

# SCIENCE AT THE EDGE

2016 SEMINAR SERIES

Quantitative Biology Graduate Program | Gene Expression in Development and Disease

## Yu-Ping Wang

TULANE UNIVERSITY

DEPARTMENT OF BIOMEDICAL ENGINEERING,  
BIostatISTICS AND BIOINFORMATICS,  
COMPUTER SCIENCE, AND NEUROSCIENCES

### “Integration of Multiscale Imaging, (Epi)genomics, Networks and Biological Knowledge for Precision Medicine”

I will present our recent efforts on the development of computational and statistical approaches (e.g., sparse regression models) for multi-scale and multi-modal genomic and image data integration and analysis. First, I will give an overview of imaging genomics in the context of precision medicine. Then, I will present a variety of approaches to correlate (epi)genomic and image data for the detection of risk genes and link with biological knowledge database. Finally, I will show how to integrate multiple genomic, imaging and protein-protein interaction networks for biomarker detection, leading to improved diagnosis of mental illnesses (e.g., schizophrenia).

#### References:

1. Jian Fang, Dongdong Lin, Charles Schulz, Zongben Xu, Vince D. Calhoun and Yu-Ping Wang, [Joint Sparse Canonical Correlation Analysis for Detecting Differential Imaging Genetics Modules](#), *Bioinformatics* (2016) doi: 10.1093/bioinformatics/btw485 First published online: July 27, 2016
2. Dongdong Lin, H. Cao, Vince D. Calhoun, and Yu-Ping Wang, Sparse models for correlative and integrative analysis of imaging and genetic data, *J. Neuroscience Methods*, [Volume 237](#), 30 November 2014, Pages 69–78.
3. Shaolong Cao, Huaizhen Qin, Hong-Wen Deng and Yu-Ping Wang, A unified sparse representation for sequence variant identification for complex traits. *Genetic epidemiology*. 2014 Dec;38(8):671-9. doi: 10.1002/gepi.21849. Epub 2014 Sep 4.

**FRIDAY, OCTOBER 7, 2016**

**11:30AM, ROOM 1400 BPS**

*Refreshments at 11:15*