

## EINLADUNG

Zeit: Montag, 9. Juni 2008, 14.30 Uhr

Ort: Hörsaal AH II, Ahornstr. 55

Referent: Prof. Frank Dehne  
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Titel: Computational Proteomics

### Abstract:

This talk presents a recent project in Computational Proteomics, the study of protein structure, function and interaction in living cells by computational means (rather than lab experiments). Here we present the first global investigation of protein-protein interactions (PPI) in yeast *Saccharomyces cerevisiae* using re-occurring short polypeptide sequences. We performed the first all-to-all sequence-based computational screen of PPIs in yeast, in which we identify 29,589 high confidence interactions out of approximately  $2 \times 10^7$  possible pairs. Of these, 14,438 PPIs have not been previously reported. We discuss the underlying biology as well as the computational problems which are mainly due to the massive complexity of the underlying computation. Using processor clusters and state-of-the-art algorithms and data structures, we were able to perform an all-to-all sequence-based computational screen in about a week (instead of several decades). This work was done in the context of HPCVL (<http://www.hpcvl.org>), a joint high performance computing consortium between Carleton University, Queen's University and Univ. of Ottawa.