

Fondo Sociale Europeo Plus 2021/2027

FSE+

Sportello 2025 P.S. 20/24

Sostegno alla realizzazione di dottorati di ricerca

With Decree No. 9526/GRFVG of February 28, 2025, the Friuli Venezia Giulia Region published the Notice regarding the submission of operations for Specific Program No. 20/24, which aims to support higher education through the realization of PhD programs.

Specific Programme 20/24, through the funding of doctoral scholarships, contributes to the achievement of the objectives of the Sustainable Smart Specialisation Strategy (S4). It supports the development or strengthening of integration with the regional production system and/or research organisations, through coordination and collaboration mechanisms with regional enterprises or research bodies, or by leveraging the potential for technology transfer of processes, products, applications, or, more broadly, research outcomes.

- Sportello 2025
- Ciclo 41
- CUP J93C25000640008
- Progetto 2025/6525/27

Dottorato in Applied Data Science and Artificial Intelligence

“Variational inference statistical methods with application to cancer data genomics”

The research project focuses on the theoretical exploration and application of statistical variational inference (VI) methods to the analysis of genomic data in the context of cancer. The VI approach, primarily developed within the framework of Bayesian inference, allows for the inference of complex parameters from high-dimensional probabilistic models while simultaneously reducing computational complexity. However, despite the massive use of VI in various scientific fields, theoretical guarantees of convergence to the posterior distribution and detailed simulation studies on the actual "scalability" of these methods are of urgent and extreme interest for the robustness of the inferential framework. The project involves the application of these advanced techniques for the analysis of tumor genomic data, with the objective of identifying significant biomarkers, analyzing genetic mutations, and understanding the interactions between genes and tumor signals. The use of probabilistic models will be proposed using the software Stan and Pyro, capable of managing large volumes of omic data by combining Bayesian inference methods with machine learning algorithms. The main expected results include the creation of robust statistical models for the identification of genomic patterns in tumors, the improvement of therapeutic response prediction, and the discovery of new targets for personalized treatments. The proposed methods will be validated using public and clinical datasets, such as those from The Cancer Genome Atlas (TCGA). The final impact of the project will be represented by the possibility of using these advanced tools for the personalization of oncological treatments, with implications in the clinical and pharmacological fields.