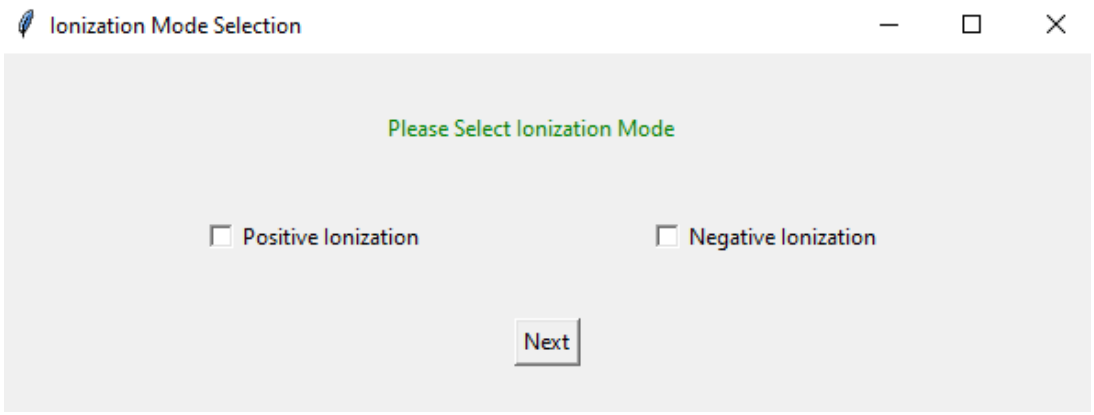
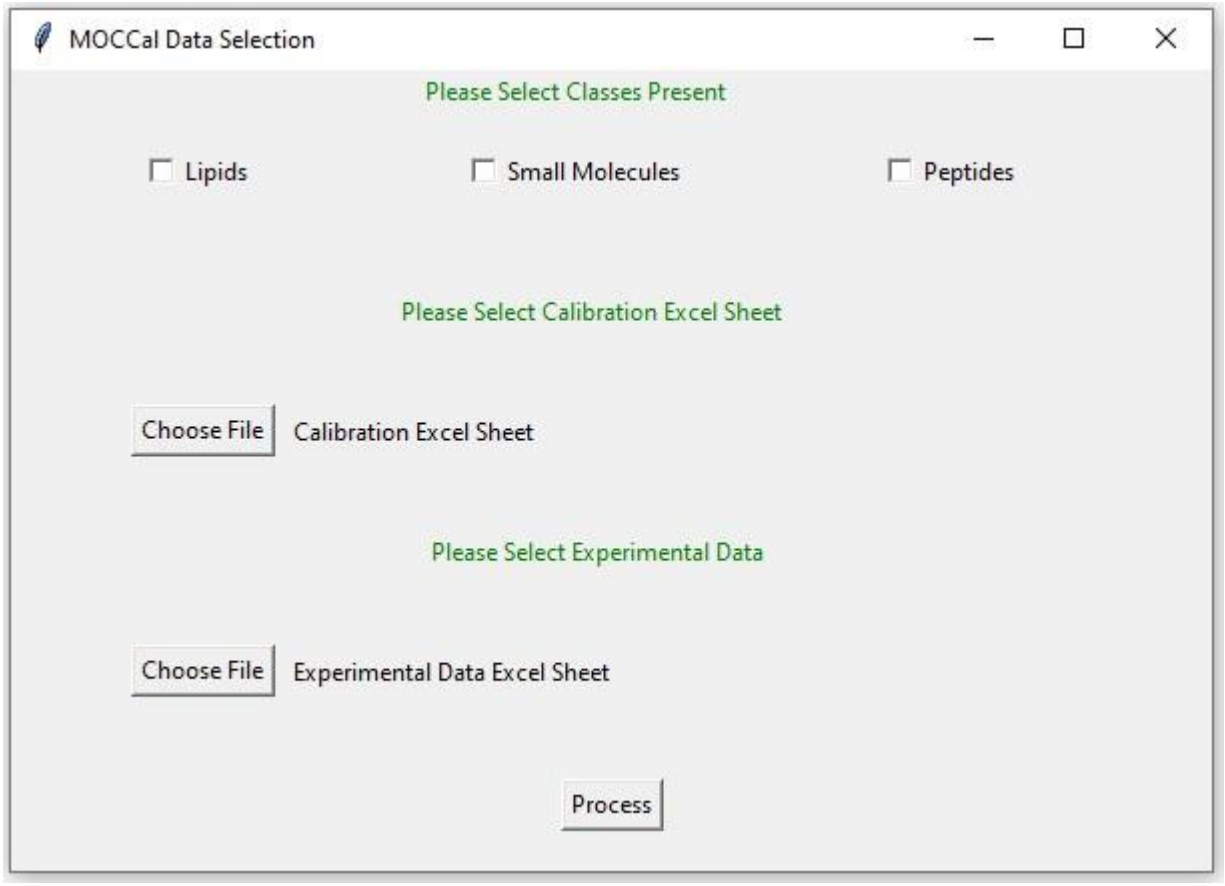
MOCCal TUTORIAL

GUI #1. The first GUI will ask you to select the ionization mode the data was collected in.

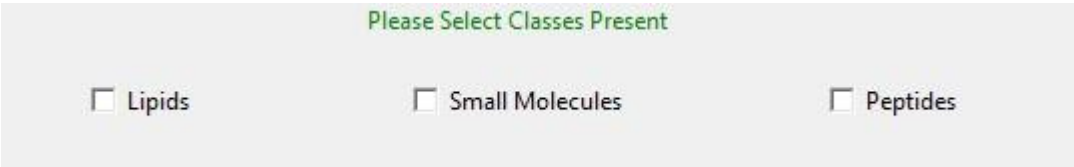


GUI #2. The second GUI will ask you for your Enhanced Duty Cycle (EDC) delay coefficient. This value is instrument-dependent and will typically fall between 1.4-1.6.

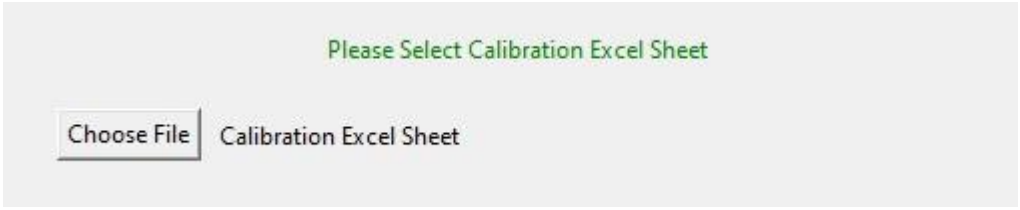
GUI #3. The third GUI will facilitate data importation. For CCS Calibration, reference standards from each biomolecular class of interest will need to be chosen. Standards should ideally cover the mass ranges of experimental analytes. Calibrant solutions should be collected via infusion



GUI #3A. The first selection option allows for you to choose which classes are present in your data. The choices are Lipids, Small Molecules, and Peptides, with "Peptides" having the functionality to calibrate singly, doubly, and triply charged peptides. Standards are required for each class chosen. You may choose any combination of these classes, as long as you have corresponding calibration data.

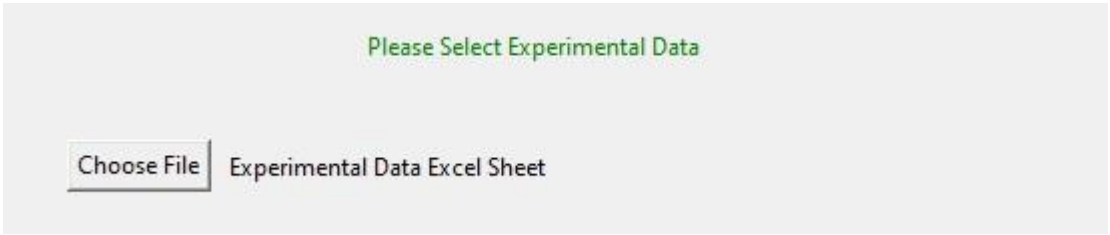


GUI #3B. For calibration data, you will need to upload an excel document containing the calibrant name, *m/z* value, drift time, reference literature ccs value, biomolecular class ("lipid", "small molecule", or "peptide"), and charge (1-3). A blank template (Calibration_Template.xlsx) and an example excel sheet (Calibration_Example.xlsx) can be found in the Templates_Examples folder.



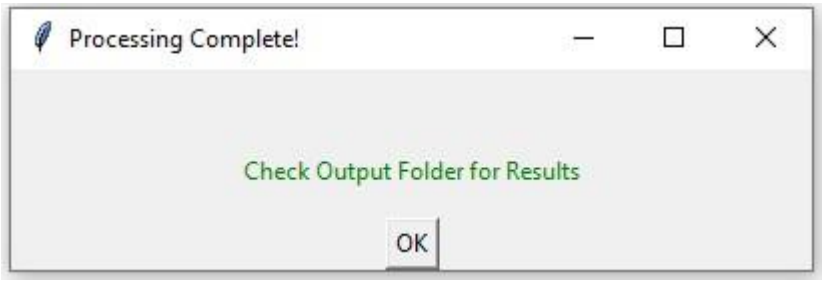
calibrant	m/z	drift time	ccs	biomolecule	charge

GUI #3C. Experimental data can be uploaded as a vendor-specific processed excel file. You will need to upload the data as an excel file containing a compound name (does not have to be a compound identity, just any data-identifying name), *m/z* value, retention time value, and drift time value. A blank template (Experimental_Data_Template.xlsx) and an example excel sheet (Experimental_Data_Example.xlsx) can be found in Templates_Examples folder.



Compound	m/z	Retention time	Drift time

GUI #4. After pressing the "Process" button, MOCCal will process the data. When the data processing is complete, the message below will pop up. There will be an excel file titled "CalibrationOutput" in the Output folder containing the processed data.



OUTPUT EXAMPLE

For every class selected in GUI #1, there will be a corresponding calibration sheet in the output excel document containing the parameters for the optimized calibration curve as well as the calculated CCS values and CCS % error (seen as residuals) as compared to the provided literature CCS values.

	parameter	values
0	A	486.3249
1	t0	0.032662
2	B	0.513517

	calibrant	mz	Drift Time	Lit CCS	Cal CCS	Residuals
0	PC 10:0	566.3763	6.44	245.4	244.88	-0.212
1	PC 12:0	622.4391	7.19	258.4	258.56	0.062
2	PC 14:0	678.4968	7.88	270.4	270.52	0.044
3	PC 16:0	734.569	8.6	282.5	282.49	-0.004
4	PE 10:0	524.3298	5.83	233	233.14	0.06
5	PE 12:0	580.3951	6.55	246.7	246.87	0.069
6	PE 14:0	636.4531	7.24	259.2	259.35	0.058
7	PE 16:0	692.517	7.93	271.5	271.28	-0.081

For experimental data, there will be a corresponding sheet in the output excel document containing the class assignment, the class-specific calculated CCS value, and the calibration effect. An example output excel sheet (CalibrationOutput_Example).xlsx can be found in the Templates_Examples folder.

Compound	m/z	Charge	Retention Time	Drift Time	Cal CCS	Class Assignment	Calibration Effect
Lipid Feature	622.4391	1	3.5	7.19	258.637	lipid	2
Small Molecule Feature	156.0755	1	6.2	1.72	131.295	small molecule	3
Peptide (z=1) Feature	729.3854	1	1.4	6.54	252.321	singly charged peptide	2
Peptide (z=2) Feature	507.2696	2	2.8	3.17	332.208	doubly charged peptide	0
Peptide (z=3) Feature	622.6627	3	4.9	4.16	578.835	triply charged peptide	0