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Strain-Level Profiling of the Hidden Diversity of the Human Microbiome

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Shotgun metagenomics has uncovered a substantial amount of diversity in the human microbiome, but a large fraction of the sequences in a metagenome remains uncharacterized. In my talk I will show how the combination of multiple reference-based and assembly-based computational approaches applied on several thousand of diverse human metagenomes led to the discovery of hundreds of previously unknown species and strain-level variants of known species. I will also discuss what are the challenges in performing comparative microbial genomics on the resulting vast catalog of human-associated microbial strains.