Project openings in the Molecular Cancer Genetics group at IGP, Rudbeck Laboratory

We are looking for students interested in improving treatment and diagnostics for cancer. Our research is focused on four main topics, (1) identification of cancer-causing mutations, (2) investigation of how specific mutations contribute to tumor development or metastasis, (3) strategies to utilize the specific genetic properties of cancer cells for targeted treatment, and (4) development of biomarkers, methods and procedures to improve cancer diagnostics.

Current project proposals:

1. **Genomic analysis of a large cohort of colorectal cancer cases.** NGS technologies are well established for characterization of genetic events involved in tumorigenesis. This project aims to increase the knowledge of colorectal cancer development through detailed characterization of the somatic genomic and transcriptomic landscapes of a large number of primary colorectal tumors from Swedish patients. This study will constitute the largest single whole genome sequencing effort in colorectal cancer to date through collaboration between the U-CAN colorectal cancer investigators at Uppsala University, Umeå University, and KTH. We are looking for students specializing in bioinformatics to participate in the data analyses. Basic knowledge of Linux and programming and scripting in Python or R is required. Previous experience with genomic data analysis or next-generation sequencing knowledge is an advantage.

2. **Biomarker discovery for early detection of cancer.** Biobank-scale proteomic analyses bring tremendous scientific potential, but also unique challenges. If you are resourceful, dexterous, and have a knack for finding creative solutions, you could help us develop improved techniques, practices and procedures for large-scale proteomic data collection efforts. The project comprises participation in the analysis of several thousand plasma samples, as part of the largest cancer-related biobank proteomic data collection effort of our knowledge. The data collected will be used towards developing biomarkers for early detection of cancer, and other translational research aims. Through participation, you will be able to analyze the workflow and set-up of the proteomic analyses, and devise improvements. The project also comprises new or revised implementation proposals of existing technology and developing proposals for new technology toward improved techniques, practices and procedures.

3. **Development of novel personalized cancer therapies.** Targeting frequent loss of heterozygosity (LOH) is an attractive strategy for the treatment of cancer, as tumors with LOH may be sensitized to certain anticancer drugs due to loss of enzyme catalytic activities that exist in normal cells. To identify potential targets under this concept, we mapped variants observed in the 1000 Genomes project and identified an enzyme important for metabolizing and eliminating a large proportion of clinically used drugs as a candidate target for novel cancer drug discovery and development. In this project we will 1) set up cell models with high or lower activity of this enzyme by stable overexpression of wild-type or mutant isoforms, 2) perform drug library screening to primarily select drug candidates which show greater potency on cells with low enzymatic activity, and 3) carry out extended studies of potential hits. Thus, we are looking for ambitious students who want to work with wet-lab techniques, such as immunoblotting, RNA/DNA isolation, PCR/RT-PCR and cell culture.

Further information and application: Professor Tobias Sjöblom (tobias.sjoblom@igp.uu.se). Read more about our research at: https://igp.uu.se/research/experimental-clinical-oncology/tobias_sjoblom/