GC-FID: Protocol for analyzing fatty acid methyl esters (FAME)

*Instrument*

Hewlett Packard HP6890 GC-FID

*Preparations*

FAME should be dissolved in hexane, in 2 mL autosampler vials. Samples should not be too concentrated (peak areas over 1000 and peak heights over 100 indicate dilution is needed).

Consider running a method blank, hexane blank, or standards along with your samples. Peaks in a method blank can indicate the introduction of contamination during your FAME extraction. Peaks in a hexane blank indicate either contaminated hexane, or contamination within the GC. Standards with known peaks are useful for identification of peaks, and can be used for quantification (a series of concentrations produces a calibration curve).

*Instrument set-up*

From the software menu, select “Sequence,” then “sequence parameters”

Do not change the operator name. Change the destination folder (probably your name). Change the date and the counter so that your data is not overwritten. Click “ok.”

From the software menu, select “Sequence,” then “sequence table”

Enter your samples, being sure to check the vial locations in the autosampler (201 – 208). Use ctrl-c and ctrl-v or “copy” and “paste” buttons in lower lefthand part of screen to copy and paste rows. You need to change only the vial location, sample name, and sample description. Everything else should remain the same.

Place your samples in the correct autosampler locations.

Fill the two rinse vials with hexane, and empty the waste vial.

Turn on the air and hydrogen cylinders. The helium and nitrogen cylinders remain open at all times.

From the software menu, select “File,” then “load method”

The default should be “FAMES4.m,” load this method.

It may take several minutes for the parameters to reach their set points. When they do, the colored blocks on the screen will all turn green.

From the software menu, select “\_\_\_\_,” then “run sequence”

If you already have data in your folder, a first pop-up window will make sure you really want to write data to that directory. A second pop-up window will appear, do NOT click anything. It will make a decision and go away by itself.

Stick around to make sure the sampler injects a sample into the inlet, and that the timer begins.

*Post-run steps*

After all samples have completed (each sample takes 85+ minutes), turn off the air and hydrogen cylinders. This is to conserve those gases. The helium remains on to provide flow through the column.

Remove your samples and replace the lids. Samples exposed to air will degrade over time. The hexane will also evaporate if there is a hole in the septum, which is particularly bad because the freezers we use for storage are not explosion proof. Other than that, the samples should keep well in the freezer (-4 or -20 Celsius are ok).

From the software, select “data analysis” from the drop-down menu towards the upper right of the screen. This will bring you into a different window. Open your samples, one at a time, to print them. Each sample requires 6 or 7 pages to print. Be sure the first page does not loop back and jam the printer. It is best to queue all the print jobs up and let it print, then tear it off once all have finished.

To save digital files, use the floppy disks labeled “use for file transfers” to save your data. Each floppy will hold data for 6 samples. The More Hall computer lab in 001 has computers with floppy drives which can be used to transfer data to a USB or the internet.