



**Postdoc position:**  
**Gene Regulatory Network Inference from Spatial and Single-cell Multi-omics data with AI and gene perturbations**

at the [Science for Life Laboratory](#) in Stockholm, Sweden, which is a strong research environment for large-scale life science research, and a joint physical center for a number of computational and life science groups at Stockholm University, KTH, and Karolinska Institutet. The research project will be supervised by Professor Erik Sonnhammer (<http://sonnhammer.org/>).

The goal of the project is to develop and apply gene regulatory network (GRN) inference methods from spatial and single-cell multi-omics data with AI and gene perturbations. By building a deep learning framework with a specialized architecture to efficiently connect data with perturbed genes, inference reliability will be boosted. To enable accurate GRN inference from spatial multi-omics data, a system will be developed for inferring the perturbation design based on gene expression and chromatin accessibility data. This way inferred region-specific GRNs can be connected to particular tissue phenotypes such as different cancer stages. The developed system will be applied to spatial liver cancer data generated by the group. Understanding cancer dysregulation can lead to new therapies needed to curb one of the major causes of death.

The project involves programming, data analysis, benchmarking, and modelling, as well as application of the developed methods to experimental data. The successful candidate should be highly motivated and have a Ph.D. in bioinformatics or related field, and good knowledge of molecular biology. Alternatively, a Ph.D. in molecular biology or related field and 2 years of postdoctoral experience in bioinformatics research and programming, documented by scientific publications. Proficiency with sequence and gene expression data analysis techniques is essential. Excellent skills in computer programming (primarily Python, Matlab, and R) and AI methods and UNIX are necessary merits.

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