

Overview of NMR of Bulk Polymers



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*“NMR Spectroscopy of Polymers”
Tutorial
ACS National Meeting*

New Orleans, April 6, 2008



Overview of NMR of Bulk Polymers



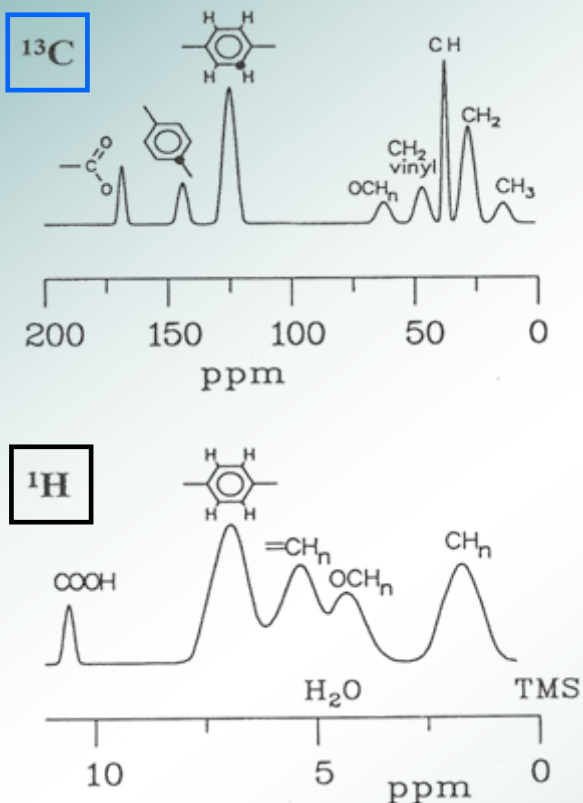
- Introduction • **Basics**
- Configuration, Conformation • **Chain Branching**
- Local Structure & Dynamics • **Amorphous & Crystalline Polymers**
- Phase Behavior • **Core Shell Structures**
- Supramolecular Organization • **Functional Polymeric Systems**
- Conclusions • **Scattering and NMR**



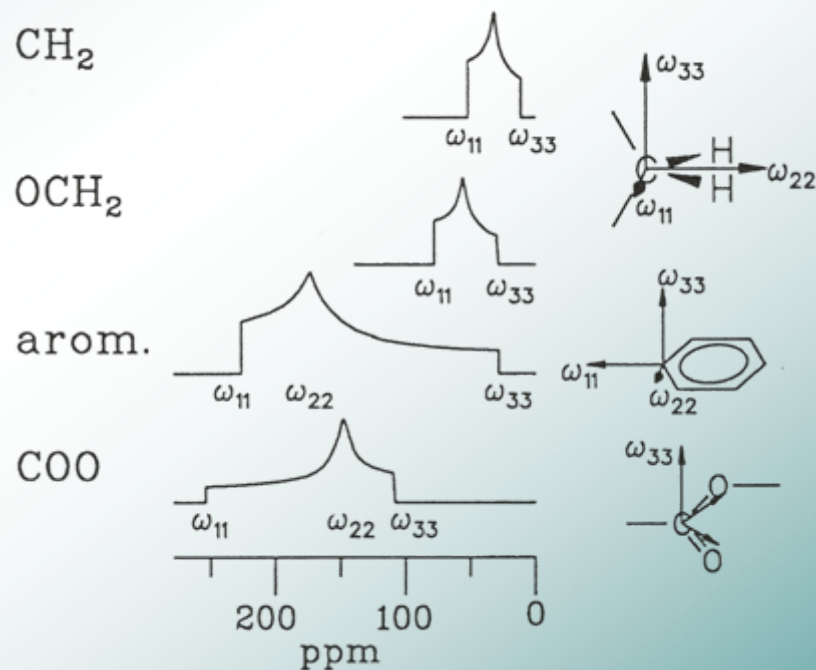
Chemical Shift Ranges for Organic Compounds



Isotropic



Anisotropic (¹³C)



Angular dependent NMR - frequency:

$$\omega = \omega_L + 1/2 \Delta (3 \cos^2\Theta - 1 - \eta \sin^2\Theta \cos 2\Phi)$$

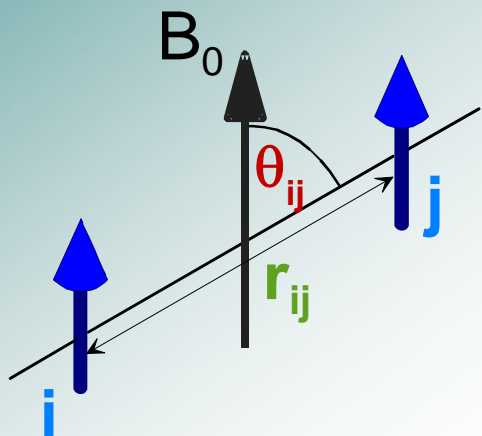
Analogous for ²H quadrupole coupling



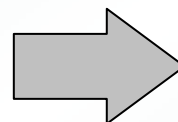
Structure and Dynamics from Solid-State NMR



Dipole-Dipole Coupling

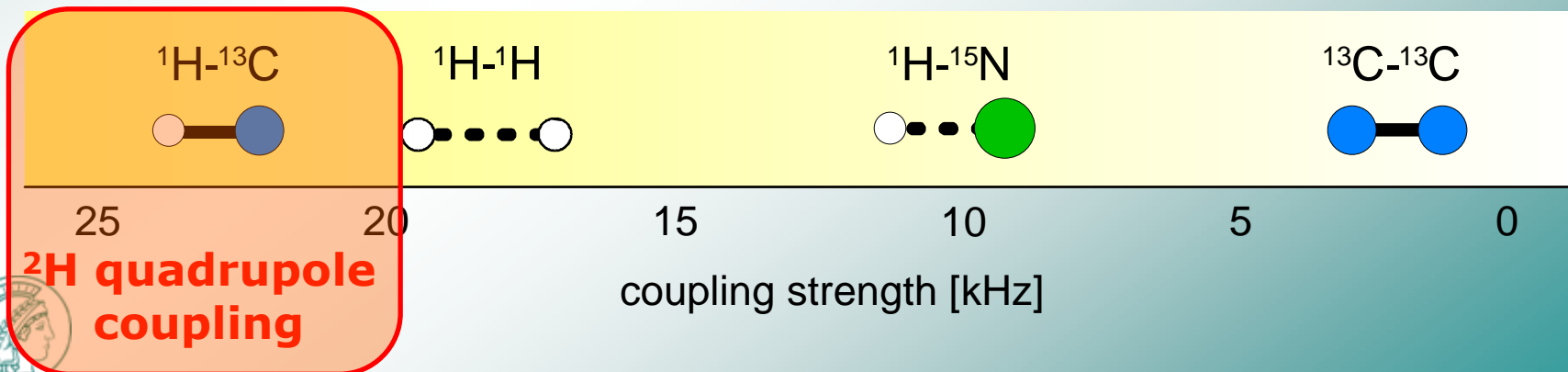


$$D \propto \frac{\gamma_i \gamma_j}{r_{ij}^3} \cdot \frac{1}{2} (3 \cos^2 \theta_{ij} - 1)$$

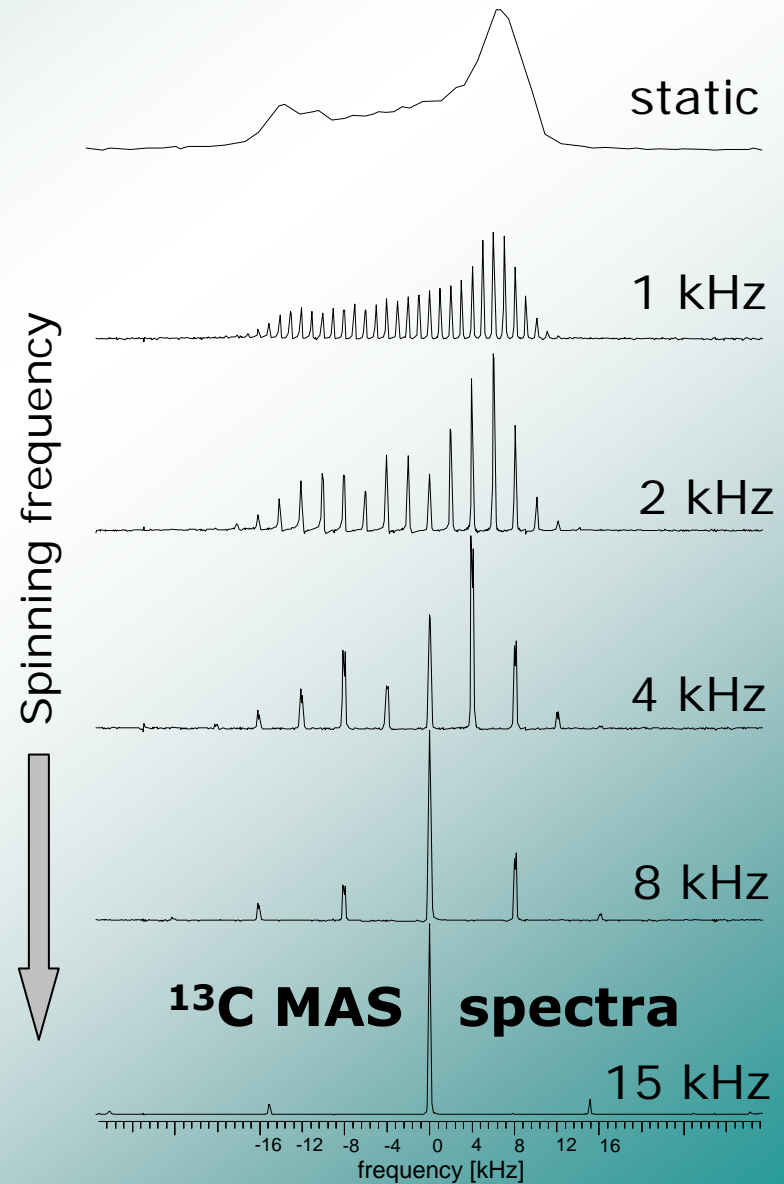
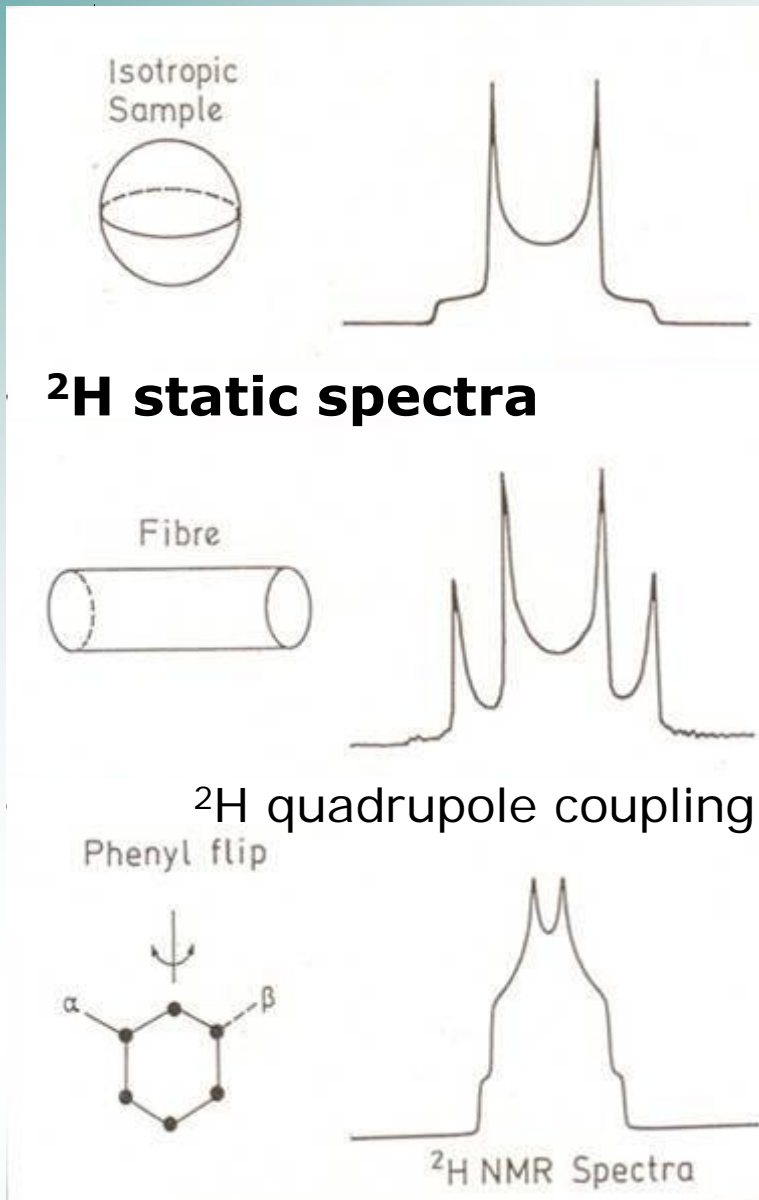


↻ **Structure**
Distance between nuclei
↻ **Dynamics**
Orientation of internuclear vector

Typical pairs of nuclei



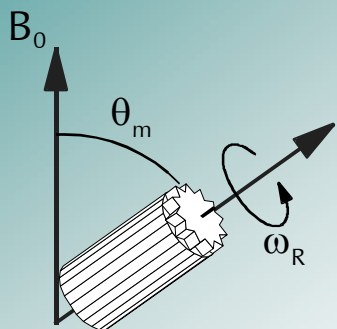
Solid State NMR Spectra



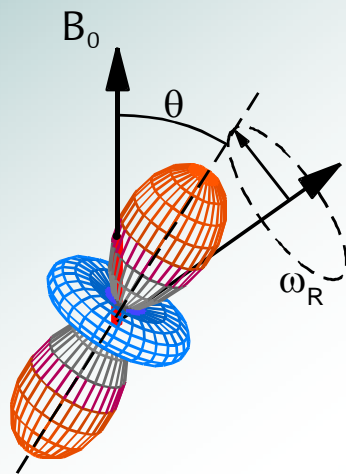
Magic-angle spinning (MAS)



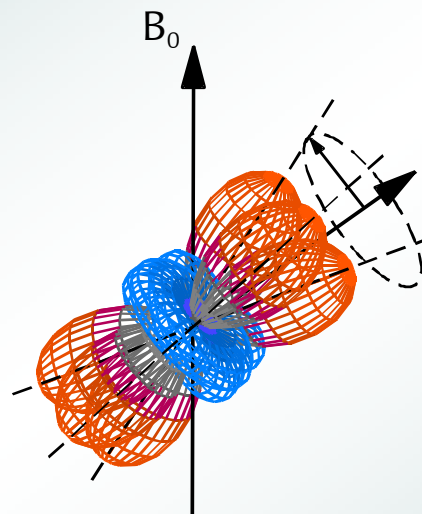
How does MAS work ?



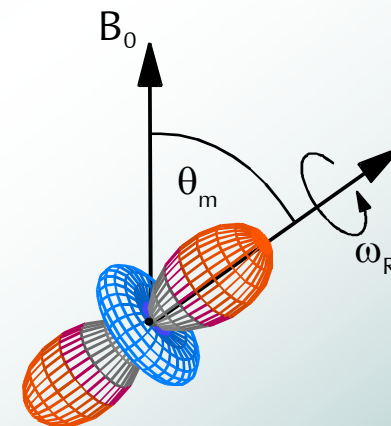
rotor is spun around an axis inclined at an angle of $\theta_m = 54.7^\circ$ with respect to B_0 .



spatial part of interaction tensor



averaging by fast rotation



resulting average tensor

in terms of coordinate transformations:

$$\frac{1}{2}(3\cos^2\theta - 1) \quad \longrightarrow \quad \frac{1}{2}\sin^2\beta \cos(2\omega_R t - 2\gamma) - \frac{1}{\sqrt{2}}\sin(2\beta) \cos(\omega_R t - \gamma)$$

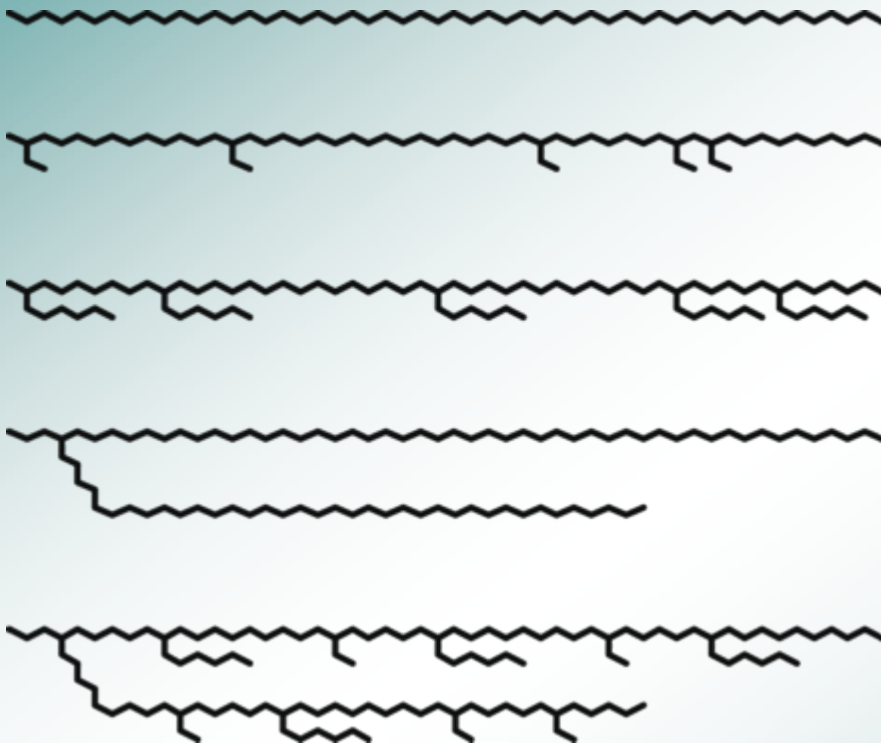
rotor modulations with frequencies $2\omega_R$ and ω_R



Polyolefin Branching

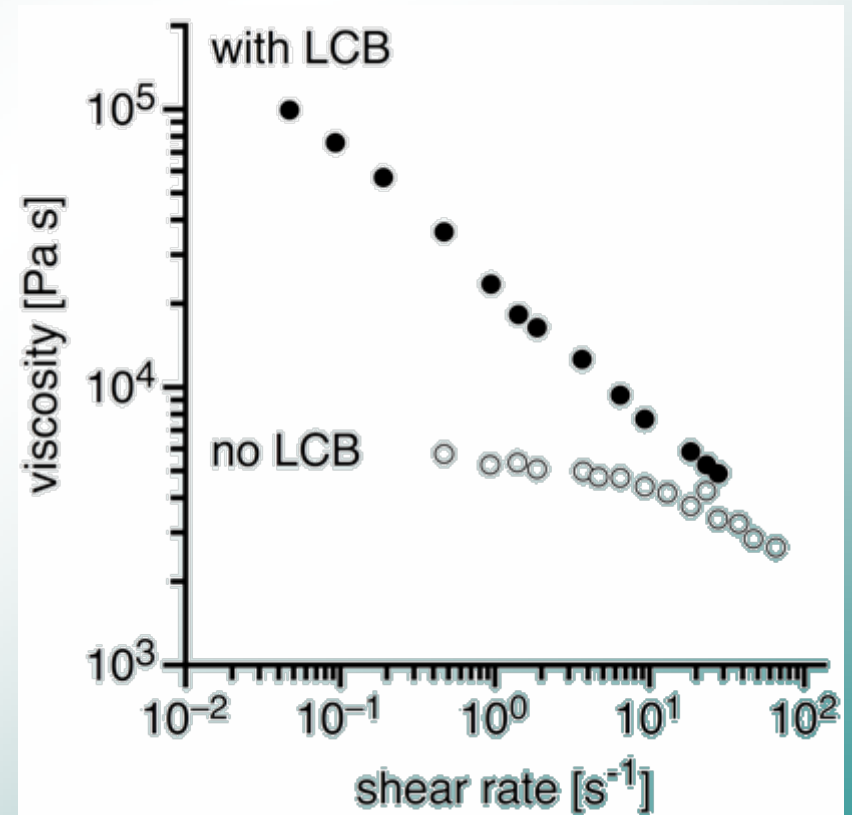


Short (SCB) < 30 C

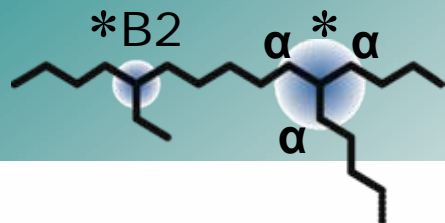


Long (LCB) > $M_e \approx 270$ C

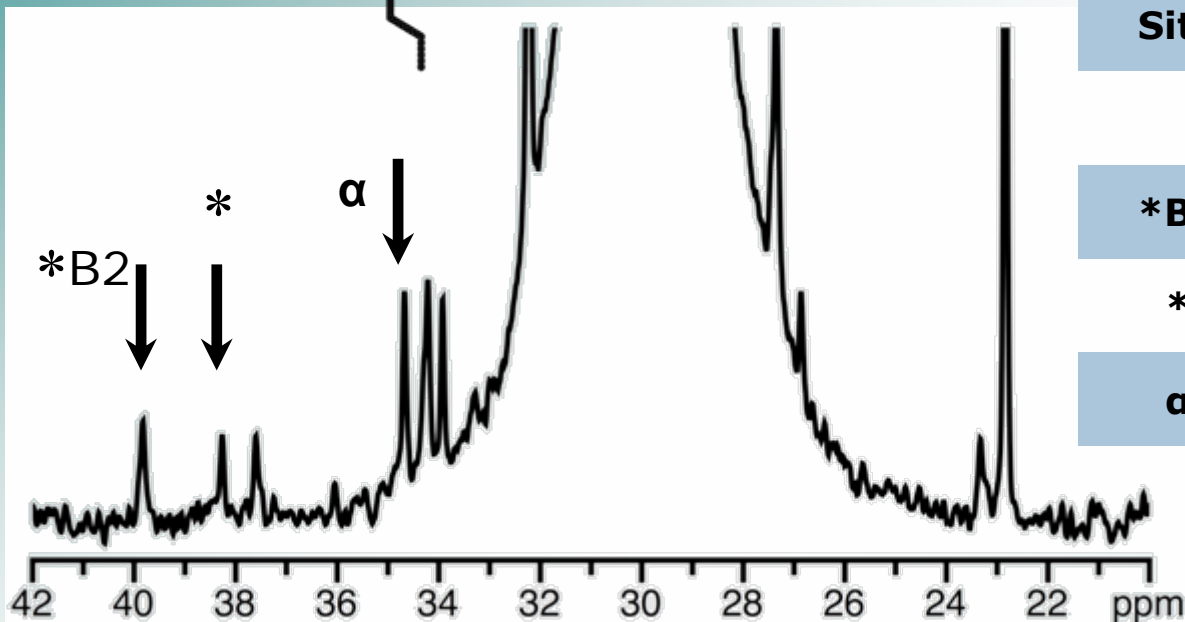
pronounced effect on
viscosity &
melt processability



MAS-NMR in Melts: Very Low Branch Contents



'Linear' PE



Site	SNR	Content per 1000 C
*B2	4.5	0.07
*	3.7	0.05
α	9.4	0.08

Sample:
R.H. Grubbs, Caltech

Quantification of 7–8 branches per 10 000 C

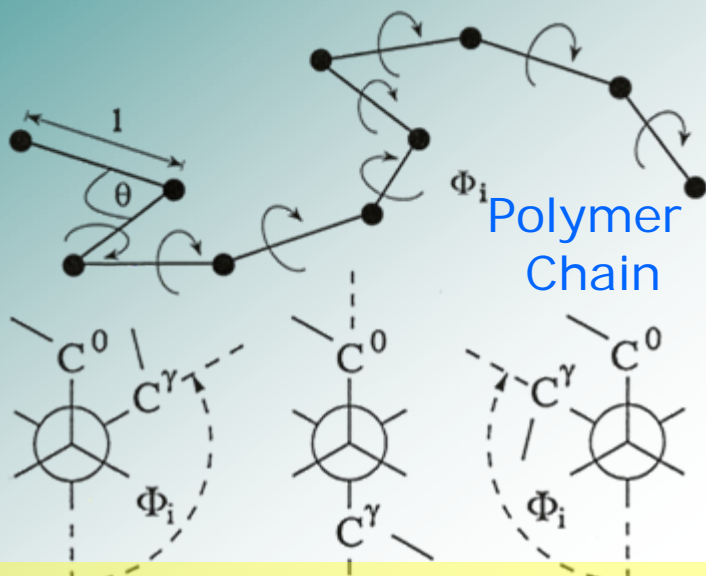
Optimised **solution** NMR:

50,000 to 2,000,000 scans (up to 60 days!)

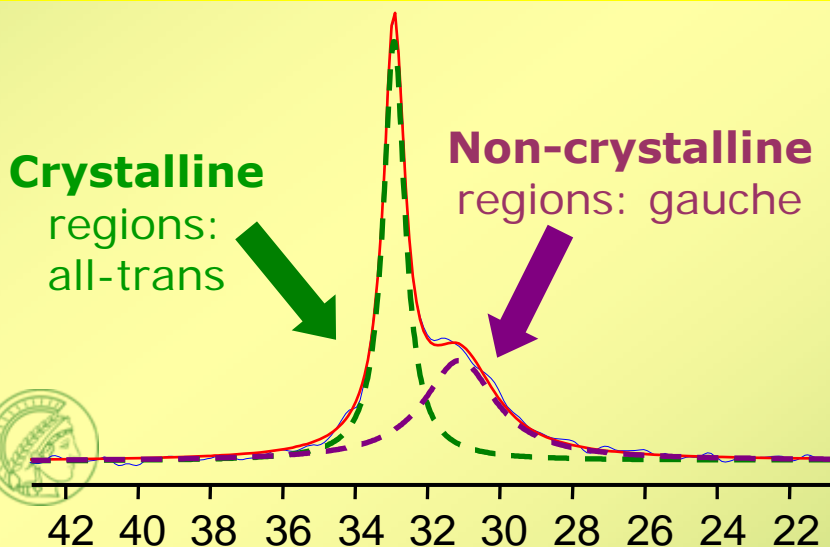
Optimised **melt-state** NMR: **21,500 scans (13 h)**



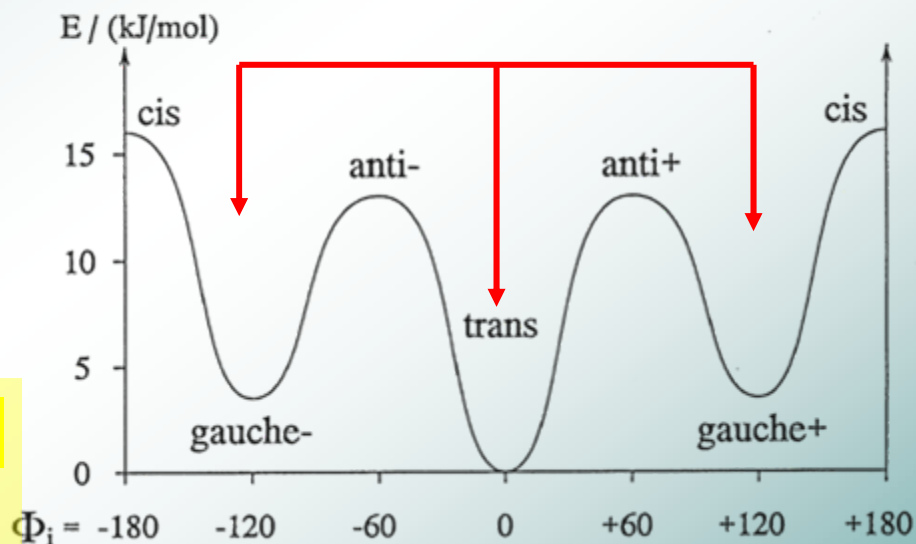
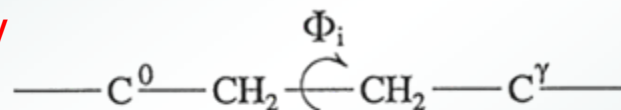
^{13}C - NMR: Conformational Effects



^{13}C NMR spectrum of PE



Potential Energy



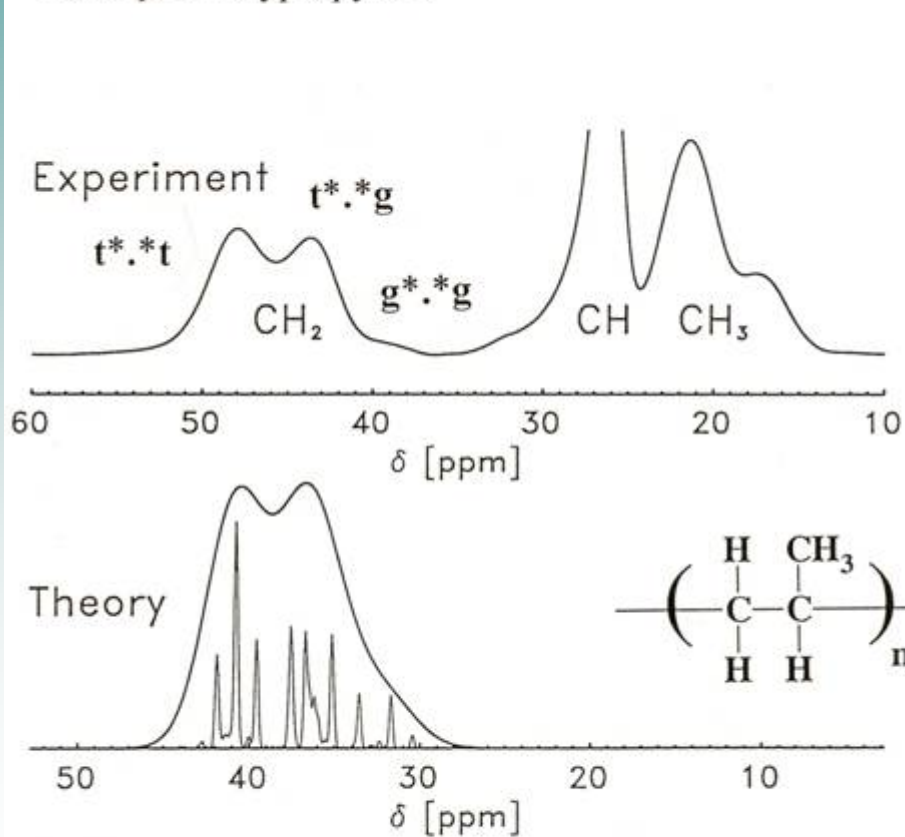
Sensitivity of ^{13}C Chemical Shifts on Conformation :

**Gamma - *gauche* effect:
- 5,2 ppm in alkanes**

Conformational Effects on ^{13}C Chemical Shifts



Example: Polypropylene

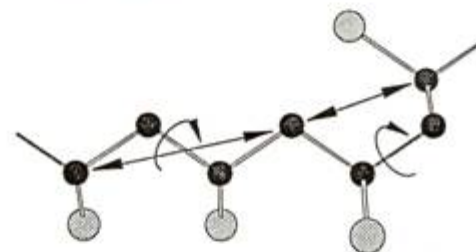


^{13}C NMR Spectrum

trans / trans ($t^*.t$)



trans / gauche ($t^*.g$)



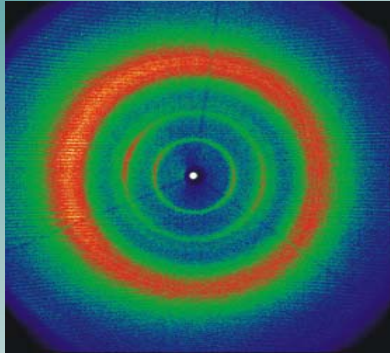
gauche / gauche ($g^*.g$)



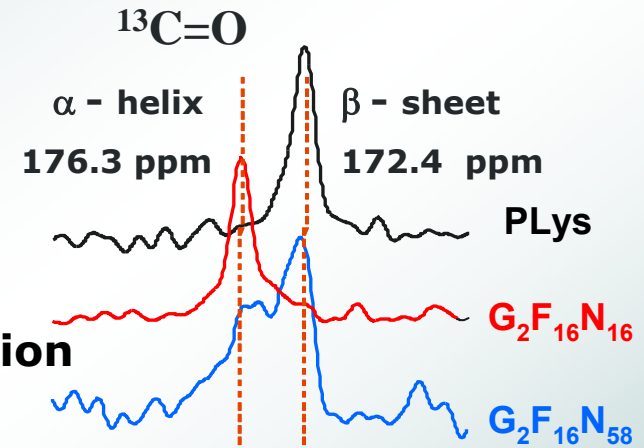
Conformations of Tetrameric Unit



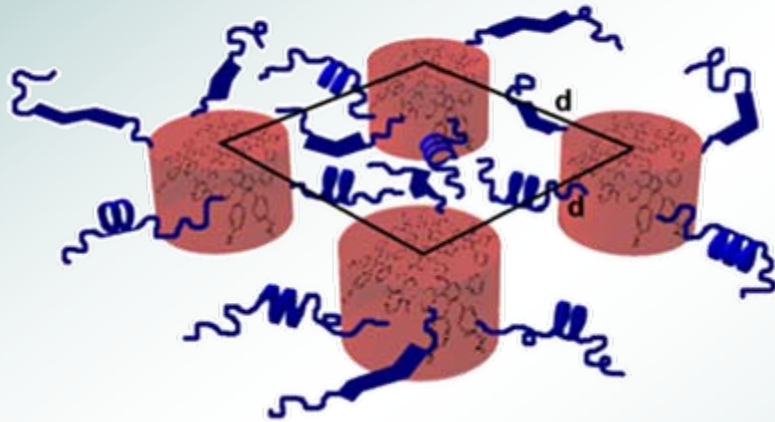
Self-Assembly and Molecular Dynamics of Peptide-Functionalized Polyphenylene Dendrimers



X-ray Scattering:
columnar order

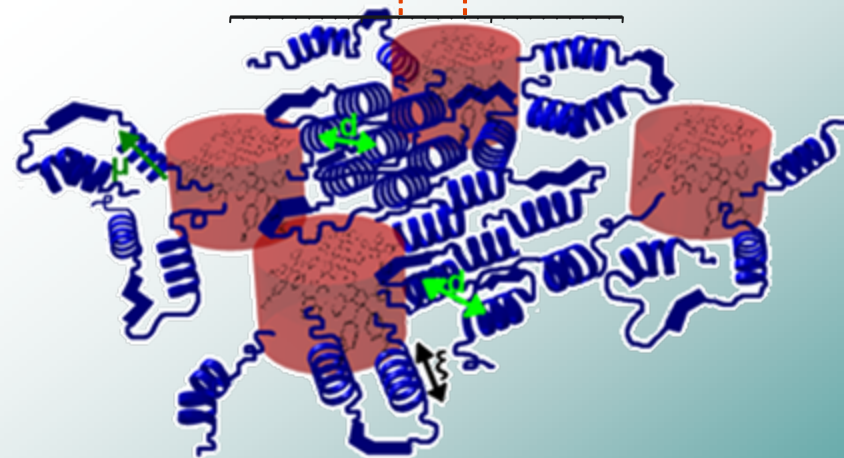


Solid state NMR:
Peptide conformation



Short polypeptides ($n < 16$)

High order of columns,
Low order of peptide chains



Long polypeptides ($n > 20$)

Low order of columns,
High order of peptide chains
(α -helices)



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- Conclusions • Scattering and NMR



Motional averaging effects



$$\mathbf{H}_{CS} = \delta \cdot \frac{1}{2} (3 \cos^2 \theta - 1 - \eta \sin^2 \theta \cos(2\phi)) \cdot \mathbf{I}_Z \quad \text{Anisotropic Chemical Shift}$$

$$\mathbf{H}_D^{(ij)} = D_{ij} \cdot \frac{1}{2} (3 \cos^2 \theta - 1) (3 \mathbf{I}_Z^{(i)} \mathbf{I}_Z^{(j)} - \mathbf{I}^{(i)} \mathbf{I}^{(j)}) \quad \text{Dipole-Dipole Coupling}$$

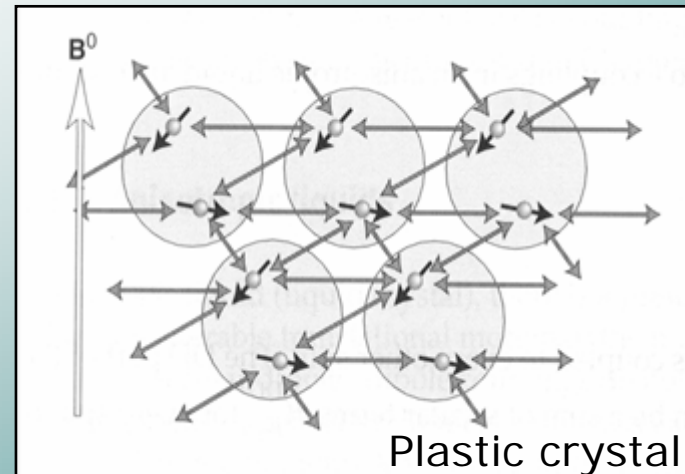
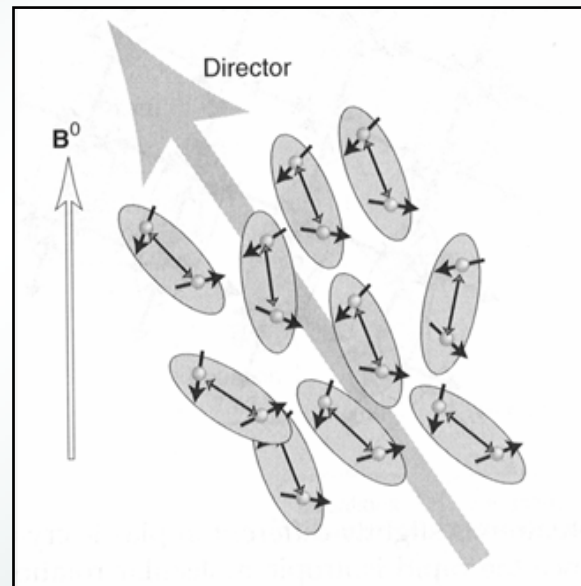
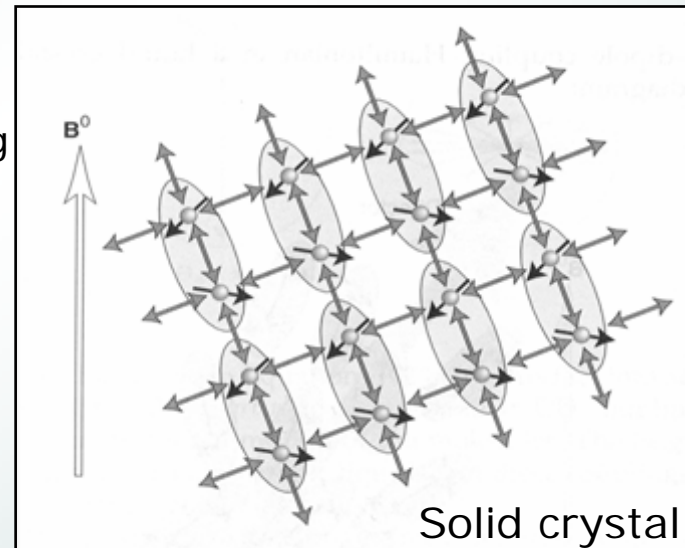
$$\mathbf{H}_Q = \frac{e^2 q Q}{2I(2I-1) \cdot \hbar} \cdot \frac{1}{2} (3 \cos^2 \theta - 1) (3 \mathbf{I}_Z \mathbf{I}_Z - \mathbf{I} \cdot \mathbf{I}) \quad \text{Quadrupole Coupling}$$

Motional averaging:

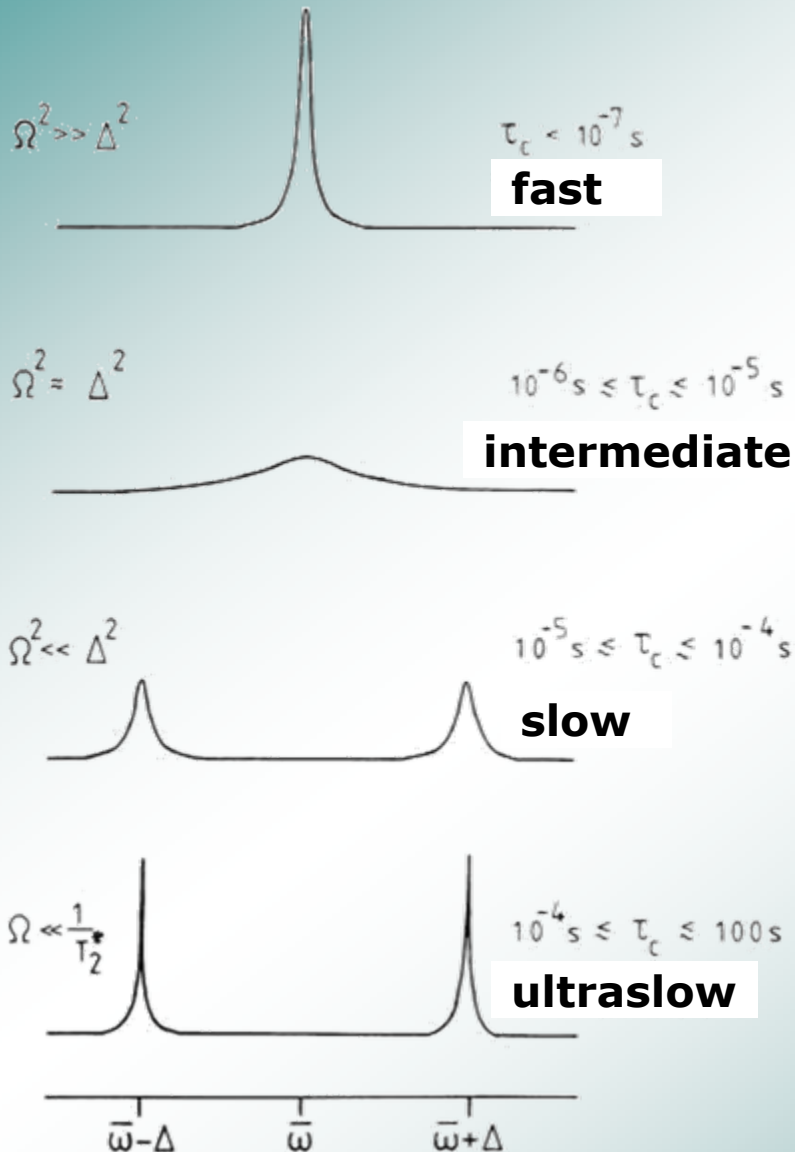
$$\int_0^\pi \int_0^{2\pi} \frac{1}{2} (3 \cos^2 \theta - 1) d\phi \sin \theta d\theta = 0$$

order parameter S_{ij} :

$$S_{ij} = \left\langle \frac{1}{2} (3 \cos^2 \theta - 1) \right\rangle$$



Motional averaging effects



Basics: Two site jumps
(analogous to chemical exchange)

Calculated NMR line shapes resulting from interchange between two NMR frequencies.

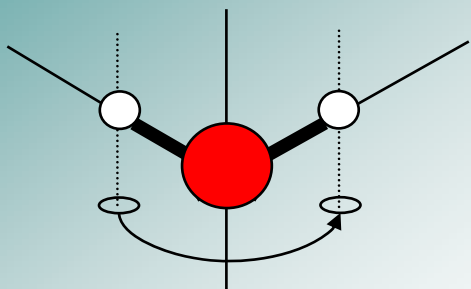
Δ : coupling strength
 Ω : exchange rate

The numerical values apply to ^2H NMR of deuterons in C-H bonds



Two-site jumps: CSA

^1H powder spectrum
of H_2O molecules
in crystalline $\text{CaSO}_4 \cdot 2\text{H}_2\text{O}$

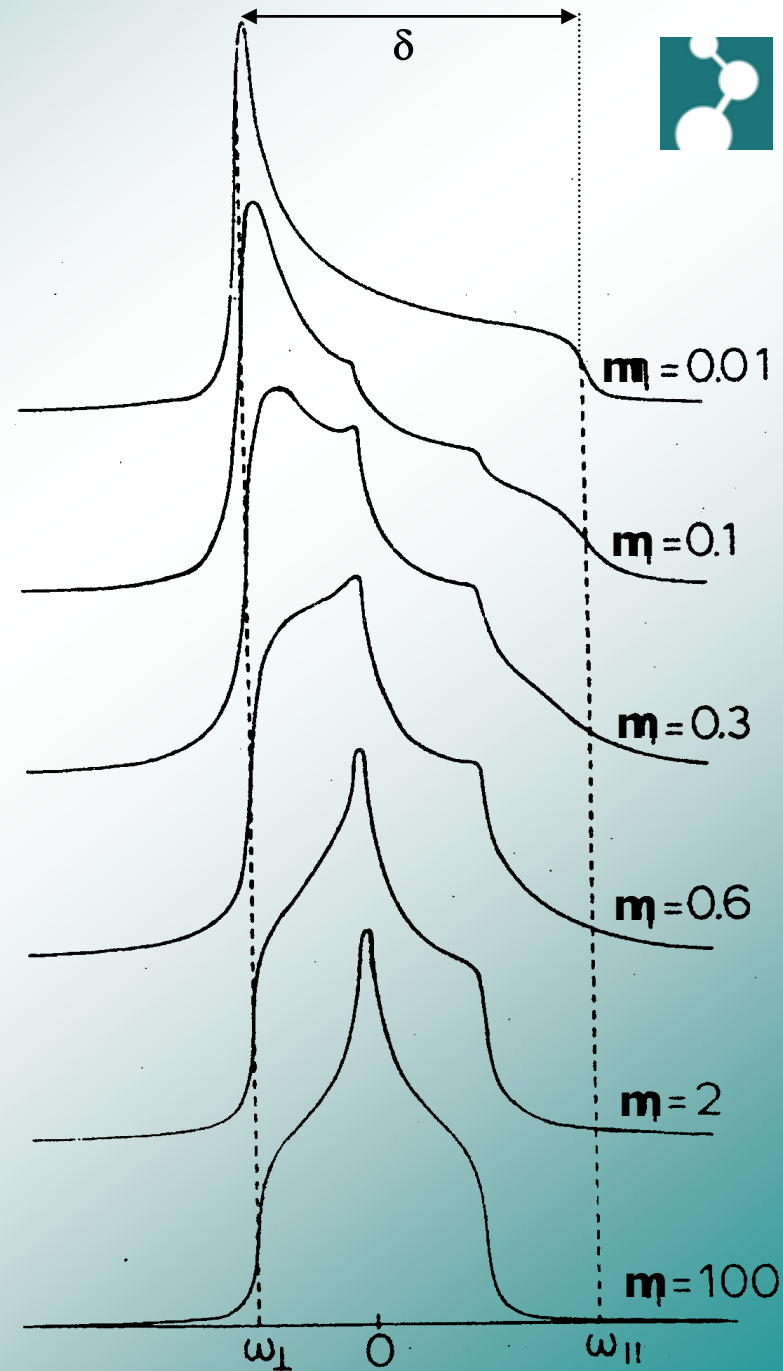


$$m = \frac{k_{\text{jump}}}{\delta} = \frac{1}{\delta \cdot \tau_{\text{jump}}}$$

Two-site jump in solid:
Different frequencies depending on orientation.

Result in fast motion limit:
Averaged interaction tensor

Line shape analysis yields both:
Timescale and geometry of motion



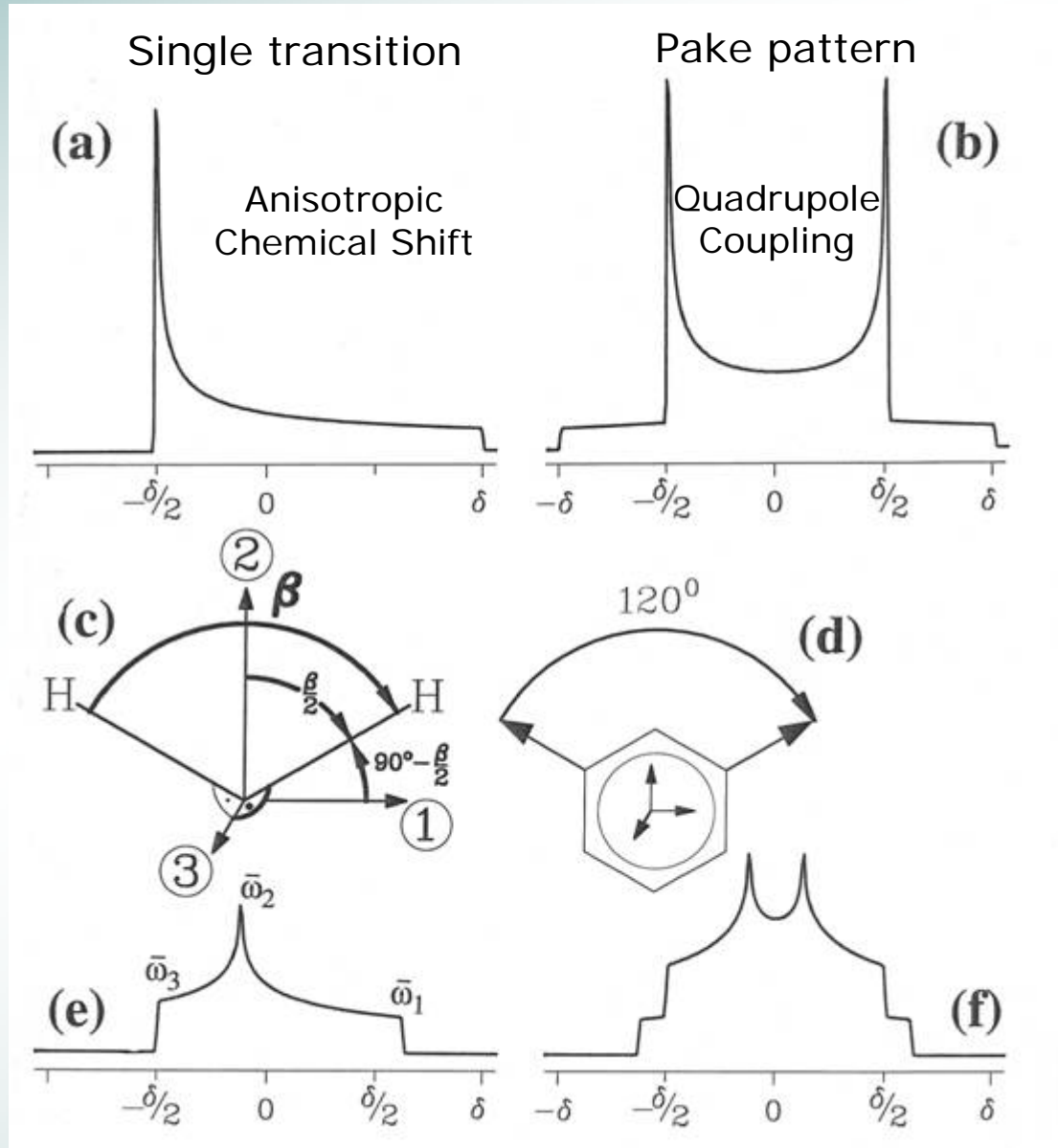
Two-site jumps: CSA, DDC and QC



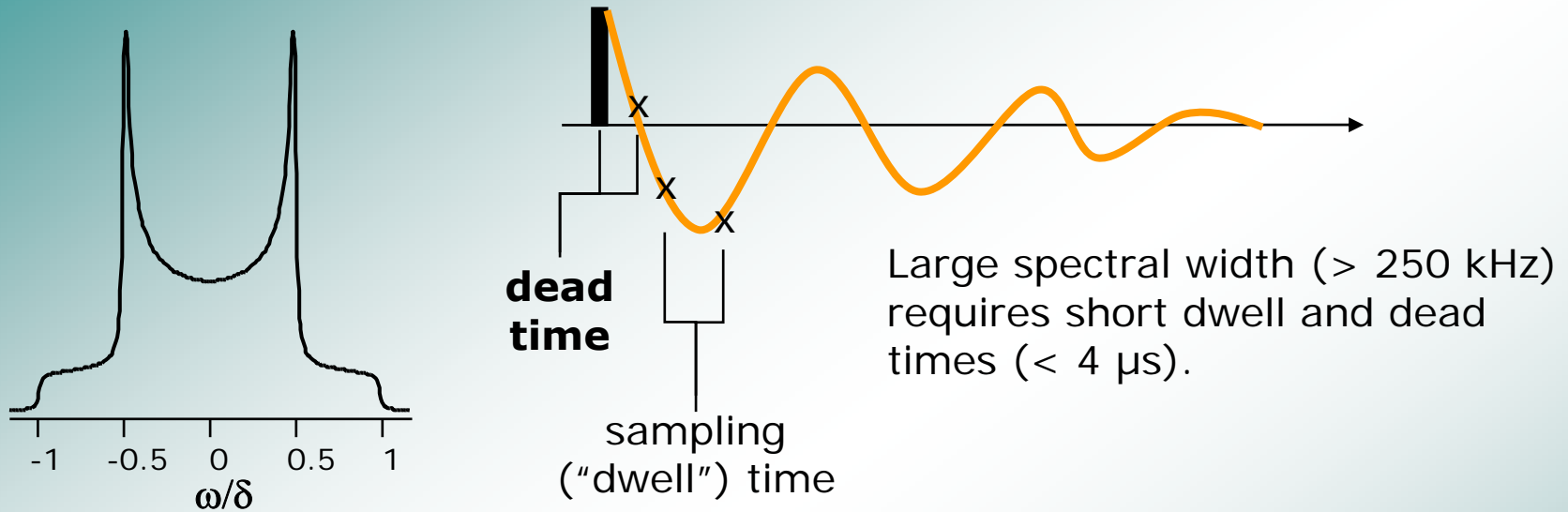
Example: Phenyl
 180° ring flip:
 Reorientation C-H bonds
 by $\beta = 120^\circ$

Averaged principal
 axes (1), (2) and (3)

$$\bar{\delta} = 5/8 \delta; \quad \bar{\eta} = 0.6$$

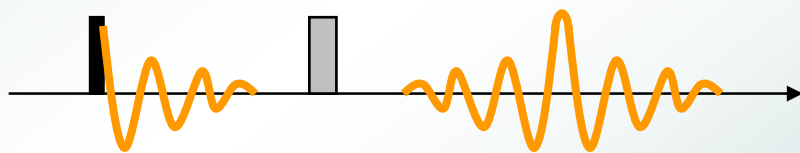


The "solid echo" experiment



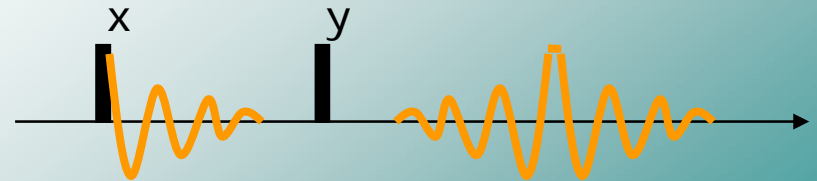
Overcoming the dead-time problem by echo experiments:

spin ("Hahn") echo



refocuses "linear-spin" interactions

solid ("Solomon") echo



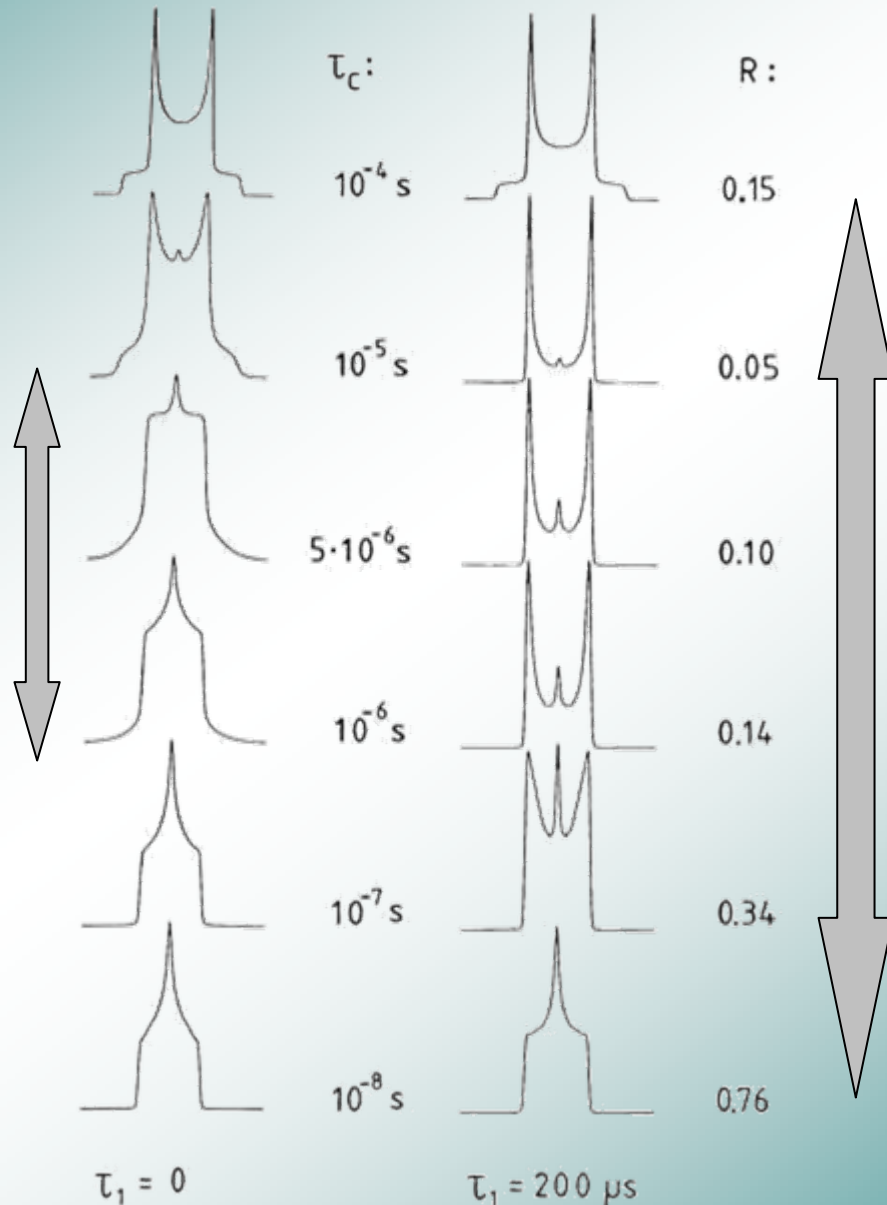
refocuses "bilinear-spin" interactions



Motions in the "solid echo" experiment: Increased dynamic range



**Absorption spectra:
Line shape changes
within one
order of
magnitude**



**Solid echo spectra:
Line shape changes
over several orders
of magnitude,
But: loss of signal!**



NMR line shapes conveniently calculated by NMR Weblab



NMR Weblab Version 4.1.1 MPIP-Mainz - Microsoft Internet Explorer

Adresse <http://weblab.mpip-mainz.mpg.de/weblab/weblab.html>

Welcome to the NMR WebLab V4.1.2
MPI for Polymer Research
V. Macho, L. Brombacher and H.W. Spiess

1D motion on a cone
 ^{13}C , ^{29}Si , ...
 ^2H

2D Exchange
 ^{13}C , ^{29}Si , ...
 ^2H

Fertig Lokales Intranet

Start April - Microsoft Outlook Complete Talks 06 NMR Weblab Version ... Microsoft PowerPoint - [L...]

18:07

<http://weblab.mpip-mainz.mpg.de/weblab/weblab.html>



NMR Weblab: How to use it




The Deuteron Weblab - Microsoft Internet Explorer

Adresse <http://weblab.mpip-mainz.mpg.de/cgi-bin/weblab41/weblab.pl>

Weblab 4.1.1 Main Menu

fast limit
general case
general case extended
sites
1 2 3 4 6

Rigid limit values of field gradient:
delta0/kHz
eta0
alpha0

 [Volker Macho](#)
[Lothar Brombacher](#)

Introduction

The NMR Weblab is the WWW-interface to our 1D- and 2D-NMR software. In this section you can simulate 1D solid echo spectra in amorphous solids of systems with nuclear spin $I=1/2$ or $I=1$ under the influence of local motions. The geometry of the motion is limited to discrete jumps or jump distributions (only for the fast motion limit) on a single cone. The simulated spectra are presented in standard graphic format and optionally as a list of xy -pairs which you can download to your site.

You need a browser that supports HTML 3.0 and JavaScript 1.0!
The calculations are performed on a HP DS20 Alpha system.

Literature:

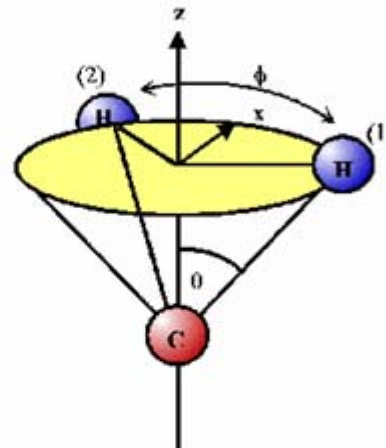
Reference to use for citation:

V. Macho, L. Brombacher, and H.W. Spiess: *The NMR-WEBLAB: an Internet Approach to NMR Lineshape Analysis*, Appl. Magn. Reson. 20,405 (2001)

Older Versions and Release Notes:

[Weblab V4.0](#)
[Release Notes 4.1](#)

Cone Model



<http://weblab.mpip-mainz.mpg.de/weblab/weblab.html>

NMR Weblab: Example phenyl flip



The Deuteron Weblab - Microsoft Internet Explorer

Adresse <http://weblab.mpip-mainz.mpg.de/cgi-bin/weblab41/weblab.pl>

Cone Menu

Cone angle θ
Flip angle ϕ
Jump angle distr
Width of distr
Population 1

to/from (+-kHz)
Lineshape
Broadening (kHz)
Show one Transition

Input parameters:
 δ_a : 120.000 kHz
 η_a : 0.000
theta: 60.000°
phi: 180.000°
site pos/deg pop
1 -90.00 0.500
2 90.00 0.500

Broadening: 3.0 kHz
Lineshape: lorentzian

Eigenvalues of averaged tensor
 V_{11} : -64.000 kHz
 V_{22} : -16.000 kHz
 V_{33} : 80.000 kHz
 δ : 80.0000 kHz
 $\delta\delta_0$: 0.6250
 η : 0.6000

Eigenvectors of averaged tensor

	*1	*2	*3
x	1.0000	0.0000	0.0000
y	0.0000	0.0000	1.0000
z	0.0000	1.0000	0.0000

Θ 90.000 0.000 90.000
 Φ 0.000 0.000 90.000
y_{max} = 0.0206
/exp/weblab05622.html

[MPiP Home Page](#) [Weblab Start Page](#)

Fertig Lokales Intranet

Start Posteingang - Microsoft ... Complete Talks 06 Microsoft PowerPoint Microsoft Word The Deuteron Weblab... 18:20

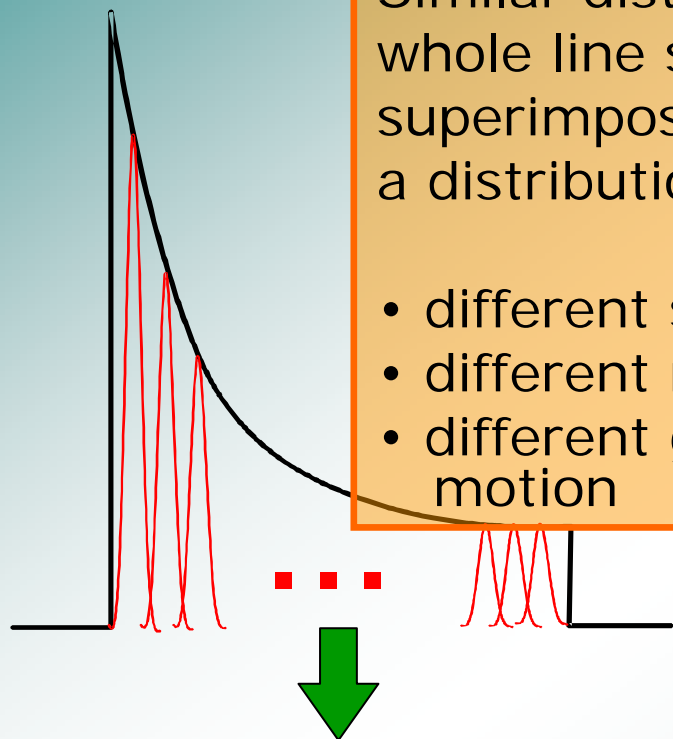


Inhomogeneous and homogeneous line broadening



Similar distinction if whole line shapes are superimposed due to a distribution of

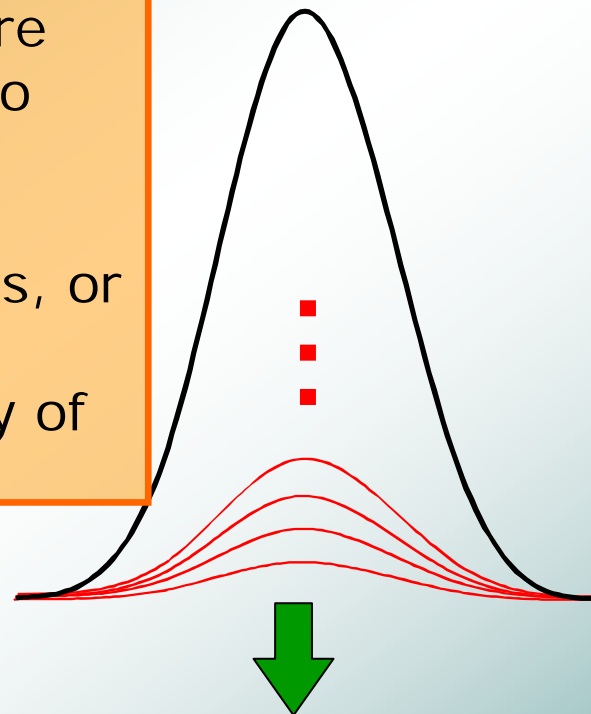
- different structures, or
- different rates, or
- different geometry of motion



Overall resonance consists of individual sharp lines and represents the sum over all different orientations

Inhomogeneous:

CSA, quadrupolar, dipolar two-spin



Due to spin-spin couplings the energy levels of single transitions (resonance lines) are no longer degenerate, but split into a multitude of levels

Homogeneous:

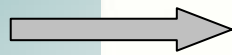
dipolar multi-spin



Example of heterogeneous rate distribution



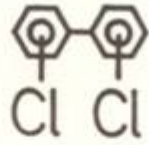
rigid limit



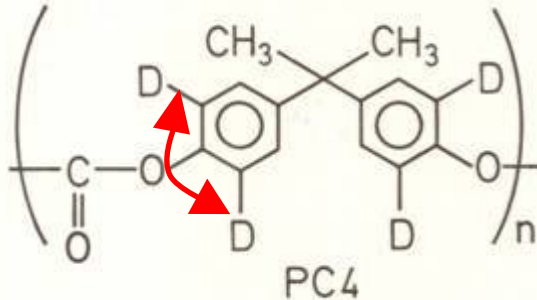
PC4

distribution

narrow

PC4 +  Cl Cl

broad



T = 199 K

T = 218 K

T = 237 K

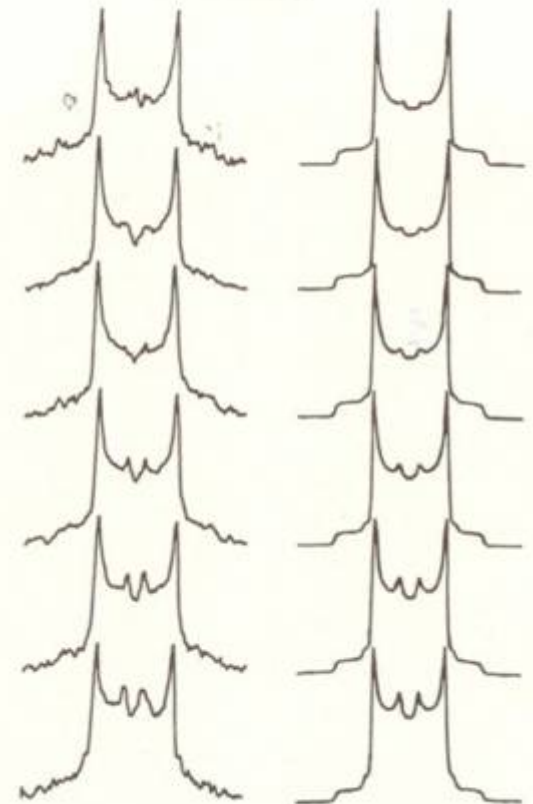
T = 255 K

T = 275 K

T = 293 K

observed

calculated

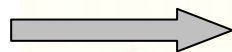


observed

calculated

100 kHz

rapid exchange



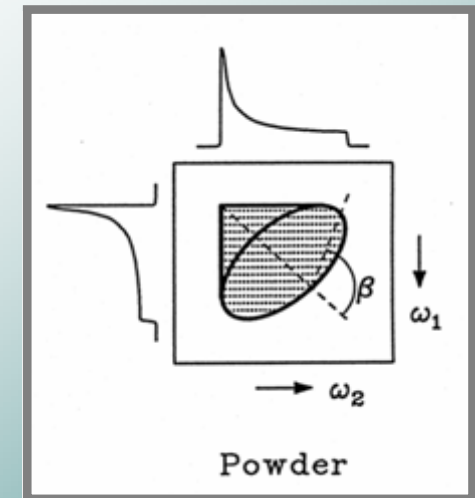
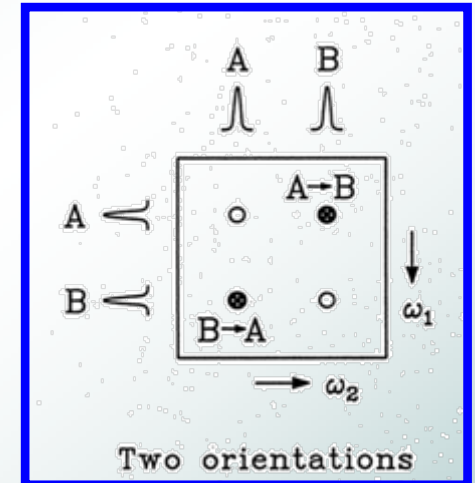
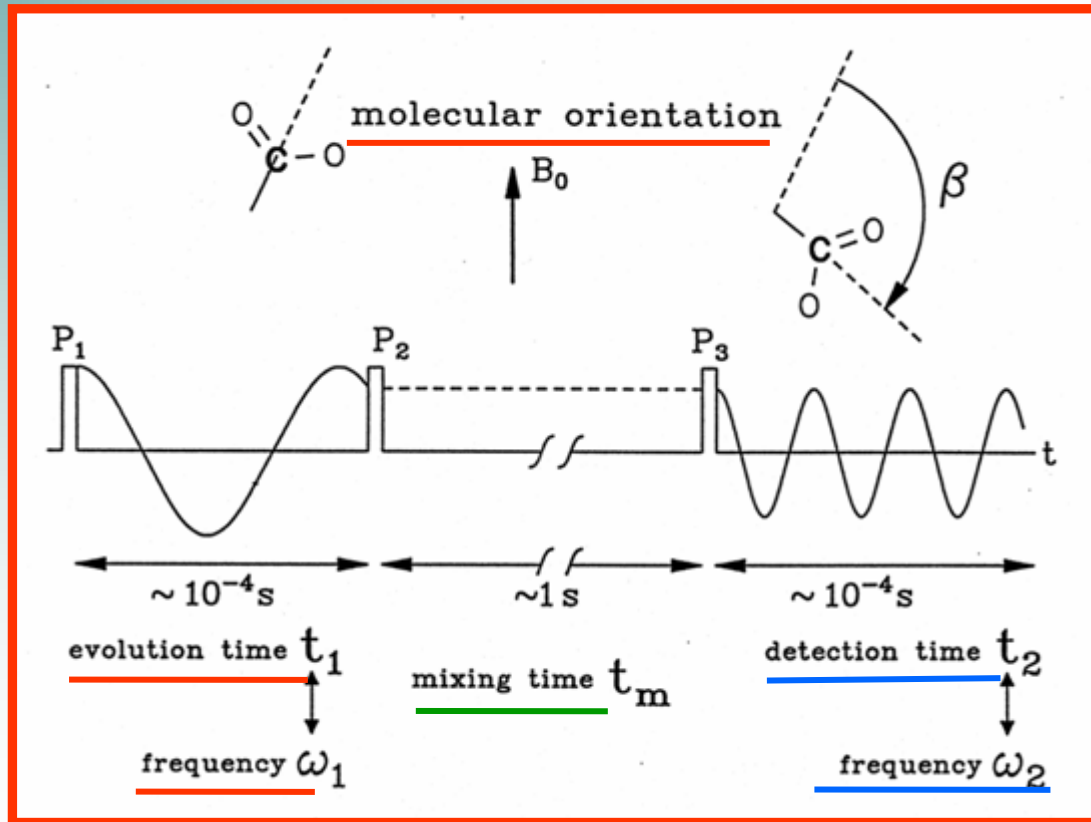
Superposition of line shapes for different rates



2D-Exchange-Spectroscopy: Simplicity



Determine geometry and time scale of motions directly and in real time



Pulse Sequence

Spectra

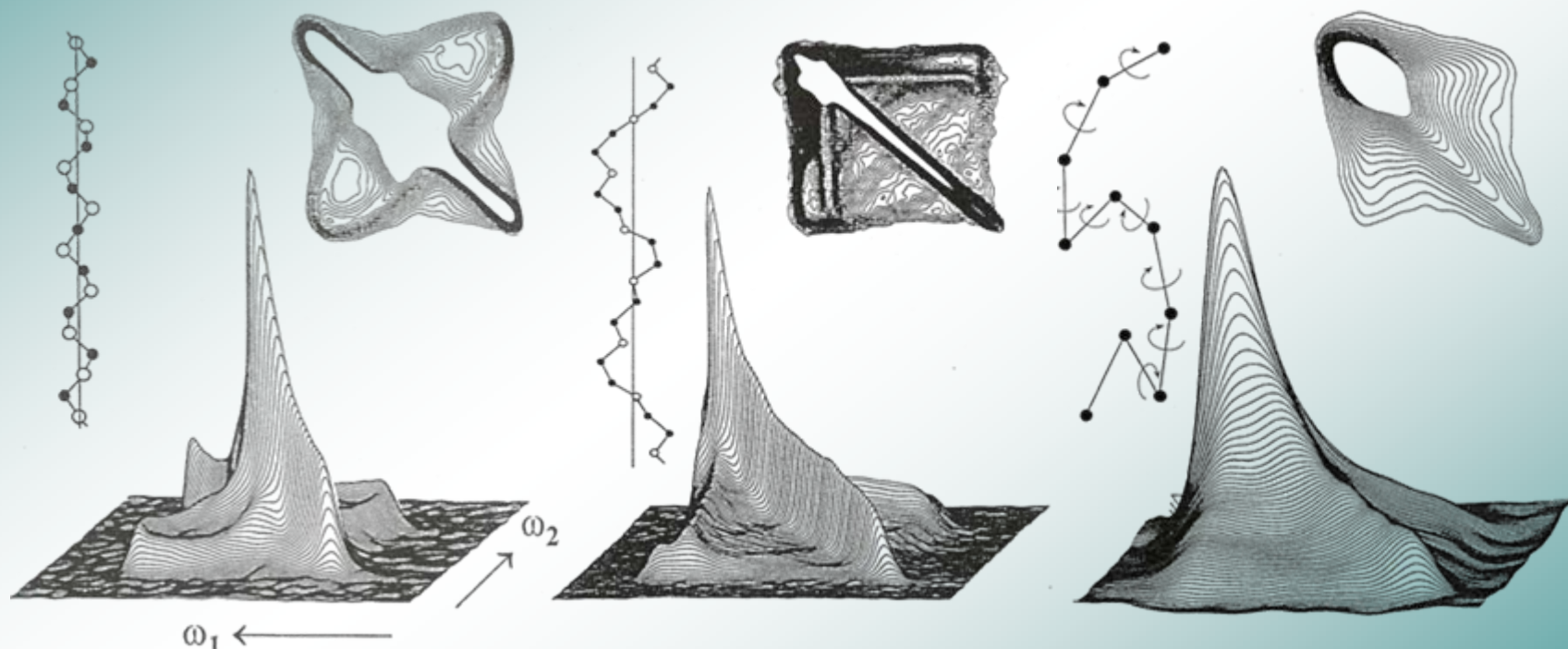
Geometry of Chain Motion in Polymers



POM (crystalline)

PEO (disordered)

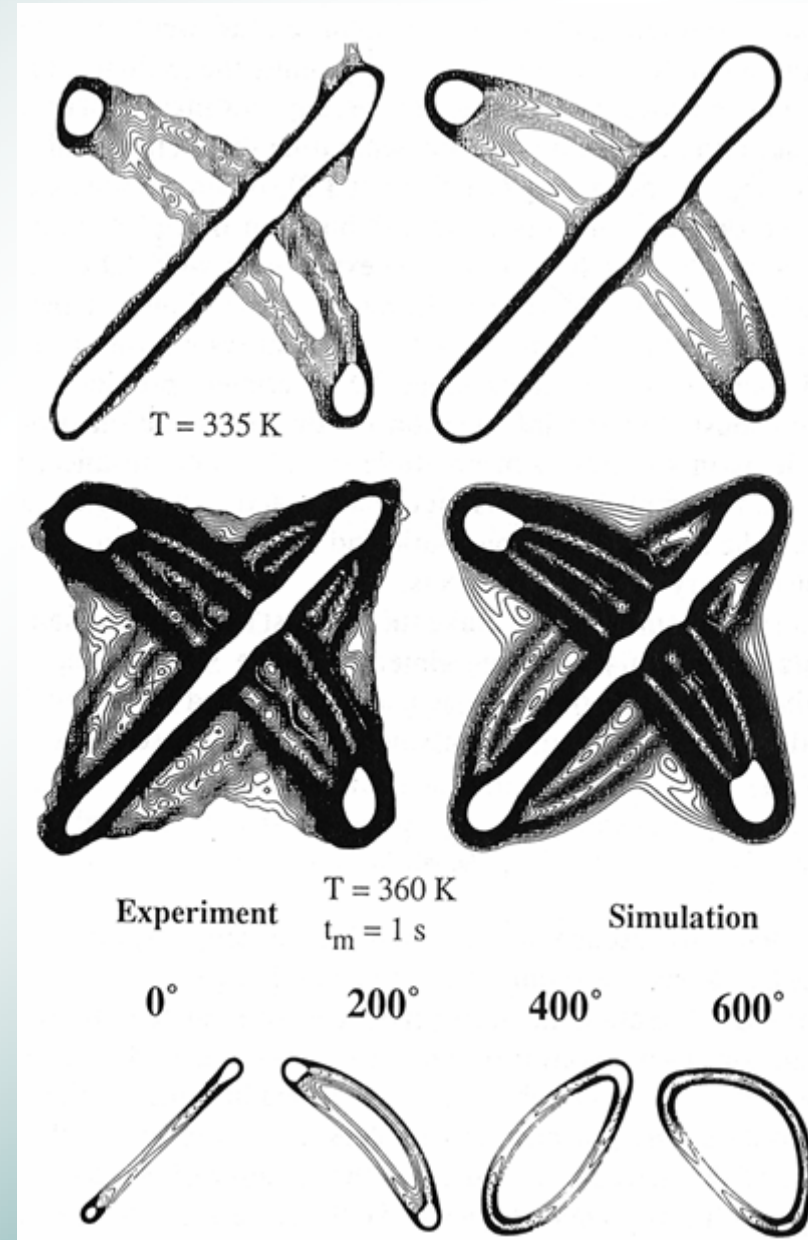
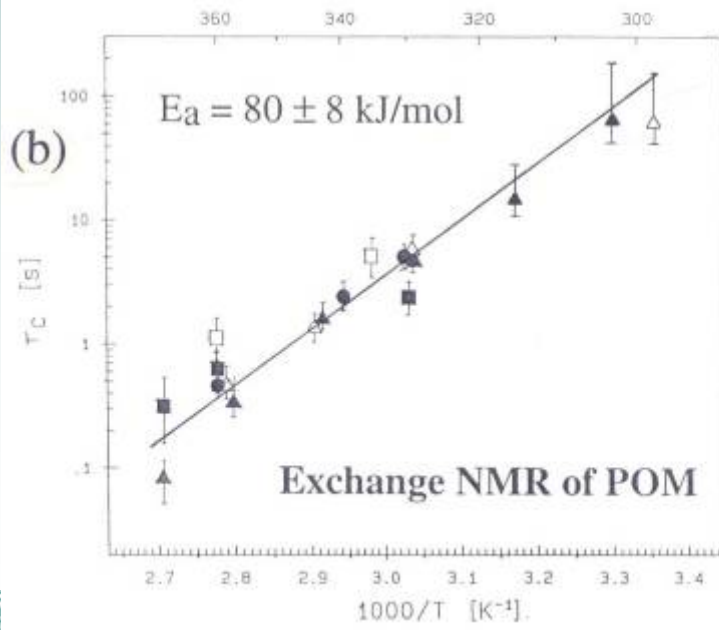
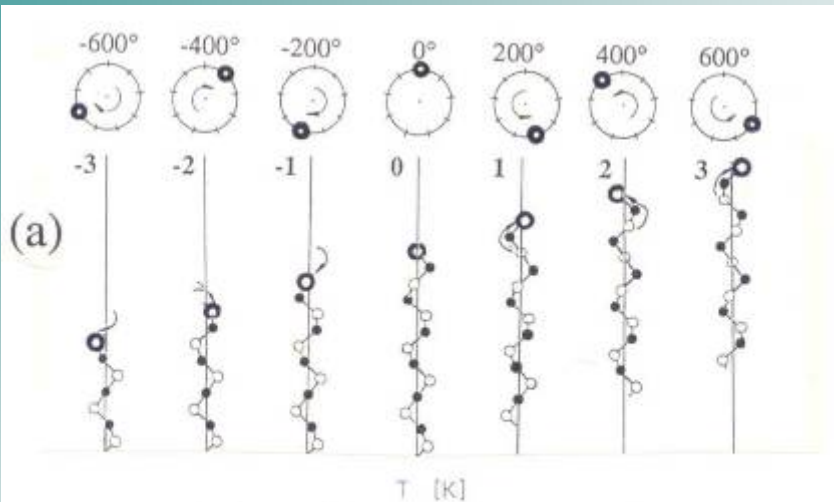
PVAc (amorphous)



^{13}C 2D Exchange NMR Spectra of Polymers
with Different Degrees of Disorder



Helical jumps in polymer crystallites: POM



Chain Folding, Chain Diffusion and Drawability



Sample:
UHMW-PE
($M_w = 3.4 \text{ M}$)

Drawability

Solution Crystallized:
Drawable

Melt Crystallized:
Not Drawable

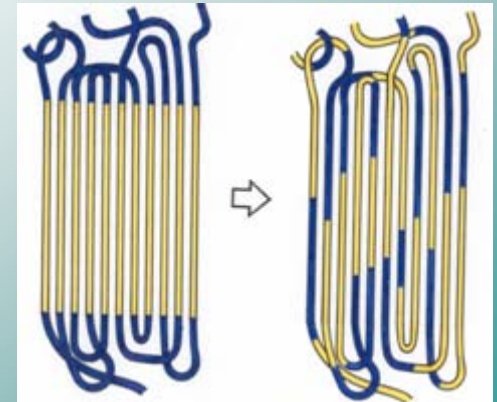
Morphology

Chain motion

Chain diffusion

Ordered

Disordered



Solution
Crystallized

Melt
Crystallized

Local

Collective

Timescales of Molecular Dynamics Accessible by NMR



Averaging of dipole-dipole couplings,
as detected by spinning sideband experiments:

C-H, N-H: REREDOR, REPT-HDOR

H-H: double-quantum

Spin-lattice relaxation:

dipole-dipole coupling,
quadrupole coupling,
anisotropic chemical shift

Destructive interference effects:
reduction and **loss** of NMR signal

Change of anisotropic interactions
during experimental "mixing time":
exchange NMR experiments
 ^2H , ^{13}C , ^{15}N : 2D, CODEX etc.

very fast

fast

intermediate

slow

10^{-9} 10^{-8} 10^{-7} 10^{-6} 10^{-5} 10^{-4} 10^{-3} 10^{-2} 10^{-1} 10^0

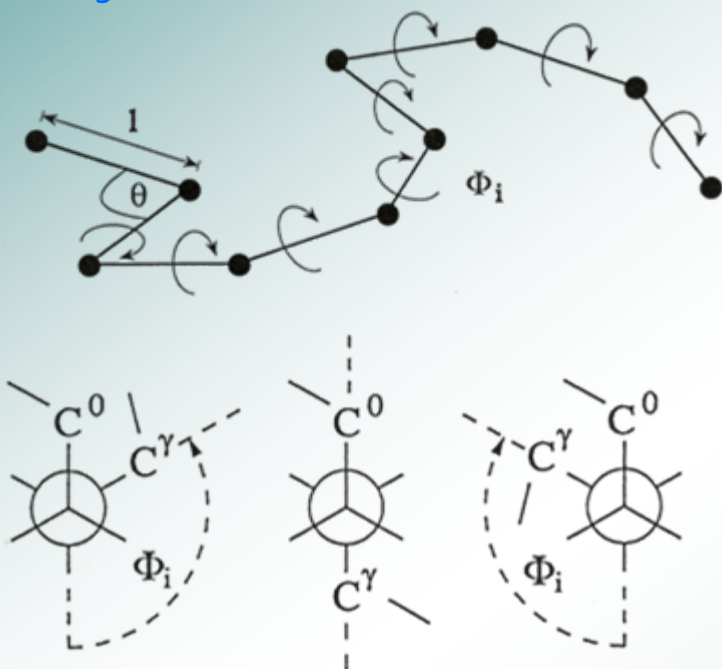
motional correlation time [seconds]



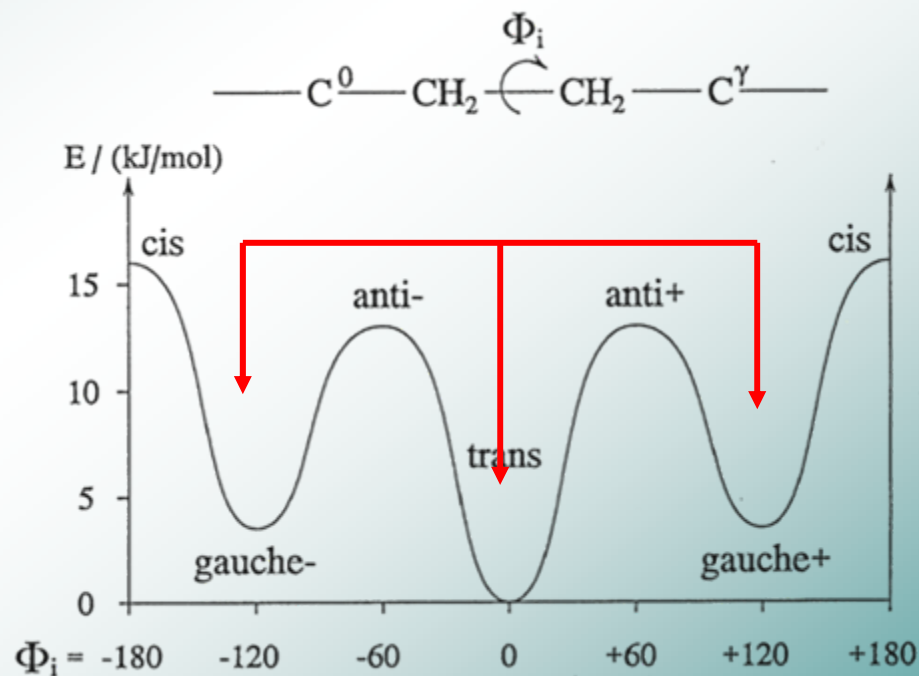
Conformational Dynamics at the Glass Transition



Polymer Chain



Potential Energy

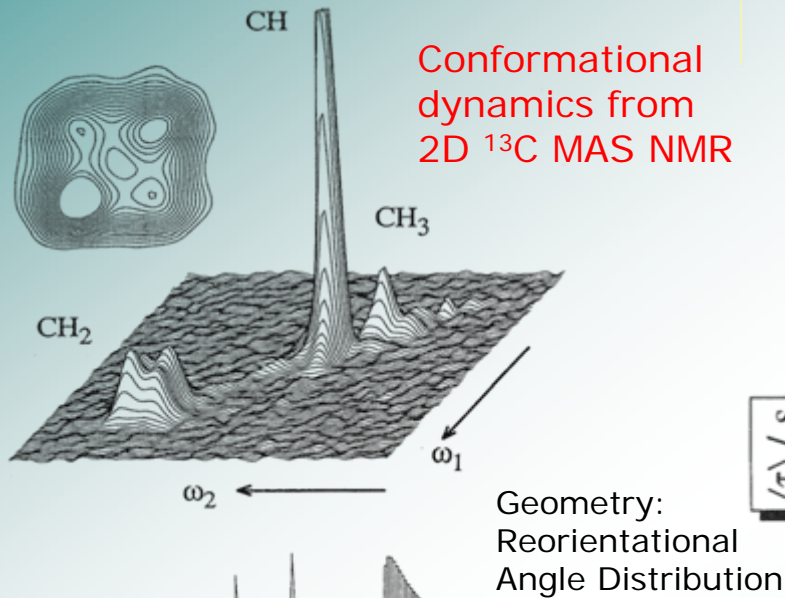


Sensitivity of ^{13}C Chemical Shifts on Conformation :

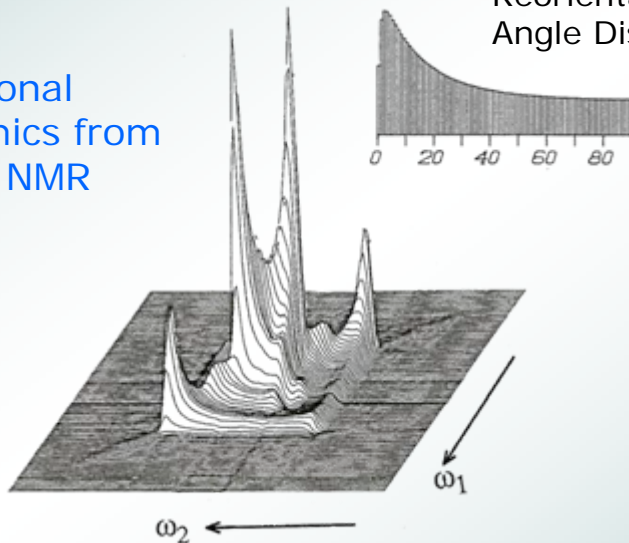
Gamma - *gauche* effect:
- 5,2 ppm in alkanes



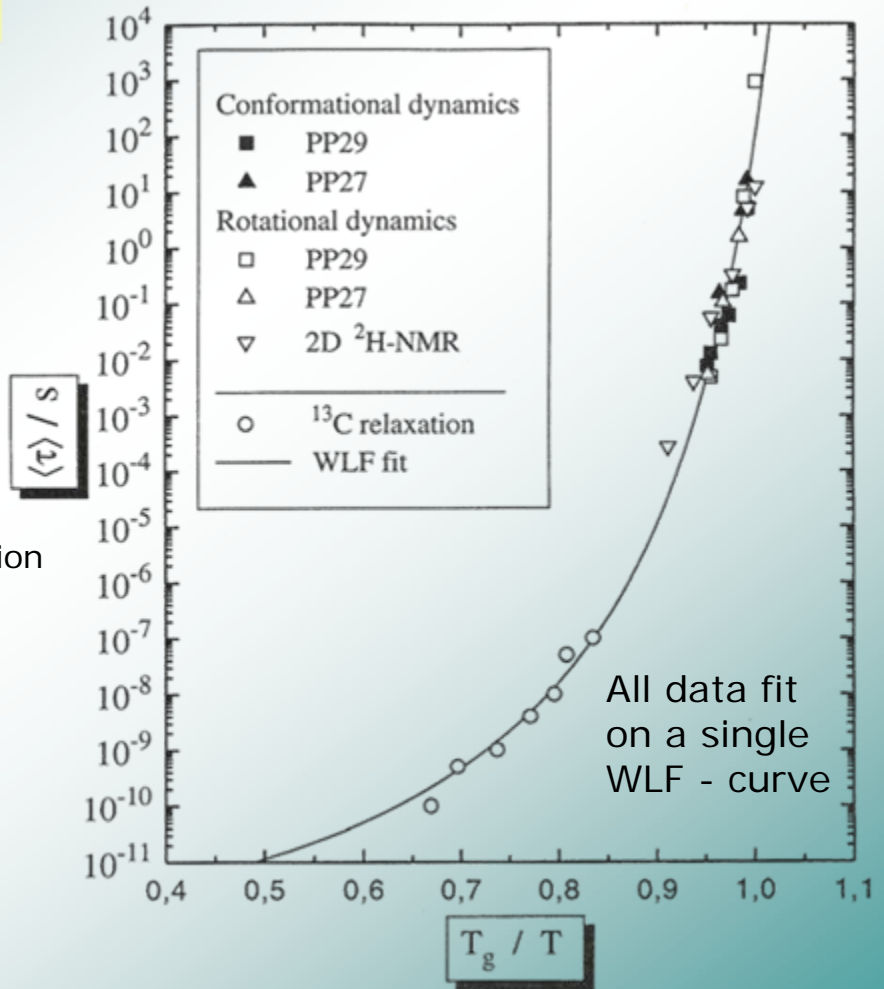
Chain Dynamics of Atactic Poly(propylene) at the Glass Transition



Rotational dynamics from 2D ^2H NMR



Conformational transitions, but no defined geometry



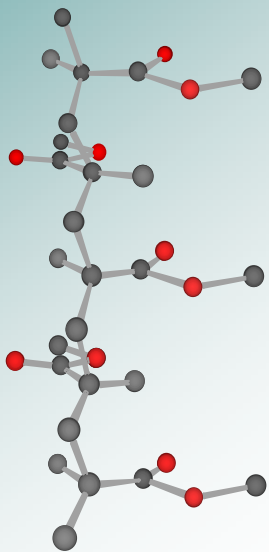
Correlation Times of Chain Motion from different NMR experiments

Structure Schemes of Syndiotactic and Isotactic Poly-(Methyl-Methacrylate)



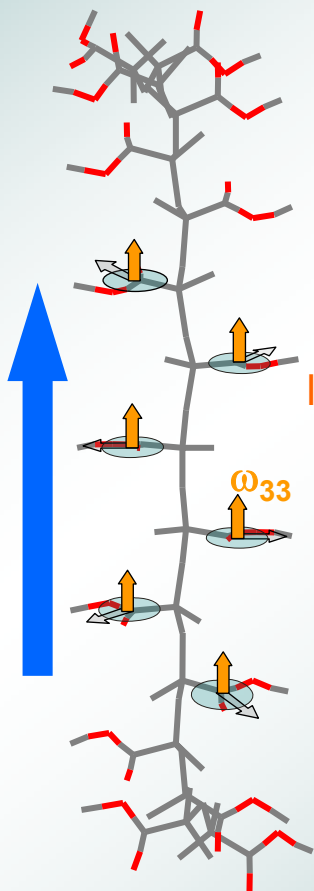
n-alkyl-methacrylates contain extended chain segments

schematic structure



local chain-axis

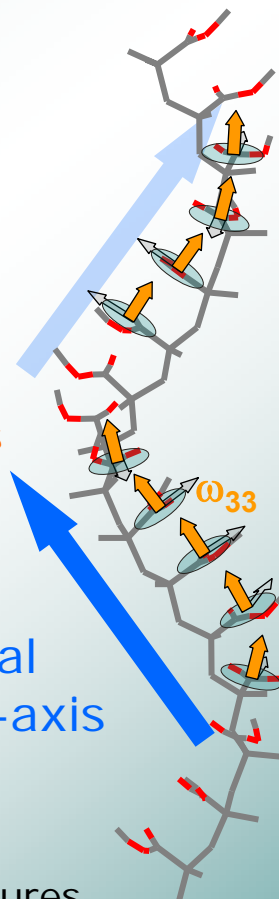
syndiotactic



Example:
PMMA

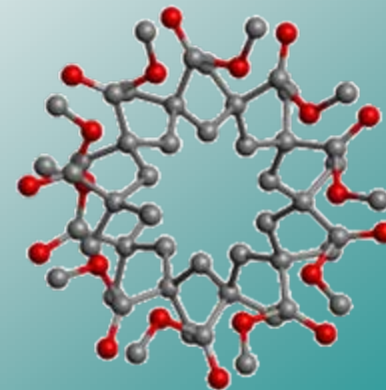
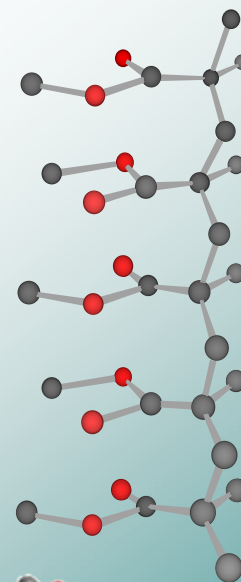
NMR probes local chain-axis through ω_{33}

isotactic



local chain-axis

schematic structure



crystal structures

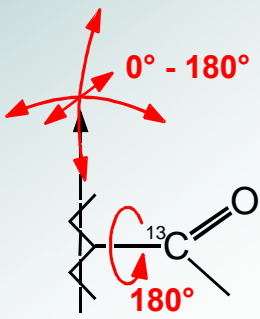
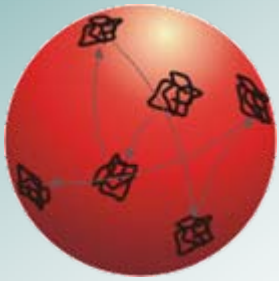


a-PEMA: Two-step Randomization of Chain Motion

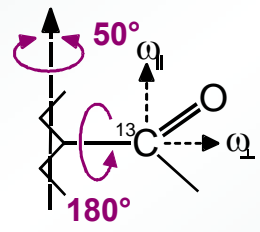
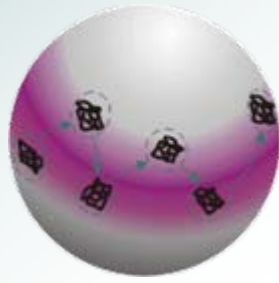


melt
melt
melt
melt
T_g glass

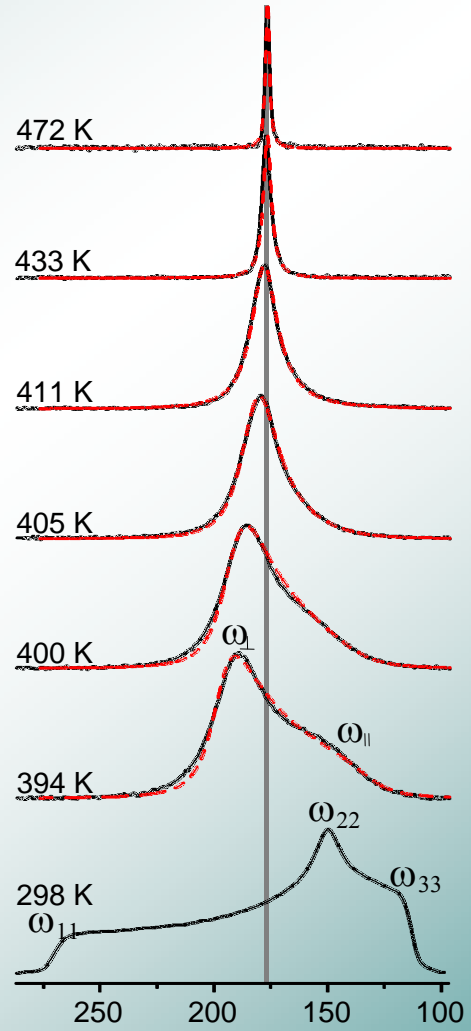
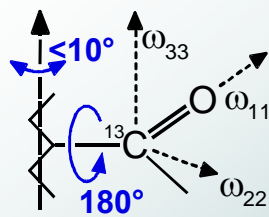
+ randomization of chain motion



+ anisotropic chain motion



rigid + fractional sidegroup flips



T_g = 354 K

1D ¹³C NMR:

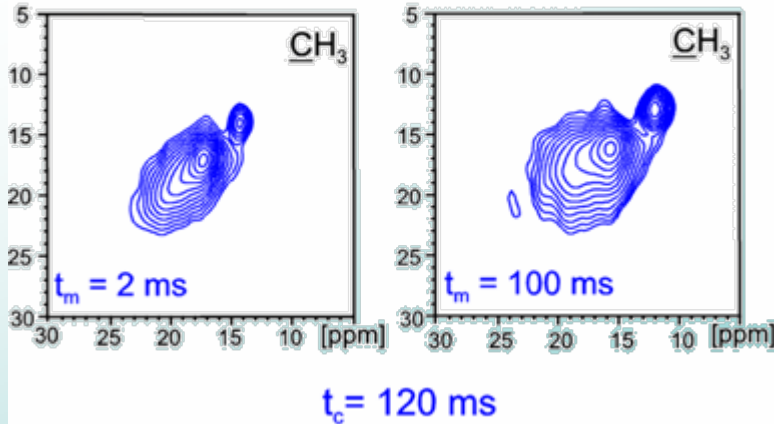
— experiment
- - - simulation



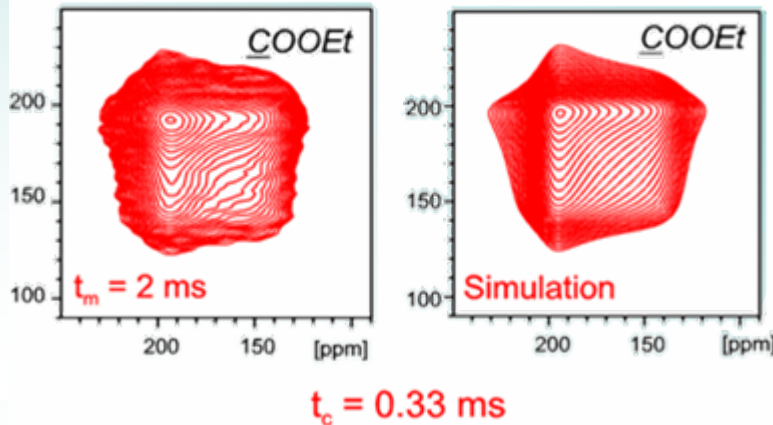
Separation of Dynamic Timescales in PEMA-Melts



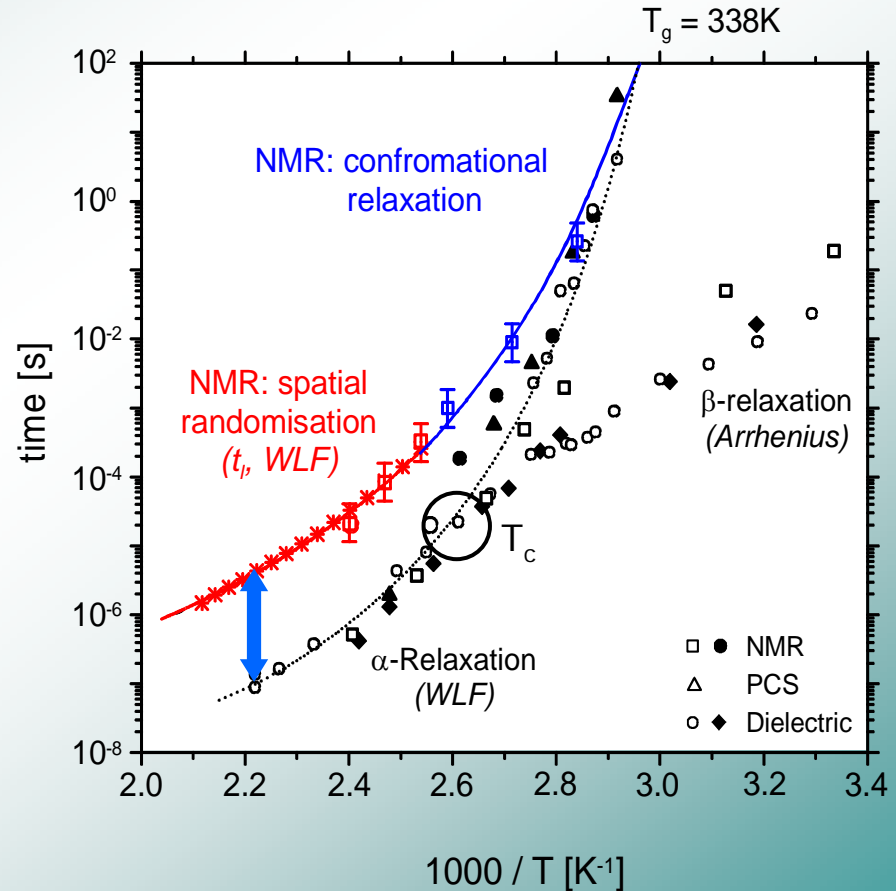
Conformational Dynamics
from ^{13}C MAS NMR ($T = 385\text{ K}$)



Randomisation from ^{13}C
2D Exchange NMR ($T = 385\text{ K}$)



Correlation Times from NMR, PCS, Dielectrics



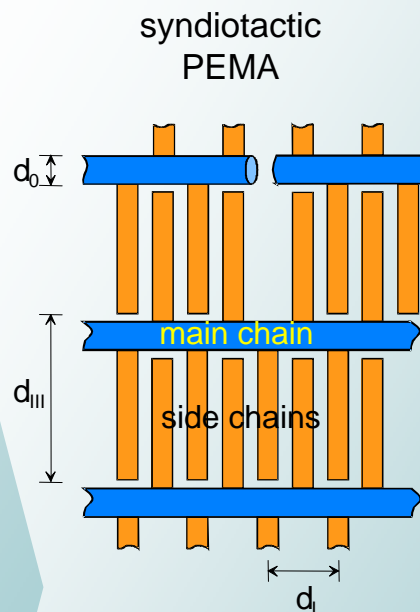
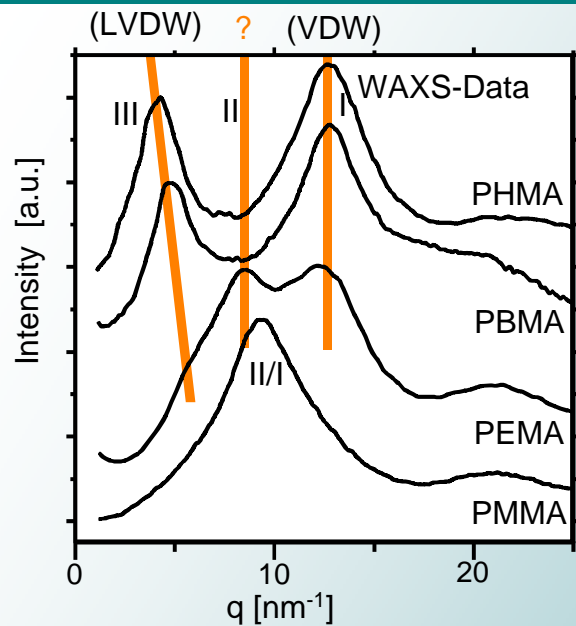
**Difference in time scale (factor 50):
consistent with length scale 7 repeat units**



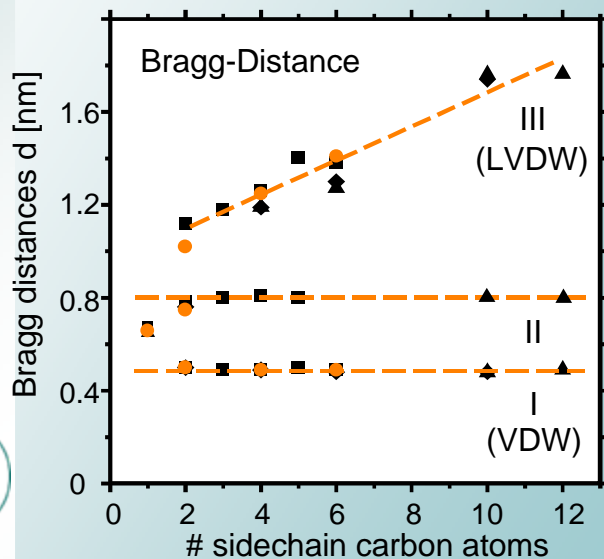
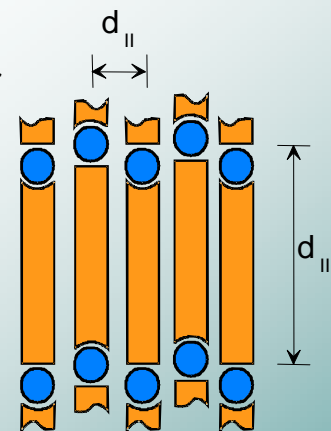
Intersegmental Order in Poly(methacrylates): WAXS



X-Ray Scattering



X-Ray patterns reminiscent of stiff macromolecules with flexible sidechains



inter layer

inter chain

intra chain

„layered nano aggregates“



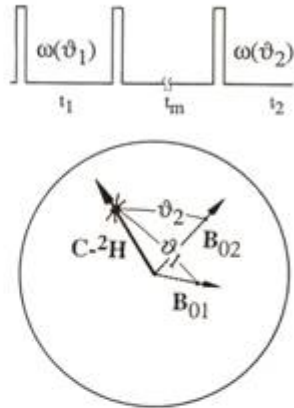
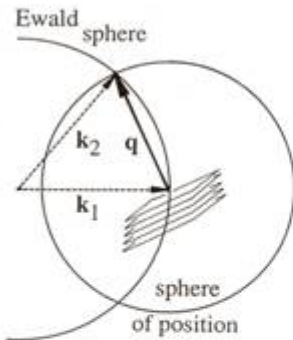
2D DECODER NMR for Ordered Systems



ANALOGY between 2D NMR and X - RAY SCATTERING

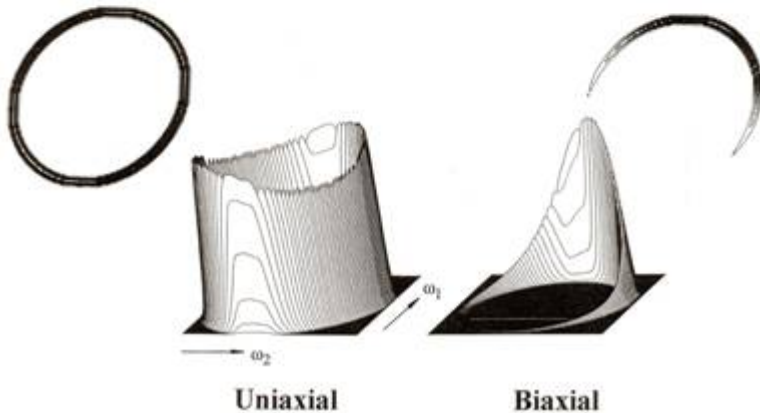
Wide-Angle
X-ray Scattering

DECODER
2D NMR



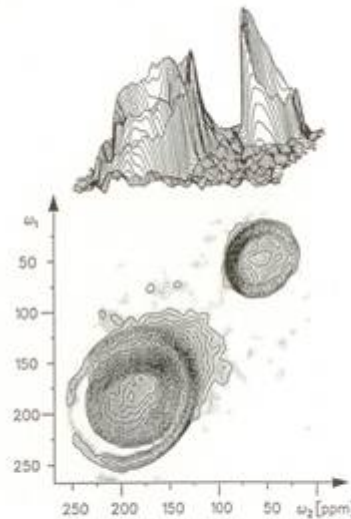
$$I_G(\mathbf{q}) \propto \left| \int \int \exp[i \mathbf{G}(\Theta, \Phi) \cdot \mathbf{r}] \exp[-i \mathbf{q} \cdot \mathbf{r}] d\Theta d\Phi \right|^2$$

$$S_B(\omega) \propto \int \int \exp[i \Omega^B(\Theta, \Phi) \cdot \mathbf{t}] \exp[-i \omega \cdot \mathbf{t}] d\Theta d\Phi$$

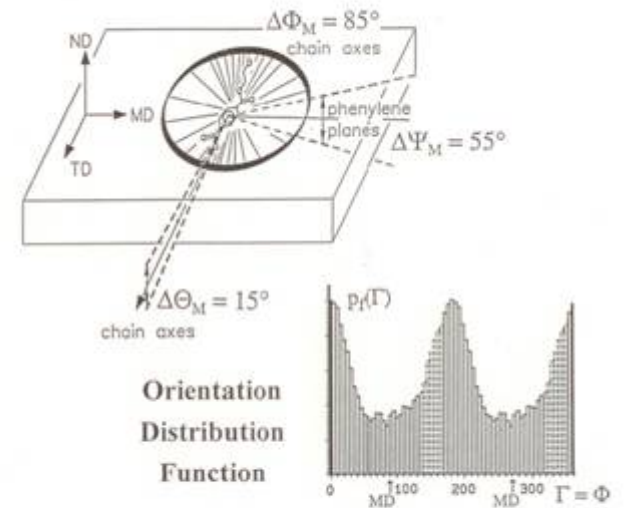


Example: Biaxially stretched PET

2D DECODER ¹³C NMR Spectra



Highly oriented PET film



Reconstruction of Orientation Distribution Function
from 2D DECODER ¹³C NMR Spectra of PET

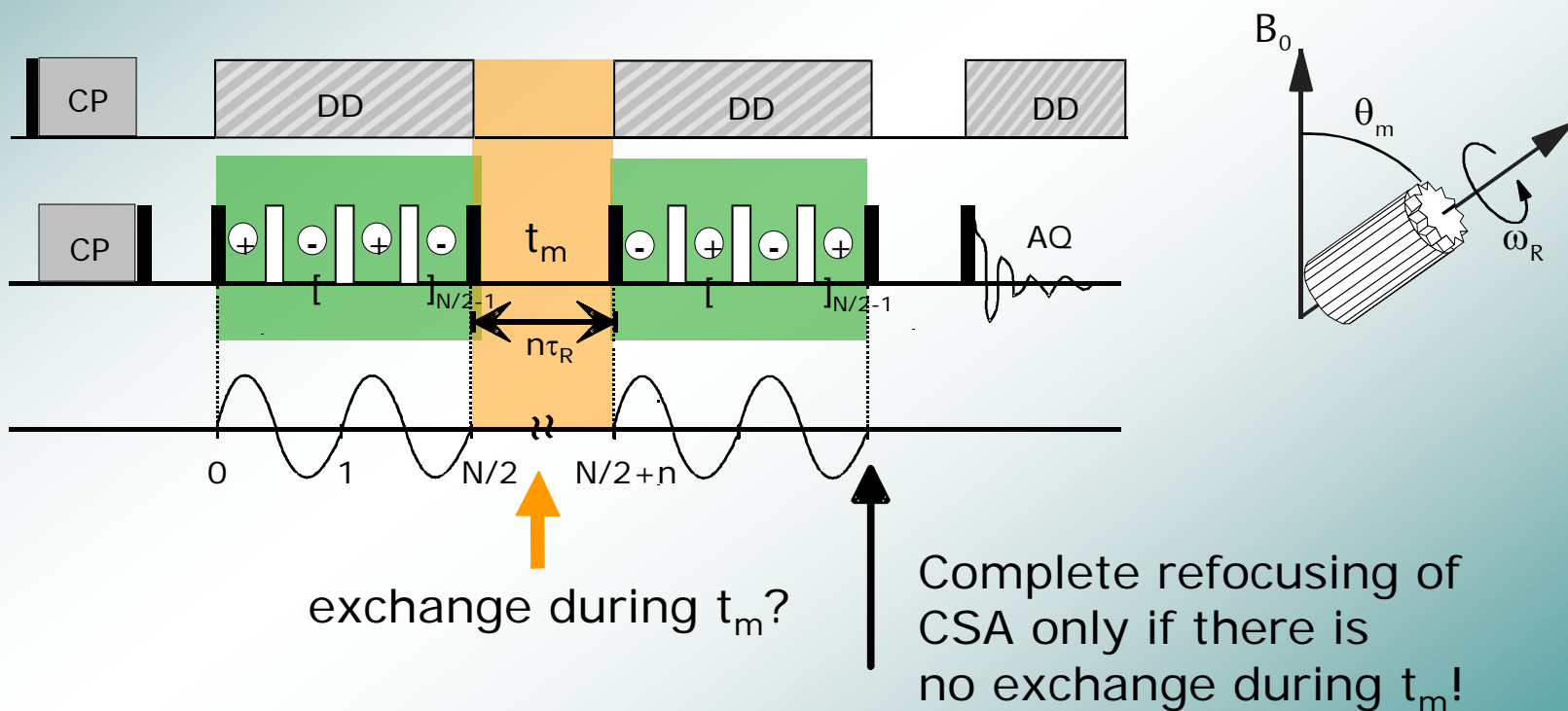
2D exchange with sample flip
rather than molecular motion

Recoupling CSA: CODEX



CODEX: Centreband-Only Detection of Exchange

Approach: Recoupling the chemical-shift anisotropy (CSA) under MAS

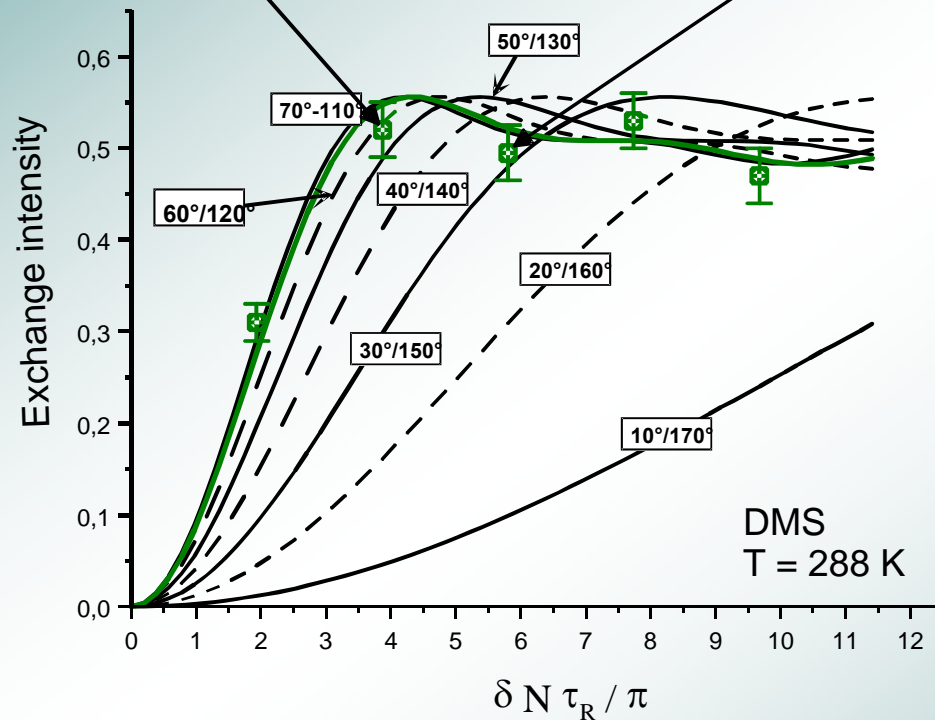


Advantages:

High spectral resolution, short measuring time compared to 2D exchange NMR



CODEX: reorientation angle



CODEX build-up curves

- exchange intensity for a given mixing time depends on the overall duration of recoupling
- shape of the curves depends significantly on the reorientation angle



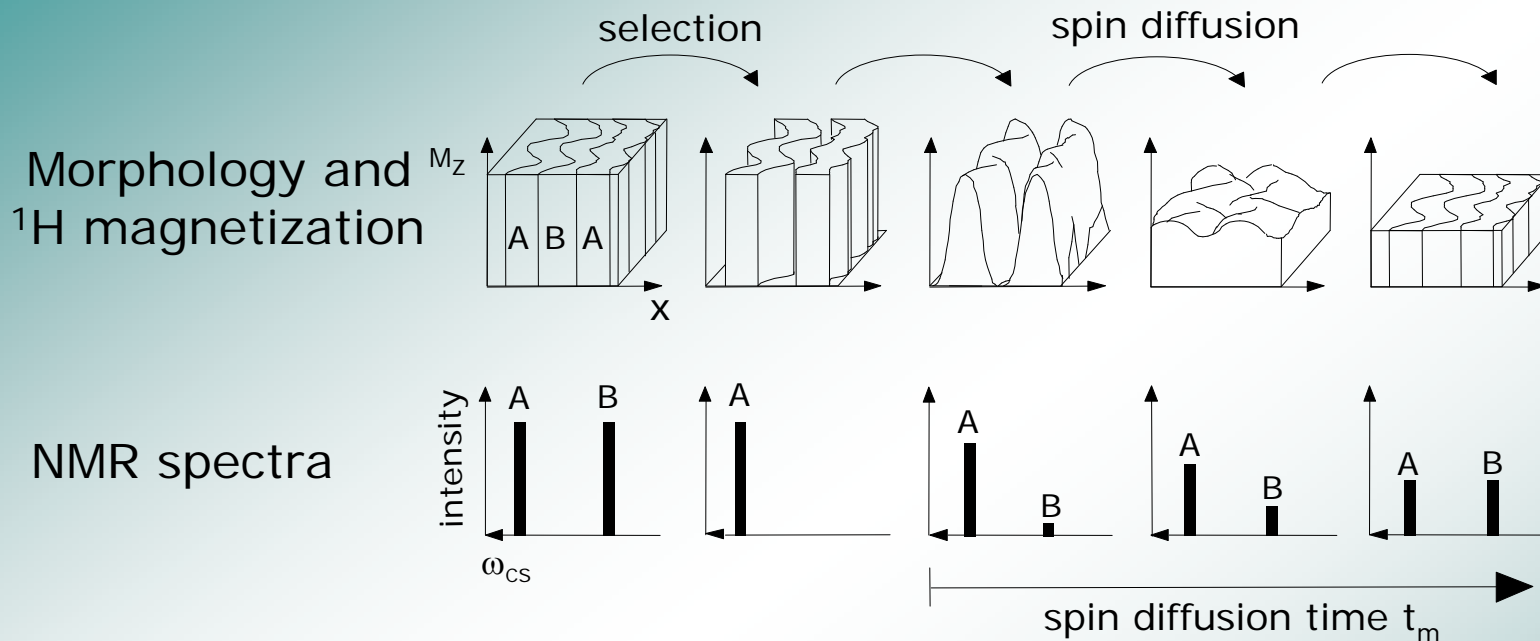
Overview of NMR of Bulk Polymers



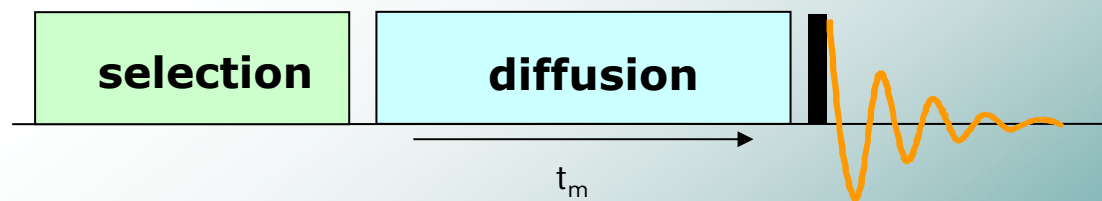
- Introduction • Basics
- Configuration, Conformations • Chain Branching
- Local Structure & Dynamics • Amorphous & Crystalline Polymers
- Phase Behavior • **Core Shell Structures**
- Supramolecular Organization • Functional Polymeric Systems
- Conclusions • Scattering and NMR



Phase Separation Probed by Spin diffusion



NMR spin diffusion experiment



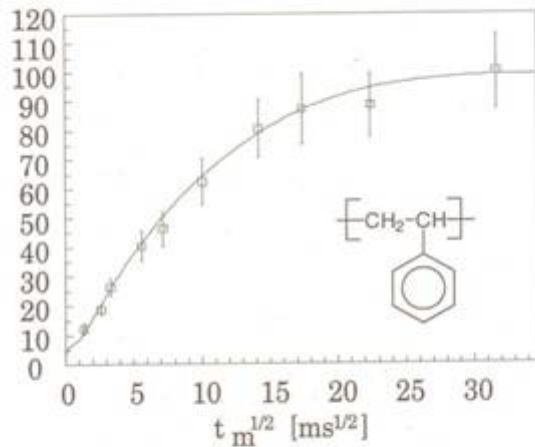
- ➡ Chemical shift filters (e.g. DANTE): spectral selection
- ➡ Dipolar filters (e.g. SR-12): motional selection



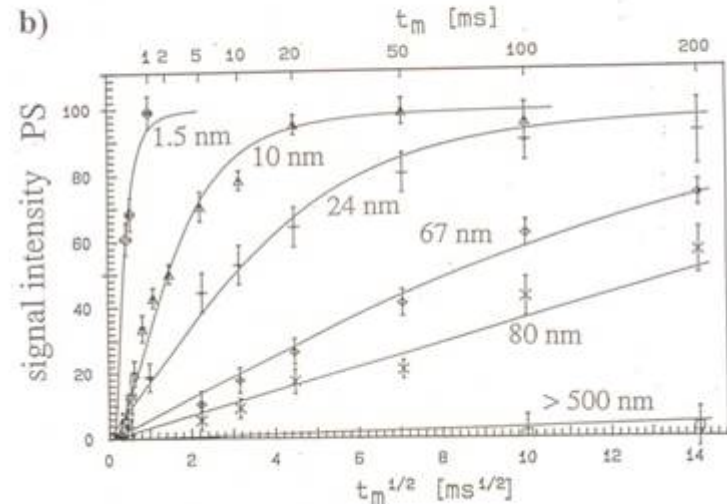
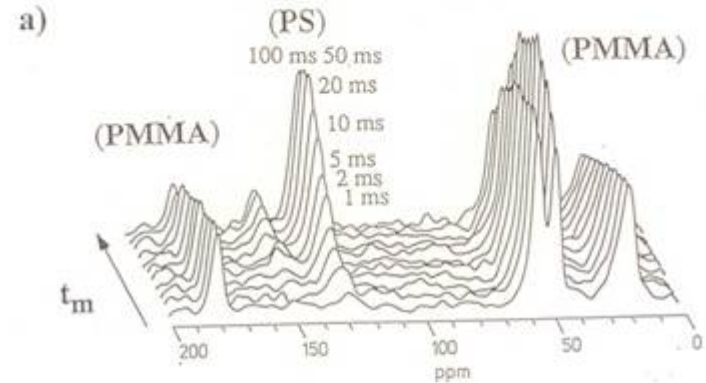
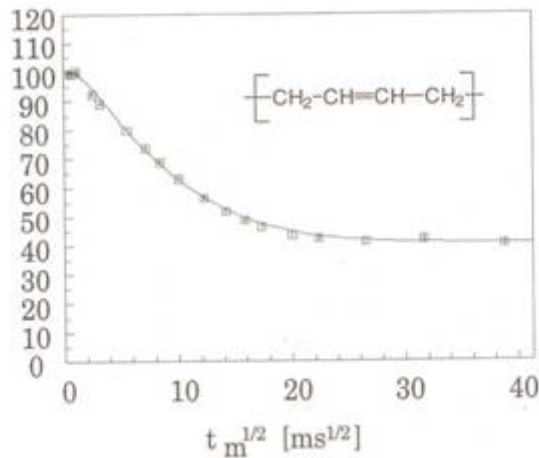
Domain Sizes in Phase Separated Polymers



Detection of rising polystyrene signal



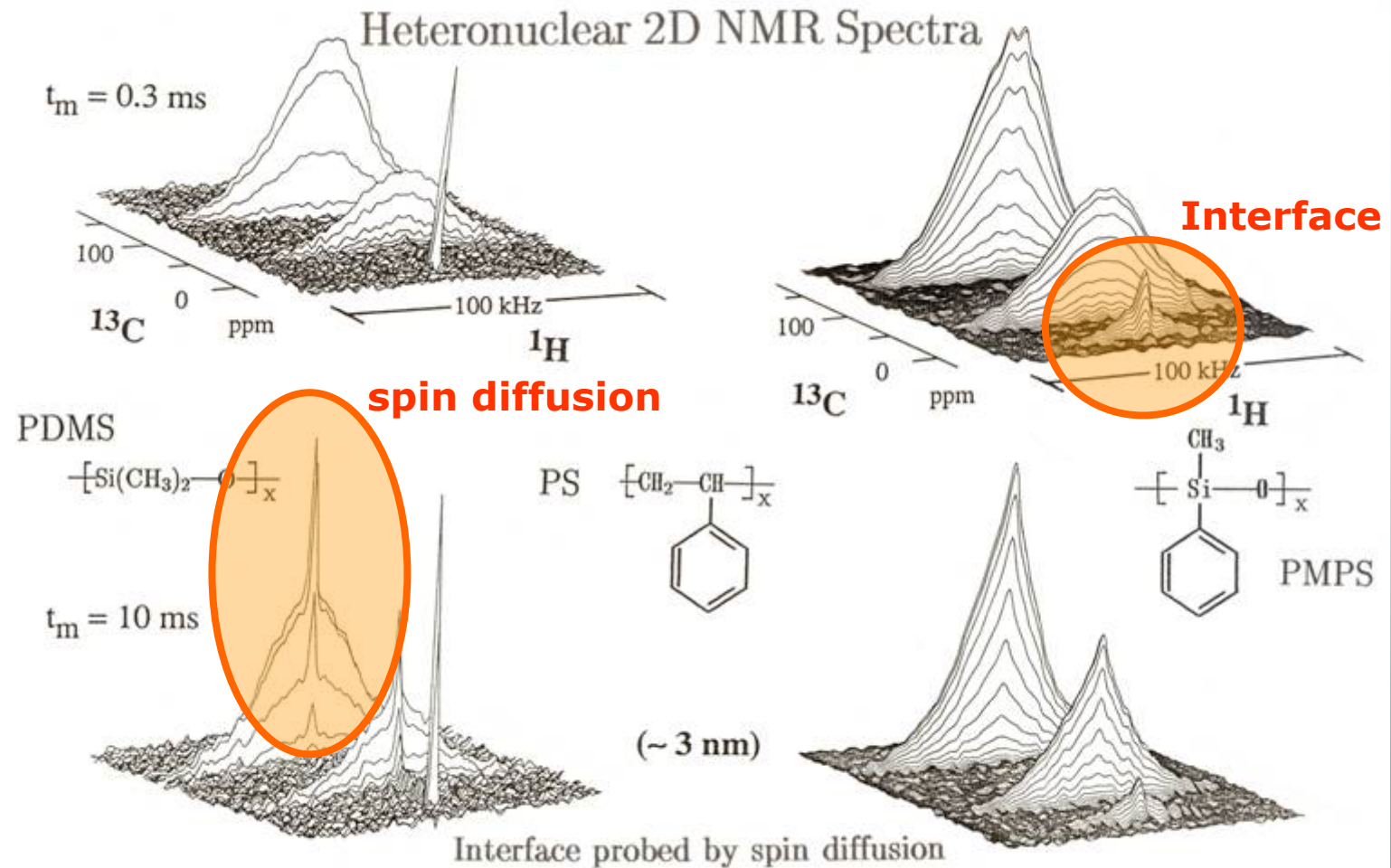
Detection of decaying polybutadiene signal



Rigid and Mobile Components

Both Components Rigid

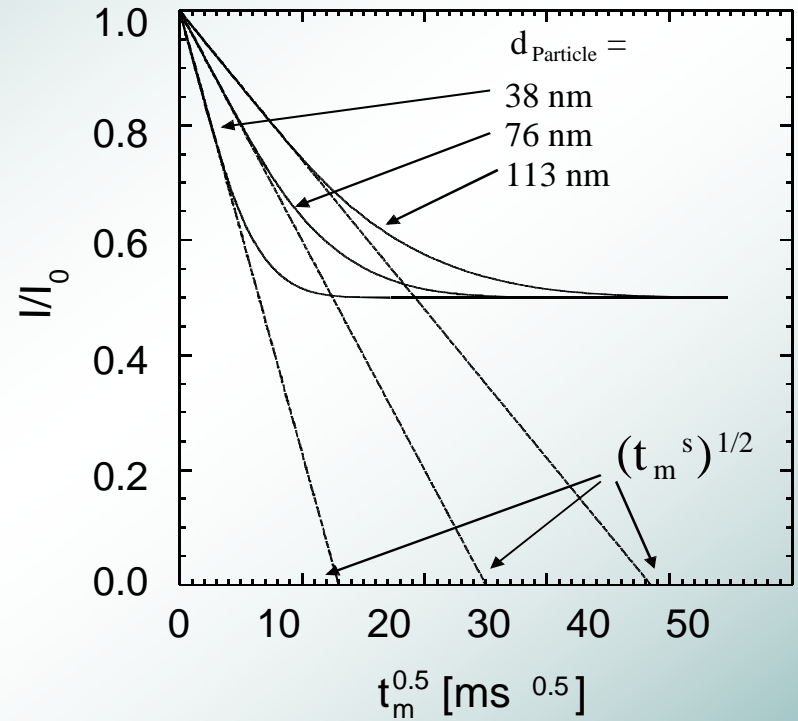
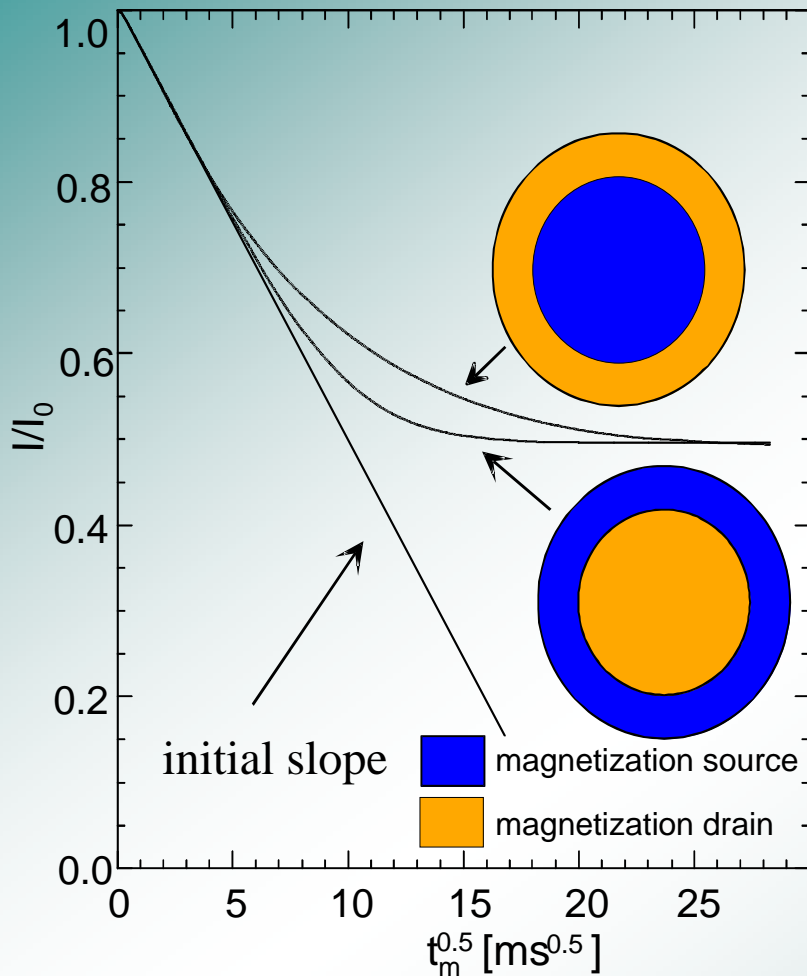
Spin Diffusion in 2D Wideline Separation Spectra



PHASE SEPARATION AND RIGID-MOBILE INTERFACES

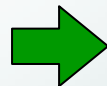


Investigating core-shell particles



contact surface: S
 source volume: V

$$S/V = \sqrt{\frac{\pi}{D_{\text{eff}} t_m^s}} \quad \text{with} \quad \sqrt{D_{\text{eff}}} = \frac{2\sqrt{D_A D_B}}{\sqrt{D_A} + \sqrt{D_B}}$$



structure and particle size can be determined



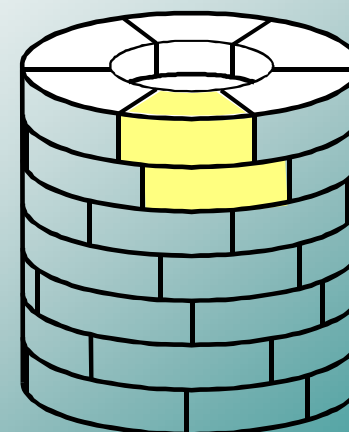
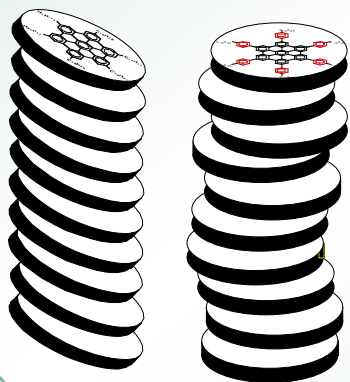
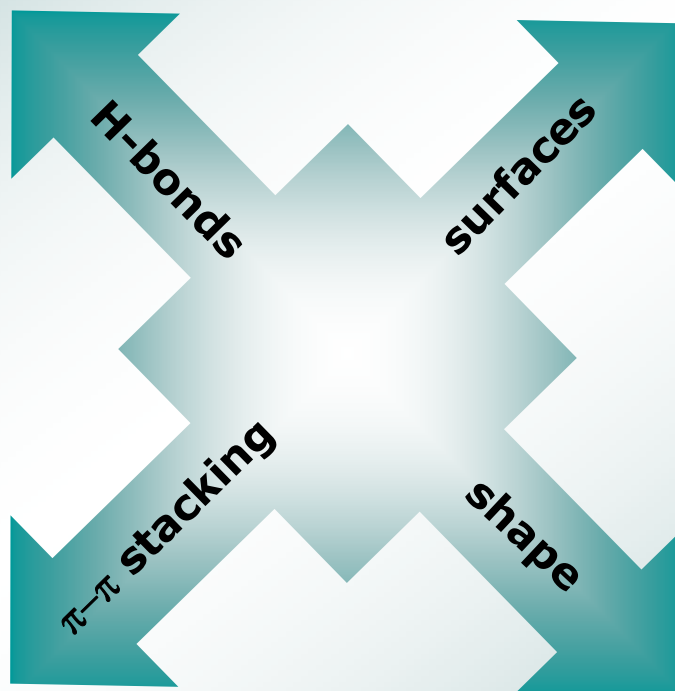
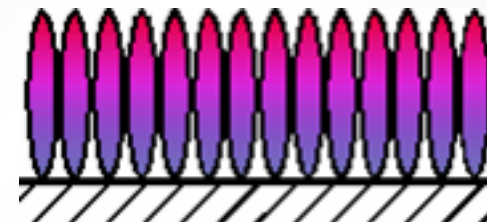
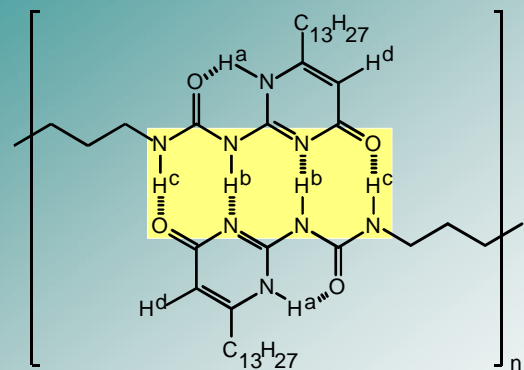
Overview of NMR of Bulk Polymers



- Introduction • Basics
- Configuration, Conformations • Chain Branching
- Local Structure & Dynamics • Amorphous & Crystalline Polymers
- Phase Behavior • Core Shell Structures
- Supramolecular Organization • **Functional Polymeric Systems**
- Conclusions • Scattering and NMR



Key Elements of Supramolecular Assemblies



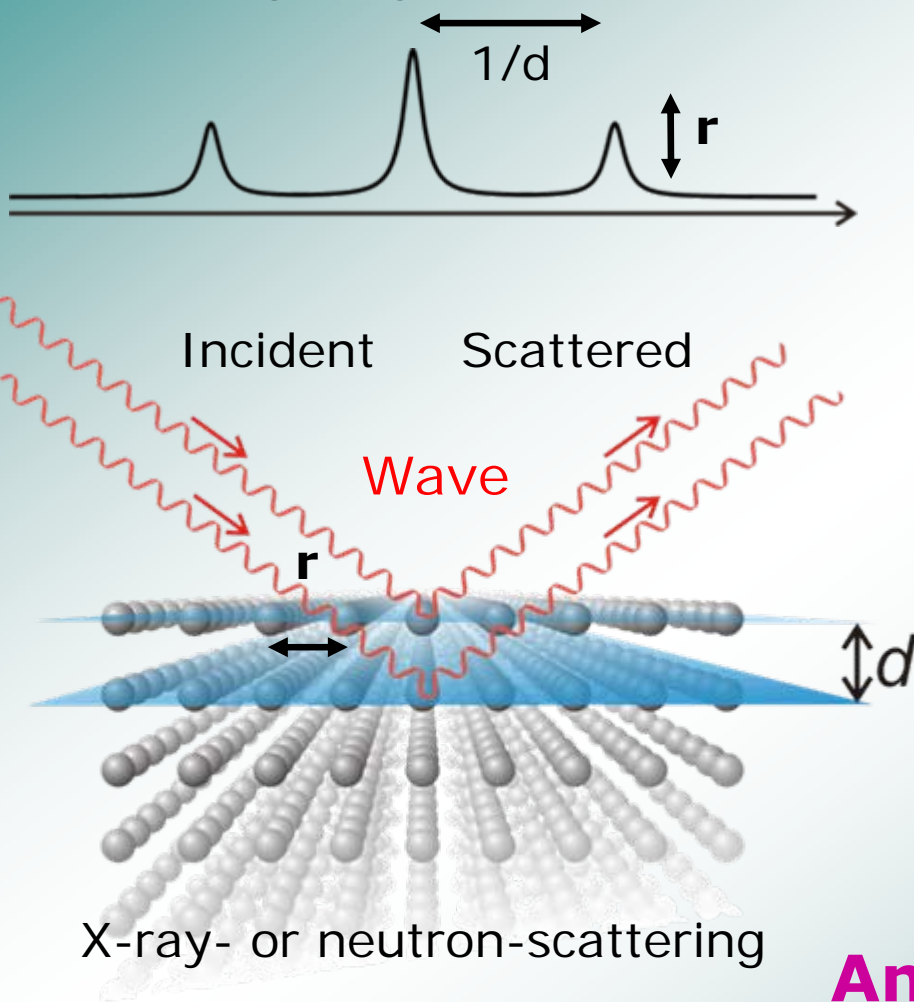
Challenge: Elucidate **Noncrystalline** Structures

Scattering

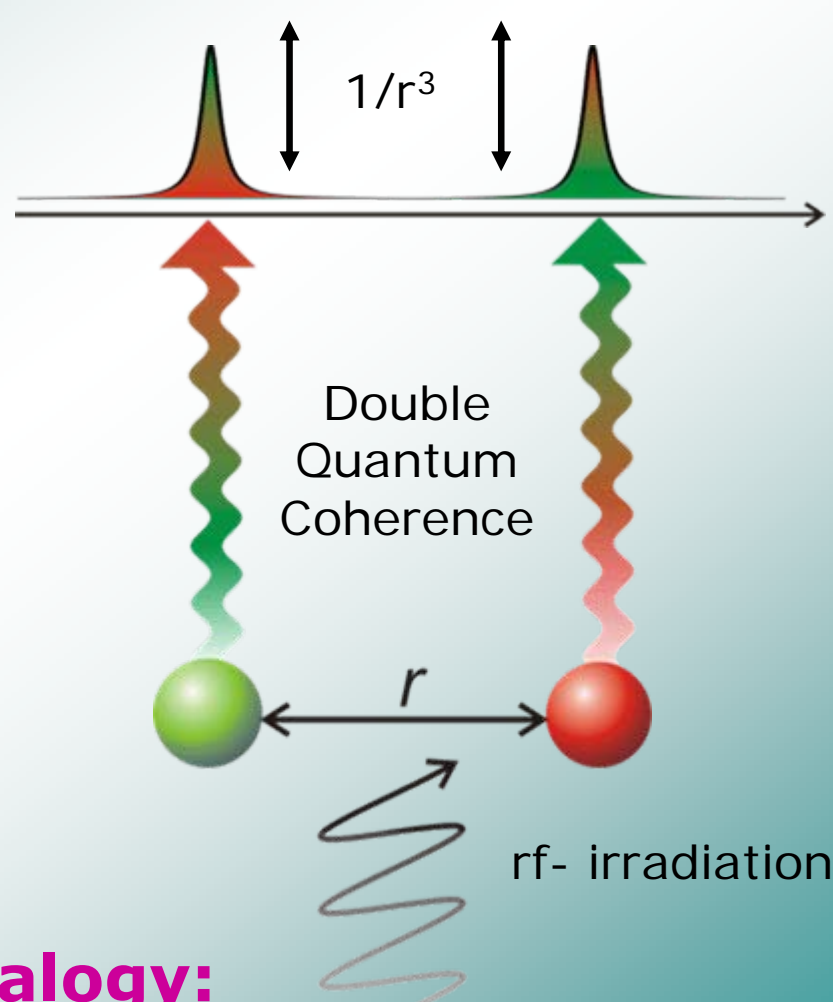
Double Quantum NMR



Scattering Diagram / (Reflections)



NMR Spectrum

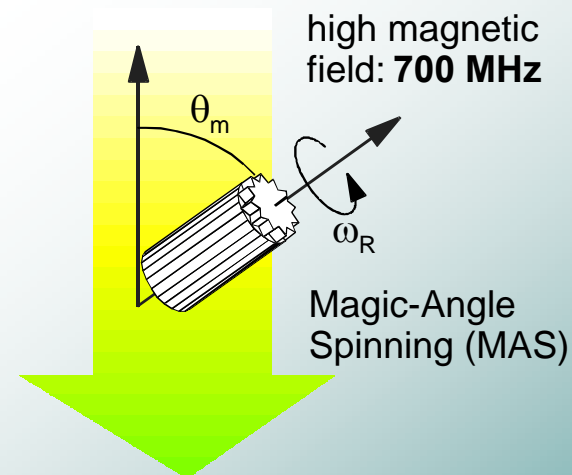
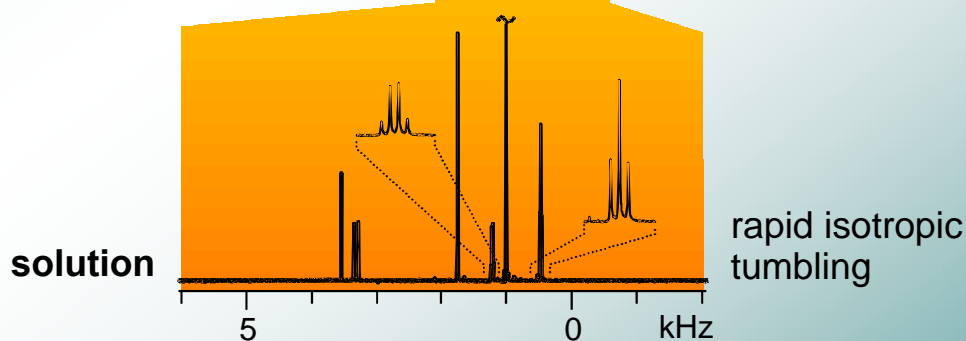
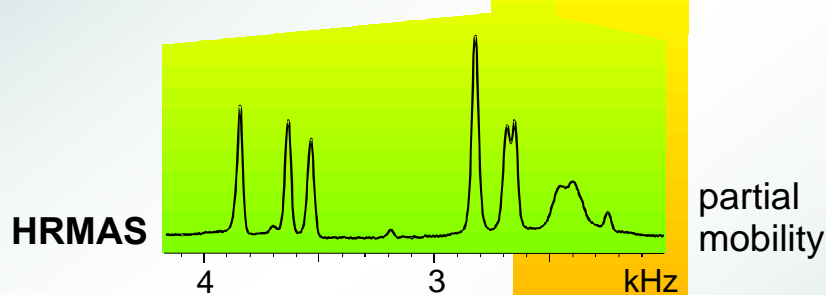
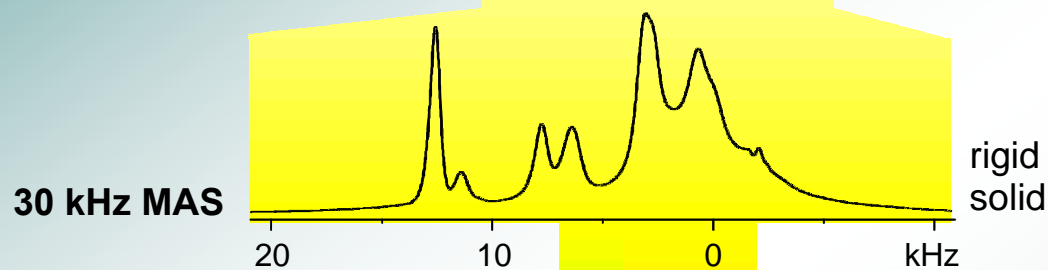
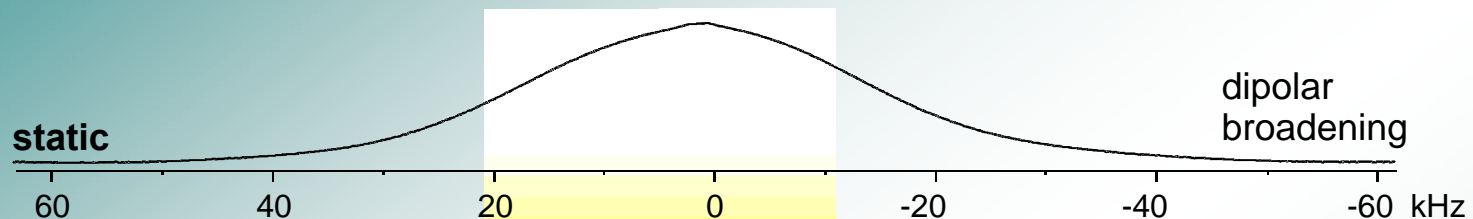


Analogy:

In both cases: coherent superposition of signals from spatially separated centers



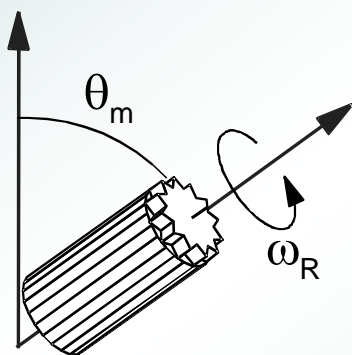
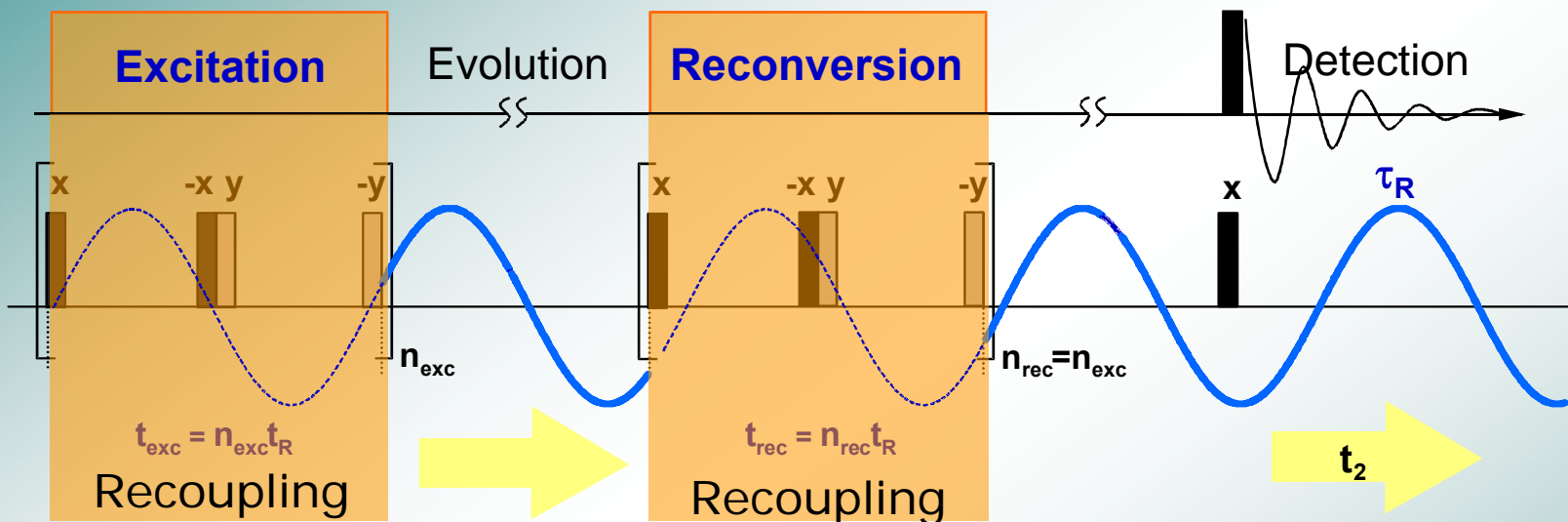
^1H NMR spectra in solid and liquid state



increasing spectral resolution



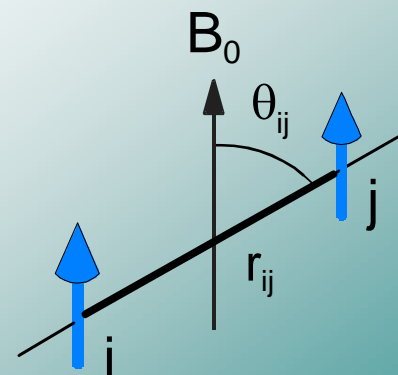
Dipolar DQ Spectroscopy of a Spin-Pair under MAS



Dipole-Dipole Coupling:

$$\hat{H} = \hat{R}_{2,0} \cdot \hat{T}_{2,0}$$

Space Spin



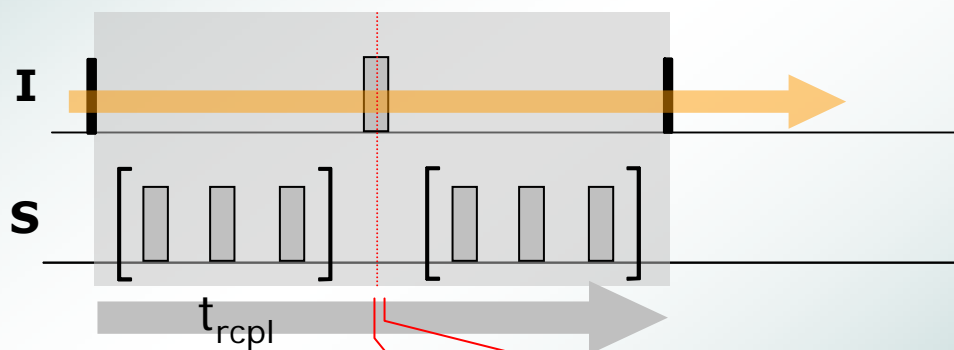
Signal build-up versus rotor-encoding



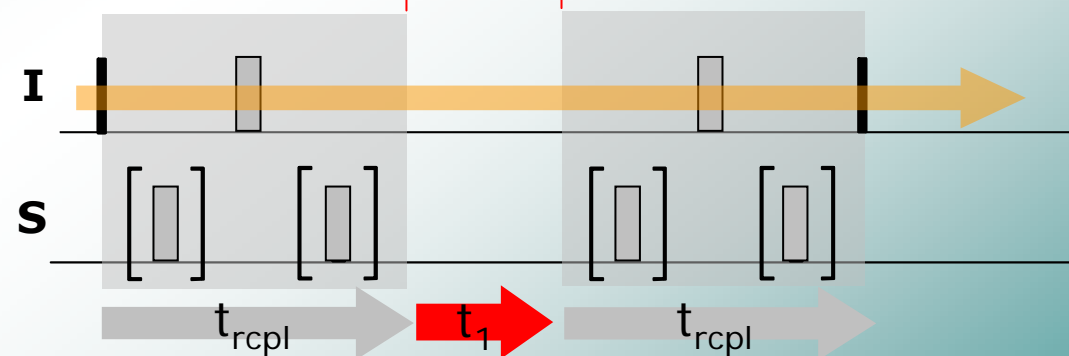
Two alternative concepts for measuring recoupled interactions:

- following the signal intensity as a function of the recoupling time (resulting in **build-up** or dephasing **curves**)
- recording **rotor-encoded** signal (resulting in MAS sideband patterns)

REDOR scheme



Rotor-encoded REDOR scheme



Rotor-encoding of dipolar Hamiltonians



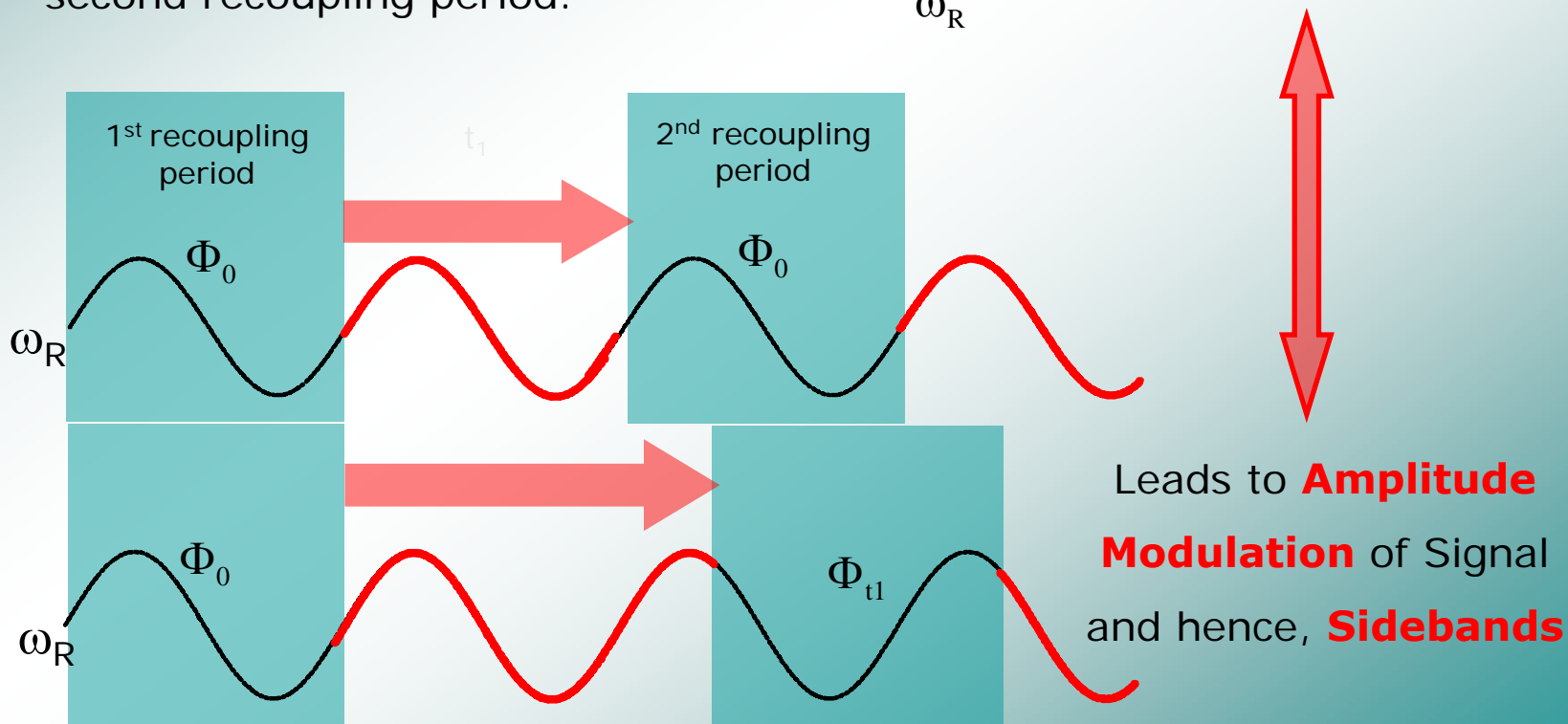
Recoupled dipolar Hamiltonian:

with dipolar "**phases**" for first recoupling period:

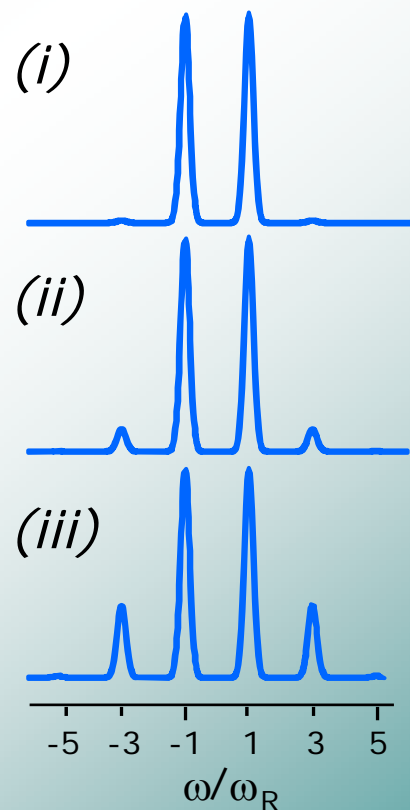
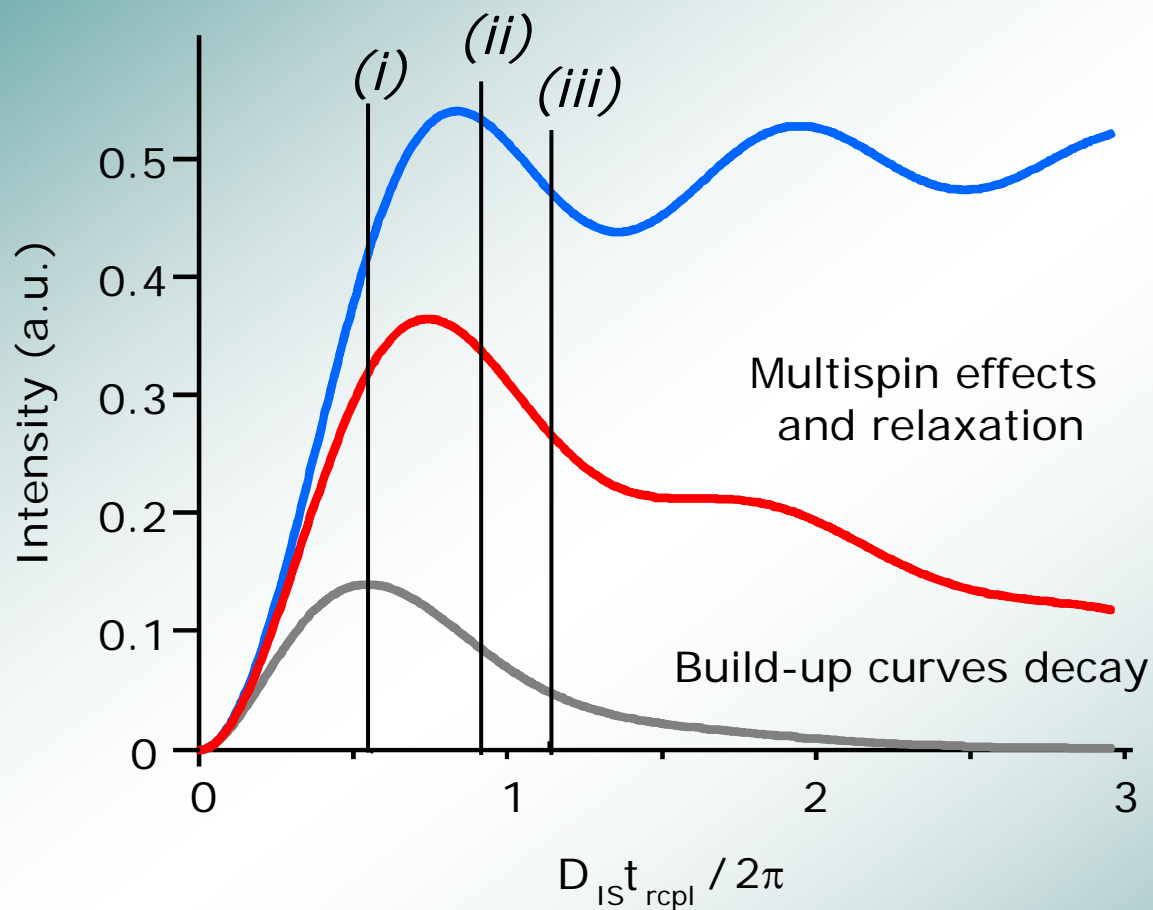
$$\Phi_0 = -\frac{D_{IS}}{\omega_R} 2\sqrt{2} \sin 2\beta \sin \gamma$$

and for "**rotor-encoded**" second recoupling period:

$$\Phi_{t_1} = -\frac{D_{IS}}{\omega_R} 2\sqrt{2} \sin 2\beta \sin(\omega_R t_1 + \gamma)$$



REDOR-type curves and sideband patterns



HDOR sideband **patterns**
robust:

Multispin effects:
additional sidebands



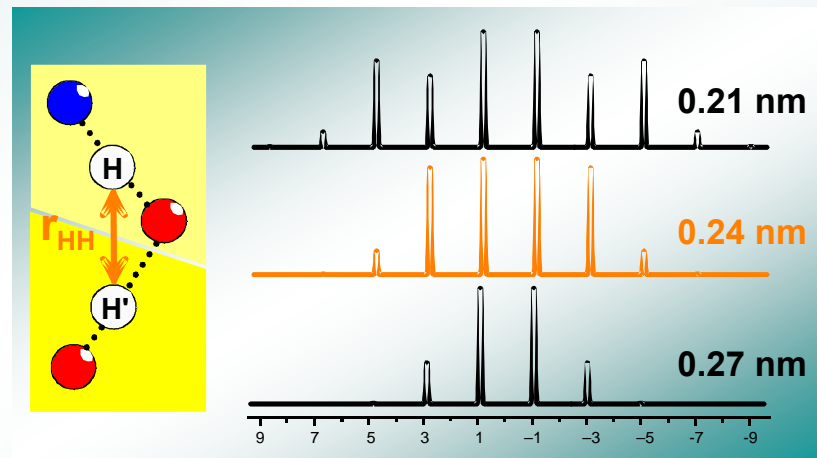
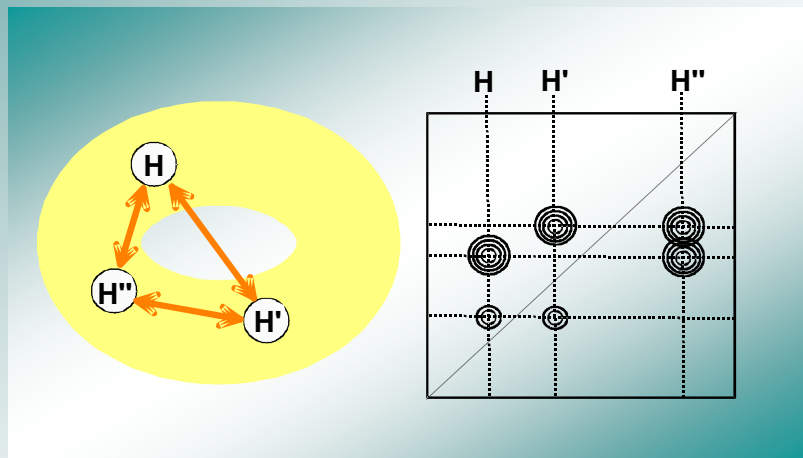
Multiple-quantum NMR methods: investigating (supra)molecular structure



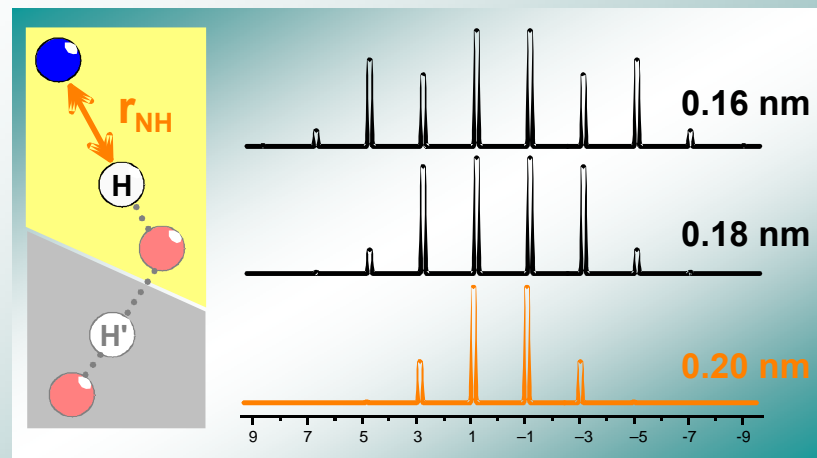
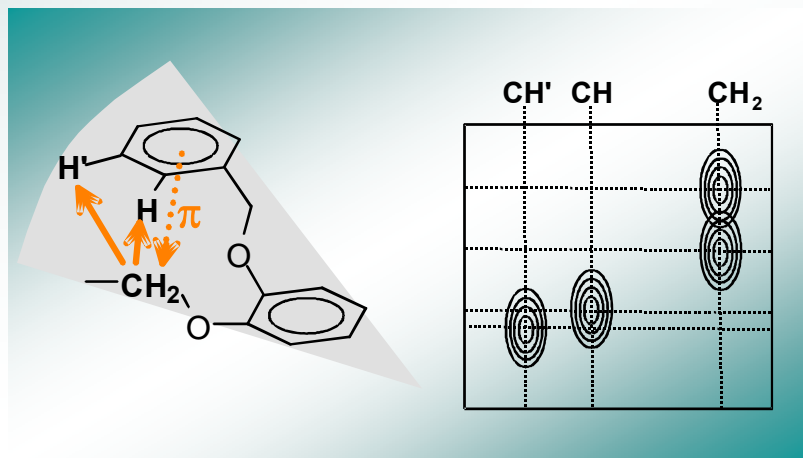
internuclear proximities,
chemical shifts and π -shifts

internuclear distances
molecular dynamics

¹H-¹H homonuclear



¹H-¹³C/¹⁵N heteronuclear



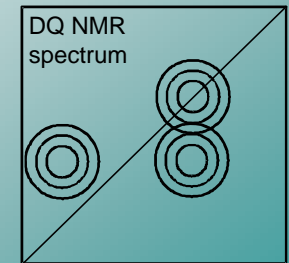
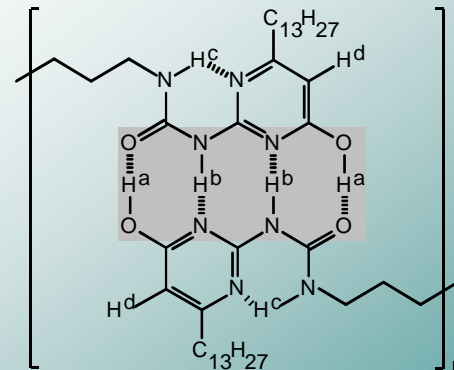
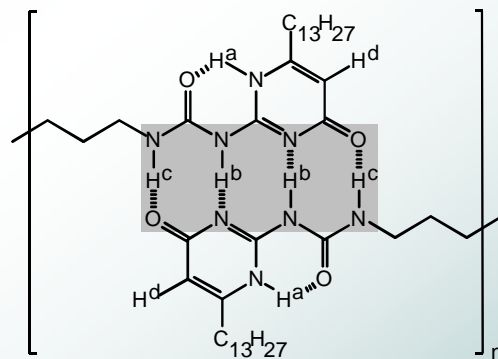
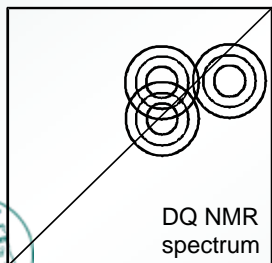
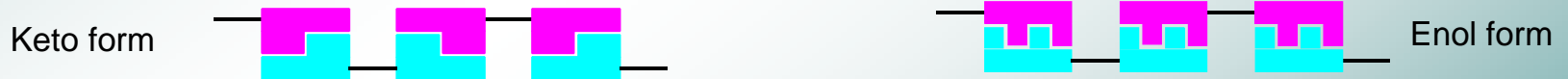
Multiple Hydrogen Bonds in Natural and Synthetic Systems



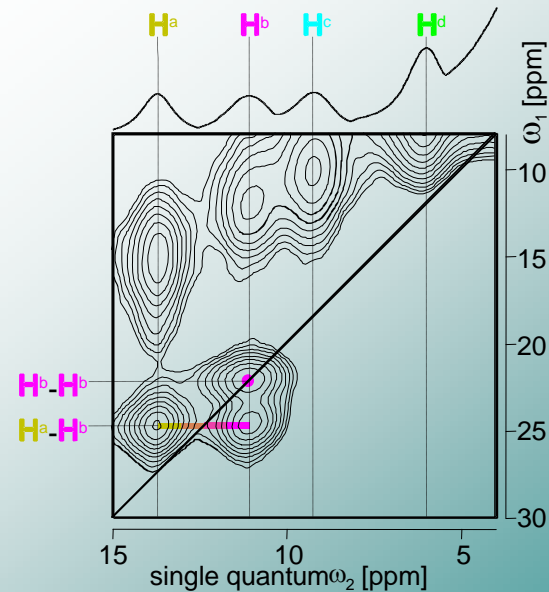
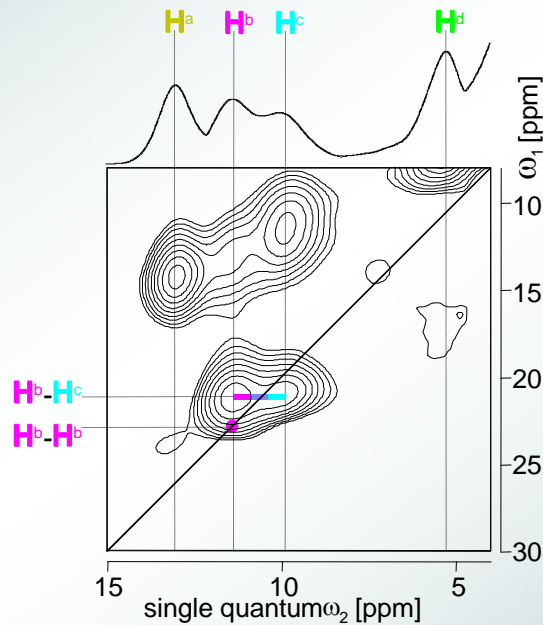
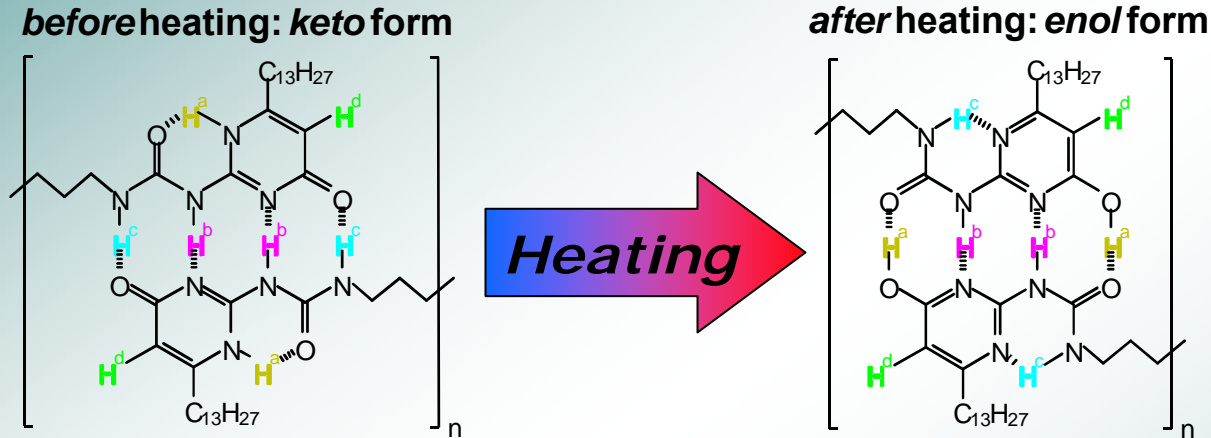
Supramolecular polymers via hydrogen bonds



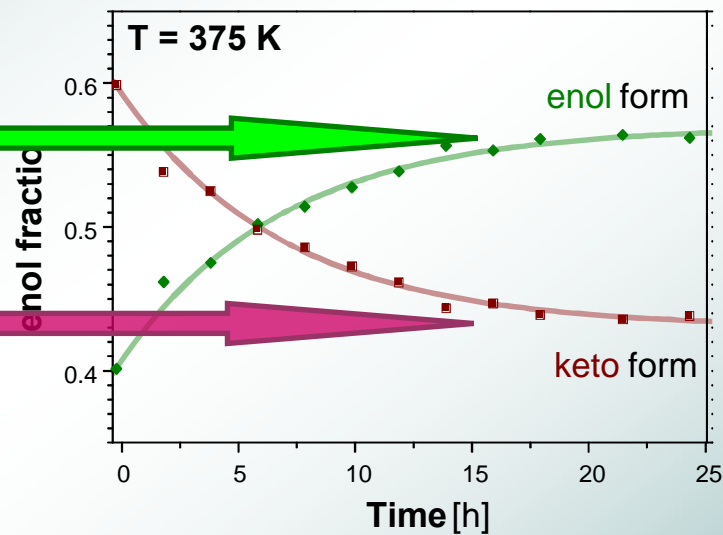
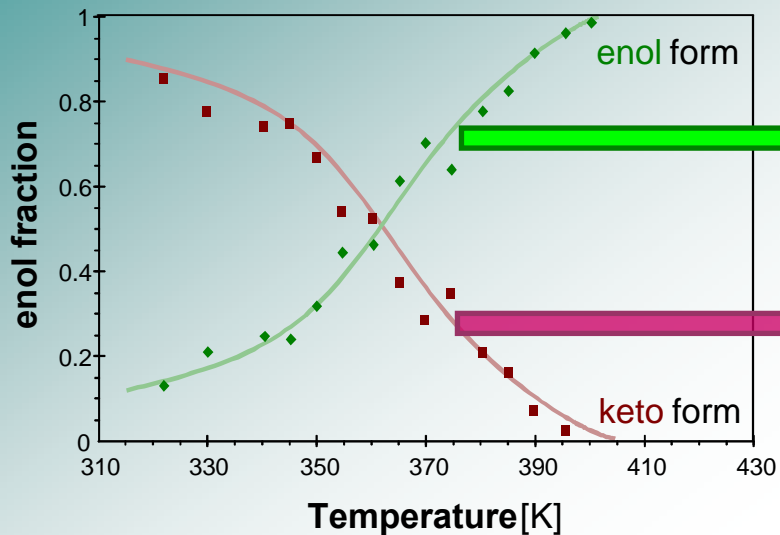
R.P. Sijbesma, E.W. Meijer et al., *Science*, 1997:
Thermoreversible linkages through quadruple hydrogen bonding



Heat-Induced Tautomeric Rearrangement: ^1H - ^1H DQ Spectra of Quadruple Hydrogen Bonds

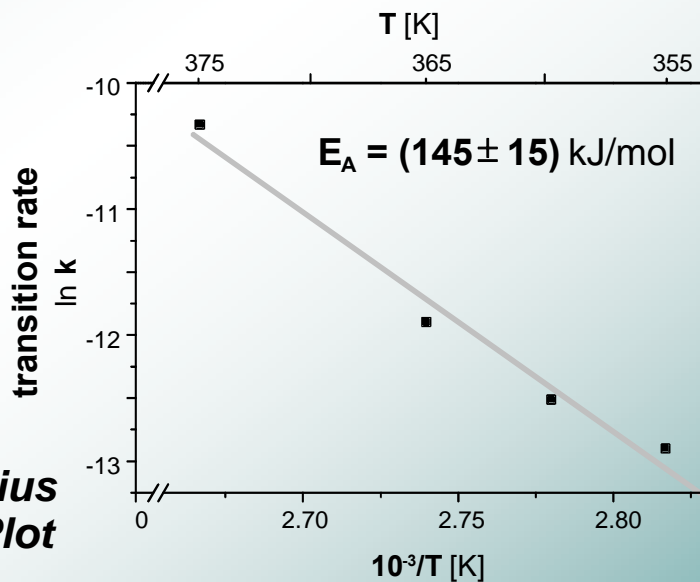


Kinetics of the Tautomeric Rearrangement



**Temperature
Dependence**

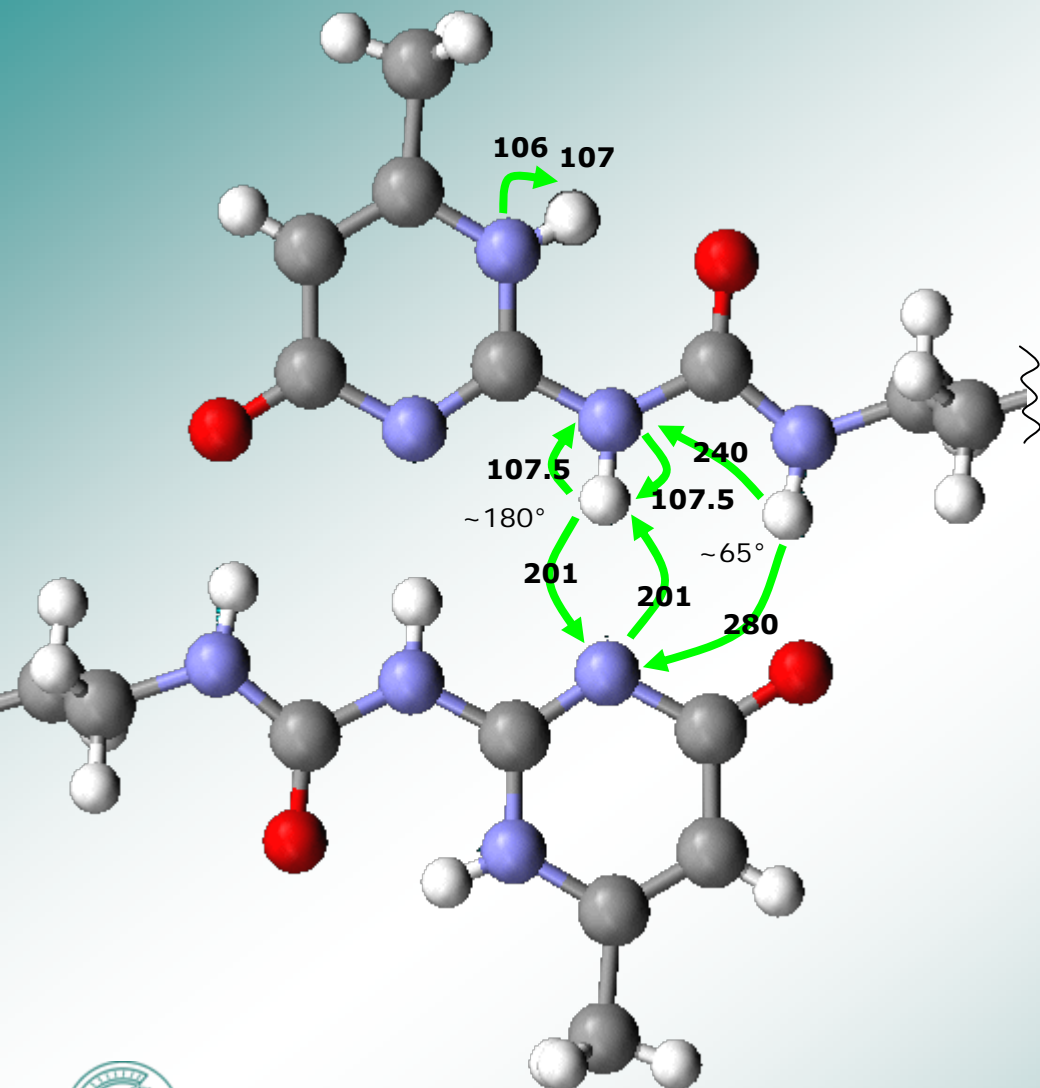
**Time
Dependence**



**Arrhenius
Plot**

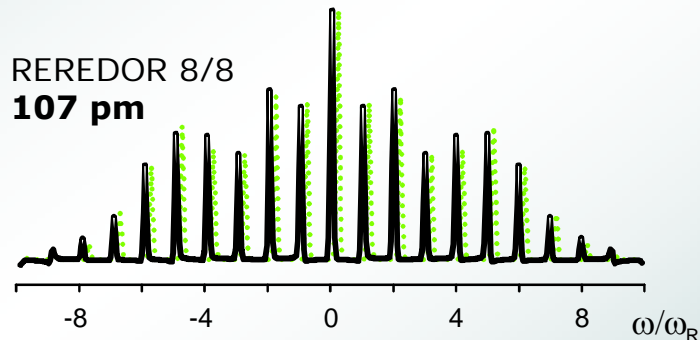


Multiple N-H Distances in the Pyrimidinone Form

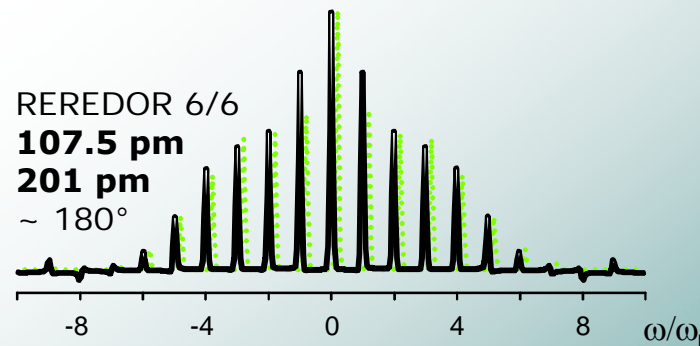


$^1\text{H}\{^{15}\text{N}\}$ recoupling: ^1H - detection

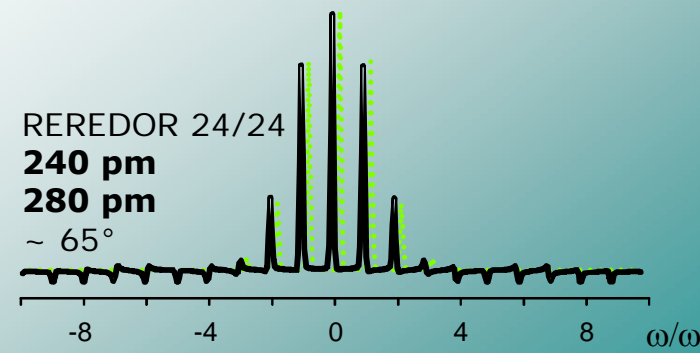
REREDOR 8/8
107 pm



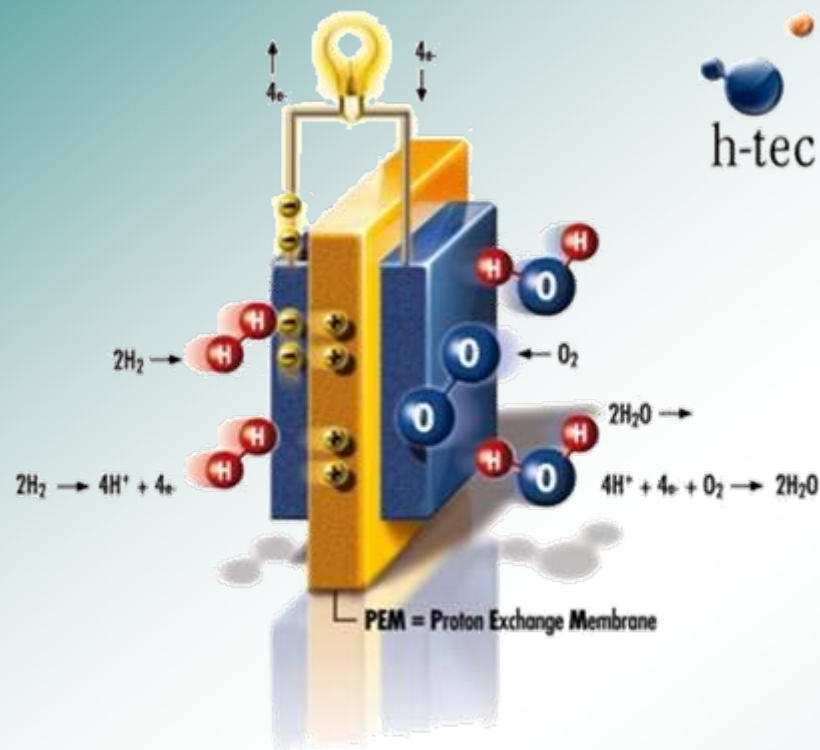
REREDOR 6/6
107.5 pm
201 pm
~180°



REREDOR 24/24
240 pm
280 pm
~65°



Separator Membranes and NMR



→ reveal details of proton conductivity on *molecular* level
(**site-selective** & **non-destructive**)



→ provide structural constraints
(proton transfer mechanism ?)



PVPA: poly(vinyl phosphonic acid)



High proton conductivity under dry conditions
at elevated temperatures

NMR probes for local structure & dynamics

³¹P NMR

↳ **phosphonic acid units**, local **dynamics**

¹H NMR

↳ backbone as well as **mobile protons** (local dynamics)

²H NMR

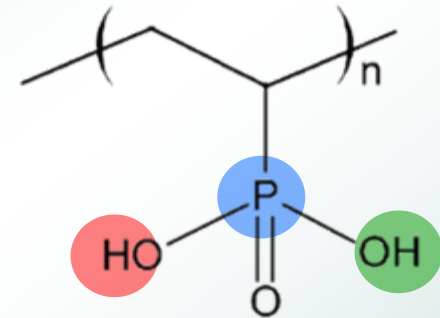
↳ **primary process**: orientation-dependent rate of movement:
time scale and geometry (multi-site jumps)

¹H-¹³C NMR

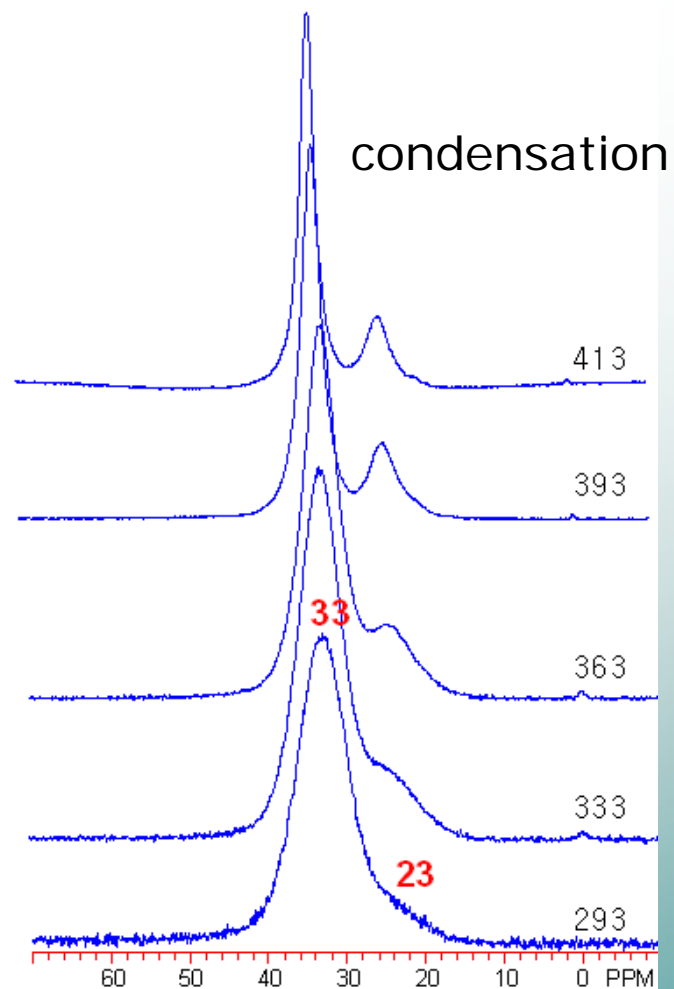
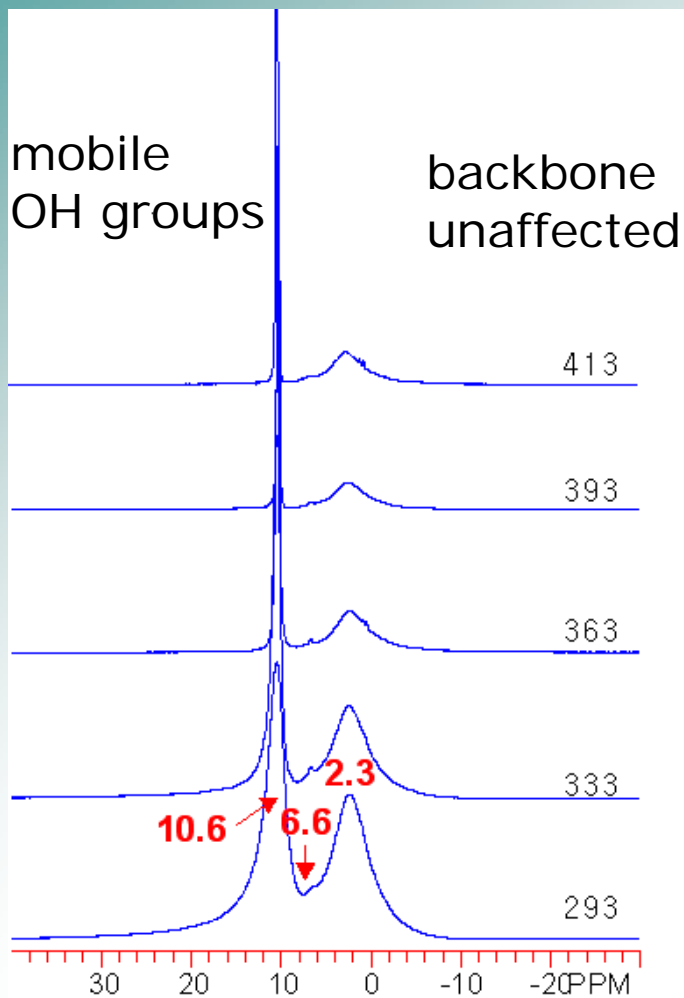
↳ segment mobilities of alkyl chains, **polyvinyl backbone**

¹H-³¹P and ¹H-¹H NMR

↳ **hydrogen bonding** at phosphonic acid units



PVPA: VT NMR motional narrowing



¹H MAS NMR

³¹P MAS NMR

very narrow lines in both ¹H and ³¹P spectra



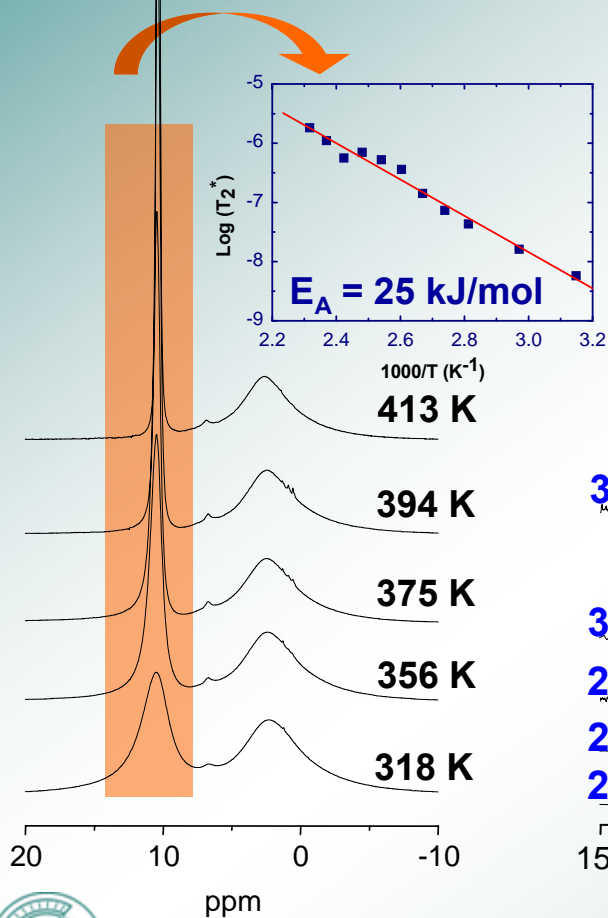
Poly(vinyl phosphonic acid): PVPA



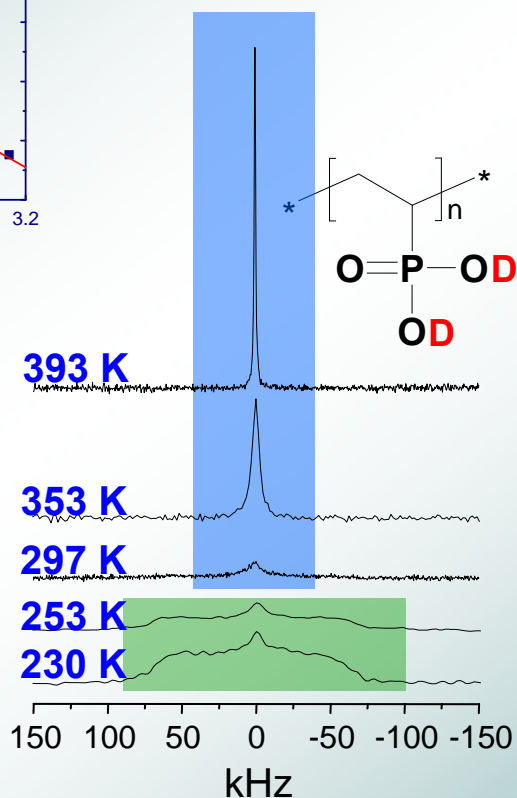
P-OH : mobile proton, hydrogen bonded
 Dynamics of motion involved in proton conduction

$^1\text{H} - ^1\text{H}$ DQ Spectra

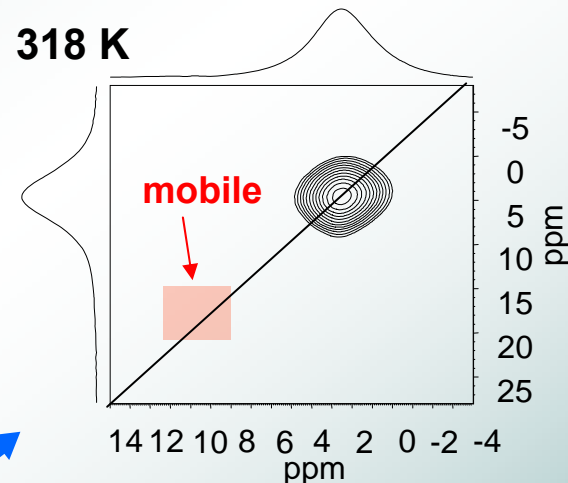
P-OH proton: mobile



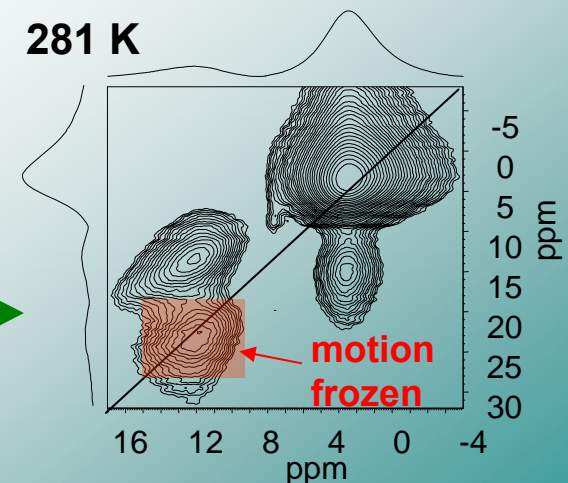
^2H solid echo spectra



318 K

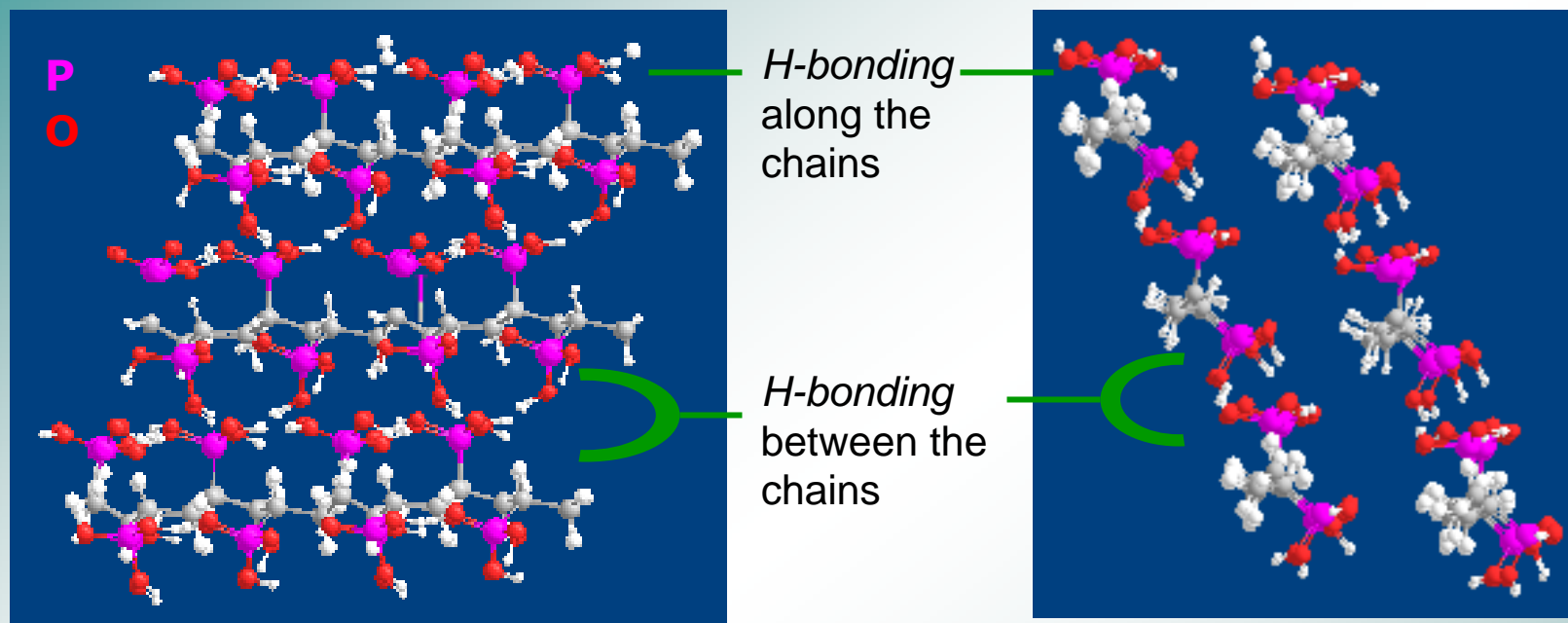


281 K



^1H MAS spectra

PVPA: *ab initio* structure (model geometry)

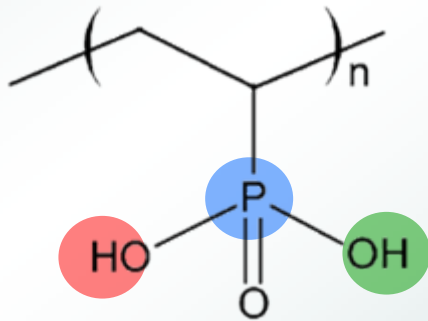
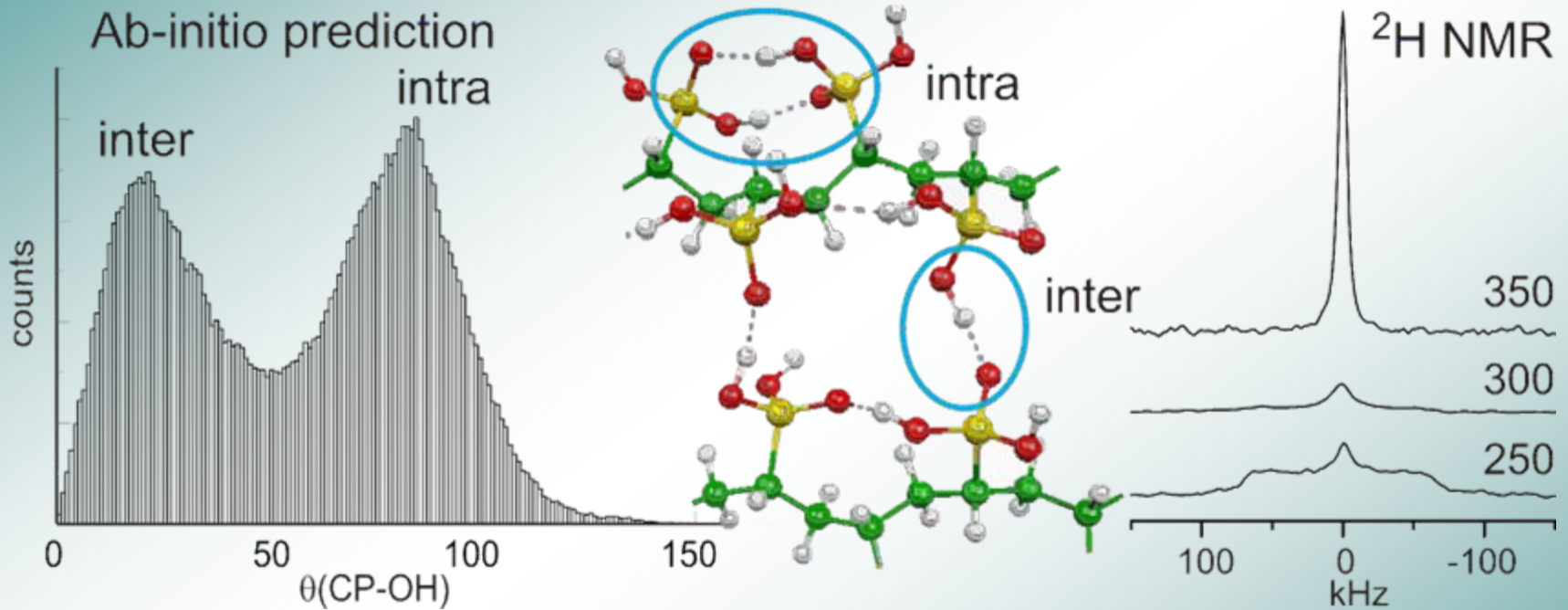


Ab initio calculation based on model geometry (CPMD):

- * Elucidation of hydrogen bondings and ^1H chemical shift calculation:
 - *H-bonding* between phosphonic acids on the *same* chains and *between* two parallel chains
 - MD: *Proton hopping* occurs along chains as well as between chains mediated by hydrogen bonds.
 - calculated $\delta(\text{P-OH}) = 9.7$ ppm (exp.: 10.6 ppm)



PVPA: Averaging of Deuteron Quadrupole Coupling



Broad distribution of angles between instantaneous O-H and C-P directions, yet
Quadrupole coupling reduced by factor 10 after CPMD run of 15 ps



Overview of NMR of Bulk Polymers



- **Introduction**
- **Basics**
- **Configuration, Conformations**
- **Chain Branching**
- **Local Structure & Dynamics**
- **Amorphous & Crystalline Polymers**
- **Phase Behavior**
- **Core Shell Structures**
- **Supramolecular Organization**
- **Functional Polymeric Systems**
- **Conclusions**
- **Scattering and NMR**



Scattering and NMR in Bulk Polymers



SCATTERING

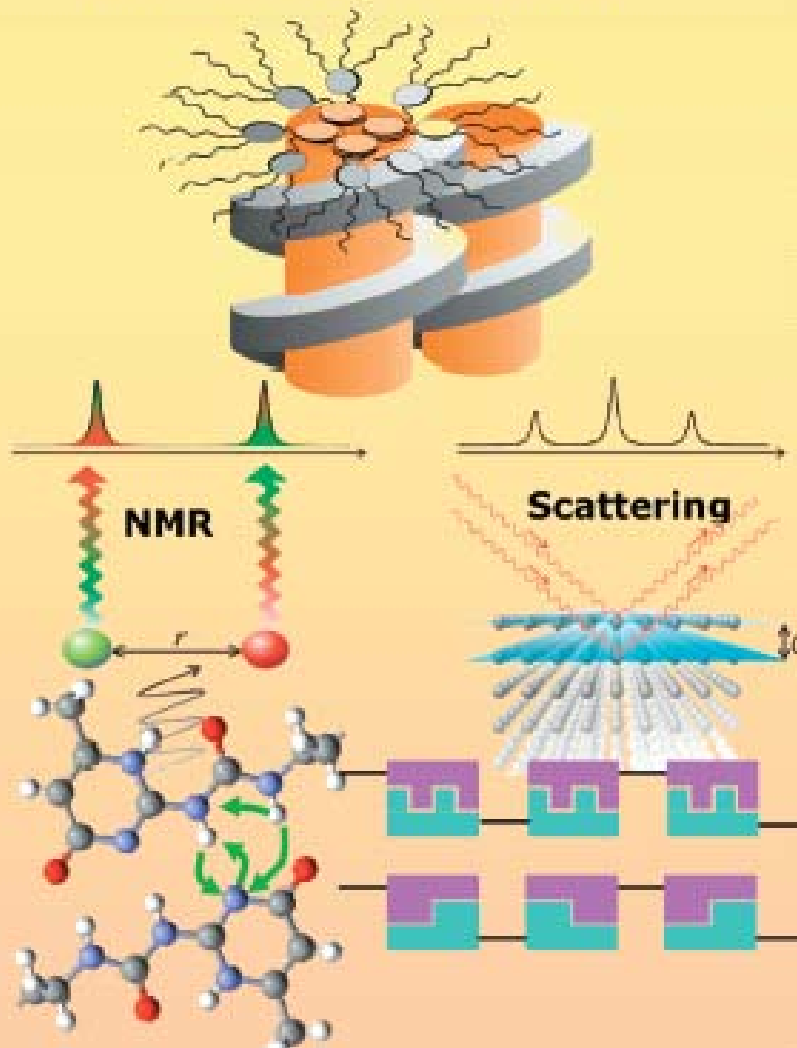
NMR

		incoherent	coherent	single quantum	double quantum
D Y N A M I C S					
	Molecular	n-quasielastic	n-quasielastic	2D-, 3D-, 4D-exchange	sidebands
	Collective		n-spin-echo	2D-exchange	decay of DQC
S T R U C T U R E					
	Molecular		WAXS, WANS	chemical shift, sidebands	2D pattern, sidebands
	Collective (packing)		X-ray pole figures, SAXS, SANS	DECODER chemical shift	2D signal pattern





Advanced Solid State NMR



Advantages of NMR:

- Selectivity, Versatility
- Detailed information on geometry and time scale of dynamics
- Large range of length- and time scales accessible
- Elucidation of supramolecular organization
- Relation between structure, dynamics and functional behavior
- Limits not reached, e.g. microcoils

References



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H. W. Spiess, *Advanced Solid-State Nuclear Magnetic Resonance for Polymer Science*;
J. Polym. Sci. **A 42**, 5031–5044 (2004).

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