

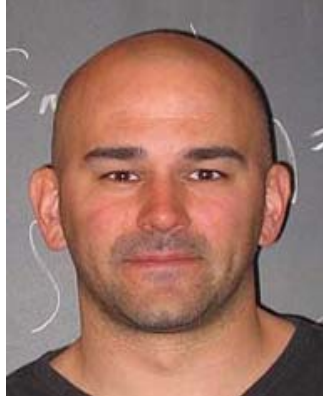
# Institute for Computational Medicine

**Date: Tuesday, March 14**

**Time: 11:00 a.m. EST**

**Location: Clark Hall 110**

Podcast available after seminar at [www.icm.jhu.edu/podcasts/index.html](http://www.icm.jhu.edu/podcasts/index.html)



*Uncovering regulatory signals in the genome using large scale structure*

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## **Abstract:**

Many of the regulatory motifs in the human genome are unknown, in part, because the genomic background is not well understood. The background is determined by selection pressures on a wide range of scales. At the largest scale are isochores, contiguous megabase length regions that have relatively high CG content. On the smallest scale are motifs consisting of a few nucleotides which include single protein binding sites. This talk is divided into two parts; the first of which analyzes the isochore structure and applies the results to predict microRNA targets. The second part is a study of the smallest scale motifs hidden within coding regions. The degeneracy of the genetic code allows for an extremely large number of sequences to code for the same protein. Hidden in the choice of sequence is a set of short functional motifs. An information theoretic algorithm is presented which finds these hidden motifs in the coding regions. Employing a set of evolutionary arguments, evidence is provided for the functionality of these motifs.