Greg Gloor, PhD.

Dr. Gloor is a Professor in the Department of Biochemistry at the University of Western Ontario. He has used DNA sequencing as a major tool for most of his career, having sequenced (by hand) part of bacteriophage Mu duing his PhD work. His group was one of the first to use high throughput sequencing platforms for bacterial genome assembly, microbial ecology and meta-transcriptomics.

Members of Dr. Gloor’s group are early adopters of compositional data analysis (CoDa) techniques to the analysis of high-throughput sequencing data. He is a founding member of the Compositional Data Analysis Society. Dr. Gloor has written several guides on how to use CoDa to analyze 16S rRNA gene sequencing data and transcriptome data, and maintains the ALDEx2 Bioconductor R package that performs differential abundance analysis using a CoDa paradigm. Dr. Gloor is developing CoDaSeq, an R package that combines and adapts a number of tools used for CoDa in other domains to the sparse, high dimensional datasets that are generated by high throughput sequencing.

In addition, to computational analysis, Dr. Gloor’s group developed a general combinatorial barcoding for the Illumina sequencing platforms that is not dependent on sample diversity. The strategy has been used to sequence amplify 16S rRNA gene fragments and many other low diversity amplicons for sequence variant detection.