Nuclear magnetic resonance (NMR)

Some concepts

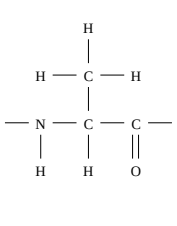
- different kinds of experiment
- spectrum interpretation:
  peak assignment, spin systems, chemical shifts
- distance restraints
- model quality

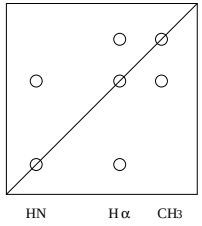
Some issues for structural bioinformatics

- structure calculation
- under- and over-constrained distance restraints
- ensembles of structures
- conformational flexibility
- identifying structural cores

COSY

- correlation spectroscopy
- magnetization can be transferred between protons on adjacent atoms





Protein NMR

Samples of purified protein in solution.

Exploits magnetic properties of certain atomic nuclei: ^{1}H, ^{13}C, ^{15}N.

Can think of “spinning spheres”.

Net excess of nuclei aligned with magnetic field.

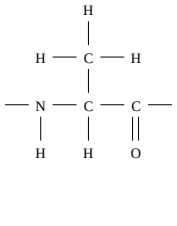
Radio frequency pulse tilts nuclear spin.

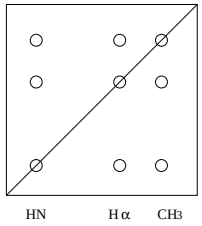
2D Proton NMR (^{1}H):
correration spectroscopy (COSY), total correlation spectroscopy (TOCSY), nuclear Overhauser effect spectroscopy (NOESY), ...

Other nuclei and higher dimensions.

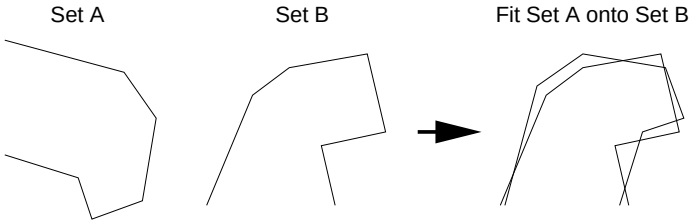
TOCSY

- total correlation spectroscopy
- magnetization can be transferred from alpha proton to beta protons, from beta protons to gamma protons, and so on, through several bonds





Comparing molecular fragments



- 3-D transformation to map Set A onto Set B
- Root Mean Square (RMS) distance

KBB056 — Methods in structural biology

Course TDA507 includes only a very light introduction to experimental methods for determining macromolecular structures, with emphasis on some of the issues that structural bioinformaticians should be aware of when using structures from the Protein Data Bank.

Course KBB056 describes these experimental methods more thoroughly:

> “This course aims to provide an understanding of the major methods for structure determination of proteins. The course will cover X-ray crystallography and Nuclear Magnetic Resonance Spectroscopy in detail, and Electron Paramagnetic Resonance and Electron Microscopy in less detail. Students will be expected to understand the steps required to solve a protien structure, and the physical concepts which underpin these methods.”