



UNIVERSITY OF
CAMBRIDGE

Department of Chemistry

Open-access experiments on Arran 700MHz cryoprobe

Peter Gierth

Senior NMR Specialist, Yusuf Hamied Department of Chemistry

University of Cambridge ptg20@cam.ac.uk

green impact

Silver Award



Rationale

- NMRKiosk will run spectra overnight (7pm-8am)
- Samples can be submitted any time to wait in the queue
- We want reasonable sample throughput
- But also better data than the current systems, particularly carbon
- Cryoprobe has ability to deal with lower concentration samples

- We are testing new methods

- Trained user access available in daytime with support from NMR team

Experiment summary – see later slides for detail

CHARACTERISATION

- Standard full char. for >5mM conc.

SHORT CARBON

- 10 minute carbon

PHIPPS UDEFT CHARAC

- Special char. for dilute/fluorinated samples

UDEFT CARBON

- Carbon for dilute/fluorinated samples

CHAR FOR ALKYNES etc

- For samples with odd C-H J coupling

CHAR FOR 90% H2O SAN

- For samples with a lot of water

Fair use rules

- We want to increase capacity for everyone
- New groups coming to the department
- Short carbon: **up to 4 per night**
- Standard char, UDEFT carbon: **up to 2 per night**
- Phipps char, H₂O/D₂O char, Alkynes char, **1 per night**
- Charging: 2 GBP for the short carbon, 4 GBP for others

2H spectrum

- For internal debugging purposes we acquire a quick 2H spectrum
- Last experiment in each case
- Mostly not interesting- just solvent peak
- But allows us to see how much deuterium is there
- If it fails to lock, might help us understand why
- Quality control of solvents can be useful...

IMPORTANT: Ionic / conductive samples

- The cryoprobe is much more sensitive to sample conductivity
- Potential tuning problems
- Potential loss of data quality due to pulse miscalibration
- If there is 50% increase in pulse length you will get a note with the data email (this will also indicate other problems that may have occurred):



Problems occurred while running this sample:

Measured proton pulse 19.30us is more than 50% longer than the reference pulse length 11.80us - data quality may be compromised.

Does your sample have high ionic strength?

Please talk to the NMR service team about whether medium or thick wall tubes are more suitable for similar samples.

Please contact the NMR service team in case of any questions!

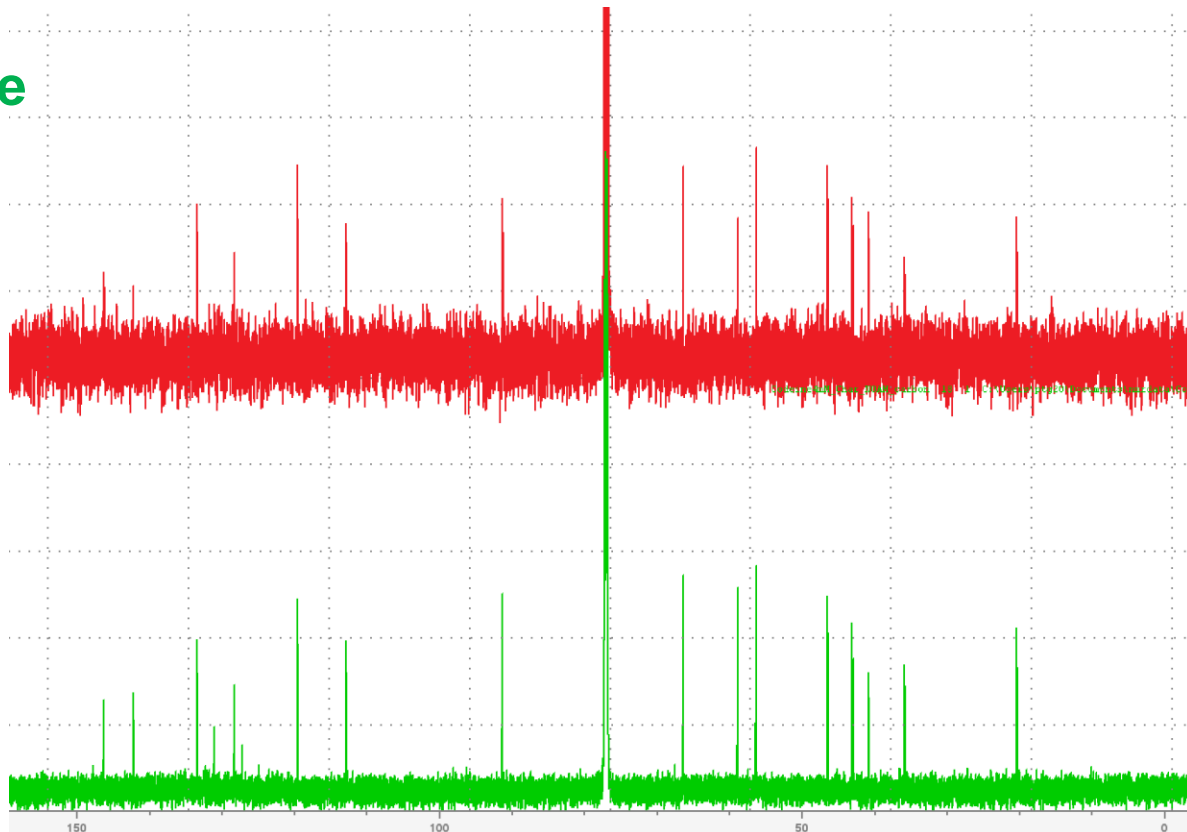
nmr@ch.cam.ac.uk

Carbon experiments

- Carbon S:N comparisons on standard ethylbenzene sample:
 - Arran, 700 MHz TXO cryoprobe: **2900:1**
 - Aberlour, service 500MHz DCH cryoprobe: 2900:1
 - Tobermory, 400MHz Prodigy cryoprobe **600:1**
 - Glenfairn, 500MHz broadband probe **360:1**
- **Experiment time $\propto (S:N)^2$ – at least 23x faster than other open access!**

Carbon experiments

- Standard long carbon on Tobermory/Glenfairn: **100 minutes**
- New standard short carbon on Arran: **10 minutes!**
- **4mM sample**



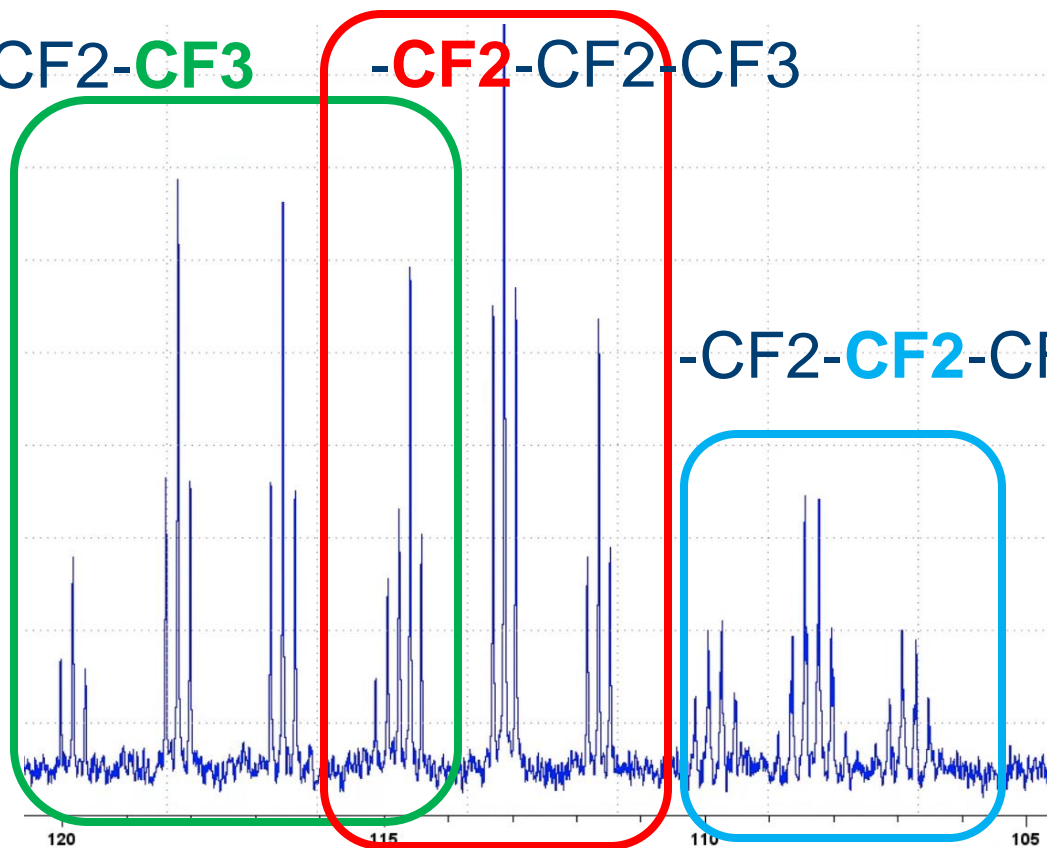
UDEFT carbon

- Example for $-C_3F_8$ moiety – 60mM concentration:



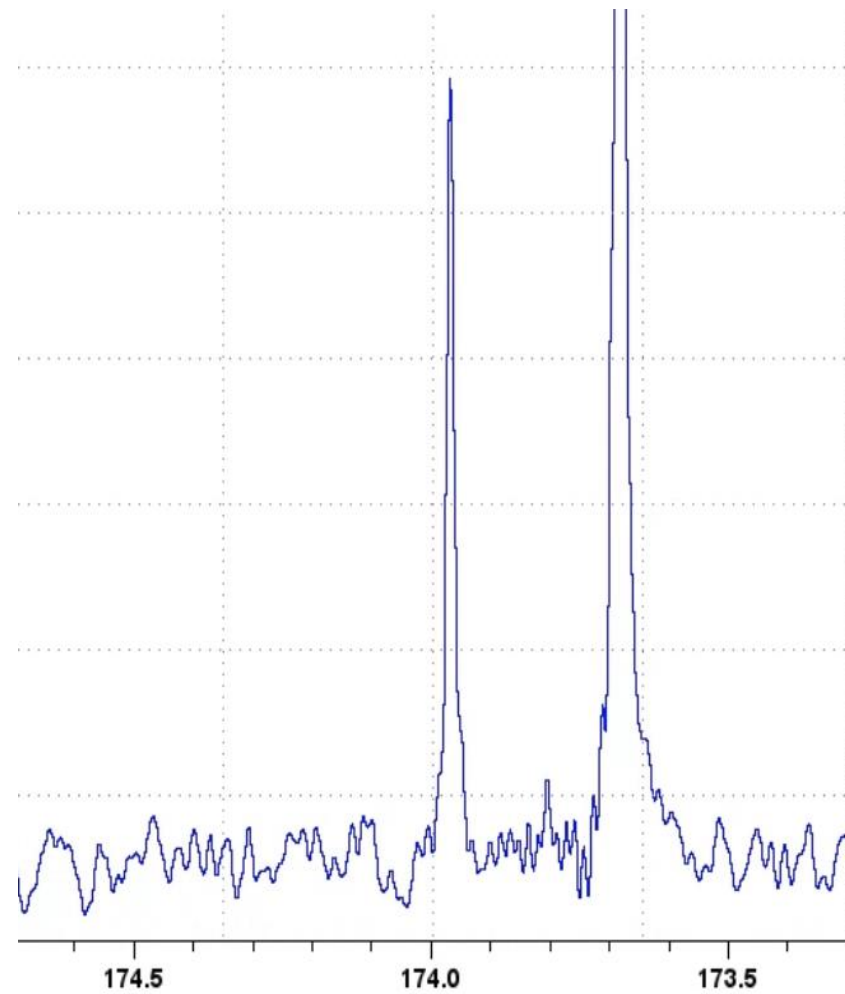
- 20mM OK for $-C_3F_8$

- Less is OK for $-C_2F_5$



UDEFT carbon: weak samples

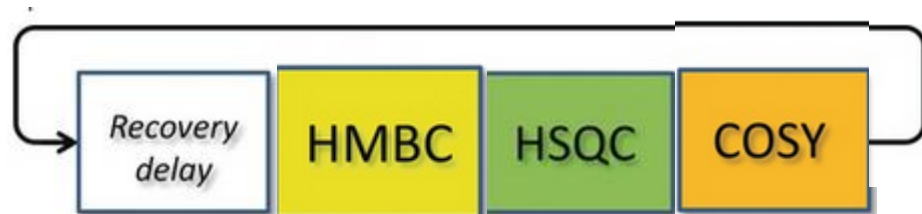
- Minor component concentration <4mM
- S:N for carbonyl ~20:1
- => **1mM** is possible



Characterisation experiments

- Speed plus sensitivity...
- Glenfairn takes **105** minutes/sample
- New char on Arran: **>30** minutes/sample
- Still, better sensitivity and resolution on Arran

Time saving by simultaneous experiments



- Time saving without losing sensitivity in HSQC/HMBC
- Generates a combined dataset (experiment 14) which is automatically split
- **Experiments 141/142/143 are HMBC/HSQC/COSY** respectively
- **Process as normal** – list of topspin processing commands in title

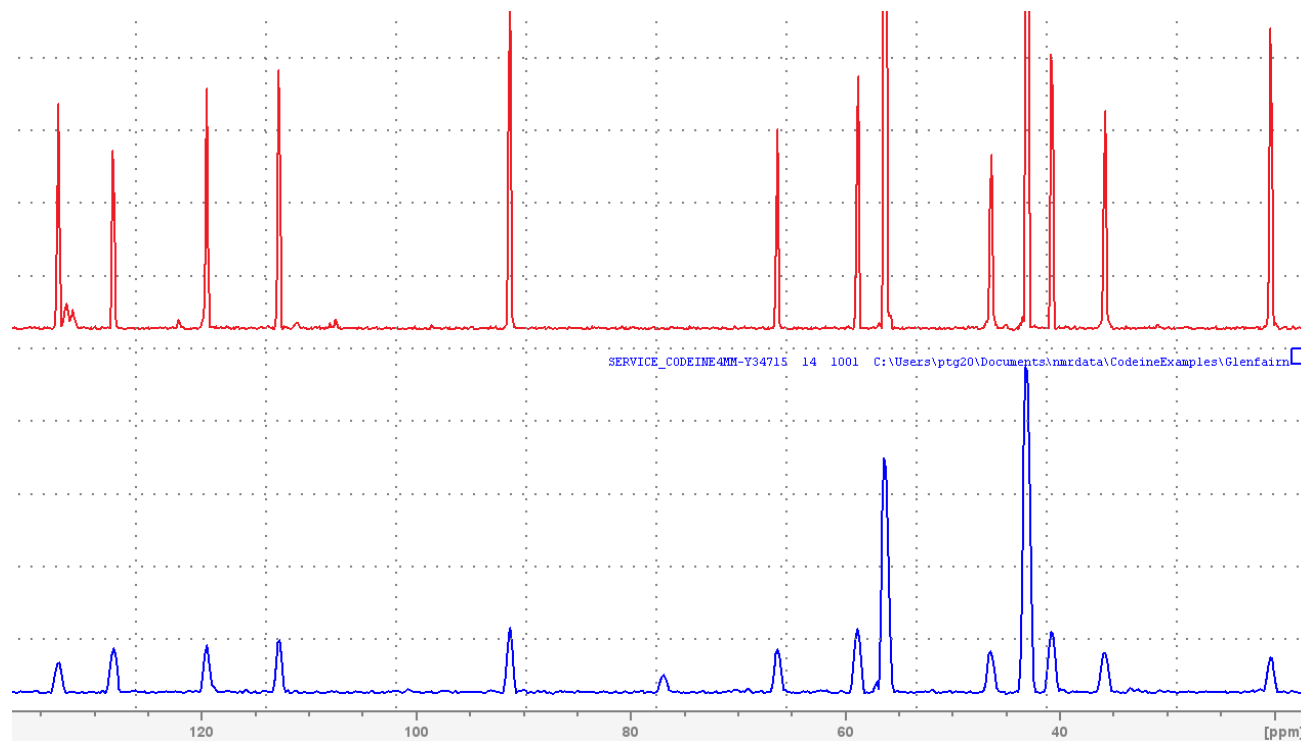
NOAH: NMR Supersequences for Small Molecule Analysis and Structure Elucidation

Dr. Ēriks Kupče ✉ Prof. Tim D. W. Claridge ✉

- <https://doi.org/10.1002/anie.201705506>

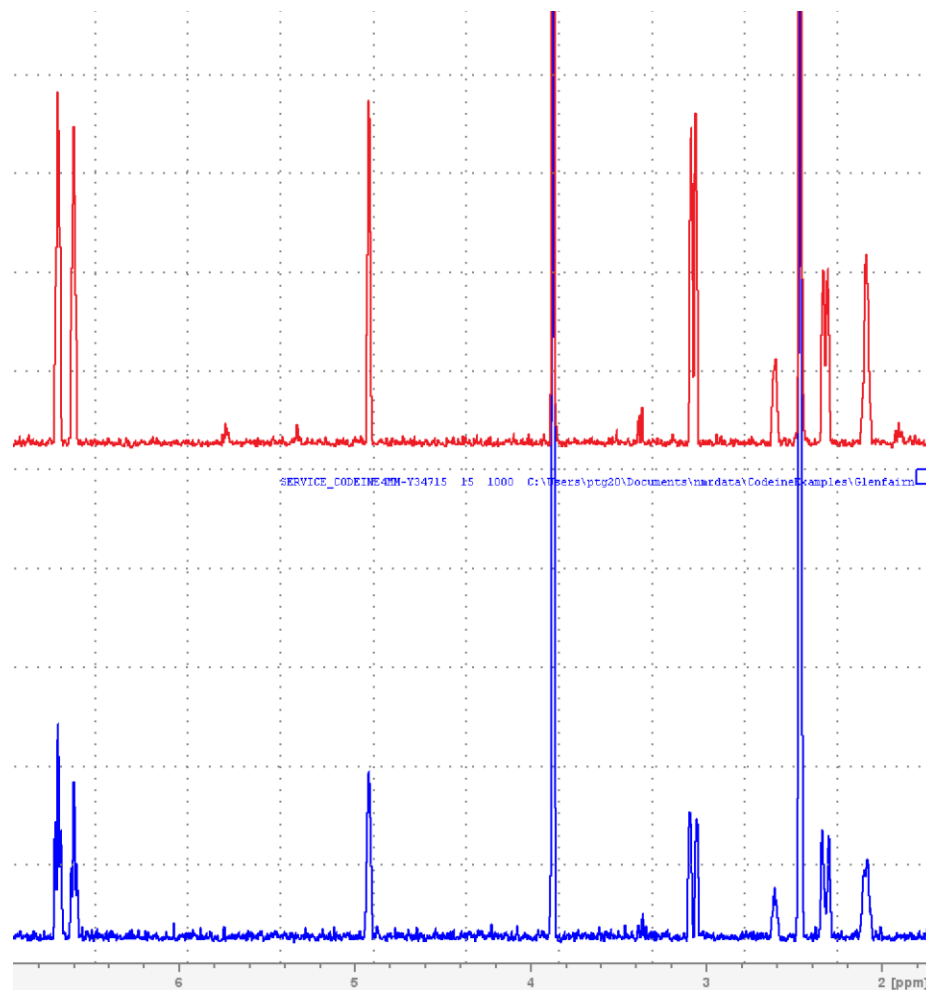
HSQC: Better sensitivity and resolution

- **Arran** vs **Glenfairn**
- Positive projection of HSQC, scaled to same noise level
- Carbon range on Arran also covers aldehydes!

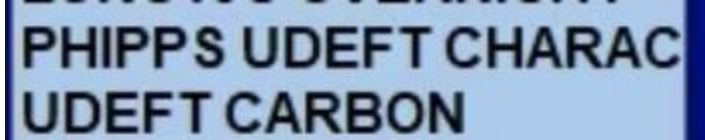


HMBC: more sensitivity

- **Arran** vs **Glenfairn**
- Positive projection of HMBC
- Scaled to same noise level



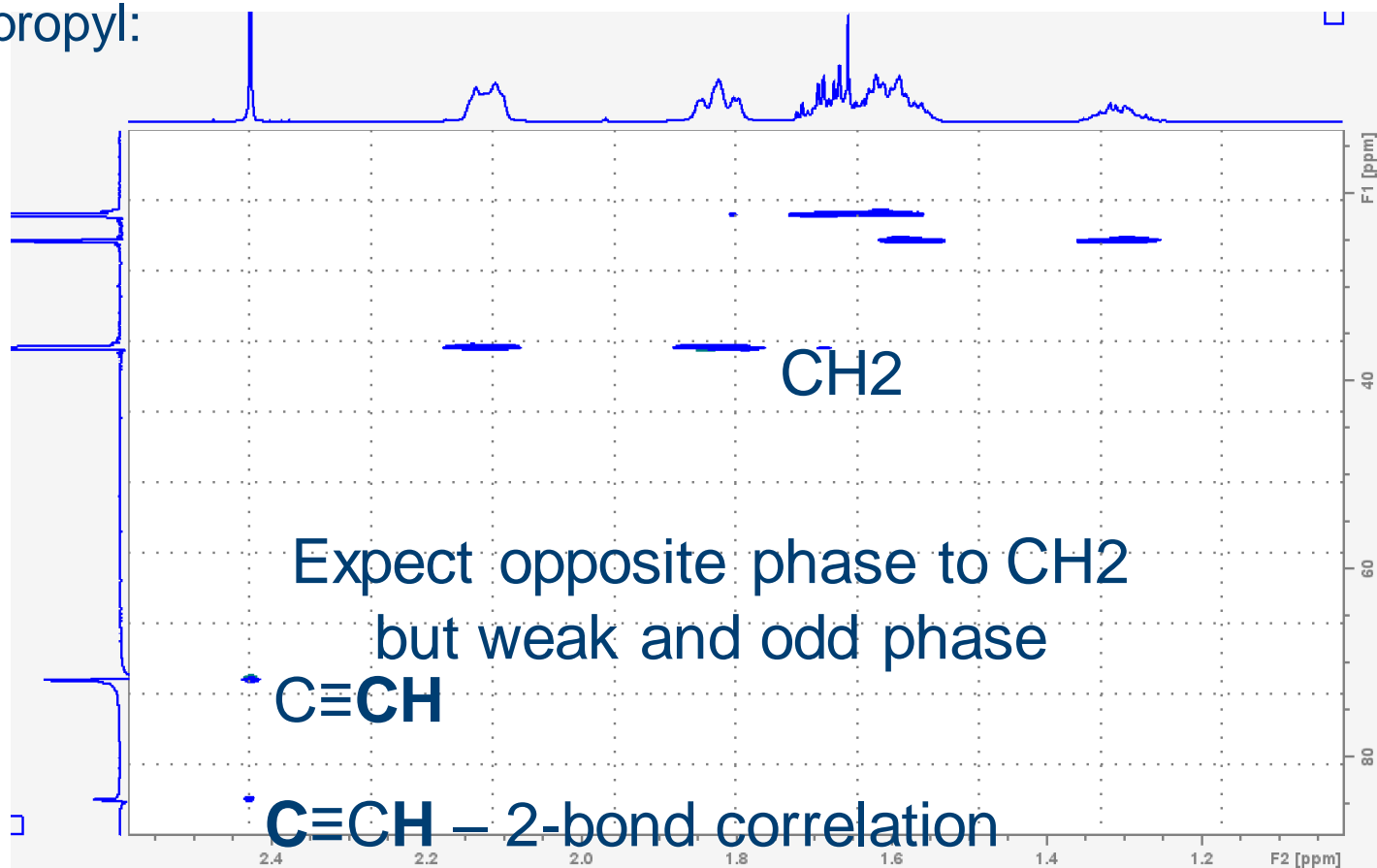
Challenging samples

- What about things you would previously submit to service?
- Concentration limits? Example sample above is **4mM**
- **For samples >5mM concentration short carbon is probably OK**
- **Likewise standard characterization**
- For weaker samples, and things with fluorine couplings in:


PHIPPS UDEFT CHARAC
UDEFT CARBON
- Slightly lower resolution carbon but better sensitivity – about **1mM concentration is possible**

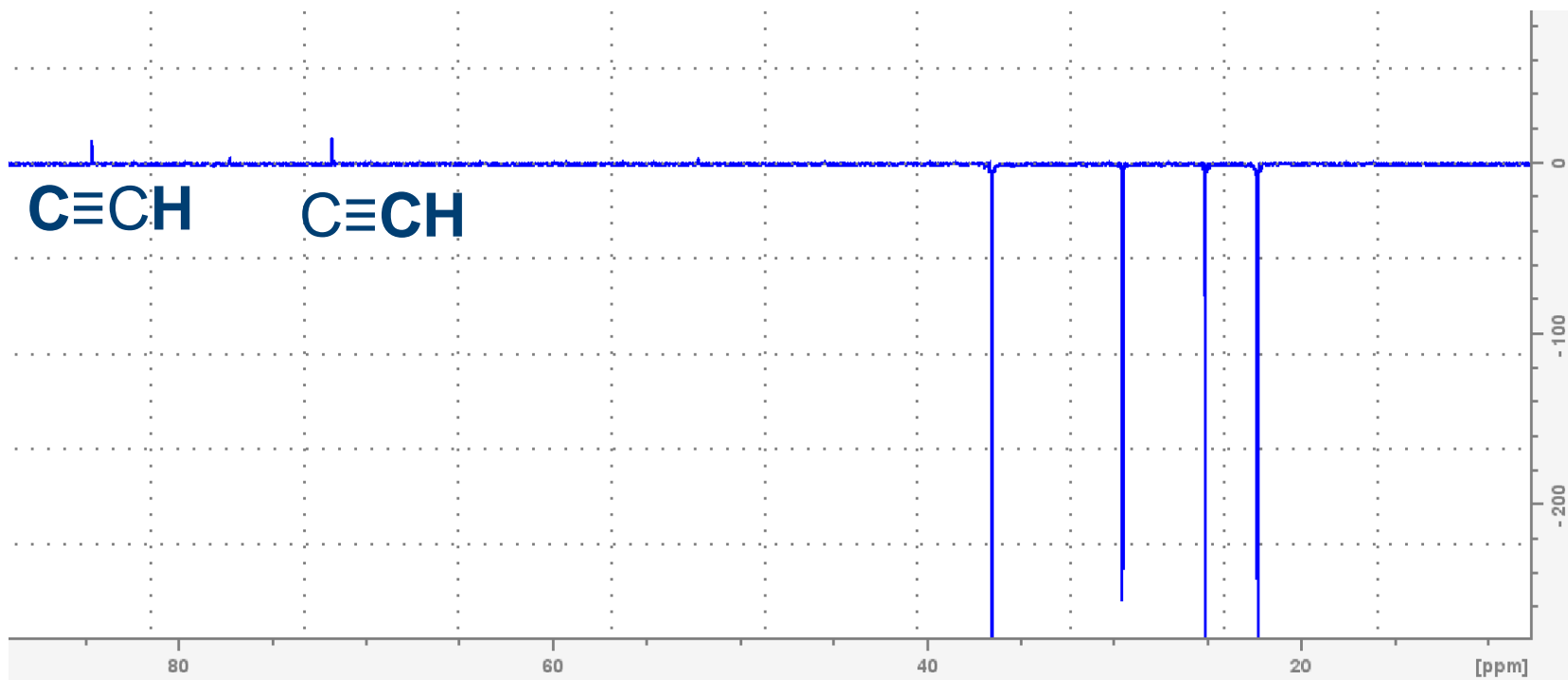
Special cases

- The way our standard HSQC/DEPT work we get odd/missing peaks for alkynes/cyclopropyl:



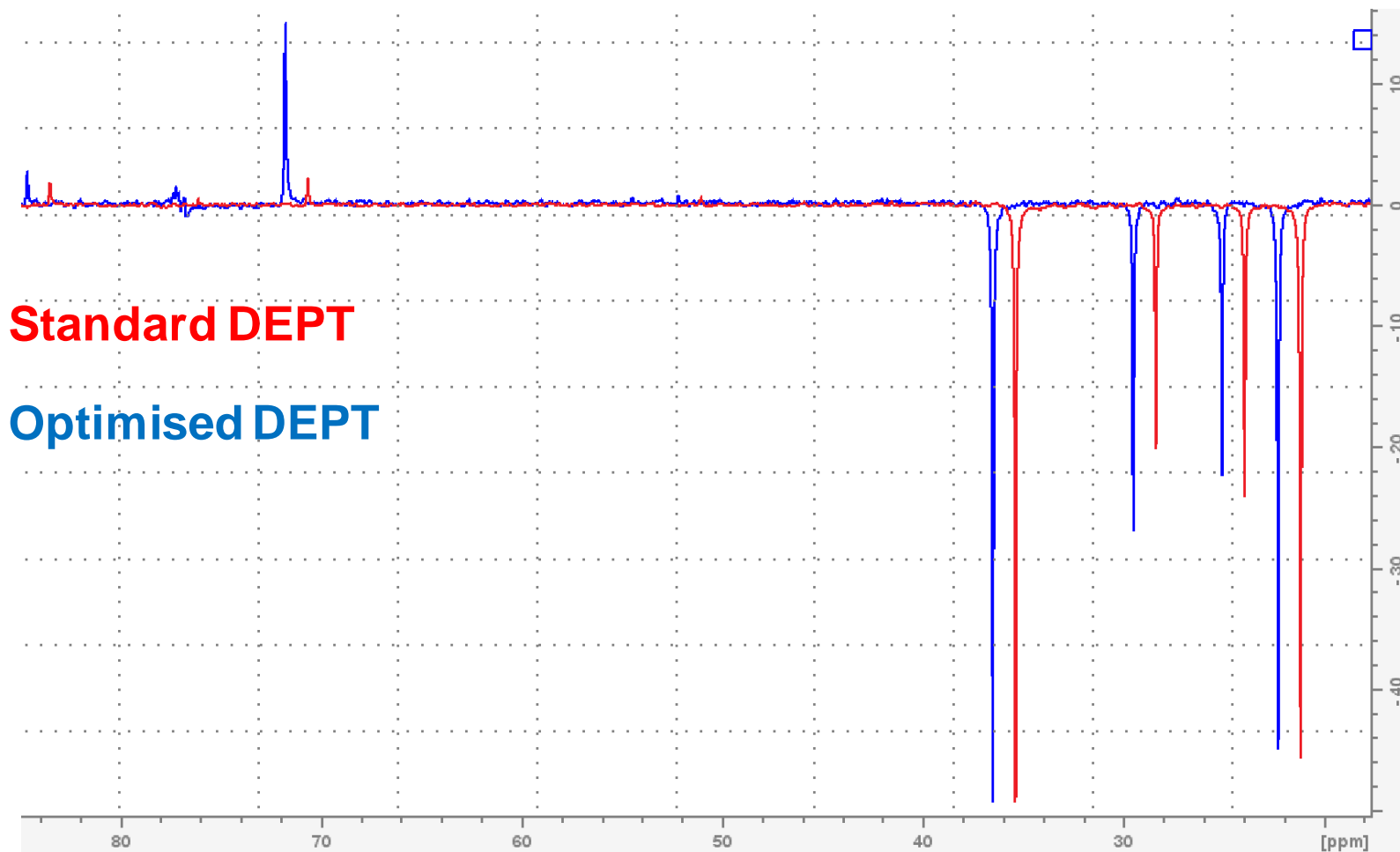
Special cases

- In DEPT, terminal and quaternary alkyne peaks show up with similar low intensity:



J-insensitive experiments: DEPT

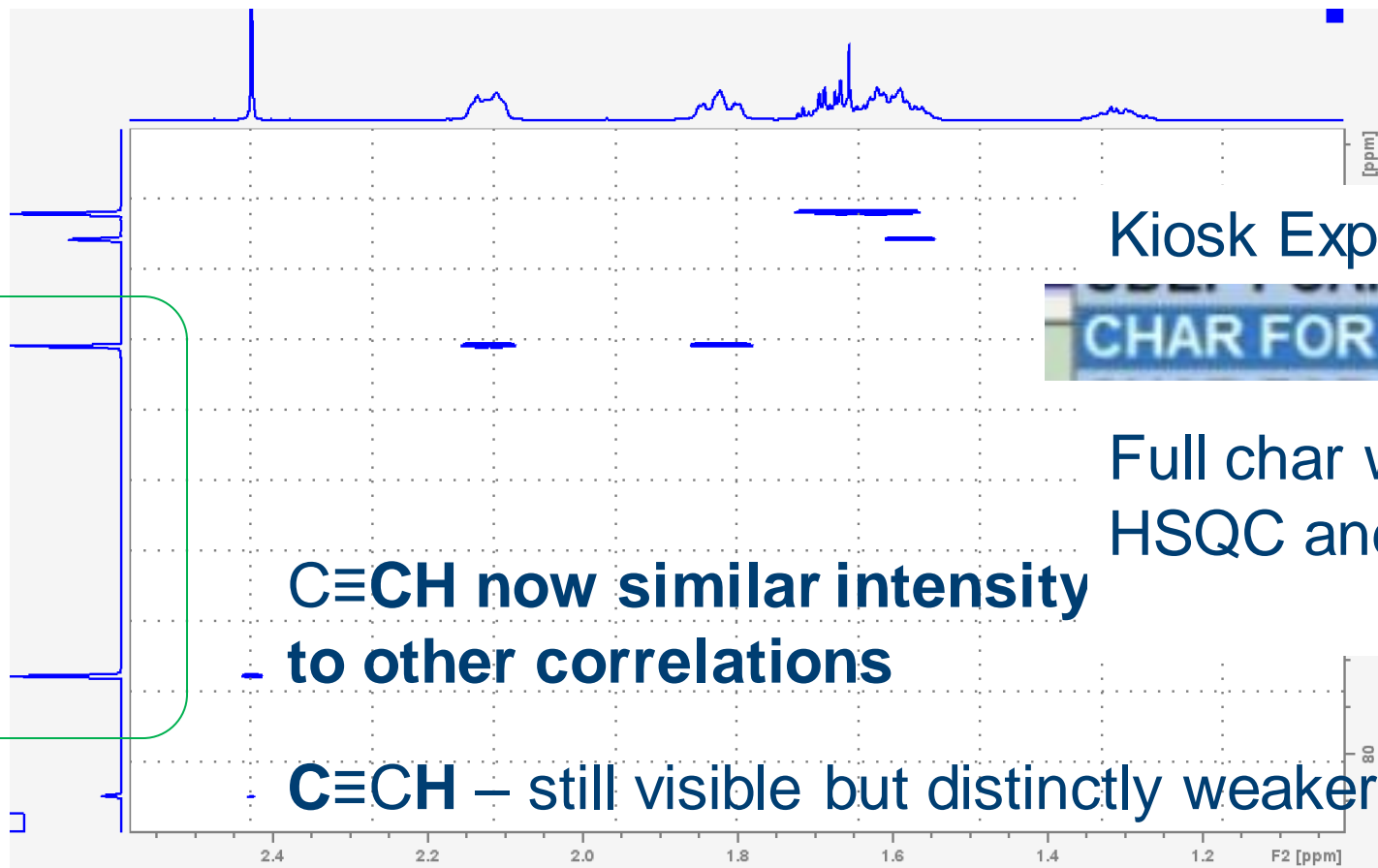
ACCORD-DEPT <https://doi.org/10.1002/mrc.2701>



J-insensitive experiments – HSQC

COB-HSQC <https://doi.org/10.1002/mrc.3846>

- HSQC, no multiplicity editing, for $J=120\text{-}250\text{Hz}$:



Samples in (mostly) protonated solvent

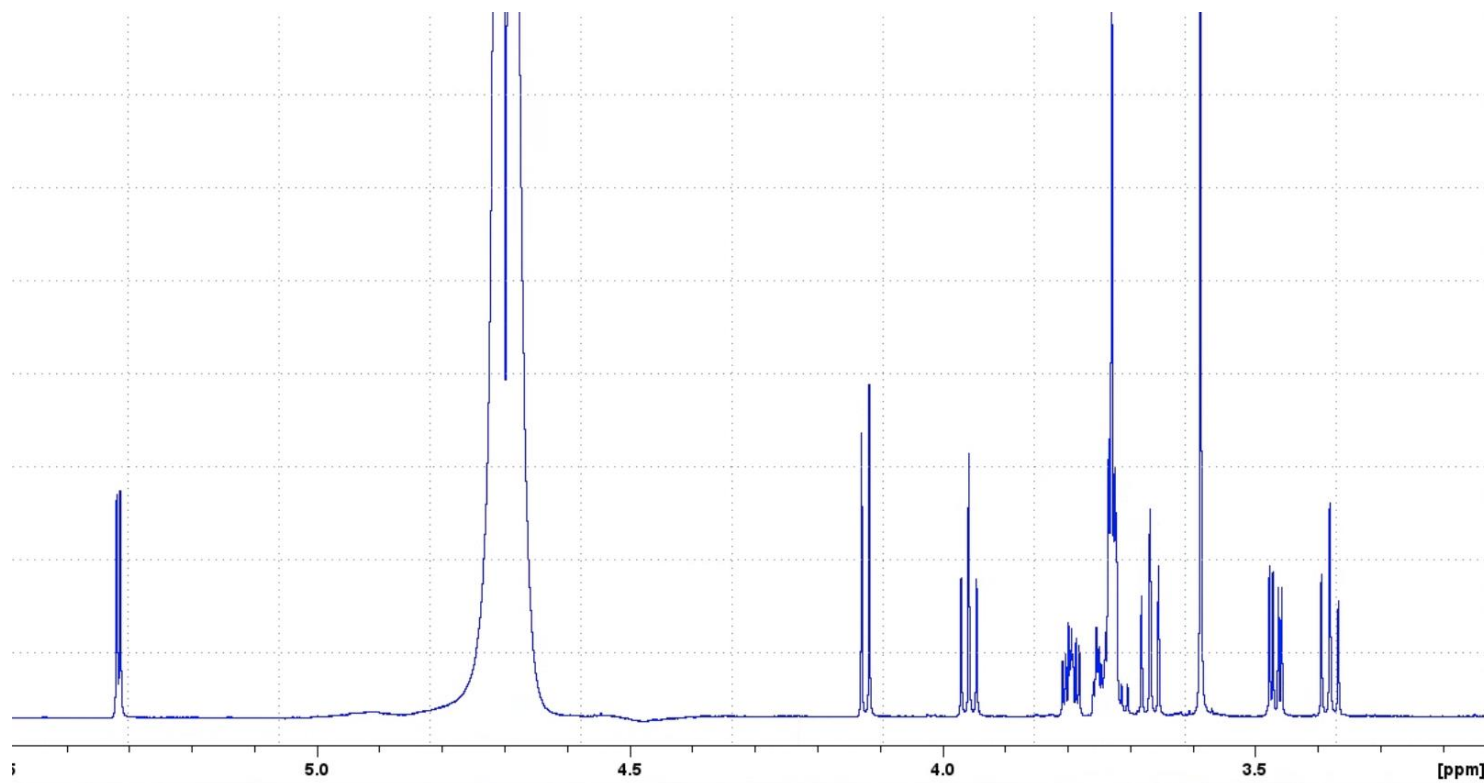
- H₂O+D₂O solvent available - some D₂O needed for lock (>5%)
- Standard parameters don't do a very good job of getting rid of water signal
- So let's try a modified experiment
- Pulse lengths will be calibrated, but if the proton pulse is too long the experiment will fail. If your sample is very ionic, may need medium wall tubes (Wilmad 524-PP)

CHAR FOR 90% H₂O SAM

- Also suitable for samples with a lot of excess water

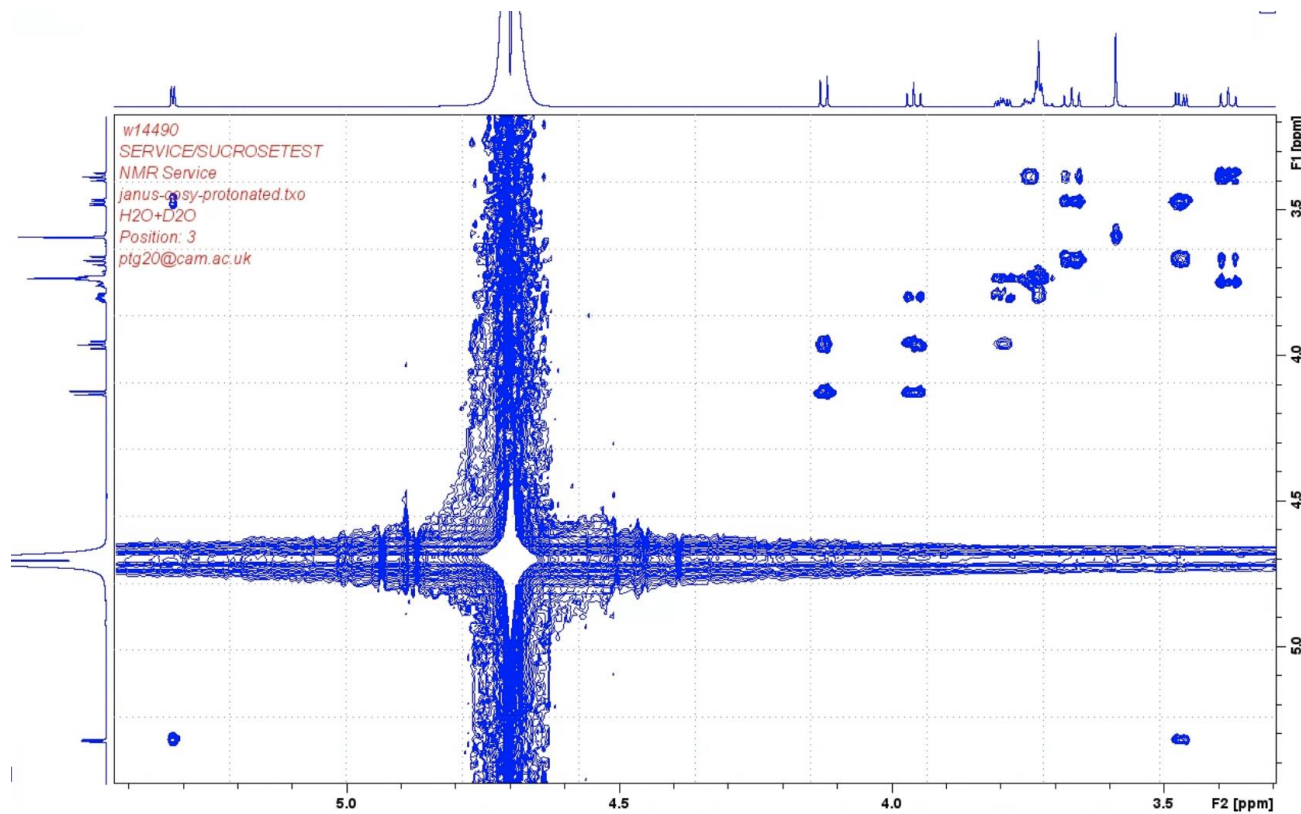
90% H₂O results, 2mM sucrose sample

- Automated solvent suppression (experiment 11):



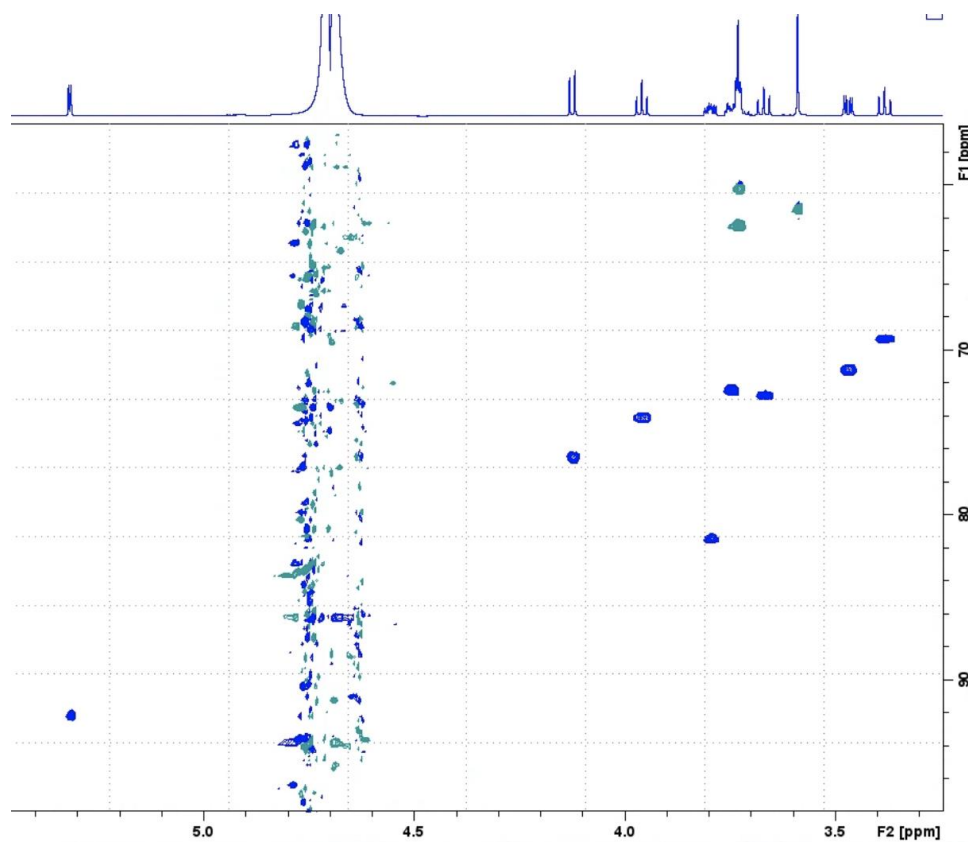
90% H₂O results, 2mM sucrose sample

- COSY, solvent suppression with only double quantum filter:



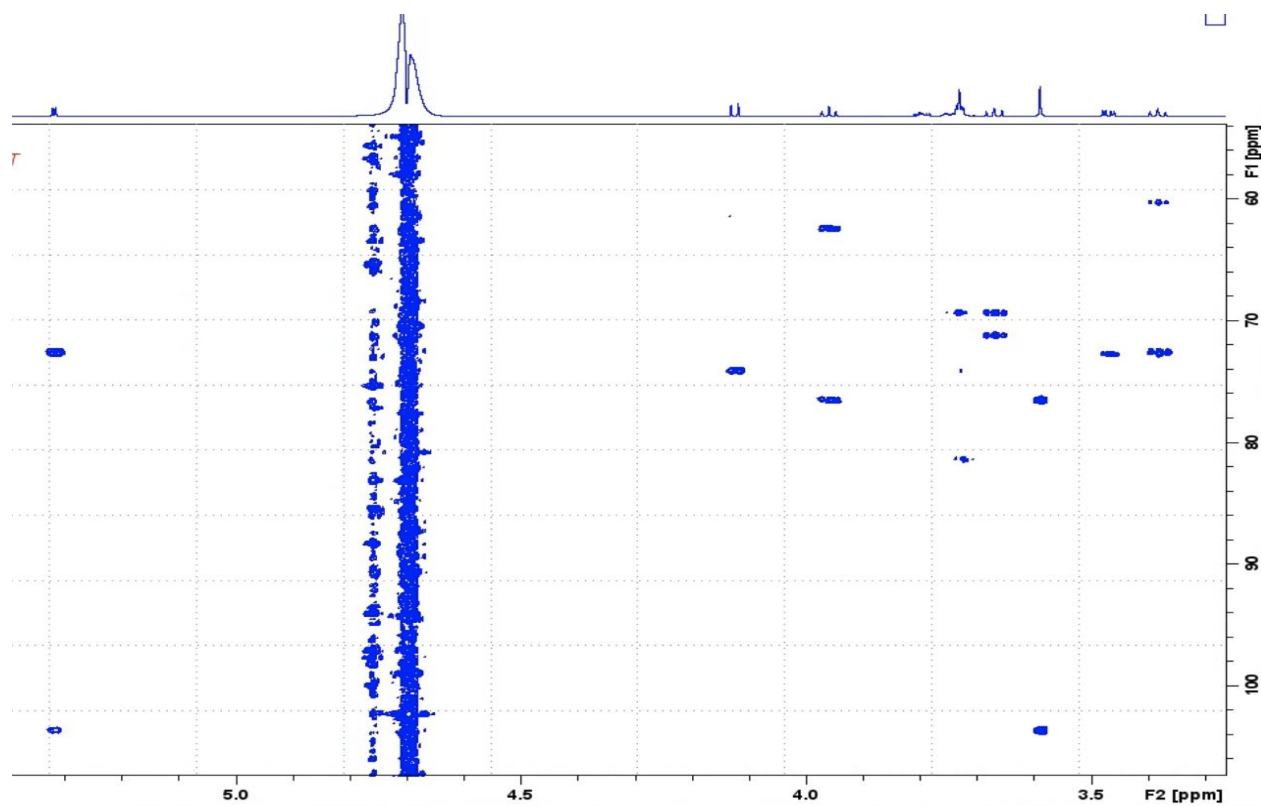
90% H₂O results, 2mM sucrose sample

- HSQC, solvent suppression by selection of only CH_n signals:



90% H₂O results, 2mM sucrose sample

- HMBC, solvent suppression by selection of only C---H_n signals:

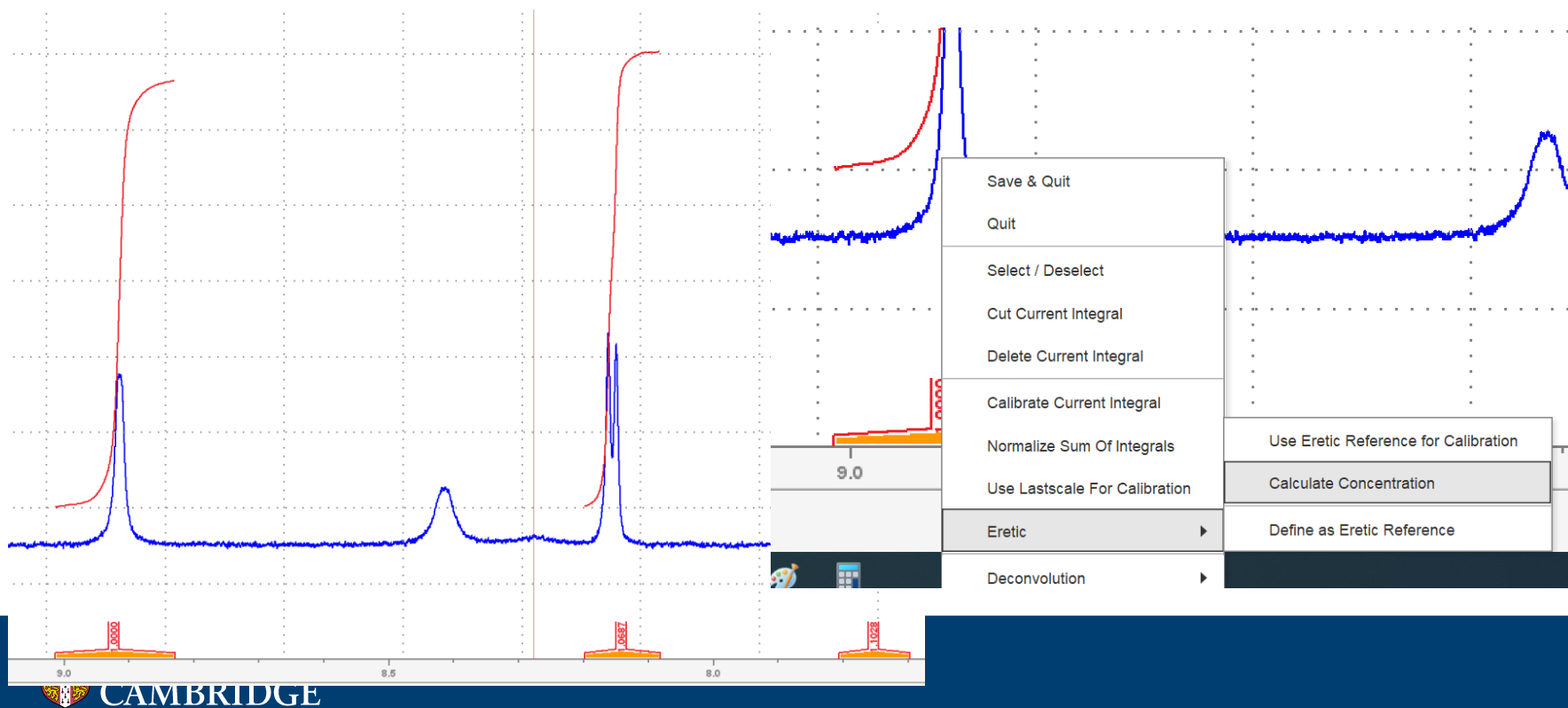


Quantitative proton

- Standard proton in experiment 10 is quantitative!
- Needs external reference data to get numbers out
- Get the zipfile from here:
- www.ch.cam.ac.uk/analytical/nmr/files/Arran_QuantRef_0.1EB_2022_09_26_CPTXO.zip
- Unzip that onto your computer somewhere useful

Quantitative proton

- Integrate peaks in your spectrum, and click to select integral of interest
 - Ctrl-click to select multiple
- Right click integral and select Eretic->calculate concentration



Quantitative proton

- Browse to the reference dataset- go into the pdata/1 folder

ERETIC2 Quantification

Reference dataset

Name

Concentration 9.4 mmol/l

Quantified dataset

Name

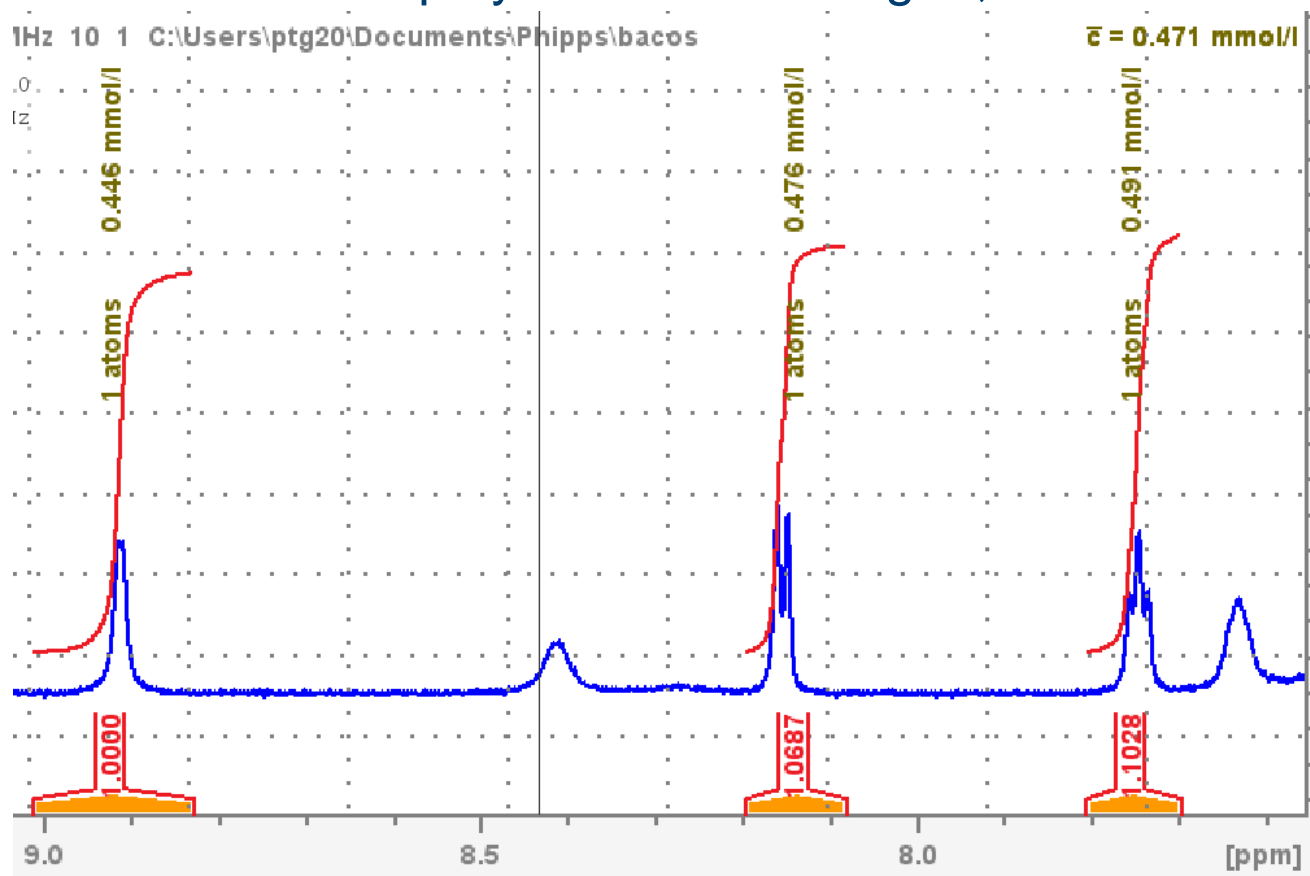
Sample volume [ml]

Number of atoms	Region start [ppm]	Region end [ppm]	Molecule name	Molar mass [g/mol]		
<input type="text" value="1"/>	<input type="text" value="9.013649"/>	<input type="text" value="8.829207"/>	<input type="text"/>	<input type="text"/>	<input type="text" value="+"/> <input type="text" value="-"/>	
<input type="text" value="1"/>	<input type="text" value="8.198394"/>	<input type="text" value="8.081617"/>	<input type="text"/>	<input type="text"/>	<input type="text" value="+"/> <input type="text" value="-"/>	
<input type="text" value="1"/>	<input type="text" value="7.806591"/>	<input type="text" value="7.697453"/>	<input type="text"/>	<input type="text"/>	<input type="text" value="+"/> <input type="text" value="-"/>	

- Set number of protons for each integral region, and click OK

Quantitative proton

- Concentration will be displayed for each integral, and an average:



Quantitative proton- limitations!

- We don't have good data on the reproducibility of the result
 - Estimate something like 10% error
 - If you want real quantification talk to us!
- Affected by ionic strength of samples:
 - Indicated concentrations will be lower than actual
 - We can work out the answer in principle...
 - This applies to any sample where the proton pulse ends up longer than normal