

**Date:** Tuesday, January 26, 2021

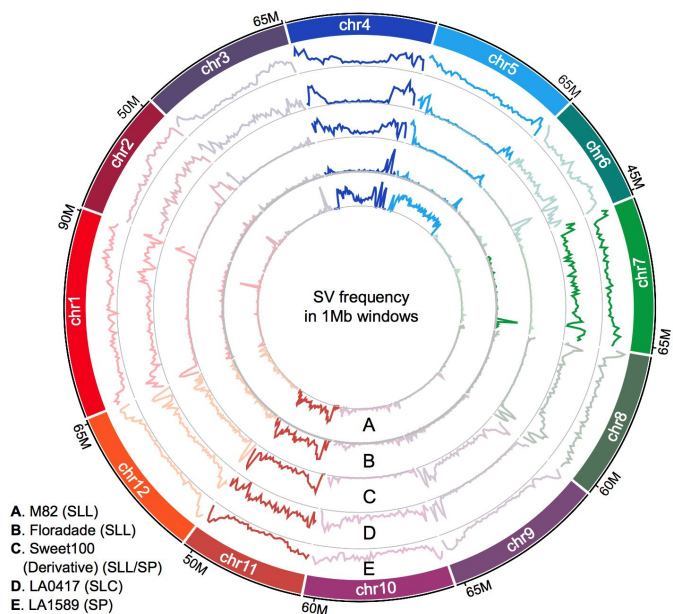
**Time:** Noon EST / 9am PST

Long-read sequencing allows for sensitive and accurate detection of structural variants (SV) which are critical to research in genomic applications such as cancer genomics, genetic disease, and crop domestication and improvement.

**Dr. Nathan Roach** (GalaxyWorks) will demonstrate analysis methods of long read data using the Oxford Nanopore (ONT) tool suite in Galaxy Pro. **Mr. Michael Alonge** (Johns Hopkins University) will highlight the application of these methods.

By sequencing 100 diverse tomato accessions with long-reads, Mr. Alonge's research has established the largest comprehensive database of SVs in any crop. He will share how this database revealed complex patterns of breeding introgression underscoring the necessity of pan-genomics for quantitative genetics research in plants.

<https://www.sciencedirect.com/science/article/abs/pii/S0092867420306164>



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