

**Title: Development of a protocol for the extraction of genomic material from fecal matter for metagenome and virome sequencing**

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With the advent of increasingly more accurate and reliable sequencing methods, the requirement for extraction methods yielding large volumes of high-quality genomic material has become progressively more significant. While the analysis of genomic material through bioinformatics can offer some methods of “cleaning” and standardizing data, it is essential that the “wet lab” aspects of data produce abundant amounts of high-quality genetic material. Therefore, the purpose of this project is to develop an optimized method of DNA extraction for fecal material sequencing in microbiome and virome investigations. The samples used for the optimized protocol are infant fecal samples collected and stored at -80°C for the purpose of performing metagenome and virome sequencing. In the course of our optimization, a number of methods have been implemented and compared from various published methodologies, papers, and industry standard kits. Finally, based on results from each method, a new methodology have been developed, resulting in the highest yield of extracted DNA, which will be used as a reference procedure for future studies aimed at characterizing the diversity of bacteria, bacteriophages and mobile genetic elements in the infant gut microbiome.