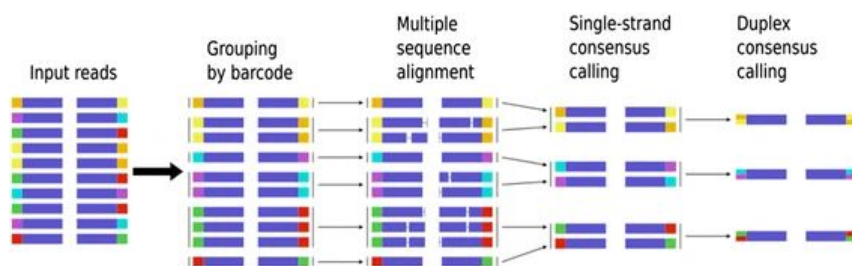


Date: Tuesday November 10, 2020

Time: Noon EST / 9am PST

Du Novo Sequencing can achieve <1% variant detection, which improves on other Duplex Sequencing analysis tools by removing reliance on a reference sequence, preserving a higher proportion of the input reads, and being available for Galaxy. We demonstrate the application of this approach by validating rare variants in the human mitochondrial genome.

Dr. Barbara Arbeithuber (Johannes Kepler University Linz, Center for Medical Research) and **Dr. Nick Stoler** (Penn State University) will present the method and applications in this webinar.



The Du Novo approach. First, reads tagged with identical barcodes are grouped into strand-specific families. Reads within each family are aligned and single-stranded consensus sequences (SSCSs) are generated. Finally, the SSCSs are reduced into duplex consensus sequences (DCSs).

<https://doi.org/10.1186/s13059-016-1039-4>

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