



Statistics in Systems Genetics

Mission:

Develop and make available data, statistical methodology and analytical tools for applying quantitative genetics and topological analysis of transcript expression to identify systems that produce disease and illuminate the path to repair of damaged systems, with a clear understanding of individual needs.

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Presentation at <http://github.com/LauraSaba>

My CV



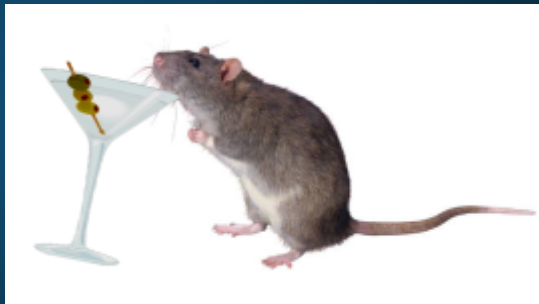
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Rocky Ford, CO



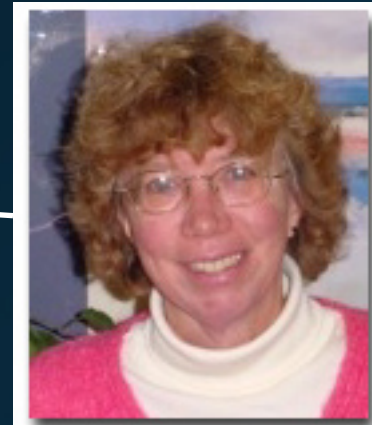
Oredigger
Chemistry Degree
from CSM



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PhD in Biostatistics



9 years studying
genetics for alcohol-
related traits



Diane Fairclough
“Latent Pattern
Mixture Models”

Collaborative Science



Dr. Boris Tabakoff
Professor
Dept Pharmaceutical
Sciences
School of Pharmacy
Pharmacologist



Dr. Paula Hoffman
Professor
Dept Pharmacology
School of Medicine
Neurophysiologist



Dr. Katerina Kechris
Associate Professor
Dept Biostatistics
School of Public
Health
Biostatistician



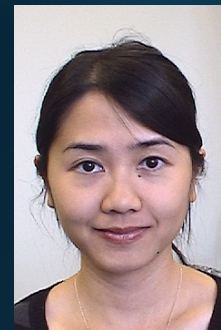
Mr. Spencer Mahaffey, ME
Computer Programmer



Ms. Lauren Vanderlinden, MS
Biostatistician



Dr. Stephen Flink
Mathematician



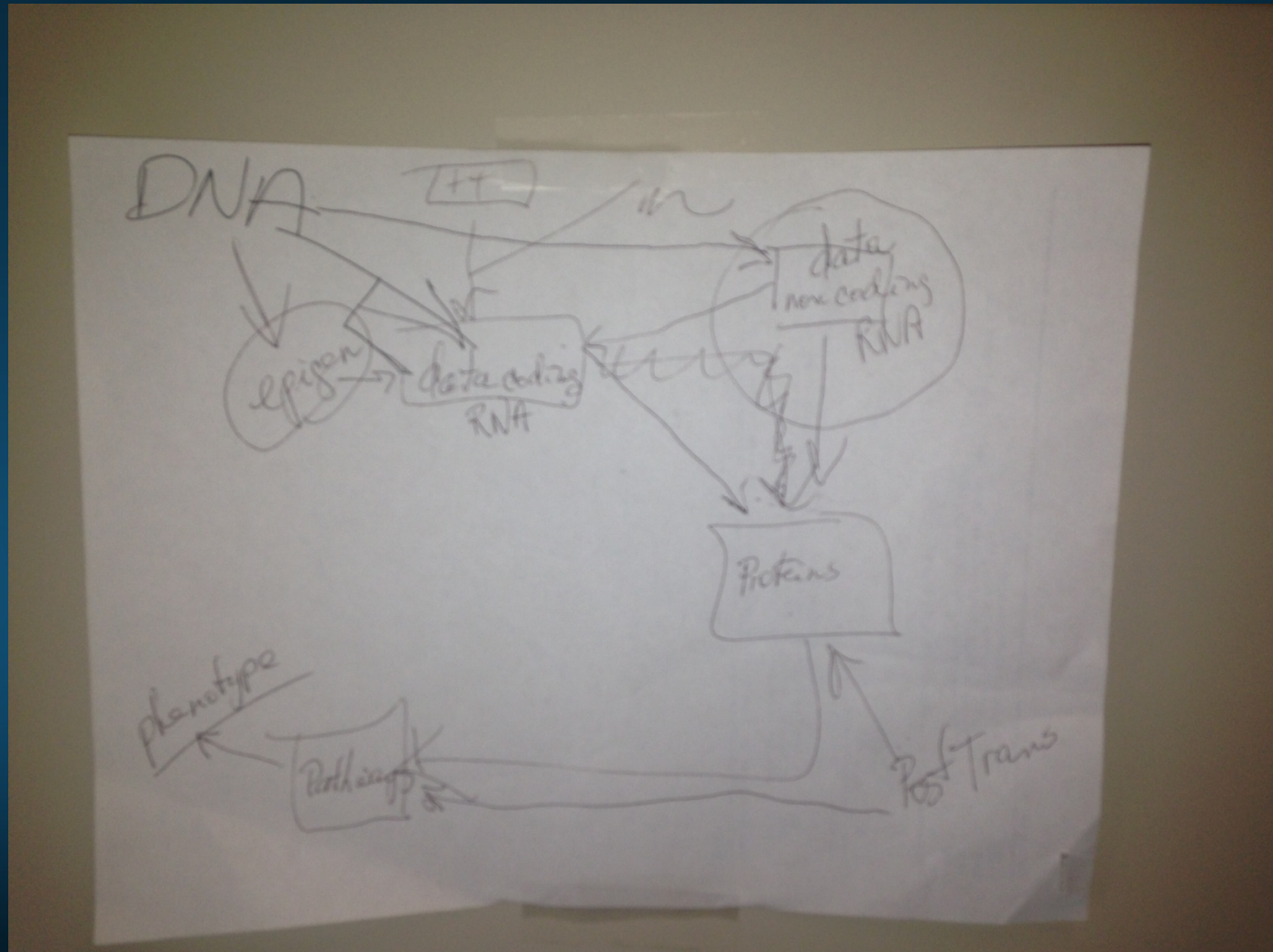
Ms. Yinni Yu, MS
Lab Manager



Systems Genetics

"The reductionist approach has successfully identified most of the components and many of the interactions but, unfortunately, offers no convincing concepts or methods to understand how system properties emerge...the pluralism of causes and effects in biological networks is better addressed by observing, through quantitative measures, multiple components simultaneously and by rigorous data integration with mathematical models" (Sauer et al., Science 2007).

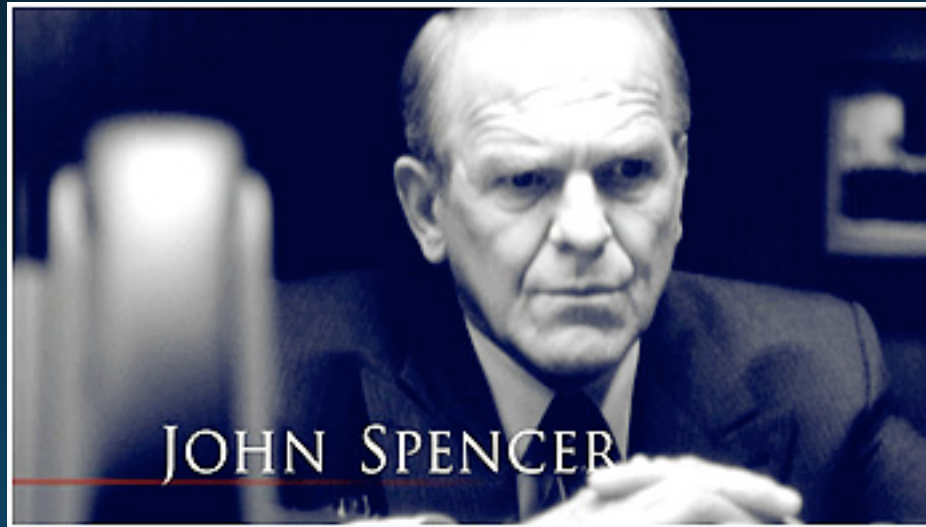
System Genetics



A vertical banner image. The left side features a blue DNA double helix structure. The right side shows a white document with faint, illegible handwriting.



Alcoholism



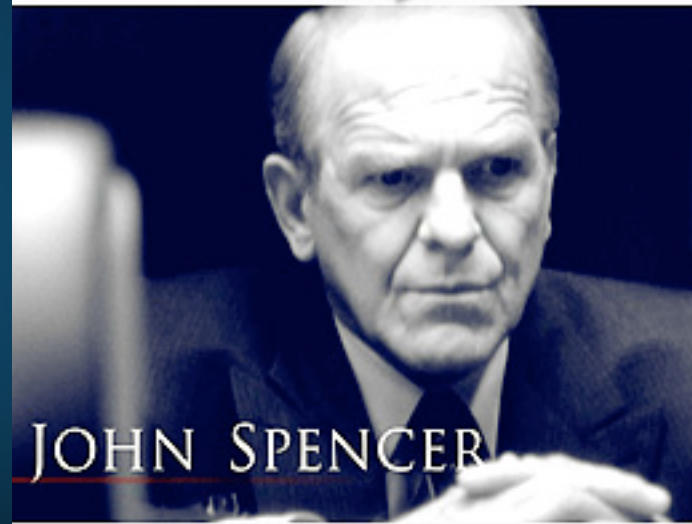
“That's because you think it has something to do with smart and stupid. Do you have any idea how many alcoholics are in Mensa? You think it's a lack of willpower? That's like thinking somebody with anorexia nervosa has an overdeveloped sense of vanity...” – John Spencer as Leo McGarry *The West Wing*

Why Did He Become An Alcoholic?

Genetics.
Leo's Dad was an
alcoholic

Past Trauma.
Vietnam War
Vet

Daily Stress.
Chief of Staff
to US
President



Neurological
Changes.
Previous
excessive
drinking leads
to biological
changes

Animal Models

Can control
their
environment

Examine biological
traits prior to and
immediately after
initial exposures

Can control
alcohol
intake

Can
control
their
genetics



Can measure
biological
traits in any
organ at any
time point

How do you measure alcoholism in animals?



Types of Data

- Phenotypes
 - free choice consumption
 - deprivation induced drinking
 - alcohol tolerance
 - alcohol sensitivity
- DNA Sequence
 - SNP arrays
 - DNA-Seq
- RNA Expression Levels and Structure
 - array or RNA-Seq
 - different tissues, tissue parts, cell types, etc.
 - alternative splice variants, untranslated regions, etc.



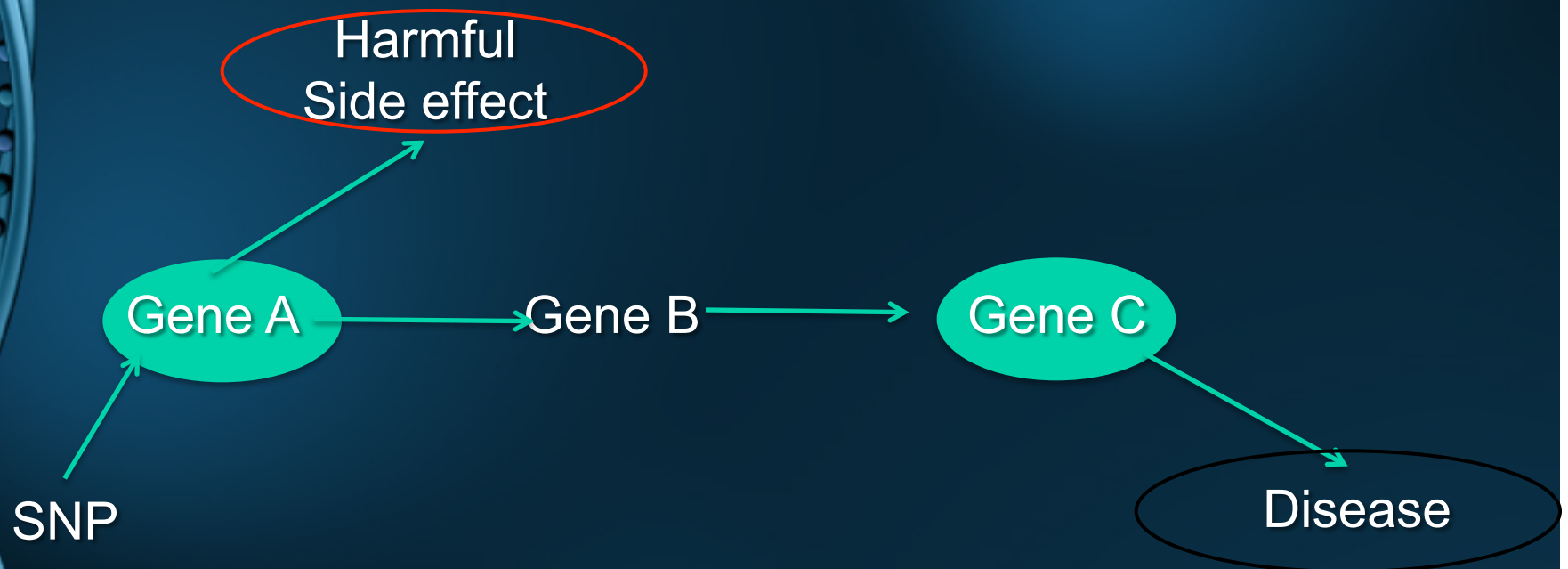
Statistics-Related Questions

Questions:

1. What are the best methods for processing data from these emerging technologies, e.g., high throughput sequencing?
2. Can we integrate data from DNA, RNA, and phenotype to identify a genetic pathway associated with disease?
3. Can we statistically merge data across species?

Drug Development

- Can we use these data to predict changes in a phenotype based on a pharmacologic manipulation of the pathway?





Current Projects

- **Massive RNA-Seq (Tabakoff/Hoffman/Saba)**
 - goal is to generate data on approximately 500 samples
 - integrating spike-in information into quantification and estimation of uncertainty
 - using reads to determine structure of unannotated genes/isoforms
- **eQTL integration across tissues and species (Kechris)**
 - Use hierarchical Bayesian modeling to leverage the abundance of data on mouse/rat RNA expression in human eQTL and GWAS studies
- **prediction with validation (Saba)**
 - evaluate prediction results/methods applied to large mouse populations by manipulating the expression of MeCP2 in regions of mouse brain and evaluating genome-wide changes in expression
- **systems genetics methods for complex traits**



For Students Interested in Statistical Genetics

- Technology outpaces statistical methods → LOTS OF OPPORTUNITIES
- Lots of publically available array and high throughput sequencing data (e.g., <http://phenogen.ucdenver.edu>)
- Mostly program in R and command line tools developed for RNA-Seq data