CASL Computational Science Seminar

Title: Quick prediction of draft protein structures by machine learning

Speaker: Dr Gianluca Pollastri (AmMBio group, UCD)

Date: Tue 6th November 2007 at 2:00PM

Location: CASL Seminar Room - Belfield Office Park

Abstract: I will describe the current state of Distill, an automated system for the prediction of protein structures from their amino acid sequences that was developed in my lab. Distill, which relies on machine learning techniques, is fast, and accurate over a broad range of proteins. During my talk I will also briefly describe an ongoing project to predict protein folding pathways based on Distill's responses, and a multi-genomic-scale prediction effort that is scheduled to begin over the next few weeks.

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