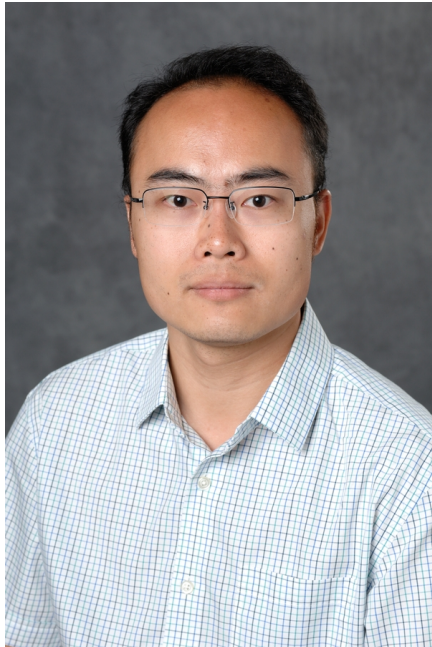




TULANE UNIVERSITY  
SCHOOL of MEDICINE



## Tulane University Center for Biomedical Informatics & Genomics

### TIIDHS Research Seminar

#### Dr. Jianrong Wang

Assistant Professor  
Department of Computational Mathematics  
Michigan State University

#### **Reconstruct the context-specific 3D human genome at high-resolution**

April 17, 2023 | 3:00PM – 4:00PM

Zoom Link

#### **Abstract**

High-resolution reconstruction of spatial chromosome organizations from chromatin contact maps is highly demanded, but is hindered by extensive pairwise constraints, substantial missing data, and limited resolution and cell-type availabilities. We have developed a new computational method, FLAMINGO, that addresses these challenges by compressing inter-dependent Hi-C interactions to delineate the underlying low-rank structures in 3D space, based on the low-rank matrix completion technique. FLAMINGO successfully generates 5kb- and 1kb-resolution spatial conformations for all chromosomes in the human genome across multiple cell-types. Compared to other methods, FLAMINGO consistently demonstrates superior accuracy in recapitulating observed structures with raises in scalability by orders of magnitude. The reconstructed 3D structures efficiently facilitate discoveries of higher-order multi-way interactions, imply biological interpretations of long-range QTLs, reveal geometrical properties of chromatin, and provide high-resolution references to understand structural variabilities. Importantly, FLAMINGO achieves robust predictions against high rates of missing data and significantly boosts 3D structure resolutions. FLAMINGO can be widely applied to large-scale chromatin contact maps and expand high-resolution spatial genome conformations for diverse cell-types.

#### **Biography**

Dr. Jianrong Wang is an Assistant Professor in the Department of Computational Mathematics, Science and Engineering (CMSE) at Michigan State University. He obtained his PhD from Georgia Institute of Technology in 2012, and did his postdoc research at MIT and Stanford University before joining MSU. He is a recipient of the NSF CAREER Award 2020. He works in the field of computational biology and functional genomics. His group focuses on developing machine learning algorithms and integrative statistical models for gene regulatory networks, 3D genome structures, epigenomics, and systems genetics.