Metabolome Intro- might fit better after transcriptome section

The metabolome of a bacterial community can be assessed by variety techniques; the most widely used being nuclear magnetic resonance (NMR), gas chromatography mass spectrometry (GC-MS), and liquid chromatography mass spectrometry (LC-MS). NMR and GC-MS are attractive methods due to the relative ease of compound identification, however the classes of molecules detected by these methods are limited in comparison to LC-MS. Conversely, while LC-MS is capable of detecting the widest range of molecules with the highest sensitively, metabolite identification is extremely challenging. In contrast to sequence-based methods, metabolites may be of bacterial or host origin or both, and it can be difficult, if not impossible to distinguish the source of many metabolites. Additionally, metabolomic data is not compositional in nature, but is a measure of absolute abundance; that is a change in the abundance of one metabolite will not affect that of another. As the absolute abundance of the microbiota cannot be measured by 16S sequencing, metagenomic or metatranscriptomics, there may be a considerable amount of disconnect between sequence and metabolomic data, which has only just begun to be addressed.