11th Berlin Late Summer Meeting 2018 – Grand BIMSB opening symposium

Report by

Dr. Simon Hastreiter, ETH Zürich, Department of Biosystems Science and Engineering in Basel (Prof. Timm Schroeder's lab)

This year's Berlin later summer meeting was a special edition: The opening of the new building for the "Berlin Institute for Medical Systems Biology (BIMSB)" was celebrated with world-leading experts from the fields of Stem Cell and Developmental Biology, Cancer Research, Systems Biology and Biophysics. The integration of those different fields at a very high scientific level and in a rather small setting made the meeting a unique event.

Personal scientific highlights:

Jürgen Knoblich (Vienna, Austria) and Hans Clevers (Utrecht, Netherlands) made clear why human organoids are such a hot topic. Knoblich presented an organoid based model for human brain cancer which gave very interesting insights into the development of this devastating cancer (apparently, neuroepithelial cells can transdifferentiate into endothelial cells). It also enables testing of new drugs including very particular ones: Knoblich presented data showing that the "Zika"-virus is not only a threat for unborn children but could be a blessing for brain cancer patients since it reduces the growth of brain tumor organoids. Clevers showed that cancer organoids derived from patient's material grow slower than healthy organoids because cell divisions are often aberrant. He also presented some evidence that the cell division rate might not be such a critical factor for the mutation rate as currently assumed.

Leonie Ringrose (Berlin, Germany) presented an interesting model suggesting that bivalent chromatin marks (H3K4/H3K27 methylation) are likely a result of dynamic switching between the two states rather than a stable state. Thus "bistable" chromatin might be a better name for this phenomenon.

A pleasure for the audience was the talk of Patrick Cramer (Göttingen, Germany) where he presented his newest structural insights into the different biochemical complexes for transcription initiation, pausing and elongation as beautiful animations. Another interesting insight was the limitation of the initiation rate by the pause duration which his group inferred from various sequencing-based measurements. Nobel Prize laureate Phil Sharp (MIT, USA) later showed an interesting concept how splice sites control the elongation of transcripts.

Fascinating new aspects of gene regulatory mechanisms were presented by Mike Levine (Princeton, USA) and again Phil Sharp (MIT, USA). The traditional model of enhancer-promoter looping might be soon replaced by a model which suggests that gene regulation occurs in phase separated condensates where enhancers and promoters are not in direct contact with each other. This allows one enhancer to activate multiple genes simultaneously. It might also lead to a more synergistic mode of gene activation or even sequester regulatory factors. Although it is not well understood how those condensates are formed and if RNA plays a major role, Phil Sharp suggested that this will be the future of cell biology research.

In his second part, Mike Levine presented a beautiful study where he used single-cell RNA sequencing to understand the embryogenesis of a very close relative of vertebrates: The tunicate Ciona. This was at the same time a feasible task due to the low cell number, but also an important one due to the evolutionary proximity of Ciona to "higher" organisms. This illustrates the power of scRNA-seq which can be applied in a lot of different contexts.

Nikos Karaiskos (BIMSB, Germany) showed fascinating data where scRNA-seq data were exploited by computational methods to map the cells in space. This approach can yield virtual in-situ-hybridization-like data, but with genome-wide information. Florian Erhard (Uni Würzburg, Germany) presented an approach which allowed him to distinguish new and old mRNA molecules in single and thus contains dynamics information. Altogether, those examples suggest that extensions of scRNA and their smart application will provide many more fantastic insights in the future which will allow us to better understand how cell states and tissues are regulated.

Another highlight was the poster session where young researcher presented their current work which I found similarly interesting as the talks. This allowed me to discuss highly debated topics like the importance of topologically-associating-domains (TADs) with people who work in that field. I also presented a poster about “pluripotency network dynamics at the single cell level” which many people found interesting including an editor of a relevant scientific journal.

I’m sure that the meeting will be helpful for my future career since I could learn new aspects about the topics I’m most interested in and I could extend my scientific network. It was also a great opportunity to make my own work more visible and discuss it with other researchers.

I would like to thank the GSCN for supporting me with this travel award and wish the BIMSB a good start in their new building.

Best regards,

Simon Hastreiter