Noel Malod-Dognin (Barcelona Supercomputing Center)

Towards a data-integrated cell(*)

We are flooded with large-scale molecular data capturing complementary aspects of the functioning of a cell. To enable new discoveries, we propose a novel, data-driven concept of an integrated cell, iCell. Also, we introduce a computational prototype of an iCell, which integrates three omics, tissue-specific molecular interaction network types: protein-protein interactions, gene co-expressions, and genetic interactions. We apply our framework and construct iCells of four cancers, breast, prostate, lung, and colorectal, as well as of the corresponding tissue controls. Comparison between cancer and control iCells allows us to uncover the most rewired genes in cancer that do not appear as different in any of the constituent data types. Many of these genes are of unknown function. We biologically validate that they have a role in cancer by knockdown experiments followed by cell viability assays. We find additional support through Kaplan-Meier survival curves of thousands of patients. Finally, we extend this analysis to twenty different cancer types to uncover new pan-cancer genes. Our methodology is universal and enables integrative omics comparisons of diverse data over cells and tissues.

* based on: N. Malod-Dognin, J. Petschnigg, S.F.L. Windels, J. Povh, H. Hemmingway, R. Ketteler, and N. Pržulj, Towards a data-integrated cell, Nature Communications 10: 805, 2019.