Whole genome sequencing (WGS) allows for more rapid, cost effective, accurate and efficient pathogen identification in a variety of environments. Next generation sequencing (NGS) allows for this to happen in a massively parallel manner and as such it is becoming more heavily relied upon in prediction of new trends, identification of food contaminants, microbiology studies and other relevant fields. To allow for precise, rapid analysis of the NGS data, the High-Performance Integrated Virtual Environment (HIVE) was developed and implemented at the FDA through a partnership with George Washington University. Having access to such a platform has allowed the development of tools that facilitate identification of metagenomic content.

NGS facilitates global outbreak investigations thus, protecting food supply and public health. The proposed pipeline allows for pathogen identification through specimen sampling and subsequently links to external resources to provide further information. This pipeline, implemented in HIVE, leverages the internally developed tool: CensuScope which allows an investigator to take a ‘sneak peak’ into the population distribution and estimate taxonomic composition and subsequently link out to other relevant sources. This allows more rapid accurate identification of food contaminants thereby ensuring greater food safety.

Acknowledgements:
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