February 7, 2024

# Experience performing an online secondment with the University of Turku

## BACKGROUND

In this blog post, I will share my experience participating in a three-month virtual secondment with a Data Science team at the University of Turku (UTU) in Finland. I will discuss the process of planning and executing my online secondment, and the research conducted.

I am a Bioinformatician and former postdoctoral researcher with the Microbial Informatics Team at the Hinxton site of the EMBL European Bioinformatics Institute (EMBL-EBI).

I have a background in Food Chemistry from the National Autonomous University of Mexico. I went on to specialize in microbiology, obtaining an MSc and PhD, with a focus on analyzing microbial communities associated with fermented foods. I used molecular and bioinformatics methods for this purpose. During my first postdoc at the Consortium for the Investigation of the Gulf of Mexico, I gained expertise in metagenomic analysis, which involves working with highly diverse environmental samples. For my second postdoc at the EBI-Sanger Postdoctoral (ESPOD) program, I explored host-associated microbes and their mobile genetic elements, working with high-quality hybrid assemblies of long and short reads.

Currently, I am working on improving my informatics skills, specifically in programming, pipeline development, and software engineering using Nextflow.

As an Early Career Researcher (ECR) in the Horizon2020 FindingPheno project, I have an opportunity to participate in a secondment opportunity provided by the project. These secondments allow ECRs to gain hands-on experience as knowledge is transferred between consortium partners, which is incredibly valuable. Being seconded for three months online with UTU is ideal as it allows me to merge my biological background with the informatics skills I have developed over the years as a MGnify Bioinformatician. Furthermore, it allows me to improve my research knowledge and skills from our computational project experts in Finland.

## VIRTUAL ENGAGEMENT
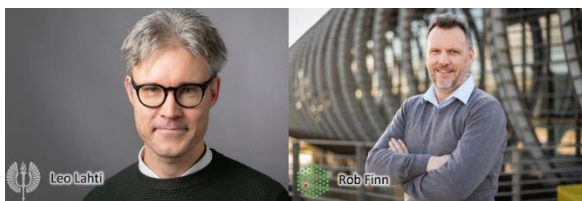


I will be doing a three-month online secondment with Professor Leo Lahti and postdoctoral researcher Matti Ruuskanen where the team focuses on the computational analysis and modeling of complex natural and social systems.

Together with Leo, Matti and my [EMBL-EBI team leader, Rob Finn](), we submitted a secondment request form establishing the "rules of engagement" between me and UTU. We also described the tasks I will engage in and how the UTU partners will supervise me to ensure our remote exchanges are successful. To make sure that everything runs smoothly, we will use online training sessions tailored to my needs, structured online self-reporting and bi-weekly check-in meetings for status updates. During these meetings, we will discuss challenges, assess workload levels, celebrate our wins, and offer ideas on moving forward. Additionally, we will use platforms like Zoom for simpler and less formal conversations, as well as time-sensitive communication.


Matti Ruuskanen

## THE SECONDMENT PROJECT

The **main objective** is to assess the feasibility of deducing functional profiles of microbial communities from low-sequencing yield shotgun metagenomesor "shallow-shotgun" sequencing. Our **methodology** revolves around indirectly gauging the metabolic potential of microbial communities by leveraging the extensive biome-specific genome catalogues available on MGnify. Our **approach** involves mapping raw reads obtained from shallow-shotgun sequencing to these genome catalogues, thereby identifying potentially present species. From there, we hope to derive the functional profile of the microbial community by analyzing the pangenomes referenced in these catalogues. This strategy allows us to infer the metabolic capabilities of the microbial community, providing valuable insights into its ecological functions and potential impacts on its environment.
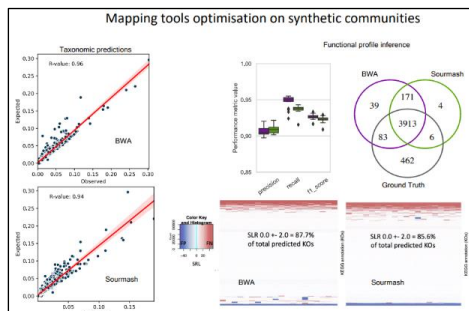


Our project will also optimize informatics tools and the rigorous evaluation of their predictive capabilities. We will conduct a comparative analysis that juxtaposes the shallow-shotgun read-mapping approach with other methods like functional inference from 16S amplicon sequencing, deep-shotgun assembly and functional annotation methodologies. This comparative analysis allows us to assess the strengths and limitations of each approach, providing a comprehensive understanding of their respective use in characterizing microbial communities and their functional profiles.

We will concentrate on **chicken gut metagenomes** as a relevant use case, with **deliverables** geared towards maximizing accessibility, transparency and reproducibility, including:

1. the development of a **publicly available Nextflow tool** tailored for mapping shallow-shotgun reads to MGnify genome catalogues.
2. **publication** of research findings in a scientific journal.
3. **comprehensive GitHub repository** housing all relevant data and scripts generated during the project for transparency and reproducibility.



## MOTIVATION FOR ENGAGING IN THE SECONDMENT PROJECT
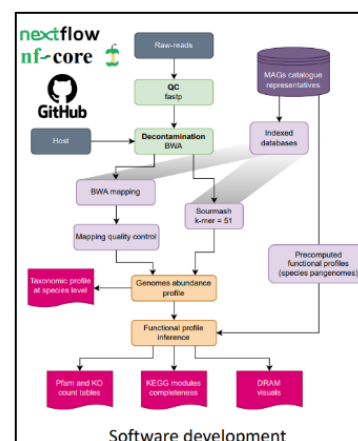
The main goal is to create a reliable bioinformatics solution for analysing low-cost sequencing data using bioinformatics. Currently, the low-cost option for studying the metabolic potential of microbial communities involves amplifying variable regions of the 16S rRNA gene and inferring functions based on taxonomic annotations. This approach suffers from limitations like low taxonomic resolution and the use of non-biome-specific genome reference databases for functional inference. Strains of the same species found in different environments can exhibit vastly different functional profiles, while species inhabiting the same biome tend to share similar functions due to their adaptation to the same environment.

Rob, Leo, Matti and I have produced promising results that showcase the effectiveness of mapping reads to a biome-specific database of microbial genomes for accurate functional predictions in synthetic microbial communities. Next we will validate the method using real shallow-shotgun data.
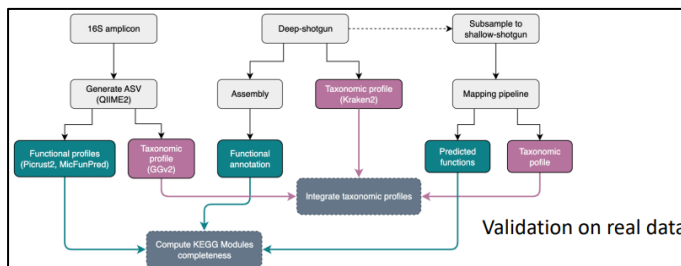


## TAKEAWAYS

I appreciate the opportunity to manage my time and research efficiently, since I have multiple deadlines to meet. This flexible work style aligns seamlessly with my role as a mother of a two-year-old child.

I believe remote work is an effective solution for overcoming barriers in professional development posed by geographical barriers, travel time and expenses. This approach has already gained popularity in various professional contexts, such as attending international conferences, workshops, meetings with collaborators, and training sessions, where professionals can participate without the constraints of physical distance. It is also proving to be an excellent fit for secondments, including my online secondment. By maintaining open lines of communication and regular progress meetings, we are ensuring that I receive valuable feedback from our collaborators, and likewise, I could share valuable knowledge with them.

## Secondment made possible with

### project:



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