Dynamic Nuclear Polarization for Neutron Scattering

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Neutron protein crystallography

- Usually, macromolecular crystallography uses X-ray facilities to measure molecular structure
 - Modern light sources have incredibly high flux
- Using neutrons for crystallography has pros/cons:
 - Comparatively low flux
 - Sensitivity of the neutron cross section to lighter elements (especially hydrogen)
 - Sensitivity to isotopes
- NPX is a unique experimental tool for the experimental location of key hydrogen atoms and water molecules in biological macromolecules.



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HIGH FLUX ISOTOPE

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- NPX is a unique experimental tool for the experimental location of key hydrogen atoms and water molecules in biological macromolecules, but use is limited by requirement for huge crystals.



Community Scientific Needs: Smaller Samples and Faster Data Collection



Grand Challenges in Biological Neutron

Scattering

Workshop Report University of California San Diego, January 17th – 18th, 2014

Organizers: Susan Taylor (University of California San Diego) and Heidi Hamm (Vanderbilt University) Grand Challenges: Cold neutron flux:

"Radically increase the flux of neutron beam lines at long wavelengths in particular for small angle scattering, crystallography, and spin echo."

Gains Required

- Data set in 1 day x20
- Reduce crystal size to 0.001mm³ x100
- How can we accomplish this without building a new facility?

At the workshop, 37 invited leading researchers from more than 20 different universities and institutes joined 5 participants from the Neutron Sciences Directorate of ORNL to map out 10 grand challenges that we face in biological research over the next 10 years.



Spin Dependence of Neutron Scattering

- For a lattice of identical atoms with non-zero spin, the incoherent and coherent cross section for neutron scattering has a dependence on the spin alignment of the neutron and the struck nucleus
- Control over spin orientation gives control over scattering.
- Neutron Polarization is well developed
 - Supermirror polarizers
 - 3He filters
- Nuclear Polarization is more challenging

$$\left(\frac{d\sigma}{d\Omega}\right)_{inc} = \frac{b^2}{4} \{I(I+1) - pPI - P^2I^2\};$$

$$\left(\frac{d\sigma}{d\Omega}\right)_{coh} = \left\{b_0^2 + bb_0 IpP + \frac{I^2 P^2 b^2}{4}\right\};$$



Spin Dependence of Neutron Scattering from Hydrogen

- Hydrogen is a special case
 - The spin dependence of the hydrogen cross section is very large
 - Looking for hydrogen locations is a primary motivation for Neutron Protein Crystallography
- Incoherent scattering can be removed entirely (true for any nucleus)
- Coherent scattering can be increased by a factor of 7 (or 20)
- An increase in signal to noise enters squared into the calculation figure of merit
 - Factor of 10 in signal to noise is a factor of 100 in flux/sample size/data collection time
- The hydrogen nucleus is polarizable



Coherent, incoherent and total scattering cross section of hydrogen as a function of the proton polarization for fully polarized neutrons.

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Tests at IMAGINE







Refrigerator and Magnet

- Stock Dilution Refrigerator from Bluefors
 - 400µW@100mK
 - >1mW@1K
 - Base temperature (unmodified) ~7mK
 - Cryogen Free
- 5T Solenoid
 - Warm 100mm bore
 - Cryogen Free







NMR

- Absolute polarization measurements are challenging
 - Target sizes are generally <1mm³
 - TE signals are extremely small
- Liverpool Q-meter almost works
 - With sufficient gain and careful work, a decent TE can be measured
 - Error is high
 - Still hard to trust
 - Sensitive to very small contaminations
- In general, absolute polarization measurement is not needed
 - The higher the better
 - Absolute numbers may be extracted from diffraction data
 - Large solution samples are used to test performance



Microwave System

- Here, small sample size is helpful
 - Very low microwave power needed because the sample is tiny
- VDI diode based microwave source
 - Low cost
 - 300mW of power @140GHz
 - Ease of use
 - USB control
 - Incredibly stable frequency
 - No high voltage or cooling





Sample Interface

- Requirements
 - Cannot put the sample in the mixing chamber
 - 3He captures neutrons
 - Allow crystal rotation
 - Fit in 100mm space
 - Load sample cold
 - Crystals cannot warm past ~150K
- Sample located in a Kel-F chamber, surrounded by superfluid
 - Not sealed space
 - Large cryogenic load from 4He film/vapor
 - Hard to get repeatable temperatures
 - Sample temperatures vary from 300mK to 150mK



Paramagnetic Labeling in Protein Crystals

- Strategies
 - Site specific
 - Non-specific
- Site specific labeling (Intrinsic)
 - Mutagenesis for intrinsic/site specific labels
 - Spin-labeled mutants T4 lysozyme constructed, expressed, crystallized
 - X-ray and first neutron structures determined
- Non-specific
 - Crystals soaked in a solution with paramagnetic label



HIGH FLUX



MTSL

T4 Lysozyme Results

- Doped with TEMPO
- "Large" crystals
 - ~0.5mm-1.0mm on edge
- Detector was uncalibrated, and shifted between frames
- Short hold times in "frozen spin" mode
 - ~60-180 min T₁
 - Very high temperatures
 - ~230 mK
- Measured diffraction pattern change
- Enhancements of 2-3 in integrated diffraction pattern for anti-aligned spins
 - The enhancement of individual reflections depends varies depending on the relative contribution of hydrogen
- Consistent with maximum polarizations of around 50%





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Moving Forward

- New Scattering data will be taken starting in November 2018
- System has been updated with ¼" VCR based cold seal at the top of the sample stick
 - Seal made at low temperature using 0.005" KELF gasket
 - Appears to be very reliable and require little torque
 - Relaxation times improved by factor of 1.5-2.2
- Improved (existent) DAQ software
 - Will allow the crystal orientation to be determined
 - Allow extraction of polarization from scattering data
- New detector
 - Same design concept, but lower noise

Conclusion

- The nuclear spin dependence of neutron scattering can be used to manipulate scattering
- Polarized hydrogen has a large potential benefit to protein crystallography
 - Could allow the use of sustainably smaller samples or greatly reduced data collection time
- DNP is an effective means to polarize the hydrogen within a sample
 - Sample preparation and sample environment requirements are substantial



Application to SANS Contrast Matching

Deuteration

- The unpolarized coherent scattering length of hydrogen is -3.74 fm
- The unpolarized coherent scattering length of deuterium is 6.674 fm
- Polarization
 - Positive polarization: 10.82 fm
 - Negative polarization: -18.3 fm
 - Can be changed in-situ
 - Requires a single sample reparation
 - Work done by Stuhrmann et al
 - Current work by Kumada et al. (also working on DNP for reflectometry)





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Advanced Techniques: Localized Polarization

- If the center is an attached spin label, then the location of the polarized region can be controlled
 - Attached to a specific site on a macromolecule
 - Size and rate of propagation has been studied with SANS (van den Brandt 2006)
- Alternatively, different components of a composite sample could be selectively polarized
 - One layer of a sample for example





Advanced Techniques: Difference Measurements

- All that is required is to change the microwave frequency to change polarization sign
 - Field remains constant
 - Temperature remains constant
- Adiabatic Fast Passage or neutron spin flipper can reverse polarization more quickly
- Only thing that changes is the cross section for the nuclei, and that changes in a predictable manner
- This can be used to highlight specific structures





Spins Anti-aligned



Other Nuclei

- All non spin zero nuclei will polarize
- Polarization will be different for different nuclei
 - 15N and 13C polarize well, are used for DNP enhanced MRI and NMR measurements
- Spin dependent scattering lengths are different for each nucleus
 - 15N and 13C have very little spin dependence
- Difference measurements may still be possible
 - Different nuclei species could be selectively polarized/depolarized/flipped using a combination of NMR and DNP techniques

$$a = b_0 + b\boldsymbol{I} \cdot \boldsymbol{s}$$

$$b = \frac{2(b_+ - b_-)}{(2I+1)}$$

$$\begin{pmatrix} d\sigma \\ d\Omega \end{pmatrix}_{inc} = \frac{b^2}{4} \{ I(I+1) - pPI - P^2 I^2 \};$$
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