HTS - High-Throughput Sequencing Data Analysis

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Job description: Massive amounts of genomic data are being generated, such as the high-throughput data sets released by the ENCODE consortium (http://www.nature.com/encode/). A major bottleneck is the lack of computational methods to analyse the data sets efficiently and in a biologically meaningful way. We are thus seeking for a student interested in developing new integrative and probabilistic bioinformatics methods. During the summer internship, a student can work on e.g. development/comparison of epigenetic or transcriptome data analysis methods (details will be decided based on student’s preferences). The project requires good knowledge of mathematics, statistics/machine learning, programming skills (e.g. R/Python) and interest in bioinformatics/molecular biology.

Additional information: http://research.ics.aalto.fi/csb/