2D NMR spectroscopy

- So far we have been dealing with multiple pulses but a single dimension that is, 1D spectra. We have seen, however, that a multiple pulse sequence can give different spectra which depend on the delay times we use.
- The 'basic' 2D spectrum would involve repeating a multiple pulse 1D sequence with a systematic variation of the delay time t_D, and then plotting everything *stacked*. A very simple example would be varying the time before acquisition (*DE*):



• We now have *two time domains*, one that appears during the acquisition as usual, and one that originates from the variable delay.

2D NMR basics

- There is some renaming that we need to do to be more in synch with the literature:
 - The first perturbation of the system (pulse) will now be called the *preparation* of the spin system.
 - The variable t_D is renamed the *evolution time*, t₁.
 - We have a *mixing* event, in which information from one part of the spin system is relayed to other parts.
 - Finally, we have an *acquisition period* (t₂) as with all 1D experiments.
- Schematically, we can draw it like this:



- t₁ is the variable delay time, and t₂ is the normal acquisition time. We can envision having f₁ and f₂, for both frequencies...
- We'll see that this format is basically the same for all 2D experiments (and nD, for that matter...).

A rudimentary 2D experiment

 We'll see how it works with the backbone of what will become the COSY pulse sequence. Think of this pulses, were t₁ is the preparation time:



• We'll analyze it for an off-resonance (ω_o) singlet for a bunch of different t_1 values. Starting after the first $\pi / 2$ pulse:



The rudimentary 2D (continued)



- The second π / 2 pulse acts only on the y axis component of the magnetization of the <xy> plane.
- The **x** axis component is not affected, but its amplitude will depend on the frequency of the line.

$$\left(\mathbf{A}(\mathbf{t}_1) = \mathbf{A}_o * \mathbf{cos}(\boldsymbol{\omega}_o * \mathbf{t}_1)\right)$$

The rudimentary 2D (...)

• If we plot all the spectra in a stacked plot, we get:



- Now, we have frequency data in one axis (f₂, which came from t₂), and time domain data in the other (t₁).
- Since the variation of the amplitude in the t₁ domain is also periodic, we can build a pseudo FID if we look at the points for each of the frequencies or lines in f₂.
- One thing that we are overlooking here is that during all the pulsing and waiting and pulsing, the signal will also be affected by T₁ and T₂ relaxation.

The rudimentary 2D (...)

Now we have FIDs in t₁, so we can do a second Fourier transformation in the t₁ domain (the first one was in the t₂ domain), and obtain a two-dimensional spectrum:



 If we had a real spectrum with a lot of signals it would be a royal mess. We look it from above, and draw it as a *contour plot*. We chop all the peaks with planes at different heights.



• Each slice is color-coded depending on the height of the peak.

The same with some real data



The same with some real data

• Now the *contour-plot* showing all the *cross-peaks*:



- OK, were the heck did all the *off-diagonal* peaks came from, and what do they mean?
- I'll do the best I can to explain it, but again, there will be several black-box events. We really need a mathematical description to explain COSY rigorously.

Homonuclear correlation - COSY

- **COSY** stands for **COrrelation SpectroscopY**, and for this particular case in which we are dealing with homonuclear couplings, *homonuclear correlation spectroscopy*.
- In our development of the 2D idea we considered an isolated spin not coupled to any other spin. Obviously, this is not really useful.
- What COSY is good for is to tell which spin is connected to which other spin. The off-diagonal peaks are this, and they indicate that those two peaks in the diagonal are coupled.
- With this basic idea we'll try to see the effect of the COSY
 90_y t₁ 90_y t₁ pulse sequence on a pair of coupled spins. If we recall the 2 spin-system energy diagram:



 We see that if we are looking at I and apply both π / 2 pulses, (a pseudo π pulse) we will invert some of the population of spin S, and this will have an effect on I (polarization transfer).

Homonuclear correlation (continued)

- Since the I to S or S to I polarization transfers are the same, we'll explain it for I to S and assume we get the same for S to I. We first perturb I and analyze what happens to S.
- After the first π / 2, we have the two I vectors in the x axis, one moving at ω_I + J / 2 and the other at ω_I J / 2. The effect of the second pulse is that it will put the components of the magnetization aligned with y on the -z axis, which means a partial inversion of the I populations.
- For t₁ = 0, we have complete inversion of the I spins (it is a π pulse and the signal intensity of S does not change. For all other times we will have a change on the S intensity that depends periodically on the resonance frequency of I.
- The variation of the population inversion for I depends on the cosine (or sine) of its resonance frequency. Considering that we are on-resonance with one of the lines and if $t_1 = 1 / 4 J$:



Homonuclear correlation (...)

 If we do it really general (nothing on-resonance), we would come to this relationship for the change of the S signal (after the π / 2 pulse) as a function of the I resonance frequency and J_{IS} coupling:

$$\begin{aligned} \mathsf{A}_{\mathsf{S}}(\mathsf{t}_{1}, \mathsf{t}_{2}) &= \mathsf{A}_{\mathsf{o}} * \mathsf{sin}(\ \omega_{\mathsf{I}} * \mathsf{t}_{1}\) * \mathsf{sin}(\mathsf{J}_{\mathsf{IS}} * \mathsf{t}_{1}\) \\ &* \mathsf{sin}(\ \omega_{\mathsf{S}} * \mathsf{t}_{2}\) * \mathsf{sin}(\mathsf{J}_{\mathsf{IS}} * \mathsf{t}_{2}\) \end{aligned}$$

• After Fourier transformation on t_1 and t_2 , and considering also the I spin, we get:



• This is the typical pattern for a doublet in a *phase-sensitive* **COSY**. The sines make the signals dispersive in f_1 and f_2 .

Heteronuclear correlation - HETCOR

- The COSY (or *Jenner experiment*) was one of the first 2D experiments developed (1971), and is one of the most useful 2D sequences for structural elucidation. There are thousands of variants and improvements (*DQF-COSY*, *E-COSY*, etc.).
- In a similar fashion we can perform a 2D experiment in which we analyze heteronuclear connectivity, that is, which ¹H is connected to which ¹³C. This is called *HETCOR*, for *HETeronuclear CORrelation spectroscopy*.
- The pulse sequence in this case involves both ¹³C and ¹H, because we have to somehow label the intensities of the ¹³C with what we do to the populations of ¹H. The basic sequence is as follows:



HETCOR (continued)

 We first analyze what happens to the ¹H proton (that is, we'll see how the ¹H populations are affected), and then see how the ¹³C signal is affected. For different t₁ values we have:



HETCOR (...)

- As was the case for COSY, we see that depending on the t₁ time we use, we have a variation of the population inversion of the proton. We can clearly see that the amount of inversion depends on the J_{CH} coupling.
- Although we did it on-resonance for simplicity, we can easily show that it will also depend on the ¹H frequency (δ).
- From what we know from SPI and INEPT, we can tell that the periodic variation on the ¹H population inversion will have the same periodic effect on the polarization transfer to the ¹³C. In this case, the two-spin energy diagram is for ¹H and ¹³C:



Now, since the intensity of the ¹³C signal that we detect on t₂ is modulated by the frequency of the proton coupled to it, the ¹³C FID will have information on the ¹³C and ¹H frequencies.

HETCOR (...)

• Again, the intensity of the ¹³C lines will depend on the ¹H population inversion, thus on ω_{1H} . If we use a stacked plot for different t_1 times, we get:



• Mathematically, the intensity of one of the ¹³C lines from the multiplet will be an equation that depends on ω_{13C} on t_2 and ω_{1H} on t_1 , as well as J_{CH} on both time domains:

 $A_{13C}(t_1, t_2) \propto trig(\omega_{1H}t_1) * trig(\omega_{13C}t_2) * trig(J_{CH}t_1) * trig(J_{CH}t_2)$

HETCOR (...)

• Again, Fourier transformation on both time domains gives us the 2D correlation spectrum, in this case as a contour plot:



- The main difference in this case is that the 2D spectrum is not symmetrical, because one axis has ¹³C frequencies and the other ¹H frequencies.
- Pretty cool. Now, we still have the J_{CH} coupling splitting all the signals of the 2D spectrum in little squares. The J_{CH} are in the 50 - 250 Hz range, so we can start having overlap of cross-peaks from different CH spin systems.
- We'll see how we can get rid of them without decoupling (if we decouple we won't see ¹H to ¹³C polarization transfer...).

HETCOR with no $J_{\rm CH}$ coupling

• The idea behind it is pretty much the same stuff we did with the refocused INEPT experiment.



- We use a ¹³C π pulse to refocus ¹H magnetization, and two delays to to maximize polarization transfer from ¹H to ¹³C and to get refocusing of ¹³C vectors before decoupling.
- As in INEPT, the effectiveness of the transfer will depend on the delay Δ and the carbon type. We use an average value.
- We'll analyze the case of a methine (CH) carbon...

HETCOR with no J_{CH} coupling (continued)

• For a certain t₁ value, the ¹H magnetization behavior is:



 Now, if we set Δ₁ to 1 / 2J both ¹H vectors will dephase by by exactly 180 degrees in this period. This is when we have maximum population inversion for this particular t₁, and no J_{CH} effects:



HETCOR with no J_{CH} coupling (...)

• Now we look at the ¹³C magnetization. After the proton π / 2 we will have the two ¹³C vectors separated in a 5/3 ratio on the <z> axis. After the second delay Δ_2 (set to 1 / 2J) they will refocus and come together:



 We can now decouple ¹H because the ¹³C magnetization is refocused. The 2D spectrum now has no J_{CH} couplings (but it still has the chemical shift information), and we just see a single cross-peak where formed by the two chemical shifts:



Long range HETCOR

- The Δ_1 and Δ_2 delays are such that we maximize antiphase ¹³C magnetization for ¹J_{CH} couplings. That is, Δ_1 and Δ_2 are in the 2 to 5 ms range (the average ¹J_{CH} is ~ 150 Hz, and the Δ_1 and Δ_2 delays were **1 / 2J**).
- This is fine to see CH correlations between carbons and protons which are directly attached (¹J_{CH}). Lets see what this means for camphor, which we discussed briefly in class:



 An expansion of the HETCOR spectrum for carbons a and b would look like:



Long range HETCOR (continued)

- The problem here is that both carbons **a** and **b** are pretty similar chemically and magnetically: From this data alone we would not be able to determine which one is which.
- It would be nice if we could somehow determine which of the two carbons is the one closer to the proton at C_c, because we would unambiguously assign these carbons in camphor:



- How can we do this? There is, in principle, a very simple experiment that relies on long-range CH couplings.
- Apart from ¹J_{CH} couplings, carbons and protons will show long-range couplings, which can be across two or three bonds (either ²J_{CH} or ³J_{CH}). Their values are a lot smaller than the direct couplings, but are still considerably large, in the order of 5 to 20 Hz.
- Now, how can we twitch the HETCOR pulse sequence to show us nuclei correlated through long-range couplings?

• The key is to understand what the different delays in the pulse sequence do, particularly the Δ_1 and Δ_2 delays. These were used to refocus antiphase ¹³C magnetization. For the ¹H part of the sequence:



• For the ¹³C part:



In order to get refocusing, i.e., to get the '-3' and the '+5' vectors aligned, and in the case of a methine (CH), the Δ₁ and Δ₂ delays have to be 1 / 2 * ¹J_{CH}. So, what would happen if we set the Δ₁ and Δ₂ delays to 1 / 2 * ²J_{CH}?

 To begin with, Δ₁ and Δ₂ will be in the order of 50 ms instead of 5 ms, which is much longer than before. What will happen now is that antiphase ¹³C magnetization due to ¹J_{CH} couplings will not refocus, and will tend to cancel out. For the ¹H part of the refocusing:



 The delay values are now way of the mark for ¹J_{CH}, and we do not have complete inversion of the ¹H populations. Now, for the ¹³C part:



At the time we decouple ¹H, we will almost kill all the ¹³C signal that evolved under the effect of ¹J_{CH}...

• In the end, we'll se that most of the magnetization that evolved under the effect of different ${}^{1}J_{CH}s$ will be wiped out. On the other hand, ${}^{13}C$ antiphase magnetization that originated due to ${}^{2}J_{CH}$ will have the right Δ_{1} and Δ_{2} delays, so it will behave as we saw before. For ${}^{1}H$:



• For ¹³C:



 So in the end, only 13C that have 2JCH couplings will give rise to correlations in our HETCOR and we will be able to achieve what we wanted

• If we take our HETCOR using this values for Δ_1 and Δ_2 , and if we consider everything working in our favor, we get:





- Great. We can now see our long-range ¹H-¹³C coupling, and we can now determine which CH₂ carbon is which in camphor. Note that we did the whole explanation for CHs for simplicity, but the picture is pretty much the same for CH₂s.
- As usual, things never go the way we want. This sequence has several drawbacks. First, selecting the right Δ_1 and Δ_2 to see ${}^2J_{CH}$ over ${}^1J_{CH}$ is kind of a crap-shot.
- Second, we are now talking of pretty long delays Δ_1 and Δ_2 on top of the variable evolution delay (which is usually in the order of 10 to 20 ms). We will have a lot of relaxation, not only of the ¹³C but of the ¹H, during this time, and our signal will be pretty weak.
- Furthermore, since ¹H relaxes considerably, the inversion will vanish away and we don't get strong correlations.

COLOC-HETCOR

- How can we avoid these problems? If we want to keep the idea we have been using, i.e., to refocus ¹³C magentization associated with ${}^{2}J_{CH}$, we need to keep the Δ_{1} and Δ_{2} delays.
- Then the only delay that we could, in principle, make shorter is the variable evolution delay, t₁. How do we do this, if we need this delay to vary from experiment to experiment to get the second dimension?
- The solution is to perform a *constant time* experiment. This involves to have an evolution time t1 that is overall constant, and equal to Δ₁, but have the pulses inside the evolution progress during this time. The best example of such a pulse sequence is called *Correlations via LOng-range Couplings*, or *COLOC*. The pulse sequence is:



COLOC-HETCOR (continued)

- As you see from the pulse sequence, the Δ_1 period remains the same, as so does the total t_1 period. However, we achieve the evolution in t_1 by shifting the two 180 pulses through the t_1 period constantly from one experiment to the other.
- We can analyze how this pulse sequence works in the same way we saw how the regular HETCOR works. We'll see the analysis for a C-C-H. The first ¹H 90 puts ¹H magnetization in the <xy> plane, were it evolves under the effect of J_{CH} (²J_{CH} in the case of C-C-H) for a period t₁ / 2, which is variable.
- The combination of 180 pulses in ¹H and ¹³C inverts the the ¹H magnetization and flips the labels of the ¹H vectors:



COLOC-HETCOR (...)

- Now, after Δ₁ t₁/2, the magnetization continues to dephase. However, since the total time is Δ₁, we will get the complete inversion of ¹H magnetization, we have the maximum polarization transfer from ¹H to ¹³C, and we tag the ¹³C magnetization with the ¹H frequency (which gives us the correlation...).
- Since we always have complete inversion of ¹H magentization and refocusing, we won't have ²J_{CH} spliting in the ¹³C dimension (f₁).
- Finally, over the Δ_2 delay we have refocusing of the ¹³C antiphase magnetization, just as in the refocused HETCOR, and we can decouple protons during acquisition:



 The main advantage of this pulse sequence over HETCOR is that we accomplish the same but in a much shorter time, because the Δ₁ period is included in the t₁ evolution.
 Furthermore, instead of increasing t₁ from experiment to experiment, we change the relative position of the 180 pulses to achieve the polarization transfer and frequency labeling.