



STSM: Molecular profiling of FFPE tissue samples

Biomedical Research Foundation Academy Of Athens

22.10.-27.10.2023.

COST Action CA21165 PerMediK

Vesna Coric, MD, PhD

Sub-specialization in *Laboratory diagnostics in Oncology diseases*
Faculty of Medicine, University of Belgrade, Serbia
2022

Specialization in *Laboratory medicine*
Faculty of Medicine, University of Belgrade, Serbia
2018

PhD in Molecular medicine
Faculty of Medicine, University of Belgrade, Serbia
2017

Medical Doctor
Faculty of Medicine, University of Belgrade, Serbia
2010



Academic mobilities

STSM COST Action CA16113 CliniMARK

- WG2 “Biomarker clinical feasibility study design”
- Training in sample preparation and statistical and bioinformatics analysis of proteomics data
- **July 2021**

ERAWEB (ERASMUS–WESTERN BALKANS)

- 3-month period on a short-term academic exchange program at the Department of Oncology, Faculty of Medicine, University of Torino (Italy), project entitled “Optimization of the oncological therapy: new drugs against Multidrug Resistance”
- **2013**

SFRR-E/IUBMB

- *7-day Summer School 2012 "Dietary factors and redox signalling", Spetses, Greece*
- **2012**

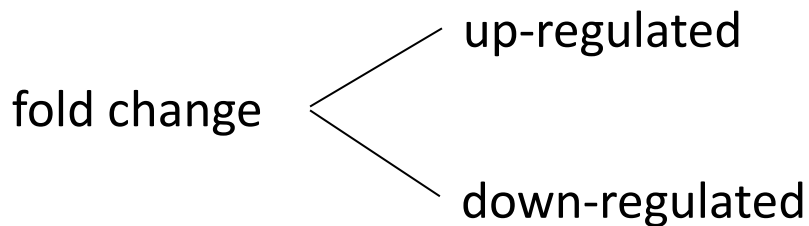
LC-MS/MS, statistical and bioinformatic analysis

STSM 2023

LC-MS/MS with Tims-ToF

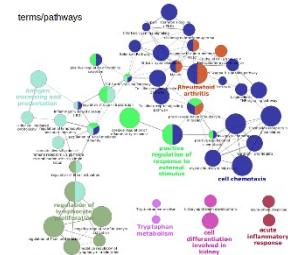


Differentially expressed proteins



STSM 2021

Pathway analysis



ClueGO plug-in in Cytoscape 3.5.1.

PCA and Heatmap analysis

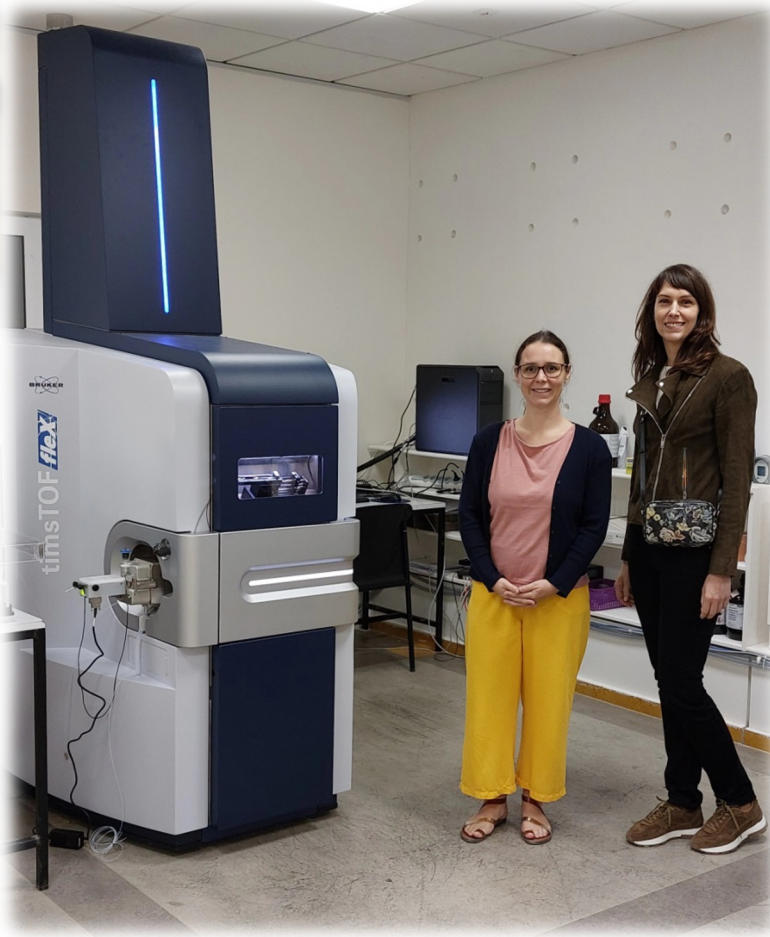


The purpose of the STSM 2023

- Dr Vesna Coric (the applicant) was **methodologically trained** in certain steps of proteomics analysis such as:
 1. *hands-on* training on sample preparation for quantification of protein biomarkers via mass spectrometry,
 2. the statistical and bioinformatics analysis of the *omics* acquired data
- The aforementioned steps were tailored to fit the the objective of **COST Action CA21165 PerMediK**

The purpose of the STSM 2023

- Dr Vesna Coric (the applicant) was **methodologically trained** in certain steps of proteomics analysis such as:
 1. *hands-on* training on sample preparation for quantification of protein biomarkers via mass spectrometry,
 2. the statistical and bioinformatics analysis of the *omics* acquired data
- The aforementioned steps were tailored to fit the the objective of **COST Action CA21165 PerMediK**



Lab work at BRFAA

with Julie Courraud
At University of Athens

The purpose of the STSM 2023

- Dr Vesna Coric (the applicant) to be **methodologically trained** in certain steps of proteomics analysis such as:
 - 1. *hands-on* training on sample preparation for quantification of protein biomarkers via mass spectrometry,
 - 2. the statistical and bioinformatics analysis of the *omics* acquired data
- The aforementioned steps were tailored to fit the the objective of **COST Action CA21165 PerMediK**

- Dr Coric was trained for analyzing proteomics **data** and graphically present them using:
- basics of the R statistical functions
- data reduction methods such as *principal component analysis* (PCA)
- exploratory data analysis such as *Clustering*
- gene set enrichment method such as *gene set variation analysis* (GSVA)
- correlation matrix for R *ggplot2* package in order to produce *Heatmaps* and *Volcano* plots
- *Cytoscape* and *Metascape*, an open source software platforms for assessing pathway enrichment and protein:protein interactions, using *ClueGO* plug-in for specifically gene ontology enrichment and visualization
- In addition, Dr Coric acquired skills in obtaining proteomics and transcriptomics datasets from available Open Access databases (PRIDE, ProteomeXchange, Nephroseq, etc.) for the purpose of their annotation and subsequent reanalysis.

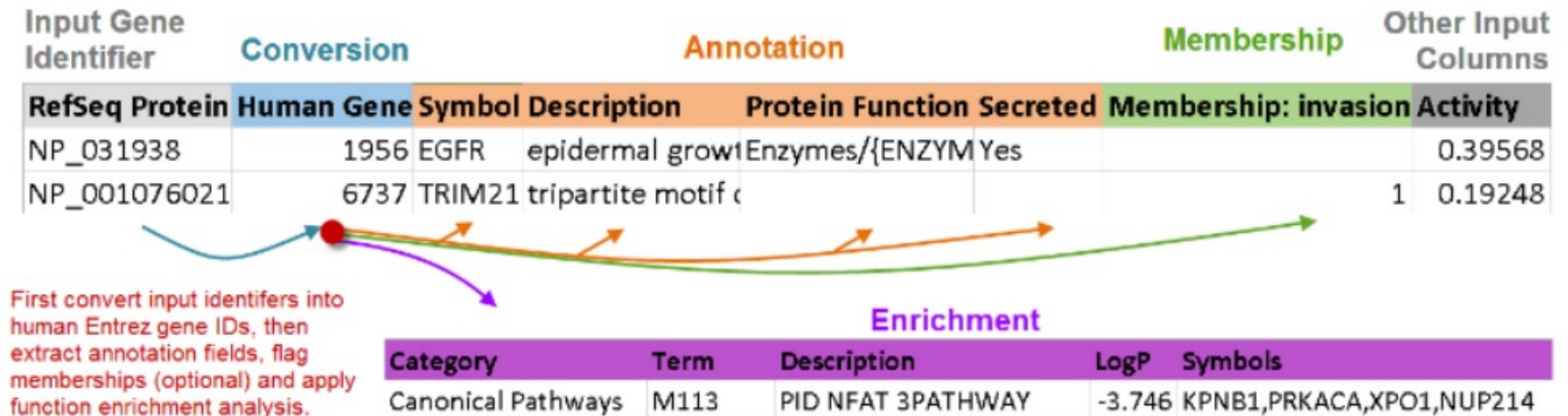
Transferable skills for data acquisition, analysis and its visualization



Metascape

Metascape - CAME analysis workflow

- C** ID Conversion -- convert input gene identifiers into Entrez gene IDs of a target species, as subsequent analyses rely on Entrez gene IDs.
- A** Annotation -- extract annotation columns for the gene list, including gene descriptions, functions, and protein classes.
- M** Membership -- flag genes of interest, e.g., flag genes which fall under GO biological process terms that contain "invasion" as a keyword.
- E** Function Enrichment analysis of the gene list -- identifying pathways that have statistically significant p-values. This step also includes protein network analysis, which can be used to identify densely-connected protein network components and their biological roles.

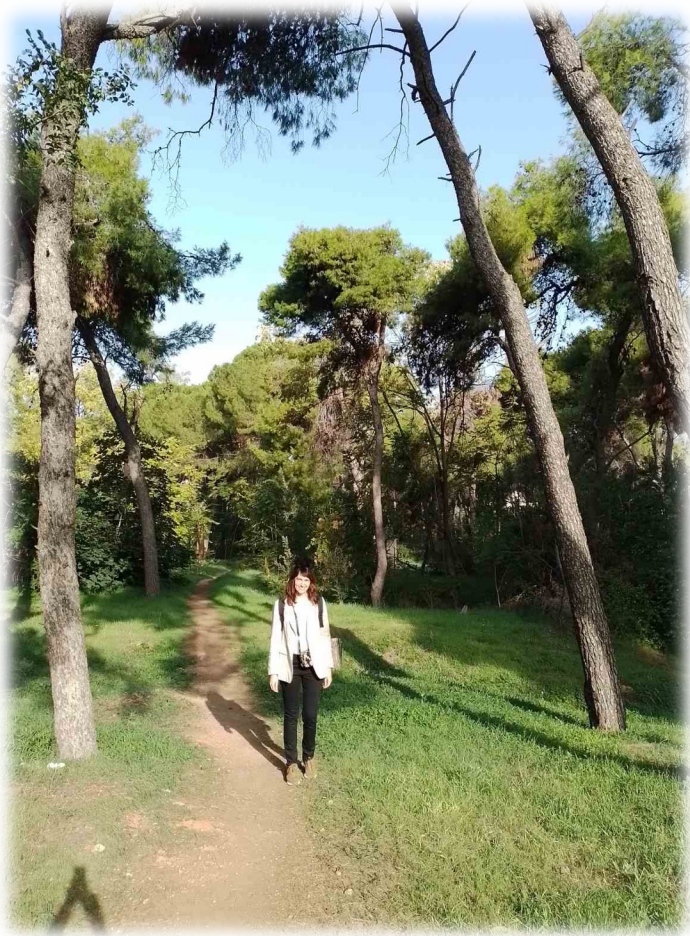


Other activities

- Additionally, Dr Coric attended the Journal Clubs and Laboratory meetings
- Regular lab meetings (*Microsoft Teams*) on MONDAYS
 - ✓ Reports from the previous week
 - ✓ Reports regarding the progress of current projects
 - ✓ Plans for the ongoing week
- Regular Journal clubs (*Microsoft Teams*) on TUESDAYS
 - ✓ host of the Journal Club
 - ✓ journal, monthly issue

The establishment of future collaborations for submitting manuscripts and research proposals is envisioned

FUTURE PERSPECTIVES



On my way to BRFAA



With BRFAA group