PIMS Mathematical Biology Seminar

Monday, February 11, 2007
3 pm – 281 CAB
Please note the room number

Gustavo Carrero
Athabasca University

Mathematical analysis of FRAP data reveals a differential response of histone H1 variants to the anticancer drug TSA

Histones are abundant nuclear proteins that bind to the chromatin structure (DNA and associated proteins), regulating its organization and DNA accessibility to transcription factors. It is known that hyperacetylation caused by Trichostatin A (TSA) reduces histone H1 binding affinity to the chromatin structure, facilitating the access of transcription factors responsible for apoptosis to DNA.

In this work, we assess the effect of TSA on the binding affinity of the different histone H1 variants by interpreting FRAP (Fluorescence Recovery After Photobleaching) experimental data with a linear reaction-diffusion equation. Data analysis of the estimated kinetic parameters reveals a differential response of histone H1 variants to TSA treatment. The results allow us to group the variants into two distinct groups that may link histone H1 structure with their binding affinities. Possible implications for drug resistance are discussed.

Join us for refreshments in CAB 549 immediately following the seminar

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