

NIDA Core Center of Excellence in Omics, Systems Genetics, and the Addictome (OSGA)

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Barriers To NIDA Researchers

Generating, normalizing, and combining massive genome, transcriptome, behavior, and health record datasets

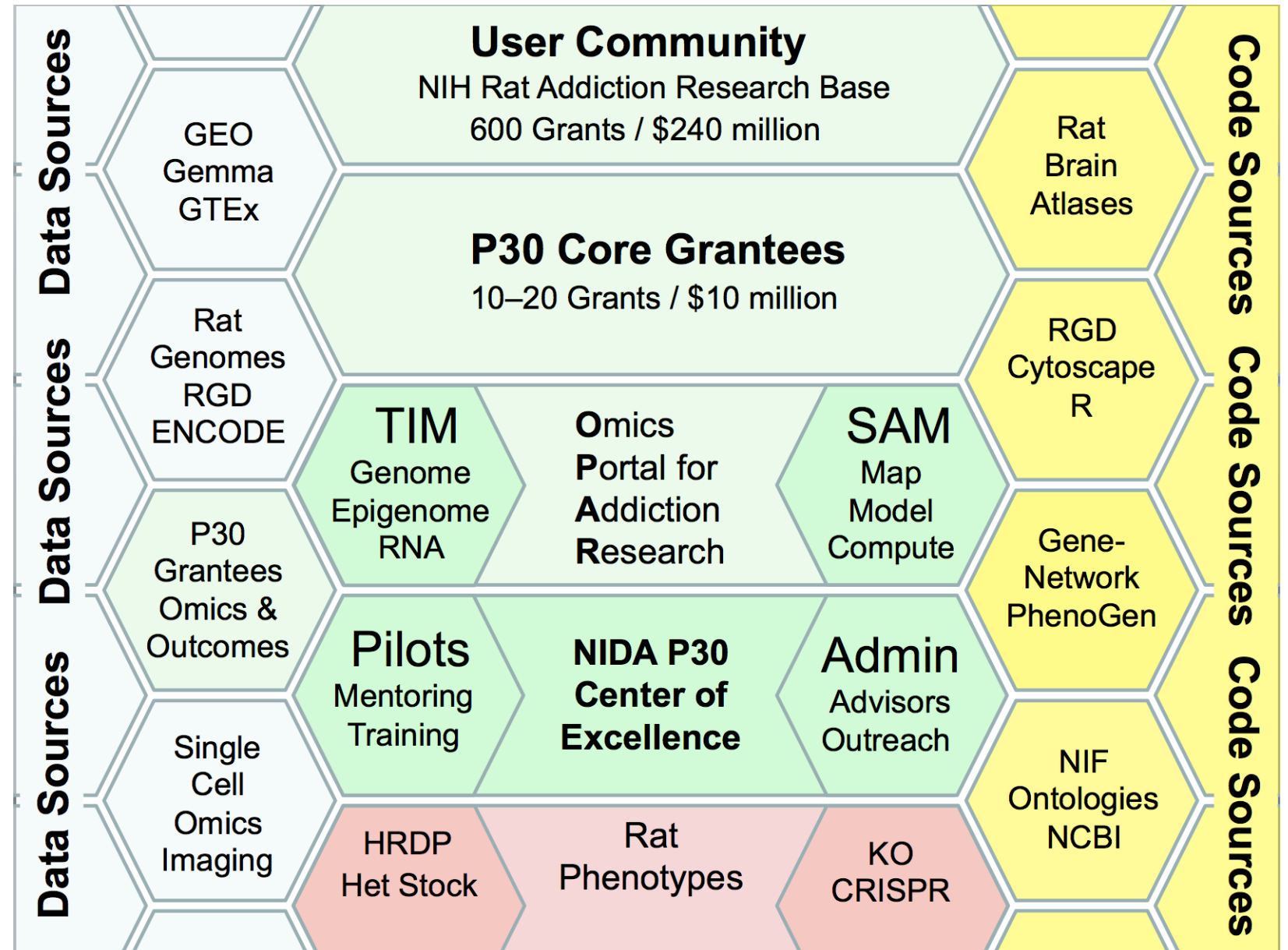
- Gaining access to high-end computational resources and appropriate analytic frameworks is usually beyond R01 teams.
- Finding bioinformatics/biostatistics collaborators with the domain expertise to handle high-dimensional datasets (epigenomes, proteomes, images, metagenomes, single-cell assays) related to addiction is also challenging.

Purpose of the Center

The long-term goal of this *NIDA Core Center of Excellence in Omics, Systems Genetics, and the Addictome* 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.

Our Approach

- Omics Portal for Addiction Research (OPAR)
- Methods, software, and dataset development for omics analyses
- Training in Systems Genetics, RNA-Seq, and Web-based Rat Genomics/Genetics Resources
- Funding for pilot grants



Omics Portal for Addiction Research

Omics Portal for Addiction Research

- Access to curated data
- Access to tools
- Access to gene level reports
- More intuitive search/question capabilities

OPAR

where is Gnb1 expressed

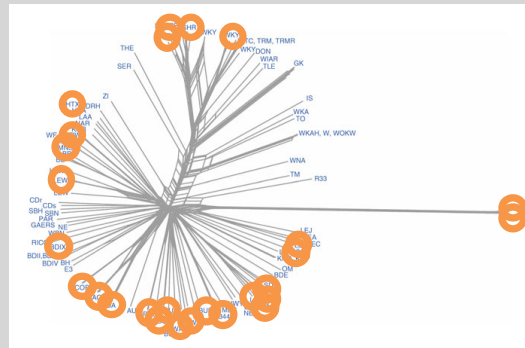
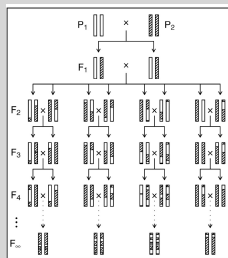
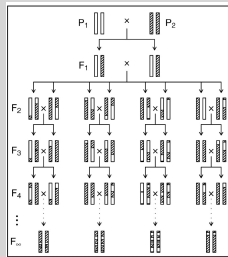
Google Search

I'm Feeling Lucky

The Rat Addictome

Hybrid Rat Diversity Panel

NIAAA/NIH (R24AA013162)

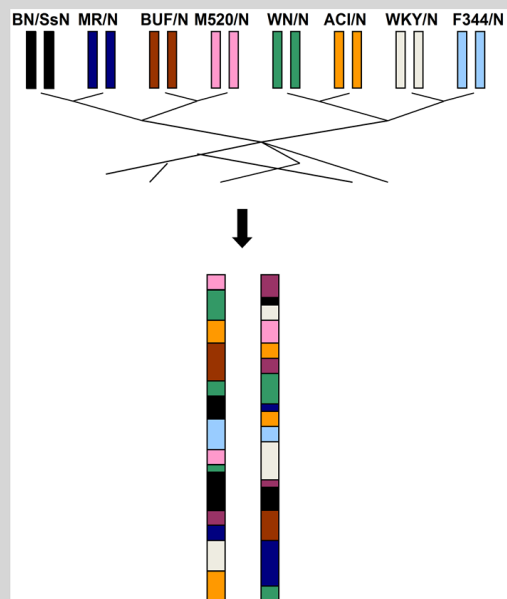


- **Past:** Rat addiction related data sets (GEO and GEMMA)
- **Present:** Two foundational rat populations
- **Future:** Data direction from NIDA/NIAAA researchers

NIH

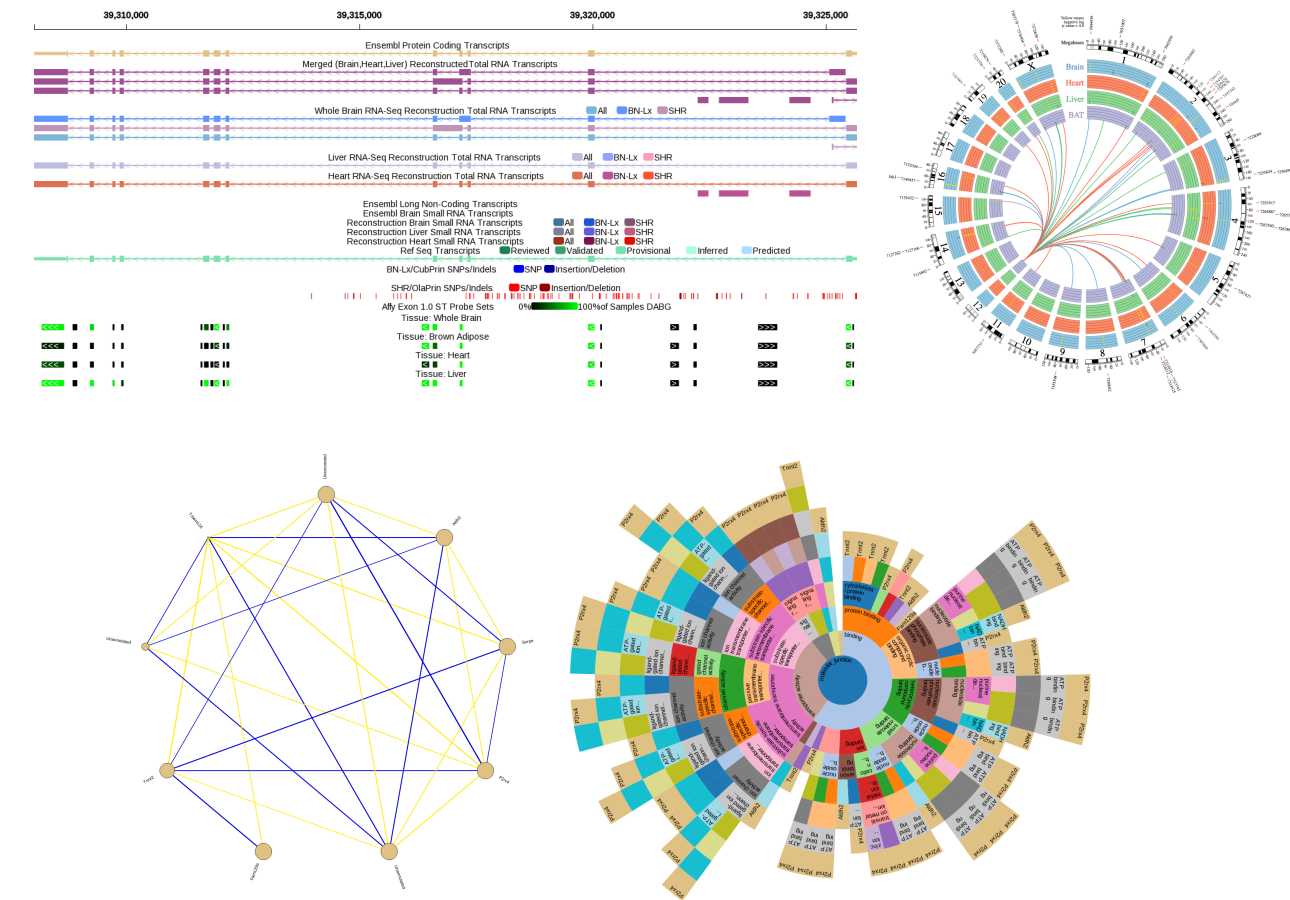
Heterogeneous
Stock

NIDA/NIH (P50DA037844)



PhenoGen Informatics

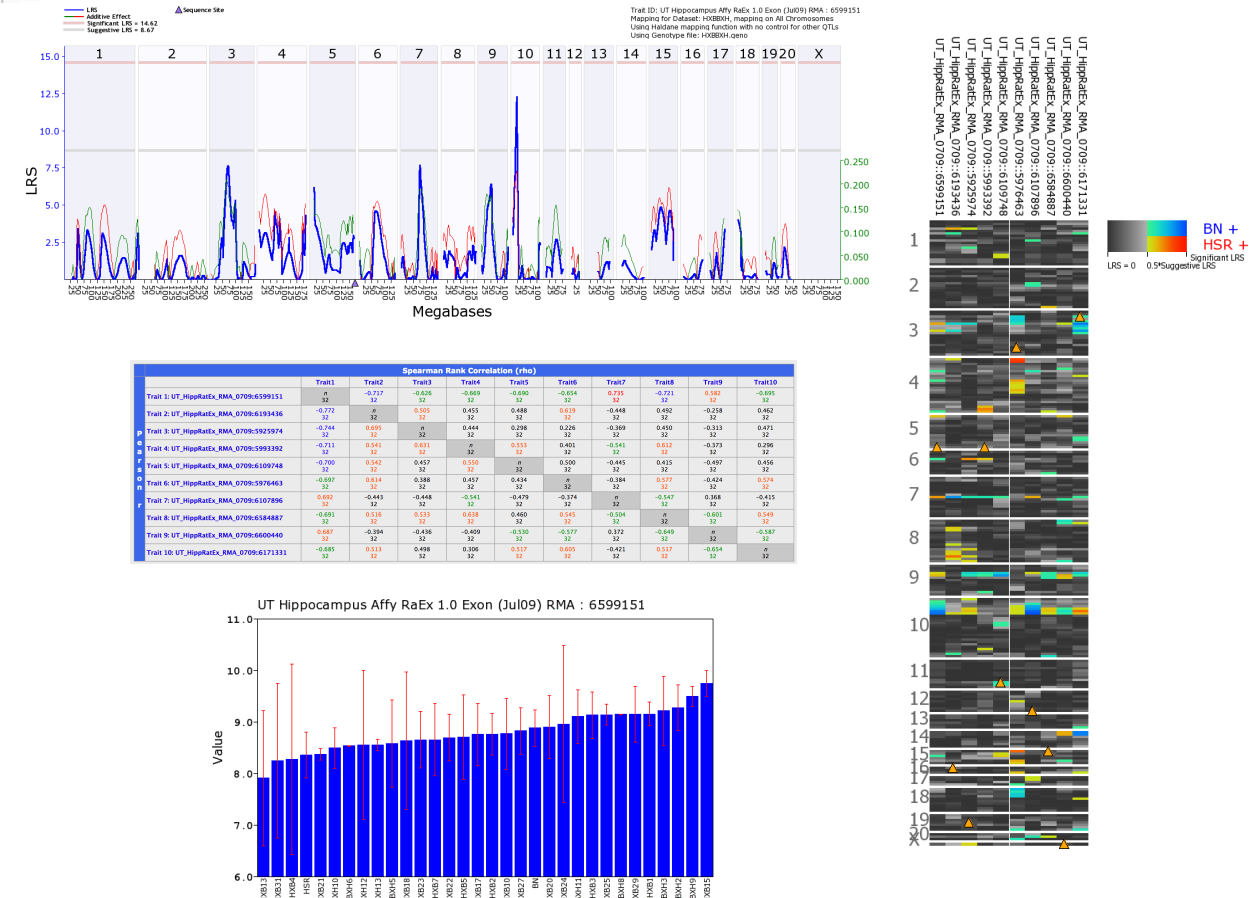
The site for quantitative genetics of the transcriptome.



GeneNetwork

University of Tennessee: www.genenetwork.org

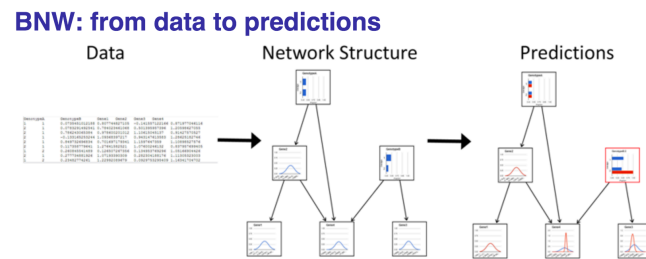
Use GeneNetwork 2



GeneWeaver.org

A system for the integration of functional genomics experiments

Home Search Manage GeneSets Analyze Ge



A Smarter Search

**Where is the brain is
P2rx4 expressed?**

**What rat genes are
expressed in
hippocampus within
10 Mb of my QTL?**

**What other genes and
traits are associated
with P2rx4?**

**Is P2rx4
genetically
controlled?**

**Are there multiple is-
forms of P2rx4 in the
nucleus accumbens?**

**What genes expressed
in the VTA have a
binding site for mir-23?**

Methods, Software, and Database Development

Systems Analytics and Modeling (SAM) Research Support Core

(Core Lead - Dr. Saunak Sen at UTHSC)

- Smart search capabilities to connect investigators queries with relevant information across rat genetics websites and databases
- Fast linear mixed model computations for QTL analyses with population structure
- Matrix linear models for mapping multivariate traits
- Methods/workflow for single cell RNA-Seq data

Transcriptome Informatics and Mechanisms (TIM) Research Support Core

(Core Lead - Dr. Laura Saba at CU-AMC)

- Processing of brain and liver RNA-Seq data from the Hybrid Rat Diversity Panel (Tabakoff, Hoffman, Saba; NIAAA/NIH R24AA013162)
- Processing of RNA-Seq data from 5 brain regions of the heterogeneous stock (HS) rats (Palmer; NIDA/NIH P50DA037844)
- Identification and evaluation of novel brain and liver rat transcripts (mRNA, ncRNA, snoRNA, miRNA)
- Development of methods for systems genetics and for exploring the genetic control of transcription levels and characteristics

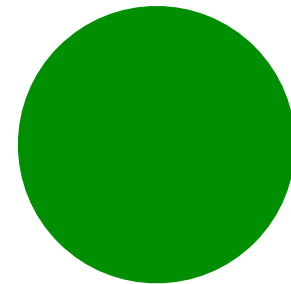
Current Training Opportunities

Training in Web-based Rat Genomics/Genetics Resources

Integrated training on:

- OPAR
- PhenoGen
- Rat Genome Database
- GeneNetwork/
GeneNetwork2
- GeneWeaver
- Chilibot
- Allen Brain Atlas

Beginner



**Low
Intensity**

**NO EXPERIENCE
NECESSARY**

**First timers
welcome**

Summer of Rat Genomics (SuRGe) Workshop

- Friday and Saturday (August 2nd and 3rd; 8am to 5pm)
- Skaggs School of Pharmacy and Pharmaceutical Sciences on the University of Colorado Anschutz Medical Campus in Aurora, CO
- First 20 out-of-state participants will receive travel funds to cover lodging costs
- All participants will be FED!
- Participants are asked to come with a gene or set of genes and a region of the genome relevant to them to investigate using the various tool

SuRGe Workshop Format

Three sections:

1. Identifying a genomic region of interest
2. Interrogating a genomic region
3. Examining your favorite gene(s)

Within each section and each web tool:

- 15 minutes of instruction
- 45 minutes of hands-on activities with multiple “coaches” available for individual consultation

Who should come?

- All levels welcome!
- Registration at: http://bit.ly/OSGA_2019
- GitHub Repository: https://github.com/OSGA-OPAR/SuRGe_2019
- Email Laura.Saba@cuanschultz.edu with questions

Future Training Opportunities

RNA-Seq Processing and Analysis

(researchers generating transcriptome data for the first time)

- On-site training upon request
- Short course in Colorado and/or Tennessee

Intermediate



**Moderate
Intensity**

**EXPERIENCE
RECOMMENDED**

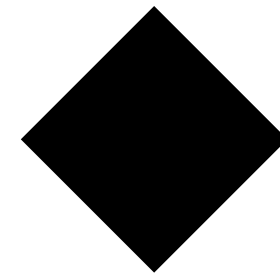
**Some physical
ability required**

Systems Genetics

(researchers with multiple types of omics data for integration)

- On-site training upon request
- Short course in Colorado and/or Tennessee

Advanced



**High
Intensity**

**EXPERIENCE
RECOMMENDED**

**Need agility, good
balance, & strength**

Pilot Funding Program

Purpose/Structure

Our pilot program was designed to entice investigators to explore the role of genetics in addiction using rat models by reducing eliminating some of the barriers and to promote the development of collaborative, inter-disciplinary teams.

Provide funding/support for:

- Researchers to help establish collaborations (across at least two institutions and/or disciplines)
- \$20,000 per year for up to 2 years
- e.g., studies that provide proof that genetic variation contributes substantially to a complex addiction-related trait and/or that a new omics technology can capture a critical missing piece of the mechanistic model of disease

What comes with it?

1. **Financial resources.** One of the charges of the pilot research project core is to provide financial support to generate this preliminary evidence.
2. **Networking opportunities.** Once a researcher is awarded pilot funding they will be required to attend our Annual Center Meeting.
3. **Mentoring and guidance.** The goal of the research pilot core is to nurture the best and the brightest addiction researchers interested in systems genetics by providing them with both the financial means and the guidance to be successful in the field.
4. **Statistical genetics expertise and computational resources.** Participation in the Center through the Pilot program provides access to statistical genetics expertise and computational resources through the OPAR and the SAM and TIM cores.

Application Process

- Rolling Deadline until 9/1/19:
applications are reviewed within 2
months of receipt
- Details available at the OPAR website
(<http://opar.io>)

Feedback

Methods for providing feedback

- Email us at rwilliams@uthsc.edu or Laura.Saba@cuanschutz.edu
- Contact us via twitter @OPARProject