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SIX-MONTH SECONDMENT AT Eli Lilly

Over the past few months, I have been doing my secondment at Eli Lilly (July 2021 – January 2022) in David Collier's group. Overall, the aim of this placement is to identify novel targets that underlie degenerative symptoms in Fabry disease. To achieve this goal, we performed single cell RNA sequencing from hippocampal samples followed by bioinformatics analysis using 10X genomics and Seurat package in R software. The first thing I learned in my secondment was how to interact with an HPC (High Performance Computing) system and it took me some time to familiarize myself working on command line. At the same time, I was learning little by little this new language and am fully motivated to increase my knowledge in bioinformatics.

Our workflow for this scRNAseq analysis included Cell ranger pipelines to perform alignment, filtering, barcode and counting. Downstream analysis was completed in R using Seurat library, which was designed for exploration of single-cell transcriptomic data. As we had tree conditions, integration pipeline was run from the beginning. Following quality control, we reduced the dimensionality of the data by UMAP clustering to classify the cells according to conserved markers of each cell population. In addition, we identified dysregulated genes in the clusters of interest that could be potential novel targets.

Although this secondment has been conducted online due to COVID travel restrictions, I have been 100% supported by David's group and available to work remotely. Even we (George ESR1 and I) were invited to attend the Genetics and Informatics annual strategy meeting, where scientific discussions were held within an innovation and therapeutic context. I have to admit that my bioinformatics knowledge is growing exponentially in this secondment and I am excited to continue with further analyses to conclude these results.



This project has received funding from the European Union's Horizon 2020 research and innovation programme under the Marie Skłodowska-Curie Grant Agreement No 764860