

UAB
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ALABAMA AT BIRMINGHAM
Knowledge that will change your world

Introduction to metabolomics research

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Targeted
Metabolomics &
Proteomics
Laboratory

Course goals

1. To understand the **vital** roles of metabolites
 - To provide energy for the chemical and enzymatic processes of life
 - To provide the building blocks for the macromolecules (DNA, RNA, proteins, carbohydrates, lipids)
 - As co-factors
 - As signaling molecules
 - As biomarkers for disease

Course goals

2. To understand the **origins** of metabolites

- Produced by (human) cells
- Produced by **the things that we eat (the food-ome)**
 - Plants (wheat, corn)
 - Fruits (apples, oranges, strawberries)
 - Vegetables (rice, potatoes, broccoli, peas)
 - Dairy products, including fermented forms
 - Meat from other animals
 - Xenobiotics
- Produced by **microorganisms** in our bodies
- Therapeutics, smoking, household chemicals

Course goals

3. To understand that a metabolomics experiment is **high dimensional**

- i.e., it compares the intensities of hundreds, if not thousands, of distinct species
- Very important statistical consequences
- Cannot afford to do a robust experiment that fully satisfies theoretical statistical principles
- Very important to sit down with a statistician prior to executing an experiment

Dr. Hemant Tiwari

Course goals

4. To select the appropriate method for extracting/recovering metabolites

- **Metabolites encompass an enormous range of chemistries**
 - Gaseous (H₂, H₂S)
 - Volatile (butyric acid, acetone, skatole)
 - Hydrophilic (glucose)
 - Charged-positive/negative (amino acids, nucleotides, organic acids, amines)
 - Hydrophobic (lipids, steroids, hydrocarbons)
- **No single method suitable for all metabolites**

Dr. Prasain and Barnes

Course goals

5. Selecting the analytical approach

- ***In situ* analysis**
 - Laser ablation of frozen tissue
 - Other desorption methods
 - Magic angle spinning NMR
 - Other spectroscopic methods
- **Extracted samples**
 - NMR
 - GC-MS (1- and 2D chromatography and MSMS)
 - LC-MS (1- and 2D chromatography and MSMS)
 - CE-MS
- **Targeted vs untargeted analysis**

Drs. Petit and Barnes

Course goals

6. Analysis of the data

– Data alignment

- NMR methods
- LC-MS and GC-MS methods (XCMS; ADAP)

– Statistical evaluation

- Univariate and multivariate analysis (MetaboAnalyst)
- XCMSonline
- Mummichog

– Data visualization

- XCMSonline
- Mzmine

Dr. Barnes and UNC-CH team

Course goals

7. Identifying the “interesting” metabolites

– Use of MS (absolute mass)

- METLIN
- Mummichog
- ChemSpider

– MSMS (fragmentation spectra)

- METLIN

– Metabolite standards

– Importance of retention time

- Multiple column conditions

Dr. Barnes and Prasain

Course goals

8. Pathways and applications

- Mummichog
- KEGG pathway mapping
- Applications to:
 - Adverse cardiovascular risk
 - Diabetes
 - Lens and kidney diseases
 - Cancer

What is “Metabolomics”?

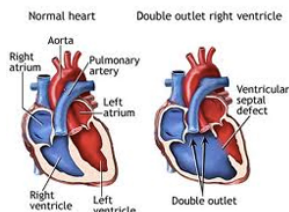
- Metabolomics is like other types of –omics analysis (microarray, RNA-Seq, proteomics, etc.)
 - Offers a “comprehensive” view of all detectable chemicals (not just metabolites)
 - Can be applied to body fluids
 - Plasma/sera, urine, saliva, tears, fecal water, etc.
 - Also to tissues
 - Liver, lung, heart, kidney, brain, eyes, etc.
 - And to single cells
 - Human, rodent, yeast, bacteria, etc.

Defining who we are chemically


- Are we “*Living in the Promisedland*” as per Willie Nelson’s song?
- Does an understanding of the functions of human genes define the chemical make up of our body fluids and tissues?
- How does metabolomics provide information on the circulating chemicals?
- Are the detected chemicals metabolites produced by human enzymes?
- So, what are we really exposed to? And does it make a difference?

A great deal of emphasis is being placed on the importance of DNA sequencing

CDH This model works for congenital diseases

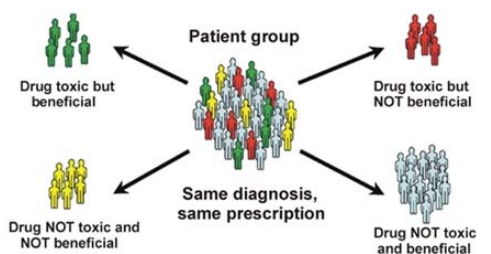


Biliary atresia



<https://loveyabeckett.files.wordpress.com>

This has evolved into precision medicine and optimization of therapy

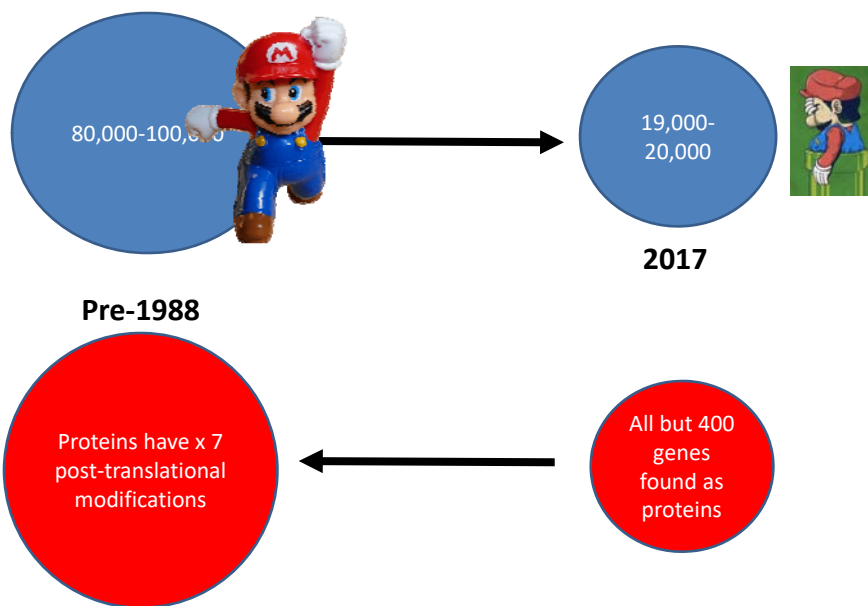


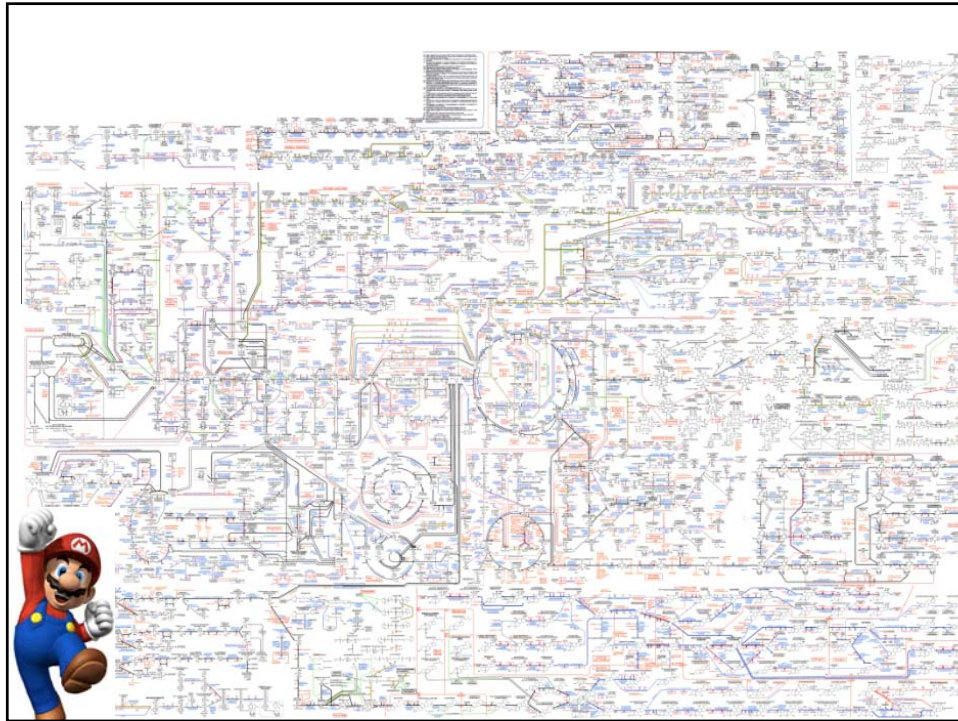
<http://personalizedmedicineproject.weebly.com/>

Metabolomics in the newborn

Dr. Dan Sharer

Genes failed to meet expectations





The Undiagnosed Disease Network

Dr. Bruce Korf

Where does the metabolome come from?

- It starts with what fixes CO₂ and N₂



Trees convert CO₂ to organic compounds



Field of soybeans – they fix N₂ because of nitrogen-fixing bacteria in their root nodules

Plants have more genes than humans

- Why? Plants can't run away!!
- Instead, they have to practice chemical warfare to prevent attack by aphids and microorganisms
- Many plants are poisonous to us
- Understanding which plants were safe to eat, or were so if cooked, represented the rise of agriculture and civilization



Compounds in plants and fruits

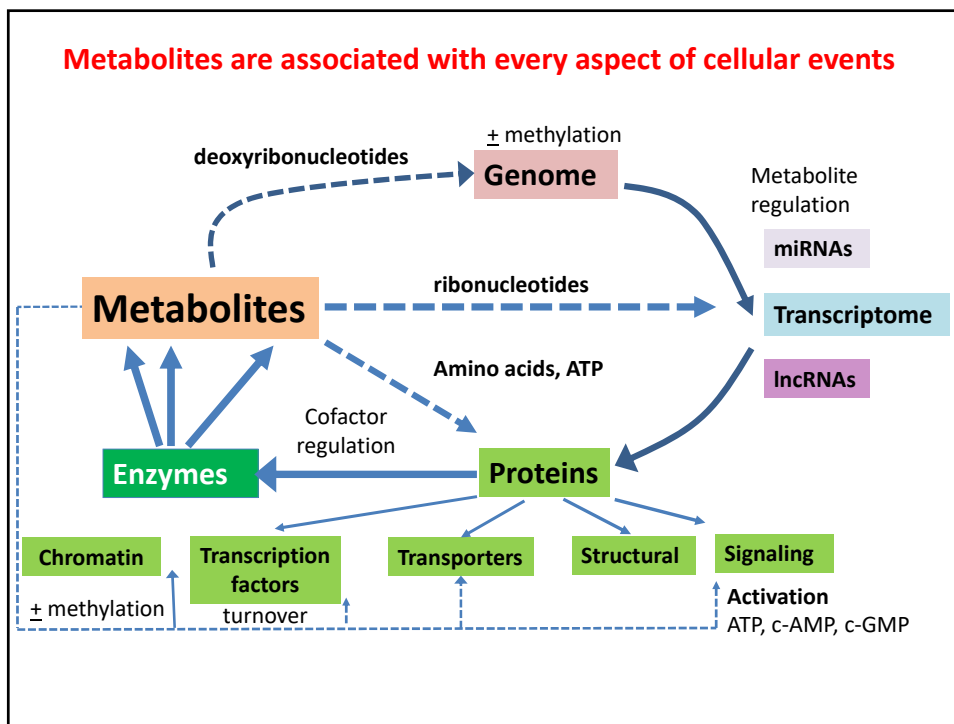
- Carotenoids
- Many vitamins
- Polyphenols and anthocyanins
- Not made by human cells



Other sources of body chemicals

- **The microbiomes**
 - Humans are not single organisms
 - Instead, we are super-organisms
 - The gut microbiome has 10 times the number of cells found in the rest of the (human) body
 - It makes novel compounds that are absorbed, enter the blood stream and tissues
- **Chemicals from the environment**
 - industrial contaminants, therapeutics, supplements
- **Interactions between the xenobiotics and the human enzyme systems**

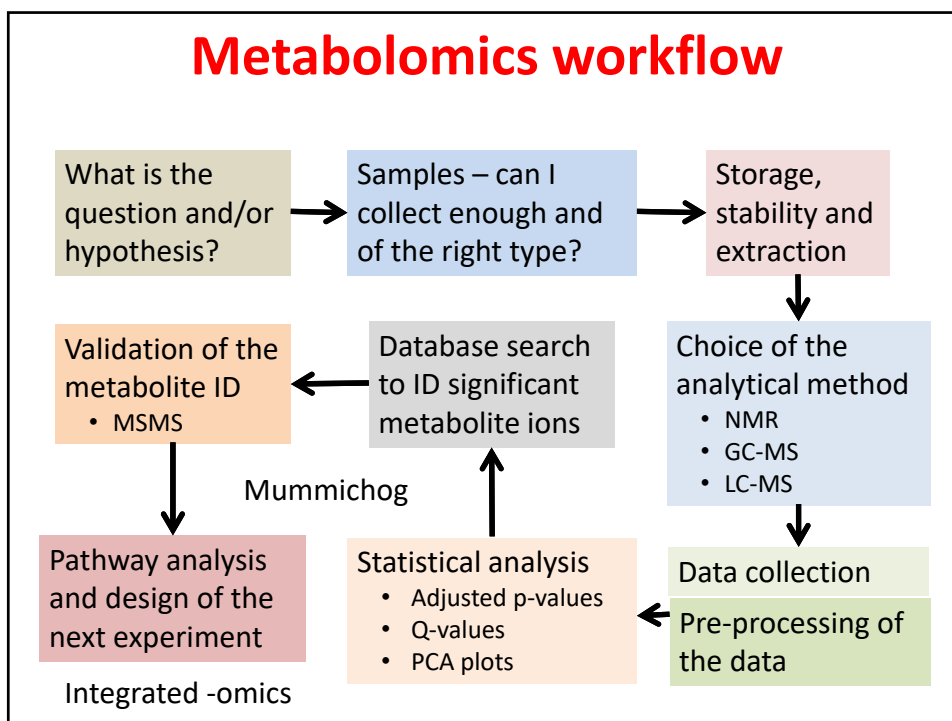


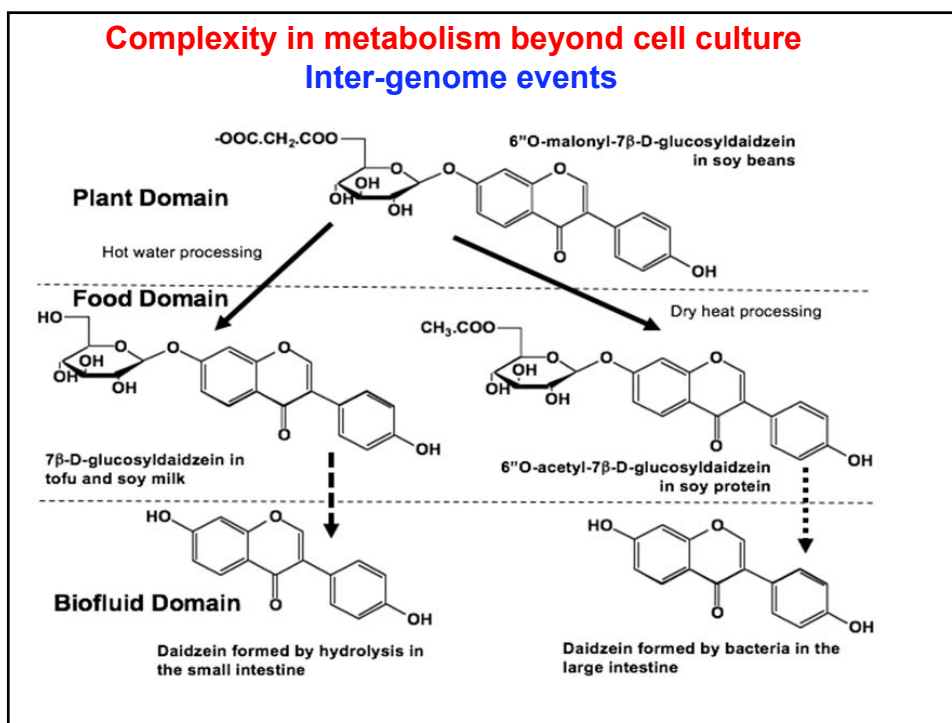


The metabolome is very complex!



Metabolomics workflow





Where did metabolomics come from?

Transition of mass spectrometry to biology



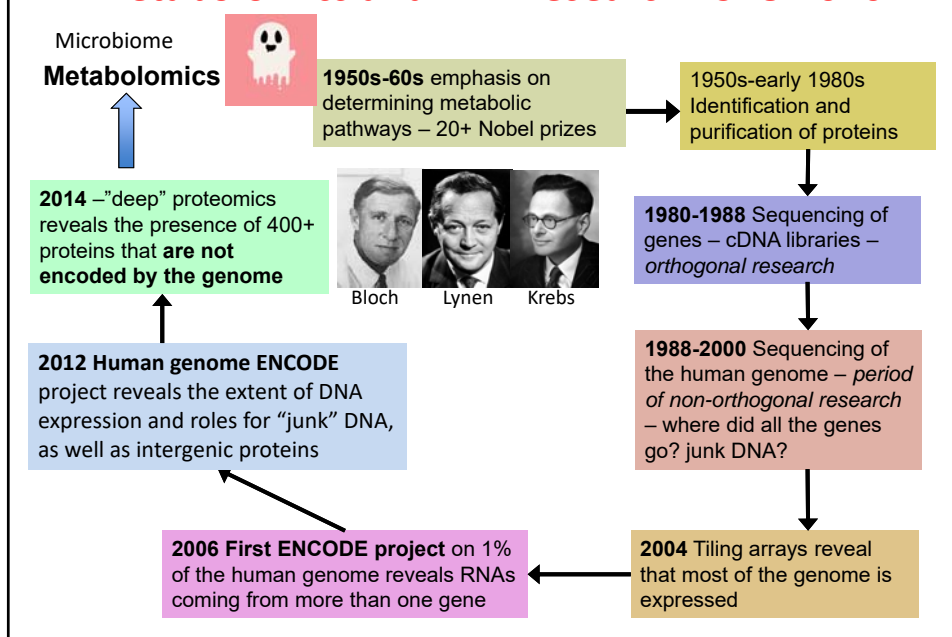
Ralf Schoenheimer



David Rittenberg

- While the politicians, tyrants, dictators and despots were salivating at the thought of developing nuclear weapons from unstable isotopes in the early part of the 20th Century, two scientists began the pursuit of the peaceful use of stable isotopes, initially deuterium (²H), and later carbon (¹³C) and nitrogen (¹⁵N), to study biochemical pathways
- Understanding the pathways of metabolism was born

Metabolomics and NIH Research 1948-2016



Progress in LC-MS

- Commercial HPLC appeared in the early 1970s to separate thermally stable and unstable molecules
- The challenge remained to find a way to get the unstable compounds into the gas phase
 - Applied to macromolecules (peptides, proteins) as well as metabolites
- Thermospray had some initial success
- **Electrospray ionization** and **chemical ionization** radically changed analysis, allowing compounds to go into the gas phase at atmospheric pressure and room temperature

LC-MS

- Suddenly, there were what appeared to be no limits (or very few) to what could be analyzed
- Unheard of, robust mass spectrometers came into play
 - “A reliable mass spectrometer” was considered in 1990 to be an oxymoron

Types of LC-MS analysis

Single quadrupole
LC-MS analysis

LC-time-of-flight
(TOF)-MS

FT-ICR MS

Orbi-trap

Triple quadrupole
LC-MS analysis

Multiple reaction
monitoring (MRM)

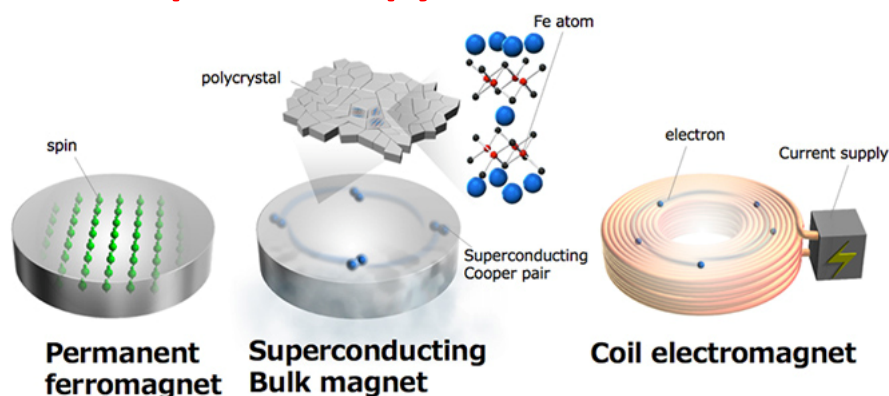
Q-TOF

TripleTOF



Ion Mobility

NMR spectroscopy and metabolomics

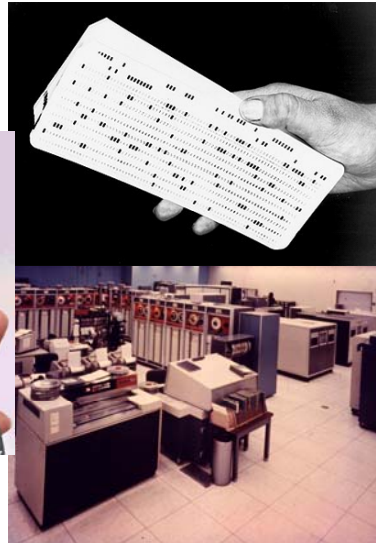
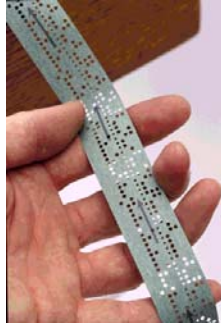


https://nationalmaglab.org/images/news_events/news/2015/october/pnictide_magnetism_1oct2015.jpg

NMR has had several critical development steps – Fourier Transform analysis of collected data, increase in field strength with superconducting magnets, micro-coil, cryogenic analysis, hyperpolarization.

Changing times in Computing

- 1950 The Cambridge colleagues of Watson and Crick calculated the structure of DNA by putting data onto punched cards and taking them by train to London for analysis – and to the fog – the “cloud” in 1950s
- 1964 Seymour Cray develops the CDC 6600 (1 Mflops)
- 1967 I used paper tape to collect data from a radio gas chromatograph and then submitted them via a terminal reader to the CDC 6600 at the University of London



Today in Computing



On my desk in 2018

- The Apple MacBook Air with 2 quad core Intel i7 processors
 - Operates at 2.0 GHz
 - Memory of 8 GB
 - Access 1.333 GHz
 - 512 GB Flash memory storage
 - 10 Gbs Thunderbolt I/O
- Also cost ~\$2,000



Cheaha high-performance computing

- Initially IBM Blue-Gene operating at 4.733 Tflop/s
- Replaced by Cheaha, in its current configuration it has 2800 conventional CPU cores and 6.6 PB raw storage
- It operates at 468 Tflop/s (max)

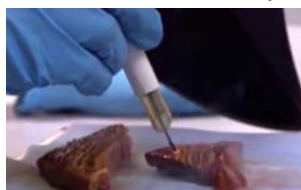
MRC-NIHR National Phenome Centre



600 MHz NMR instruments in surgical suite



Mass spectrometers (10 Q-TOFs) each dedicated to one assay format



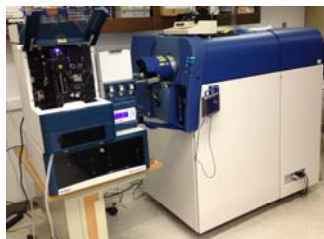
Iknife - revolutionizing surgery

This is Next-GEN precise medicine

The UK National Phenome Center, LC-MS labs



UAB capabilities in metabolomics

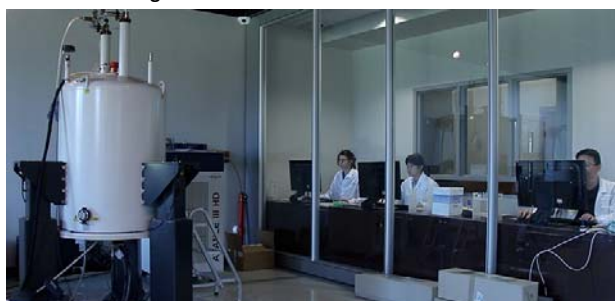


SCIEX 5600 TripleTOF
with Eksigent nanoLC

TMPL mass spec lab
MCLM 459/427
Stephen Barnes, Director
205-934-7117/3462



SCIEX 6500 Qtrap with SelexION



Central Alabama NMR facility
Chemistry Bdg
William Placzek, Director
205-934-2465

Great challenges in metabolomics

- The extent of the metabolome
 - From gaseous hydrogen to earwax
- Having complete databases
 - METLIN has 220,000+ metabolite records, but your problem always creates a need to have more
 - Improvement in the size of a MSMS database
- Storing and processing TBs of data
- Standards and standard operating procedures
- Being able to do the analyses in real time

NIH Common Fund Metabolomics Program

- **Metabolomics Workbench:**
<http://www.metabolomicsworkbench.org/>
- **Regional Comprehensive Metabolomics Research Centers**
 - University of Michigan: <http://mrc2.umich.edu/index.php>
 - UC Davis Metabolomics Center: <http://metabolomics.ucdavis.edu/>
 - UNC-CH: <http://www.uncnri.org/wp-content/uploads/2016/12/NIHERCMRC.pdf>
 - SE Center for Integrated Metabolomics: <http://secim.ufl.edu/>
 - Resource Center for Stable Isotope Metabolomics:
<http://bioinformatics.cesb.uky.edu/bin/view/RCSIRM/>
 - Mayo Clinic Metabolomics Resource: <http://www.mayo.edu/research/core-resources/metabolomics-resource-core/overview>