

Meeting november 5th

BIOINFORMATICS –From Sequences to Systems Biology and Beyond

Title 1: EPipe - a meta-server for differential predictions from sets of amino acid sequences (abstract below)

Speaker: Henrik Nielsen, Associate professor, Center for Biological Sequence Analysis, Technical University of Denmark

When and where: Tuesday 2013-11-05 at 13.00-14.00 at the Pufendorf Institute, Stora Hörsalen, Biskopsgatan 3, Lund

Title 2: Prediction of variant effects. From tolerance to mechanisms

Speakers: Abhishek Niroula and Mauno Vihinen, Department of Experimental Medical Science, Lund University

When and where: Tuesday 2013-11-05 at 14.15-15.15 at the Pufendorf Institute, Stora Hörsalen, Biskopsgatan 3, Lund

EPipe - a meta-server for differential predictions from sets of amino acid sequences

Henrik Nielsen, Associate professor, Center for Biological Sequence Analysis, Technical University of Denmark

Current high-throughput technologies including sequencing methodologies are generating vast amounts of individual genetic variation data, that needs to be analysed, classified, and prioritized. For coding non-synonymous variants, it is desirable to know whether the amino acid changes have consequences for the structure and function of the proteins in which they occur.

Many bioinformatics methods for predicting functional and structural properties of proteins from their amino acid sequences have been developed, and they might carry important information about consequences of amino acid sequence changes. However, submitting a set - or several sets - of sequence variants to all available servers, collecting their outputs, and analyzing them for differences in predicted properties is a tedious task.

To automate this process, we are developing a meta-server and difference seeker named EPipe. EPipe takes as input one or more sets of amino acid sequences, for example versions of the same genes differing by SNPs, indels, or isoforms, or groups of orthologs from different organisms. If requested, EPipe aligns each set, and then EPipe launches the selected predictors, remaps the output to the alignments, and mines the results for differential predictions, which are presented in both graphical and tabular formats.

Importantly, EPipe differs from known SNP effect predictors such as SIFT, SNAP, Polyphen, PhD-SNP etc. by mapping the biological feature space rather than relying on patterns of amino acid conservation. Since EPipe looks at specific features that might be disrupted as a result of a mutation, results can be directly translated into biological hypotheses.

The current version of EPipe contains 230 predictors, of which 197 are regular expressions from the ELM (Eukaryotic Linear Motifs) database. A beta version is online (www.cbs.dtu.dk/services/EPipe/), but work is still ongoing on various aspects of the server, especially the output interface.

We do appreciate a notification, since coffee will be served.

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