Reasonable names and reasonable terms for *Bacteria* and *Archaea*.

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One of the principle goals of metagenomics studies is to better understand the complex relationships that exist between microbial communities and the environments in which they are found. A complicating factor is that each exerts an influence on the other in significant but poorly understood ways that are often in a state of flux. To gain useful information from such studies, one must understand not only the community composition, but also the metabolic capabilities of the community members under the observed conditions. High throughput sequencing, coupled with various ordination and phylogenetic methods provides a way of uncovering interesting patterns in the data, but extraction of knowledge from the data requires integration with other databases and the literature, both of which are typically accessed based on inferred identity of community members. For such inference to be meaningful, one must have a fundamental understanding of both the nomenclature and the terminologies that are used to describe unambiguously the species of interest, preferably in a manner that is amenable to automation. This presentation will focus on the development of a generalized semantic model that has been developed to disambiguate biological nomenclature and to provide both humans and machines with direct access to the correct information about all of the validly named prokaryotic taxa. Current research efforts on developing an ontology of microbial phenotypes, which supports machine reasoning, will also be discussed.