



# **Metabolomics: quantifying the phenotype**



# Metabolomics Promises Quantitative Phenotyping

What can happen

**GENOME**

**Bioinformatics**

What appears to be happening

**TRANSCRIPTOME**

What makes it happen

**PROTEOME**

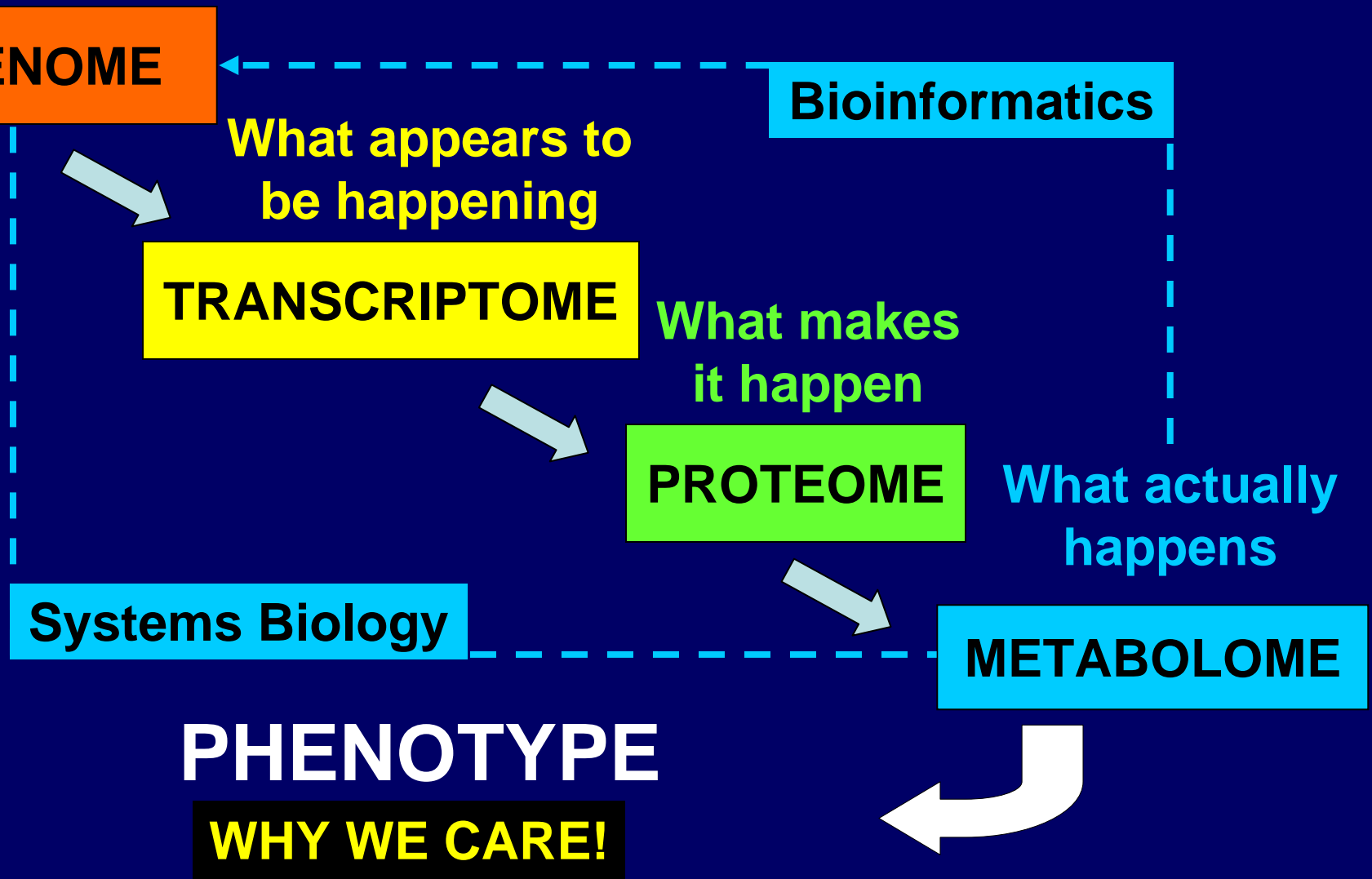
What actually happens

**Systems Biology**

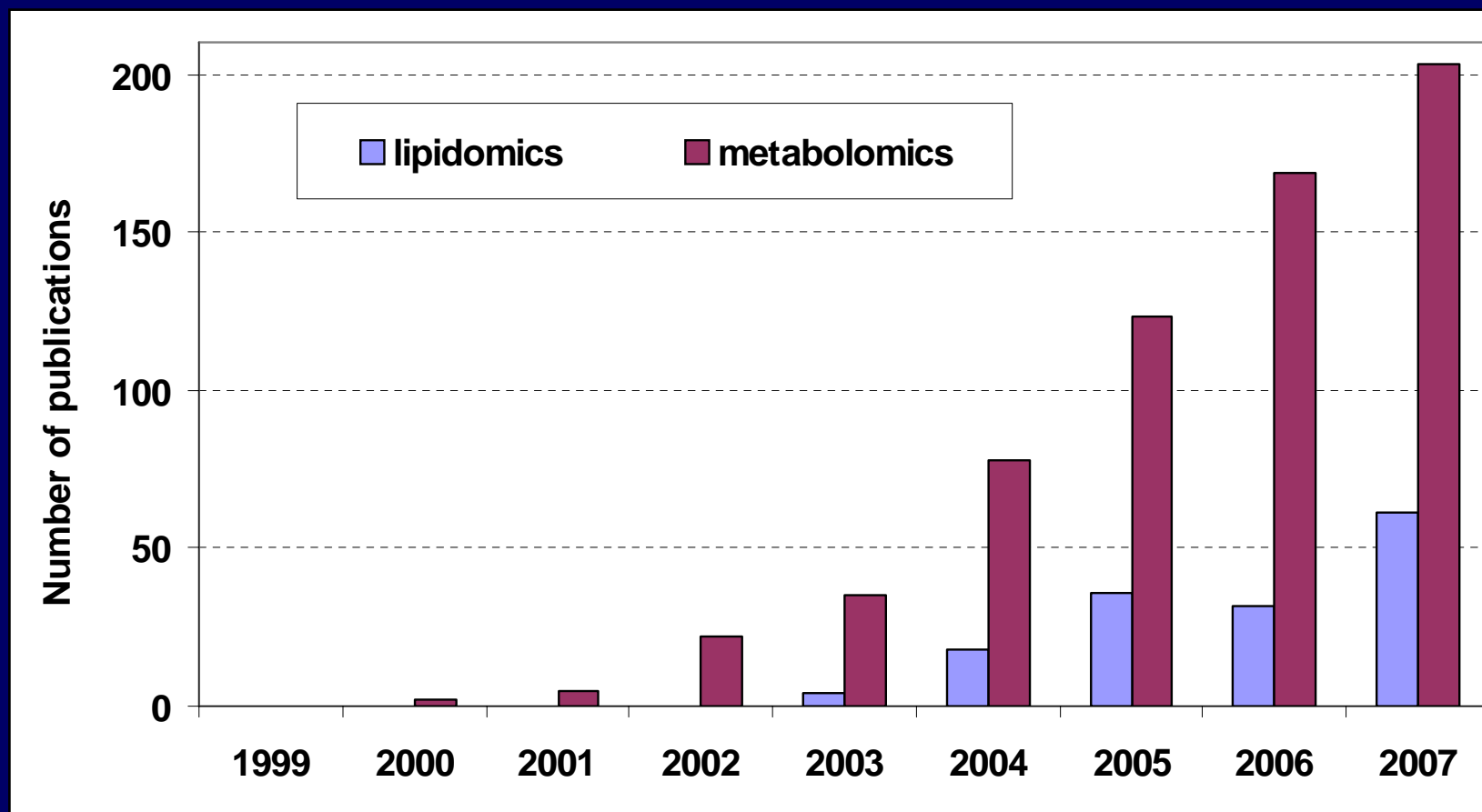
**METABOLOME**

**PHENOTYPE**

**WHY WE CARE!**



# Metabolomics publications in Pubmed



↑  
First  
"metabolomics"  
publication

↑  
First  
"lipidomics"  
publication

# History of metabolomics

## **Quantitative Analysis of Urine Vapor and Breath by Gas–Liquid Partition Chromatography**

*(orthomolecular medicine/vitamins/controlled diet)*

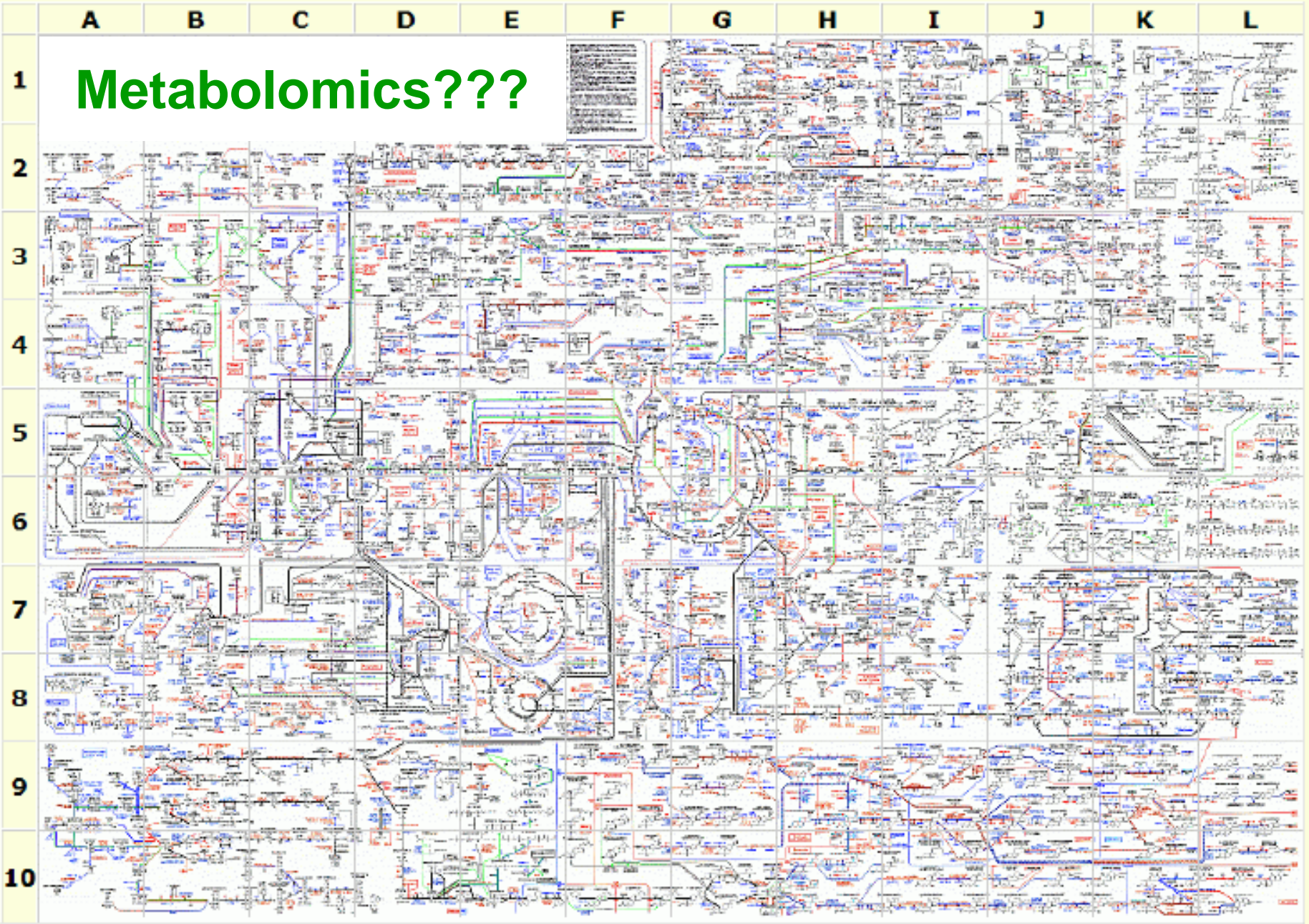
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\* Department of Chemistry, Stanford University, Stanford, California 94305; and † Western Regional Laboratory, U.S. Department of Agriculture

*Contributed by Linus Pauling, July 29, 1971*

- **metabolomics developed by Pauling in 1970**
- **the term metabolomics first used in 1998**
  - **Oliver SG et al (1998). Trends Biotechnol 16:373**
- **Metabolomics Society founded 2004**
- **January 23rd, 2007 first draft of the human metabolome “completed”**

# Metabolomics???



# Approaches to Investigating the Metabolome

- **Metabolic Fingerprinting**
  - **Pattern recognition** to classify samples by shifts in “global” metabolite composition.

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- **Metabolic Targeting**
  - **Quantification** of a small number of known compounds.
- **Metabolic Profiling**
  - **Quantification** of a group of related compounds or metabolites within a specific metabolic pathway.

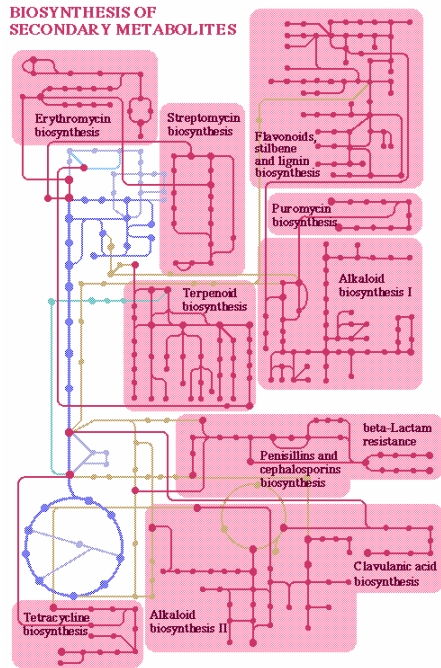


## Metabolomics

- **Quantification** of “all” metabolites at a defined time under specific environmental conditions.

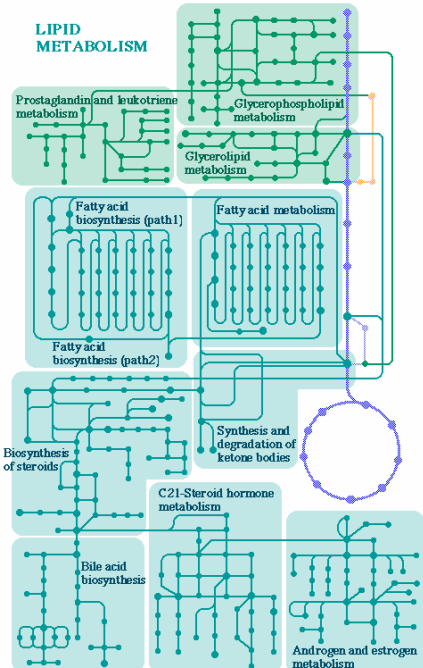


**BIOSYNTHESIS OF SECONDARY METABOLITES**



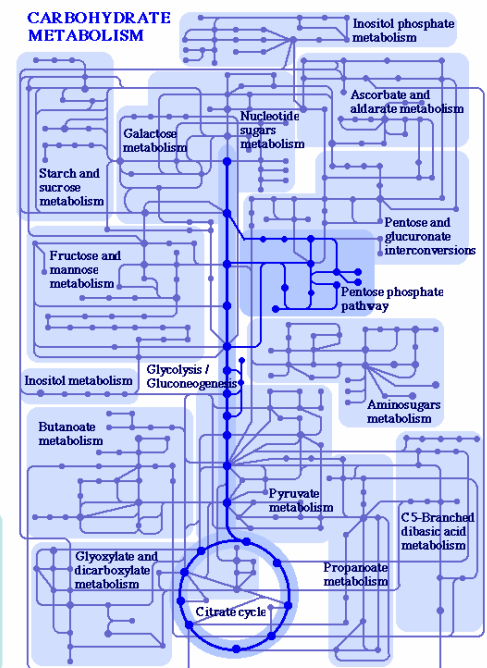
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**LIPID METABOLISM**



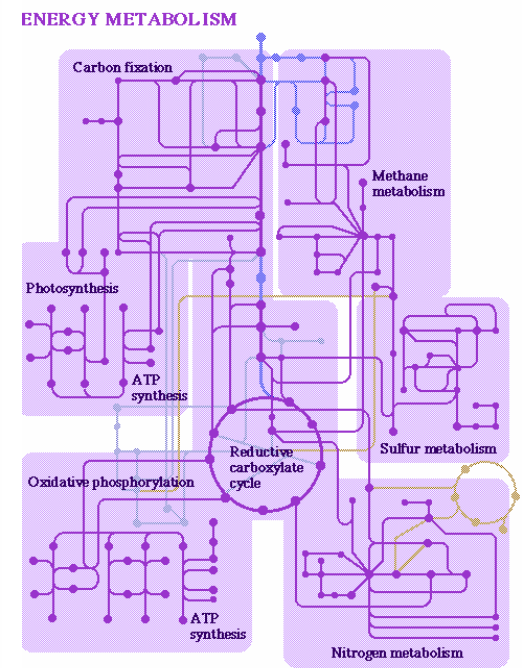
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**CARBOHYDRATE METABOLISM**



110 R11

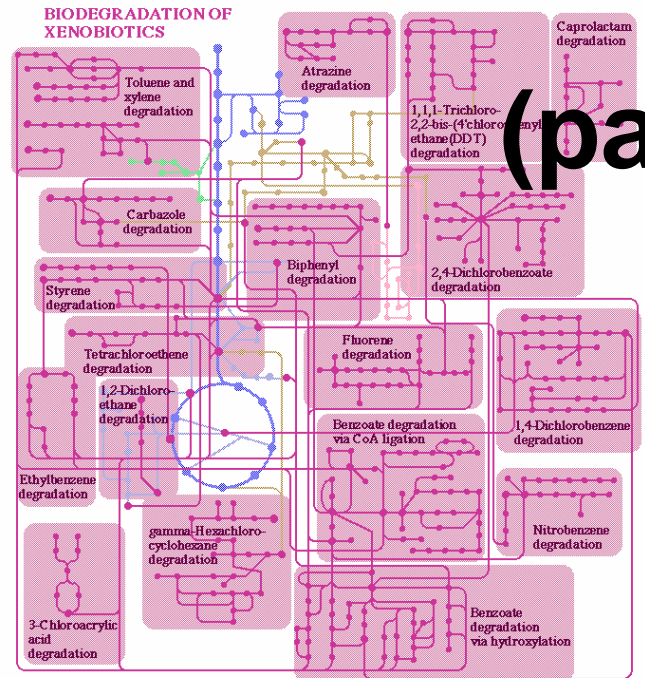
**ENERGY METABOLISM**



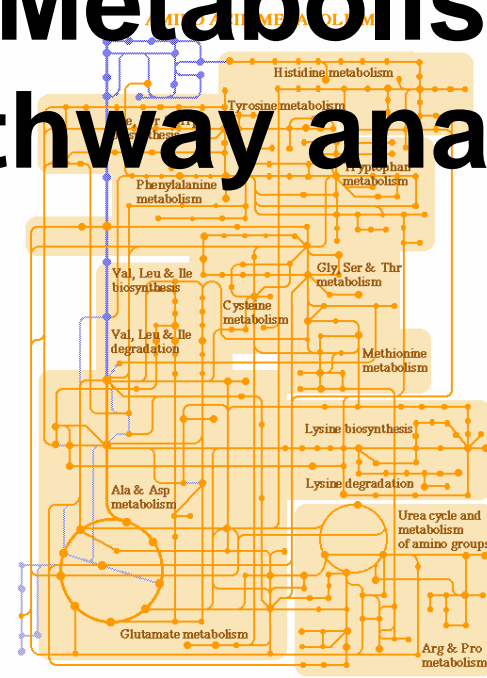
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# Metabolism (pathway analysis)

**BIODEGRADATION OF XENOBIOTICS**

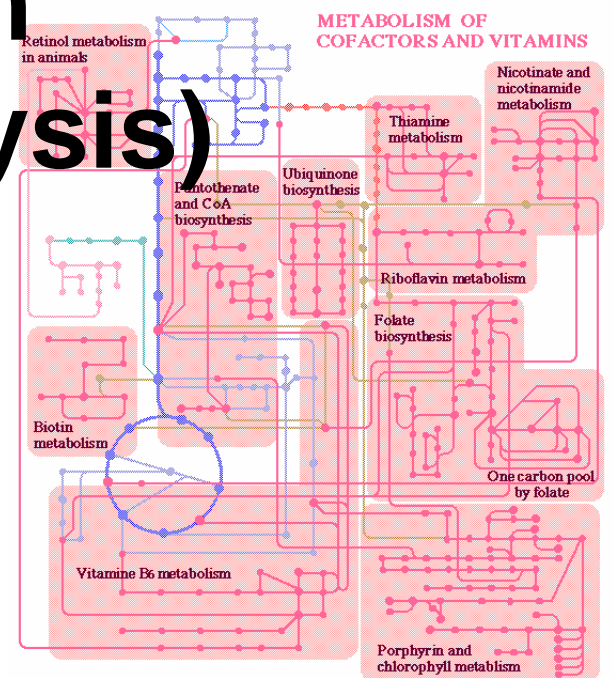


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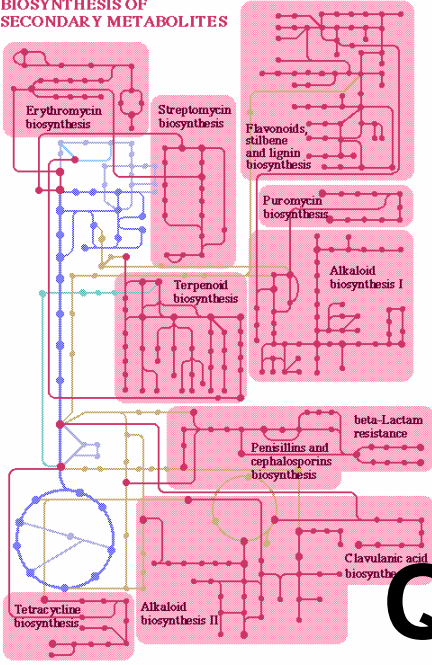
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**METABOLISM OF COFACTORS AND VITAMINS**

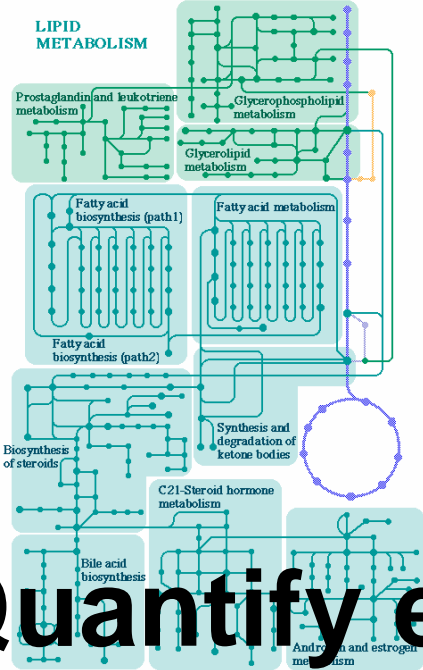


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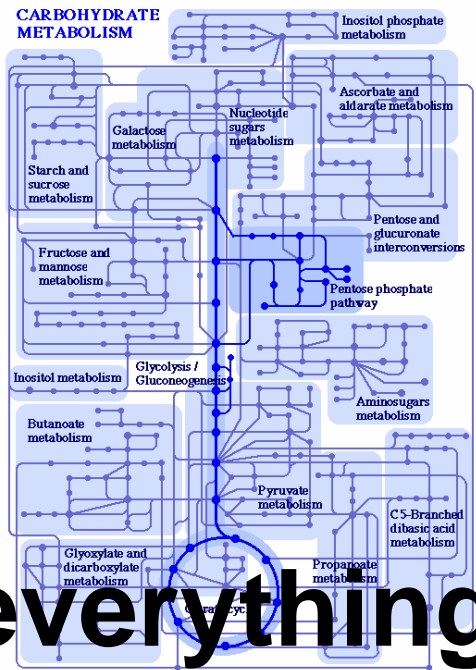
**BIOSYNTHESIS OF SECONDARY METABOLITES**



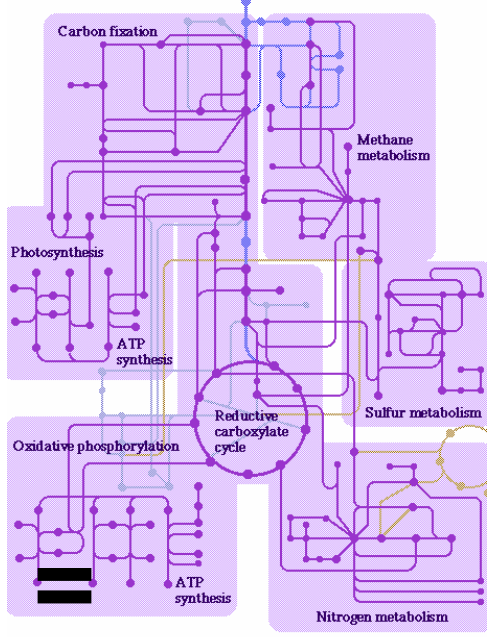
**LIPID METABOLISM**



**CARBOHYDRATE METABOLISM**



**ENERGY METABOLISM**

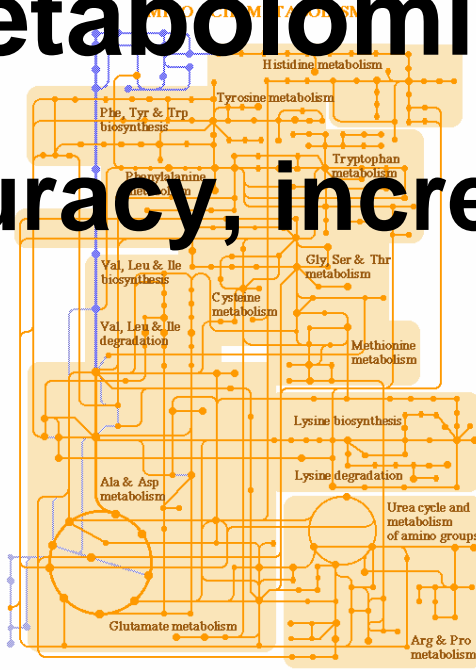
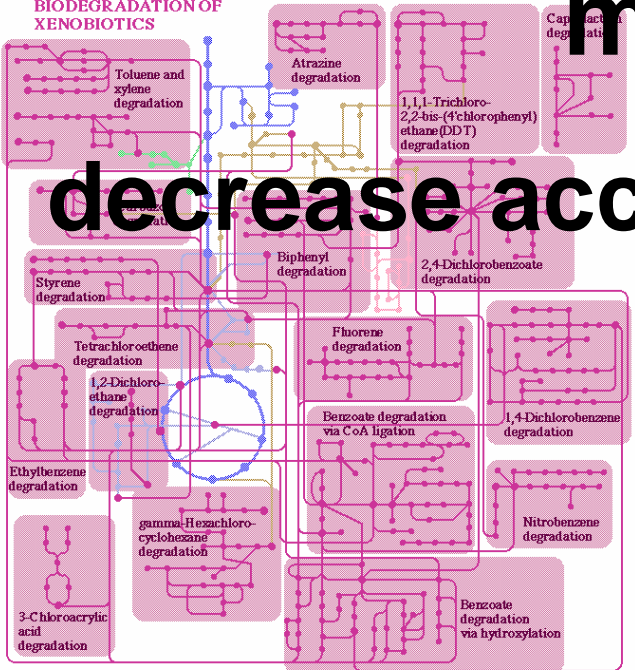


**Quantify everything =**

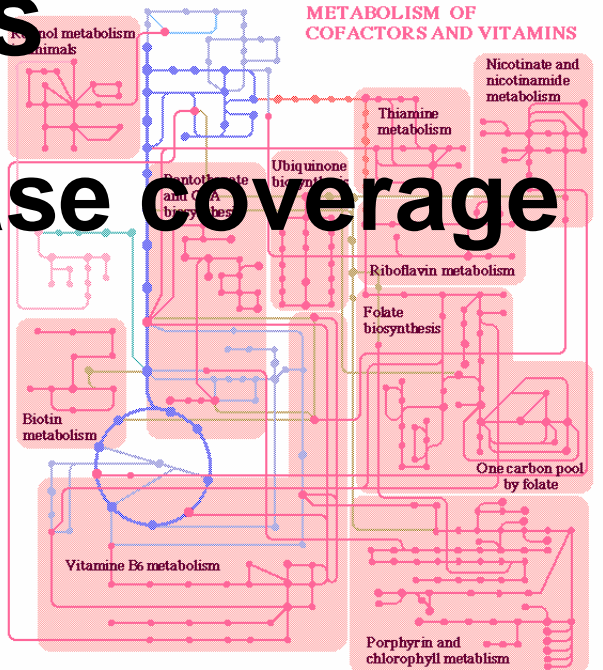
**metabolomics**

**decrease accuracy, increase coverage**

**BIODEGRADATION OF XENOBIOTICS**

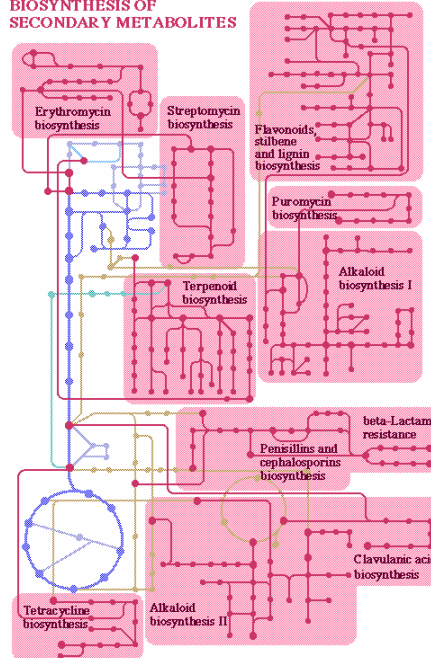


**METABOLISM OF COFACTORS AND VITAMINS**



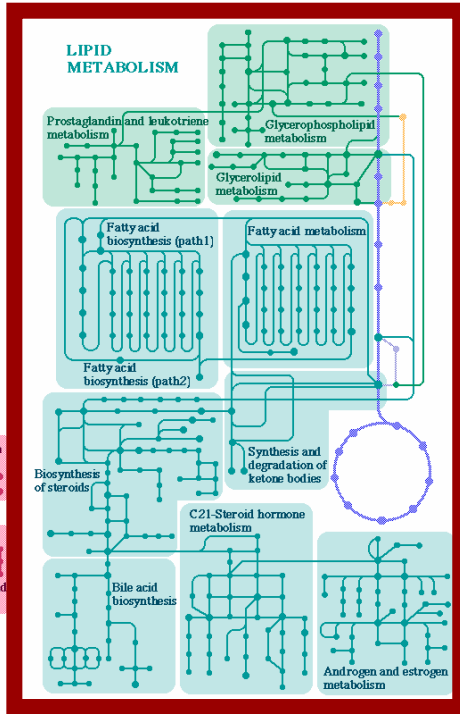


**BIOSYNTHESIS OF SECONDARY METABOLITES**



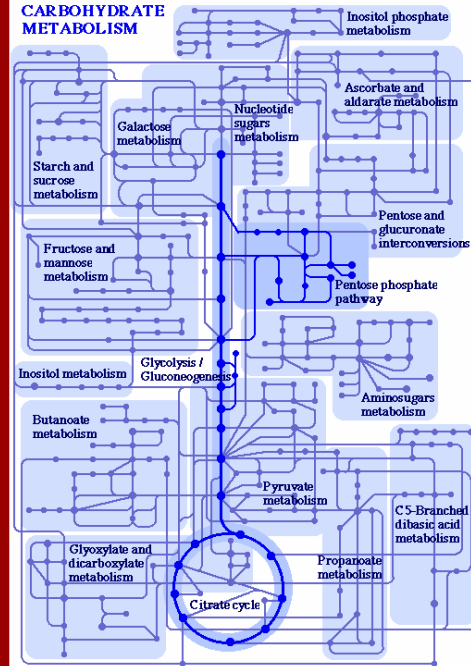
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**LIPID METABOLISM**

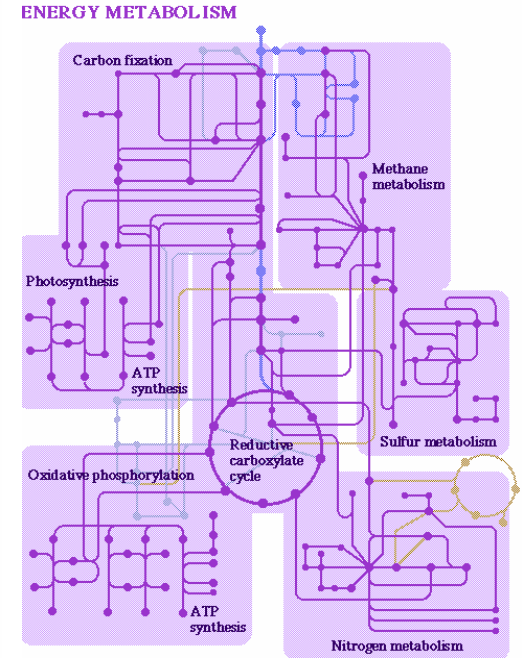


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**CARBOHYDRATE METABOLISM**

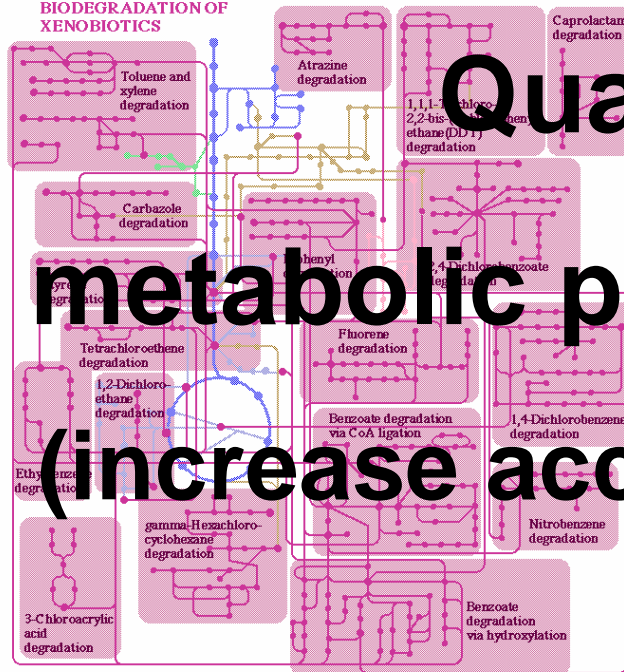


**ENERGY METABOLISM**



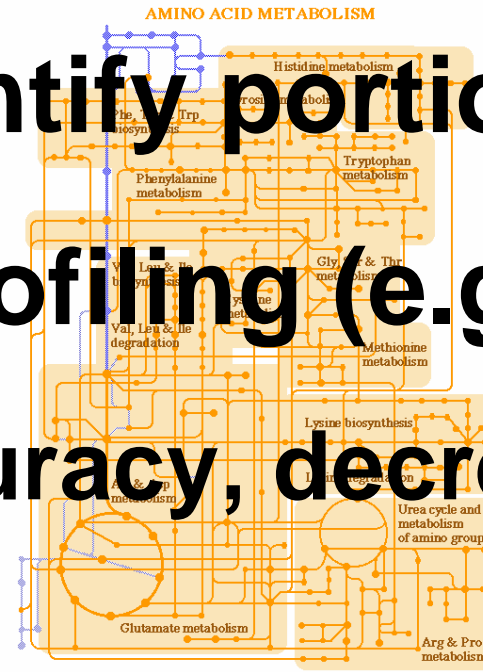
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**BIODEGRADATION OF XENOBIOTICS**



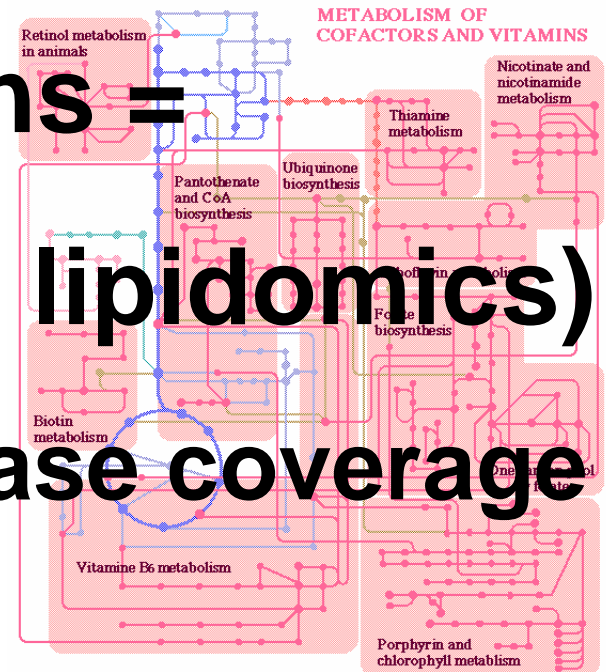
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**AMINO ACID METABOLISM**



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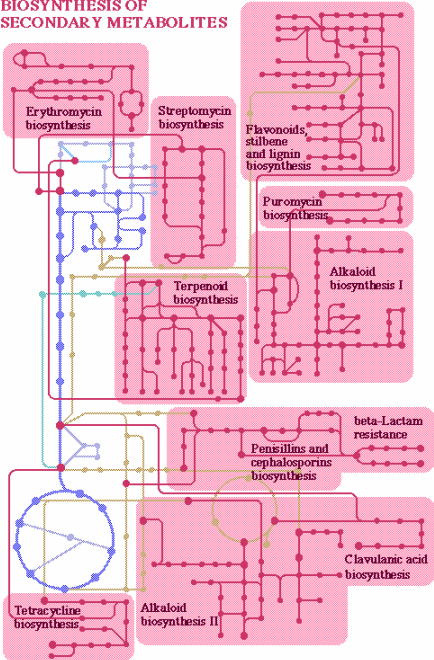
**METABOLISM OF COFACTORS AND VITAMINS**



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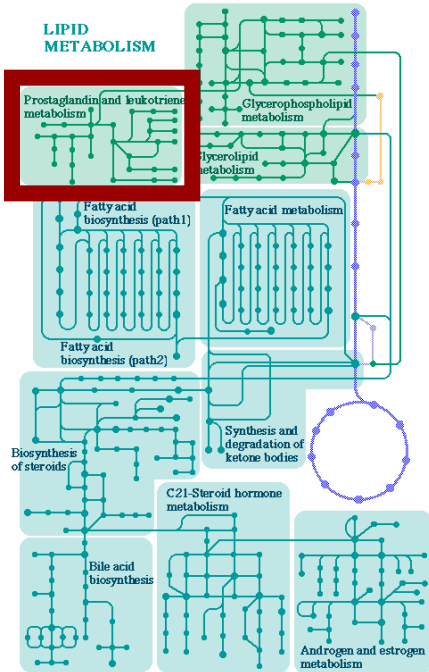
**Quantify portions = metabolic profiling (e.g. lipidomics) (increase accuracy, decrease coverage)**

**BIOSYNTHESIS OF SECONDARY METABOLITES**



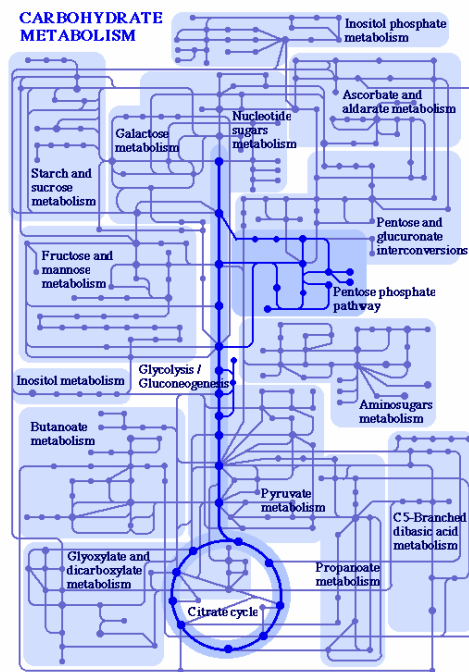
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**LIPID METABOLISM**



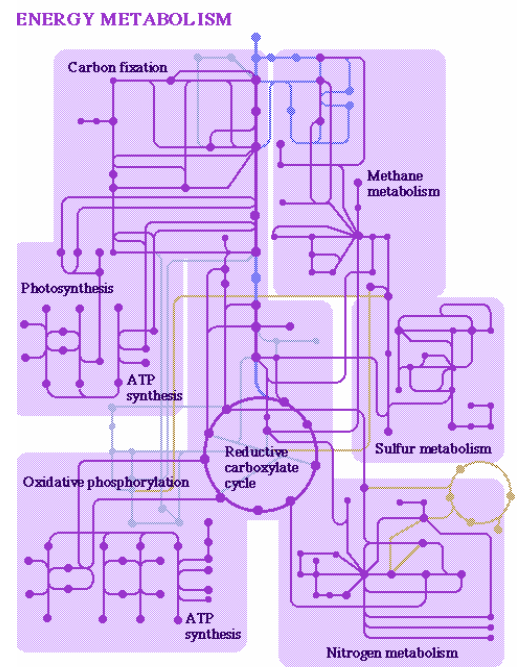
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**CARBOHYDRATE METABOLISM**



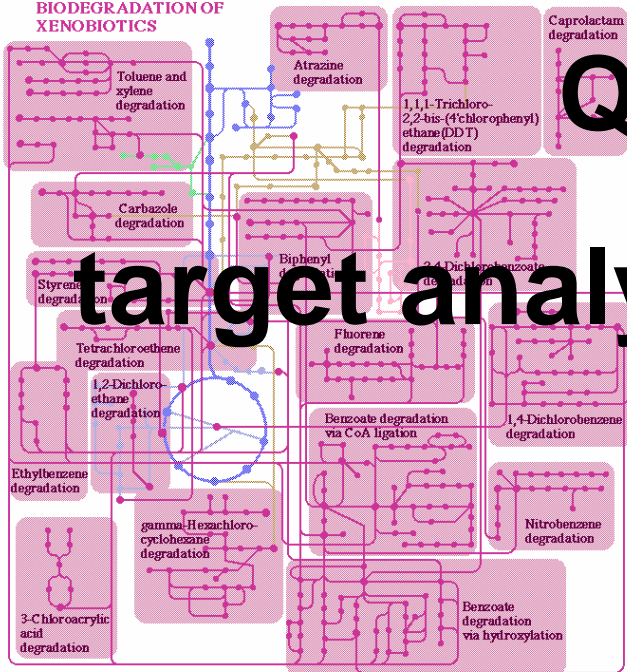
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**ENERGY METABOLISM**



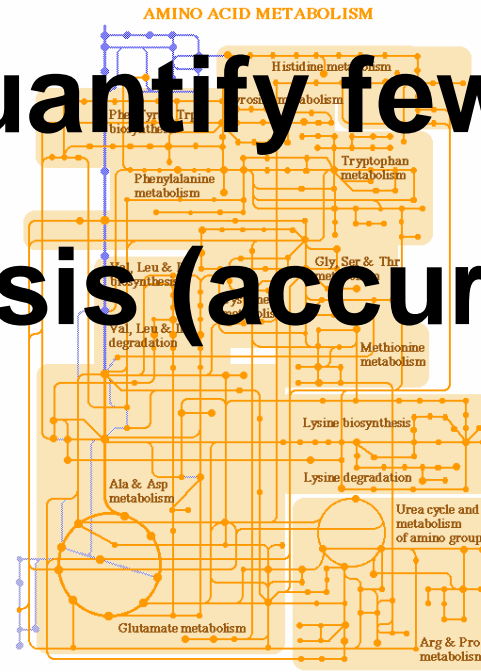
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**BIODEGRADATION OF XENOBIOTICS**



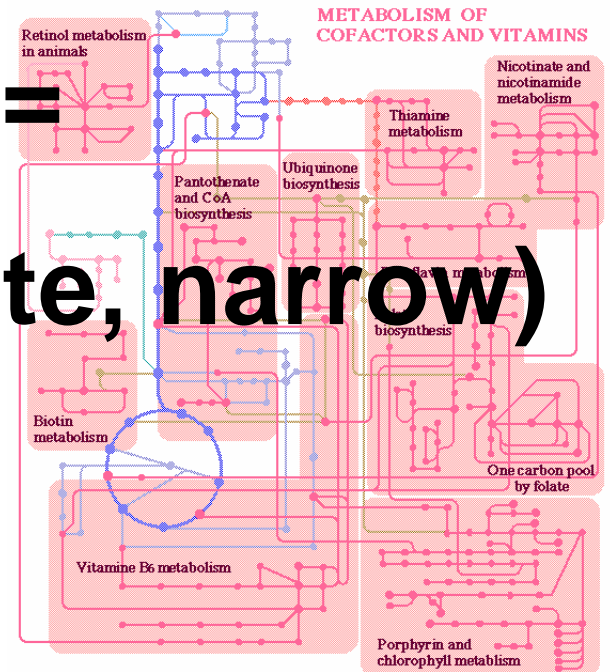
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**AMINO ACID METABOLISM**



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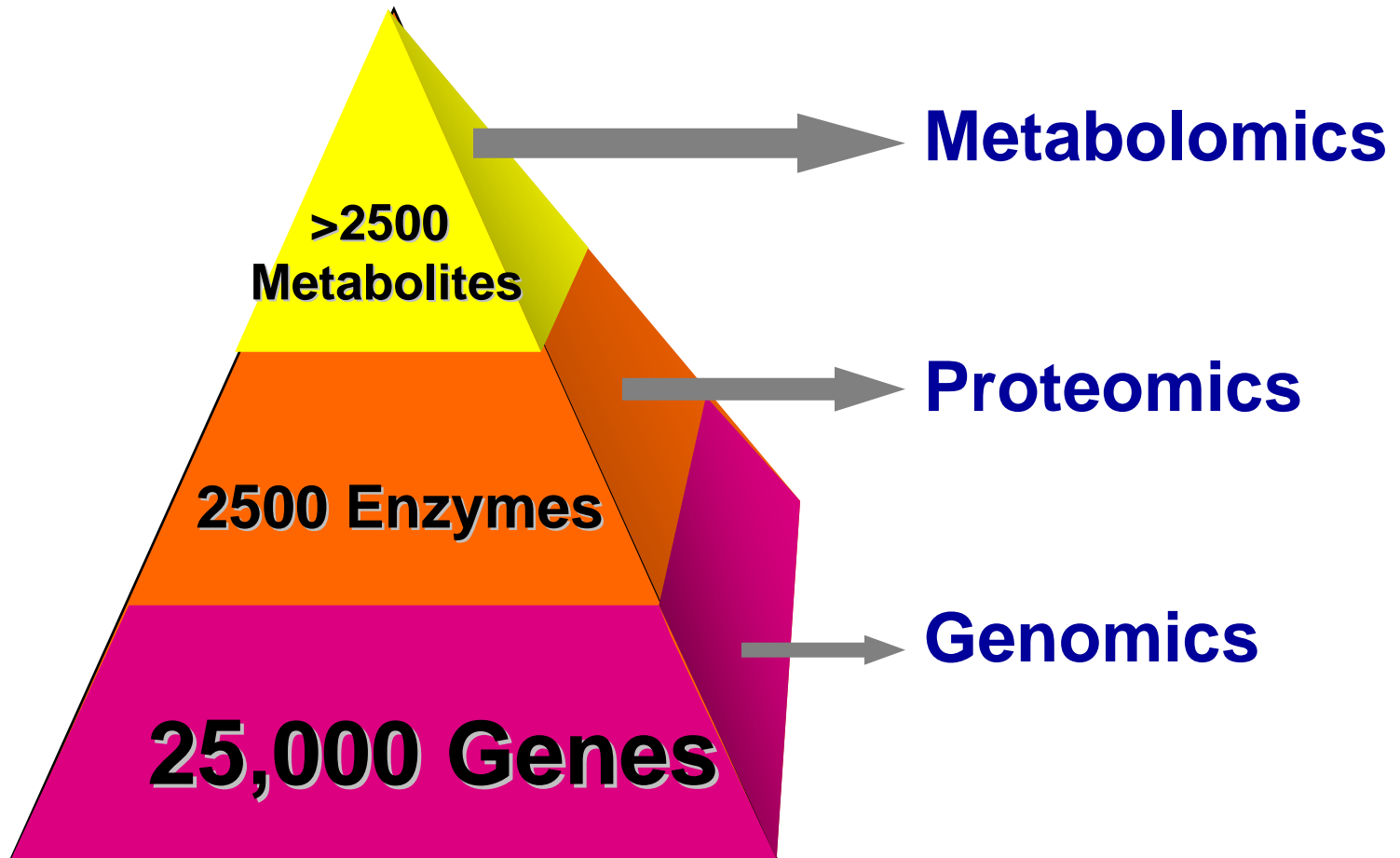
**METABOLISM OF COFACTORS AND VITAMINS**



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**Quantify few = target analysis (accurate, narrow)**

# The Pyramid of Life



From the Human Metabolome Project: <http://metabolomics.ca/>

# What is metabolomics?

A comprehensive quantitative analysis of all metabolites in the metabolome under a given set of conditions

## What is a metabolite?

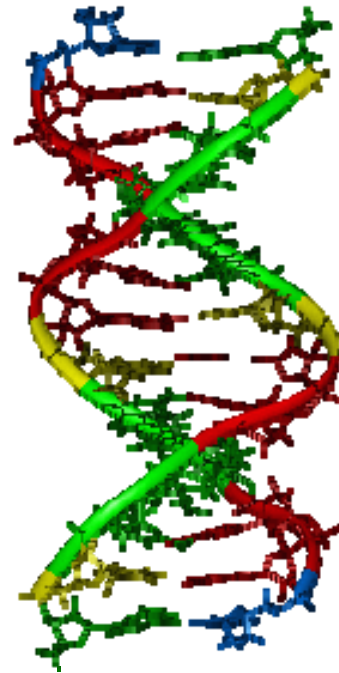
- Substance involved in metabolism
- A by-product of the breakdown of either food or medication by the body
- Compound produced from the chemical changes of a drug in the body
- Any compound detected in the body <1500 Da

Substance produced in or by biological processes

# What is a metabolite?

- peptides
- oligonucleotides
- sugars
- nucleosides
- organic acids
- ketones
- aldehydes
- amines
- amino acids
- lipids
- steroids
- alkaloids
- drugs
- xenobiotics

# Why Are Metabolites Relevant?

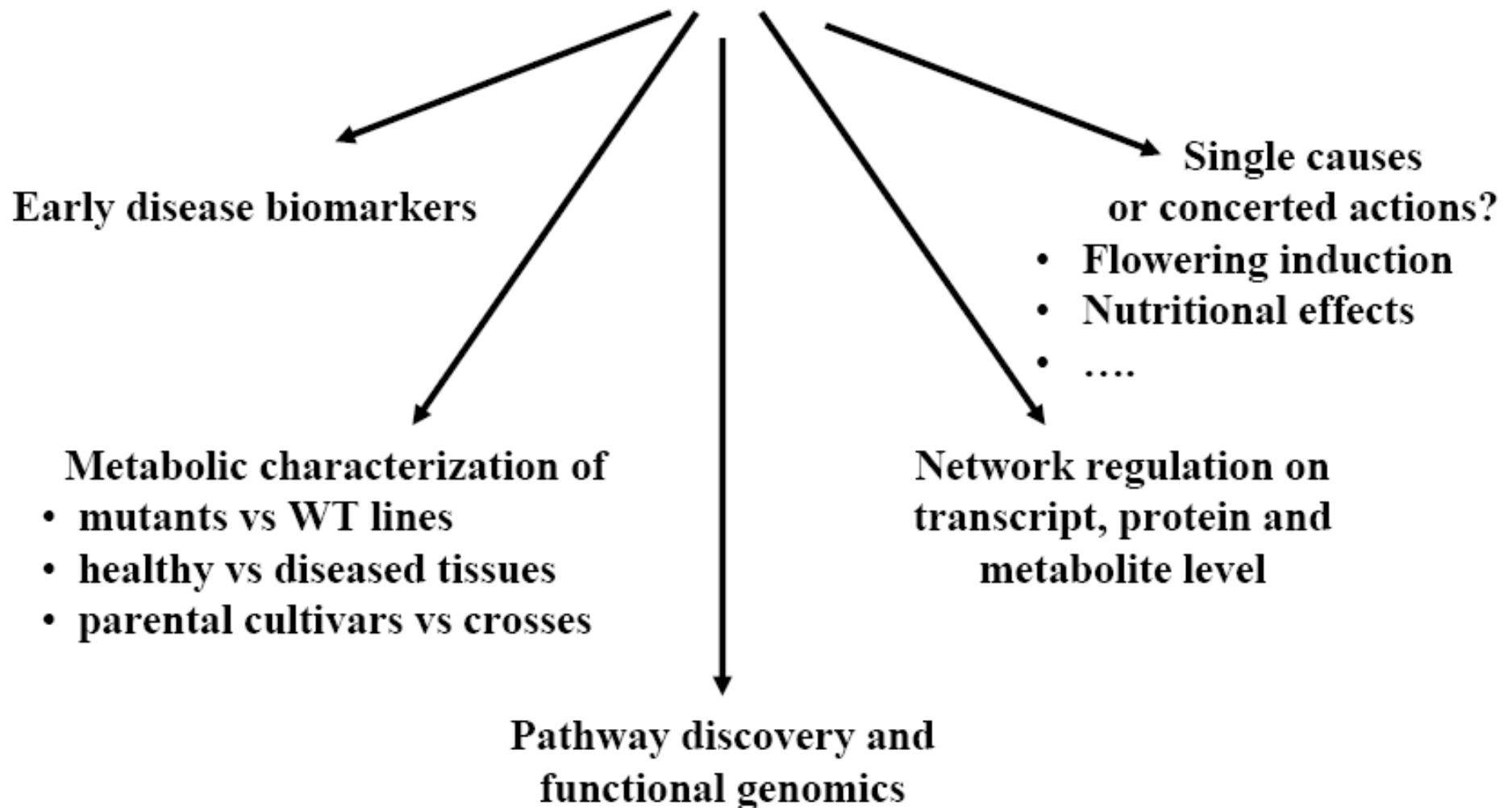


**Metabolites are the Canaries of the Genome**

# Why measure metabolites?

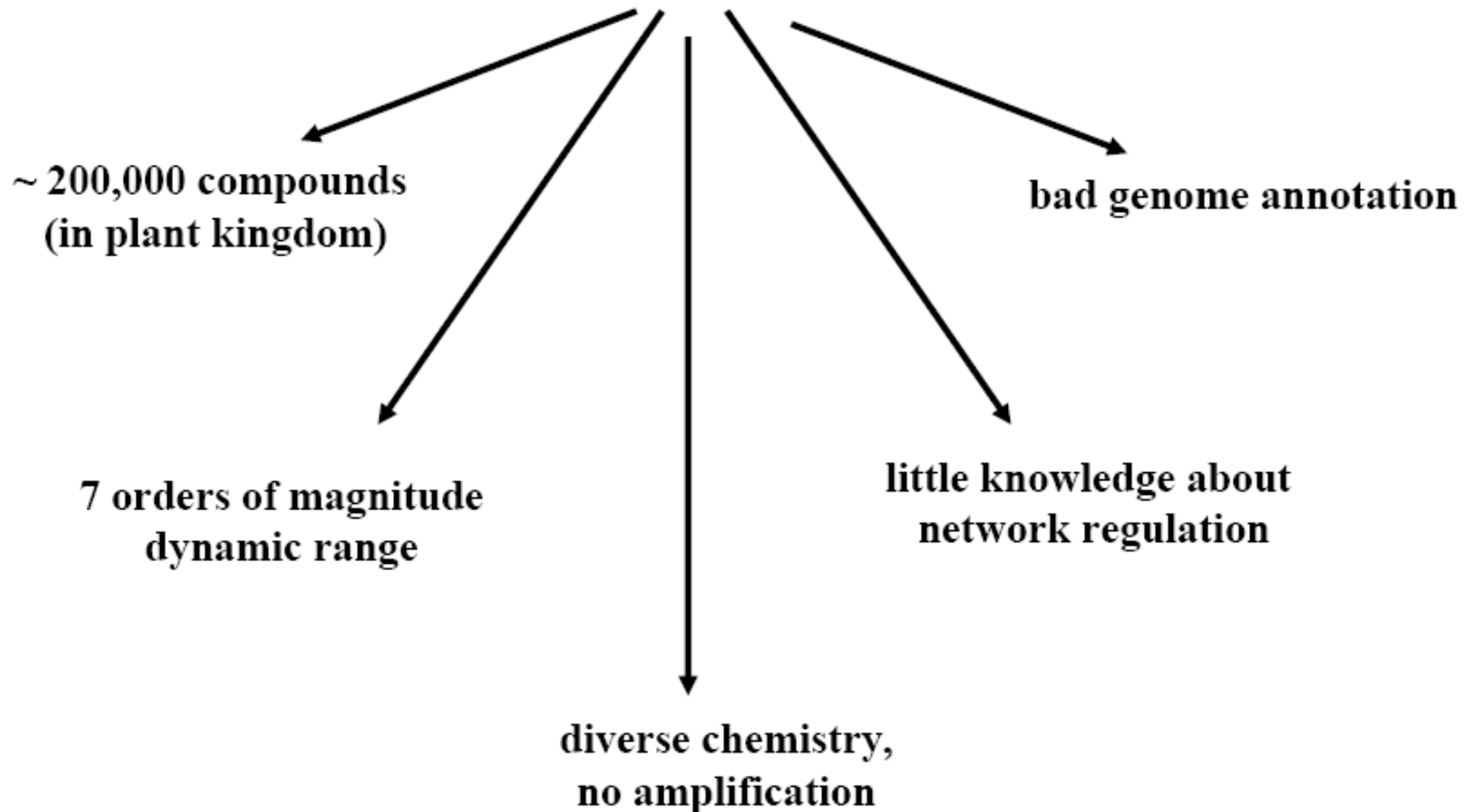
- **Simple answer**
  - Readout of underlying molecular network
  - Infer enzyme activities
  - Reflective of any observable phenotype
  - Diagnostics, functional genomics
- **Not so simple answer:**
  - Not victims, but actors
  - A cause somewhere in the network can have effects elsewhere

**Use of metabolomic approaches:  
'Detect the unexpected'**





# **‘Complexity’**



# **‘Complexity’**

**Soga et al., 3x CE/MS:  
~ 1,500 compounds  
in B. subtilis**

**B. subtilis genome annotation:  
computation of ~650 compound  
metabolome**

**Metabolome cannot be  
computed from genome**

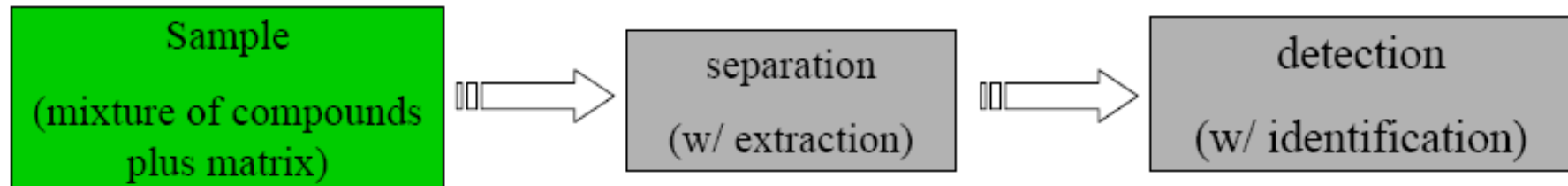
The diagram illustrates the discrepancy between experimental and computational metabolome data. At the top, the word 'Complexity' is written in red. Two black arrows point downwards from it to two text blocks. The left block describes experimental data from Soga et al. (3x CE/MS) showing ~1,500 compounds in B. subtilis. The right block describes genome annotation data for B. subtilis, showing a computation of ~650 compound metabolome. Two thick grey arrows point from the bottom of these two blocks towards a central conclusion at the bottom: 'Metabolome cannot be computed from genome'.

Metabolomics is a branch of  
**Analytical Biochemistry**

Analytical biochemistry is the analysis of material samples to gain an understanding of their biochemical composition and structure.

**Qualitative analysis** seeks the presence of a given functional group or organic compound in a sample.

**Quantitative analysis** seeks the amount of a given compound in a sample.



**separation types:**

**(a) physicochemical (b) biochemical properties**

(a) electrical charge, lipophilicity, hydrophilicity, volatility, size...

(b) binding, metabolism, precipitation...

**detection types:**

**(a) physicochemical (b) biochemical properties**

(a) mass, vibration, rotation, magnetic resonance, radiation absorption/fluorescence/scattering  
redox potential, thermal conductivity, refractive index...

(b) antibody, protein folding/binding → FRET

# Metabolomics experiment

- 1. Extraction from biological tissues**
- 2. Separation**
  - chromatography
- 3. Detection**
  - mass spectrometry
- 4. Identification & quantification**

# Metabolomics methods

## Separation methods

- **Gas chromatography (GC)**
  - one of the most widely used and powerful methods
  - high chromatographic resolution
  - compounds must be volatile (or derivatized)
- **High performance liquid chromatography (HPLC)**
  - lower chromatographic resolution
  - wider range of analytes can be analyzed (polar)
- **Capillary electrophoresis (CE)**
  - higher theoretical separation efficiency than HPLC
  - suitable for wider range of metabolites than GC
  - most appropriate for charged analytes (electrophoretic technique)

# Metabolite detection techniques

## Physical Property

- mass
- rotation, vibration
- $h\nu$  absorbance
- $h\nu$  emittance
- spin
- volatility
- hydrophobicity
- charge
- size

## Method

- mass spectrometry
- infrared spectrometry
- ultraviolet-visible spectroscopy
- fluorescence spectroscopy
- nuclear magnetic resonance
- gas chromatography
- liquid chromatography
- capillary electrophoresis
- size-exclusion chromatography

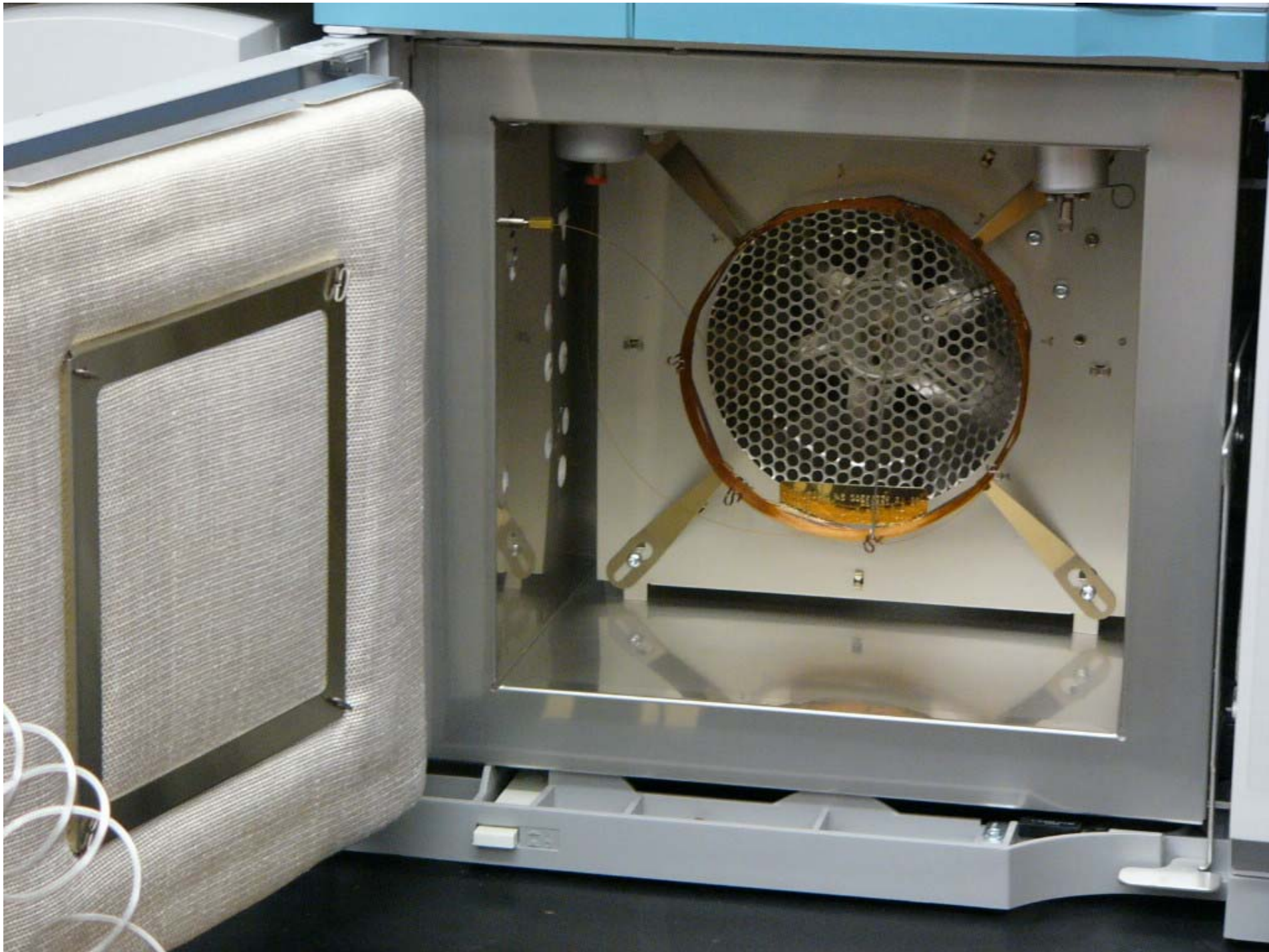
# Gas chromatography

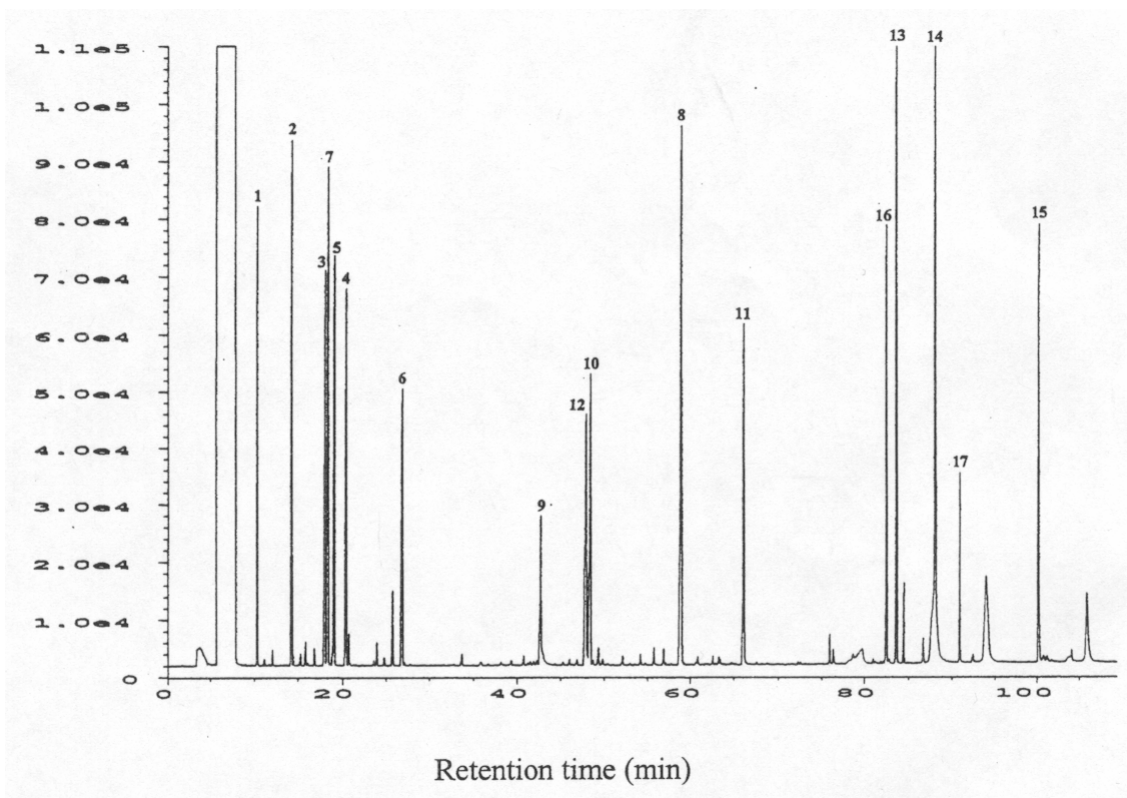
- **Advantages**
  - Very high chromatographic resolving power
  - Good selection of stationary phases
  - Wide dynamic range
- **Disadvantages**
  - Compounds must be sufficiently volatile (derivatized)
  - Compounds must be thermally stable
  - Limited to nonpolar and slightly polar molecules











# Liquid chromatography

- **Advantages**

- Capable of analyze wide range of metabolites
- (thermally labile, polar, high molecular mass)
- Good selection of stationary phases

- **Disadvantages**

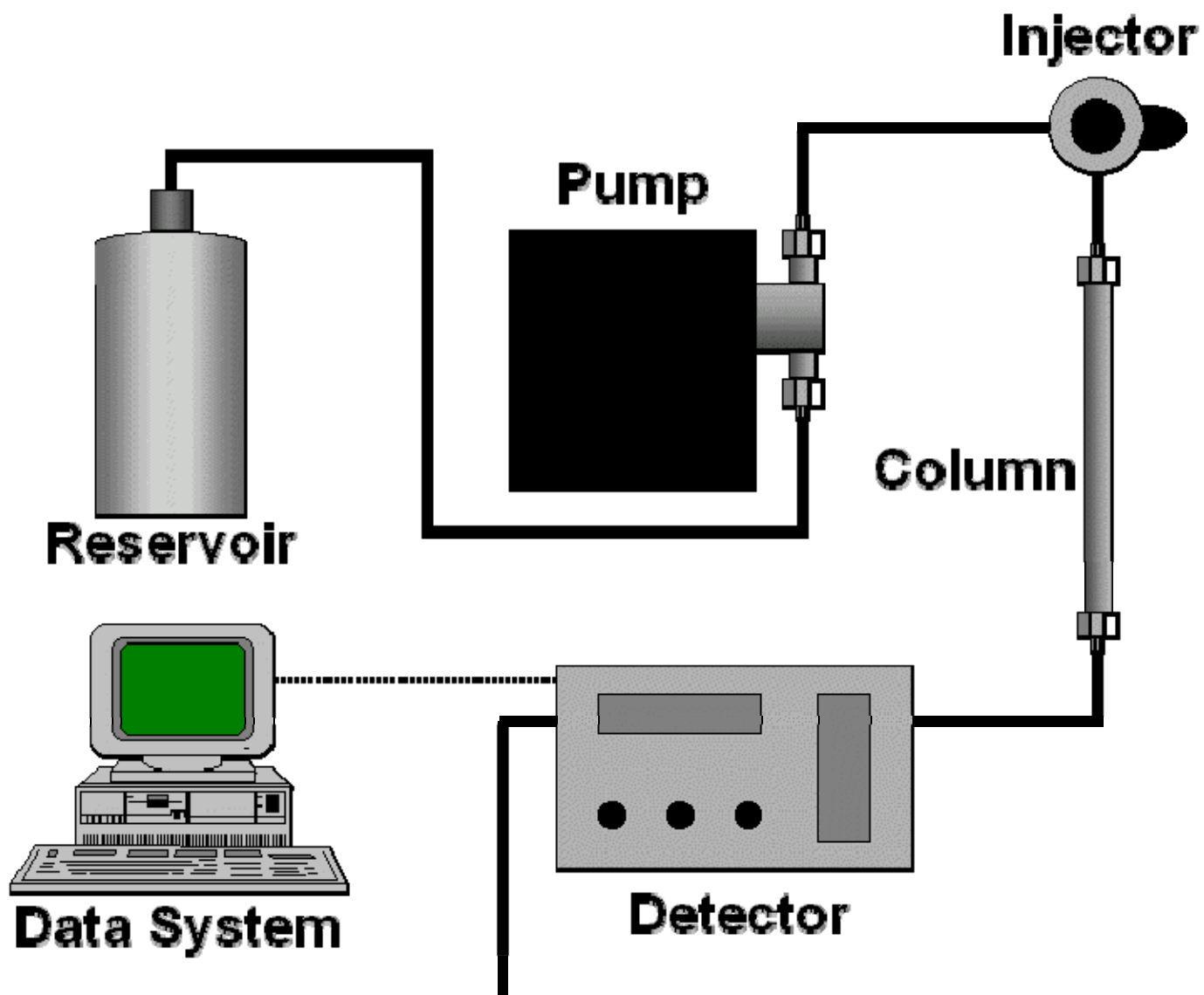
- Fragmentation rules not well-established
- No MS fragmentation libraries
- Limited resolution (but UPLC is an improvement)

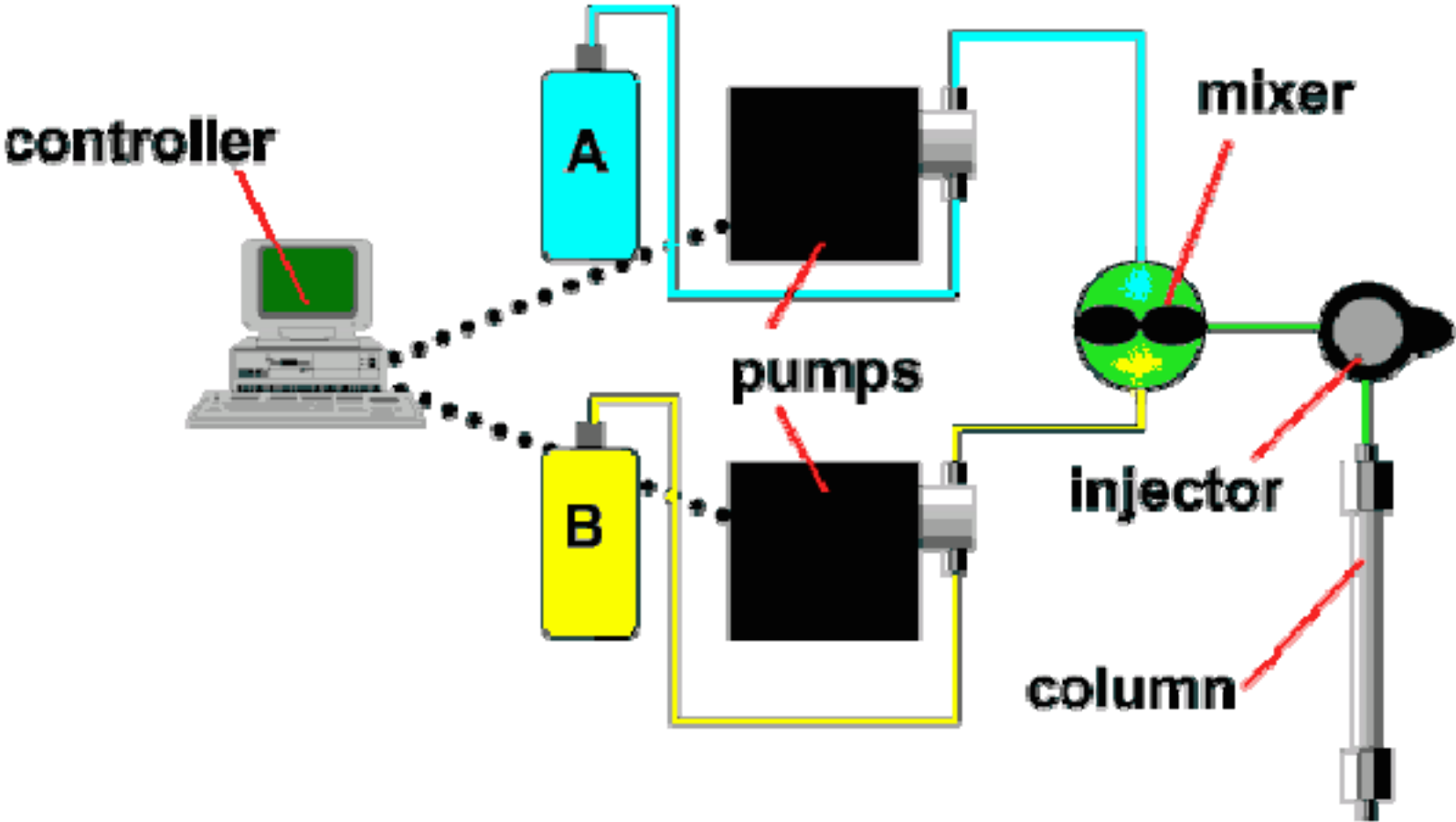


# HPLC

## high performance liquid chromatography

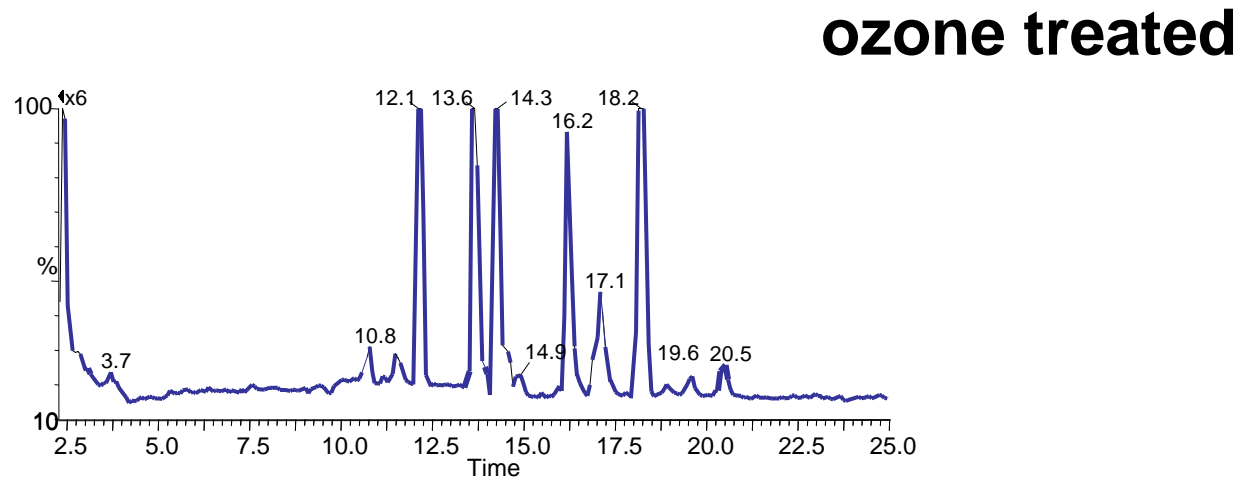
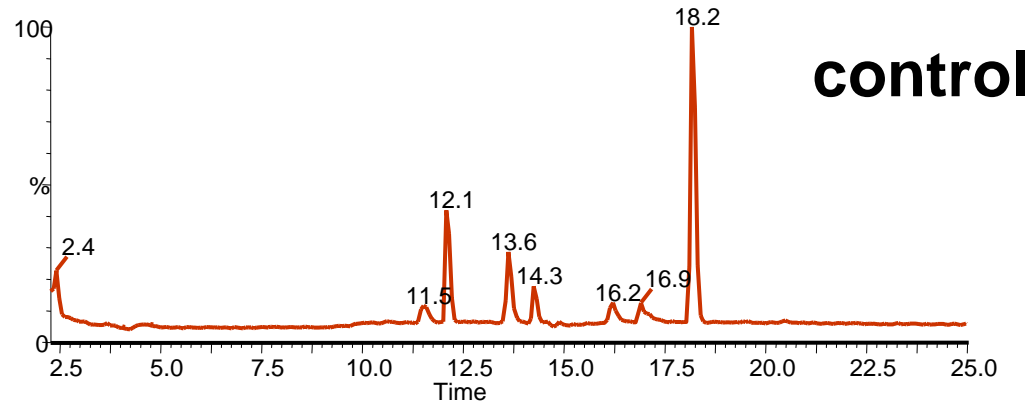








# Metabolic Fingerprinting – MS Analysis

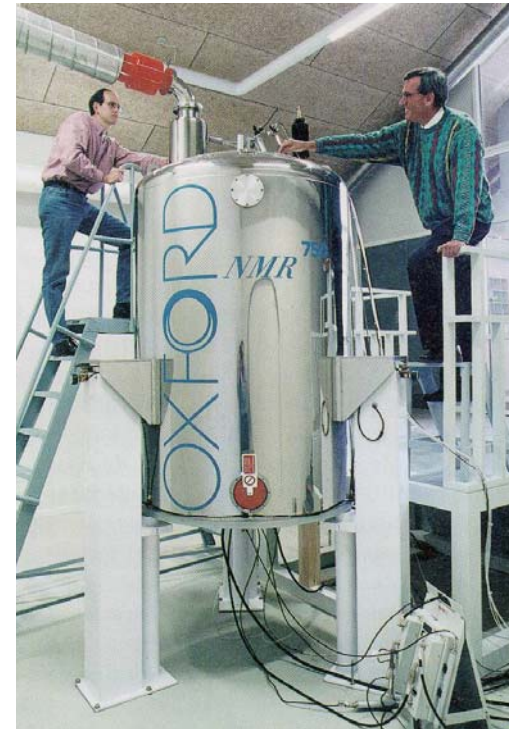


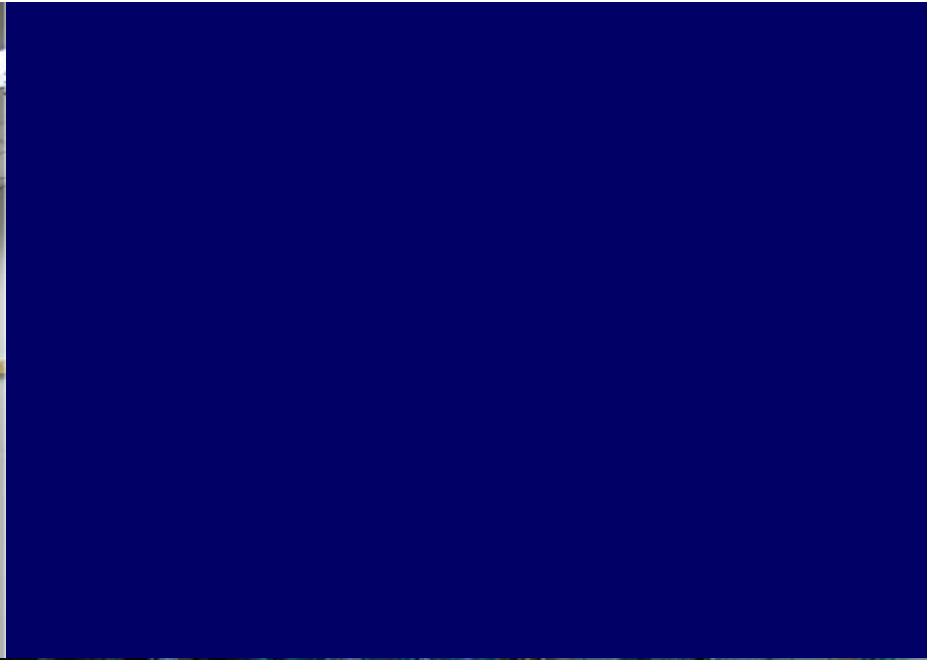
Online SPE-HPLC-TOF-MS analysis of 20  $\mu$ L bronchiolar alveolar lavage fluid



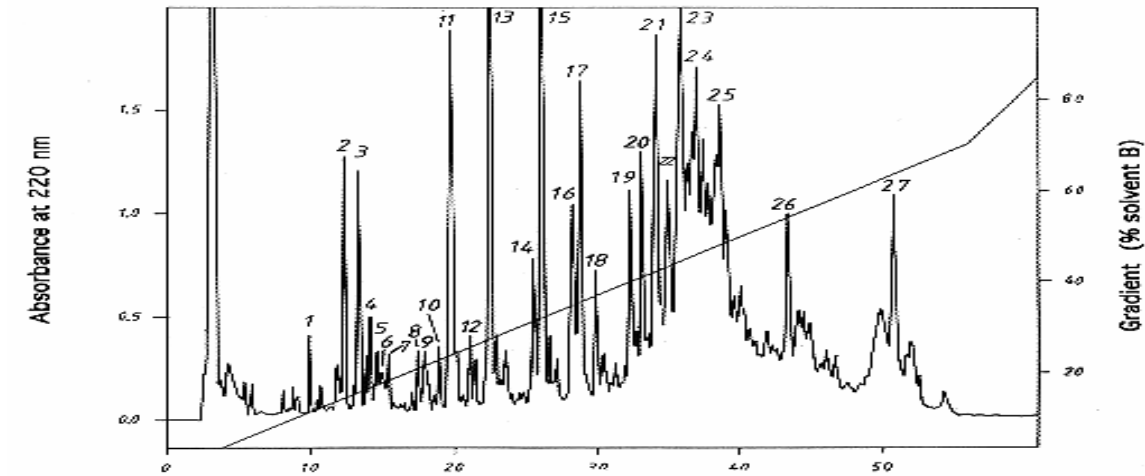
# NMR

- **Advantages**
  - No sample separation necessary
  - Essentially universal detector
  - Non-destructive
- **Disadvantages**
  - Low sensitivity
  - Results difficult to interpret
  - Decreased quantification
  - Expensive

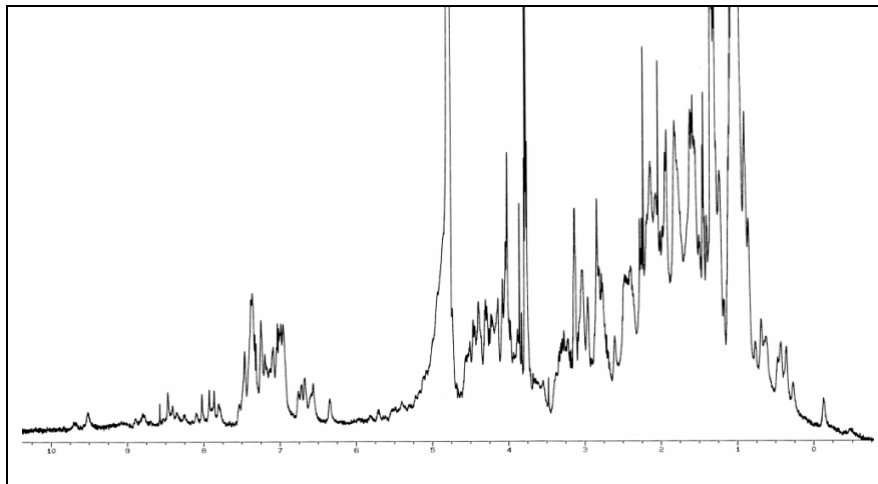




# Why NMR?



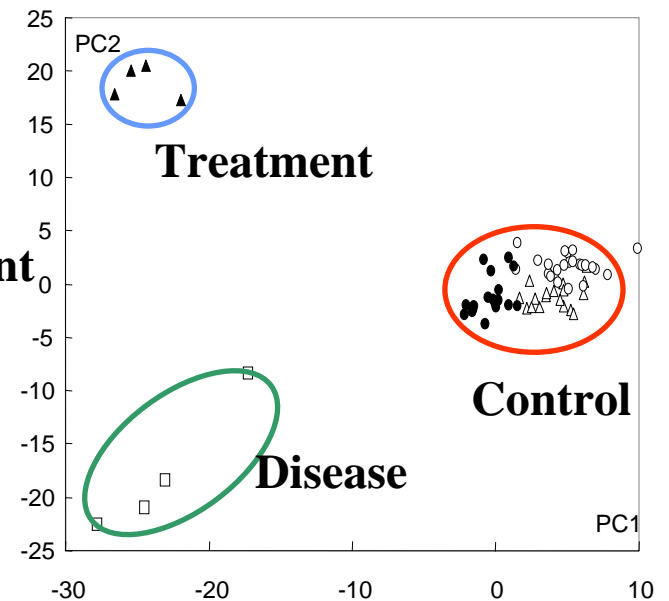
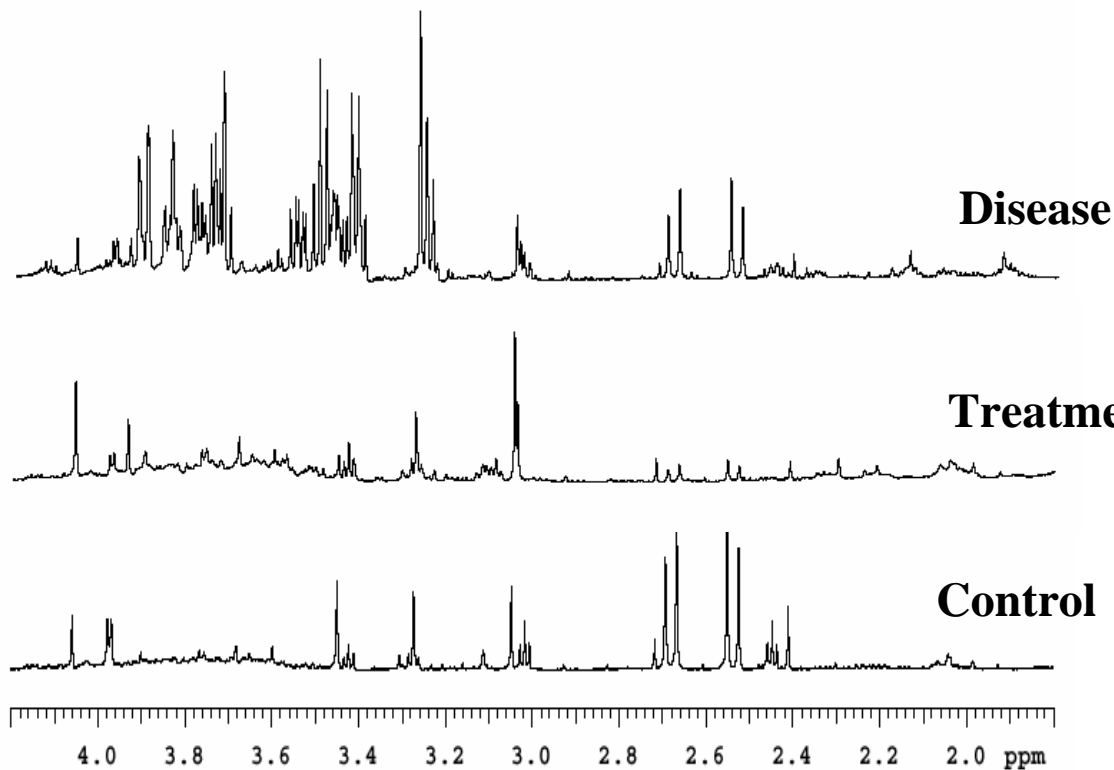
**Mixture separation  
by HPLC (followed  
by ID via Mass Spec)**



**Mixture separation  
by NMR (simultaneous  
separation & ID)**

**Chemical Shift  
Chromatography**

# NMR Metabolic Profiling and Drug Toxicology



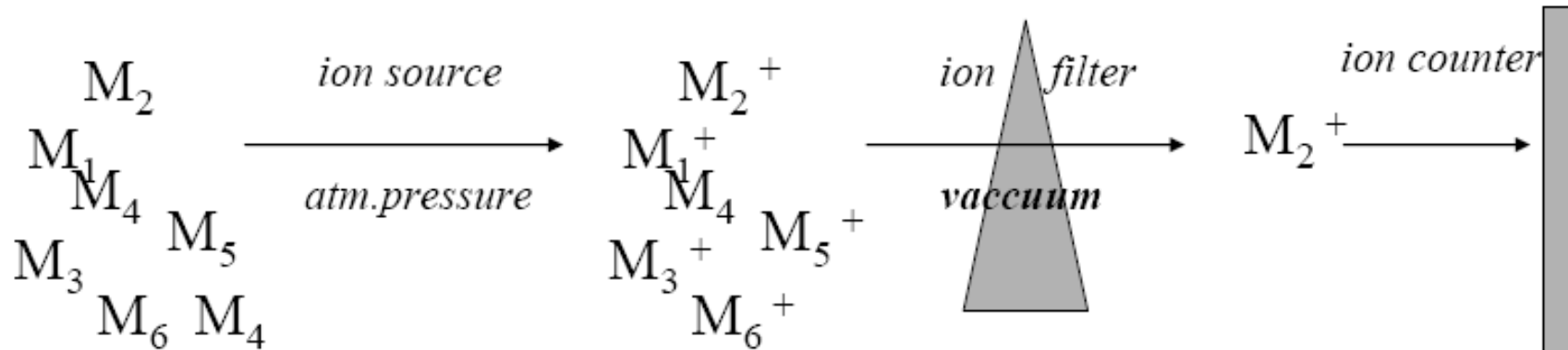
**Principal Component Analysis**

# Mass spectrometry

- *chemical analysis technique to measure the mass of molecules by ionizing, separating & detecting ions according to their mass-to-charge ratios.*
- *involves the study of ionized molecules in the gas phase with the aim of one or more of the following:*
  - **Molecular weight determination**
  - **Identify unknown compounds**
  - **Structural characterization**
  - **Qualitative and quantitative analysis of mixtures**
  - **Carbon dating**

- **What is ionization?**
- producing an electrically charged molecule from a neutral molecule by adding protons or removing electrons.
- **Why is ionization of sample required in mass spectrometry?**
- sample to be analyzed by mass spectrometry must be ionized to separate ions according to their mass-to-charge ratio
- **What is the "mass-to-charge" ratio of an ion?**
- The mass of the ion divided by the charge on the ion.
- The charges on an ion are always positive integers (1, 2, 3, ...).
- Charged ions are produced by ionization.
- Ions charged by adding a proton or by removing an electron.
- **For example:**
  - molecule  $C_2H_6$  with mass of  $(2 \times 12) + (6 \times 1) = 30$  Da.
  - can acquire a charge of 1 unit in 2 ways:
    - losing an electron (mass-to-charge ratio =  $30/1 = 30$ )
    - accepting a proton (mass-to-charge ratio =  $(30+1)/1 = 31$ )

# What is mass spectrometry????



# Ion sources used in metabolomics

## HPLC

ESI – electrospray ionization (Nobel prize in 2002)

API – atmospheric pressure ionization

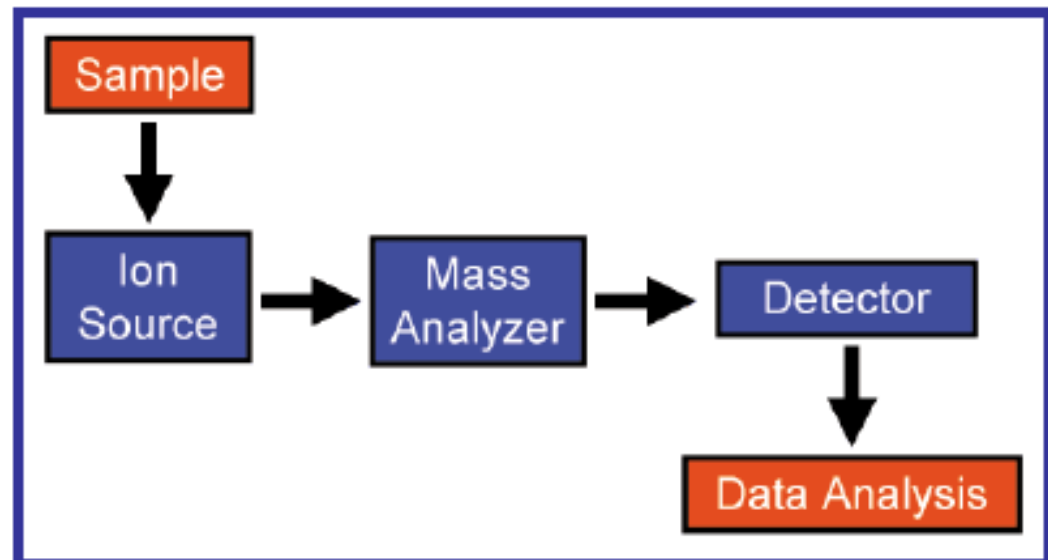
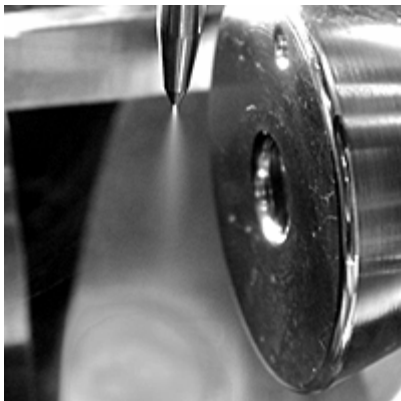
MALDI – matrix-assisted laser desorption ionization

ICP – inductively coupled plasma

## GC

EI – electron impact ionization

CI – chemical ionization

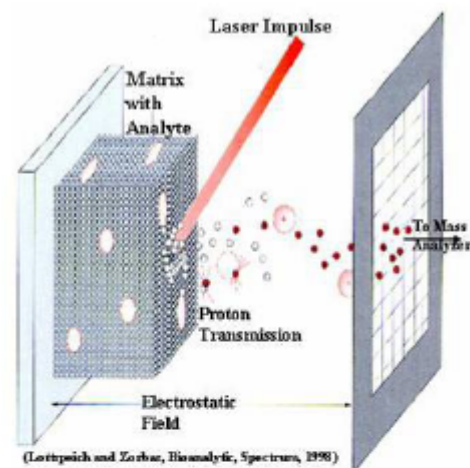




# Three most common types of ionization

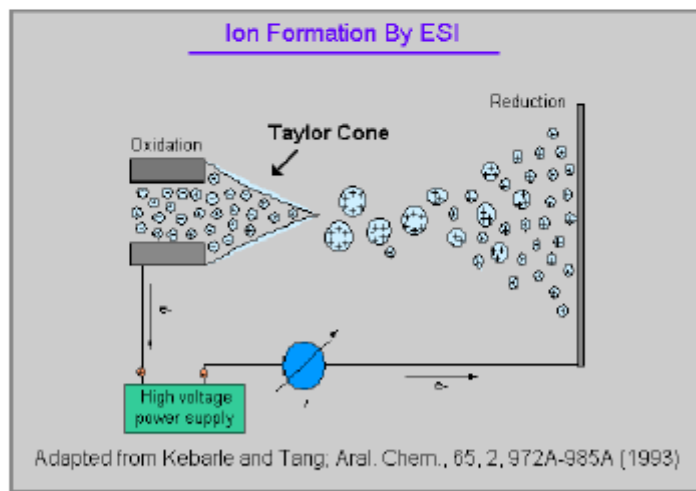
## MALDI-MS

Matrix Assisted Laser  
Desorption Ionization



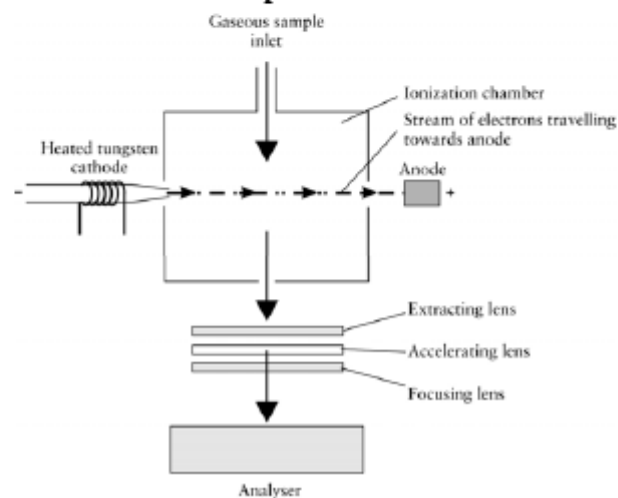
## LC/ESI-MS

Electrospray Ionization



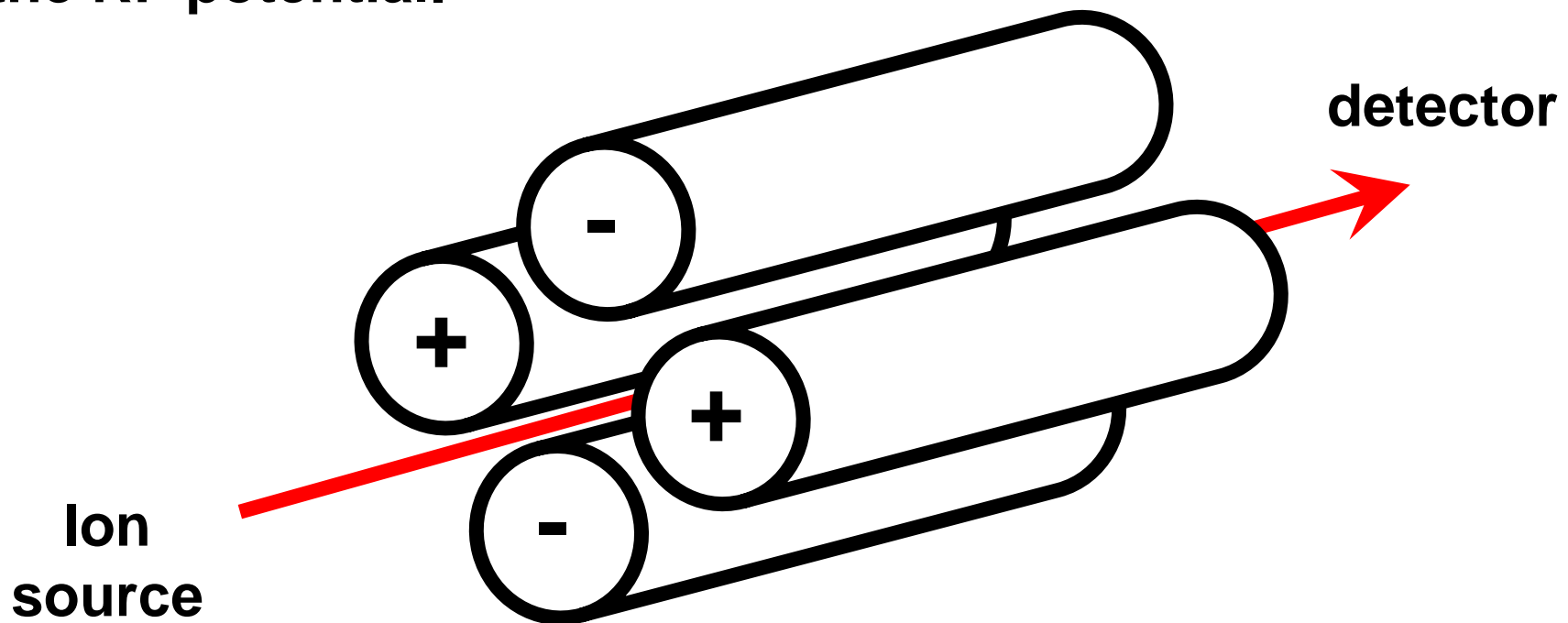
## GC/EI-MS

Electron Impact Ionization

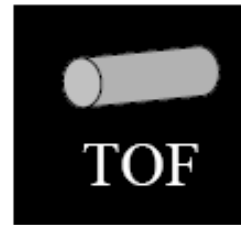
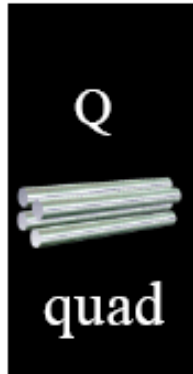


# The basic unit of mass filtering is a quadrupole

- The quadrupoles are 4 parallel rods controlled by DC voltage & an RF potential.
- Ions with specific  $m/z$  ratios separated by controlling the RF potential.



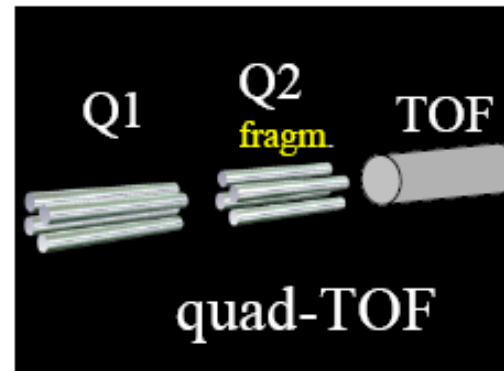
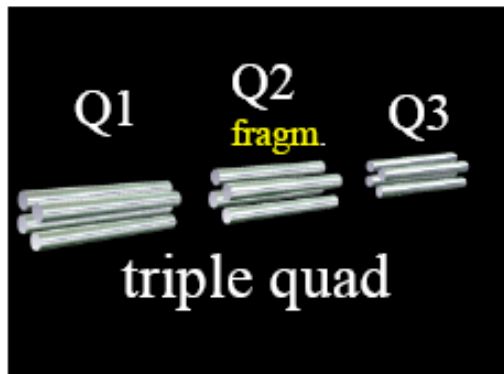
# Types of Mass Spectrometers (‘ ion separators ‘)



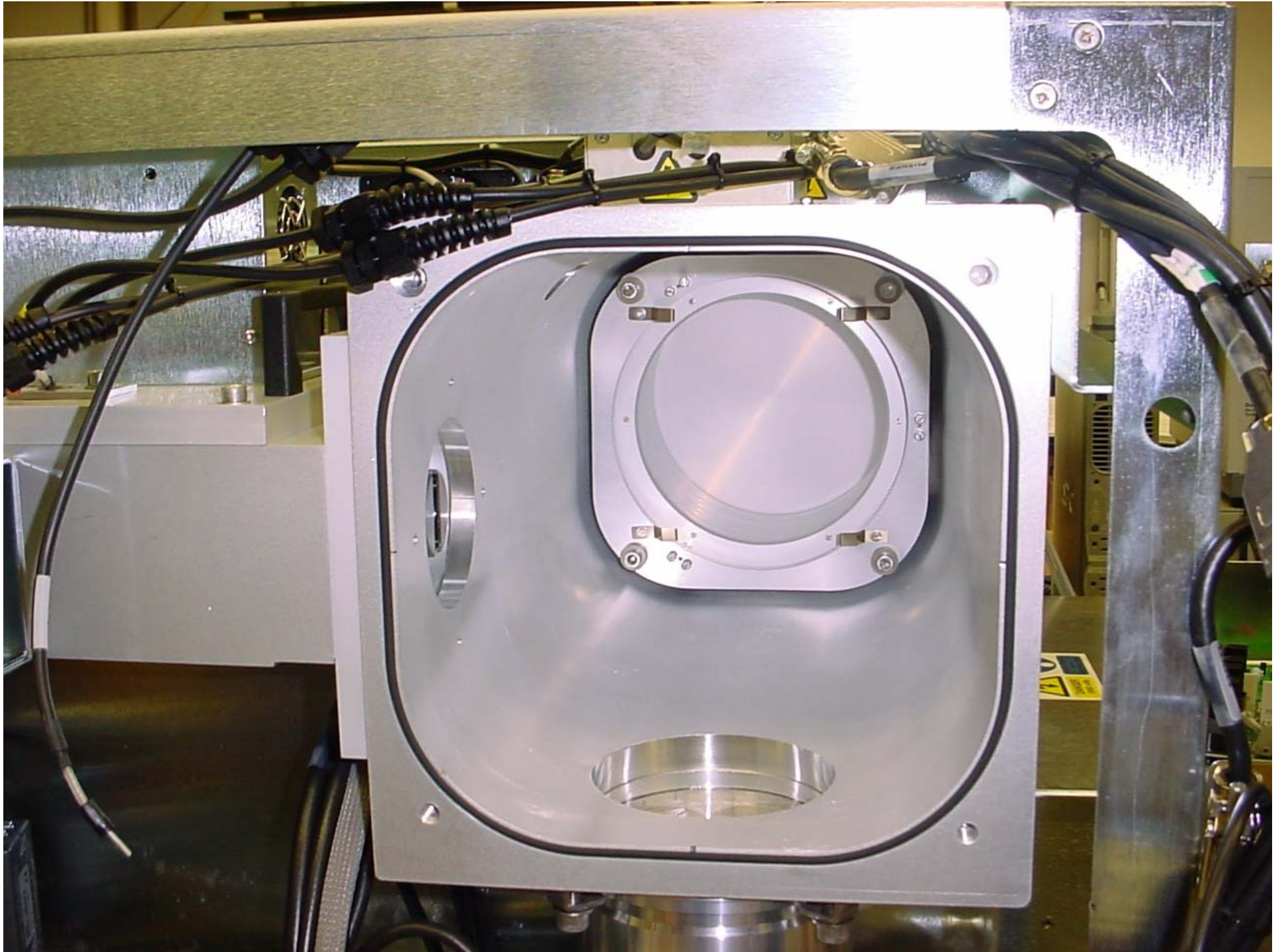
mostly without MS/MS fragmentation

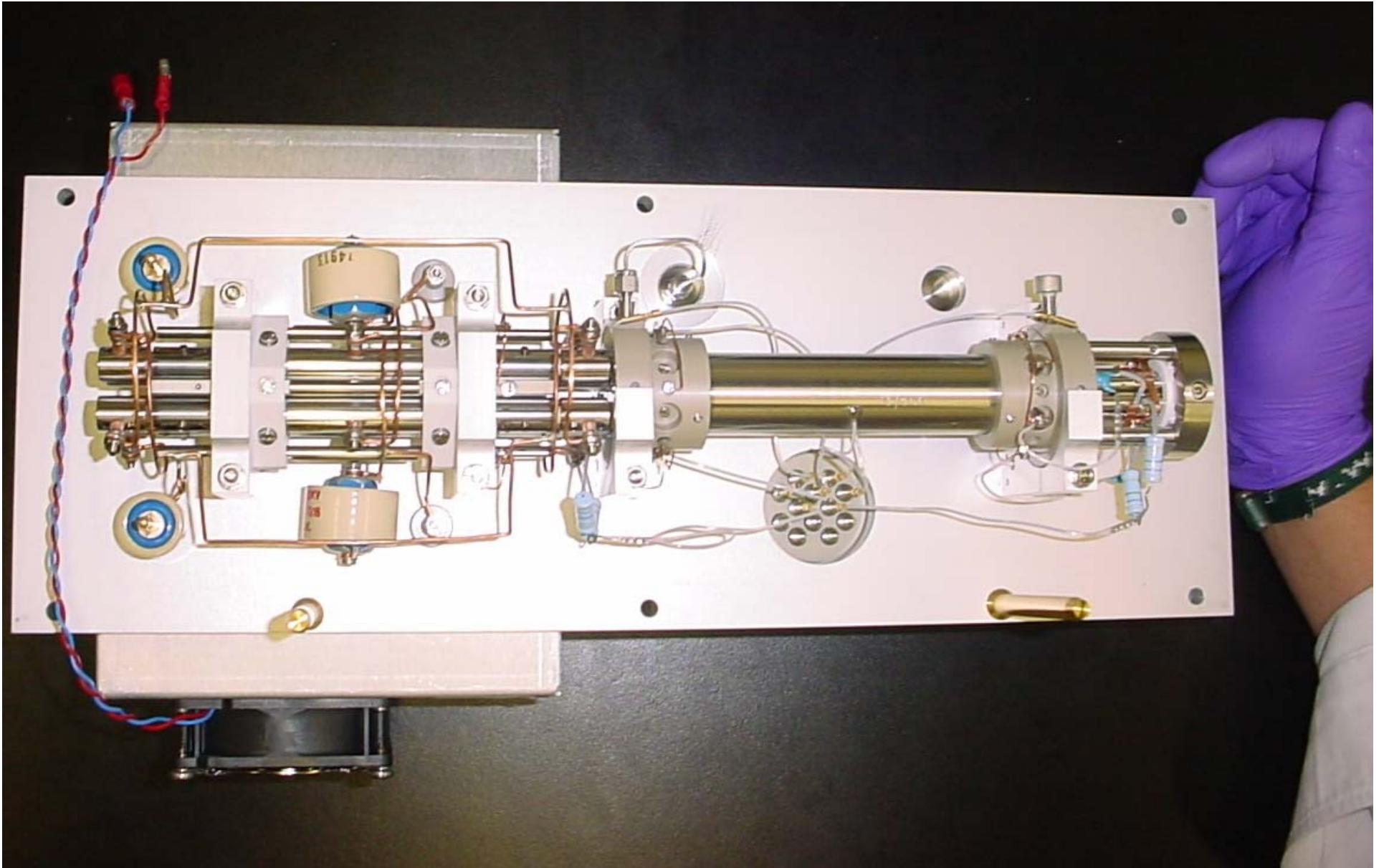
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mostly with MS/MS fragmentation





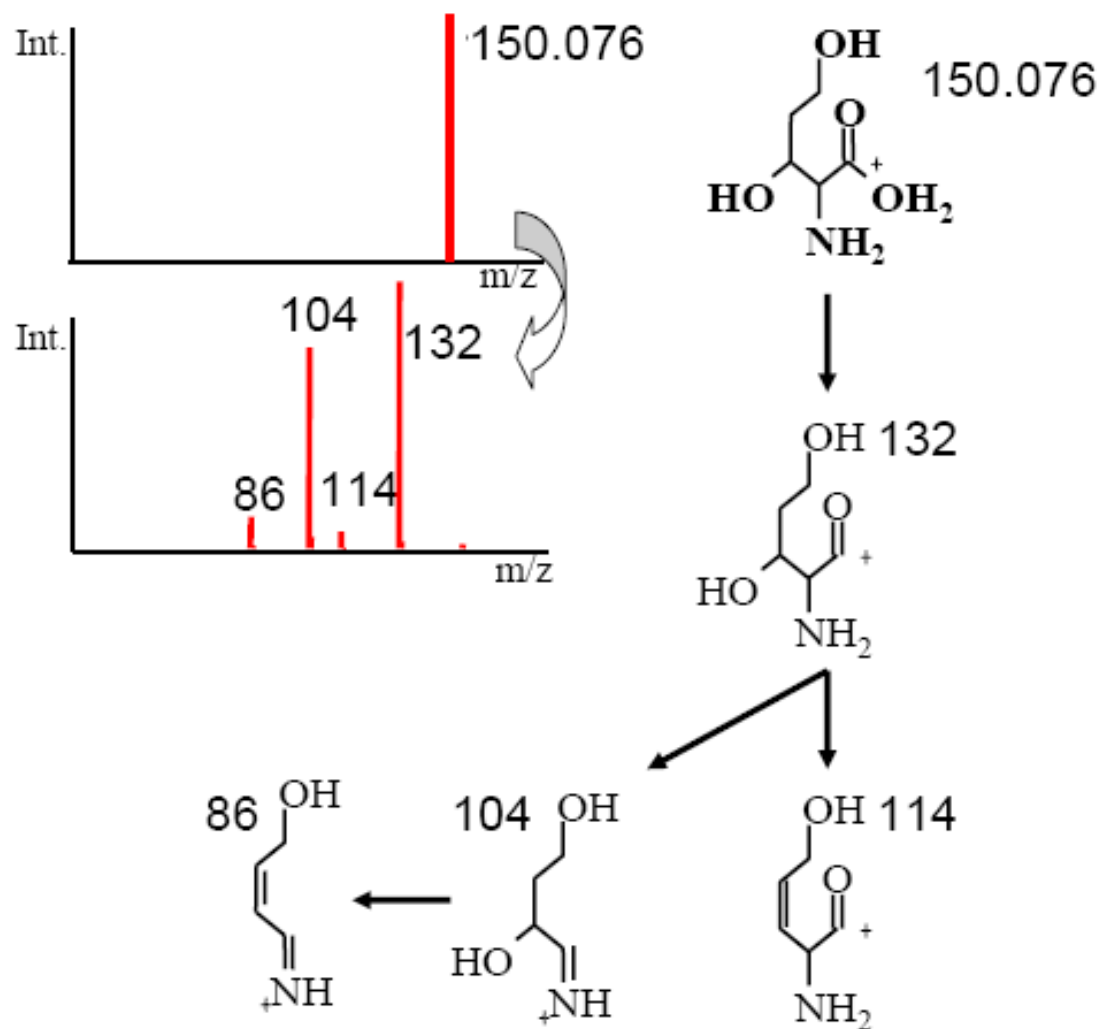




## Qualitative analytical biochemistry: metabolite identification in LC/MS

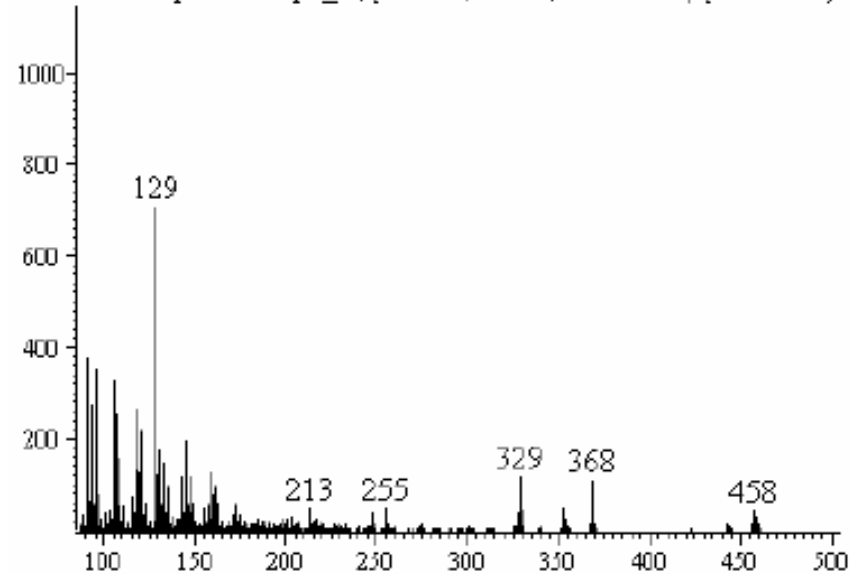
### MS/MS

(ion trap, Q3,  
ICR, QTOF)

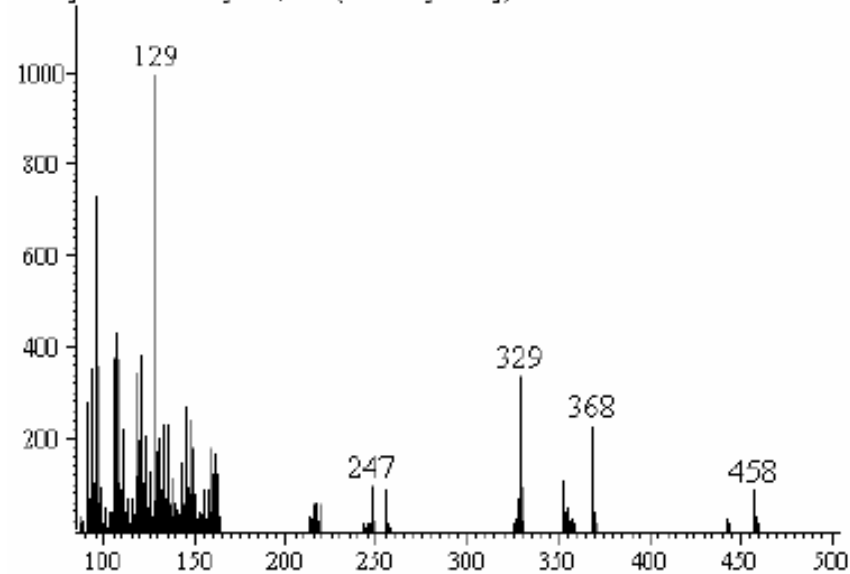


# Qualitative analytical biochemistry: metabolite identification in GC/MS

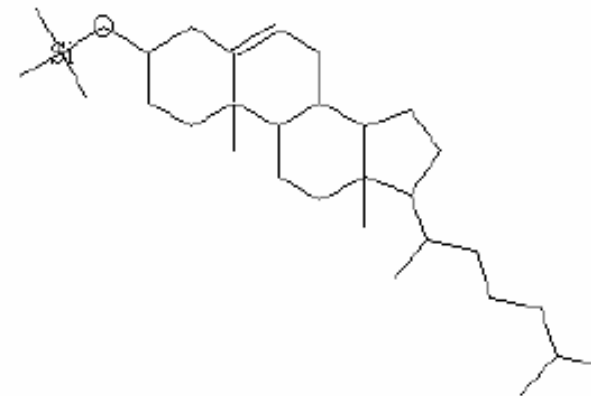
Peak True - sample "2287eq01\_1", peak 131, at 1186,33 seconds (Spec # 17124)



Library Hit - similarity 873, "3-(Trimethylsiloxy)cholest-5-ene"



cholesterol TMS  
mw=458 Da

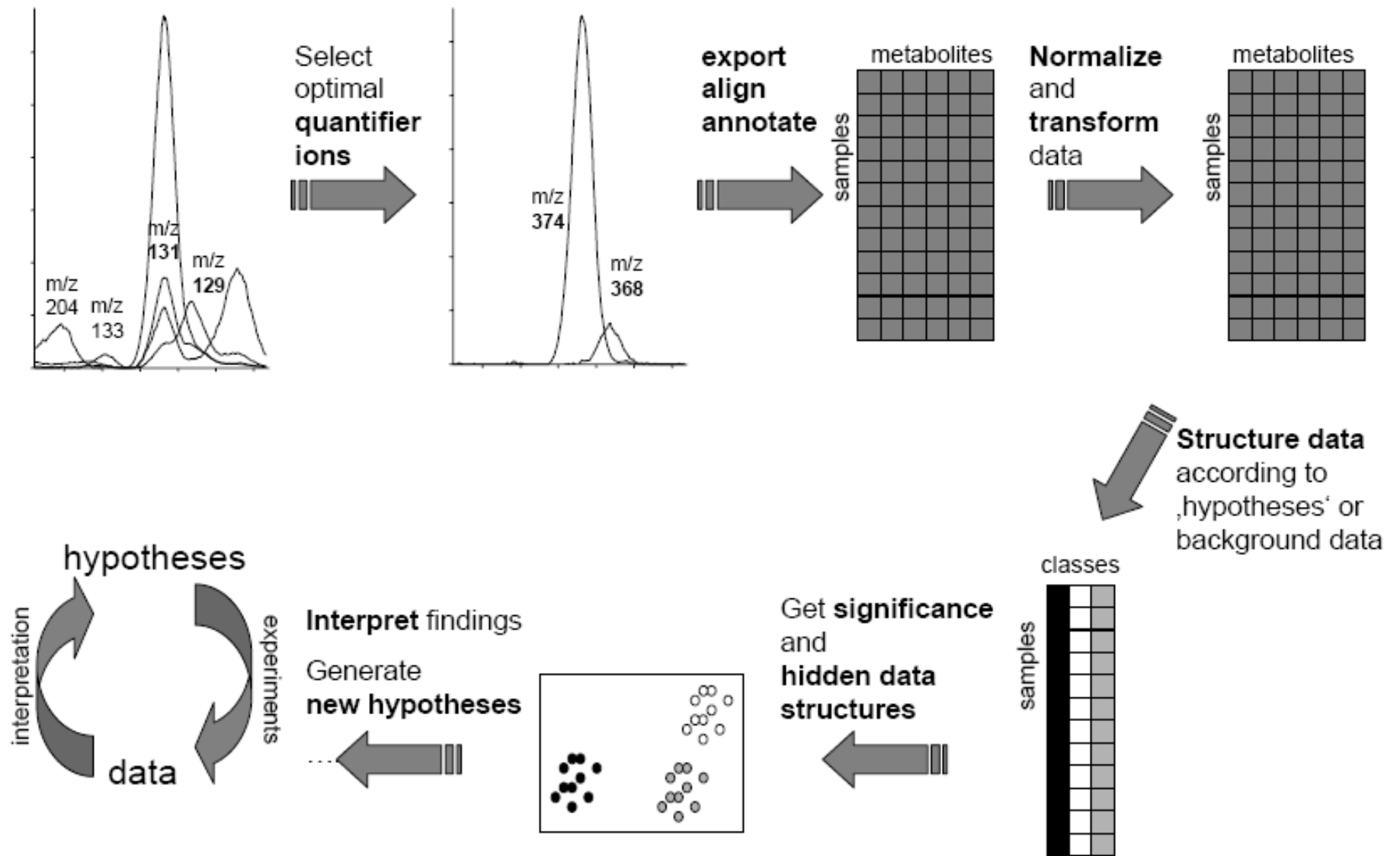




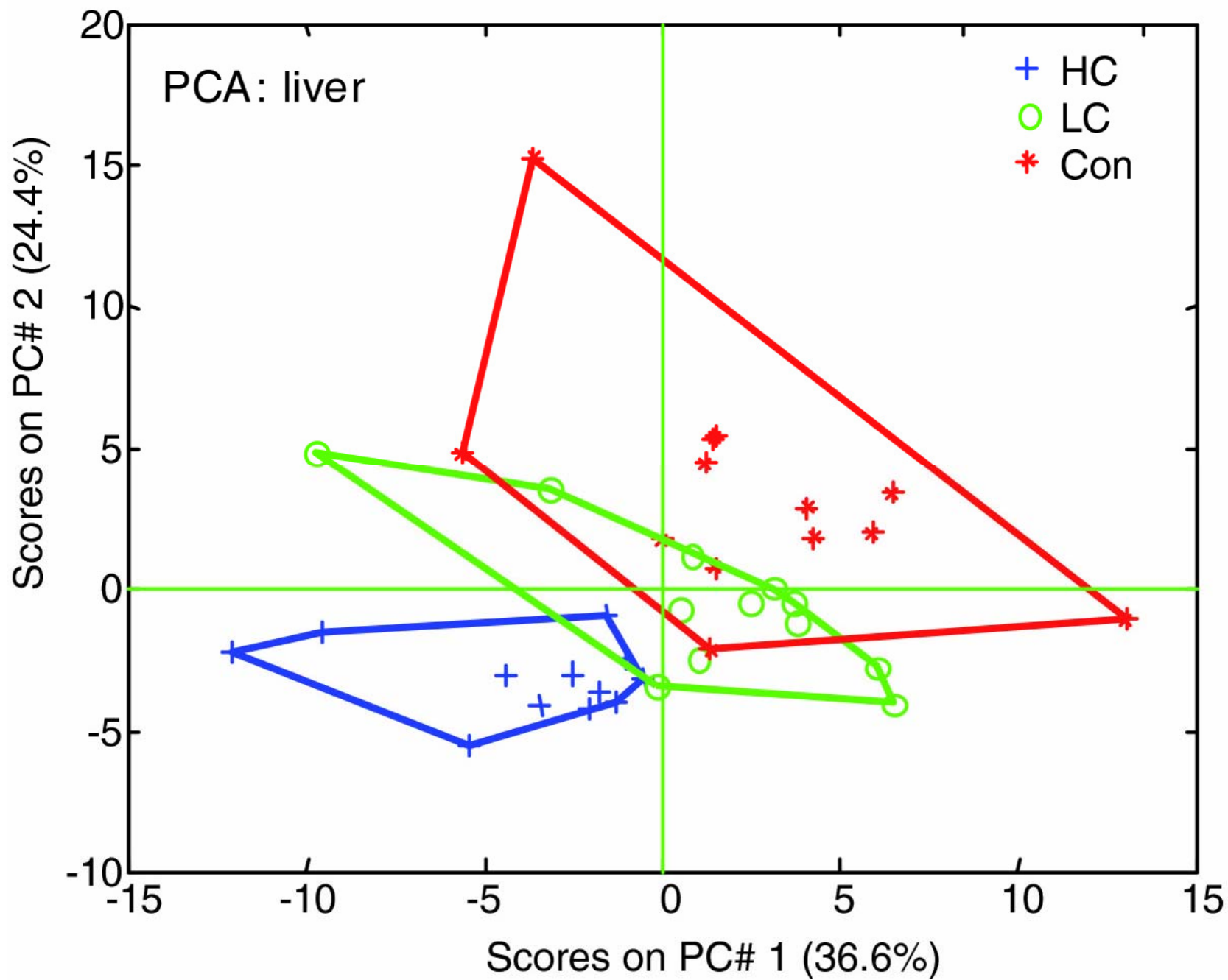
# Metabolomics experimental design

- **If classification is most important aim, get as many samples as possible & run fingerprints!**
- **If you have no clue what to expect, combine GC/MS, LC/MS and 2D-NMR data**
- **IF you have valid hypotheses in mind, use metabolite profiling (e.g. lipidomics)**
- **Use more than one statistical tool to be certain**
- **Biological variance has different sources, but is usually larger than analytical error**
- **Metabolomics is suggestive of phenotype**

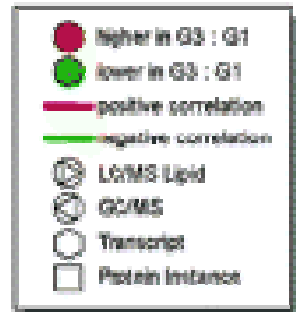
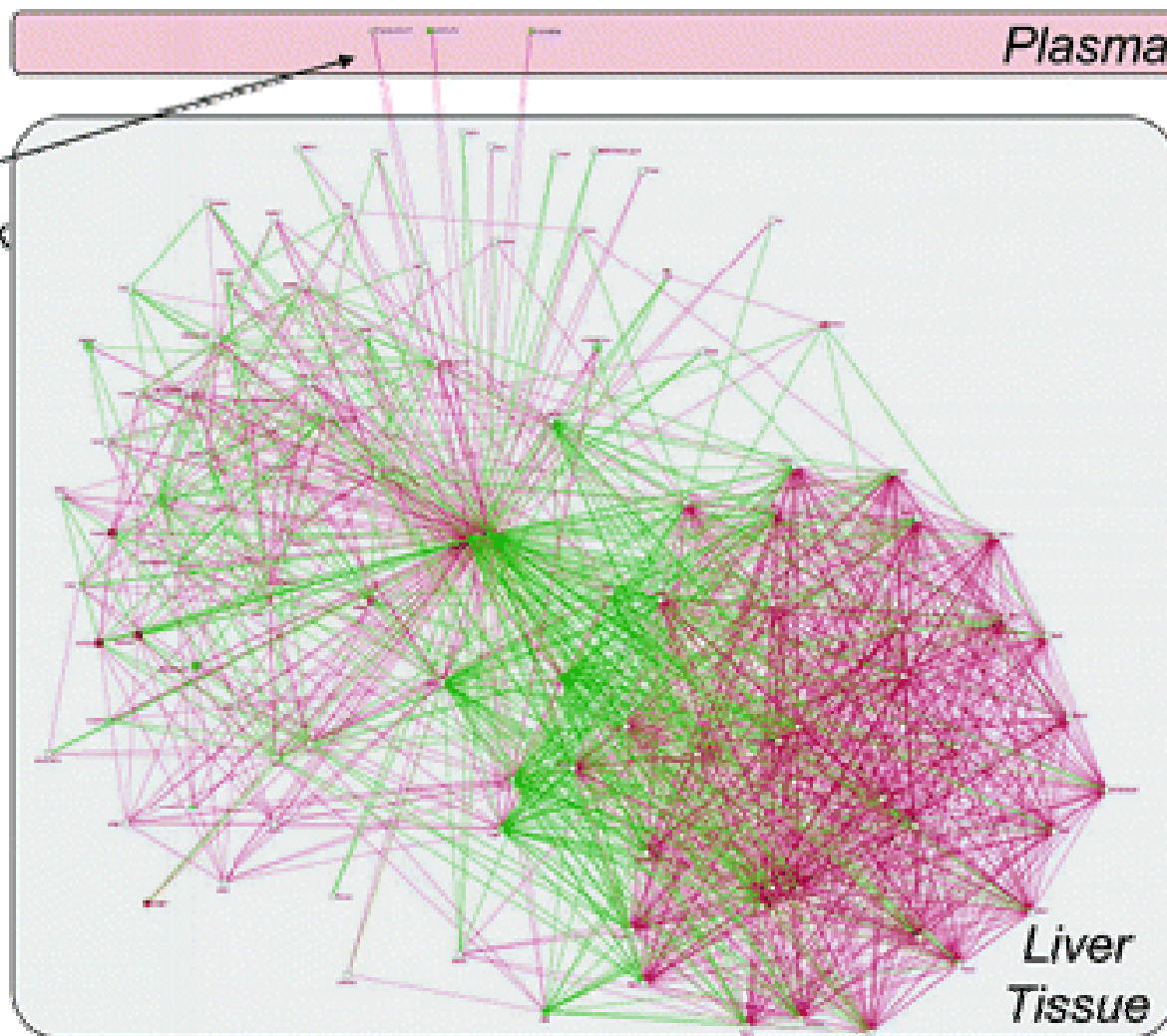
# Metabolomic experiment flowchart



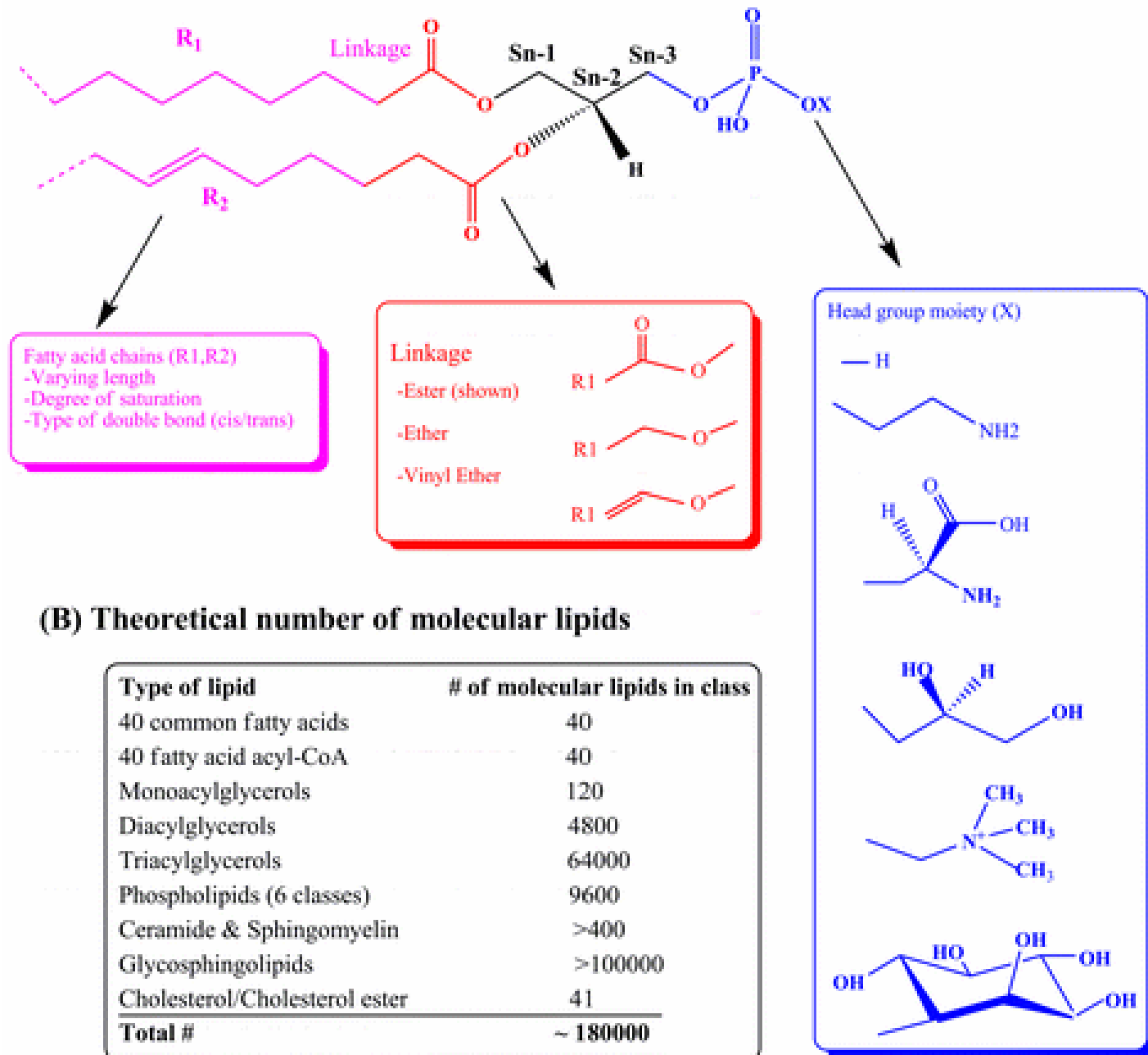
Scores for PC# 1 versus PC# 2



C23:0 SPM,  
C20:3 TG,  
GC/MS peak

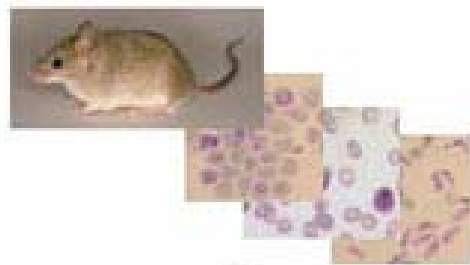


## (A) Glycerophospholipid Structure



## (B) Theoretical number of molecular lipids

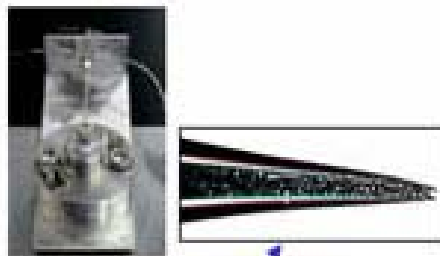
Type of lipid	# of molecular lipids in class
40 common fatty acids	40
40 fatty acid acyl-CoA	40
Monoacylglycerols	120
Diacylglycerols	4800
Triacylglycerols	64000
Phospholipids (6 classes)	9600
Ceramide & Sphingomyelin	>400
Glycosphingolipids	>100000
Cholesterol/Cholesterol ester	41
<b>Total #</b>	<b>~ 180000</b>



Extraction of metabolites



Selective enrichment using various StageTips

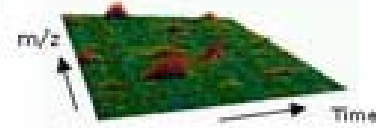


nanoLC-MS with Arch-stone columns

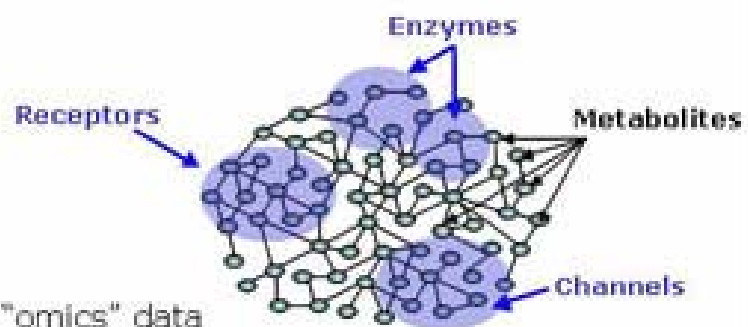
Raw data

Transcriptome

Proteome



Data management system

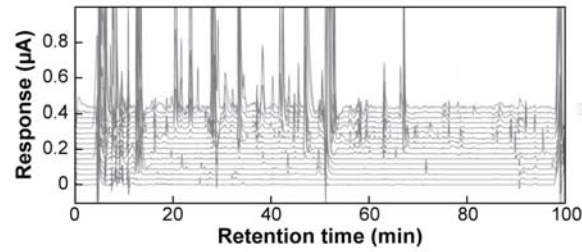


Mapping all "omics" data

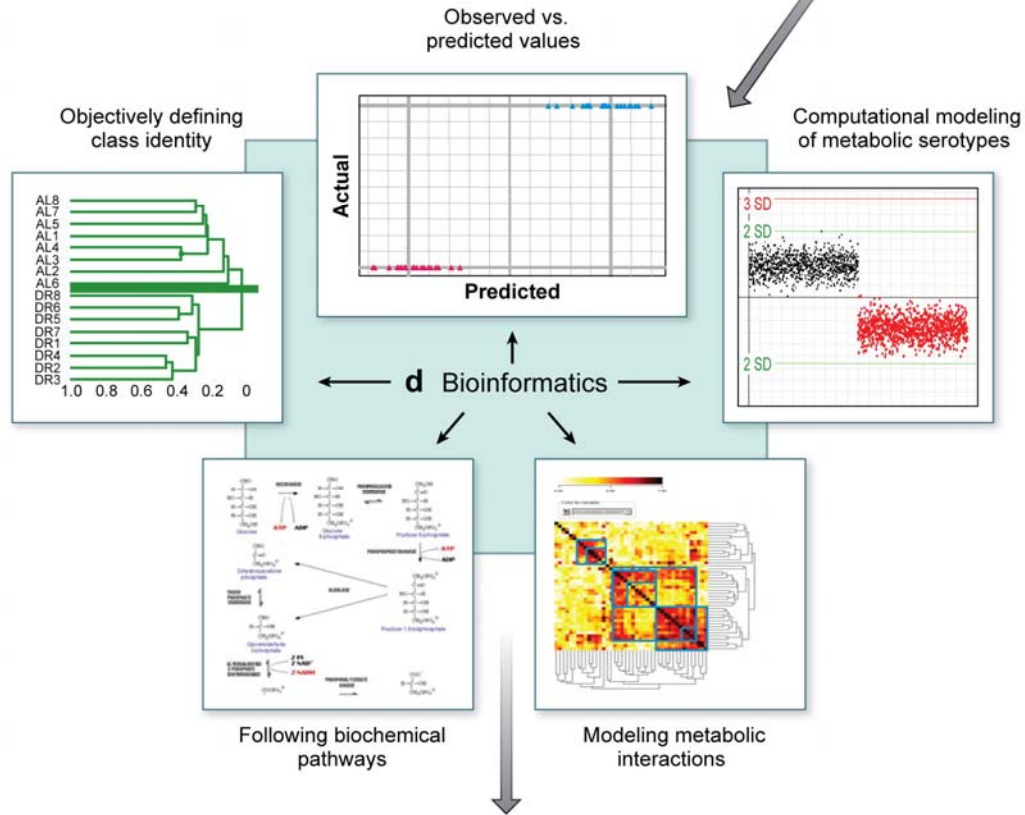
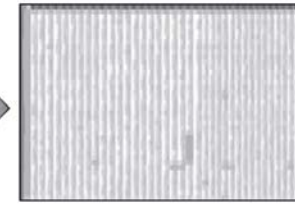
**a** Sample collection



**b** Sample analysis



**c** Database curation



- Mechanistic insight
- Drug development
- Toxicology
- Classification
- Prediction
- Functional genomics
- Sub-threshold studies
- Others

# Metabolic Profiling: The Possibilities

- Toxicology Testing
- Clinical Trial Testing
- Fermentation Monitoring
- Food & Beverage Tests
- Nutraceutical Analysis
- Drug Phenotyping
- Water Quality Testing
- Petrochemical Analysis
- Genetic Disease Tests
- Nutritional Analysis
- Clinical Blood Analysis
- Clinical Urinalysis
- Cholesterol Testing
- Drug Compliance
- Dialysis Monitoring
- Forensics



# Human Metabolome Database

The screenshot shows the Human Metabolite Database (HMDB) website. The browser window is titled "Metabolomics Toolbox - Netscape". The website header includes "Metabolomics Toolbox" and navigation links: "About Us", "Project Info", "News & Events", "Related Links", and "Metabolite Database". A search bar is present in the top right. The main content area is titled "Metabolite Database" and "Human Metabolite Browser". A sidebar on the left provides a description of the database and lists tools like "Metabolite Search", "Data Extractor", "Chemical Query", and "BLAST Search". The main content area shows a table of metabolites, sorted by common name. The first entry is (R)-3-Hydroxybutyric acid, with CAS Registry number 625-72-9, chemical formula C<sub>4</sub>H<sub>8</sub>O<sub>3</sub>, and molecular weight 104.1045. The table is sorted by common name in ascending order, displaying 20 items per page. The page number is 1 of 10.

Metabolite Database

The Human Metabolite Database acts as an electronic repository for identifying, quantifying, and characterizing small molecule metabolites.

In total there are an estimated 1400 endogenous metabolites that can be found in urine, blood, CSF and white blood cells at concentrations greater than 1 micromolar.

Metabolite Database

Metabolite Search

Data Extractor

Chemical Query

BLAST Search

Human Metabolite Browser

Sorted By Common Name

Sort By: Common Name Ascending Display: 20

Page 1 of 10: 1 2 3 4 5 6 7 8 9 10

CAS REGISTRY	COMMON NAME	CHEMICAL NAME	MOLECULAR FORMULA	MOLECULAR WEIGHT
625-72-9 MetaboCard	(R)-3-Hydroxybutyric acid	(R)-3-Hydroxybutyric acid	C <sub>4</sub> H <sub>8</sub> O <sub>3</sub>	104.1045

www.hmdb.ca

# More than one method needed for metabolomics

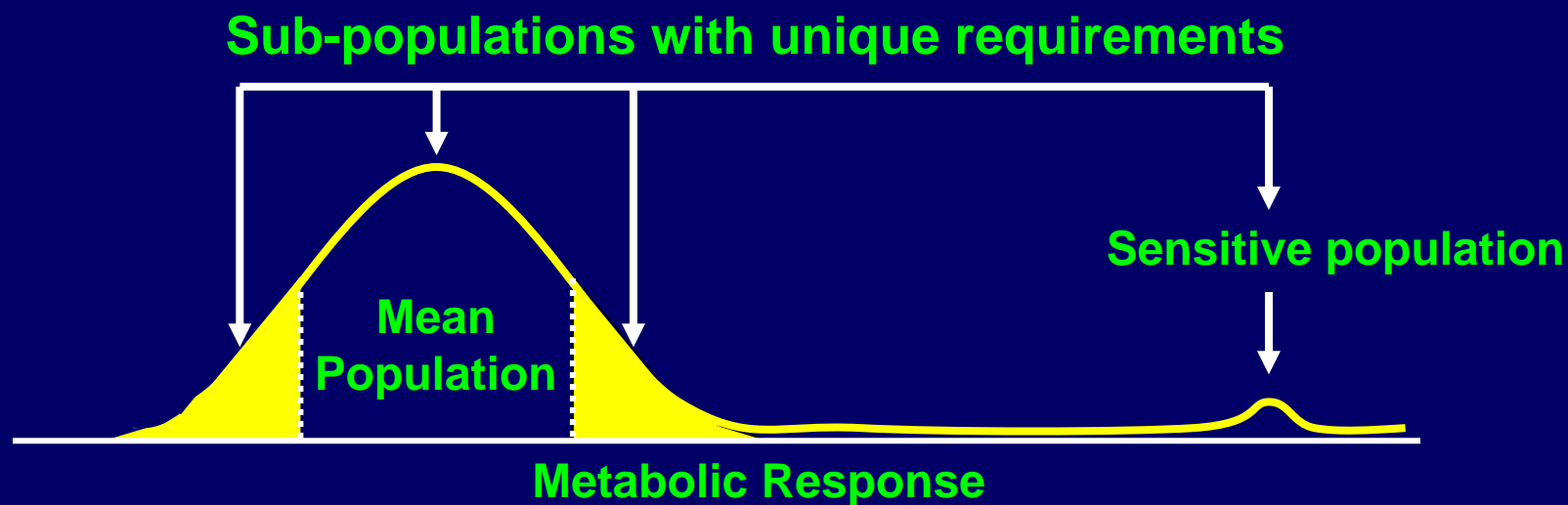
- **NMR or MS fingerprinting**
  - **Very robust, 500-10,000 variables**  
**high-throughput**  
**5-50 identified compounds**
- **GC/MS**
  - **Robust, ~500-1000 primary metabolites <550 Da**  
**high-throughput**  
**50-200 identified compounds**
- **LC/MS**
  - **Not as robust, ~50-70 secondary metabolites <2500 Da**  
**low-throughput**  
**20-100 identified compounds**

- **Exciting methodology that can provide quantitative phenotyping**
- **Important step in the omics cascade**
- **Leads to personalized medicine**

# What is the pay off from metabolomics?

Mechanistic Insight into Biological Processes

A Step Towards Personalized Medicine



**We are not all the same!**



***And we do not want to be the same!!!!***



*Sports Illustrated 2002*

**Thank you for your attention**



