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MOVING METABOLOMICS FROM THE BENCH TO THE BEDSIDE.

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Metabolites are sometimes called “the canaries of the genome”. Indeed, a single base change to a gene can lead to a 10,000X fold change in the concentration of a given metabolite. This sensitivity exists because metabolites represent the sum of all cellular and physiological activities encoded by the genome, the transcriptome and the proteome. This makes the measurement of metabolites (i.e. metabolomics) particularly appealing for clinical applications. Indeed, metabolite measurements have been used for more than 100 years to detect, diagnose or even predict disease. However, for metabolite measurements to be used in the clinic, they have to be measured by tools or technologies that are cheap, quantitative, fast and reliable. Unfortunately, most of the tools and technologies used in metabolomics today are not cheap, nor are they particularly quantitative, fast or reliable. In this presentation I will describe some of the work my laboratory is undertaking to make metabolomics more useful for clinical applications. In particular, I will describe some of the data resources and computational tools we have developed to facilitate both compound identification and biomarker selection. I will also describe some of the technologies and software we have created to make metabolomics much faster and far more quantitative. In doing so, I will also provide some examples of clinically useful and clinically validated biomarkers that we have discovered via metabolomics. Finally I will describe some novel technologies that we, and our collaborators, are developing to make metabolomic devices much cheaper, far more portable and potentially far more friendly for clinical applications.