LUXEMBOURG INSTITUTE OF HEALTH
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LECTURE SERIES & WORKSHOPS

TRANSLATIONAL BIOINFORMATICS AND SYSTEMS BIOMEDICINE

26

JUNE 2018
Tuesday

LECTURE

📍 **Maison des Sciences Humaines**
"Blackbox" room
(11, Porte des Sciences L-4366 Esch-sur-Alzette)

4.00 - 5.00 pm

MEET THE SPEAKER*
Light snacks provided
Maison des Sciences Humaines
Room N°0.202

5.00 - 6.30 pm

| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |

*Please register by sending a mail to florence.henry@lih.lu

QUANTIFYING INTRATUMORAL HETEROGENEITY AT SINGLE CELL LEVEL

SPEAKER
Dr Andrei ZINOVYEV

Scientific coordinator of Computational Systems Biology of Cancer group, Bioinformatics department of Institut Curie, Paris, France

HOST:
LIH
RESPONSIBLE SCIENTISTS:
Francisco Azuaje
(francisco.azuaje@lih.lu)
Petr Nazarov
(petr.nazarov@lih.lu)

ABSTRACT

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. In this talk, I will present several methods for dealing with large and complex single-cell RNASeq datasets, including Independent Component Analysis for identification of hidden factors shaping cell populations and ElPiGraph method for quantifying branching or circular pseudo-time. 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.

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