

Name of the MSC Fellow: Bence Gálik

Nationality: Hungarian

Host organization: Medical University of Bialystok (MUB)

Country of the Host: Poland

Project Acronym: ImPRESS

Project start and end date: 1.02.2018-31.01.2023

***MSC Fellows project start and end date: 1.10.2018-30.09.2022**

Type of MSC action, H2020: COFUND

Project objectives and research field:

The aim of my project conducted within ImPRESS is to create a novel model for personalized tumor diagnostics based on an integrated analysis of multi-omics and clinical data. The results of combined analyses of genomic, transcriptomic, proteomic and metabolomic biomarkers and PET/MRI images performed on patients with non-small cell lung cancer will be a reference model of tumor diagnosis.

Tell us why your topic is important and/ or how it brings to advancement in your research field:

The applied omic-platforms (genomic, transcriptomic and epigenomic) can help to better understand the biology of cancer. The Whole Genome Sequencing has produced an explosion in the context and complexity of cancer genomic alterations, including point mutations, small insertions or deletions, copy number alterations and structural variations. With an integrated multi-omics approach, we will be able to obtain a much more precise view of genome than by standard analysis methods. The whole transcriptome approach can not only quantify gene expression profiles, but also detect alternative splicing, RNA editing and fusion transcript. In addition to mRNA, the study of microRNAs (miRNAs) and DNA methylation and their roles in regulating the expression of specific genes in cancerous cells is rapidly expanding our comprehension about this aspect of cell biology.

What are the benefits of participating in a MSC action?

I will design and implement analytical pipelines for NGS data analysis as well as perform comprehensive analysis of data produced within the project. This includes the following technologies, their intersections and downstream analyses: RNA-Seq, smallRNA-Seq, methylated DNA and genome sequencing. New pipelines will be used to detect polymorphisms further correlated with phenotypical data (drug resistance, prognosis, etc.). As a result, we will be able to detect genes and isoforms that are up- and downregulated depending on tumor stage and phenotype. This allows for both better understanding of cancer biology and discovery of new biomarkers. In parallel with that a unique software platform is being developed for the collection, integration and analysis of omics and clinical data. A reference model of personalized tumor

diagnosis will be created. Furthermore, a similar approach may be easily scaled and applied in e.g. metabolic and cardiovascular diseases or other lifestyle diseases.

Did you encounter any challenges during application/ implementation and did you get any help?

The biggest challenge of the project could be collecting every necessary data from the different groups involved in the experiment. I can ask help from the Bialystok University of Technology which is one of the partners of the MOBIT project (*Development of Personalized Diagnostic of Malignant Tumors based on tumor heterogeneity and integrated genomic, transcriptomic, metabolomic and imaging PET/MRI analysis. Getting Ready for Individualized Therapy* - a MUB project which is a source of data I am working with). They developed a SmartBioBase where they collected all sort of data (e.g. PET/MRI images, metadata) from all patients. I can do different queries to extract the necessary data in the right format. Also, I can run some additional analyses in the database which is very helpful, for instance clustering and statistical tests.

Why did you choose a widening country as a Host? What was the reason that convinced you? What is making you professionally happy here?

Previously, I was collaborating with MUB and was partly involved in one of their projects. Working on it I realized how important is to be much closer to the raw data source and expertise, especially when you have to deal with human medical data. I saw really good examples for well-designed heterogeneous projects, where different fields of science had to cooperate. Also, the goals were clear, apart from the complexity, but not unrealistic with important milestones. Statistics and modelling are very strong at MUB, therefore it is a great opportunity to extend my basic knowledge in these fields collaborating with them. Now I have the chance to work on proteomic and metabolomic data, not just genomic ones. Furthermore, I can learn different approaches how to integrate particular datasets and generate a model out of it to support physician decisions and predict prognosis for instance.

Would you recommend others to apply? What useful advice/ tips can you give them?

I highly recommend others to apply to COFUND projects or other MSC Actions, but also to visit the Medical University of Bialystok. You can personally meet the experts of different fields of medicine. Even if your project is quite complex the clinicians are very helpful and you can get acquainted with all aspects related to your project e.g. wet lab or data analysis. You can easily ask advice if you are stuck with your project, for example, the Centre for Bioinformatics and Data Analysis (CBI) can help you in downstream analysis of your project e.g. statistics.