

## Overview of OSGA Cores

### Systems Analytics and Modeling (SAM) Research Support Core

The SAM Research Support Core, led by Dr. Saunak Sen ([www.senresearch.org](http://www.senresearch.org)), has three main goals:

1. To support researchers analyzing complex addictome data-essentially to amplify their efforts by embedding their data in the Omics Portal for Addiction Research (OPAR)
2. To integrate a wide range of software for open-access analytics to enable researchers without advanced computational skills to address complex questions using vetted methods and interfaces
3. To develop new methods to dissect genotype-to-phenotype (G2P) relations in model organisms-rats in particular

### Transcriptome Informatics and Mechanisms (TIM) Research Support Core

The TIM Research Support Core, led by Dr. Laura Saba ([www.thesabalab.com](http://www.thesabalab.com)), has three main goals:

1. Providing databases in a format that is easily utilized for systems genetics research
2. Centralizing the labor- and computationally-intensive tasks of processing RNA-Seq data
3. Sharing our statistical and computational expertise through improved analysis pipelines and effective visualizations of systems genetics analysis results.

## Memphis

### Workshop location:

71 S. Manassas Street  
(TSRB Room 100)  
Memphis, TN 38163

**Map URL with 71 S Manassas**

May is one of the best times to visit Memphis. Temperatures are expected to be pleasant, and the Memphis in May (<https://www.memphisinmay.org/>) festival brings a lot of cultural activities and visitors to the city. Consider visiting:

- National Civil Rights Museum (<https://www.civilrights museum.org/>)
- Graceland (<https://www.graceland.com/>)
- Beale Street (<http://www.bealestreet.com/>)
- Big River Crossing (<https://www.bigrivercrossing.com/>)
- Sun Studios, only a 1 minute walk (<https://www.sunstudio.com/>)
- Bass Pro Pyramid (free)

### Where to stay:

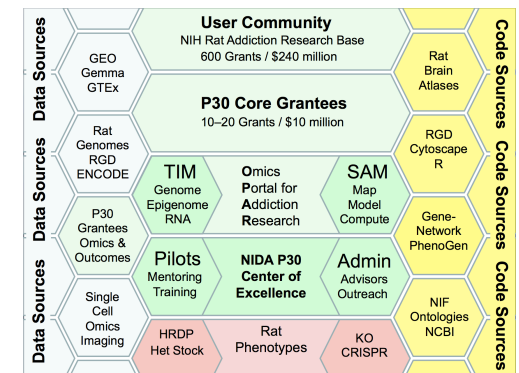
- DoubleTree Hilton (~\$125)
- Best Western Gen X Inn (~\$125)
- La Quinta Inn & Suites (~\$150)

**Local hosts:** Rob Williams (901 604-4752), Saunak Sen ([sen@uthsc.edu](mailto:sen@uthsc.edu)), Tamara Brock ([tbrock5@uthsc.edu](mailto:tbrock5@uthsc.edu))



# NIDA Center of Excellence in Omics, Systems Genetics, and the Addictome

The long-term goal of the NIDA Center of Excellence in Omics, Systems Genetics, and the Addictome (OSGA) is to empower current and future researchers supported by NIDA and NIAAA to analyze the interwoven roles of genetic, epigenetic and environmental variation on drug abuse risk, relapse, and treatment.



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## Workshop Details

**Target Audience:** Researchers working with Hybrid Rat Diversity Panel/Heterogeneous Stock or similar populations that are new to QTL mapping

**Recommended skills:** R experience helpful; basic knowledge about model organisms including a familiarity with HS/HRDP rats

**Expert Instructors:** Dr. Saunak Sen (UTHSC), Dr. Robert Williams (UTHSC; founder of GeneNetwork and GeneNetwork2); Dr. Pjotr Prins (UTHSC); Dr. Laura Saba (UC AMC)

**Cost:** There is no fee for this workshop but participants will need to pay for their own travel and lodging in Memphis.

**Registration:** <http://opar.io/surge2020/registration.html>, limited to the first 20 registered participants

### Relevant Websites:

- GN2 (<http://gn2.genenetwork.org/>)
- R/qtl2 (<https://kbroman.org/qtl2/>)
- Jupyter Notebooks (<https://jupyter.org/>)

**Recent Protocol Paper:** Mulligan et al. 2017 (PMID:27933521)

## OSGA Training - Summer of Rat Genetics/Genomics (SuRGe) 2020

May 19th and 20th, 2020  
University of Tennessee Health Science Center  
Memphis, TN

### Quantitative Trait Loci Mapping in Model Organisms

**Workshop Objectives:** By the end of the workshop participants will be 1) understand the genetic concepts behind QTL mapping, 2) be able to map a phenotype using GeneNetwork2, 3) be able map a phenotype from a complex population using software such as R/qtl2, and 4) practice reproducible research using a Jupyter Lab Notebook



## Tentative Schedule

The workshop will consist of short lecture-style introductions with hands on demonstrations where participants are given a problem(s) to work through based on the lecture portion. Solutions to the problem will then be reviewed with all participants. The Hybrid Rat Diversity Panel and Heterogeneous Stock rats will be used for all demonstrations.

### Tuesday, May 19th, 2020

- 9 am Introduction to QTL analysis
- 10 am GeneNetwork2 demonstration and hands on application
- 12 pm Lunch provided by workshop
- 1 pm Introduction to Jupyter notebooks
- 2 pm Mapping traits - Data wrangling
- 3 pm Mapping traits - R/qtl2
- 5 pm Group dinner provided by workshop

### Wednesday, May 20th, 2020

- 9 am Interpreting and reporting results
- 10 am From QTL to candidate genes/networks
- 12 pm Lunch provided by workshop
- 1 pm Group time to prepare for participant presentations based on results achieved during workshop
- 2 pm Participant presentations
- 3 pm Close of workshop