



## Altitude Training with a Mass Spectrometrist

Anyone listening to **Corey Broeckling** launch into an enthusiastic description of his research feels like they are trailing a runner—which they are. One of Broeckling's favorite spins is a half marathon that takes place a mile above sea level and includes 2,000 feet change in altitude.

Broeckling is newly-appointed Director of the Proteomics and Metabolomics Core Facility at Colorado State University (CSU) where, over the last decade, numerous projects have benefitted from his background in biology and analytical chemistry. Most recently, he made a significant contribution to metabolomics after seeing a hole in the set of tools available for data analysis and teaching himself to code to fill that hole. His new data processing pipeline is now published as open-source software [[github.com/cbroeckl/RAMClustR](https://github.com/cbroeckl/RAMClustR)] and has led to more accurate and efficient analysis of the signals obtained after a sample is run on a mass spectrometer.

"There is so much potential for mass spectrometry," he says. "There are so many actual results already, but the potential is still even more exciting."

Broeckling is an author on over 70 highly-cited peer-reviewed publications. As a graduate student, he won the 2001 President's Prize for Student Paper Competition at the National Meeting of the Entomological Society of America, and he is a member of the Computational Mass Spectrometry Task Group of the Metabolomics Society.

### What is your current position like?

My position is a little unique. I am not a professor; I am a research scientist in a core facility under the Office of the Vice President for Research at CSU. Our lab is designed to be a collaborative center of instrumentation and knowledge for all on campus who need access to instrumentation that they wouldn't be able to purchase on their own or expertise they do not have.

### What excites you most about your current research?

Our lab offers an opportunity to work with all kinds of people and on all kinds of questions, from metabolites in beer that predict flavor stability [Heuberger, A.L., *et al.*, *Food Chemistry* **2016**, *200*, 301-307] to dietary supplements that alter gut bacteria [Sheflin, A.M., *et al.*, *Molecular Nut. & Food Res.* **2017**, *61*, 1500905] in cancer survivors. We have a collection of instruments and figure out how to best use them to answer a particular research question, balancing it against budgets. It is a very creative process.

When I first started, our metabolomics service was running sample sets, detecting signals, and then handing a big massive excel sheet off to the researchers. I don't think a single one of the early projects was published because the biologists didn't know what to do with the information. I have no training in informatics, but I recognized what the field needed—that one of the biggest holes in metabolomics was processing—and have dedicated a lot of my research effort to learning and developing tools, which required learning and writing code. I have had a very supportive supervisor, Jessica Prenni, who recognizes that there are times when we need to balance short term needs, or 'I need to return this data,' with long term goals, or 'I need to make every data set better.'

The results have been very fruitful. We designed open-source software [Broeckling, C.D.; *et al.*, *Anal. Chem.*, **2014**, *86*, 6812–6817] that processes data to efficiently [Broeckling, C.D.; *et al.*, *Anal. Chem.*, **2016**, *88*, 9226–9234]



“ I have had many supportive supervisors that have given me opportunities past my job title – ”

Photo : Colorado State University

get more chemically meaningful data back to the researchers. In a core facility, this is important because it makes our job easier: we can return structures instead of lists of masses that are not interpretable to the standard biologist. The more that we annotate, the more likely the researchers get answers that are meaningful, relevant and reproducible.

**How did you start down the research path?**

My first forays into the hands-on analytical world used gas chromatography to look for trihalomethanes, or toxic compounds that form with drinking water chlorination, and to study how insects communicate chemically. I then got a Masters in Entomology, generating knowledge to support the development of a sampling method for biological controls used on a pest species of eastern hemlock. This was very fundamental work with a potential application because it is important to know if a population of biological control becomes established. We discovered a potential trapping tool using olfaction because we found that volatile cues [Broeckling, C.D.; Salmon, S.M., *Phytochemistry* **2003**, 62, 175–180] were used by the pest to find their food.

**How did you get into metabolomics?**

I was fortunate to be in the right place at the right time. I followed my wife to the Noble Foundation in Oklahoma and ended up getting a metabolomics job (at a time early in the life of metabolomics) with Lloyd Sumner for three years where I had my first real hands-on mass spectrometry experience. We developed software, and performed some studies characterizing cell culture metabolism [Broeckling, C.D.; *et al.*, *J. Exp. Botany* **2005**, 56 323–336] and looking for transcription

factors to improve drought tolerance [Zhang, J.Y.; *et al.*, *The Plant Journal* **2005**, 42, 689-707]. I continued to use metabolomics during my Ph.D. in Cellular and Molecular Biology where I looked at plant-plant competition and the role of phytochemicals in ecological interactions. One of my more highly cited papers looked at how the microbial community in the soil changes [Broeckling, C.D.; *et al.*, *App. & Env Microbiology* **2008**, 74, 738-744] with the application of compounds that the roots from different species of plants excrete to soil. Despite the long term consensus that the microbial community is limited by carbon, we showed that the microbial community responds to the composition of the carbon—what molecular form the carbon is in.

Metabolomics has been a great fit; I would have it no other way even though my career path was not the way most advice is given: ‘think where you want to get in 10 years, and get there.’ That is a great theory, but life intervenes. I have had many supportive supervisors that have given me opportunities past my job title – I am very fortunate for those experiences.

**Aside from running, what do you like to do when away from the office?**

We do a lot of hiking as a family, my wife and two daughters, and a fair amount of camping. I also love to read. There are so many perspectives in the written word, there is not enough time to read everything. I read science as well as literature. One of the more clever, creative, thought-provoking books that I have ever read is *Infinite Jest* by David Foster Wallace. Honestly, getting through it was a bit of a battle—it is massive—but every page was a treat and there has probably not been a book that I have not thought more about since finishing it.