Introducing the *NIDA Core Center of Excellence in Omics, Systems Genetics, and the Addictome*

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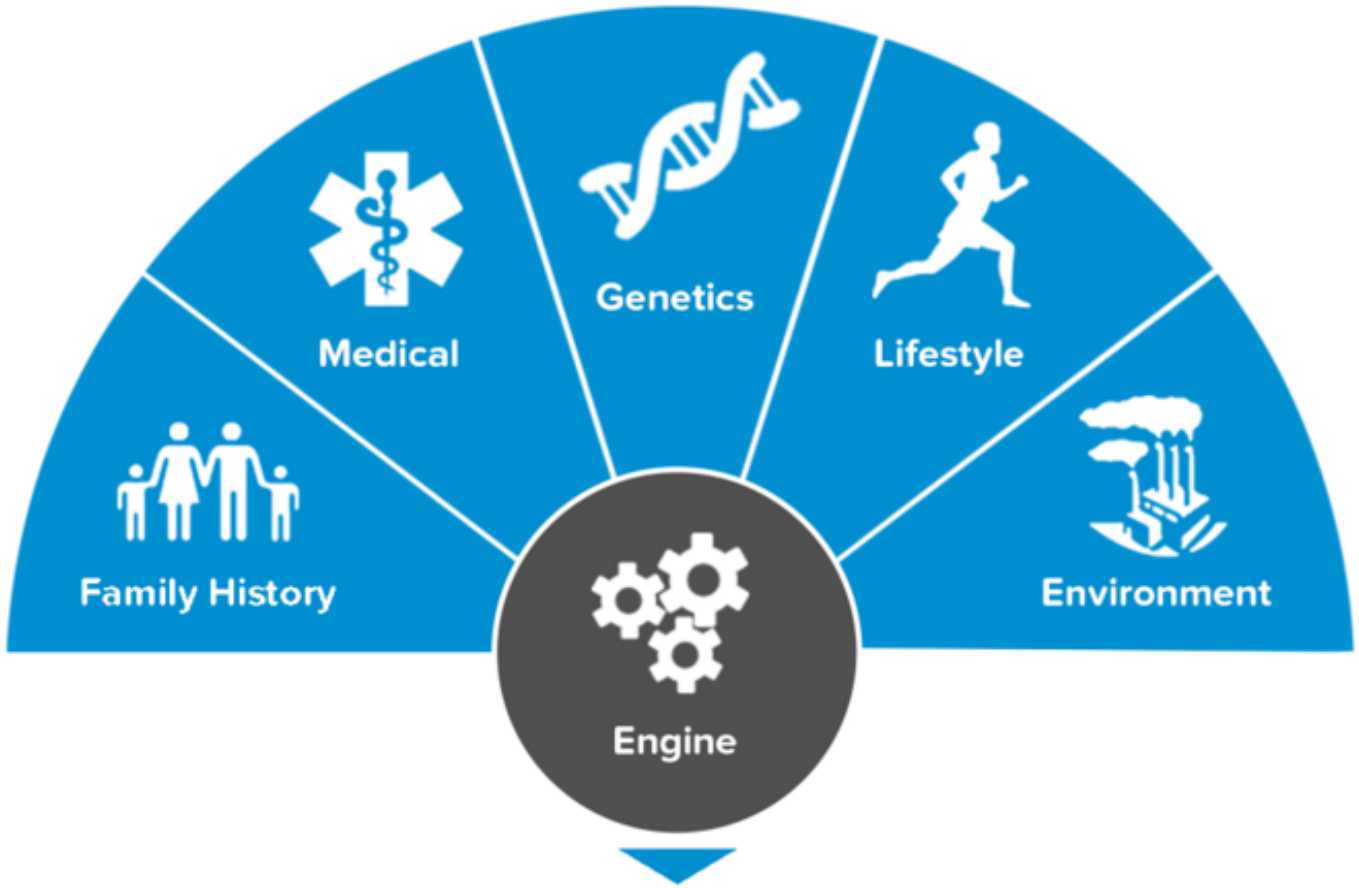
Funded by NIDA P30DA044223



The Power of Precision Medicine

http://hitconsultant.net/2016/09/20/dignity-health-chi-launch-precision-medicine-alliance-5-things-know/

Starting with the Rat

- 16.5% of all current, funded NIDA grants include ‘rat’ in the project description
- ‘Rat’ NIDA grants currently receive a total of current fiscal year costs of $215 million
- Only 8% of NIDA Rat grants, also include ‘genetics’ in the project description

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.

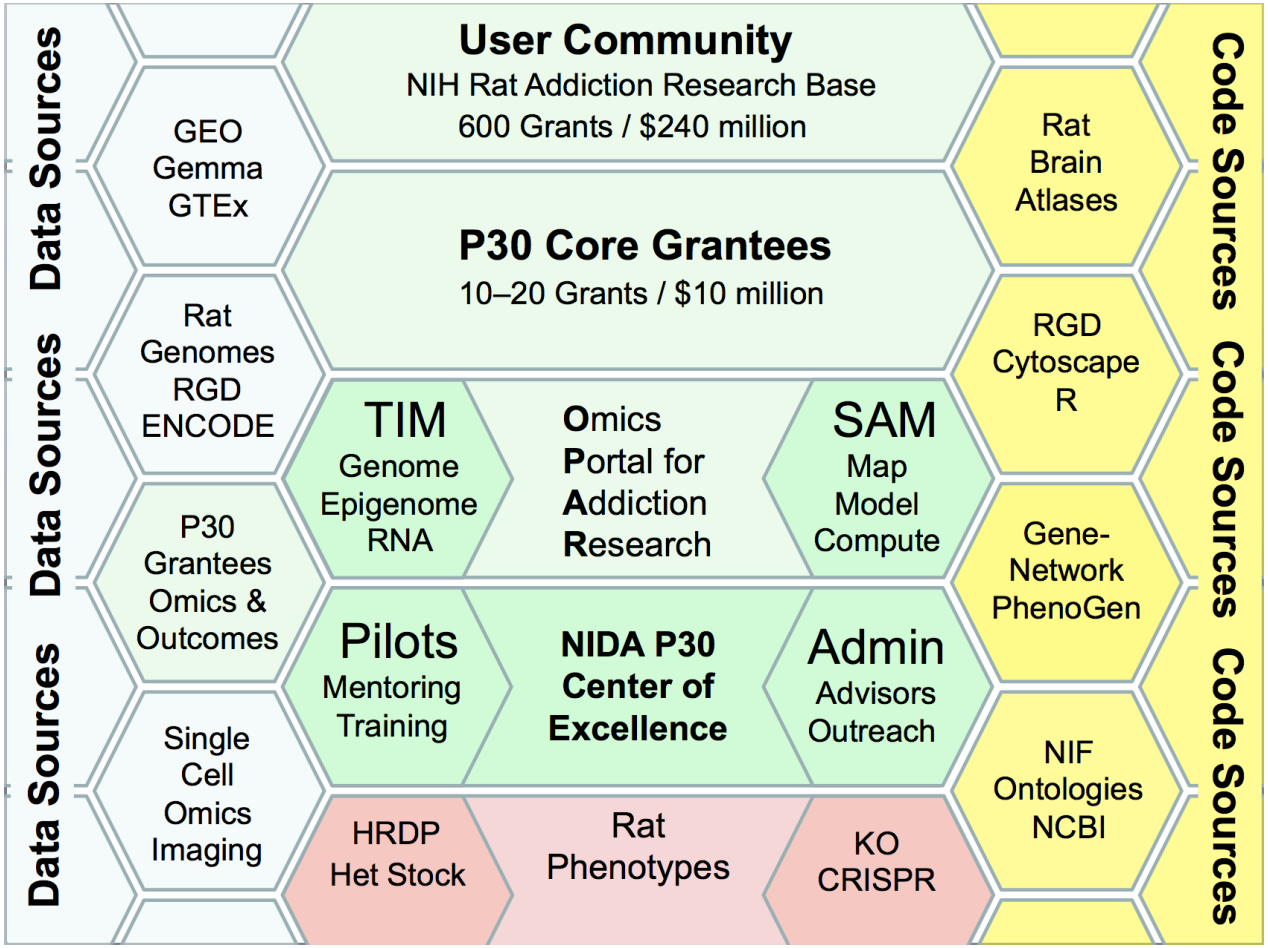
- Finding *bioinformatics/biostatistics collaborators* with the domain expertise to handle high-dimensional datasets (epigenomes, proteomes, images, metagenomes, single-cell assays) related to addiction is also challenging.

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

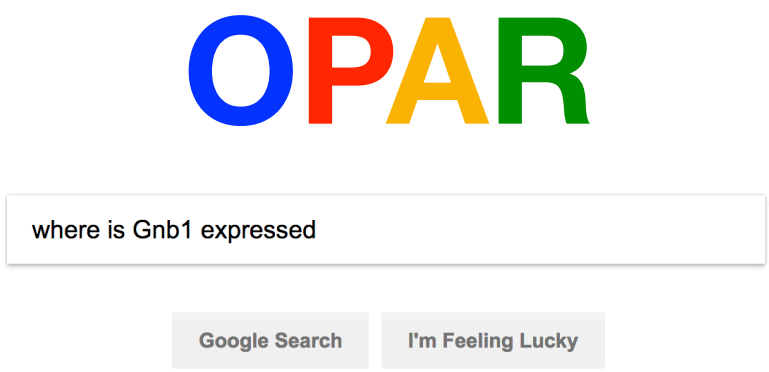
- Omics Portal for Addiction Research (OPAR)
- Study design and RNA-Seq analysis services
- Training in Systems Genetics, RNA-Seq, and OPAR usage
- Funding for pilot grants



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



A Smarter Search

Where in 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?

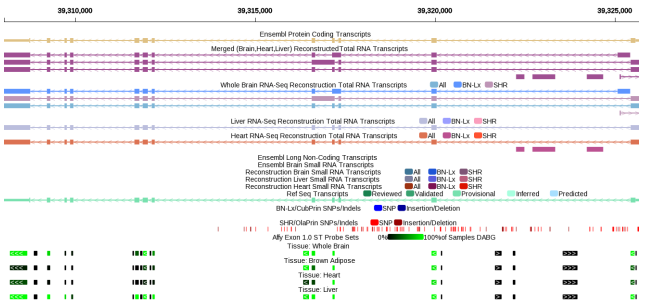
Are there multiple is-forms of P2rx4 in the nucleus accumbens?

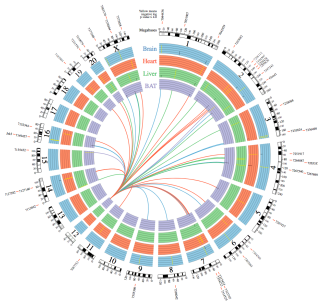
What genes expressed in the VTA have a binding site for mir-23?

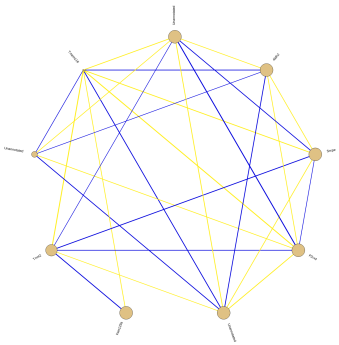
Bringing Together The Best Tools

PhenoGen Informatics

The site for quantitative genetics of the transcriptome.



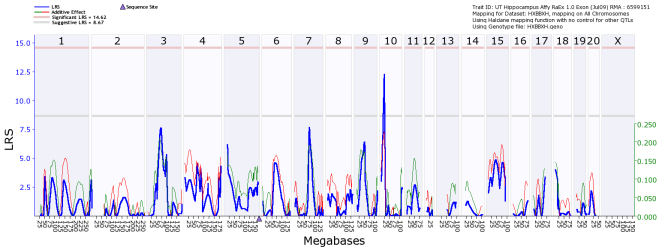


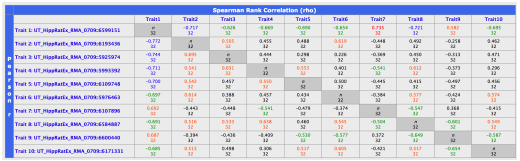


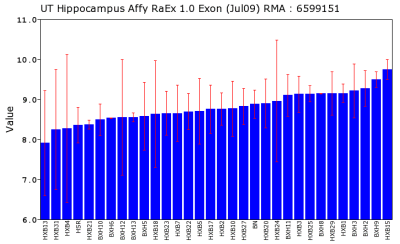
GeneNetwork

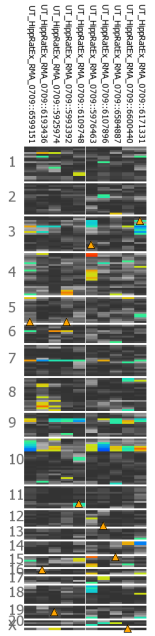
University of Tennessee: www.genenetwork.org

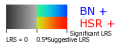
Use GeneNetwork 2









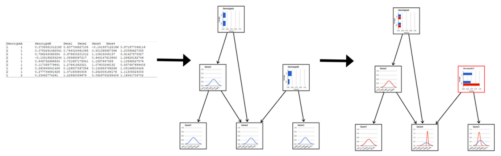


GeneWeaver.org

A system for the integration of functional genomics experiment

Home Search ▼ Manage GeneSets ▼ Analyze Ge

BNW: from data to predictions



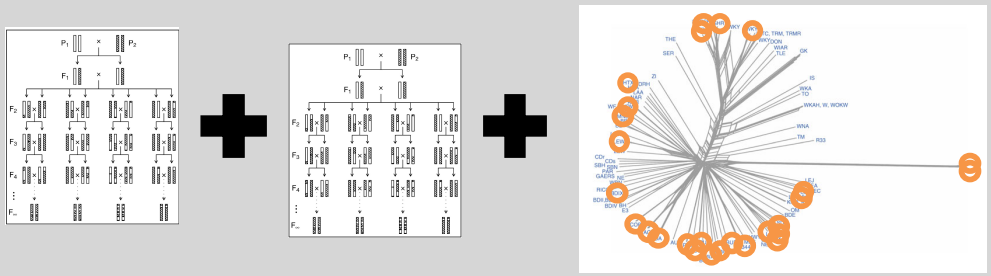
RGD

Gemma

The Rat Addictome

Hybrid Rat Diversity Panel

NIAAA/NIH (R24AA013162)



NIH Heterogeneous Stock

NIDA/NIH (P50DA037844)

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

Proposed Center Services

Study Design Consultation

- Speak with individual researchers about types of genetic populations
- Advise on how to design their study to capitalize on available public data
- Work to connect researchers

RNA-Seq Data Processing

- Quantitation and initial analysis of smaller studies upon request
- Provide access and documentation to standard pipelines
- Collaborate for bigger projects including those that will eventually become crucial data in OPAR

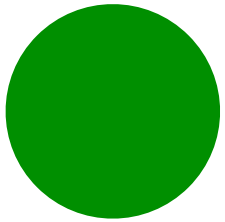
Proposed Training Opportunities

OPAR Usage

(meant for new users)

- Workshops at meetings
- Webinars
- On-site training by request

Beginner



Low Intensity

NO EXPERIENCE NECESSARY

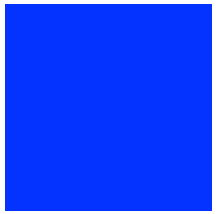
First timers welcome

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

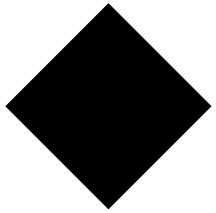
Some physical ability required

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 early career investigators to explore the role of genetics in addiction by reducing eliminating some of the barriers and to promote the development of collaborative, inter-disciplinary teams.

Provide funding/support for:

- Early career researchers (post doc and assistant professors) to help establish collaborations (across at least two institutions)
- $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

Important Dates

- Official call for applications: March 1, 2018
- Applications due: May 1, 2018
- Funds distributed: July 1, 2018

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.

Feedback

Methods for providing feedback

- Stop either Rob or me today.
- Email us at rwilliams@uthsc.edu or laura.saba@ucdenver.edu
- Contact us via twitter @OPARProject

Acknowledgements

- **Center Leadership**
  - Rob Williams (Co-Director)
  - Saunak Sen (Core Lead - Systems Analysis and Modeling Core)
- **Center Team**
  - *University of Colorado Anschutz Medical Campus*
    - Spencer Mahaffey, Harry Smith, Lauren Vanderlinden
  - *University of Tennessee Health Science Center*
    - Arthur Centeno, Hao Chen, Pjotr Prins, Zachary Sloan, Lei Yan, Siamak Yousefi
- **Collaborators**
  - Boris Tabakoff and Paula Hoffman - HRDP/PhenoGen, UCD-AMC
  - Abraham Palmer - HS Rats, UCSD
  - Elissa Chesler - GeneWeaver, Jackson Laboratories
  - Paul Pavlidis - Gemma, UBC
  - Yan Cui and Jesse Ziebarth - BNW, UTHSC
- **Funding**
  - NIDA - P30DA044223
- **Computational Resources**
  - UNLV National Super Computing Institute (Joseph Lombardo)
  - ACF Super Computing Facility