

7<sup>th</sup> Polish Illumina SymposiumThursday 12<sup>th</sup> & Friday 13<sup>th</sup> October 2017

Adam Mickiewicz University, Faculty of Biology

ul. Umultowska 89

61-614 Poznań

Venue: Aula

Event location: Collegium Biologicum

**Thursday 12<sup>th</sup> October****SEMINAR SCHEDULE****09:30 Registration****10:00 Welcome and introduction****10:05 Updates and new developments****Florian Graedler, Illumina****10:50 Sexual dimorphism in the dioecious tree *Taxus baccata*****Emilia Pers-Kamczyc, Department of Dendrology, Polish Academy of Sciences, Kornik****11:20 Coffee break****11:50 What can we learn about host-microbiome interactions from a chicken in vitro model?****Anna Sławińska, Department of Animal Biochemistry and Biotechnology, University of Science and Technology, Bydgoszcz****12:20 Single cell RNA-Seq of oocytes and preimplantation porcine embryos****Piotr Pawlak, Department of Genetics and Animal Breeding, University of Life Sciences, Poznan****12:50 Gene expression changes in fast-growing chicken hypothalamus during ontogenesis****Kacper Żukowski National Research Institute of Animal Production, Cracow - Balice****13:20 Lunch****14:00 NGS-based comparative analysis of aDNA damage patterns in mitochondrial and nuclear DNAs****Ireneusz Stolarek, Institute of Bioorganic Chemistry, Polish Academy of Sciences, Poznan****14:30 Genetic association of FTO/IRX region with obesity and overweight in the Polish population****Słomka Marcin, Biobank, University of Lodz**

<b>15:00</b>	<b>Personal identification process: from exhumation to Massively Parallel Sequencing</b>	<b>Maria Szargut, Department of Forensic Genetics, Pomeranian Medical University, Szczecin</b>
<b>15:30</b>	<b>Using Illumina Next-generation Sequencing to Explore the Heterogeneity and Clonal Evolution of Colon Tumours</b>	<b>William Cross, University of Oxford</b>
<b>16:10</b>	<b>Coffee break</b>	
<b>16:25</b>	<b>Deciphering aggressive CpG Island Methylator Phenotype in adrenocortical carcinoma</b>	<b>Gwenneg Kerdivel, INSERM, Paris</b>
<b>17:05</b>	<b>Analysis of ChIP-seq profiles sheds light on the epigenetic heterogeneity of neuroblastoma cells</b>	<b>Valentina Boeva, INSERM, Paris</b>
<b>17:45</b>	<b>Departure for a dinner</b>	

Friday 13<sup>th</sup> October

## SEMINAR SCHEDULE

09:15	Organizational issues	
09:20	NGS in Transcriptomics - From classical gene expression analysis to gene regulation, gene fusion and single cell genomics	Illumina
09:50	SMARTer <sup>®</sup> way for RNA-Seq from single cells and other challenging samples	BIOKOM
10:00	Genome-wide characterization of STAT1 in VSMC-specific and non-specific gene expression in vascular inflammation	Anna Piaszyk-Borychowska, Department of Human Molecular Genetics, Adam Mickiewicz University, Poznań
10:30	Workshop 1: Primary analysis of ChIP-seq data and quality control using the Nebula framework	Gwenneg Kerdivel, Valentina Boeva
12:00	Coffee break	
12:15	Workshop 2: Analysis of DNA Methylation in eukaryotic cells: an overview	Gwenneg Kerdivel, Valentina Boeva
13:45	Lunch	