Organic Chemistry II
Supplementary Laboratory Handouts

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Laboratory Schedule

For a color-coded standard calendar view of the schedule, see:
http://homepages.gac.edu/~bobrien/OrganicII_Lab/Fall.2004.calendar.150.final.pdf

Week	Lab Dates	Experiment	Report Due
9/13	9/13-9/16 (M,T,W,R)	Isolation of Essential Oils from Cumin Seeds or Caraway Seeds	
9/20	9/20-9/23 (M,T,W,R)	Spectroscopy of Terpenes and Essential Oils: IR, ^{1}H, ^{13}C and DEPT NMR Experiments	
9/27	9/27-9/30 (M,T,W,R)	Preparation of 1-Bromobutane	9/27-9/30 Terpenes
10/4	----------	Nobel Conference Week: "The Science of Aging," Oct. 5 and 6 Lab Does Not Meet	
10/11	10/11-10/14 (M,T,W,R)	Grignard Synthesis of an Alcohol	
10/18	10/18-10/21 (M,T,W,R)	Isolation and Purification of the Alcohol	
10/25	10/27-10/28 (W,R)	Catalytic Transfer Hydrogenation of Cinnamate Derivatives	10/27-10/28 Grignard
11/1	11/1-11/2 (M,T)	Catalytic Transfer Hydrogenation of Cinnamate Derivatives	11/1-11/2 Grignard
11/1	11/3-11/4 (W,T)	Characterization of Hydrogenation Products	
11/8	11/8-11/9 (M,T)	Characterization of Hydrogenation Products	
11/8	11/10-11/11 (W,R)	Oral Presentations – Hydrogenation Products	
11/15	11/15-11/16 (M,T)	Oral Presentations – Hydrogenation Products	
11/15	11/17-11/18 (W,R)	Preparation of Iododurene	11/17-11/18 Hydrogenation
11/22	----------	Thanksgiving Week Lab Does Not Meet	
11/29	11/29-11/30 (M,T)	Preparation of Iododurene	12/1-12/2 Hydrogenation
11/29	12/1-12/2 (W,R)	Isolation of Caffeine from Tea Leaves	12/1-12/2 Iododurene
12/6	12/6-12/7 (M,T)	Isolation of Caffeine from Tea Leaves	12/6-12/7 Iododurene
12/6	12/8-12/9 (W,T)	Check Out	12/8-12/9 Caffeine
12/13	12/13-12/14 (M,T)	Check Out	12/13-12/14 Caffeine

Laboratory Notebooks

Disclaimer: This document is meant to supplement the information in your lab text: *Experimental Organic Chemistry* by Mohrig, Hammond, Morrill and Neckers. Please consult your lab manual *in addition to* this document before preparing your laboratory notebook.

Since chemistry is primarily an experimental science, *your* observations are of crucial importance during the course of an experiment. Things that seem insignificant at the time may be very important in understanding your results later, especially when things don't turn out exactly as expected. Accordingly, you should keep a careful record in a laboratory notebook of what you do and what occurs in lab during an experiment.

Your laboratory notebook is the definitive record of your ideas and thoughts while working in the laboratory. Note all of your observations carefully in your notebook *in ink* and at the time you make the observation (not two hours later). Your notebook should be organized and written in such a manner that someone else could understand and repeat your experiments, if necessary. It is better to include too much information than too little. Your notebook should be organized and legible, but it need not be a work of art. As long as someone else could follow what you have done it's good enough.

A proper record of your experimental results must answer certain questions. When did you do the work? What are you trying to accomplish? How did you do the experiment (are you following a procedure from your lab manual)? What did you observe and what was the result? How do you explain the observations and results? *Your notebook must be accurate and complete.* It is interesting to note that scientific notebooks are considered to be legal documents and are admissible as evidence in courts of law.

At times, you will be working with other people for the laboratory experiments. Although you are working together, you each still must record all ideas and results into your notebook. The exception would be if you clearly did two separate projects, and then discussed your results with one another in order to draw conclusions. It is important to acknowledge the contributions of others to your work. Therefore, always include your partner's name, when appropriate. Also, if you receive help with certain problems that stump you, acknowledge the person or literature resource that you consulted to assist you with your analysis. There is nothing wrong with obtaining help! This is how we all learn, but you should properly acknowledge the help you receive.

This notebook outline should be followed as closely as possible for each experiment. However, depending on the particular experiment, some of the suggested items will not be included. Sometimes for a multiple-week experiment it will be appropriate to prepare only one "prelab" for all the weeks and other times a separate prelab for each week will be useful. In any case, only one conclusion section is appropriate for a multiple-week experiment. Use your best judgement in following this format.

Reserve two or three pages at the beginning of your notebook for a **table of contents**. **Number** every page in your notebook before starting the first laboratory, and **date** all notebook pages as you add data to your notebook. Always use a pen when writing in your lab notebook. All observations should be recorded

directly into your notebook. NEVER EVER write information down on scratch paper with the intent to copy it neatly into your notebook at a later time.

1. Experiment **title and a statement of purpose** (brief).
2. A *brief* **description** of the method used, **or a balanced equation** representing the reaction to be performed. This should not be a regurgitation of the lab manual.
3. A **table** of physical properties of reagents, and molecular masses, quantities, and moles of reagents used under the equation for the reaction. You may need to use a resource other than your laboratory manual to locate information such as boiling point or density. See Mohrig, et. al., pp 5-9 and this document for a list of useful literature resources.
4. Method of yield calculation and the **theoretical yield** (for synthesis labs).
5. **Procedure** and pre-lab questions.
6. A **running account** of what was done in the lab. Anticipate the data you will collect and, when appropriate, set up in advance a suitable tabular format that makes it easy to record the data and to evaluate it later. The running account should be written in ink while the work is being done. Especially important are:

a. All measurements that you make (i.e. masses and volumes). When measuring by difference, both initial and final measurements must be included.

b. Instruments and settings used to acquire data.

c. Appropriate units of measurement for all numbers, whether quantities or data. Numbers also should be represented with the correct number of significant figures.

d. Thin layer chromatography plates should be drawn to the exact size in the notebook, including origin, spots and solvent front. In addition, solid support, eluent composition, visualization method and R_f calculations should be included.

e. Observations you make of colors, physical states and behavior of a reaction, especially changes in any of these properties.

7. **Evaluation** of data, including calculations, estimated uncertainty, interpretations drawn from data, and a neat concise presentation of your calculated results (when appropriate). **Explanation** of observations you made in your running account. An account of the **mechanism** of the reaction performed, where appropriate. **Discussion** of possible sources of error.

Laboratory Reports

In addition to the lab notebook you will prepare a separate report, which is due at the beginning of the lab period one week after the experiment was completed (see schedule for dates). This will be turned in to your teaching assistants. Reports turned in up to one week late will be penalized by up to one grade level. After one week, reports will not be accepted for credit.

The reports need not be typewritten, but they should be written legibly in blue or black ink on paper with clean-cut edges and the pages should be stapled together. They should be succinct, yet written using complete sentences. (Items 1 through 4 below should consist of about one typewritten page or about two handwritten pages.) A complete report includes:

1. **The title of the experiment and a brief statement of purpose** (three sentences, maximum).
2. **Experimental:** A brief description of the experiment performed; for a synthetic procedure, write the equation representing the chemical transformations you accomplished. List masses and volumes of starting materials and products, melting points or boiling points of products, and any *important* observations you made during the laboratory period. Try to put much of the numerical information in a table. In this section, touch on the highlights of the experiment and ignore the mundane. Keep it about one paragraph in length.
3. **Results and Discussion:** Calculate the percent yield, analyze spectral data, and write a mechanism for the reaction you performed, when relevant. Discuss any unusual occurance(s) and provide an explanation of it (them). This section should be one to two paragraphs.
4. **Conclusions:** A brief statement of what was accomplished and a statement of what might be important or interesting to do if the experiment were to be continued. For example, is there a result that needs to be verified or can you propose an additional experiment that would address questions raised by your work? This should be about one paragraph.
5. **Supplementary Information:** Attach answers to any assigned questions at the end of your report. Attach and label the IR and/or NMR spectra of your compounds, or xerox copies of them.

Your grade on these reports will reflect the completeness of the report and the quality and thoroughness of your data evaluation.

Standard Laboratory Reference Sources

A number of useful references for the organic lab, as well as references for other classes and specific chemical, physical, and biological topics, are kept in the room outside Gretchen's office, Room 303. The reference books should never be removed from the room. PLEASE do not write in the reference books. With the exception of the Aldrich Catalog, of which there are several copies, books should not be used in the laboratory. If they are taken there, it is nearly inevitable that they will become disfigured from spills, splatters, etc.

References in the Organic Lab (Room 303)

CRC Handbooks; various editions and formats.
These contain physical data such as melting and boiling points, solubilities, and densities, in addition to a large amount of other types of physical and chemical information.

The Merck Index is an excellent reference; the data for compounds that are included is exceptionally thorough, and includes uses, toxicity data, references to synthesis, historical nomenclature, and other items, in addition to data such as solubility, density, etc

Aldrich Chemical Company Catalog; various editions. There are several of these to be found in the organic lab, the chemistry library, and the chemistry office. They are useful sources for data such as molecular masses, melting points, and densities.

Spectrometric Identification of Organic Compounds, Robert M. Silverstein, G. Clayton Bassler, and Terence C. Morill, Wiley, 1974. This is a good reference for various spectroscopic techniques. It is especially relevant to our class for its sections on IR and NMR spectroscopy. A more up-to-date edition is available from Dr. O'Brien.

References in the Bernadotte Library

The Aldrich library of ^{13}C and ^{1}H FT NMR spectra, edited by Charles J. Pouchert & Jacqlynn Behnke. LOCATION: Bernadotte Library REFERENCE QC462.85 .A44 1993. This is a library of NMR spectra of every compound that the Aldrich Chemical Company sells. When you are faced with analyzing an NMR spectrum of an unknown compound, this is an invaluable reference.

Web Sites
http://www.indiana.edu/~cheminfo/ is a wonderful site for all kinds of chemical information.

http://www.chemfinder.camsoft.com is a good site for looking up physical properties of compounds. You must register (they will then also send you junk e-mail).

http://webbook.nist.gov/chemistry/ contains MS and IR data that may be searched by formula, name, CAS #, and several other options

http://www.aist.go.jp/RIODB/SDBS/menu-e.html has an extensive database of NMR (H-1 and C-13) and mass spectra (NIMC =National Institute of Materials and Chemical Research in Japan)

Isolation and Characterization of Essential Oils;
Spectroscopic Analysis of Terpenes

The first two laboratory sessions will concern the isolation and characterization of the terpenes present in the essential oils of cumin and caraway seeds. The first week will be spent isolating either cumin seed oil or caraway seed oil, and the second week will entail spectroscopic analysis of the oils, pure terpenes present in these oils, and other terpenes.

Week 1—Isolation of the Essential Oils of Cumin and Caraway Seeds

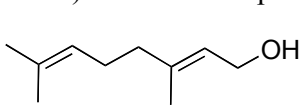
Pre-lab

Reading: Read pp 54-60 in Mohrig, et al. and review the techniques of steam distillation (pp 796-798) and extraction (pp 724-731).

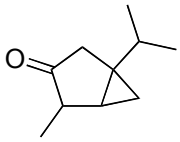
Notebook: Make sure that your notebook has an up-to-date table of contents and numbered pages. Write an experiment title and brief purpose, followed by descriptions of the general procedure to be used. Draw the structures of the major component of caraway seed oil, (S)-(+)-carvone, and the major component of cumin seed, cuminaldehyde (4-isopropylbenzaldehyde), in your notebook, along with their physical properties (boiling point, density, optical rotation). Also include the physical properties of water and dichloromethane. As the experiment progresses, record pertinent observations in you notebook.

Questions: Answer the following questions on a separate sheet of paper and turn them into your TA upon entering the laboratory.

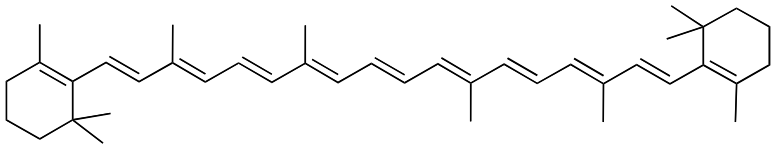
1.) Show the isoprene units in each of the structures listed below.



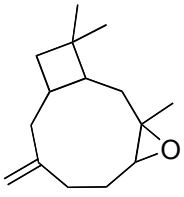
geraniol



thujone



β-carotene



caryophyllene oxide

2.) Why is the distillation temperature of the system constant?

3.) Will dichloromethane constitute the top or the bottom layer in your separatory funnel?

4.) How will you know when you have evaporated all of the dichloromethane away from your essential oil?

Experimental Instructions

You will be assigned either cumin seed or caraway seed to extract. Once you know which substance you are working with, follow the procedure in Mohrig, et. al., described on pp 59-60, **with the following exceptions**: *You will not be making a semicarbazone derivative of carvone. You will not use gas chromatography or polarimetry to analyze your products, but rather IR and NMR spectroscopy (described below).* Save your product in your drawer, **tightly stoppered,** for the second week.

Week 2—Spectroscopy of Terpenes

Although the essential oils that you isolate will contain one major component, either carvone or cuminaldehyde, there will also be other terpenes present in your product. The purpose of the second week's experiment is to evaluate the purity and identify the components of the essential oils of cumin and caraway seeds using IR, ^{1}H NMR, and ^{13}C NMR spectroscopy. In this process, you will assign spectral absorbances to particular structural features of the terpenes under consideration, and you will learn how to use and interpret spectra from a DEPT (Distortionless Enhancement by Polarization Transfer) NMR experiment.

Before reading the rest of this laboratory experiment, review Chapter 13 of Brown and Foote, closely reading sections 13.13 and 13.14.

You are already familiar with interpreting IR and ^{1}H NMR spectra in order to identify the structure of unknown compounds. Sometimes ^{1}H NMR spectra are too complicated to accurately identify and assign all of the signals—this is particularly true for many natural products and polymers. In this case, investigation of the proton-decoupled ^{13}C NMR (^{13}C{^{1}H}) NMR spectrum can yield greater insight into the actual compounds structure and purity.

The ^{13}C NMR spectra are simpler than the proton spectra because the complex splitting due to neighboring proton nuclear spins is removed by decoupling. In addition, the coupling between neighboring ^{13}C nuclei is not observed because of the very small chance that two ^{13}C atoms will be neighbors in any given molecule. (Remember, the natural abundance for the ^{13}C isotope is only 1.1%.) In general, one single resonance is observed for each chemically distinct carbon in the molecule. The trend in relative chemical shifts of carbons, measured in ppm relative to TMS (tetramethylsilane), closely matches that observed from proton NMR. For example, aliphatic carbons resonate farthest upfield, carbons attached to polar functional groups resonate farther downfield, aromatic carbons resonate even farther downfield and carbonyl carbons resonate the farthest downfield from TMS.

Because the proton decoupling can affect the intensity of the ^{13}C signals, we do not normally integrate carbon spectra. Some useful information can be gleaned from relative intensities, however. When comparing resonances due to similar carbons (for example, if you compare resonances due to aliphatic CH_3 groups with one another, it is reasonable to interpret two signals that are in a 2:1 ratio as representing a 2:1 ratio of carbon atoms in the molecule. It is not possible to compare intensities of two different types of carbon atoms (for example, don't compare CH_2 carbon intensities with CH carbon intensities). Also, quaternary carbon atoms (sp^3 carbons bearing no hydrogens) and other carbons with no hydrogens, such as those contained in a benzene ring and bearing a substituent, can often be identified because they generally produce the least intense signals in the ^{13}C{^{1}H} NMR spectrum.

How do you know which signals are due to primary (CH_3), secondary (CH_2), tertiary (CH) or quaternary carbons? The DEPT (distortionless enhancement by polarization transfer) experiment is a useful NMR experiment that provides information on the number of protons

attached to the various ^{13}C resonances in a carbon NMR spectrum. In a DEPT experiment, the spins of both ^{1}H and ^{13}C nuclei are manipulated, through a sequence of carefully timed delays and RF pulses, so as to cause enhancement of the intensities of the ^{13}C signals. In addition, the experiment is designed to manipulate the phase of each ^{13}C signal so as to allow differentiation of the signals according to the number of attached hydrogen atoms. The behavior of the ^{13}C spectrum in three differently configured DEPT experiments is outlined below.

DEPT 45

This experiment provides a ^{13}C spectrum that is missing signals from carbon atoms that have no attached hydrogen atoms (directly bonded hydrogen atoms are necessary for the polarization transfer to occur). The phases of all of the ^{13}C signals in the DEPT 45 experiment are positive, giving rise to normal (+) peaks in the frequency spectrum. The DEPT 45 spectrum thus allows one to identify, through comparison with the normal ^{13}C NMR spectrum, quaternary carbon atoms, alkene, and aromatic carbon atoms which do not have attached hydrogen, and non-aldehydic carbonyl groups. Chemical shift information is, of course, used in conjunction with the DEPT data.

DEPT 90

This experiment provides a ^{13}C spectrum that contains only the signals from carbon atoms that are bonded to a single hydrogen atom (methine, aromatic, and olefinic C-H, aldehyde). The signals have the normal (+) phase, and thus give rise to normal peaks in the frequency spectrum. Signals from CH_2 and CH_3 groups do not appear (the signals are nulled). It should be noted that careful adjustment of both ^{13}C and ^{1}H pulse lengths is necessary for exact nulling of the methylene and methyl signals. If either of these parameters is improperly set, small residual signals from the CH_2 and CH_3 carbon atoms will appear in the spectra.

DEPT 135

This experiment provides a ^{13}C spectrum that contains signals, as does the DEPT 45 spectrum, from all carbon atoms that are bonded to any number of hydrogen atoms. In the DEPT 135 experiment, however, the phases of the signals from CH_2 carbons are inverted, and thus give rise to negative peaks in the frequency spectrum.

When you view the DEPT experiment data, three separate data sets, one each for 45, 90, and 135, will be plotted. By evaluating the resonances in each data set, whether they are positive, negative, or null, you can identify the number of protons attached to each carbon. This information will then provide evidence for the most likely structure(s) that can be assigned to the compound in question.

Pre-lab

Notebook: Include a title and statement of purpose, and a brief description of the procedure (a list of steps you will perform is sufficient). It might be useful to reference an explanation of the spectroscopic techniques you will employ.

Procedure

There are five major tasks to accomplish during this laboratory:

1. Analyze the DEPT NMR spectra of five terpenes (page 11-structures and pages 17-26-spectra) so that you can assign the spectra to particular terpene structures.

2. Combine your essential oil with that of two other lab students who isolated the same material, and prepare a sample for obtaining a ^{13}C NMR spectrum in $CDCl_3$.

3. Obtain a ^{13}C NMR spectrum of your product on the Varian 300 MHz NMR instrument in NHS 306A, along with your two partners, and make five copies to share with your benchmates.

4. Obtain an IR spectrum of your product on the IR instrument in NHS 306A

5. Download the ^{1}H NMR spectra of carvone and cuminaldehyde using the PC-based program, MestRe-C.

At the end of the laboratory period, you should have the following information:

1. IR and ^{13}C NMR spectra of cumin seed oil and caraway seed oil.

2. IR and ^{1}H NMR spectra of carvone and cuminaldehyde.

3. DEPT and ^{13}C NMR spectra of the five terpenes drawn below (including carvone and cuminaldehyde).

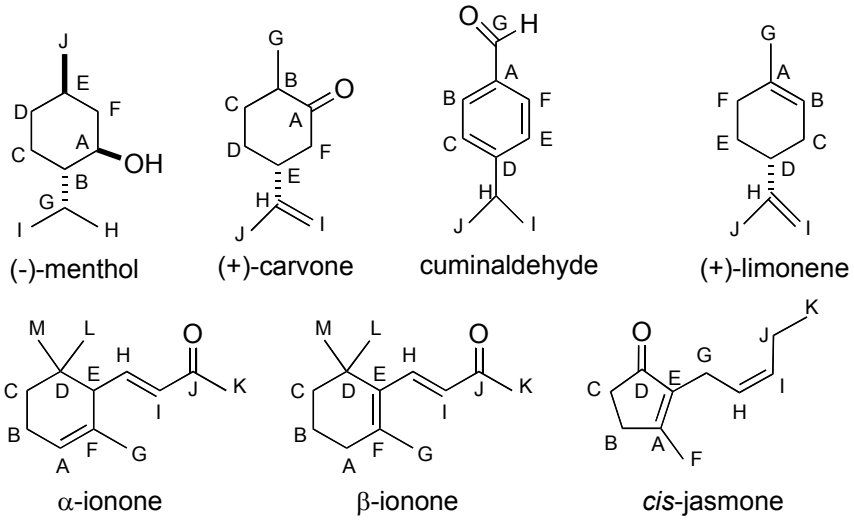
Detailed Instructions:

Review the procedures found in Appendix I (IR instructions) and Appendix II (MestRe-C instructions).

DEPT Spectra

The following five terpene structures all have the same number of carbon atoms. If you inspect the structures carefully, you will notice that they have different numbers of primary, secondary, tertiary and quaternary carbons, however. Therefore, the DEPT spectra should enable you to distinguish these compounds from one another. Copies of DEPT and ^{13}C NMR spectra labeled "Terpenes A-E" are provided at the end of this laboratory experiment (pages 18-27) Begin analyzing the number of each type of carbon present in each spectrum, according to the explanation of each DEPT experiment described above. After matching the terpene structure with its respective ^{13}C NMR spectrum, label the ^{13}C resonances according to the letters used to label the individual carbon atoms in the structure.

Terpene Structures:



^{13}C NMR Spectrum

1. Prepare a ^{13}C NMR Sample

You will be running three samples: the oil which you isolated by steam distillation, pure carvone, and pure cuminaldehyde. DEPT spectra will be obtained for the latter two. All samples will be dissolved in deuterochloroform ($CDCl_3$). This solvent will serve both as the source for the deuterium lock signal and as an internal reference (δ ^{13}C = 77.0 ppm). Your instructors will show you how to measure appropriate volumes of both solvent and solute. The volume of solvent is critical--too much solvent not only dilutes the ^{13}C spins, but also greatly increases the difficulty of shimming the sample. It is imperative that the sample be dry and free of solid impurities. Should either water or insoluble material be present, it must be removed before running the spectrum. Techniques for both drying and filtering of the samples can be demonstrated by your instructors if necessary.

2. Use the Varian NMR Spectrometer to Obtain a ^{13}C NMR Spectrum

- Be careful to wait for the instrument to respond to the command you have given before giving the next command. Sometimes the computer can be slow and try your patience. If you aren't patient, the computer may hang up or crash.
- Throughout this document, commands that you type in are denoted in **`bold courier font`** and the symbol ↵ indicates a return.
- The left mouse button is the normal operator, except in a few cases such as increasing lock or shim values, changing from axial z to z0, and manipulating the spectrum. During some operations you will see three yellow boxes lined up at the bottom of spectrum window. The codes in these three boxes indicate the functions of the left, middle, and right mouse buttons.
- In the VNMR program, to move a window to the 'front' simply place the cursor on one of the edges of the window (the arrow cursor becomes an open circle on the very edge of a window) and click the left mouse button.

• Most of the commands you need for routine operation can be performed by clicking on a series of 'buttons' in the menu bar above the spectrum window. However, all of these commands can also be entered directly by typing the command code into the cursor window above the menu bar. Sometimes, a particular operation can only be performed by typing in the command. If you are looking to do something different, check the 'Command and Parameter Reference' book located by the instrument—chances are, you will find the command you are looking for. Also, it is possible to string commands together on one line, separated by spaces. Type return at the end of the line to execute your commands.

• Click on main menu to get back to the highest level of "buttons" on the menu bar.

1. Login to the computer and find your lab section subdirectory within the 2003 and terpene subdirectories.

When you approach the NMR computer, the screen may be blank. If so, you can turn on the screen by pressing the return key or moving the mouse.

A. LOGIN as **`ochemII`** and enter the password (fall2003) at the prompt. This will automatically open Solaris, and dump you into the VNMR operating system. What you will see is a series of windows open. The upper left-hand window will have two rows of "buttons" (the menu bar) along the bottom.

B. When you login to the computer, you will end up in a directory with the following pathname: **`/home/woodward/ochemII`**, which indicates that **`ochemII`** is a subdirectory of **`woodward`**, which is a subdirectory of `home`. All of the user accounts are found in the /home directory. You can move up and down in the directory system in the VNMR program by clicking on the File "button". To move down a directory click on the directory of interest and click on the Set Directory and then Change buttons. To move up a directory click on the Parent button. The UNIX command **`pwd`** is useful to determine where you are (just type it in followed by return). Change into the terpene subdirectory, and then the subdirectory appropriate for your lab section (monday, tuesday, wednesday, thursday) and check your pathname by typing **`pwd`** . Your pathname should now read **`/home/woodward/ochemII/2003/terpene/monday`** (for someone in the Monday section).

   As a member of the nmrgroup (a UNIX distinction) all nmr user accounts have permission to access and read anyone else's files; however, you cannot alter other user's files (of course, this isn't true of the files of other members of your user account, so be careful). You can call up other user's files, save them in your directory and alter them as you like, but you cannot alter the original file. To look at other user's files, simply move through the directories as discussed above.

2. Lock and shim your sample.

The sample must be inserted into the magnet probe, the deuterium lock signal located and optimized, and the local field around your sample adjusted to make it as homogeneous as possible (the latter process is called 'shimming', within the

context of NMR jargon). Your instructors will show you how to do this after insertion of your sample.

3. Set-up the experiment and obtain spectral data.

Note: Main Menu is the highest level among the menu boxes.

The NMR spectrometer must be set to the proper frequency for ^{13}C and appropriate parameters for ^{13}C signal acquisition must be entered. The parameters are contained in a table within the computer, and are loaded by clicking on the 'setup' button, followed by clicking on the appropriate combination of nucleus and solvent $^{13}C/CDCl_3$ for our measurements).

A. SETUP THE EXPERIMENT that you want to do with the left mouse button, by clicking on setup and choosing appropriate buttons in the command bar above the spectrum window ($^{13}C/ CDCl_3$ for our measurements). Type **nt=128**↵ to set the number of scans to 128.

B. TYPE **su**↵. This sets up the experiment, by adjusting the hardware for observing the particular nucleus you have chosen. To display the chosen parameters below the spectrum window, type **dg**↵.

C. TO BEGIN ACQUISITION, type **ga**↵, or use ACQUIRE menu and click on the appropriate box (e.g. GO, with FT).

D. To monitor the status of the experiment you can look at the acquisition status window. To check your spectrum after 16 scans, type **wft**↵ after 16 scans have been obtained. A spectrum should appear.

E. AFTER ACQUISITION IS COMPLETE, use the full box to see the full spectrum and PHASE it by typing **aph**↵.

4. Transform, phase, integrate, save and print the ^{13}C spectrum, and then obtain a peak print-out of the ppm values of the resonances.

A. You should now have the raw data, which will need to be transformed. If you would like to view the raw data, type **df**↵. The decaying sine wave (free induction decay, or FID) will show up, which is the so-called 'time domain' for your data. To view the data in the 'frequency domain', type **wft**↵ for 'weight fourier transform' and you will see something that looks more like a spectrum, although it may be out of phase. This will also dump you into a subroutine, which I call the 'display interactive mode'. If at any time you are unable to manipulate spectra according to the following directions, click on MAIN MENU, followed by the DISPLAY and then the INTERACTIVE buttons. (cr (cursor), vs (vertical scale) and delta (distance between cursors) at the bottom of the spectrum refer to the three mouse buttons.).

B. Click on the FULL box to see the full spectrum and phase it by typing **aph**↵.

C. Use the right and left mouse buttons to put the cursors around the triplet of peaks corresponding to $CDCl_3$. Click on the button EXPAND on the button bar. This should enable you to clearly see all three peaks. Place the cursor, using the left mouse button, on the center peak and set the position of the *reference* by typing **rl(77.00p)**↵.

D. DISPLAY the spectrum as you would like to plot it. Go back to the full spectrum by clicking on the full button and then place the cursors on either side of the region of the spectrum that you would like to plot. You can display the scale by typing **dscale**↵ or use the NEXT box to display the DSCALE box and click. You can switch from pip to Hertz by typing **axis='h'**↵ or **axis='p'** ↵. Check the intensity of the spectrum to make sure it is not off scale or too small. Use the middle mouse button and click and drag to adjust. This is a touchy adjustment, so be patient. You may also type **vs=150**↵ and the computer will set the tallest peak of your spectrum to 150 mm.

E. INTEGRATE the spectrum or a portion of the spectrum by typing **region**↵ with the appropriate portion of the spectrum displayed. Then click on the PART-INTEGRAL box in the DISPLAY INTERACTIVE menu, to see the integrals.

F. To LIST THE PEAKS on the spectrum or in a table you will want to set the *peak threshold*. Click on the NEXT, then TH buttons and set the yellow line using the left mouse button and clicking or clicking and dragging. Any peak above the line will be recognized as a peak on your spectrum or in your line list. Any peak below this line is considered noise.

G. To give your spectrum a title, type **atext ('your title')**↵.

H. Now SAVE the spectrum in your own subdirectory, by first moving to that subdirectory using the MAIN MENU, FILE, SET DIRECTORY buttons as described earlier. Then type **svf**↵ and the computer will prompt you for a name to use to save your file. Or, you may click the FILE, DATA, and then SAVE.FID buttons. To re-display your spectrum, type **ds**↵.

I. To send your spectrum to the PLOTTER, you may type the commands **pl pscale pap ppf**↵ or use MAIN MENU, DISPLAY, and PLOT buttons; then hit PLOT (again), SCALE, ALL PARAMS and PEAKS. The **ppf** command (or peaks button) is optional if you don't want to plot the peak frequencies.

J. To PRINT what's been sent to the plotter, click the page box, or type **page**↵. Nothing will come out of the plotter without entering the page command. Everything you send to the plotter in the interim will be put onto the same sheet of paper. Don't forget this command.

5. How to Run DEPT

A. Set up for ^{13}C in chloroform

B. nt=128

All other parameters should be fine.

C. Acquire data....analyze, set reference peak for chloroform (rl=77.0p), no integration, set threshold as usual.

D. Give spectrum a title (see **4.G** above).

E. Save spectrum to proper directory (see **4.H** above).

F. Plot the spectrum.

G. Type in **dept** to set dept experiment parameters.

H. Type- **mult=0.5,1,1.5**

This sets up parameters for dept 45, 90, and 135:

Change the following parameters by typing in commands below:

sw=18761.7 **pw=10**

pp=(ask your instructor) **nt=(ask your instructor)**

I. Acquire data as usual.

J. To view one spectrum by itself, type **ds(1)**, **ds(2)**, or **ds(3)** for the first, second or third acquisition, respectively.

To view all spectra in a vertical array (stacked atop one another), type **dssa**. This is the most useful format. If the spectra need to be expanded to full size, type **ds(1)**, then **wc=400p** before using the **dssa** command.

To view all spectra side by side, type **dssh.**

K. To plot, type **pscale stacked plot** or **pscale pl('all') page**

5. Log out properly.

A. After you are through collecting data, remove your sample and insert the standard sample into the probe. LOCK & SHIM ON THE STANDARD SAMPLE!! Disconnect from the acqui window.

B. To exit vnmr, click on the `MAIN MENU` box, then click on the `MORE` box. Finally click on the `EXIT VNMR` box. This will quit VNMR.

C. To LOGOUT, put the cursor on the wallpaper, hold down the right mouse button, and move the mouse to select **exit**. The computer will ask you to confirm the exit. Click the `CONFIRM` button.

<u>^{1}H NMR Spectra</u>

Use the program MestRe-C (see Appendix II) on the PC computers in the general chemistry lab or Nobel computer lab to download ^{1}H NMR spectra of cuminaldehyde and carvone and plot them with integration values. Plot expansions as needed.

Lab Report

Your report should include the items listed below. Items I-IV can be completed by writing on the relevant spectra. Item V should be written on a separate sheet of paper. All items should be stapled together, in order, with your name on the top sheet.

I. Assign each DEPT/^{13}C NMR spectral data set (A-E) to one of the terpenes listed on p. 11. Then assign the resonances in each ^{13}C NMR spectrum according to the lettering scheme in the figures on p. 11. In cases where signals lie close together, if it was possible to assign them with reasonable certainty, be sure to explain how they were differentiated. If you are unable to assign such signals, this should also be stated clearly. Your rationales can be written on the spectra themselves.

II. Each student should make assignments of the ^{1}H NMR signals for carvone and cuminaldehyde. In cases where signals are overlapping, if it was possible to assign them with reasonable certainty, be sure to explain how they were differentiated. If you are unable to assign such signals, this should also be stated clearly. Your rationales can be written on the spectra themselves.

III. Students should provide one another with data (^{13}C NMR) from the two oils that were isolated by steam distillation. Each student should then independently analyze the data, and assign, to the extent possible, the ^{13}C signals of the oil, based on ^{13}C NMR analyses of carvone, cuminaldehyde, and limonene done in parts (I) and (II). The relative concentration of carvone and cuminaldehyde in each oil sample should be roughly calculated, by comparing the integration values of similar carbons from cuminaldehyde or carvone with those of the limonene component.

IV. Analysis of the IR spectra of cuminaldehyde and carvone should be carried out. Assignments of peaks, which can be made directly on the spectra, should include C=O stretching, C-H stretching of various types (alkyl, vinyl, aromatic, aldehyde), and C=C stretches.

The IR spectra of cumin seed oil and of caraway seed oil should be compared, respectively, with the IR spectra of pure cuminaldehyde and pure carvone, and any major differences noted.

V. Use the mass of oil that you isolated from either cumin or caraway seeds to calculate the percent by mass of steam-distillable oil in your original sample of seeds.

Grignard Laboratory Report Instructions

The Grignard lab report should contains five sections, as described below:

1. The title of the experiment and a brief statement of purpose.

2. Experimental: A brief description of the experiment performed; for the synthetic procedure, write the equation representing the chemical transformations you accomplished. List masses and volumes of starting materials and products, melting points or boiling points of products, and any *important* observations you made during the laboratory period. Try to put much of the numerical information in a table. In this section, touch on the highlights of the experiment and ignore the mundane. Keep it about one paragraph in length.

1. Results and discussion:
    a. Calculate the percent yield
    b. Analyze spectral data (the most challenging part of this lab)
        i. Bromobutane NMR
        ii. Product IR
        iii. Product NMR
    c. Mechanisms for reactions
    d. Discuss any unusual occurrences and provide an explanation of them.

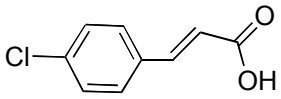
2. Conclusions: A brief statement of what was accomplished and a statement of what might be important or interesting to do if the experiment were to be continued. For example, is there a result that needs to be verified or can you propose an additional experiment that would address questions raised by your work?

3. Supplementary information:
    Answer questions 5, 6, 8, and 10 in your laboratory textbook (pp 381).

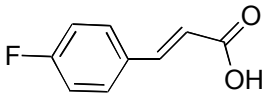
Catalytic Transfer Hydrogenation

of Cinnamate Derivatives and of Chalcone

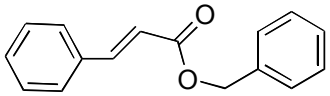
Organic synthesis is more complicated than discovering and using reagents that will accomplish desired transformations. This is because synthetic intermediates and targets are usually polyfunctional molecules, and a reagent may react with more functional groups in a substrate than were intended by the synthetic chemist. Therefore, a significant effort by synthetic chemists is spent developing new methods and finding new reagents that will be **chemoselective**, or able to transform one functional group in a polyfunctional molecule and leave the remaining ones untouched.



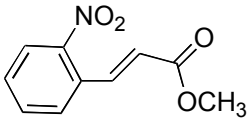
4-chlorocinnamic acid



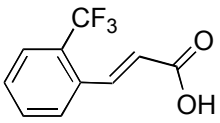
4-fluorocinnamic acid



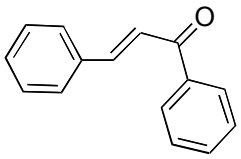
benzyl cinnamate



methyl *o*-nitrocinnamate

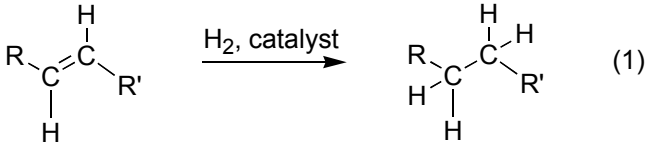


2-trifluoromethylcinnamic acid



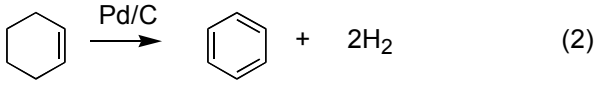
chalcone

This week in the laboratory you will explore and evaluate the chemoselectivity of palladium catalyzed transfer hydrogenation of derivatives of 3-phenylpropenoic (cinnamic) acid (see structures above) and the structurally related ketone, chalcone. You have learned that hydrogen can be added across a carbon-carbon double bond in the presence of a suitable catalyst to give the corresponding alkane (eq 1).



(1)

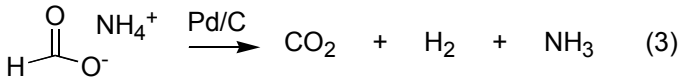
Other methods exist for accomplishing this type of reduction that make use of organic molecules as the source of hydrogen. One example of such a "hydrogen donor" is cyclohexene, which can be easily dehydrogenated by the catalyst, palladium on carbon (Pd/C) (eq 2).



(2)

If this reaction is carried out in the presence of another alkene, the hydrogen from cyclohexene can be transferred to the alkene to effect its reduction. Such reactions are known as transfer hydrogenations. The driving force for this particular reaction is the formation of the aromatic ring (i.e. benzene).

Another hydrogen donor used in transfer hydrogenation reactions is ammonium formate, which in the presence of Pd/C, generates hydrogen, ammonia and carbon dioxide (eq 3).



(3)

This is the reagent that will be used in this set of experiments.

WEEK 1--Synthesis

You will work in a groups of three or four, as assigned by your laboratory instructor. Each group should work with one substrate (which will be assigned during the lab period) but each student in the group should perform his/her own experiment. This means that each group will reproduce the experimental result several times.

Prelab: Include all relevant physical data, structures, and molecular weights of the compounds involved in this experiment. In addition, assign the ^{1}H and ^{13}C NMR spectra of the starting materials, provided as part of this packet (pp 39-48) and write out the particular transfer hydrogenation reaction that you will perform in the laboratory.

Waste Disposal: Place all organic solvent and aqueous waste in the appropriate containers. Place the pipettes used for filtering the palladium on carbon in the specially labeled containers found in the fume hoods. This material will be recycled.

Safety Notes: You will be doing the hydrogenation reaction in the hood. Hydrogen is also being generated in these reactions, so be especially careful to have no flames during this lab period. Be careful with the palladium catalyst. If the dry catalyst comes into contact with the methanol vapors, it can ignite the vapors. **Therefore, be sure to add the catalyst to your reaction flask first, *before* adding the methanol.** Also, be sure to clean up any spilled catalyst with a wet paper towel, then rinse the paper towel with plenty of water before discarding it. Do not place your face over the reaction flask when you are sampling for TLC. Ammonia is being generated and can be quite irritating. All of the substrates and their resultant reaction products are mild irritants and therefore dermal contact should be minimized.

Procedure

1. Weigh out 150 mg of the substrate you have been assigned and place it in a 17 x 150 mm test tube. Label the test tube with your last name and the name of your substrate. Add 30-40 mg of 10% palladium on carbon and 7.5 molar equivalents (based on moles of your substrate) of ammonium formate, followed by 2 mL of methanol. Swirl the mixture to dissolve the substrate. (If your substrate is chalcone, half of your group should use 95% ethanol as a solvent in place of methanol, and then you should compare the outcome of the reaction in methanol versus ethanol in your analysis.)

2. Spot the reaction mixture on a TLC plate and call this t = 0. Tape a micropipette to a boiling stick to allow you to reach the reaction mixture. You can re-use this pipette by dipping it in some clean acetone and blotting on a paper towel or tissue

(2 or 3 times). On the same plate you should have a spot of authentic starting material, prepared by dissolving a small amount in methanol and spotting with the micropipette. All TLC plates of cinnamic acid derivatives should be developed in 98:2 ethyl acetate:acetic acid and all plates of chalcone should be developed in 70:30 ethyl acetate:hexane. Sometimes, methanol as a developing solvent provides better resolution of the fluorinated and chlorinated starting materials and their respective products. The compounds can be visualized with UV light.

3. Start heating the test tube in the test tube heater (set at 80°C) that you will find in the hood. The reaction will start bubbling (even before reflux) due to the decomposition of the ammonium formate according to eq 3. The methanol reflux level should come about halfway up the test tube.

4. Monitor the reaction every 10 min by TLC (you may have to use additional plates). Probably you will want to remove your tube from the heater before you remove the sample (caution: the bottom of the test tube will be hot). When the reaction is complete (by TLC), remove the reaction mixture from the test tube heater and let it cool to room temperature. Filter the reaction mixture through a Pasteur pipette fitted with a piece of glass fiber filter into a **large** test tube (about 1/4 of a glass fiber disk is enough--share the rest with your neighbors). Rinse the reaction flask with an additional 0.5 mL methanol and pass this through the filter. Cool the filtrate in an ice bath for 10 min.

5. Place the catalyst-filled pipette in the designated beaker in the hood.

6. Remove the methanol by evaporation with a gentle stream of air and/or gentle heating over a steam bath. Do not overheat. Your product may be an oil which should not be mistaken for residual methanol. Add 4.5 mL of 1M HCl to the flask, followed by 10 mL of ether. Swirl the contents of the flask until everything has dissolved. Transfer this mixture to a separatory funnel, shake and separate the organic layer (Save the organic layer in a small Erlenmeyer flask.). Extract the *aqueous* layer with an additional 5 mL of ether. Dry the combined organics with sodium sulfate. (It is convenient to spot the compound on a TLC plate while it is still dissolved in ether.) Filter the dried organics through a pipette fitted with a small plug of cotton into a tared Erlenmeyer flask, containing a few boiling chips. Evaporate the ether in the hood over a steam bath and/or with a gentle stream of air, and determine the mass of your product. If you obtain a solid product after evaporation of the ether, obtain a melting point.

7. Using the ether solution of your product, compare the TLC retention factor (R_f) of your product with the starting material by preparing a plate with three lanes: one product, one starting material and one co-spotted product and starting material. Compare this information with your group members.

8. When you agree that you all have the same product, prepare NMR samples of your compounds. Each person should prepare his/her own ^{1}H NMR sample and each group should prepare just one concentrated sample for a ^{13}C NMR spectrum for the whole group. For the ^{1}H NMR sample, dissolve 10-20 mg product in 0.5 mL $CDCl_3$ in an NMR tube. If the product is insoluble in $CDCl_3$, add DMSO-d_6 dropwise, until the sample is homogeneous.

WEEK 2--Spectroscopy and Analysis

1. Prepare a concentrated NMR sample of your product for obtaining a ^{13}C NMR spectrum. Use 100-200+ mg of material for the ^{13}C NMR sample. You may need to combine the products from several group members to get enough material for a good ^{13}C NMR sample, but make sure they are really the same before combining them (Run them side-by-side and co-spotted on a TLC plate and compare melting points by obtaining a mixed melting point).

2. As further spectroscopic information would be useful for determining the structure of the reduction product, each group will also obtain an IR spectrum and a mass spectrum of their product.

WEEK 3--Presentation of Results

Each group will make an oral presentation to its lab section that summarizes the outcome of the transfer hydrogenation the members have performed. This must include the reaction (written on the board) and a discussion of the spectral data the led to the identification of the reaction product. You need not discuss all of the spectra if they are not relevant to your conclusion. It is sometimes important to consider the spectra of the starting material and compare them to the product in order to convince other members of the class of the conclusions you have reached (e.g. disappearance of peaks, etc.). Each member of the group must present some aspect of this information. You will find it helpful to prepare transparencies of several spectra for your presentation. These can be made using the xerox machine in the chemistry department, with the help of Nadine (the department secretary) or one of your TAs or instructors. Presentations should take approximately 20 minutes (including questions from the audience).

Write-up

Your laboratory notebook will be collected and graded, according to the usual criteria. This should include your in-lab observations and a short discussion. This is a regular *individual* write-up.

In addition to your individual lab notebook, each group will submit *one* typewritten report summarizing the **outcome of the reactions of all the groups in your lab section**. Include a brief summary of the results of each group, a chemical equation that represents each outcome, and reasonable mechanisms for reactions where a significant transformation has occurred. In addition, provide a *detailed* analysis of the spectra (assign peaks) related to your group's substrate. Remember that the overall purpose of this experiment is to evaluate the chemoselectivity of transfer hydrogenation involving ammonium formate as the hydrogen donor; therefore, a discussion that compares functional groups and their relative reactivities is necessary for full credit. Your grade for this report will combine both the oral and written components.

This laboratory was originally developed by Professor Steven F. Pedersen,

The University of California, Berkeley

Appendix I:

Instructions for the Bruker Tensor 27 FT Infrared Spectrometer

1.) Double click on the Opus 4.0 icon.
2.) Log in: Administrator
3.) Password: OPUS (all caps)
4.) The 'About Opus' screen comes up-click OK.
5.) The Opus screen opens, click on the icon that looks like a test tube containing a green solution, this is where you will set up your experiment.
6.) Click 'Basic'
    a.) Operator name: yourname
    b.) Sample name: cumin or caraway oil
    c.) Sample form: liquid
7.) Click 'Advanced'
a.) Filename: yourname
    b.) Path: :\STUDENT DATA ATR\Organic II\Monday (or Tuesday, Wed, Thurs depending on your lab day).
8.) Click 'Basic'
9.) Open lid of FT-IR instrument
10.) If the 'sample clamp' is touching the metal base of the ATR, turn the black knobs on each side of the sample clamp away from you. This will lift the sample clamp off of the metal base of the ATR.
11.) Wash the metal base by squirting a little isopropyl alcohol onto a KimWipe and wipe down the metal base and tip of the sample clamp.
12.) Turn the black knobs toward you until the plunger touches the metal base and 'springs' down into place. At this point, the knobs will no longer turn.
13.) Close the lid of the FT-IR.
14.) Under the 'Basic' screen, click 'background single channel'. This will collect a background spectrum to store in the computer.
A green box will open on the bottom of the screen and indicates that background scans 1-5 are being collected. When the scanning is finished, the words 'no active task' will appear on the bottom of the screen.
15.) Open the lid of the FT-IR.
16.) Turn the black knobs away from you so that the sample clamp rises off of the metal base.
17.) Take a glass pipette and using capillary action with your finger, pipet one drop of your essential oil onto the germanium cell (the circle in the center of the metal plate). You only need a very small amount of the oil.
18.) Turn the black knobs toward you until the sample clamp 'springs' in the down position, touching the metal plate and your sample.
19.) On the 'Basic' window, click 'sample single channel'. The collection of scans will begin (green box at bottom of screen will indicate collection of 1-5 scans, then will read 'no active task'. At this point, scanning is finished and your sample spectrum will pop onto the screen.)
20.) To scale your spectrum, right click in the y-axis and select 'maximize spectrum'.
21.) To pick peaks, click on the red icon with yellow lines underneath the peaks.
a.) Select your file for peak picking....:\STUDENT DATA ATR\ORGANIC II\MONDAY (TUESDAY, WED, THURS)\yourname.
b.) Click 'start interactive mode'.
    c.) A slide will appear on the left side of your spectrum, as you move the slide up and down, peaks will be picked (as indicated by a vertical line underneath each picked peak) or 'de-selected' (disappearance of the vertical line).
    d.) As soon as you have adjusted the slide threshold, so as to have all of the major peaks picked, click 'store' and the frequency of your peaks will appear at the bottom of your spectrum.
22.) To print your spectrum (you don't need to save because it is already saved on the hard drive), click on the print icon at the top of the screen.
23.) After you are finished printing, in the left frame of the screen, left click on the title of your spectrum file, then right click and select 'unload file'. This will unload your file from the desktop, but will not delete your file from the hard drive.

24.) To clean up, open the IR lid. Lift the sample clamp off of the metal plate (turn knobs away from you), squirt a little isopropyl alcohol onto a Kim Wipe and wipe off the metal base and tip of the sample clamp. Then put the sample clamp back into the 'down' position, so that dust does not get onto the germanium cell.

25.) If you are the last IR group for the day, close the Opus software.

Appendix II

Guide to NMR Data File Transfer and *Magnetic Resonance Companion*(MestRe-C)

Brenda S. Kelly

(Throughout this guide, use the left mouse button unless stated otherwise).

Transfer of NMR data from the Gustavus NMR spectrometer computer to PC's in the computer lab on the first floor of Nobel Hall.

1. Choose the **LeechFTP** icon under the Programs and Internet directories.

2. In the FTP program, choose "Connect" from the "File" pull-down menu. For host, enter **woodward.chem.gac.edu**, for username, enter **ochemII** for password, enter **fall2002**. Choose okay. You will be connected to the NMR computer, from which you will transfer your data. It might take a minute for the connection to be made.

3. Note the format of the window which appears: the middle window shows the local location where your files will be transferred, the left half of the window (Local System) is where the transferred files will show up and the right window (Remote System) is the NMR computer set to the directory containing your data (e.g. /home/woodward/ochemII). Your NMR data is in one of the **folders** in the right window.

Make sure that you are in the Temp folder on drive C in the Local window. You need to go up to the highest level on drive C and then choose the Temp folder by double-clicking.

4. In the right, Remote System, window, double click on the **2002** folder, followed by **grignard,** then **Monday/Tuesday/Wednesday or Thursday** for your lab day, and finally **your name**.

5. Clicking on your folder should have caused four new files to appear in the right window. Use the mouse to **highlight all four files** (left mouse button (+ shift key for each additional file), named *fid*, *log*, *procpar*, and *text*.

Note that four files with these same names may also appear in the left window (usually in the aaanmr subdirectory). These are the files of the last person who transferred data, since everyone is transferring files with the same four names. It is extremely important to ensure that these files are overwritten and replaced by your files. You can check this by reading the comments in the scroll screen after downloading your files. Also, it is important to do this data transfer before going into MestRe-C to work up the NMR data, or you will be processing someone else's data!

6. After selecting your files, transfer your data to the PC by clicking the download button (to the right of the magnifying glass) on the toolbar. You want to click on the button that shows an arrow pointing down toward a hard drive icon. Your files are now copied to the ***C: /Temp/aaanmr*** folder. **If files with the same names were already on the Local System folder, make sure they have been overwritten with your data.**

7. Close the connection to the NMR computer by quitting the FTP program. Just click the "**X**" box in the upper right corner of the window, as with any Windows program.

Starting MestRe-C

1. Choose the **Mestrec1.exe** icon under **Programs**.

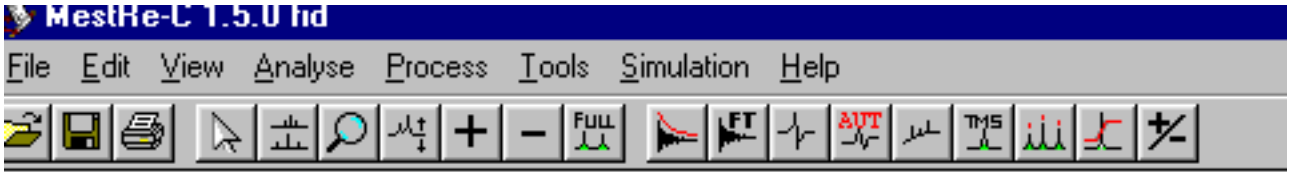
2. Since the data you transferred is not MestRe-C data, you will need to *Import* your data to the MestRe-C program: **FILE/IMPORT** (i.e. select **IMPORT** under the **FILE** menu).

3. A dialog box will appear asking you what type of data you want to import. Select the *Varian VRX/Unity* file type; click **OK**.

4. A dialog box appears that you will use to select a file to be opened. Go to the ***C: /Temr*** folder where you saved your data. Once you get there the four files you transferred, *fid, log, procpar, text,* should appear in the window. Double click on the *fid* file (or highlight it and click the Open button). Your FID will now appear in the window.

Processing Your FID

Most of the commands you need to process routine data can be accessed through the buttons on the toolbar that runs across the top of the spectrum/FID window in MestRe-C. The toolbar is shown below, with numbers assigned to each button for easy reference. When a button is referred to in this document, its number is always given in bold in parentheses.



Step-by-Step Data Processing

1. First you must perform the Fourier Transformation (FT) calculation to convert the FID into the spectrum. Click the **FT** button (**12**) and click OK in the dialog box that appears.

2. Your spectrum is likely to appear with very small peaks. Click on the + and – buttons (**8** and **9**) to increase and decrease the vertical scale.

3. You will need to *phase* the spectrum if the baseline around the peaks is not flat. You can let the program autophase your spectrum with the **Autophase** button (**14**). It is likely that you will still need to do a little manual phasing to get a good baseline. To do so, select the **phase correction** button (**13**). A dialog box appears with slide bars to adjust the zero-order and first-order phase corrections. A red cursor line (pivot) also appears on the tallest peak in your spectrum. If it is not already located at one end of your spectrum, move this pivot to any tall peak near one side of the spectrum or the other. Use the **Displace Pivot Point** slide bar to make this movement. Use the **order-0** phase correction bar to flatten the baseline around the peak with the pivot. Don't worry about the phasing of the other peaks at this point. You may find it useful to greatly increase the vertical scale of the peaks (+ and – buttons; **8** and **9**) to get a good look at the baseline. When you are satisfied with the phasing of the peak with the pivot on it, use the **order-1** phase correction to adjust the phasing of other peaks of your spectrum (do NOT move the pivot). Usually the peaks farthest away from the peak with the pivot will be most in need of the first-order phase correction. When you are satisfied, click the Apply button to apply the phasing corrections you made to the spectrum. If the spectrum looks good, exit the phasing routine by clicking the OK button. If not, continue the phasing process until you are satisfied.

4. This program prints exactly what you see on the screen, so you will probably want to move the spectrum down in the window, so that it sits about an inch above the ppm scale on the bottom of the window. To do this, click the **Vertical Shift** button (**7**). In this mode, the baseline of the spectrum moves to the point where you place the cursor and click the left mouse button. You can also hold down the left mouse button and move the black line that appears to where you would like the baseline of the spectrum to be located. At this point release the mouse button. Leave room for the integral values to be printed below the baseline. To fully exit this vertical shift mode, click the **Default Mode** button (**4**). The program stays in the vertical shift mode until you explicitly exit this

mode (button **4**). **It is not a bad idea to click this button (4) after each major manipulation, just so that you exit fully the previous mode in which you were operating.**

5. To expand around a region of interest in your spectrum use the Zoom button (**6**). In this mode, you can use the left mouse button to drag a box around the region of interest. Releasing the mouse button causes the expansion to occur. Exit the Zoom mode by clicking the Default Mode button (**4**).

6. To set the ppm scale, expand (step 5) around the TMS peak (or any other reference peak). Select the Spectrum Reference button (16 - labeled with TMS). In this mode, the arrow cursor becomes a cross hatch. Place the cross hatch on the reference peak and click left mouse button. A dialog box appears. Enter the desired ppm for this peak in the "New Reference" entry (0 ppm for TMS, 7.24ppm if you are using the residual chloroform peak) and click **OK**.

6. To get back to the full spectrum click the Full button (**10**).

7. Now expand around the peaks you wish to plot.

9. Before putting the integral lines on the spectrum you will want to correct the integral baseline. If you don't do this you get poorly phased integrals with poor baselines (and bad integral values!). So, to correct this before you display the integral, go to the **Tools** menu. In the **Integral Options** entry, select **Baseline Correction**. Your integral lines should appear nicely phased when you display them in the next step.

10. To enter the integration mode click the Integrate button (**18**).

11. To integrate individual peaks, drag a box (left mouse button) around each peak, one at a time. After you release the mouse button after making a box around a peak, the integral line will appear and an integer value for this resonance appears under the peak. Do this for each peak of interest. Note that the program sets an integral value of 1 to the first peak you integrate; the integral value of all other peaks are set relative to this first peak. So, if you suspect that one of your peaks is due to a single proton, integrate it first. You can always start over by selecting the **Delete Integrals** entry under the **Tools** menu.

11. To set the vertical offset of the integral segments (i.e. where you want the integral baseline to be), use the scrollbar on the right side of the spectrum window.

12. You can control the vertical scale of the integral lines with the **arrow up** and **arrow down** keys on your keyboard. Set the largest integral line to a size that fills most of the page.

13. When the integrals are displayed as you would like them to be, exit the Integrate mode by clicking the Default Mode button (**4**).

14. To add a title, go to the **Edit** menu and select **Inset Comments**. In the dialog box that appears, enter your title or any other comments you wish to make. Click **OK** and your comments/title will appear on the left side of the spectrum.

15. To Print your spectrum, select the print button (**3**). **Before** clicking **OK**, you must set the paper orientation to **Landscape**. To do this, click on the **Properties** button in the upper right corner of the Print dialog box. Click on the orientation box and select the **Landscape** orientation and click **OK**. Now, click **OK** in the Print dialog box to print your spectrum.

18. When you are done, quit the application. You will be asked if you want to save the spectrum; usually just click the **NO** button. If you want to save your work, save it on a floppy...but there is no need to do this; the data remain on the NMR computer and can always be re-transferred to the PC's.