**Pre-program Winter School Systems Immunology**

**Dec 12-16, 2022**

Every day from 9:00 to 17:00

**Day 1. Gene expression/RNA-seq approach/Phantasus**

*Alexey Sergushichev (Washington University/ITMO)*

a. General introduction on gene expression analysis and bulk RNA-seq

b. Data exploration (using the web tool Phantasus)

c. Differential expression/pathway analysis (Phantasus)

d. Working with public datasets (Phantasus etc)

**Day 2. scRNA-seq from basics to applications, single-nuclei and Cite-seq**

*Maxim Artyomov and Konstantin Zaitsev (Washington University /LP2M, Nice)*

a. General introduction on scRNA-seq approaches

b. Data exploration (using scNavigator)

c. Example of cancer immunology

d. Example of CITE-seq from human scRNA-seq in aging

**Day 3. Immunometabolism computational and applications**

*Alexey Sergushichev (Washington University/ITMO) and Maxim Artyomov (Washington University /LP2M, Nice)*

a. Introduction on Immunometabolism

b. Working with network analysis (example of macrophage activation)

c. Metabolic analysis of single-cell RNA-seq data

d. Example of itaconate and immunometabolic regulation

**Day 4. Genetics**

*Nikita Artyomov (Nationwide Childrens Hospital/OSU)*

a. Introduction on genetics

b. Introduction on GWAS, exome sequencing, whole genome sequencing

c. Immunological traits seen from human genetics

d. Example of genetic overlap between melanoma and vitiligo

**Day 5. Epigenetics – chromatin and DNA methylation**

*Maxim Artyomov (Washington University /LP2M, Nice)*

a. Introduction into chromatin modifications and accessibility (chipseq/atac-seq)

b. Examples of chromatin modification and changes in activated immune cells (atac-seq pipeline)

c. Example of epigenetic regulation of dendritic cell development via specific enhancer

d. Introduction on DNA methylation and example from aging