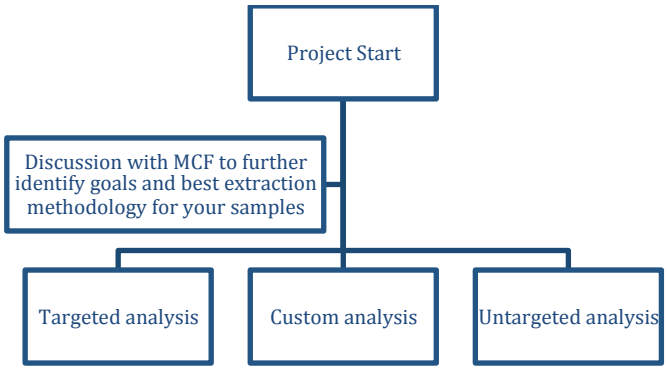
Terms of Use

Revision 4: September 24, 2013

The Metabolomics Core Facility (MCF) is a Canadian funded facility for use by academic, government and industrial researchers. Users of the facility may submit samples to the facility for analysis or Goodman Cancer Research Centre scientists may be trained by MCF staff to collect and analyze their own data. Researchers may request sample analysis or training by contacting the MCF manager (daina.avizonis@mcgill.ca). The MCF has adopted a collaborative approach with its users to help ensure the highest quality analysis.

General workflow

Due to the unique nature of a metabolomics facility, and the complexity of analyses performed, a project is first opened via discussion, email contact or our sample submission form. Once in contact with the MCF, the project may be further discussed to clearly identify the objectives of the work with the MCF. A sample extraction protocol may be suggested at this point. We offer three general areas of service / collaboration: targeted analysis, custom analysis and untargeted analysis. For the targeted analyses a pilot study consisting of 2-4 samples will be planned (free of charge) to ensure that we can detect the metabolites of interest. After a successful pilot study, a larger analysis will be arranged for which the researcher will be charged (cost estimates will be provided via website, email or pdf document). The researcher will remit payment promptly upon billing. For more collaborative projects we must invoice for staff and instrument time to cover the facility's expenses.



MCF Authorship & Acknowledgment

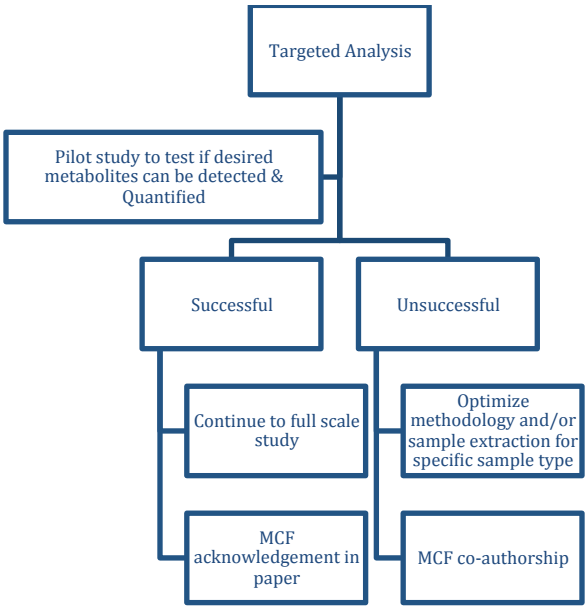
In order to set expectations, we recommend the following rules for when it is appropriate to simply acknowledge the MCF for its work or when it is appropriate to include the MCF as co-authors. Below are three flow charts or scenarios that show potential benefits from working together.

Targeted analysis

For most targeted analyses our protocols are well established. In this situation you may simply acknowledge the MCF for its contribution with the following statement:

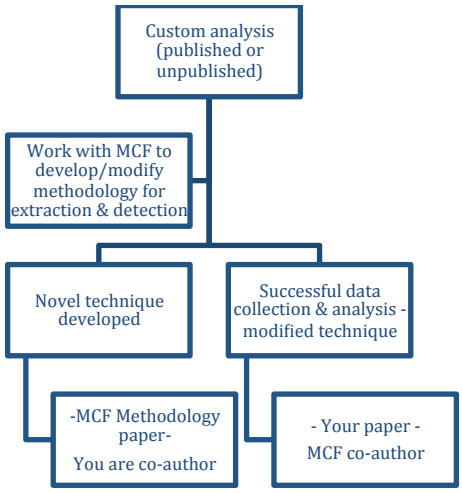
Metabolite measurements were performed at the Rosalind and Morris Goodman Cancer Research Centre Metabolomics Core Facility supported by the Canada Foundation for Innovation, The Dr. John R. and Clara M. Fraser Memorial Trust, the Terry Fox Foundation (TFF Oncometabolism Team Grant 116128), and McGill University."

Note that the MCF staff is always happy to help write the experimental section, just ask! In the situation where the MCF needs to develop an extraction technique or modify LC/MS or GC/MS detection protocols for your particular samples then co-authorship would be required since this represents work requiring additional expertise. Please refer to the flow chart below:



Custom Analysis

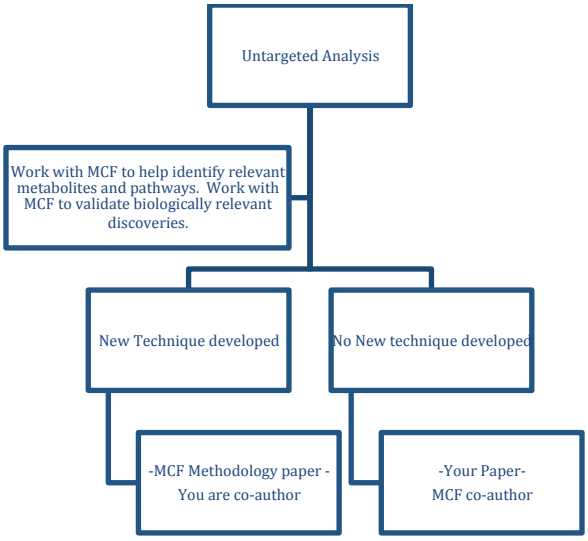
The MCF staff is happy to develop custom metabolite analyses for you. We will invoice for staff and instrument time to cover our costs. Even if a protocol or methodology for extracting and detecting the metabolites of interest is published, it must be tested and refined for our systems and your samples. You should expect to work closely with the MCF to obtain authentic metabolites, and to refine extraction protocols to detect the metabolites of interest in your samples. During this process the MCF may develop an entirely new, and better methodology. In this case, the MCF will want to publish the new methodology, including you as co-author. When only methodology modifications were made, the MCF staff should be included as co-authors on your publication, write the modified experimental or analytical methodology and carefully review the article before submission to ensure the best presentation of data acquired at the MCF. Please refer to the flow chart below:



Untargeted Analysis

The workflow for untargeted analysis requires close collaboration between you and the MCF. The MCF is developing untargeted workflows for NMR, GC/MS and LC/MS. These workflows should always be considered "under development" because they are very project specific. For example, columns must be chosen for both LC/MS and GC/MS applications while NMR is limited to primarily water-soluble metabolites. Once data are acquired, the peaks that differentiate groups must be identified and followed up with more extensive experiments (LC-MS/MS for example). The metabolites are then putatively identified and authentic standards must be obtained for validation. Metabolite confirmation is obtained by showing that the putative metabolite has the same column retention time, exact mass (in the case of QTOF) and MS/MS or NMR spectra as the authentic standard. Finally the standard should be spiked into the sample to further support its identification in the biological sample.

Once the differentiating metabolites are identified, they may be mapped to potential pathways. In the ideal situation these pathways would then be targeted and metabolite levels confirmed. Further, the pathways may be tested through the use of stable isotope tracer analysis if ^{13}C, ^{15}N or ^{2}H isotopically labeled substrates can be obtained. Clearly the untargeted analysis involves extensive interaction with the MCF and co-authorship is required.



For all situations where the QANUC NMR facility is used by the MCF for data collection, this facility must also be acknowledged with the following statement as per the QANUC terms of use requirements:

"NMR experiments were recorded at the Québec/Eastern Canada High Field NMR Facility, supported by the Natural Sciences and Engineering Research Council of Canada, the Canada Foundation for Innovation, the Québec ministère de la recherche en science et technologie, and McGill University"

The MCF is happy to provide you with written experimental sections and help with data interpretation whenever possible.

Intellectual Property, Patents and Licensing

Any intellectual property developed jointly with the MCF will include the appropriate MCF staff as co-inventors and conform to the McGill Intellectual Property policy: http://www.mcgill.ca/files/international/ipcorrectfinal.pdf