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Decoding the accessible genome with single molecular long reads sequencing

Location

We are located at the Department of Immunology, Genetics and Pathology

Project

In our group, we are fascinated by why cells in our body contain the exactly same DNA sequence but turn into different fates, e.g, some cells in the human bodies become cancer not the others; stem cells could differentiate into totally different cell types. We are aiming to understand the role of epigenetic in controlling the cell fate in the human disease. The fundamental mechanisms that generate variability from identical DNA sequences in the same cell types remains elusive. The recent advances in functional genomics studies have indicated the epigenetic status, particularly the chromatin structure, as the switch to turn on and off hundreds to thousands genes at different physiological environment. In the last decades, extensively genome wide studies have shed light that most of regulatory elements are located in accessible chromatin loci.

We are looking for a highly motivated master student or project student to join us. In this project we are going to use nanopore sequencing to decode the accessible genome with single molecular long reads sequencing. We will develop new chemical tricks to decode “chromatin accessibility” and how DNA is folded around histones in individual cell types. You would learn how to use nanopore sequencer and computational biology. You would also learn the recent advances of single cell epigenetics.

Group website link:
http://igp.uu.se/research/molecular_tools/xingqi-chen/

Please contact PI for the detail of the project, xingqi.chen@igp.uu.se, if you are interested.