



Moving beyond a single reference genome: GenoMAGIC™, a novel solution to describe and manage genomic variation

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NGS technologies have opened the door to multiple genome analyses and an increased understanding of the variations present in populations. To date, most of the germplasm analyses have relied on the comparison of sequence reads to one reference genome assembly, limiting our understanding of genomic variation.

NRGene has developed novel analytics and approaches to efficiently de-novo assemble genomes and describe the relevant variation across germplasm using a pan-genome approach.

Using this approach, we are able to perform critical analyses including, haplotype imputation from sequence based genotyping and marker selection for array design to aid in molecular breeding and gene discovery.

Wednesday, Nov. 8th, 2:00-4:00 PM
The Stephens Room
3503 Thomas Hall

*Refreshments will be provided

Please RSVP to David Neuman - ndavid@nrgene.com