

NMR Training: Metabolite ID

UAB Metabolomics Training Course
July 17-21, 2017

Wimal Pathmasiri

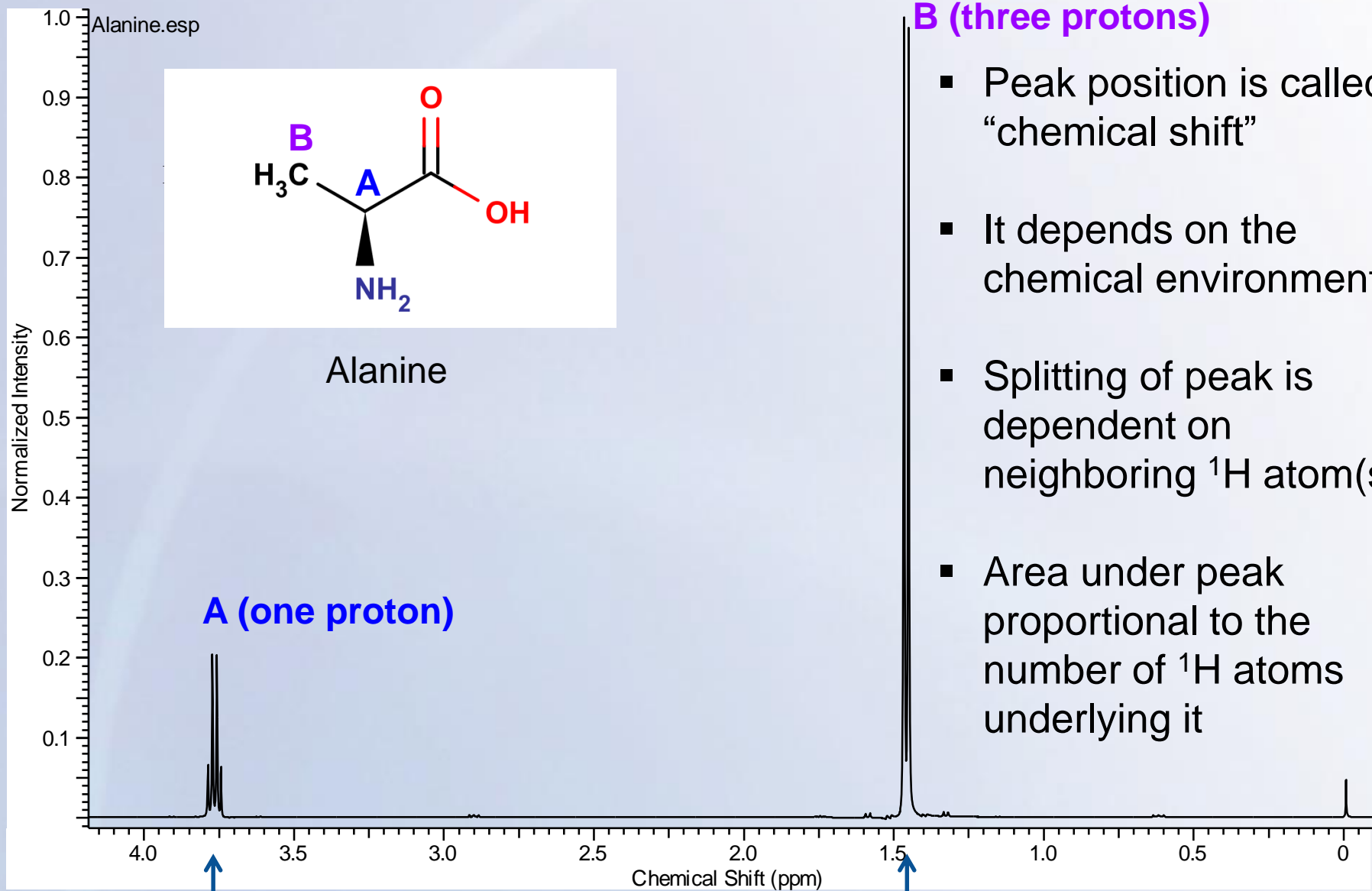
NIH Eastern Regional Comprehensive Metabolomics Resource Core
(ERCMRC)

Department of Nutrition – Nutrition Research Institute
University of North Carolina at Chapel Hill

Outline

- Information that NMR Spectroscopy data can provide
 - Chemical shift, J-coupling, chemical structure
- Available NMR methods
 - 1D NMR: ^1H , ^{13}C , ^{15}N , ^{31}P
 - 2D NMR: COSY, TOCSY, HSQC, HMBC, NOESY, INADEQUATE
 - Selective 1D: 1D TOCSY, 1D HSQC
- Spectral editing methods
 - CPMG, Diffusion, JRES, DEPT (DEPT 45, DEPT 90, DEPT 135)
- NMR Libraries, software, and databases
 - AMIX, BBREFCODE (Bruker), BATMAN, Chenomx, COLMAR, HMDB, BMRB, Birmingham Metabolite Library, NMR Shift DB
- Other complementary methods
 - Eg. STOCSY, STORM, RANSY
 - MUMA Package (R Based) for STOCSY and STORM
- Tagging, Spike-in of metabolites, Predicting Spectra

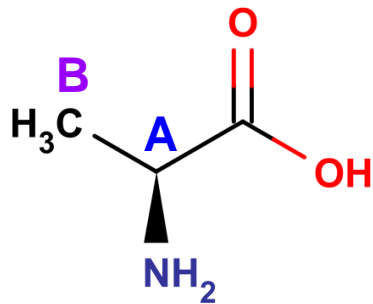
NMR Chemical Shift



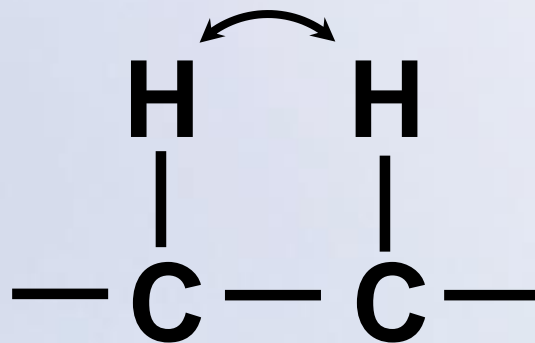
Chemical shift of CH
4 lines (quadrat)

Chemical shift of CH_3
2 lines (doublet)

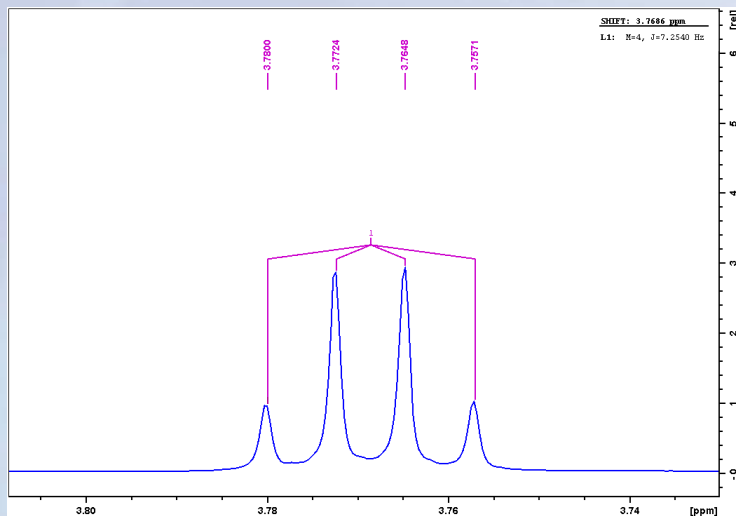
NMR J-Coupling



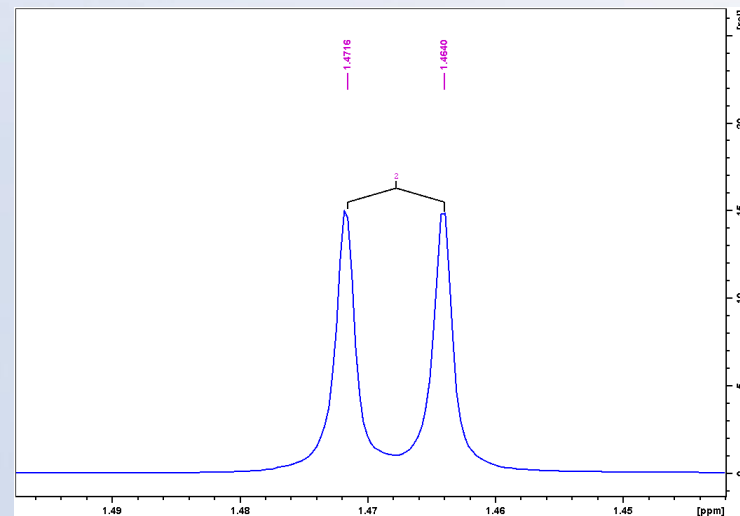
Alanine



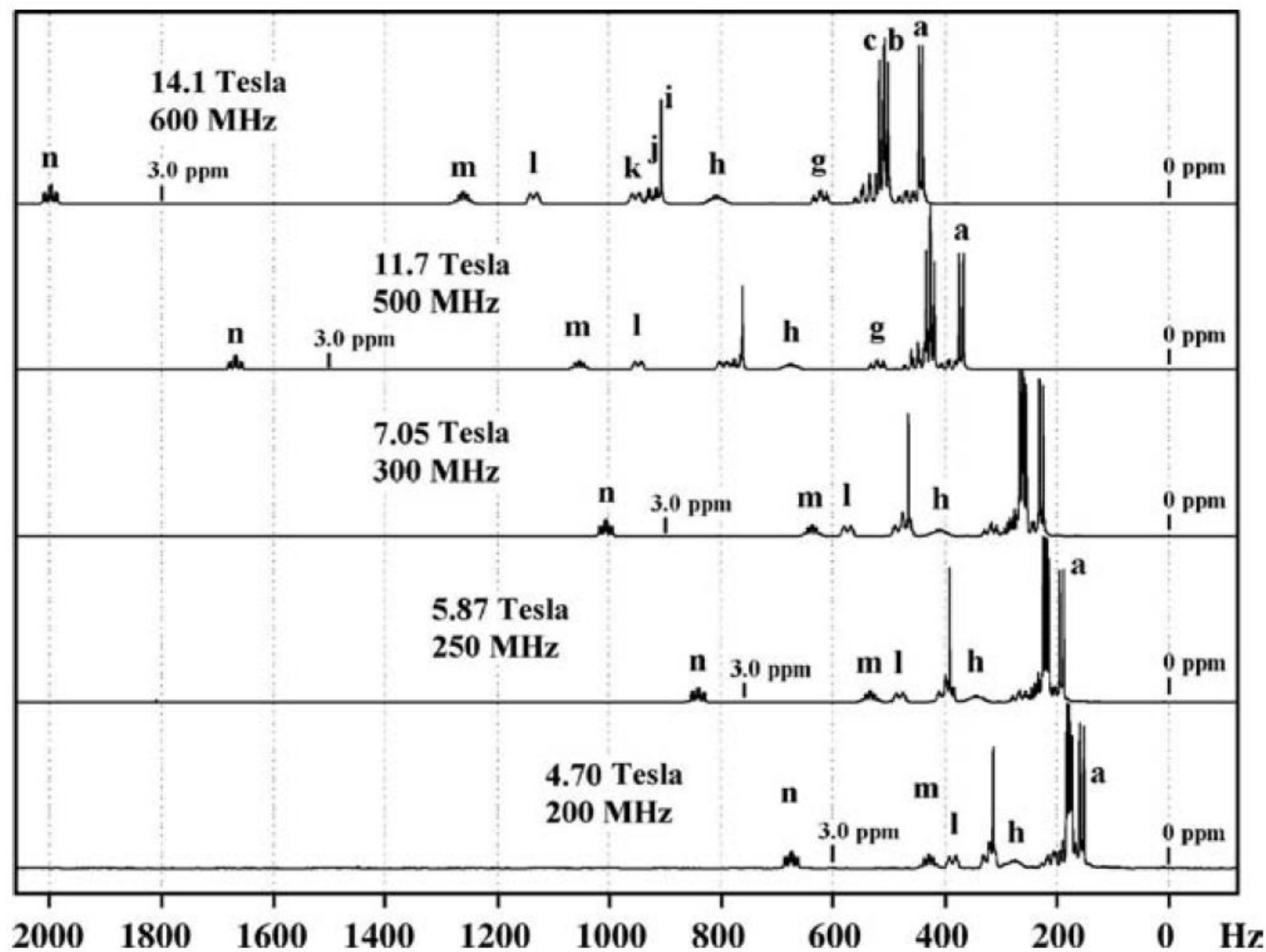
J = 7.2 Hz



J = 7.2 Hz

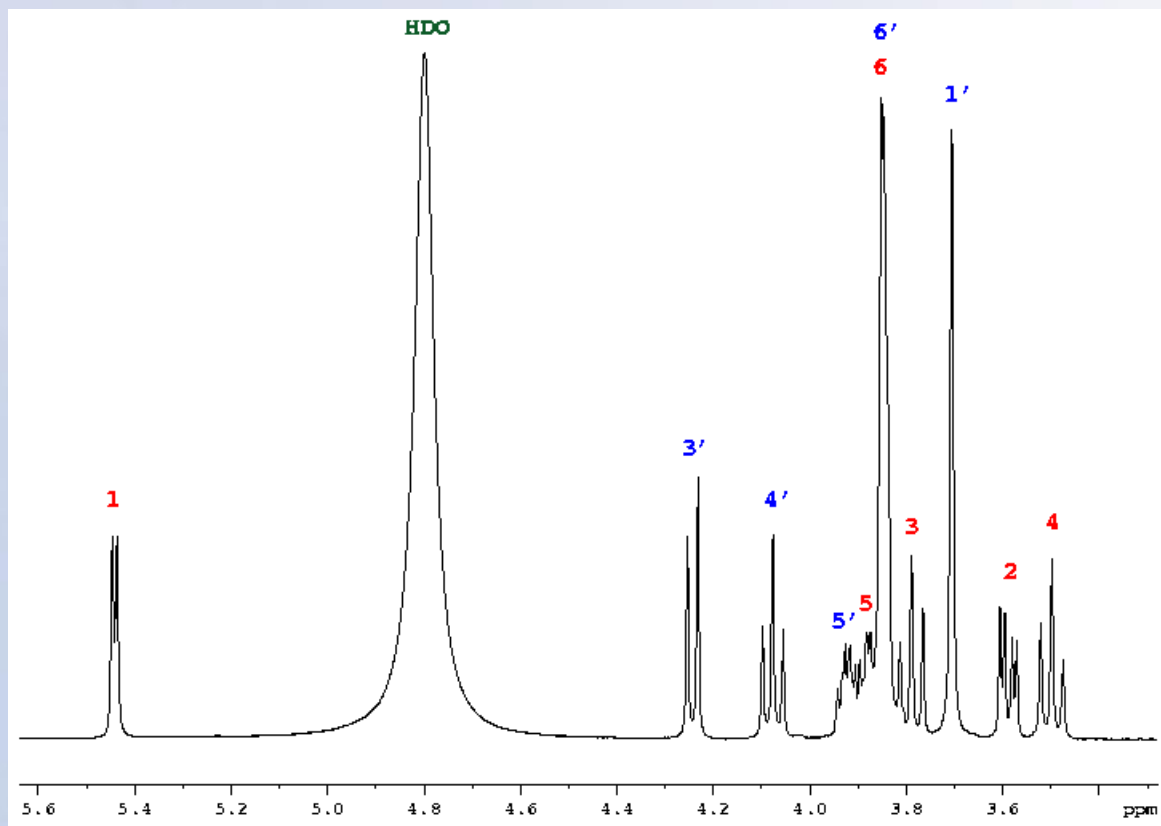
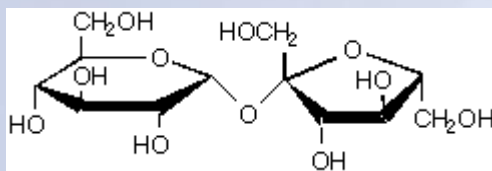


Dispersion of NMR Signal with Magnetic Field Strength

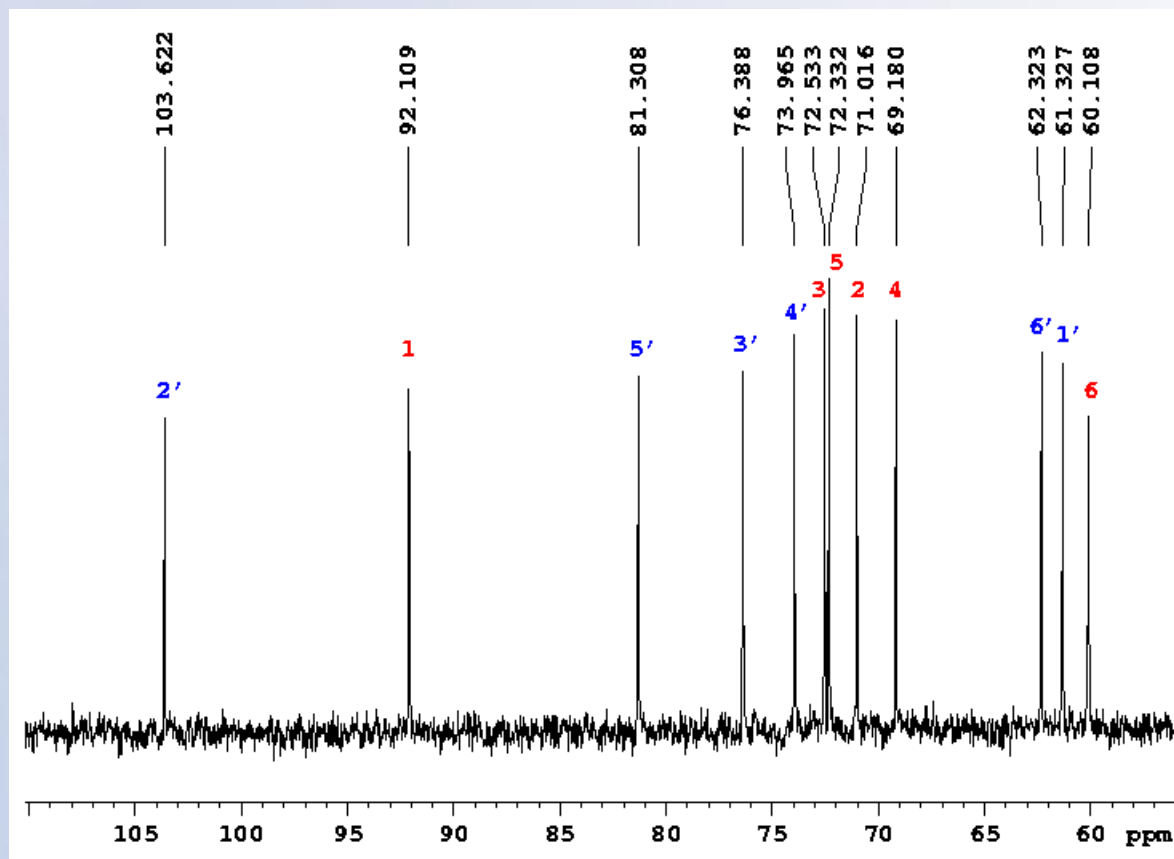
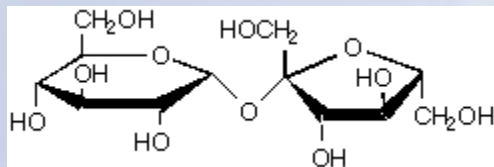


1D and 2D NMR Methods

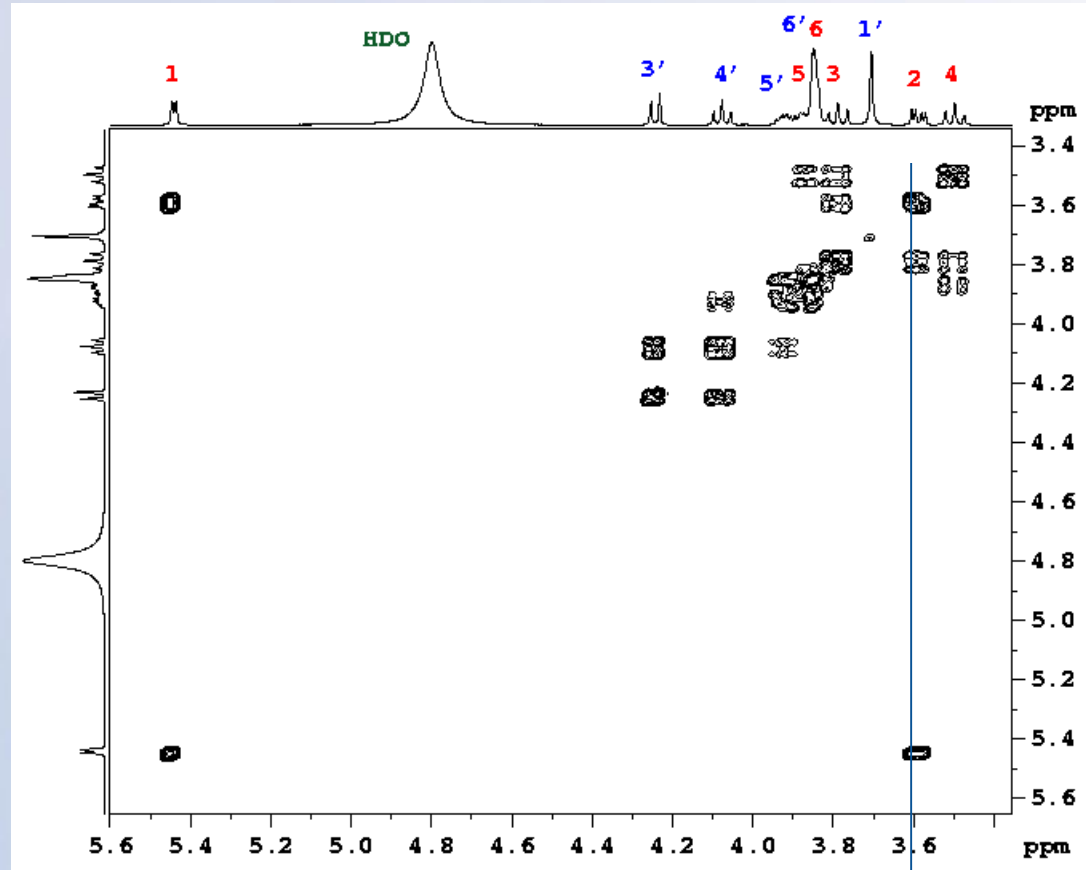
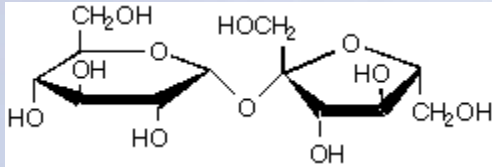
^1H NMR: Sucrose



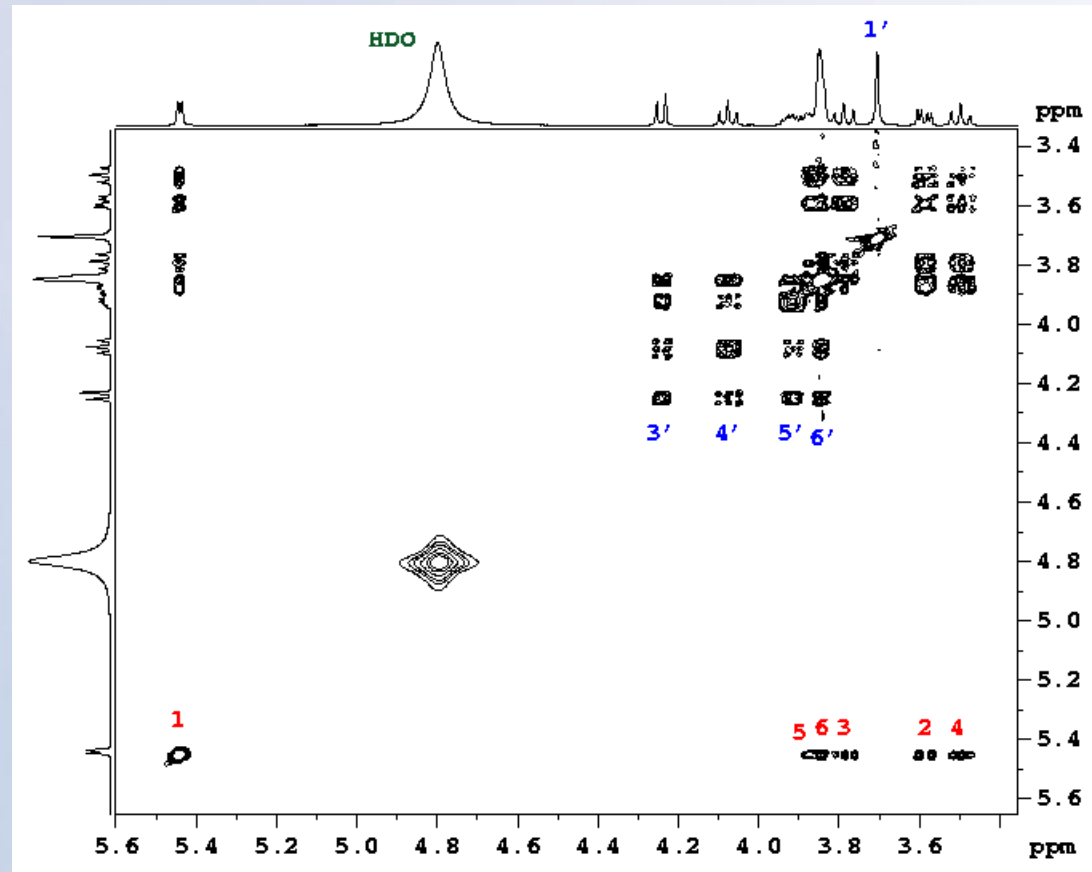
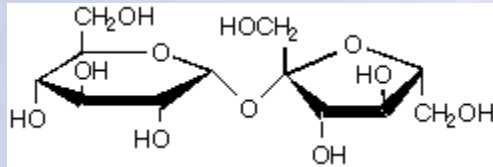
^{13}C NMR: Sucrose



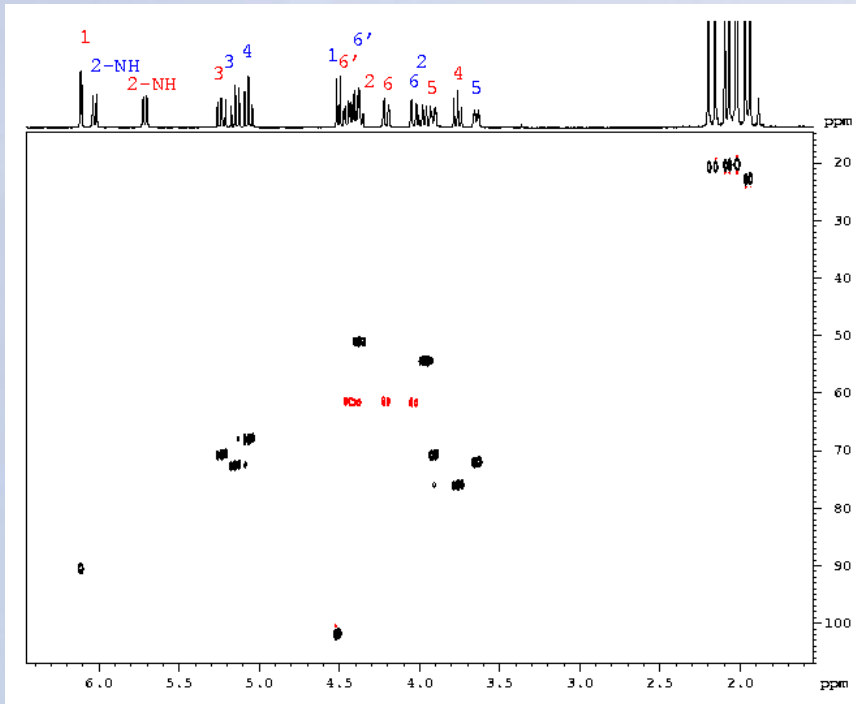
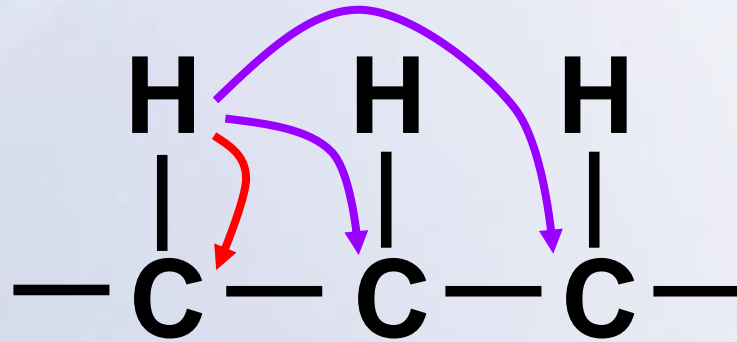
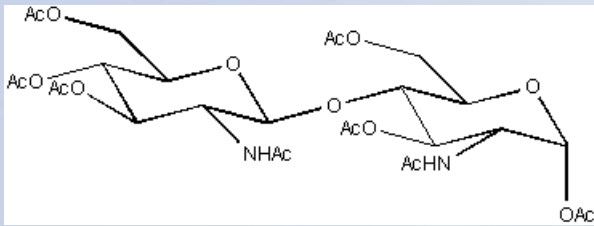
COSY: Sucrose



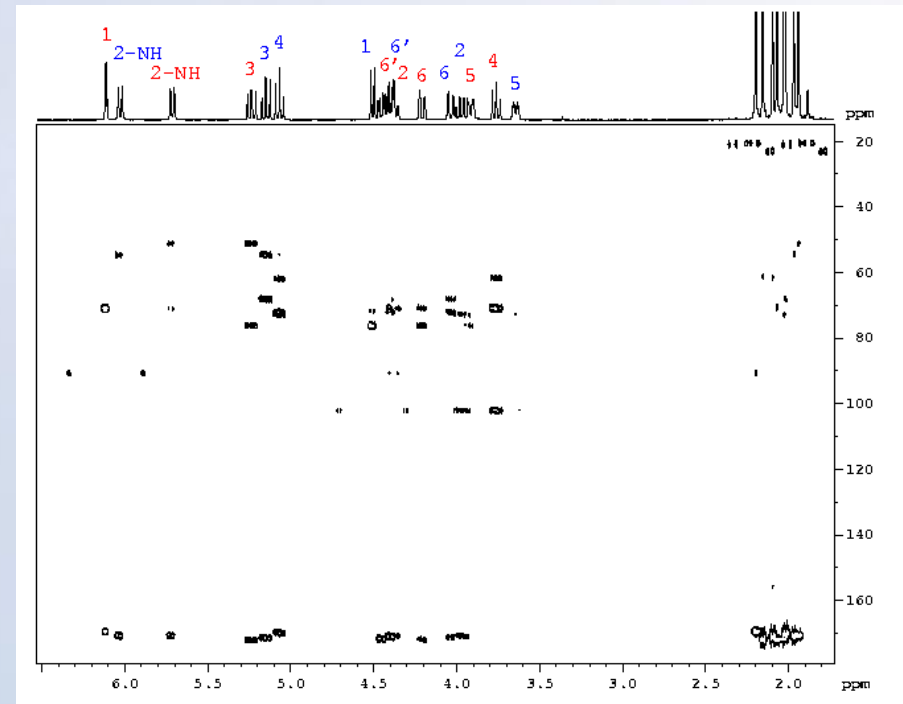
TOCSY: Sucrose



Chentobiose

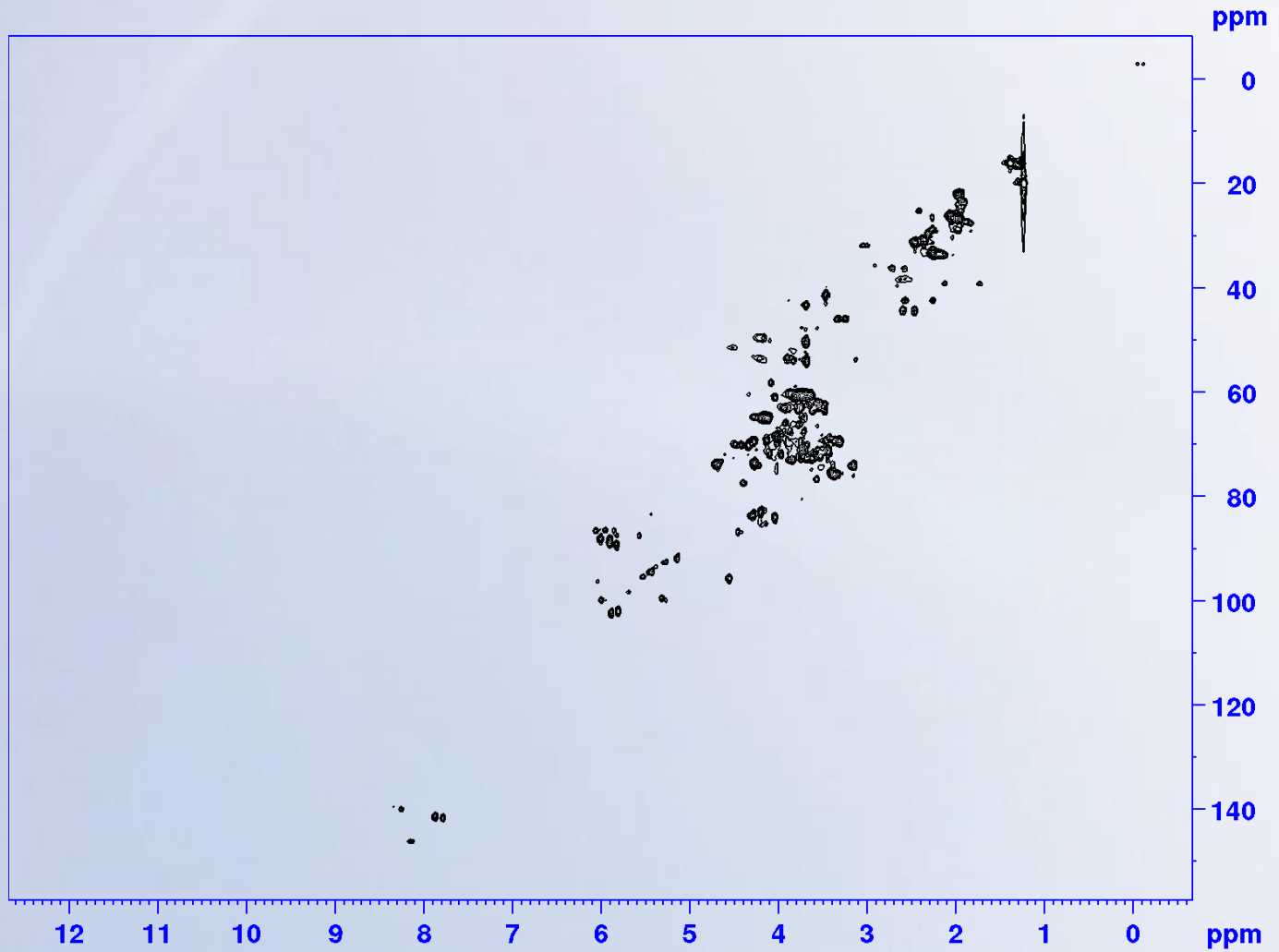


HSQC ($^1J_{CH}$)



HMBC ($^2J_{CH}$, $^3J_{CH}$)

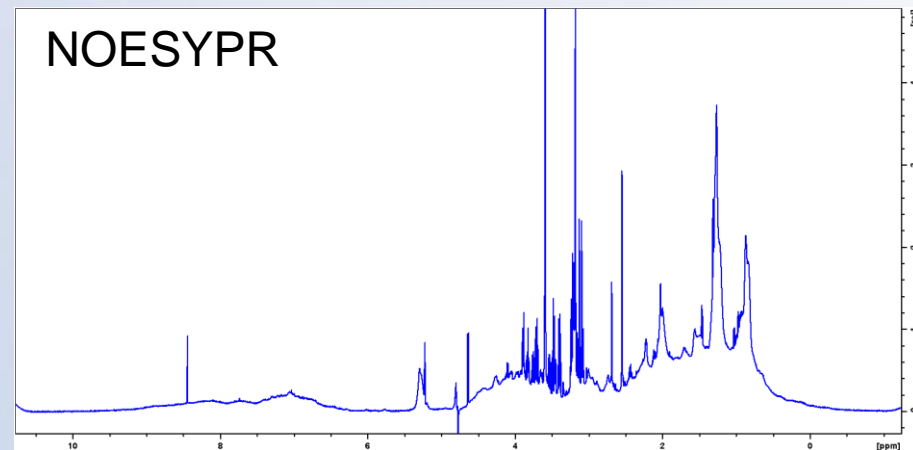
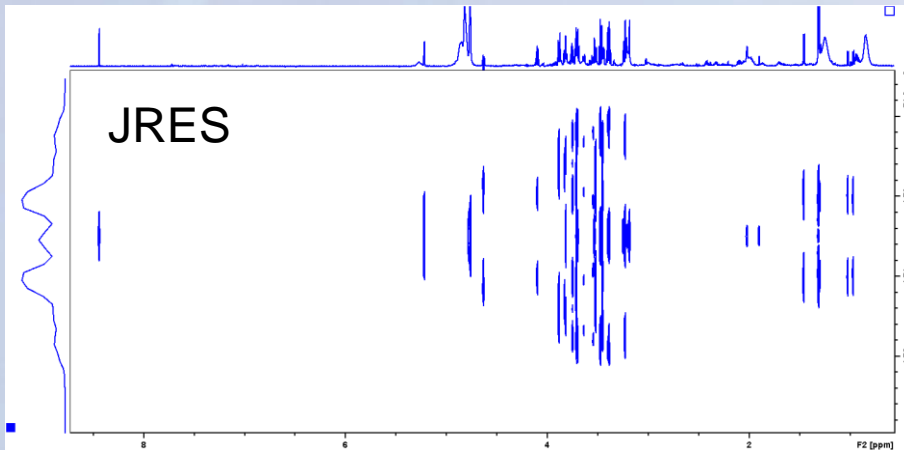
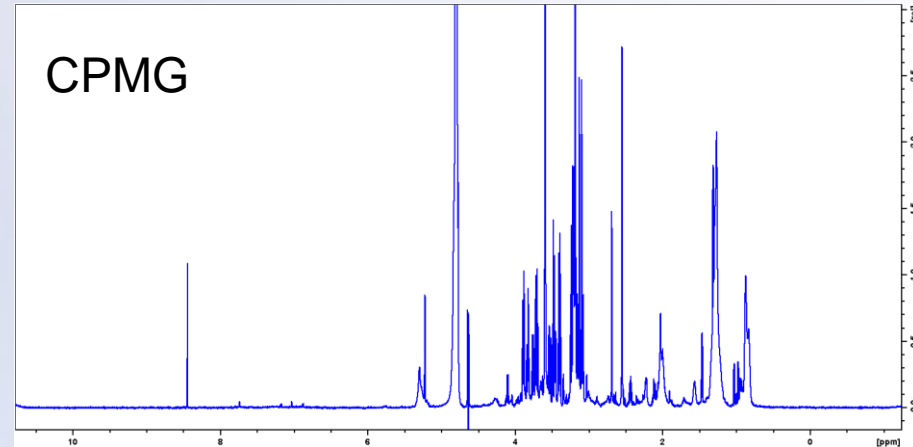
^1H - ^{13}C HSQC Spectrum of Cell Extract



Spectral Editing

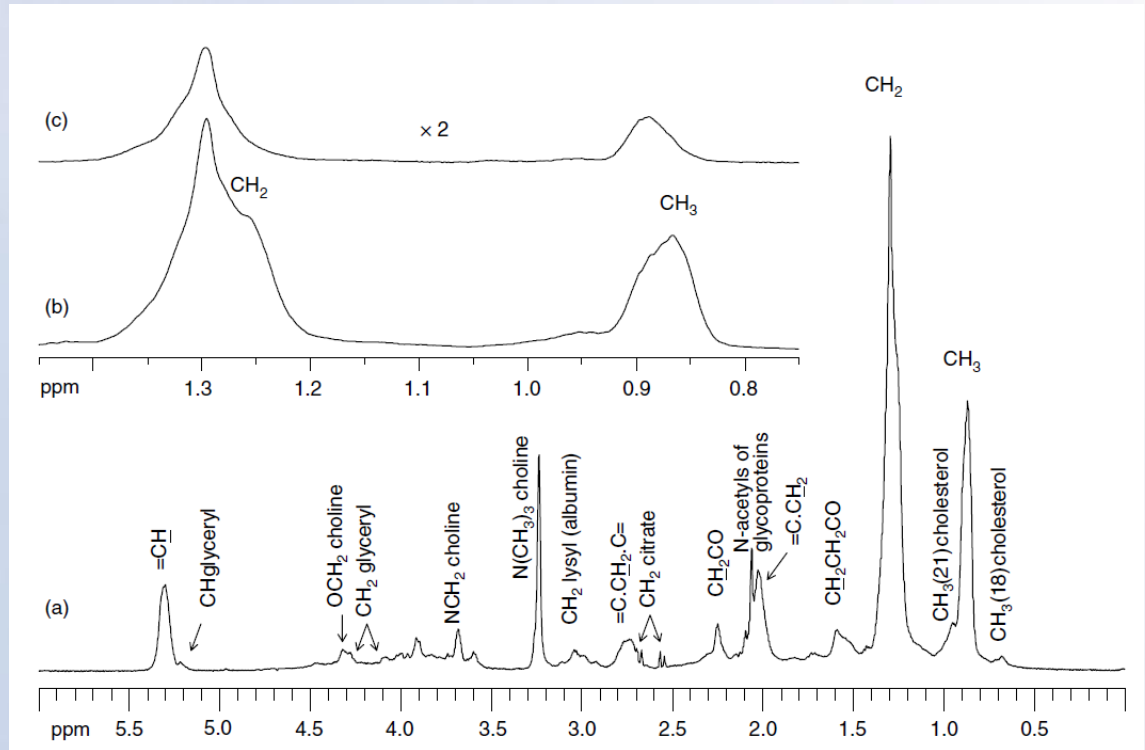
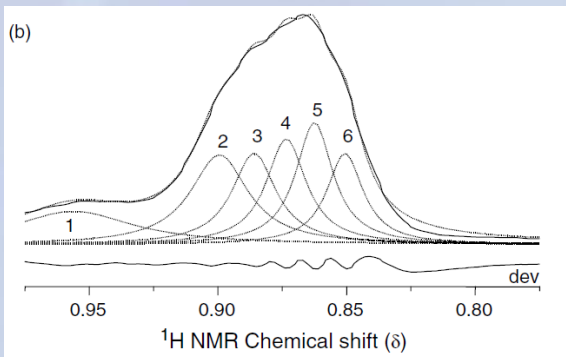
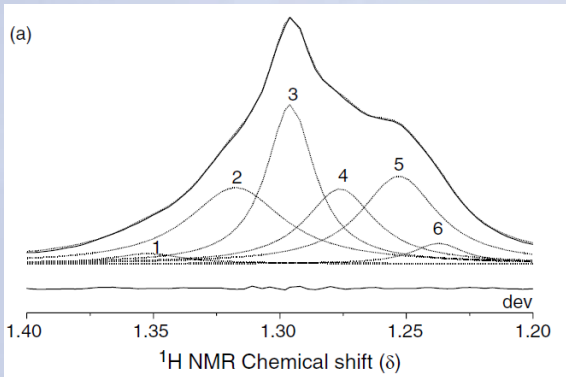
Spectral Editing

- Relaxation editing
 - CPMG Pulse sequence
- J- Modulated
 - J-RES



Analysis of Lipoproteins

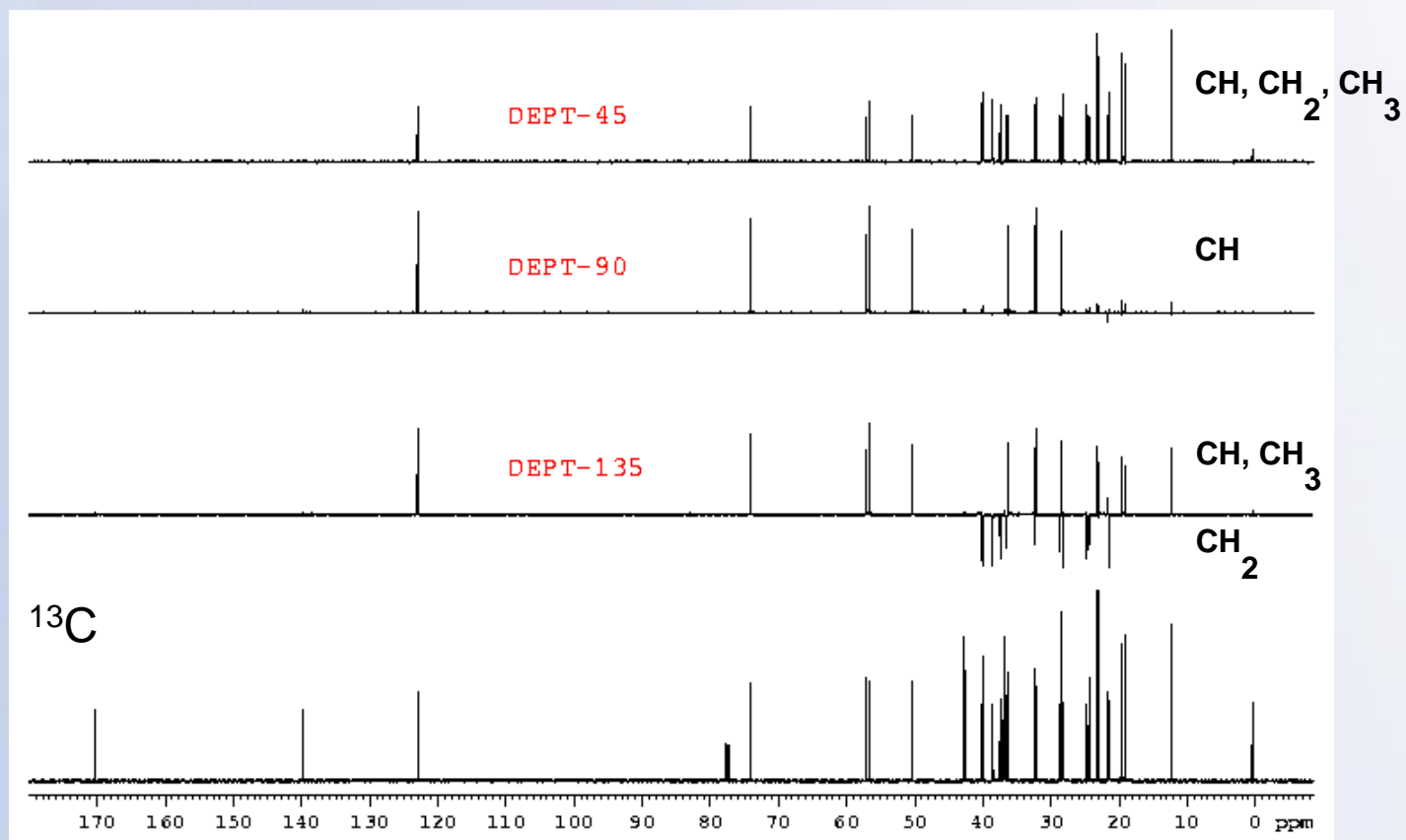
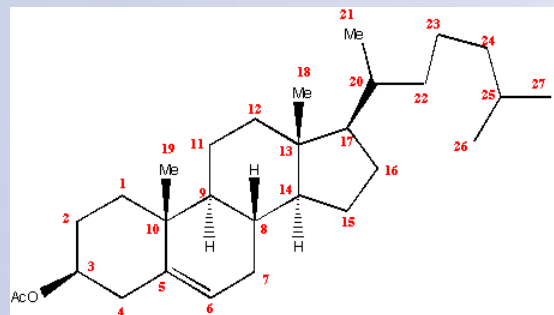
- Lipoproteins are classified based on their size and density (VLDL, LDL, HDL)
- Lipoproteins can be assigned to these sub fractions by deconvoluting the CH_3 and $(\text{CH}_2)_n$ in diffusion edited spectra



Diffusion Edited NMR Spectra

Peak	δ (ppm)	Width (Hz)	D (cm ² s ⁻¹ × 10 ⁷) ^a	Area (%) ^b	Assignment
(CH ₂) _n 1	1.353	19.7	2.72	2.3	LDL + VLDL
(CH ₂) _n 2	1.317	28.0	1.98	26.4	VLDL
(CH ₂) _n 3	1.296	14.0	1.85	27.9	VLDL
(CH ₂) _n 4	1.276	17.8	3.15	15.5	LDL
(CH ₂) _n 5	1.255	20.5	5.19	19.9	HDL(60.6%) + LDL(39.4%)
(CH ₂) _n 6	1.240	18.4	5.96	7.9	HDL
CH ₃ 1	0.956	33.9	3.77	15.8	VLDL + HDL
CH ₃ 2	0.899	16.4	1.70	20.6	VLDL
CH ₃ 3	0.886	12.4	1.84	15.9	VLDL
CH ₃ 4	0.873	11.3	3.07	16.7	LDL
CH ₃ 5	0.862	10.5	4.51	17.9	HDL(40.8%) + LDL(59.2%)
CH ₃ 6	0.851	10.2	7.11	13.1	HDL

DEPT: Cholesterol



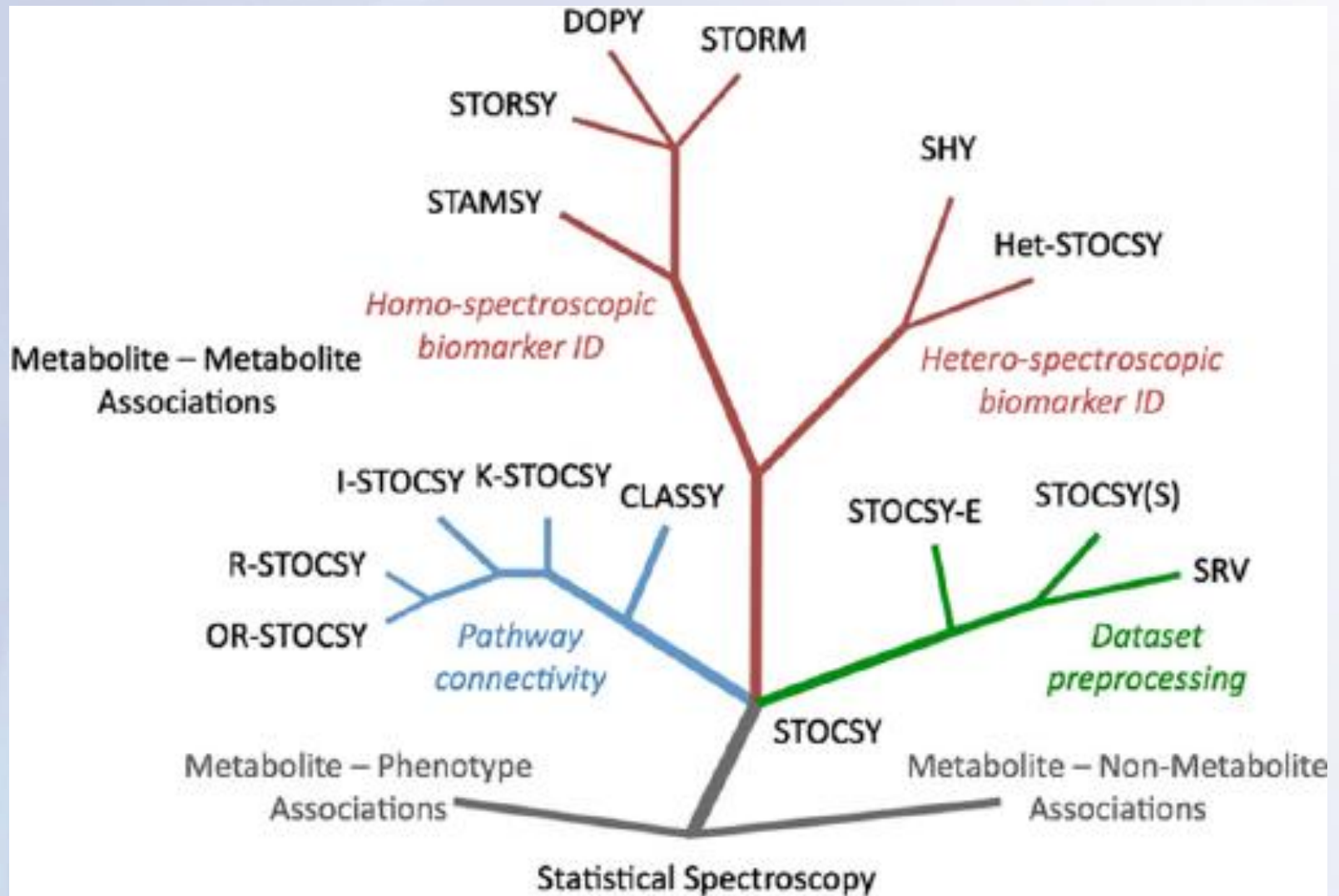
NMR Libraries, Software and Databases

NMR Libraries and Databases

- Continuously emerging
- Databases
 - HMDB (<http://www.hmdb.ca/>)
 - Birmingham Metabolite Library (<http://www.bml-nmr.org/>)
 - BMRB (<http://www.bmrwisc.edu/>)
 - NMRShift DB (<http://nmrshiftdb.nmr.uni-koeln.de/>)
- Online Software
 - COLMAR (<http://spin.ccic.ohio-state.edu/>), Bayesil (<http://bayesil.ca/>)
- Standalone Software
 - Chenomx (<http://www.chenomx.com/>)
 - AMIX/ ASSURE/BBREFCODE
<https://www.bruker.com/products/mr/nmr/nmr-software/software/amix/overview.html>
 - BATMAN (<http://batman.r-forge.r-project.org/>)
 - CCPN Metabolomics (<http://www.ccpn.ac.uk/collaborations/metabolomics>)
 - rNMR (<http://rnmr.nmrwisc.edu/>)

Other Complementary Methods

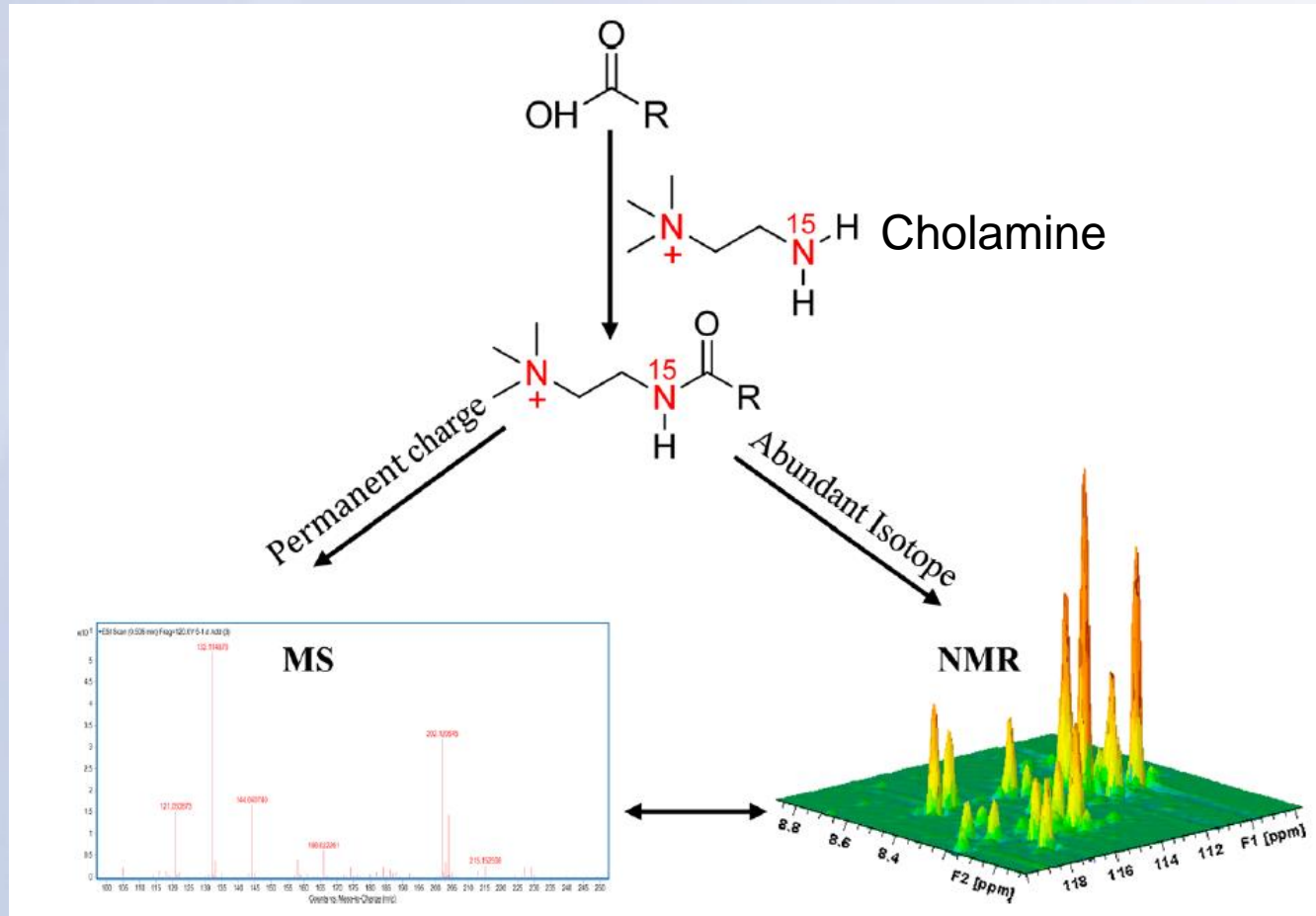
Statistical Spectroscopic Tools



Robinette, S. L., J. C. Lindon and J. K. Nicholson (2013). "Statistical spectroscopic tools for biomarker discovery and systems medicine." *Anal Chem* 85(11): 5297-5303.

Tagging

Smart Tagging

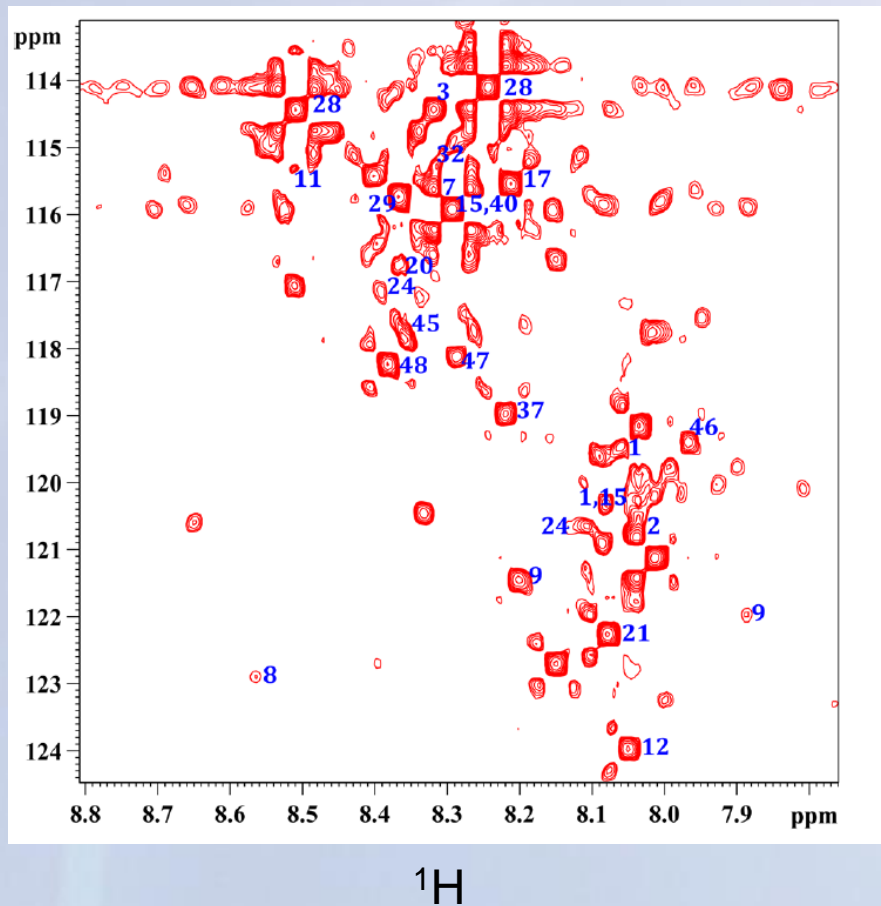


Tayyari, F., G. A. Gowda, H. Gu and D. Raftery (2013). "¹⁵N-cholamine--a smart isotope tag for combining NMR- and MS-based metabolite profiling." *Anal Chem* **85**(18): 8715-8721

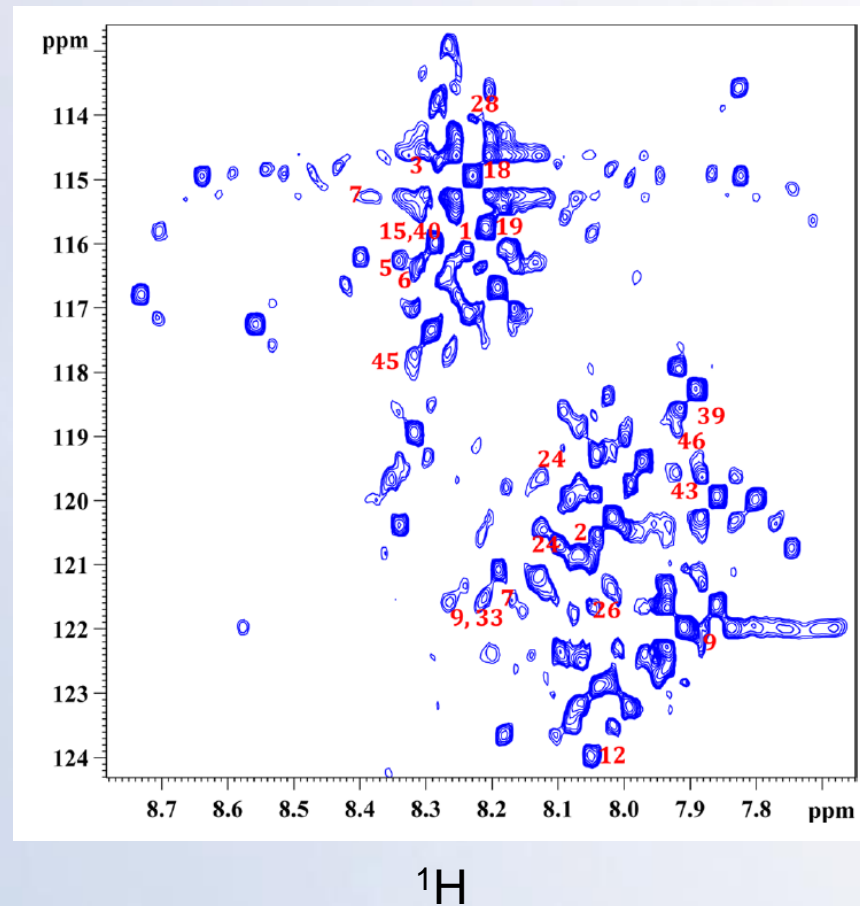
Smart Tagging

^1H - ^{15}N HSQC

Human Serum



Human Urine



Tayyari, F., G. A. Gowda, H. Gu and D. Raftery (2013). " ^{15}N -cholamine--a smart isotope tag for combining NMR- and MS-based metabolite profiling." *Anal Chem* **85**(18): 8715-8721

References

- Beckonert, O., H. C. Keun, T. M. Ebbels, J. Bundy, E. Holmes, J. C. Lindon and J. K. Nicholson (2007). "Metabolic profiling, metabolomic and metabonomic procedures for NMR spectroscopy of urine, plasma, serum and tissue extracts." *Nat Protoc* 2(11): 2692-2703.
- Cloarec, O., M. E. Dumas, J. Trygg, A. Craig, R. H. Barton, J. C. Lindon, J. K. Nicholson and E. Holmes (2005). "Evaluation of the Orthogonal Projection on Latent Structure Model Limitations Caused by Chemical Shift Variability and Improved Visualization of Biomarker Changes in ^1H NMR Spectroscopic Metabonomic Studies." *Analytical Chemistry* 77(2): 517-526.
- Lindon, J. C. and J. K. Nicholson (2008). "Spectroscopic and Statistical Techniques for Information Recovery in Metabonomics and Metabolomics." *Annual Review of Analytical Chemistry* 1(1): 45-69.
- Posma, J. M., I. Garcia-Perez, M. De Iorio, J. C. Lindon, P. Elliott, E. Holmes, T. M. Ebbels and J. K. Nicholson (2012). "Subset optimization by reference matching (STORM): an optimized statistical approach for recovery of metabolic biomarker structural information from ^1H NMR spectra of biofluids." *Anal Chem* 84(24): 10694-10701.
- Robinette, S. L., J. C. Lindon and J. K. Nicholson (2013). "Statistical spectroscopic tools for biomarker discovery and systems medicine." *Anal Chem* 85(11): 5297-5303.
- Sands, C. J., M. Coen, T. M. Ebbels, E. Holmes, J. C. Lindon and J. K. Nicholson (2011). "Data-driven approach for metabolite relationship recovery in biological ^1H NMR data sets using iterative statistical total correlation spectroscopy." *Anal Chem* 83(6): 2075-2082.
- Wei, S., J. Zhang, L. Liu, T. Ye, G. A. Gowda, F. Tayyari and D. Raftery (2011). "Ratio analysis nuclear magnetic resonance spectroscopy for selective metabolite identification in complex samples." *Anal Chem* 83(20): 7616-7623.
- Tayyari, F., G. A. Gowda, H. Gu and D. Raftery (2013). " ^{15}N -cholamine--a smart isotope tag for combining NMR- and MS-based metabolite profiling." *Analytical Chemistry* 85(18): 8715-8721.

Chenomx Exercise

Chenomx Exercise

- Save the folder called “Chenomx_Tutorial.zip onto your computer
 - Sample files
 - Chenomx NMR Suite Tutorial.pdf
- We will use Processor and Profiler in the exercise
- Processor
 - Sample.fid
- Profiler
 - Basic Start, Basic End
 - Advanced Start, Advanced End
 - Batch fitting

ERCMRC at UNC Chapel Hill



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



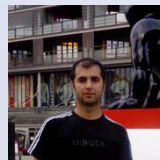
Wimal Pathmasiri
NMR & GC-TOF-MS



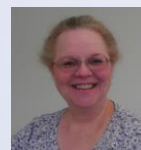
Delisha Stewart
NMR and LC-TOF-MS



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



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

RTI



Jessica Gooding
LC-MS



Rod Snyder
NMR and LC-MS



Courtney Whitaker
LC-MS

Scott Watson
Neurotransmitter
LC/MS



Colin Kaye
NCSU
6500 Sciex
Triple Quad

DHMRI

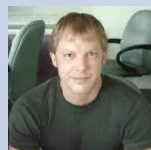


Kevin Knagge
700 and 950 MHz NMR

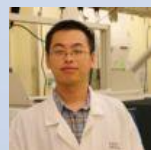
Jason Winnike
NMR
2D-GC-TOF-MS



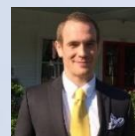
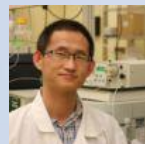
David Kirchner
LC-MS/MS



Huiyuan Chen
GC-MS
GC-TOF-MS



Huadong Chen
LC-MS
LC-TOF-MS



Owen Myers



XiuXia Du

Aleksandr
Smirnov



UNC-G
Q-Exactive

UNC Charlotte Bioinformatics