

Postdoctoral Position Available

Statistical and Computational Methods for the Study of Alternative Splicing using High-Throughput Sequencing

Research Groups of Steven Brenner and Sandrine Dudoit
University of California, Berkeley



Project background and description

The goal of the modENCODE Project (<http://www.modencode.org>) is to identify all functional sequence elements in the model organisms *Caenorhabditis elegans* and *Drosophila melanogaster*. As part of the modENCODE Consortium, we aim to characterize all functional elements associated with the transcriptome in *D. melanogaster*, focusing specifically on sequence elements involved in RNA splicing regulation.

Splicing factors are proteins that bind to specific sequences on a target pre-mRNA and either inhibit or promote spliceosome assembly—usually at a nearby splice site. To discover putative splicing regulatory elements, we identify sequence motifs enriched near splicing events affected upon RNAi depletion of 125 known and putative splicing factors. Changes in splicing upon knock-down of each splicing factor are assayed by high-throughput sequencing of the transcriptome (RNA-Seq) using the Illumina Genome Analyzer system.

High-throughput sequencing (e. g., Illumina's Genome Analyzer, Applied Biosystems' SOLiD, Helicos BioSciences' HeliScope, and Roche's 454 Life Sciences). is rapidly replacing microarrays as the approach of choice for genome-wide expression studies. These novel assays have already been applied to monitor transcription levels (RNA-Seq), DNA-protein interactions (ChIP-Seq), chromatin structure, and DNA methylation. High-throughput sequencing studies raise similar as well as new statistical and computational challenges, in areas such as image analysis, base-calling, read-mapping, and (differential) expression inference.

The appointed researcher will develop and apply statistical and computational methods for the identification alternative splicing events and the inference of isoform-level expression, based on high-throughput sequencing data. These data will be used to discover the mechanisms by which splice factors regulate mRNA splicing.

Position requirements

The candidate should have a Ph.D. (in statistics, biostatistics, computational biology, or a related field) with a strong publication record and strong professional references. The ideal candidate should have demonstrated interests and experience in the analysis of genomic data, ideally recent high-throughput sequencing data from the Illumina Genome Analyzer; strong knowledge of molecular biology; extensive programming experience pertinent to the analysis of large and diverse datasets (UNIX operating system; R, C/C++, Java, Perl/Python languages; MySQL database); work well in a multi-disciplinary team. Excellent communication skills are required for effective interaction with the multidisciplinary cohort of researchers in our laboratory and with collaborators.

The Berkeley academic environment

This joint postdoctoral position between the Brenner and Dudoit groups seeks to leverage the power of high-throughput sequencing to investigate gene regulation by alternative splicing. The postdoctoral researcher will be part of an interdisciplinary team comprising prominent researchers in computational and statistical analysis of alternative splicing and high-throughput genomic data and would benefit from the resources of the UC Berkeley Center for Computational Biology (<http://ccb.berkeley.edu/ccb>). We are associated with the Division of Biostatistics, the Department of Plant and Microbial Biology, the Department of Bioengineering, the Department of Molecular and Cell Biology, the Biophysics Graduate Group, and Lawrence Berkeley National Lab. Our key collaborators on this project are Brent Graveley's group at the University of Connecticut Health Center and the fly transcriptome modENCODE group (<http://www.modencode.org/Celniker.shtml>)

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Interested applicants should have statement of interest, CV, transcript, and at least three letters of reference sent to
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