





EURO-CHOLANGIO NET COST ACTION MULTI-OMICS TRAINING SCHOOL

Date: 2-3 June 2022

Location: Krakow, Poland

Outline:

To give a general understanding of easy-to-use tools and public data sets for basic analysis in your own study.

Training objectives:

Main objective: to get a general overview of multi-OMICs data and to analyze them.

The topics that will be covered during the Training School are:

- Genomics
- Metagenomics
- Transcriptomics
- Proteomics

The specific learning objectives are:

- 1 Get to know the available repositories of various OMIC datasets
- 2 Conduct genomic analysis of CCA tumors (identify and classify recurrent mutations, associations with prognosis, essentiality and druggability of genes)
- 3 Gain insights on differential gene expression analysis
- 4 Learn how to do create a heatmap and how to perform clustering of samples and/or features
- 5 Perform gene ontology (GO) and gene set enrichment analysis (GSEA)
- 6 Get in touch with the important tools to know your gene/protein of interest







DAY 1

08h00 – 08h45: Arrival and registration

08h45 - 09h00: Welcome

Vincenzo Cardinale, Jesus M. Banales, Rui E. Castro, Jesper B. Andersen, Marcin Krawczyk, Piotr Kuśtrowski, Jerzy Kotlinowski, Jolanta Jura and Melissa Kerr

09h00 - 12h00: Genomics

09h00 – 09h15: Applications of genomics in cholangiocarcinoma research

Prof. Jesper B. Andersen (Copenhagen, Denmark)

09h15 – 10h30: Examples and practical exercises I

- i) Check expression of your gene(s) in Tumor vs surrounding liver
- ii) Investigate genomic alterations (mutations, copy number variations, methylation) of your gene of interest and associate genomic alterations with patients' survival
 - iii) Stratify patients based on your gene(s) of interest and generate KMplots

10h30 - 10h45: Coffee break

10h45 – 12h00 - Examples and practical exercises II

- iv) Investigate the relative importance of your gene of interest for tumor cell survival
- v) Assess the druggability of your gene of interest and investigate the sensitivity of CCA cells to targeted therapies against druggable genes of interest.

12h00 - 13h00: Lunch

<u>13h00 – 15h30: Metagenomics</u>

13h00 – 13h15: Metagenomics and hepatobiliary tumors

Prof. Marcin Krawczyk (Homburg, Germany)

13h15 – 15h30: Examples and practical exercises

- i) Taxonomic & Functional Profiling of a Human Sample
- ii) Cohort Study: compute alpha-diversity, beta-diversity, and detect differential abundances between two classes on a prepared abundance table

15h30 - 16h00: Coffee break









16h00 - 19h00: Transcriptomics

16h00 – 16h15: Applications of transcriptomics in cholangiocarcinoma research *Prof. Rui E. Castro (Lisbon, Portugal)*

16h15 - 17h30: Examples and practical exercises I

- i) Sequencing basis, Data upload, Quality control, sequence trimming and mapping
- ii) Use **GEO2R** to perform differential expression analysis in deposited microarray datasets (we let galaxy time to map sequences)
- iii) Quantify gene expression and prepare formats for differential expression analysis

17h30 - 17h45: Coffee break

17h45 - 19h00 - Examples and practical exercises II

- iv) Perform differential expression analysis and visualize differentially expressed genes and sample grouping with PCA
- v) Perform gene set enrichment analyses (GSEA) overrepresentation analysis
- vi) Discover expression of your gene in single-cell RNAseq dataset(s).

DAY 2

<u>09h00 – 12h00: Proteomics</u>

09h00 – 09h15: Applications of proteomics in cholangiocarcinoma research

Prof. Jesus M. Banales (San Sebastian, Spain)

09h15 - 10h30: Examples and practical exercises I

- i) Set up the proteomic processing of raw data downloaded from PRIDE
- ii) Protein interaction and post-translational modifications (PTM)

10h30 - 10h45: Coffee break

10h45 - 12h00 - Examples and practical exercises II

- iii) Get to know the characteristics of your protein of interest
- iv) Study the involvement of your protein/gene of interests in distinct type of cancers and know in which human organs (multi-organ RNA-seq) and which cell types (sc-RNAseq of healthy tissue) is your gene being expressed

12h00: Farewell and lunch