

Student Project

Shiny App Development for Visualization of Medical Data

Main area: Bioinformatics

Student's background: Bioinformatics, Computer Science, or other fields with coding or programming experience. Knowledge of R or Python, and basic Linux command line is required.

Type of project: MSc student project

Project description: CHIP/PERSIMUNE houses a large amount of clinical and human genetics data for use in personalized medicine research. We are seeking a student to create a Shiny app that will allow researchers and collaborators to explore our in-house data for the purposes of conducting project feasibility (e.g. variable availability and completeness, sample sizes, power calculations, etc.) and generating hypotheses for new projects. The project will primarily focus on our HIV cohorts and will involve linking SNP microarray genotype data (vcf format) and clinical variables. The app will be tested by internal users prior to sharing with external collaborators. This project will give the student an opportunity to work on real medical data alongside experienced bioinformaticians, data managers, researchers and medical doctors to develop a tool to be used by a large network of international researchers.

Methods used: The student will become familiar with the in-house data sets and hold discussions with future app users to make decisions on data inclusion and the user interface design for the initial and subsequent iterations of the app. Assistance will be provided with data preparation to allow the student to focus on building the app, which can be either R or Python-based. The app should be able to present data in the form of summary tables and plots, and to output reports. Thorough code and user-focused documentation will be an important part of the app development process.

About PERSIMUNE: PERSIMUNE (www.persimune.dk) is a multidisciplinary centre of excellence embedded within CHIP (chip.dk) and funded by the Danish National Research Foundation. PERSIMUNE works from the hypothesis that across patients with impaired immune function, there is a common pattern of un-discovered risk factors explaining the variation in risk of infectious complications. We aim at understanding the mechanisms explaining the variation in risk using a diverse set of methodologies, including pattern recognition from big data from routine clinical care, studies of host and microbial genetics, imaging, and immunological characterization. These data will be used to develop clinical algorithms aimed at improving the clinical outcomes in patients with various immune dysfunction.

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Deadline for application: January 31 2024

Project start time: flexible depending on the student's availability