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Sivan Leviyang* (sr286@georgetown.edu) and **Igor Griva**. *Haplotype Reconstruction Using Next Generation Sequencing Data with Applications to Acute HIV Infection*.

In recent years, HIV studies have increasingly used next generation sequencing (NGS) technologies to characterize viral diversity and evolution. NGS datasets contain a large number of sequence reads, allowing for a more precise estimation of viral population genetics than previously possible, but NGS sequence reads are very short, creating challenges in correlating genetic information across different sites in the viral genome. In this talk, we will give an outline of NGS methods as applied to HIV and explain the mathematical challenges, in particular, of using NGS datasets to understand acute HIV infection, a period of time composing the first few months of infection. We will then present a novel approach to analyzing NGS data and compare the approach to existing methods. (Received September 05, 2016)