



CASL Computational Science Seminar

Title: Going from large databases of human and pathogen protein sequences to experimental testing for short bioactive peptides: computational and statistical issues.

Speaker: Professor Denis Shields, Conway Institute, School of Medicine, and CASL, UCD

Date: Tue 8th May 2007 at 2:00PM

Location: CASL Seminar Room - Belfield Office Park

Abstract: Short regions of proteins (3-12 residues) sometimes have biological activity on their own, independent of the whole protein (30 residues to 10,000 residues long). Our objective is to identify such regions from human proteins, and from the pathogens of humans. We use computational predictions followed by experimental evaluation (see Nature Chemical Biology Feb '07 issue). Computational issues include: how do we identify shared short motifs among unrelated proteins? How do we compare significance of putative motifs from large datasets of functionally grouped proteins? How do we infer interesting motifs from evolutionary patterns? How do we find compounds (including drugs) that resemble these short motifs? How do we design efficient experiments to discover how those peptides interact with different factors in a signalling system?

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