

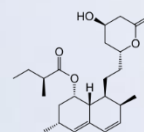
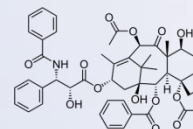
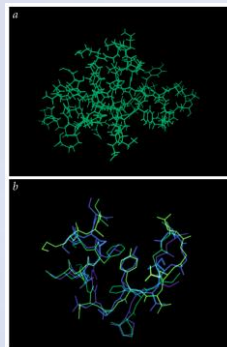
# NMR Hands On

UAB Metabolomics Training Course  
July 17-21, 2017

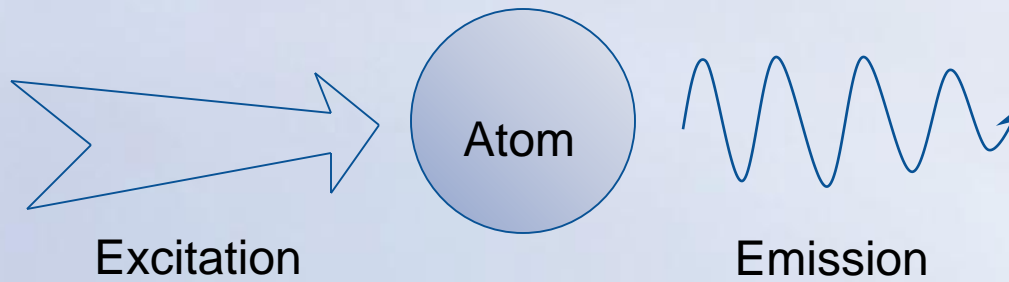
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NIH Eastern Regional Comprehensive Metabolomics Resource Core  
(ERCMRC)  
Department of Nutrition – Nutrition Research Institute  
University of North Carolina at Chapel Hill

# Nuclear Magnetic Resonance (NMR) Spectroscopy

- Detects NMR active nuclei
- Robust and highly reproducible
- Non-destructive
- Quantitative
- Used in
  - Structure elucidation
    - Small molecules
    - Macromolecules (DNA, RNA, Proteins)
  - A number of techniques
    - 1D , 2D, 3D
  - Molecular motion and dynamics
- Similar method used in Imaging (MRI, fMRI)



# NMR Spectroscopy



# NMR Frequencies

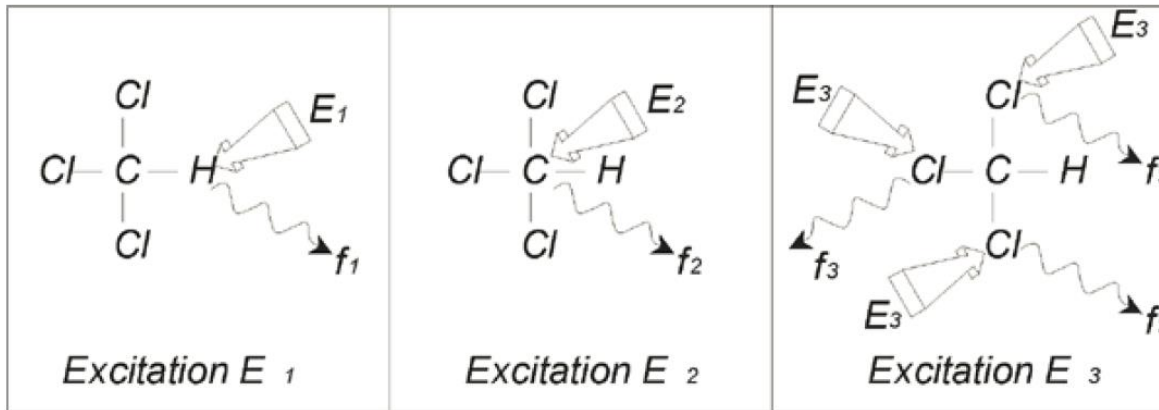


Figure 3.3: NMR Analysis of  $\text{CHCl}_3$

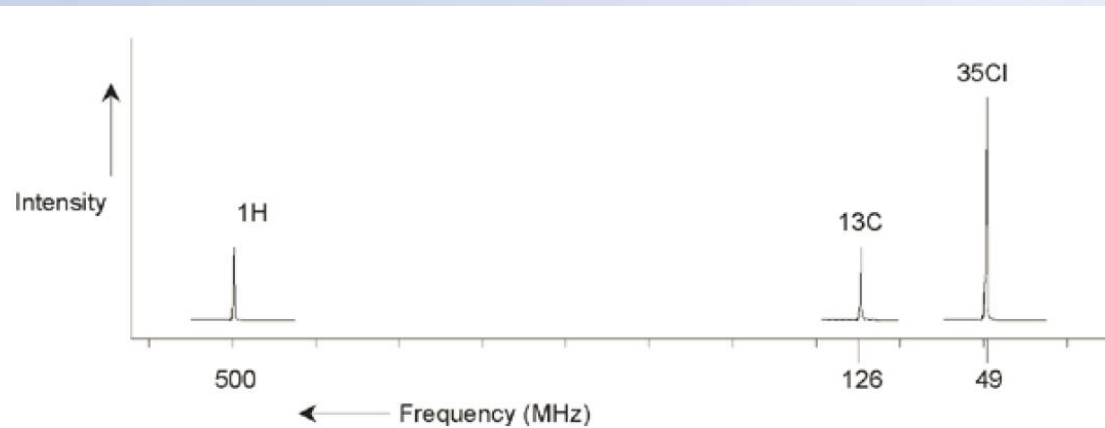


Figure 3.4: NMR Signals Emitted by  $\text{CHCl}_3$

# NMR Spectroscopy

Frequencies in 11.7T magnet

Nucleus	Basic Frequency (MHz)	Natural Abundance (%)
$^1\text{H}$	500	100
$^2\text{H}$	77	0.015
$^3\text{H}$	533	0.005
$^{13}\text{C}$	126	1.11
$^{35}\text{Cl}$	49	75.53
$^{37}\text{Cl}$	41	24.47
$^{15}\text{N}$	50	0.37
$^{19}\text{F}$	470	100
$^{31}\text{P}$	202.5	100
$^{57}\text{Fe}$	16.25	2.20

AVANCE Beginners User Guide 004 (Bruker, Germany)

NMR Spectroscopy Explained : Simplified Theory, Applications and Examples for Organic Chemistry and Structural Biology: Neil E Jacobsen, John Wiley & Sons, Inc. 2007, ISBN 978-0-471-73096-5

# NMR Spectrometer

## NMR Console

Computer



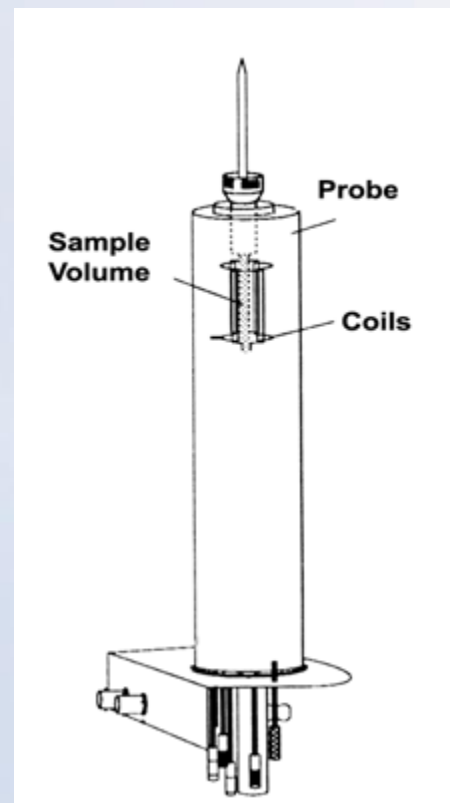
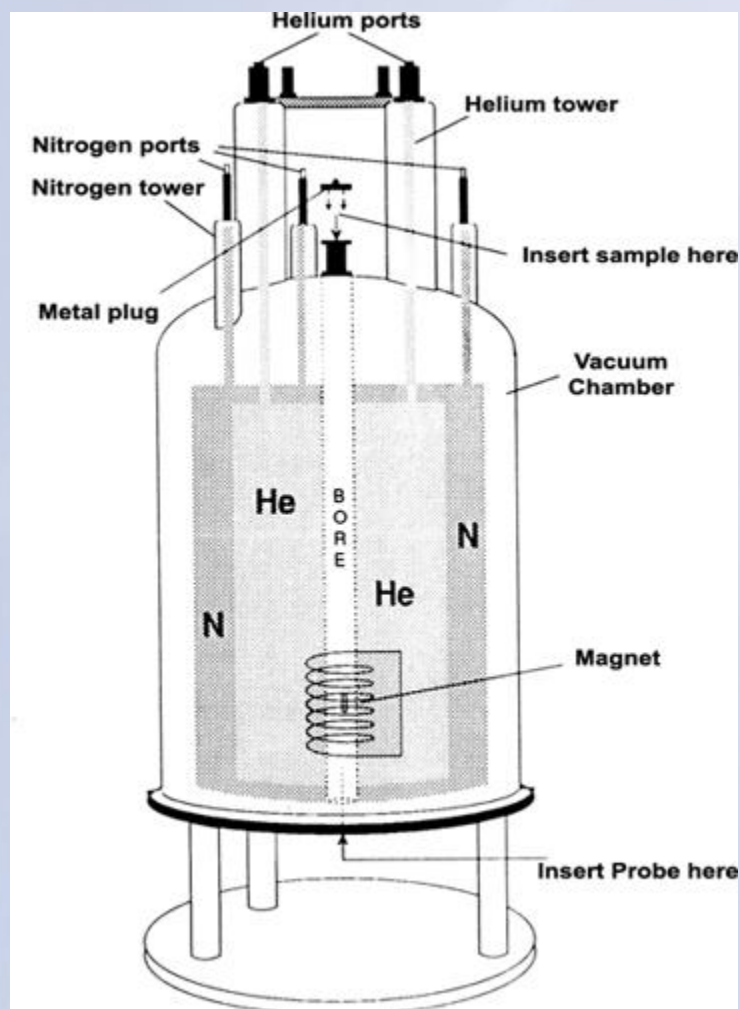
Magnet

Pre-amplifier



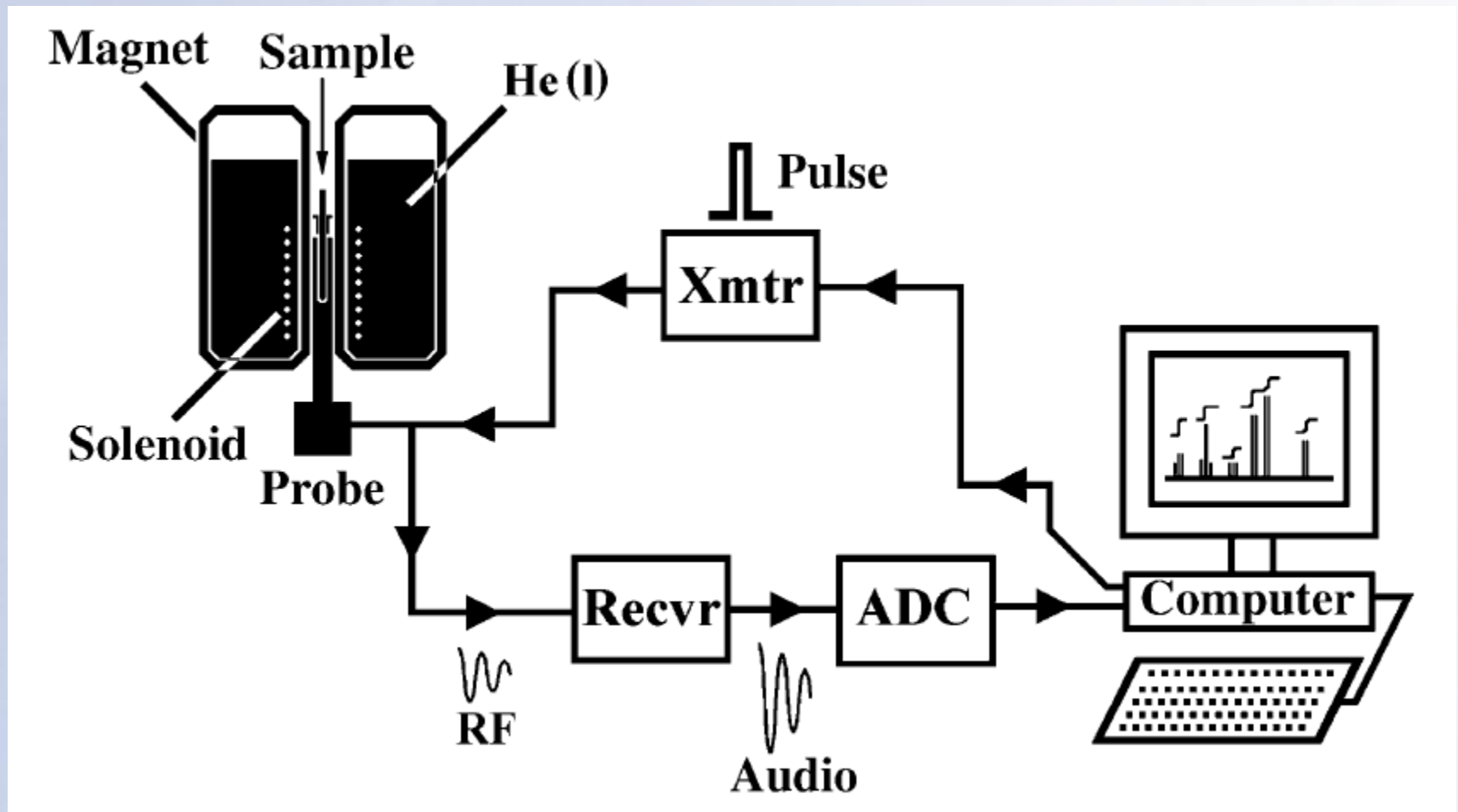
Probe and shim system

# NMR Magnet and the probe



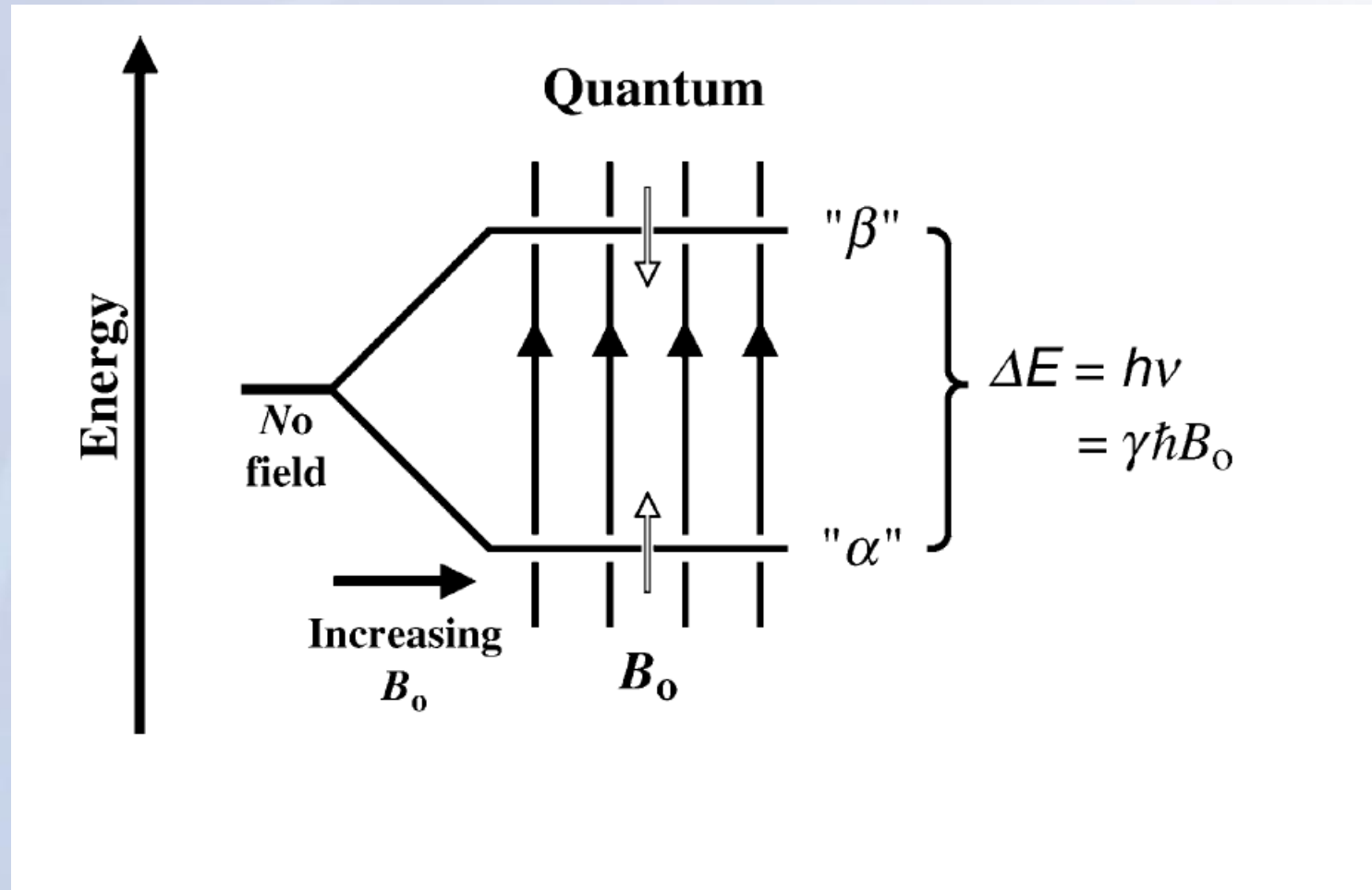
Sample is positioned on the probe using a spinner.

# NMR Experiment

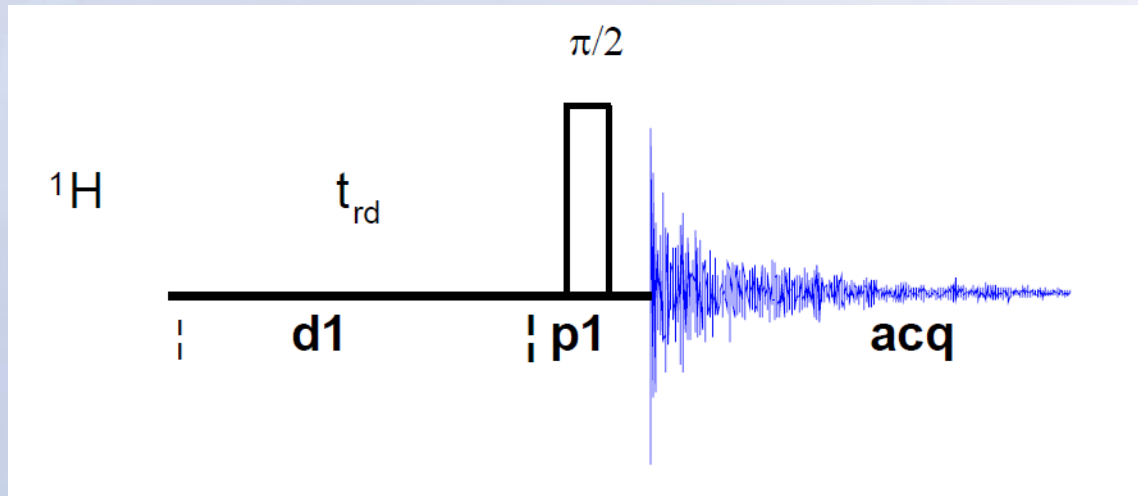




# NMR Spectroscopy



# Basic $^1\text{H}$ Experiment

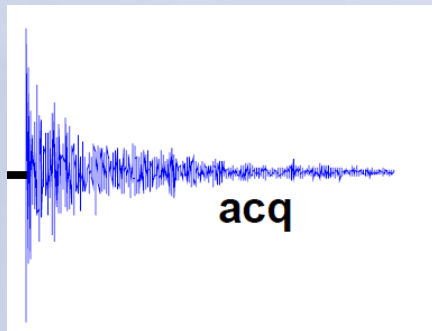


$d1$  = delay

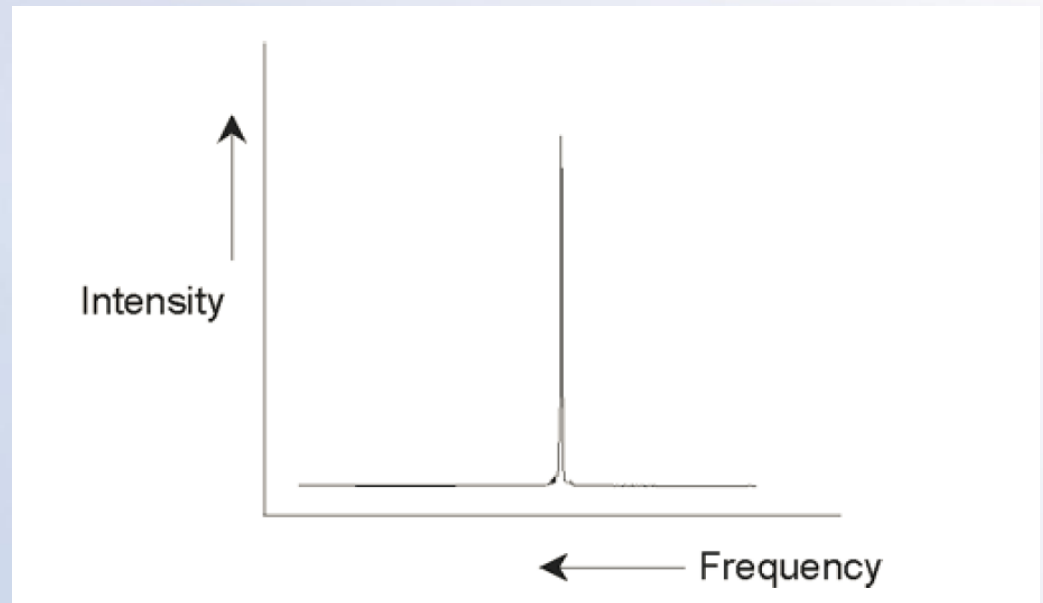
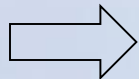
$p1$  = pulse width

$acq$  = acquisition time

# NMR Signal

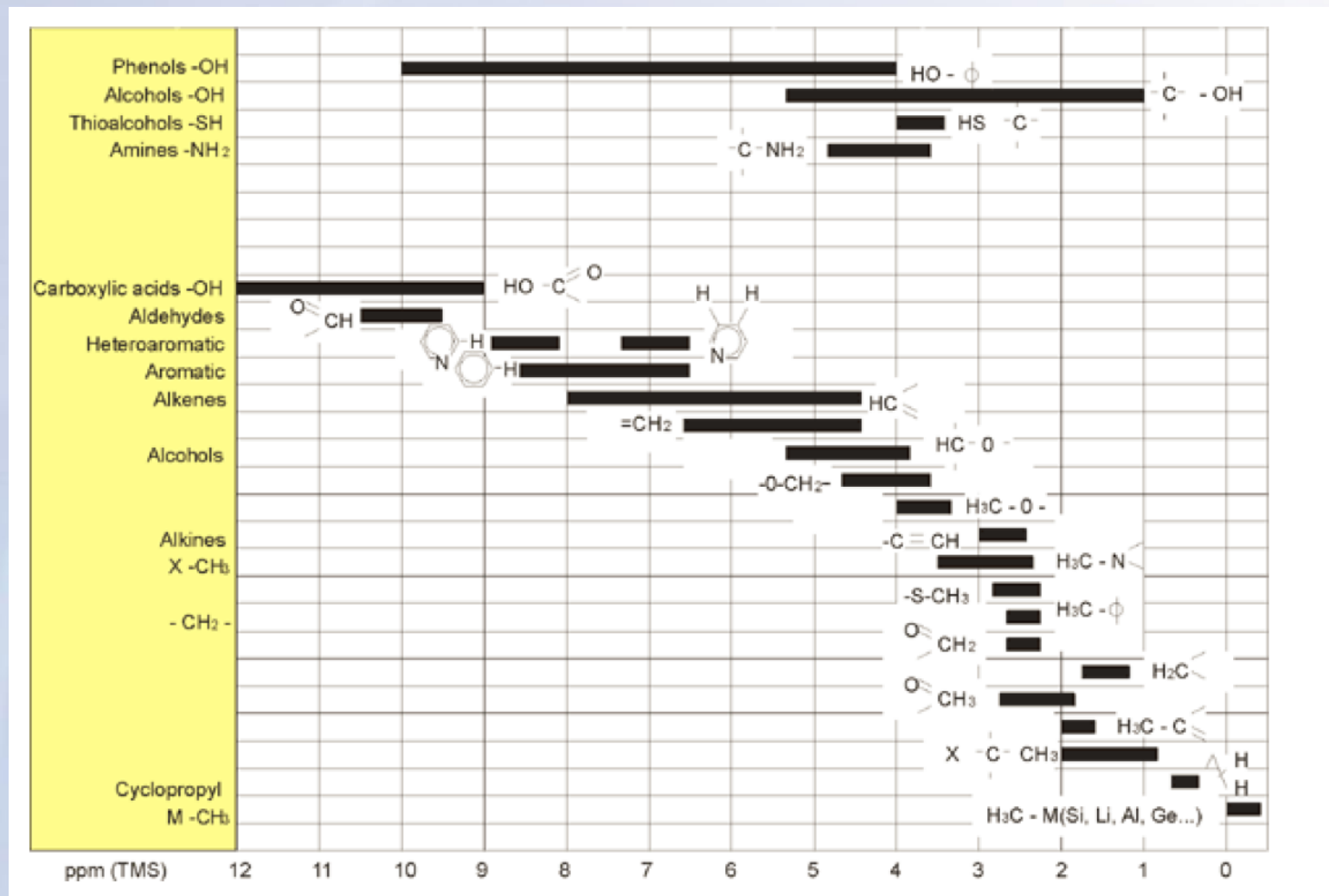


Fourier  
Transform

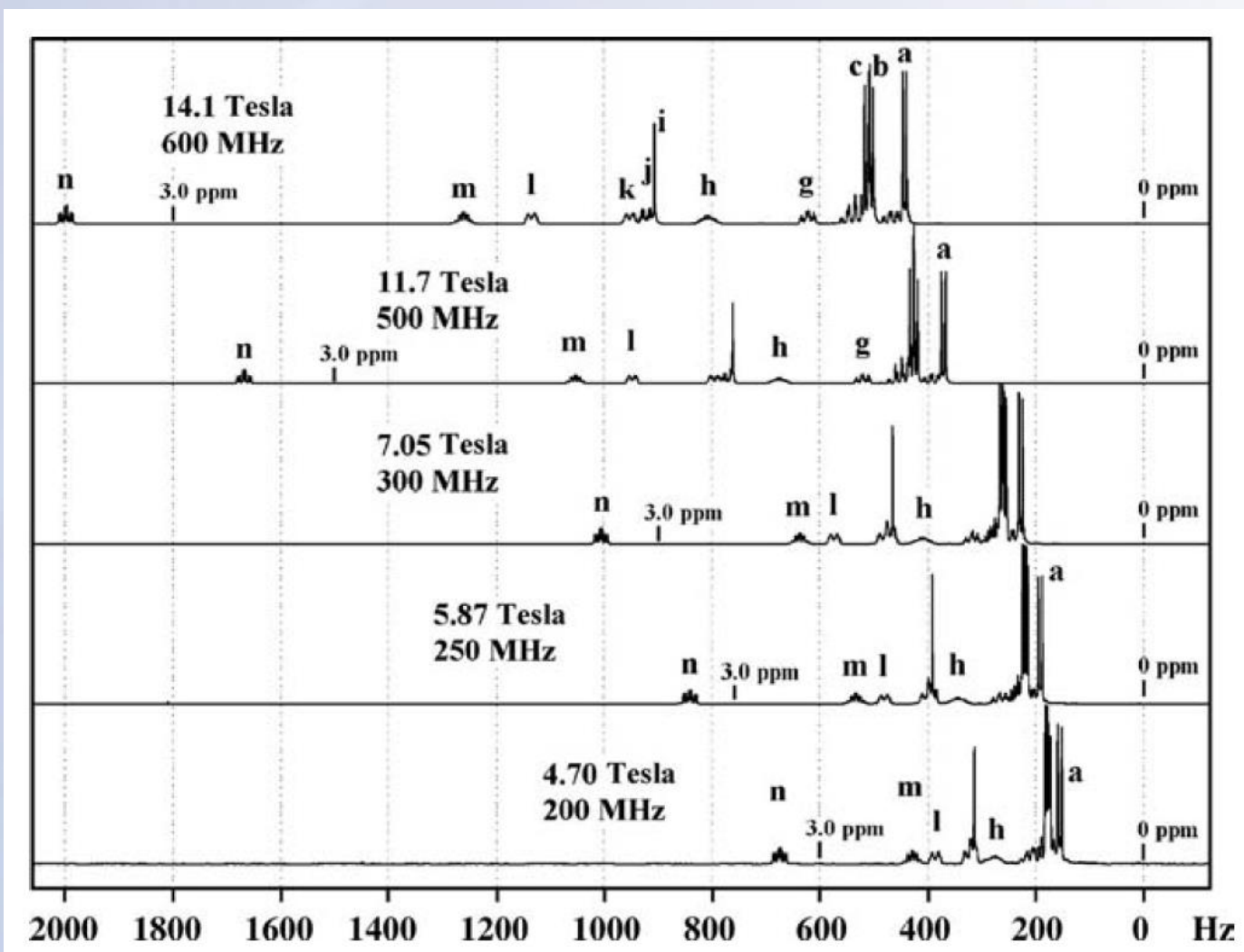


Chemical shift (ppm scale) = frequency / Spectrometer Frequency (MHz)

# Chemical Shift of molecules



# Static Magnetic field strengths



# Sample Preparation for metabolomics

- Balance and calibration check
- Prepare samples on ice, Minimize freeze thaw cycles
- Dilution
  - Using D<sub>2</sub>O or Buffer (0.2M Phosphate)
- Extraction
  - MeOH or MeOH/ Water
  - MeOH/ CHCl<sub>3</sub>/ H<sub>2</sub>O (Folch Method)
  - 50% Acetonitrile in Water
  - Dry the sample
  - Reconstitute in D<sub>2</sub>O or 0.2M Phosphate Buffer
- Internal standards
  - Chemical shift reference (DSS, also for line shape)
  - pH reference (Imidazole)
- Pooled QC Samples
- Consistency across the whole study is very important

# Sample Preparation for Metabolomics Analysis

Current sample preparation practices (in brief)

- **Biofluids**

- Dilute with D<sub>2</sub>O/ buffer/ 0.9% Saline
- Add internal standard (ISTD, eg. Chenomx) solution or formate (for serum).
- Centrifuge and transfer an aliquot into NMR tube

- **Tissue and Cells**

- Homogenization performed in ice cold 50/50 acetonitrile/water
- Supernatant dried down (lyophilized)
- Reconstituted in D<sub>2</sub>O and ISTD (eg. Chenomx) solution

- **Pooled QC Samples (Sample Unlimited)**

- Mix equal volume of study samples to get pooled QC samples
- 10% QC samples

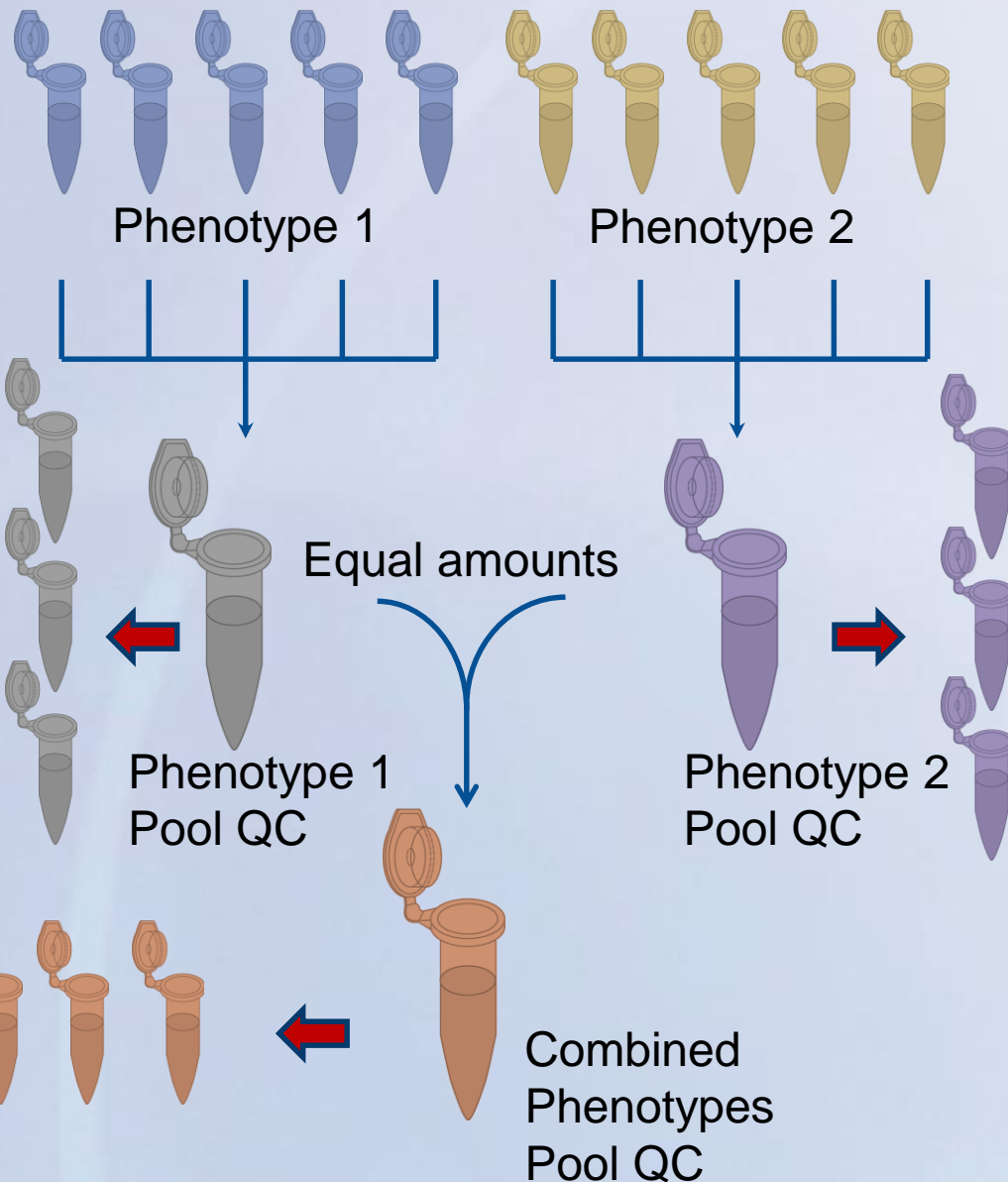
- **Pooled QC Samples (Sample Limited)**

- Use independent pool of similar samples
- 10% QC samples

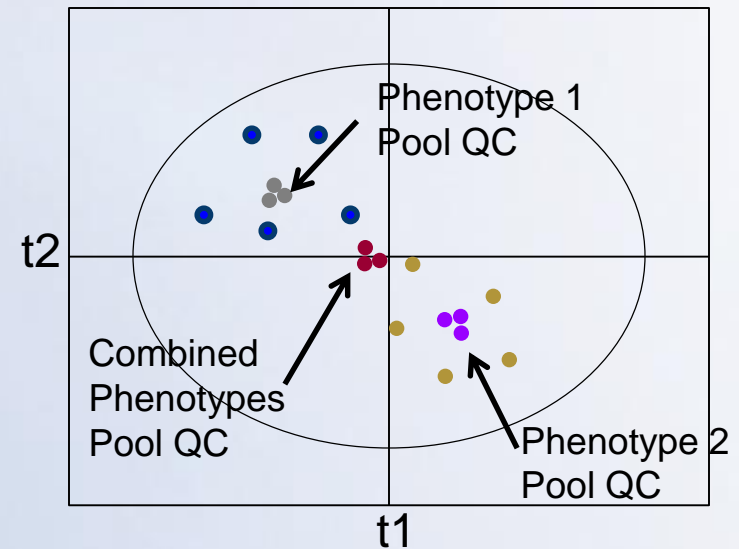
- **Daily balance and pipette check**

**Samples are randomized for preparation and data acquisition**

# Pooled QC Samples



- Aliquots from each sample in the study phenotype are pooled (phenotypic pool)
- Equal amount of each phenotypic pools are pooled (Combined phenotypic pool)
- Replicates of pools are prepared
- Pool samples are prepared along with the study samples



**Pooled samples  
should cluster tightly**

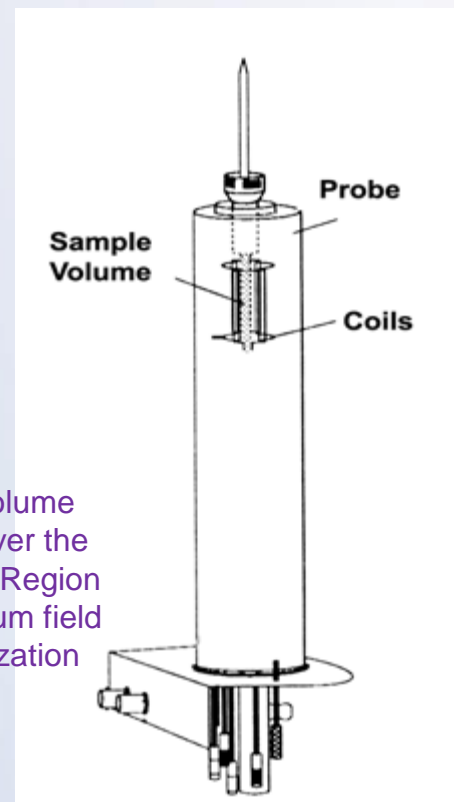
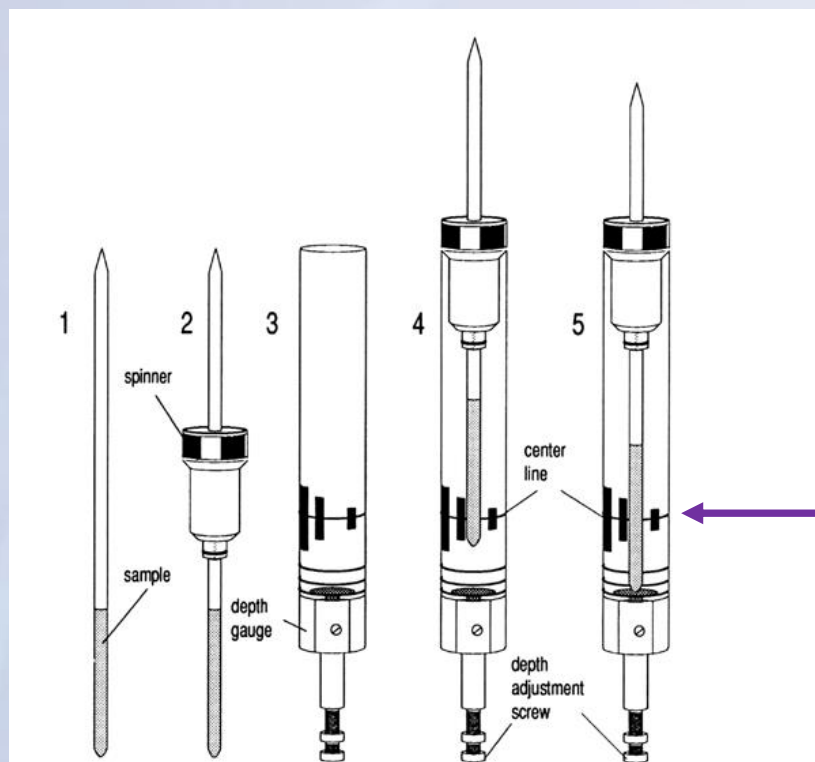


# NMR Data Acquisition

- 1D NMR
  - 1<sup>st</sup> increment of NOESY
    - noesyprid (Bruker)
  - CPMG (serum or plasma)
    - cpmgpr1d (Bruker)
    - To remove broadening of signals due to macromolecules (eg. Proteins and lipids)
- 2D NMR (for structure elucidation)
  - 2D J-Resolved
  - COSY
  - TOCSY
  - HSQC
  - HMBC



# Sample Amount in NMR tube



Sample volume should cover the NMR Coil Region For optimum field homogenization

- At least 10% D<sub>2</sub>O in the sample
- Optimum volume
  - 550 – 600  $\mu$ L (5mm tube)
  - 200  $\mu$ L (3 mm tube)
- Sample gauge is used

**For very small sample amounts, a NMR with a microcoil probe is an option.**

# Steps in Data Acquisition

- Place the sample in the spinner
  - Use sample gauge
- Tune and match the probe
  - Automatic in new instruments
- Lock and shim the instrument
  - Gradient shimming
- Create and set up NMR parameters
- Acquire data
- Process the NMR spectrum

# ERCMRC at UNC Chapel Hill



Yuanyuan Li  
LC-MS/MS  
LC-TOF-MS



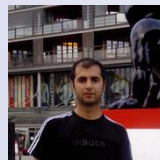
Wimal Pathmasiri  
NMR & GC-TOF-MS



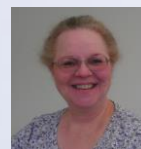
Delisha Stewart  
NMR and LC-TOF-MS



Maria Moreno  
NMR and LC-MS/MS



Reza Ghanbari  
Postdoctoral Fellow



Rose Ewald  
Graduate Studies



Susan Sumner  
PI, ERCMRC



Susan McRitchie  
Program Coordinator  
Data Analysis

## NCRC



Nick Gillitt  
Dole  
700 MHz NMR  
6500 Sciex LC-MS



Colin Kaye  
NCSU  
6500 Sciex  
Triple Quad



UNC-G  
Q-Exactive



Debby Reed  
GC-MS  
GC-TOF-MS



Stephen Orena  
LC-MS/MS



Martin Kohlmeier  
Training



Tim Fennell  
Director,  
Analytical Chemistry &  
Pharmaceutics



Yan Lan Yueh  
LC-MS



Jessica Gooding  
LC-MS



Rod Snyder  
NMR and LC-MS



Courtney Whitaker  
LC-MS

## RTI

## UNC Charlotte Bioinformatics

## DHMRI

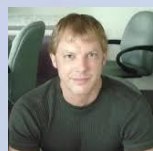


Kevin Knagge  
700 and 950 MHz NMR

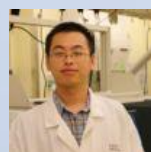
Jason Winnike  
NMR  
2D-GC-TOF-MS



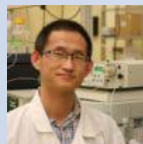
David Kirchner  
LC-MS/MS



Huiyuan Chen  
GC-MS  
GC-TOF-MS



Huadong Chen  
LC-MS  
LC-TOF-MS



Owen Myers



XiuXia Du

Aleksandr  
Smirnov

