MSc position available focused on digital image processing in the Bienko lab for Single-Cell Biology of the Nucleus

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SciLifeLab

Karolinska Institutet

A master student position in Quantitavive Biology is available from January 2015 in the newly established Bienko's Laboratory for Single-Cell Quantitative Biology of the Nucleus at the Department of Medical Biochemistry and Biophysics.

The Bienko's group will work at the leading edge of research on chromosome organization and gene expression regulation, developing and applying state-of-the-art quantitative methods to measure DNA and RNA molecules at high-resolution in hundreds of single cells. The group will build upon powerful methods for in situ quantification of DNA and RNA molecules in cells and tissues, and integrate them with newly developed single-cell genomic assays to measure chromosome positioning, epigenetic states, and gene expression in a high-throughput fashion.

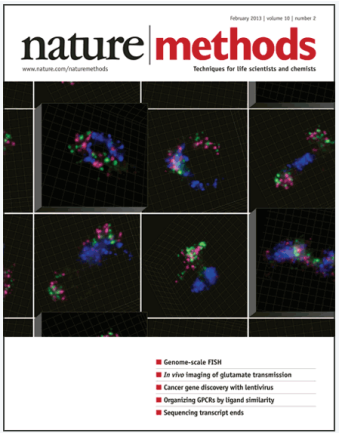
Our lab will be located in the newly established SciLifeLab laboratories in the Karolinska Institute campus, which are equipped with top-notch instruments and are home to the second largest sequencing facility in Europe. SciLifeLab Stockholm is a joint effort between Karolinska Institute, the Swedish Royal Institute of Technology (KTH) and Stockholm University, and hosts a multitude of research groups with diverse background and expertise, including basic biology, drug discovery, genomics, bioengineering, and translational medicine.

Job assignment: The successful candidate will use and develop tools for image processing of data obtained using fluorescence microscopy and Fluorescence in situ Hybridization (FISH) methods, where single molecules of RNA and DNA are visualized simultaneously in the same cells as diffraction-limited dots. The analysis will include correct identification of positive signals, single-cell quantification of the signals, precise measurement of xyz coordinates, measurement of reciprocal distances as well as assessment of nuclear localization of the FISH signals. The goal of the project is to understand the interplay between chromatin architecture and gene expression by using as a model system cells from patients affected by tri-nucleotide repeats expansion syndromes, such fragile-X syndrome, Huntington disease and Myotonic Dystrophy. We will look at how repeat expansions affecting the 3D organization of certain gene loci influence their expression. We will aim at obtaining a comprehensive view on how results of such measurements depend on the specific expansion type as well as the severity of the mutation (the length of the expansion), comparing cells from various patients. This work will be held in collaboration with the lab of Prof. Carolina Wählby and the lab of Prof. Cynthia McMurray at Berkeley, CA.

Qualifications: The candidate should have a strong background in mathematics or physics with a strong interest in biology and desire to improve existing analysis tools and develop her/his own. A completed course in Image Analysis I and Image Analysis II is required. A strong motivation to work in a highly interdisciplinary and collaborative environment is expected.

To express your interest, send a letter of motivation and a CV to mgbienko@gmail.com

To learn about our methods visit:



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