

You are cordially invited to a talk in the Edmond J. Safra Center for Bioinformatics Distinguished Speaker Series.

The speaker is Prof. David Liberles, Department of Biology and Center for Computational Genetics and Genomics, Temple University, USA.

Title: "Lineage-specific processes of genome diversification"

Time: Sunday, 30 November 2014, at 10:15 sharp

Place: Britania building, room 222

Host: Prof. Tal Pupko, talp@tauex.tau.ac.il, Cell Research and Immunology Department, Life Sciences Faculty, Tel Aviv University

Abstract: Computational genomics is now generating very large volumes of data that have the potential to be used to address important questions in both basic biology and biomedicine. Addressing important biological questions becomes possible when mechanistic models rooted in biochemistry and evolutionary/population genetic processes are developed. Examples are described on problems involving the inference of duplicate gene retention mechanisms to apply in a gene tree/species tree reconciliation setting and towards understanding the role of gene duplication and deletion in cancer progression. Additionally, two classes of models for characterizing amino acid transitions during protein evolution are presented, one rooted in population genetics and the other rooted in protein physical chemistry. Ultimately, the development of such models adds to our tool box to enable inference of lineage-specific processes in comparative genomics.