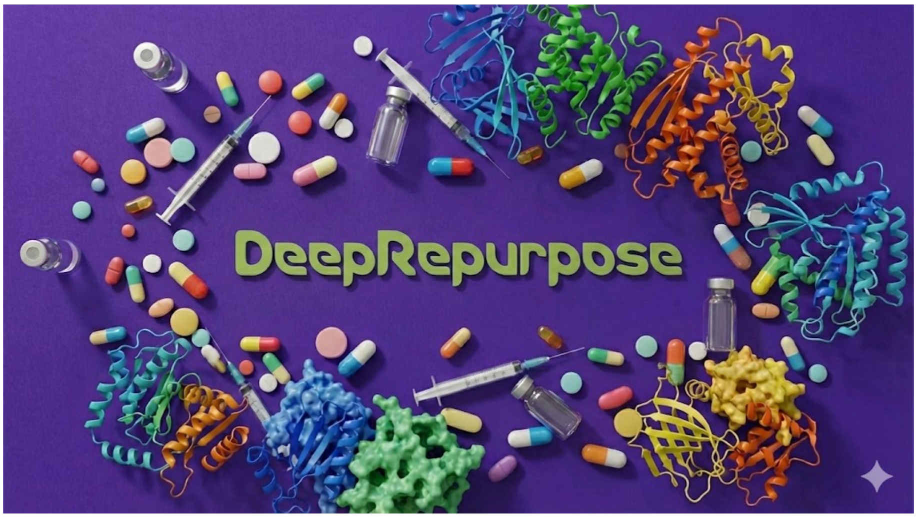

Postdoc in bioinformatics:
Deep learning modeling of spatial biology data for expression profile based drug repurposing

This industry postdoc project is a collaboration between Stockholm University and Merck AB. The project will have a base in the Sonnhammer group at 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 and Dr. Dimitri Guala.

A new exciting opportunity is combining spatial biology with AI-driven modeling of gene expression responses to drug treatment in the field of drug repurposing. Drug repurposing involves identifying new therapeutic uses for existing medications, a strategy that can significantly reduce the time and cost required to bring a drug to market. The project will use AI models such as CycleGANs, that by learning from complex spatial gene expression profiles and cellular heterogeneity within tissues can predict how existing drugs might act on previously uncharacterized disease mechanisms or cellular subtypes. These models will be employed to translate spatial gene expression profiles from healthy tissues to disease states, and vice versa. This capability allows researchers to simulate the effects of drug treatments on spatially resolved gene expression without the need for extensive experimental data. By learning the underlying mappings between these domains, synthetic data will be generated that reflects potential drug responses, thereby enhancing the predictive power of our models.

The project involves programming, modelling, and data analysis. The PostDoc should have a PhD in bioinformatics or related fields. Alternatively, a PhD in molecular biology or related field and 2 years of postdoctoral experience in bioinformatics research and programming, documented by scientific publications. Extensive experience with Python, deep learning techniques, and good UNIX knowledge are essential skills. Knowledge of Matlab, R, bash scripting and familiarity with biological omics data analysis techniques are desirable merits.

To apply, follow the instructions https://www.scilifelab.se/data-driven/ddls-research-school/ddls-research-school-postdoc-call-2026/. For further information about the research project, contact Erik.Sonnhammer@scilifelab.se or Dimitri.Guala@scilifelab.se. See http://sonnhammer.org