

## **Biological networks help unraveling tumoral heterogeneity at single cell level**

Andrei Zinovyev

*Institut Curie/INSERM, Paris, France*

Single cell measurements change the modern biology due to bringing the 'Big Data'-related approaches and challenges to the studies of normal physiology and diseases such as cancer. A number of novel computational methods and paradigms have emerged to deal with complexity of single cell genomic and epigenomic data. I will present our recent single cell study of heterogeneity of tumors of Ewing sarcoma, starting from characterizing the cell cycle-independent transcriptional program of EWS/FLI-1 oncogene in inducible cell line and finishing by the analysis of patient-derived xenografts profiled with 10x Genomics platform. Our study shows that the tumors of Ewing sarcoma are characterized by intratumoral heterogeneity strongly associated with activity of the EWS/FLI-1 oncogene, with existence of tumor cell subpopulations characterized by specific and unexpected biological properties. Interestingly, projecting the results of single cell data analysis on top of the biological network maps allowed us to obtain insights into the mechanisms shaping intratumoral heterogeneity at single cell level.