



Highly Accurate Consensus Sequence and Genome Assembly using PacBio® RS Sequence Data



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ABSTRACT

Pacific Biosciences' single molecule real-time (SMRT®) DNA sequencing platform provides extremely long read lengths and a rich profile of DNA template modifications, enabling advances in de novo genome assembly and epigenetic studies. In this talk I will discuss some of the basic mathematical models behind genome assembly, and then give an overview of our hierarchical genome assembly procedure (HGAP). After a brief overview of the properties of PacBio sequence data, I will describe our algorithm, Quiver, for highly accurate consensus sequence determination, which can generate finished assemblies with accuracies exceeding 99.999%.

Host: Van Savage, Ph.D.

To receive e-mail seminar notices, contact David Tomita (dtomita@biomath.ucla.edu)

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