Fourier Transform Infrared Spectroscopy

Description of Instrument

Mattson Instruments Genesis II FTIR spectrometer system designed for routine sample analysis in the QA/QC environment. The Genesis II is the next generation in the Genesis Series and incorporates the best design features of the original system; including it's ease-of-use, compact size, ruggedness and reliability.

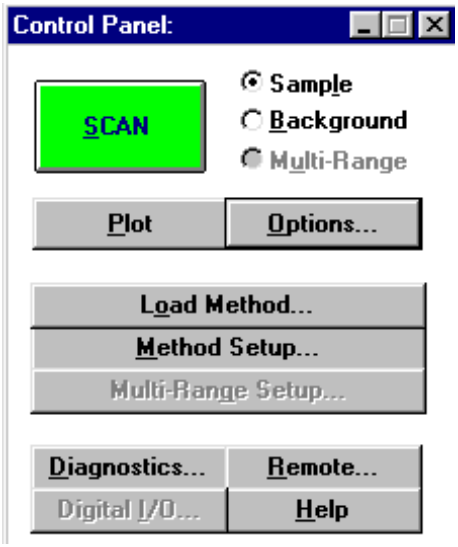
New advanced electronics on the Genesis II provide higher signal to noise ratio and additional scanning velocities; improving system performance and sampling time. The Genesis II features 1 cm^{-1} resolution in either near or mid infrared configurations with the choice of **room temperature (which we have)** or liquid nitrogen cooled detectors. If higher spectral resolution is needed, 0.50 cm^{-1} resolution is available as an option either at time of system purchase or later. For easy access, a new sample hatch was added to the sliding sample compartment cover. A user changeable detector is now standard extending the ease of system maintenance.

Genesis II FTIR spectrometer is compatible with all standard sampling techniques for powders, liquids and gases to provide additional flexibility. The optional Genesis Validator software provides full IQ, OQ and PQ validation for laboratories subject to regulatory review.

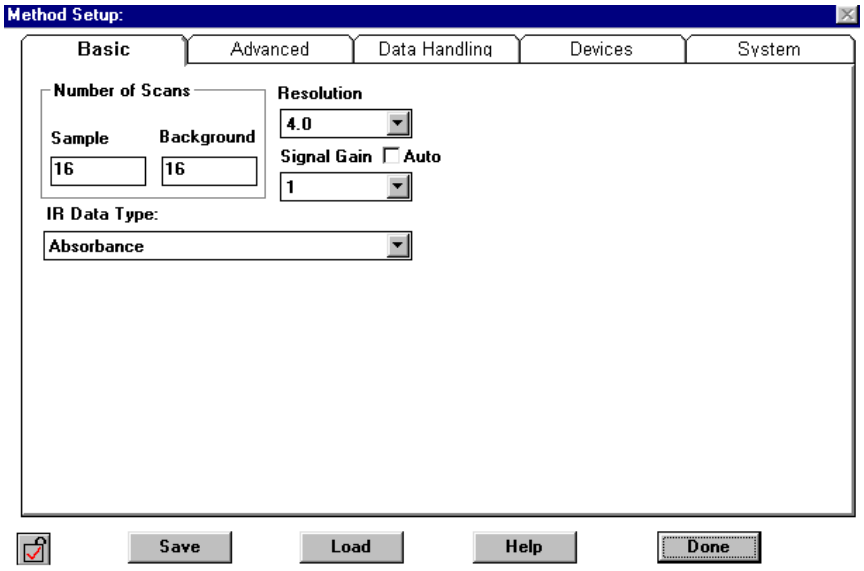
How to Run Mattson Instruments Genesis II FT-IR Instrument

Procedure:

1. **Sign on the log book.**
2. **Turn on the computer.**
3. **Turn on the FTIR Spectrometer switch at the back of the instrument.**
4. **On the computer screen "Cancel" the login to network option.**
5. **Load Win1st by clicking on the blue icon**  **on the screen following screen will appear.**
6. **Click on Load method and select upali.ini file and press ok!**



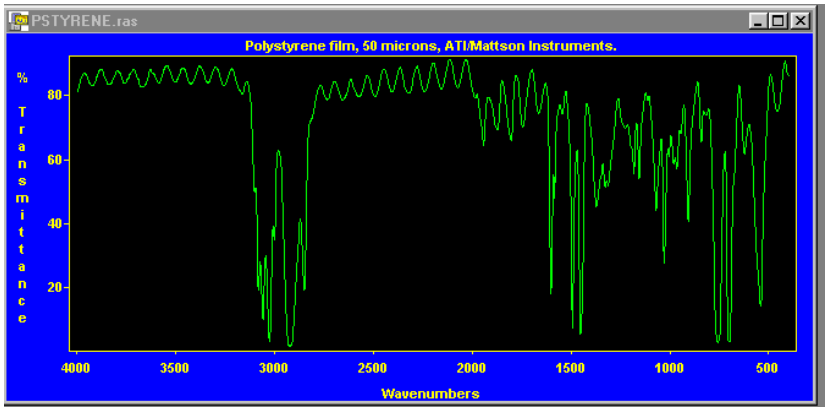
7. **Then press method setup if you need to change number scans (normally below 25) or press advanced to change scan range (400-4000 default) .**



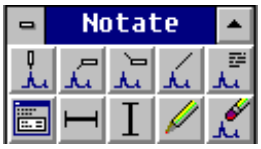
8. **Go back to control panel and select background radial button. After making sure nothing is in the sample path press SCAN. Answer ok to questions and background will be displayed!**

9. **The go back to control panel and select sample and place sample in the beam path and press SCAN.**

10. **The data display window will appear automatically at the end of the scans and you are ready to work on the spectrum; labeling the spectrum and annotating the spectral values to peaks,**



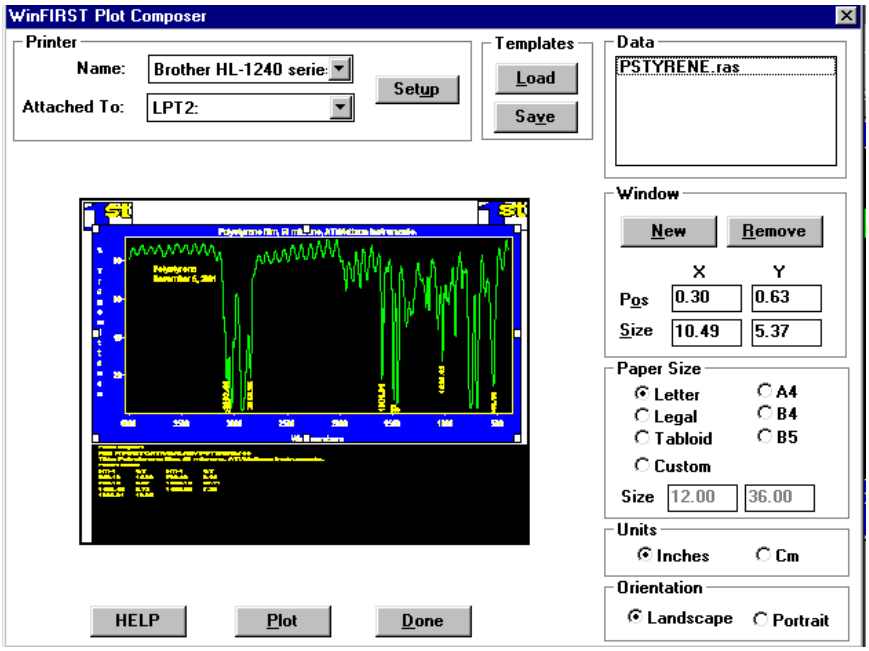
11. **Go to tools in main menu and select annotate:**



12. **Go to math in the main menu and select peaks and select threshold and stretch the rubber band where you want the threshold to be by selecting two points. Peaks will be labeled. To place text on the spectrum click on the top first button on the right and press ok. Then you can enter you text any where on the the spectrum.**

13. **Then press go to file in the main menu and select plot to print the spectrum.**

14. **Select the printer and press plot.**



15. **To save your data file go to file in the main menu and select save sample and select a name and drive and press ok!**

16. **Once you are finished with the instrument exit from WIN1st software, remove all samples from sample chamber and turn off the FTIR spectrometer. Please sign off on the log book. Thanks!**

CHARACTERISTIC INFRARED ABSORPTION FREQUENCIES		
Bond	**Compound Type**	**Frequency range, cm^{-1}**
C-H	Alkanes	2960-2850(s) stretch
		1470-1350(v) scissoring and bending
	CH_3 Umbrella Deformation	1380(m-w) - Doublet - isopropyl, *t*-butyl
C-H	Alkenes	3080-3020(m) stretch
		1000-675(s) bend
C-H	Aromatic Rings	3100-3000(m) stretch
	Phenyl Ring Substitution Bands	870-675(s) bend
	Phenyl Ring Substitution Overtones	2000-1600(w) - fingerprint region
C-H	Alkynes	3333-3267(s) stretch
		700-610(b) bend
C=C	Alkenes	1680-1640(m,w)) stretch
C≡C	Alkynes	2260-2100(w,sh) stretch
C=C	Aromatic Rings	1600, 1500(w) stretch
C-O	Alcohols, Ethers, Carboxylic acids, Esters	1260-1000(s) stretch
C=O	Aldehydes, Ketones, Carboxylic acids, Esters	1760-1670(s) stretch
O-H	Monomeric -- Alcohols, Phenols	3640-3160(s,br) stretch
	Hydrogen-bonded -- Alcohols, Phenols	3600-3200(b) stretch
	Carboxylic acids	3000-2500(b) stretch
N-H	Amines	3500-3300(m) stretch
		1650-1580 (m) bend
C-N	Amines	1340-1020(m) stretch
C≡N	Nitriles	2260-2220(v) stretch
NO_2	Nitro Compounds	1660-1500(s) asymmetrical stretch
		1390-1260(s) symmetrical stretch

v - variable, m - medium, s - strong, br - broad, w - weak