



SCHOOL OF

**INFORMATICS, COMPUTING, AND ENGINEERING**



## Precision Health Initiative Colloquium

# Can Alkan

Bilkent University, Ankara, Turkey

Wednesday, April 4<sup>th</sup>

Luddy Hall, 1106

12:00 PM

### **Characterization of Genome Structural Variation and Large Inversions Using High Throughput Sequencing**

**Abstract:**

Structural variation, in the broadest sense, is defined as the genomic changes among individuals that are not single nucleotide variants. Rapid computational methods are needed to comprehensively detect and characterize specific classes of structural variation using next-gen sequencing technology. We have developed a suite of tools using a set of aligners and algorithms focused on the characterization of structural variants that have been more difficult to assay, including complex rearrangements. This talk will be in two parts. First, I will briefly summarize our previous work towards the discovery of structural variation. Then I will introduce our more recent work that integrates different sequencing technologies for the characterization of large inversions and interspersed segmental duplications that are not detectable by traditional read-pair analyses. The algorithms we have developed will provide a much needed step towards a highly reliable and comprehensive structural variation discovery framework, which, in turn will enable genomics researchers to better understand the variations in the genomes of newly sequenced human individuals including patient genomes.

**Bio:**

Can Alkan is currently an Assistant Professor at the Department of Computer Engineering at Bilkent University since January 2012, and a Visiting Professor (on sabbatical) at ETH Zurich since February 2018. He received his Ph.D. in Computer Science from Case Western Reserve University in 2005 after a brief visit to Simon Fraser University. During his Ph.D. he worked on the evolution of centromeric DNA, RNA-RNA interaction prediction and RNA folding problems. He then joined the Department of Genome Sciences of the University of Washington as a postdoctoral fellow. Since then his work includes computational prediction of human genomic structural variation, and characterization of segmental duplications using high throughput sequencing data.



INDIANA UNIVERSITY

**SCHOOL OF INFORMATICS,  
COMPUTING, AND ENGINEERING**