

Lab 1
Processing 1D NMR Data Offline
Report Due: Friday, October 12

Introduction

NMR spectroscopy is an extremely common tool for chemists who synthesize molecules. Researchers at the University of Minnesota will often run multiple NMR experiments every day. It is possible to process and print NMR data in the NMR facility, but it is sometimes easier to work up data on your own (or your research group's) computer. The purpose of this lab is to have you download, process and print NMR spectra from a remote computer. To do this, you will learn how to:

1. Save .fid folders from a remote location to your local machine;
2. Use an NMR processing program to work up your data; and
3. Use the resulting spectrum to help identify an unknown.

Software

Groups at the University of Minnesota primarily use one of three software packages to remotely process and print NMR data:

ACD/NMR Processor (PC). ACDLabs has recently made its NMR analysis software free to all academic users, and this software will be described in these instructions. Browse to http://www.acdlabs.com/resources/freeware/nmr_proc/index.php to install the software on your own computer, or you may also use it pre-installed in the Microcomputer Lab (101D Smith). Andy is familiar with this software, so you can ask him questions about it.

iNMR (Mac). Groups that use Macs primarily use iNMR (<http://www.inmr.net/>). This program can also do everything that you need for this course. The full version of the software costs money, but the trial version is free and appears to work the same as the full version except for occasional reminders to upgrade (which don't seem to stop you from using the software anyway). I won't be explaining this program in these instructions, but it works almost identically to all other NMR processing programs. So, try to figure out how to do the same things that I describe here if you choose this program.

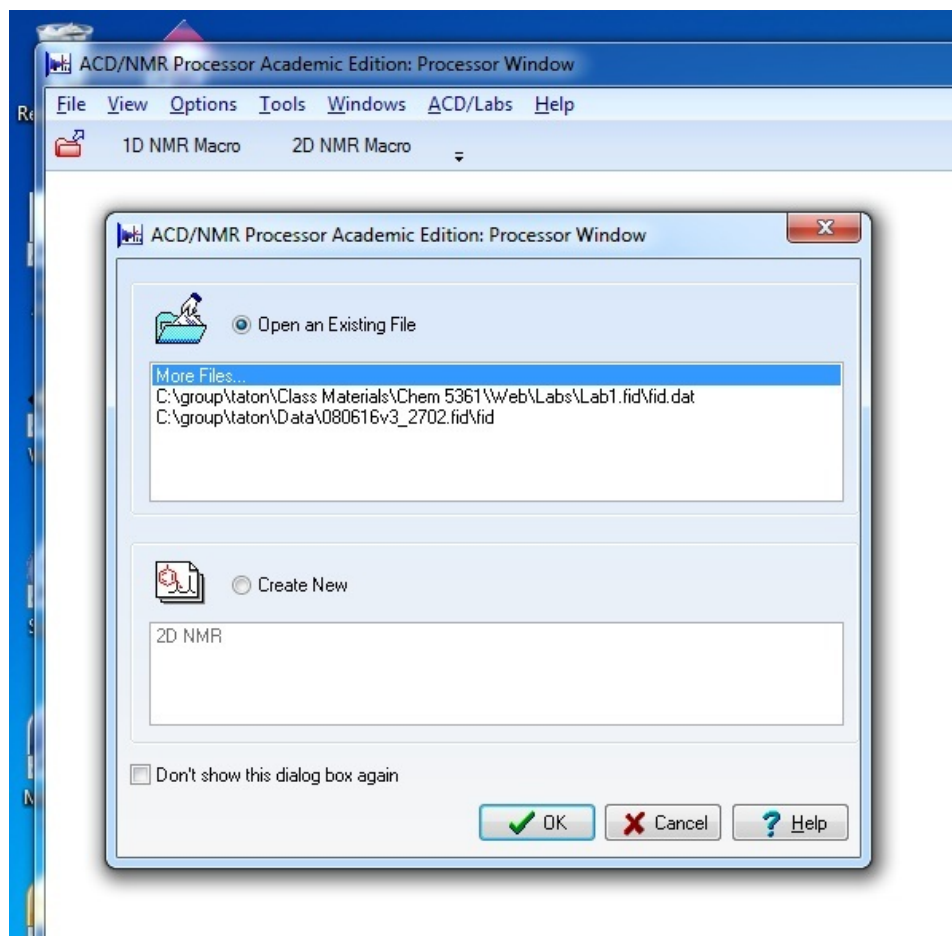
MNova/MNova Lite (PC). The University of Minnesota has unlimited academic licenses to MNova Lite by virtue of its license for CambridgeSoft ChemOffice. MNova Lite can only be used to work up 1D NMR data, and lacks a few features—including resolution enhancement, covered in this lab—that the other two packages have. MNova, the full-version partner of MNova Lite, can be used to analyze 2D spectra as well as do resolution enhancement. The University of Minnesota used to have floating licenses for this software, but it no longer does. You might find labmates who still have MNova installed on their computers, but you won't be able to download it for yourself. In addition, we have documented a few cases in which some

installations of MNova cannot read FID files under certain circumstances (e.g., when they are e-mailed, or transferred between Mac and PC). I recommend *against* using either of the MNova packages for this course, and I can't help you troubleshoot them if you do. Nevertheless, if you want to install MNova Lite on your computer, first install ChemOffice (<http://sitelicense.cambridgesoft.com/sitelicense.cfm?sid=23>), and then follow the MNova Lite instructions at <http://mestrelab.com/cambridgesoft/>.

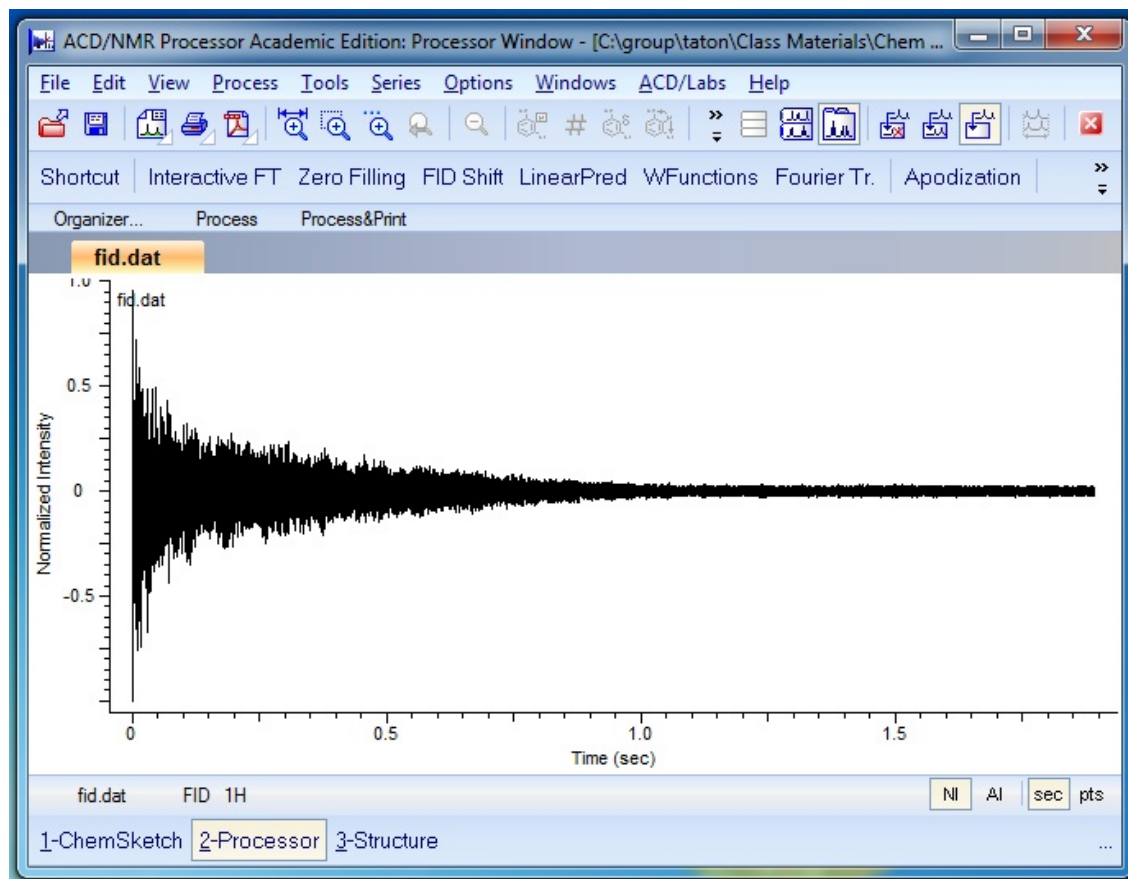
In order to transfer .fid folders from the NMR lab server to your computer, you will also need FTP client software. There are a lot of these out there. PC users can download **WinSCP** (<http://winscp.net/>) or **FileZilla** (<http://filezilla-project.org/>, also available on Microcomputer Lab workstations) for free. Mac users can also download **FileZilla** or **Cyberduck** (<http://cyberduck.ch/>) for free.

You will not need FTP software for this Lab, but you will need it for Labs 2 and 4. You can download the .fid folder you need by browsing to <http://www.chem.umn.edu/groups/taton/chem8361/Labs/Lab1.fid.zip>, saving the file to your local computer, and then unzipping the file by double-clicking it. The folder contains four files; you will be pointing your software to the *fid.dat* file for processing, but you need all four present.

Remote Processing with ACD/NMR Processor



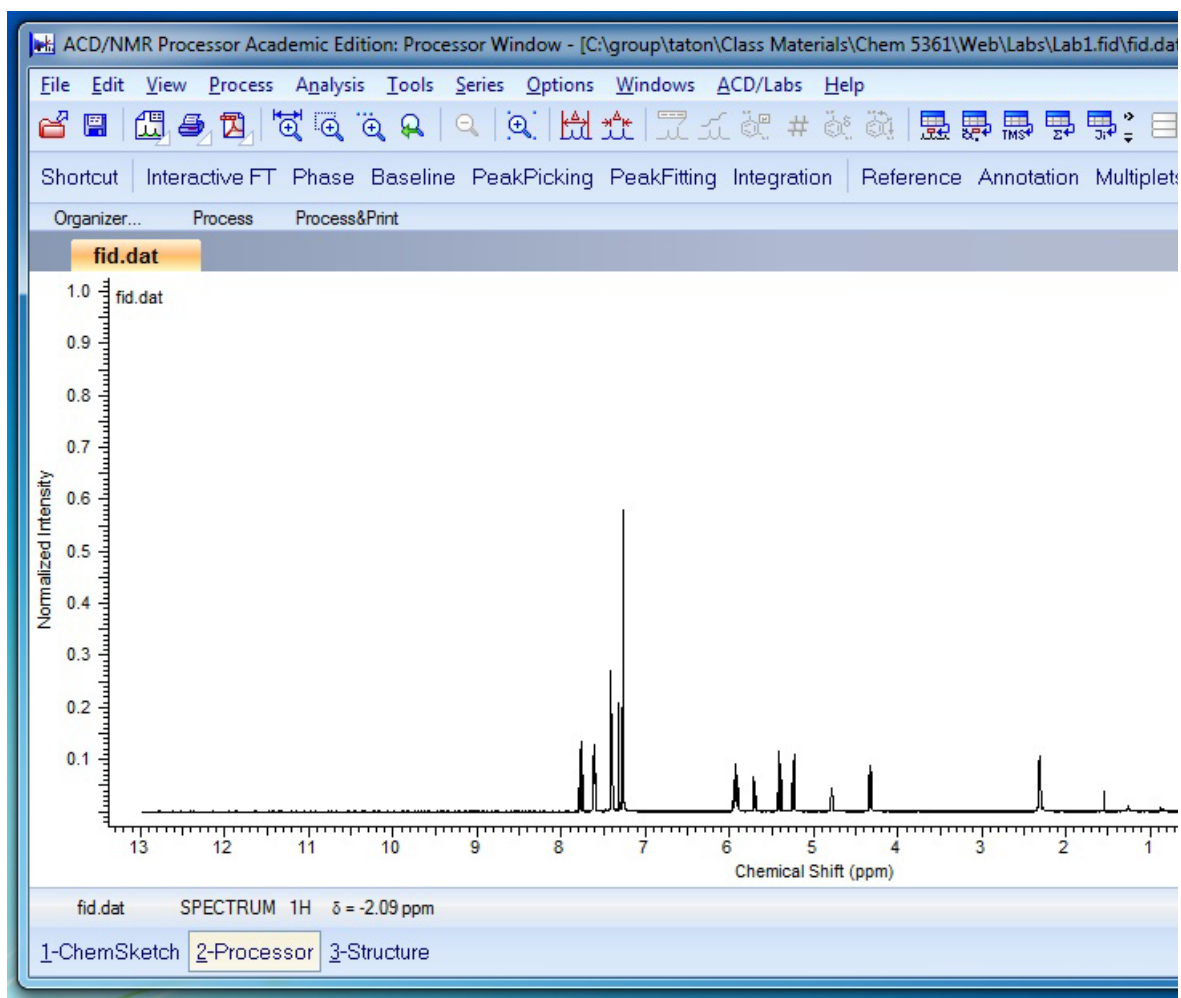
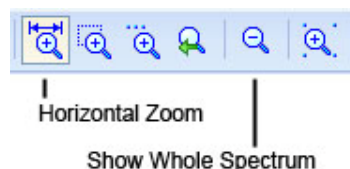
1. Start the 1D NMR Processor program, choose to **Open an Existing File**, click **More Files...**, and browse to find your *fid.dat* file. (Make sure the File Type dropdown box lists “All Files (*.*)” so you can see it.)
2. The program window will show the FID:



From here you have a couple of options. If you pick the “Shortcut” button above the FID, the program will attempt to do all of the spectral analysis for you—pick peaks, find multiplets, calculate coupling constants, etc. Most of the time it will fail, either because peaks from impurities make it over-assign the spectrum, or because it attempts to classify obviously overlapping multiplets as single resonances. I think you will find that you are much more successful at it on your own.

So, instead, I recommend that you analyze your spectrum yourself. Click **Fourier Transform** to convert your FID into a 1D NMR spectrum. The program will do a few things automatically for you; it will automatically apply a phase correction, a baseline correction, and an apodization (window) function to your spectrum. In general, the software does an excellent job of all of these things, and you may never need to change the software’s choices for these. But in case you do:

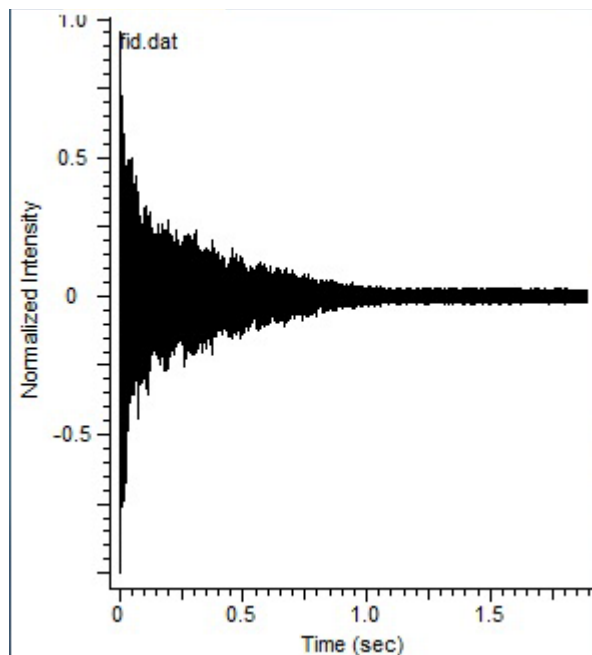
- Use the zoom buttons, and particularly the Horizontal Zoom button, to focus in on an area of the spectrum that shows some structure. Click and drag to zoom in. If you want to zoom back out, click the Show Whole Spectrum button. If you have a wheel mouse, the wheel in the center can be used to control the vertical zoom independently of the horizontal zoom.



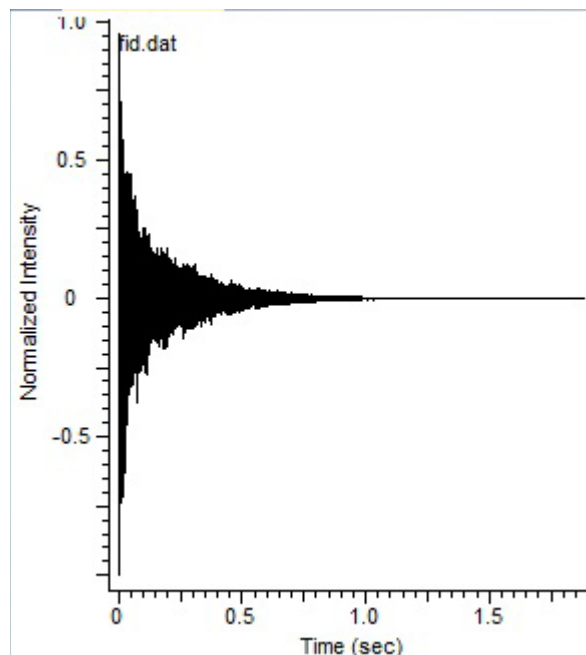
- Click **Phase** to modify the software's auto-phasing. There are two phase corrections applied, a zero-order (Ph0) and first-order (Ph1) one. The easiest way to see how this affects your spectrum is to select the **Mouse Phase** option in the command bar; in a two-button mouse, the left button controls Ph0, and the right button a combination of Ph0 and Ph1. If you don't like what you've done to the spectrum, you can always back out of the phasing menu by clicking the red X, or go all the way back the beginning with **File** → **Reopen**.

- Click **Baseline** to set baseline points; this can occasionally be useful for quantitative integration, but you probably won't ever need it.
- Click **Interactive FT** (or **WFunctions** or **Apodization** when the FID is showing) to perform resolution enhancement. Noise in the early and/or late part of the FID results in broadening of peaks in the Fourier-transformed spectrum, and so sometimes it is useful to multiply the FID by a “window” function to fix this problem.

before apodization

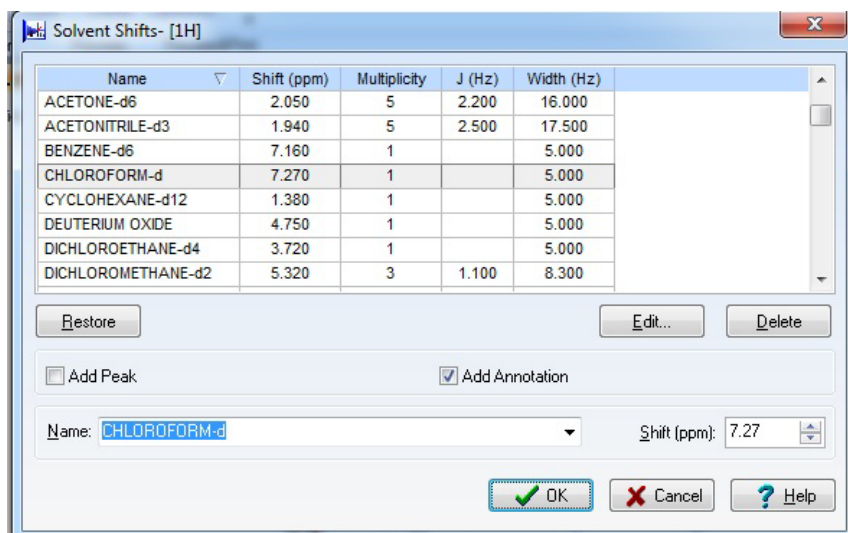


after apodization



In the Interactive FT window, you can perform “resolution enhancement” by switching the Window Function entries from Default to User, and then adjusting the given values for EM (exponential function) or GM (Gaussian function).

3. Back in the main spectrum window, click on **Reference** to make sure the chemical shift scale is correctly referenced to CHCl_3 ($\delta = 7.26$ ppm) and tetramethylsilane (TMS, $\delta = 0.00$ ppm). Because the NMR instrument's deuterium lock generally prevents the frequency from drifting, most spectra will already be extremely close to referenced. But just to make sure, move your cursor over the peak that you think to be CHCl_3 or TMS, left-click, and pick the appropriate reference frequency from the list. (See next page.)



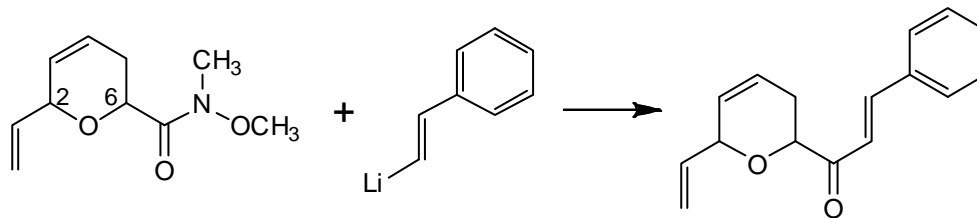
- Next, we'll work on making the spectrum presentable. In order to put chemical shift labels on the peaks, click **PeakPicking**. If you then click **Auto** to have the computer pick peaks for you, it only does an okay job. To do a better job, zoom in on each area you want to pick peaks in, click **Peak Level**, and click your cursor at the height above which you want all peaks labeled. Or, choose **Peak by Peak** and click on peaks individually. If you don't like what you've chosen, click the **Clear** button. If you do, click the green check mark to go back to the main spectrum window.

Your ^1H peak labels should show chemical shift to the fourth decimal place. If they don't, choose **Options** → **Preferences** → **Peaks** and change the **Numerical Display** option.

- Click **Integration** to set up integration ranges. If you pick Auto, the computer will not integrate intelligently—it will split up or join multiplets, and make the ranges too broad or narrow. Instead, choose Manual, and then click and drag regions of the spectrum you want integrated. If you click and drag a region that you want to serve as a reference—say a peak you know to correspond to a methyl $-\text{CH}_3$ —then right after you set that integral, type an integral (3 in this case) in the **Reference** box.
- Most of the time, steps 1-5 will be all you need to process your spectrum. At this point, you might **File** → **Print** in order to have a hard copy, or you might **Edit** → **Copy to Clipboard** so you can paste the spectrum into another document. (You'll be doing more than this with this lab, but I'll explain later.)

Assigning Your Spectrum

In this lab, you'll be analyzing a ^1H NMR spectrum collected by Matt Jansma (Hoye group). Matt was evaluating the addition of a vinyl lithium to a Weinreb amide:

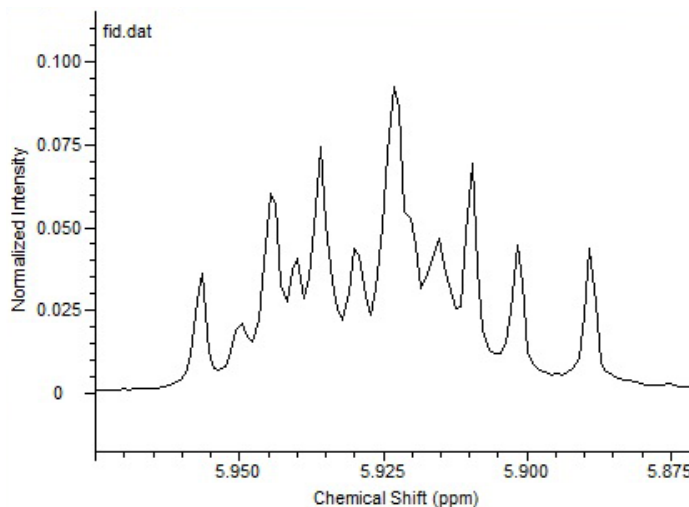


Matt had a couple of initial concerns about this reaction:

- Both the starting material and the product have two chiral centers (C2 and C6 of the dihydropyran ring), with hydrogens that might be acidic enough to exchange under the reaction conditions. Matt knew his starting material was diastereomerically pure, but he did not know the specific stereochemistry at either C2 or C6. As a result, he didn't know what to expect from the product at these positions—potentially a mixture of products, or potentially one pure product with identifiable stereochemistry.
- The *E*-vinyl lithium might not give exclusively an *E*-alkene as the product—it could potentially give a mixture of *E*- and *Z*-alkenes.

Matt ran the reaction and obtained primarily one product, which he purified by chromatography. The FID you downloaded was taken from this purified product. You will attempt to resolve Matt's questions by assigning the spectrum either to the product shown on the previous page, or to a different molecule.

One multiplet that will be challenging to assign will be the peak at $\delta = 5.90$ ppm. To start with, there are a couple of peaks in this multiplet that must belong to impurities or overlapping resonances—the multiplet isn't symmetric, even though it should be. Then, how do you decipher coupling constants from all of this? One tool that might help you is under **Analysis** → **Multiplets** → **J-Coupler**. With this tool you can guess coupling constants, and the program will show you what the multiplet would look like with the splitting pattern you give.



Report Instructions

Each student should turn in their own report.

1. Turn in a printout of the ^1H spectrum, with close-ups of regions that are too difficult to see from the whole-spectrum printout on separate pages. The spectrum should be referenced to

CHCl_3 , should have peaks picked, and should have integration regions normalized to one of the resonances that you think would correspond to one proton.

2. Did Matt make his proposed product, or did he make something else? Turn in a table assigning each of the ^1H resonances to nuclei in your proposed structure. If they are distinguishable, give separate assignments for different protons attached to the same carbon atom, and identify which proton is which. Also assign multiplicity to each resonance, and list coupling constants where you can evaluate them. Assign relative stereochemistry to the C2 and C6 protons, if you can.