Abstract: The opportunities offered by next-generation sequencing have opened up the study of non-model organisms and complex microbial communities, but primary data analysis of large sequencing data sets remains a challenge. I will discuss our approaches to de novo assembly of non-model transcriptomes and metagenomes, which are freely available and increasingly widely used. I will also talk about the next set of challenges that I see ahead of us in the sequence-focused areas of basic biology.

Biography: Titus Brown received his BA in Math from Reed College in 1997, and his PhD in Developmental Biology at Caltech in 2006. He has worked in digital evolution, climate measurements, molecular and evolutionary developmental biology, and both regulatory genomics and transcriptomics. His current focus is on using novel computer science data structures and algorithms to explore big sequencing data sets from metagenomics and transcriptomics.