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Cataloguing Human Gut Microbes in Hosts Across the Tree of Life

The human gut microbiome is the collection of bacteria, fungi, and archaea that are present in the gastrointestinal system. In 2005, the National Institutes of Health initiated a program called the Human Microbiome Project, which aims to catalog multiple microbial communities on the human body. Our study is being conducted to expand on the research already gathered by the HMP, and find all other animal hosts of the known human gut microbes. The list of all microbes in the human gut acted as the starting point of the research. A search was then conducted using GenBank, an open access database of nucleotides and proteins, to gather the 16S sequences of all related microbes, their isolation sources, and their hosts. Using Ruby computer scripting language, a tool was written that searches for these data in several biological ontologies (a structured list of terms for defining a domain). The results of these ontology searches were used to cross-reference the data found in the original GenBank search results, in order to create a list of “trusted” isolation sources and hosts. This new list of host animals and isolation sources will be analyzed and reorganized to find patterns and similarities. The intention is that medically relevant patterns will be found that may help determine appropriate animal models for medical testing.