in neural stem cells, and identified inflammatory molecules secreted by senescent cells impairing muscle regeneration in old tissues. Importantly, the development of these models aims at generating predictions to guide stem cell researchers in the design of novel regenerative medicine therapies, and to assist clinical researchers in the design of new therapeutic intervention strategies to revert disease phenotypes.

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Atrio 800
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