## Introduction to biomolecular NMR spectroscopy

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## Course outline

- Approx. 50:50 split:
  1 hr lectures,
  1 hr examples class
- Exercises from Keeler, Understanding NMR Spectroscopy, 2nd ed
- I will NOT be lecturing NMR theory directly – expect selfstudy during the week
- Excellent lectures from James Keeler are already available on YouTube: <u>http://goo.gl/PdbkUQ</u>



## Further reading

• Online lectures for those who want a deeper understanding of quantum mechanics:

http://theoreticalminimum.com



## Nuclear spin and the Zeeman effect

- Nuclear spin S = 0, 1/2, 1, 3/2, ... is a fundamental quantum mechanical property of a nucleus
- Zeeman effect: In the presence of a magnetic field, *B*, the system splits into (2S 1) energy levels

#### Magnetically-active nuclei



NMR 'friendly'

quadrupolar moment => broad lines

## Common nuclei for biomolecular NMR

	Spin	Natural abundance	γ / 10 <sup>7</sup> s <sup>-1</sup> T <sup>-1</sup>	Frequency / MHz
1H	1/2	99.985%	26.7522	700
2H	1	0.015%	4.1066	107.5
13C	1/2	1.108%	6.7283	176
15N	1/2	0.37%	-2.7126	71
19F	1/2	100%	25.18148	659
31P	1/2	100%	10.8394	283.6

frequencies calculated for  $B_0 \approx 16.4 \text{ T}$ 

#### The chemical shift

• Exact resonance frequencies are dependent on shielding by electrons at the nucleus:

#### <sup>1</sup>H chemical shifts



• NMR absorption frequencies are dependent on the field strength B<sub>0</sub>. Normalise using frequency of a reference compound to define the 'chemical shift', comparable between different NMR spectrometers:

DSS

https://www.cpp.edu/~lsstarkey/courses/NMR/NMRshifts1H-general.pdf

#### <sup>13</sup>C chemical shifts



http://chemwiki.ucdavis.edu/Physical\_Chemistry/Spectroscopy/Magnetic\_Resonance\_Spectroscopies/ Nuclear\_Magnetic\_Resonance/NMR%3A\_Experimental/NMR%3A\_Interpretation

#### 15N chemical shifts



http://chem.ch.huji.ac.il/nmr/techniques/1d/row2/n.html

#### Cutaway of an NMR spectrometer



Introduction to NMR spectrometers

http://u-of-o-nmr-facility.blogspot.co.uk









http://web.mit.edu/speclab/www/Facility/shim-probe-sample.html







## Quenching



## Sensitivity

- NMR is not a sensitive technique due mainly to the fact that the difference between energy levels is very small.
- The absolute sensitivity depends on many factors:

$$\mathrm{SNR} \propto rac{n \gamma_{\mathrm{e}} \sqrt{B_{\mathrm{0}}^{3} \gamma_{\mathrm{d}}^{3} t}}{\sqrt{R_{\mathrm{S}}(T_{\mathrm{S}}+T_{\mathrm{A}}) + R_{\mathrm{C}}(T_{\mathrm{C}}+T_{\mathrm{A}})}}$$

## Cryoprobes



## Cryoprobes



H. Kovacs et al. / Progress in Nuclear Magnetic Resonance Spectroscopy 46 (2005) 131-155

#### NMR tubes and sample volume

- Regular NMR tube: 550 600 µL
- Shigemi tube: 250 300 μL

A



600 μL adjusted to maximum depth \*Recommended\*



 $\begin{array}{c} 300 \ \mu L \\ \text{positioned too low} \\ \text{sample not in detected region} \end{array}$ 

# 

• Shigemi without plunger: 400 µL

• 3 mm tubes: 200 – 250 µL

400 μL centered in detected region acceptable but NOT recommended for normal applications; difficult to shim

#### Cryoprobes



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#### NMR tubes and sample volume



## Tuning and matching

• Probe electronics act as a bandpass filter: for optimum sensitivity, must tune and match to let your signals through!





Well Tuned and Well Matched

Poorly Tuned but Well Matched



## Locking

- Modern NMR demands highly homogeneous fields that do not vary over time
- · Lock system: 'spectrometer within a spectrometer'
- Constantly monitors <sup>2</sup>H frequency in solvent (HDO resonance) and adjusts electromagnet to compensate for any drift

# Shimming

- Process of optimising field homogeneity to  $\leq 1$  ppb (<1 Hz)
- But protein resonances are broad anyway why bother?

#### poorly shimmed magnet

magnetic field varies along nmr tube (z-axis)



#### Effect on lineshapes



## Gradient shimming

- Magnetic resonance imaging (MRI) experiment to map the water chemical shift across sample
- Shim coils then adjusted using their known profiles to obtain a homogenous field



#### Sample preparation

• Solvent: H<sub>2</sub>O / D<sub>2</sub>O?



#### Autoshim



#### Sample preparation

- Solvent: H<sub>2</sub>O / D<sub>2</sub>O?
- Choice of buffer:
  - protonation / spectral overlap?
  - ionic strength



Figure 3. One-dimensional spectra of a 1 mM lysozyme sample measured in 50 mM sodium phosphate, 50 mM HEPES/NaOH, or 50 mM MOPS/BIS-TRIS propane buffer, all pH 7, and in 50 mM MES/BIS-TRIS, pH 6.0. Only the most high-field-shifted regions of the spectra are shown.

## Effect of buffers on sensitivity

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buffer	$R_{\rm e}/R_{\rm c}$	sensitivity factor L	conductivity (mS/cm)
pentasodium tripolyphosphate	$2.71 \pm 0.04$	0.22	31.3
potassium chloride	$1.93 \pm 0.04$	0.26	23.3
disodium phosphate (Na <sub>2</sub> HPO <sub>4</sub> )	$1.89 \pm 0.04$	0.26	22.0
sodium pyrophosphate	$1.70 \pm 0.04$	0.27	20.2
sodium chloride	$1.64 \pm 0.04$	0.28	18.1
PIPES	$1.33 \pm 0.04$	0.30	14.8
$\beta$ -glycerophosphate	$1.31 \pm 0.04$	0.30	14.9
potassium phosphate (KH <sub>2</sub> PO <sub>4</sub> )	$1.25 \pm 0.04$	0.31	14.1
TRIS HCl	$1.24 \pm 0.04$	0.31	14.1
BIS-TRIS HCl	$1.12 \pm 0.03$	0.33	13.62
sodium acetate	$1.11 \pm 0.03$	0.33	12.2
sodium phosphate (NaH <sub>2</sub> PO <sub>4</sub> )	$0.95 \pm 0.03$	0.35	11.0
sodium TAPS	$0.90 \pm 0.03$	0.36	9.55
sodium MES	$0.88 \pm 0.03$	0.36	10.18
sodium MOPS	$0.88 \pm 0.03$	0.36	9.86
sodium TES	$0.84 \pm 0.03$	0.37	9.41
sodium HEPES	$0.84 \pm 0.03$	0.37	9.25
tetrabutylammonium dihydrogen phosphate	$0.69 \pm 0.03$	0.40	9.00
HEPES	$0.22 \pm 0.02$	0.62	0.06
TAPS	$0.14 \pm 0.02$	0.70	0.29
CAPS	$0.14 \pm 0.02$	0.70	0.7
TES	$0.12 \pm 0.02$	0.73	0.25
MOPS	$0.10 \pm 0.02$	0.76	0.04
CHES	$0.08 \pm 0.02$	0.79	0.06
MES	$0.08 \pm 0.02$	0.80	0.15
bicine	$0.05 \pm 0.02$	0.86	0.031
BIS-TRIS propane	$0.05 \pm 0.02$	0.86	0.022
TRIS base	$0.03 \pm 0.02$	0.91	0.1
BIS-TRIS	$0.02 \pm 0.02$	0.93	0.0236
deionized-distilled H <sub>2</sub> O	$0.01\pm0.02$	0.98	0.0023

Table 1. Rs/Rc Values, Expected Sensitivity Factor L, and Dc Conductivity of Several Different Salts, All at 200 mM Concentration

Kelly, A. E., Ou, H. D., Withers, R. & Dötsch, V. JACS 124, 12013-12019 (2002)

#### Sample preparation

- Solvent: H<sub>2</sub>O / D<sub>2</sub>O?
- Choice of buffer
- pH/temperature



#### Buffer chemical shifts as internal pH reference



Effect of pH on <sup>1</sup>H,<sup>15</sup>N HSQC spectra



## Effect of temperature on <sup>1</sup>H,<sup>15</sup>N HSQC spectra



## Sample preparation

- Solvent: H<sub>2</sub>O / D<sub>2</sub>O?
- Choice of buffer
- pH/temperature
- DSS
- Protease inhibitors
- Filtration/centrifugation

