# **IOWA STATE UNIVERSITY**

Chemical Instrumentation Facility

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## **QTOF Training Manual**

(11/1/2011 K.H.)

#### Location: 1238 Hach Hall Contact: Steve Veysey, 1234 Hach Hall; Kamel Harrata, 1236 Hach Hall Safety

All researchers working in 1238 Hach Hall must complete the EH&S courses: *"Fire Safety and Extinguisher Training"*, and *"Lab Safety: Compressed Gas Cylinders"*. When preparing samples in 1238A, please wear all appropriate personal protective equipment. Aprons, safety glasses, and rubber gloves are available.

Properly dispose of waste solvents and glass pipettes in the containers provided in 1238A. All of the data processing computers and many of the data acquisition computers in this lab have direct links from the desktop to MSDS sheets, the EH&S Laboratory Safety Manual and to the CIF Safety Manual.



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#### Important Notes:

Before starting analysis!!!!!

Samples must be completely dissolved prior to Injection. Please filter and/or centrifuge your sample. Next to the instrument there is a Vortex, Micro centrifuge, and 1,5 ml Micro centrifuge polypropylene tubes. For Flow Injection (FI) ESI work, sample concentrations of less than 100 ppm (100 ng/ul) are usually enough.







Tubes

and vials

| Actuals                  |               |  |  |  |  |  |  |
|--------------------------|---------------|--|--|--|--|--|--|
| Parameter                | Value         |  |  |  |  |  |  |
| Q-TOF: Not Ready Text Lo |               |  |  |  |  |  |  |
| Q-TOF: TOF Vac           | 2.04E-07 Torr |  |  |  |  |  |  |
| Q-TOF: Quad Vac          | 4.51E-05 Torr |  |  |  |  |  |  |
| Q-TOF: Rough Vac         | 2.10E+00 Torr |  |  |  |  |  |  |

Take a look at the pressure readings from the Acquisition software.

If any value differs greatly from those, please alert the mass spec personnel.

Make sure that the desired solvents are in the right place:

Solvent A1 is always Water (90%)/Methanol (10%)/.1% Formic Acid

Solvent B1 is always Methanol(90%)/Water(10%)/.1% Formic Acid

Solvents A2 and B2 are reserved to any other solvents. We prefer to keep B2 with Acetonitrile (90%)/Water(10%).

The instrument is always in standby mode when not used. If all solvent lines and connections are in place, open your Method File and turn on the system. Background ions are always present when the system is in the ON state. IF NO BACKGROUD ION IS PRESENT, IMMEDIATELY ALERT PERSONNEL!!!!

ESI response is concentration and sample dependant. Minimum sample concentration is strongly recommended. This will result in better data and minimal memory effects. 10 ppm (0.01 mg/ml) is a good start.

When experiments are finished, take your sample out from the tray if you want it back, otherwise it will be thrown away.

Experiments offered:

- Flow injection nominal mass measurement.
- Flow injection accurate mass measurement, better than 3 ppm.
- ESI and APCI MS/MS are performed with special request.
- House Columns include: XDB C18, Eclipse C18, Extend C18.

!!!When you finish, make sure to return the system to Standby!!!!

### **QTOF Overview:**

m/z is proportional to flight time squared. Heavy ions will spend longer time to reach the detector.



The Agilent QTOF 6540 is equipped with exchangeable ESI/APCI ion sources. The ESI source is the JetStream source. The instrument is capable of MS and MS/MS and it is using MassHunter software for data acquisition and processing. LC pumps can handle up to 8000 psi. Mass Accuracy of better than 3ppm is routinely achieved with a resolution (FWHM) of 40,000 for mass 1000. The system is capable of rapid switching between positive and negative ion modes.

### LC System Overview:



The LC system comprises: A Binary pump, Autosampler, Columns compartment, UV detector.

Typical applications are high throughput methods with fast gradients on high resolution 2.1 mm columns. The pump is capable of delivering flow in the range of 0.1 - 5 mL/min against up to 600 bar (8000 PSI) back pressures.

A switching valve located between injector and detector can be set to either column path or bypass path mode. We have set Column 1 position to column path and column 2 to bypass position. If you observe any solvent leak and/or high back pressure, please alert the mass spec lab personnel.

### **Electrospray Ionization principle:**



The formation of positive or negative ions (depending on the sign of the applied electrical field) occurs in high yield. In the positive ion mode protonated and/or alkali adduct analyte molecules are generally observed in the mass spectra. In the negative ion mode operation peaks corresponding to deprotonated analyte molecules are observed. ESI is described as a very "soft" ionization technique where the surrounding bath gas has a moderating effect on the internal and translational energies of desorbed ions.

#### Advantages of ESI:

- Soft ionization process so intact molecular ions are observed

- ESI allows production of multiply charged ions. This results in the ability of analyzing very high molecular weight species using the most available mass analyzers (e.g. quadrupoles).

- ESI is an atmospheric pressure process. This makes it easy to use and easy to interface with HPLC and CE separation techniques.



### **Atmospheric Pressure Chemical Ionization (APCI)**

APCI uses a corona discharge technique to produce ions. This ionization technique is used mostly for low molecular samples that are more or less polar. It is an excellent LC/MS interface that it's easy to use and can accommodate high flow rates. Like ESI, APCI can be used in positive ion mode or negative ion mode.

### **Tuning and Calibration**

The mass spectrometer mass accuracy is always within a one decimal place. For accurate mass measurement (4 decimal places), the mass spectrometer should be calibrated and calibration masses are always present during acquisition. It is possible to run the experiments without prior calibration. In this case, external calibration can be achieved using known accurate masses that happen to be in the mass spectral results.

Typically the instrument is set to High Resolution mode with standard mass range (3200 m/z)

If there is a need for Extended Mass Range, please inform the mass spec personnel. The instrument is capable of measuring masses up to 10,000 dalton when operated under 1 GHz conditions.

The instrument is tuned only by the mass spec personnel.

### **Calibration:**

| ESI - L Calibration lons (formerly ESI-TOF) |
|---|
| Empirical Formulas for High Resolution MS   |

| Positive Ion (m/z) | Empirical Formula    |
|--------------------|----------------------|
| 118.086255         | C5.H12.O2.N          |
| 322.048121         | C6.H19.O6.N3.P3      |
| 622.028960         | C12.H19.O6.N3.P3.F12 |
| 922.009798         | C18.H19.O6.N3.P3.F24 |
| 1221.990637        | C24.H19.O6.N3.P3.F36 |
| 1521.971475        | C30.H19.O6.N3.P3.F48 |
| 1821.952313        | C36.H19.O6.N3.P3.F60 |
| 2121.933152        | C42.H19.O6.N3.P3.F72 |
| 2421.913990        | C48.H19.O6.N3.P3.F84 |
| 2721.894829        | C54.H19.O6.N3.P3.F96 |

| Negative Ion (m/z) | Empirical Formula    |
|--------------------|----------------------|
| 112.985587         | C2.O2.F3             |
| 301.998139         | C6.H.O.N3.F9         |
| 601.978977         | C12.H.O.N3.F21       |
| 1033.988109        | C20.H18.O8.N3.P3.F27 |
| 1333.968947        | C26.H18.O8.N3.P3.F39 |
| 1633.949786        | C32.H18.O8.N3.P3.F51 |
| 1933.930624        | C38.H18.O8.N3.P3.F63 |
| 2233.911463        | C44.H18.O8.N3.P3.F75 |
| 2533.892301        | C50.H18.O8.N3.P3.F87 |
| 2833.873139        | C56.H18.O8.N3.P3.F99 |



Put the system in the ON state: In the **Context** pull down, select **Tune**.

Select calibrant **bottle B** for the calibrant mixture to flow

into the ion source. The flow stream from LC should go to waste. Select polarity. Make sure all the calibrant masses are selected.



Visually inspect the MS profile. All calibrant ions should be observed.



Verify that the resolution of mass 922.0097 (Positive ion mode) mass 1033.9881 (negative ion mode) is about 40,000 (FWHM).

| TOF Mass Calibration Autotune Manual Tune Diagnostics Instrument State | Preferences   |
|--|---------------|
| Current Mass Coefficients  |               |
| a = 3.4706364138E-01 t0 = 1.0140874292E+00 Calibrate                   | Load          |
| Default  | Save As       |
| Peak detection window %T   |               |
| Number of spectra to average 10  |               |
| Mass Time Converter  |               |
| Mass (m/z) < Convert>  | Time (usec)   |
|  | Show Extended |

From the TOF Mass Calibration menu click Calibrate.



| Calibrant Bottle | ⊙ None ⊂ A ⊂ B |
|------------------|----------------|
| LC Flow to       | ⊙ Waste ⊙ MS   |

Reset calibrant Bottle to None and LC flow to MS.

Return to Acquisition mode and proceed to acquiring data. The calibrant A (Lock masses or reference masses should be allowed in order to acquire data in high accuracy mode.

### **Data Acquisition:**

Open your Method File and your Worklist. Visually inspect all devices and vacuum status. Place your sample in the autosampler plate.

Samples can be placed in positions P1A1, P1A2 etc... It is always wise to inject blank (solvent only) first. This will constitute the instrument background that eventually can be substracted.

Note that all MS files are located in the D:\MassHunter\Data\kamel2 directory.

Data file naming is always QTOF1100001, QTOF1100002 etc... where the 11 implies the year (2011 in this case).

|                   | v          | ×                |              | Y        | v         | v                      |            |                  |       |
|-------------------|------------|------------------|--------------|----------|-----------|------------------------|------------|------------------|-------|
| Sample            | Properties | h-ALS-SL         | 1260 BinPump | Iso Pump | Column-SL | 1260 VWD               | MS Q-TOF   |                  |       |
| Sample            |            |                  |              |          |           | Run Tunnu              |            |                  |       |
| <u>N</u> ame:     | ET2111     |                  | Position:    | Vial 1   |           | n <u>u</u> ri Type.    | ļ          | Standard Start   | •     |
|                   |            |                  |              |          |           | Part of metho          | od to run: | Acquisition Only | -     |
| Custom <u>1</u> : | Elham      |                  | Custom2:     |          |           | Operator Nar           | me:        | Kamel            |       |
| – Data File       |            |                  |              |          |           | Wait Tjme fo           | r Ready:   | 10               | (min) |
| 🔽 Auto-           | increment  |                  |              |          |           | Injection <u>V</u> olu | ume:       | -1               | (µl)  |
| N <u>a</u> me:    | JQTOF110   | 1368.d           |              |          |           |                        |            |                  |       |
| <u>P</u> ath:     | D:\MassHu  | nter\data\Kamel2 | 2            |          | View Data | Comment                |            |                  |       |
|                   |            |                  |              |          |           |                        |            |                  |       |
|                   |            |                  |              |          |           |                        |            |                  |       |
|                   |            |                  |              |          |           |                        |            |                  |       |

For a single sample run you can use the following procedure or you can skip and use the worklist.

Sample information and experiment parameters field

| Fill in Sample name or ID, Injection volume h-ALS-SL; Set F | Pump conditions 1260 BinPump; Colu | ımn |
|---|------------------------------------|-----|
| bypass state Column-SL; Set UV conditions 1260 VWD          | ; Set MS Q-TOF conditions          | 1   |

All these fields are already correctly set in your Method File except Sample Name.

| Sample Properties h-ALS-SL 1260 BinPump | Iso Pump   Column-SL   1260 VWD   MS Q-TOF |
|---|--|
| Setup Timetable Options                 |  |
| Flow: 0.8 ml/min Solvent A              | Stop Time<br>No Limit<br>III I min         |
| 100.00 %<br>2: C H20                    | Post Time<br>© Off<br>© Off                |
| Solvent B<br>1: • MeOH                  | MeOH/H2O .1% FA                            |
| 2: 0  AUN _                             | ALN Min: U _ bar Max: 500 _ bar            |

Set Stop time. The stop time is usually set to coincide with the time of the total gradient LC time.

| From 1260 BinPump | and | Timetable | edit the LC gradient |
|-------------------|-----|-----------|----------------------|
|-------------------|-----|-----------|----------------------|

| Setup | Timetable | Options    |       |             |
|-------|-----------|------------|-------|-------------|
|       | Time      | <b>B</b> % | Flow  | Max. Press. |
| 1     | 0.00      | 0.0        | 0.800 | 400         |
| 2     | 5.00      | 100.0      | 0.800 | 400         |
| 3     | 5.10      | 0.0        | 0.800 | 400         |
| 4     | 11.00     | 0.0        | 0.800 | 400         |



The sample is injected, and data can be viewed in the Profile Display window and/or in the processing software.

Acquisition can be stopped manually STOP

Data can be processed in MassHunter Qual program. (See data processing)

Acquiring data using Worklists:

Open Worklist: Ctrl+W and select your worklist. You can Edit and save your worklist. A user can create only one worklist. The naming of worklist should be "USERNAME.wkl" .

Edit worklist: Sample name, Sample Position, Method File, Data File.

|   | ◄                      | Sample Name | Sample Position | Method                                | Data File                               | Sample Type |
|---|------------------------|-------------|-----------------|---------------------------------------|---|-------------|
| 1 | v                      | meOH        | P1-A1           | ESI-Kamel-100-1000-Grad1-Rich-Kemin-p | D:\MassHunter\data\Kamel1\QTOF1100539.d | Sample      |
| 2 | $\boldsymbol{\nu}_{1}$ | Se-O        | P1-A2           | ESI-Kamel-100-1000-Grad1-Rich-Kemin-p | D:\MassHunter\data\Kamel1\QTOF1100540.d | QC          |
| 3 | V.                     | Se-1        | P1-A3           | ESI-Kamel-100-1000-Grad1-Rich-Kemin-p | D:\MassHunter\data\Kamel1\QTOF1100541.d | Sample      |
| 4 | v                      | Se-2        | P1-A4           | ESI-Kamel-100-1000-Grad1-Rich-Kemin-p | D:\MassHunter\data\Kamel1\QTOF1100542.d | Sample      |
| 5 | v                      | Se-3        | P1-A5           | ESI-Kamel-100-1000-Grad1-Rich-Kemin-p | D:\MassHunter\data\Kamel1\QTOF1100543.d | Sample      |
| 6 | V.                     | L2-0        | P1-B1           | ESI-Kamel-100-1000-Grad1-Rich-Kemin-p | D:\MassHunter\data\Kamel1\QTOF1100544.d | Sample      |
| 7 | $\boldsymbol{\nu}$     | L2-1        | P1-B2           | ESI-Kamel-100-1000-Grad1-Rich-Kemin-p | D:\MassHunter\data\Kamel1\QTOF1100545.d | Sample      |
| 8 | v                      | L2-2        | P1-B3           | ESI-Kamel-100-1000-Grad1-Rich-Kemin-p | D:\MassHunter\data\Kamel1\QTOF1100546.d | Sample      |
| 9 | v                      | L2-3        | P1-B4           | ESI-Kamel-100-1000-Grad1-Rich-Kemin-p | D:\MassHunter\data\Kamel1\QTOF1100547.d | QC          |

Highlight the targeted files and click start experiment 🛅 🛍



Acquisition can be stopped manually **Stoppen** or automatically when LC gradient is finished.

After each run, enough time should be given to the starting LC conditions in order to calibrate the column. Rule of thumb the volume necessary to calibrate the column is 10 to 20 times the volume of the column.



#### **Data Processing:**

Data processing is accomplished using the MassHunter Qualitative Analysis software

The following are the essential steps to taken to obtain Chromatograph and mass spectra:



For the purpose of this training I am using "kamel-routine.xml" layout that comprises: Data Navigator, Method Explorer, Chromatogram Results, MS Spectrum Results, Formula Calculator, and Mass Calculator.



Open Data File

| Open Data File  |  |  |   |                           |                  | ? 🗙                    |
|---|--|--|---|---------------------------|------------------|------------------------|
| Look in:  | 😂 kamel2   |  |   | •                         | ← 🗈              |                        |
| My Recent<br>Documents<br>Desktop   | IH QTOF1101428           IH QTOF1101429           IH QTOF1101430           IH QTOF1101431           IH QTOF1101433           IH QTOF1101433           IH QTOF1101433           IH QTOF1101435           IH QTOF1101436           IH QTOF1101436           IH QTOF1101436           IH QTOF1101436           IH QTOF1101436           IH QTOF1101436           IH QTOF1101437           IH QTOF1101438           IH QTOF1101438           IH QTOF1101438           IH QTOF1101438           IH QTOF1101438           IH QTOF1101438 | .d<br>.d<br>.d<br>.d<br>.d<br>.d<br>.d<br>.d<br>.d | Image: Control of the state of the |                           | йи QTOF1101454.d |                        |
| My Computer   | MH QTOF1101440   | .d   | MH QTOF1101453.d  |                           |                  |                        |
| My Network<br>Places  | File names :<br>Files of type :  | QTOF1<br>Data F                                    | 101455.d<br>iles (*.d)  |                           | •                | Open<br>Cancel<br>Help |
| Options<br>C Load worklis<br>C Load results<br>Use current<br>Load result<br>Run File Op<br>selected me | t method<br>method<br>data<br>en' actions from<br>thod   |  | Sample Information<br>Sample Name :<br>User Name :<br>Sample Position :<br>Description :  | LW05.1<br>Kamel<br>Vial 1 | 016              |                        |

Double Click with left mouse button on the target data file



Left mouse button double Click will display the mass spectrum of that scan.

| 1     |  |
|-------|--|
| Шис   | Spectrum Hesults X   |
| 2 ↔   | 🗘 🔍 🔁 🚧 🕊 🛧 🔺 O O 1 💿 🖬 🔭 % 🐝 🕼 🔿                                      |
| x10 4 | +ESI Scan (2.0736 min) Frag=175.0V QTOF1100112comp.d                   |
| 5-    | 147.0449   |
| 4 -   |  |
| 3-    |  |
| 2-    | 164.0711   |
| 1-    | 118.0666   |
|       | 141.0001   |
| 0-    | 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 |
|       | Counts vs. Mass-to-Charge (m/z)  |

Left button and drag, then double click inside the shaded area to average scans.

|    | Extract MS Spectrum                       |     |
|----|---|-----|
| ~  | Extract MS Spectrum to <u>B</u> ackground |     |
| 1. | Extract UV_Spectrum                       | l ' |
|    | E <u>x</u> tract Peak Spectrum            |     |

Left mouse button and drag and release followed by Right click in the shaded area to specify the background spectrum.

| Sort by Data File          Image: Optimized state of the stat                 | 🗄 🔁 Data Navigator   | × |
|--|--|---|
| QTOF1100112comp.d      ✓ User Chromatograms      ✓ User Spectra      ✓ User Spec | Sort by Data File  | ~ |
|  | QTOF1100112comp.d      ✓ User Chromatograms      ✓ User Spectra      ✓ User Spectra      ✓ Julu + Scan (2.0736 min)      ✓ Background Spectra      ✓ Julu + Scan (1.7296-1.8442 min)      ✓ Compounds      Matched Sequences |   |

Background spectrum will be display in the Navigator window.



Right click on the averaged spectrum and select Substract Background Spectrum



Right click in Chromatogram and select Peak Integration to integrate peaks.

Also double click on any mass peak (in spectrum) to display selectively that mass in the Chromatogram (EIC)



Colors can be set by Right clicking and "Choose Define Color"

| 🚰 Method Editor: Integrate (MS)                  | × |
|--|---|
| 🚰 🔄 👻 👻 🕑 🔹 Method Items 🔹 😕 🙀                   |   |
| A Integrator A Peak Filters Results              |   |
| Integrator selection                             | ^ |
| General  |   |
| A Options  |   |
| Detector<br>Point sampling: 1 Start threshold: 1 |   |
| Smoothing Stop threshold: 0.0                    |   |
| Filtering: 5 point V Peak location: Top V        |   |
| Baseline allocation                              |   |
| Baseline reset > 10 🛕                            |   |
| lf either edge < 100 %                           |   |
| then: 💿 Drop else tangent skim 🛕                 |   |
| 🔿 Tangent skim else drop                         |   |
|  |   |
|  |   |
|  | ~ |

From Method Editor-Chromatogram-Integrate (MS), Peak Area and Heights can be manipulated.



### <u>Appendix</u>

### Common button actions in the chromatogram and spectrum view:



Reset display



Reset display without normalizing







Autoscale Y-axis during zoom

| <b>ኒ</b>        | Set Anchor display         |
|-----------------|----------------------------|
| ☆               | Separate displays          |
|                 | Overlaid displays          |
| 8               | Set number of displays     |
|                 | Range select               |
|                 | Peak select                |
| <u>.</u>        | Manual integration         |
| <mark>∕∦</mark> | Walk chromatogram          |
| 4               | Print chromatogram display |

### Additive and buffer summary:

For positive ion mode ESI use proton donor, e.g. Acetic Acid or Formic acid.

For negative ion mode ESI, use proton acceptor, e.g. TEA

Trifluoroacetic acid (<0.1 % v/v) is often used to assist the chromatographic separation.

Ammonium Acetate and Ammonium Formate are often used as buffer systems.

#### Additives considerations:

#### 1- Acids

- a- Do not use inorganic acids (may cause source corrosion).
- b- Two possible choices are:
  - 0.1 % Formic acid
  - 0.1 % Acetic acid with 0,02 % TFA
- c- Best results arise from acids stored in glass
- d- Excellent results have been found with JT Baker acids

#### 2- Surface Active Agents

Detergents and other surface active agents may suppress ionization.

### Solvents:

#### 1. Solvent Bottles

You must use your own solvents in your own bottles, or bottles that have been assigned to you. You may *never* use solvents prepared for someone else, or solvent containers that are not yours. We have a supply of 500 mL and 1000 mL bottles especially designed for use with the LCMS. These can be loaned to you for the duration of your project. The content and the owners name must be CLEARLY visible on all containers in our lab. Unlabelled containers will be discarded without hesitation.

#### 2. Solvent Filtering

Pure organic solvents do not need to be filtered prior to use. If any modifiers have been added to the organic phase, then the mixture should be filtered. The aqueous phase, regardless of the presence or absence of modifiers, should be filtered immediately prior to use. Bacterial growth, especially in aqueous solutions, can lead to clogs in the HPLC mixer, the high-pressure stainless steel tubing, or the capillary transfer tubing, as well as high background and extraneous mass peaks in the mass spectrum. As part of your training, Dr. Harrata will show you how to use the filtering apparatus located in our wet lab.



### **Samples Rules:**

#### 1. Preparation

If possible, samples should be prepared in your own lab. In emergency situations you may use the equipment in our wet lab, including the balance, centrifuge, acid-washed

glassware, and sample filtration cartridges. We do have a supply of nanopure water available. This can be used for final rinse or sample dilutions. If you use any of our glassware, *do not* return it to the glassware rack or shelf. Put it in the sink and we will eventually clean and acid wash it. At no time should phosphate detergents be brought into or used in our lab.

#### 2. Sample Filtration

All samples should be filtered through a 0.45 micron filter just prior to analysis. No exceptions. Ignoring this rule will be cause for suspension of privileges. We have a limited supply of these filters for use in cases of emergency. You should order and use your own.

#### 3. LC Columns and Syringes

You must provide your own LC column, as appropriate for your project. You must provide your own syringes (blunt-tip; especially designed for LC use). You WILL be charged for damage to rotor seals if you use sharp-tip syringes.