
Methodology and Ontology in the Human Microbiome Project

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Abstract

Session: Conceptual Challenges in the Human Microbiome Project (John Huss, Mark Borrello, Mark Sagoff (organizer); Lindley Darden, Chair; Chris Diteresi, commentator). The term "human microbiome" has been interpreted in the biomedical literature in both ecological and molecular terms. The ecological view suggests that we think of the microbiome as a microbial biome. The molecular view suggests that we think of the microbiome as the genome of our microbes, easily assimilated to the list of other "omes" and in some sense continuous with our nuclear genome, mitochondrial genome, and virome as yet another component in an apparently incomplete and emerging concept of "the" human genome. Moreover, one can view metagenomics as a set of tools either for identifying genetically the ecological actors in the human microbial ecosystem, or for arriving at a "metagenome" that black-boxes the identities of phylotypes for the sake of capturing the overall functional capacities of the microbial "community." Restricting myself to the molecular perspective, I shall examine the ontological categories that emerge from the Human Microbiome Project, for example, metagenome, "core" microbiome, and enterotype. I shall argue that these categories are artifacts of the biotechnological, conceptual, and statistical tools of investigation. The result is that the tools are supplying-not uncovering-the biological ontology, and that these methodological artifacts are on a path toward reification as units of nature.

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