

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

The speaker is **Prof. Ting Chen**, Program in Computational Biology and Bioinformatics, University of Southern California, and Department of Computer Science and Technology, Tsinghua University, and Center for Synthetic and Systems Biology, TNLIST, Tsinghua University.

Title: "Metagenomic Data Analysis and Applications in Oral Microbiome"

Time: Wednesday, **November 4** 2015, at **11:15** (refreshments from 11:00)

Place: School of Computer Science, **Schreiber building**, third floor, **room 309**

Host: Prof. Ron Shamir, rshamir@tau.ac.il, School of Computer Science

Abstract: Underlying an environmental sample from, i.e., marine, fresh water, soil and human body, the diversity of the microbial community can be answered by the identities of the operational taxonomic units (OTUs), and their abundance levels. With the advancements of next-generation sequencing technology, it is now possible to directly sequence DNAs obtained from environmental samples. Two major approaches to such studies are *targeted 16S rRNA gene sequencing* that directly profiles the diversity of the microbial communities, and *metagenome shotgun sequencing* that profiles both gene functions and the diversity of the microbial communities. In this talk, we present two methods to analyze these two kinds of sequencing data sets: an unsupervised Bayesian clustering method for Clustering 16S rRNA for OTU Prediction (CROP), and identifying the 16S rRNA gene fragments in the sequencing data and using them to estimate OTUs and their abundance levels. In addition, we will discuss our works in oral microbiome.