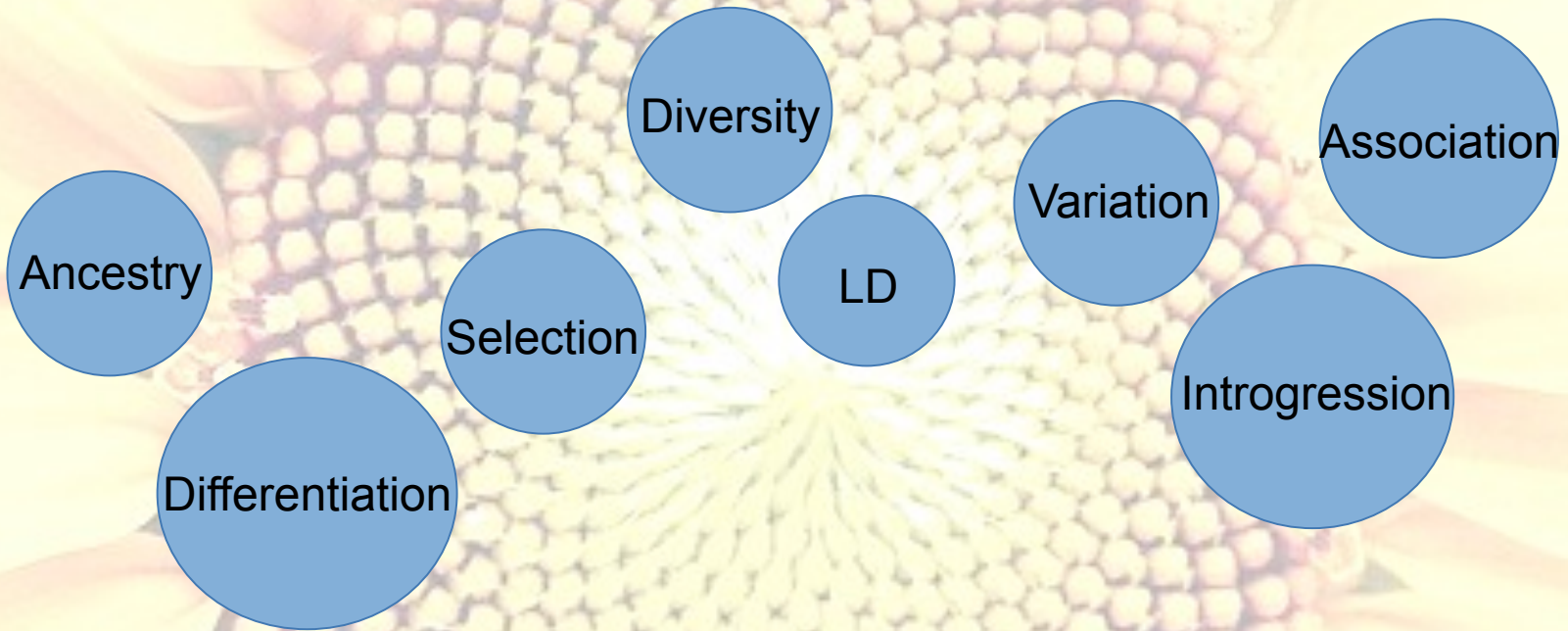


**Development of a high-throughput
analytical pipeline to explore sunflower
genomics**

Sariel Hübner

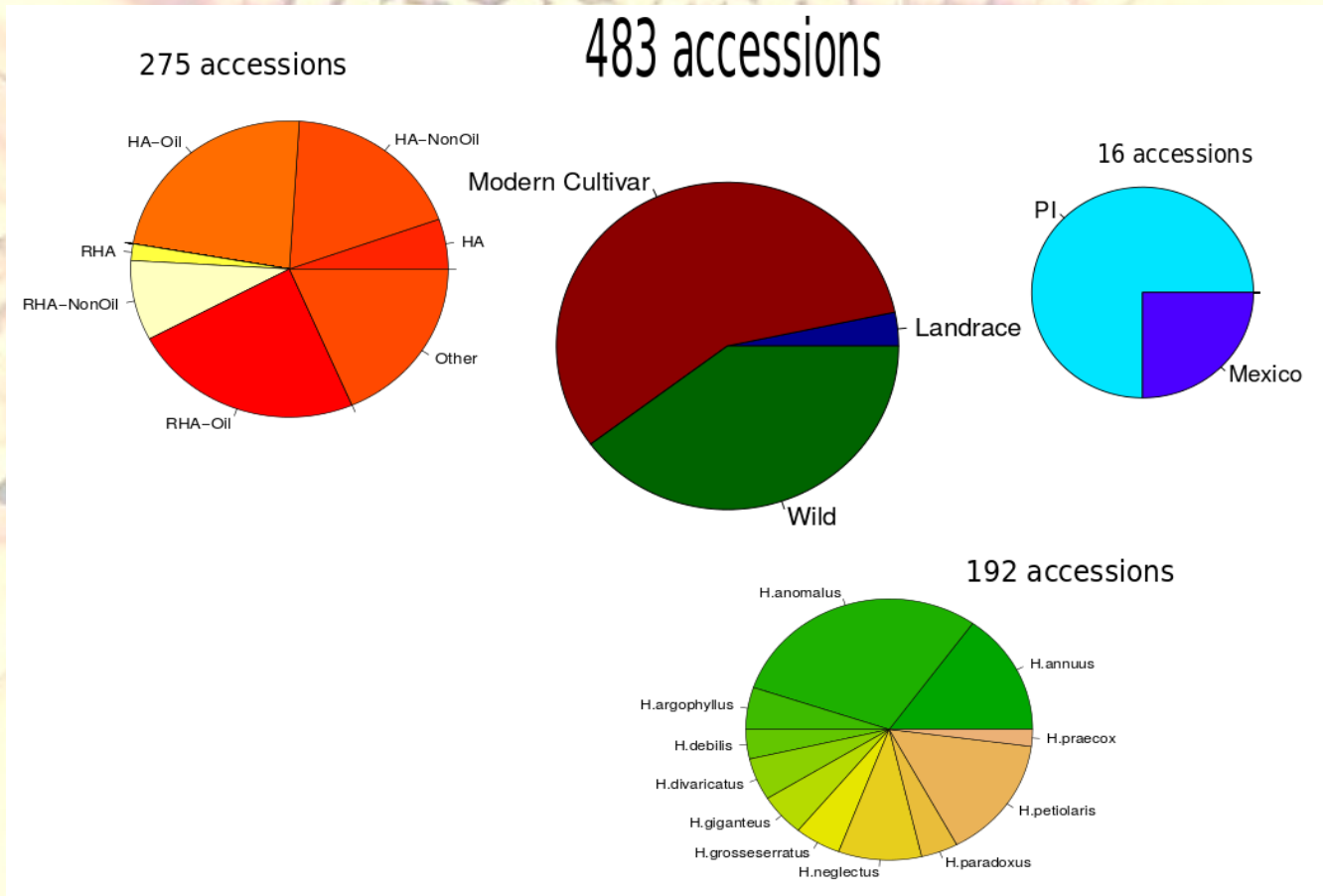
University of British Columbia

Exploring sunflower genomics



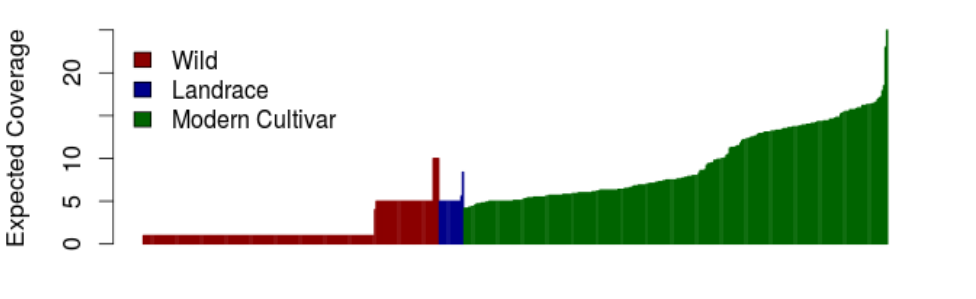
Reference Genome

Resequencing sunflower accessions



Sequence coverage across accessions

Σ



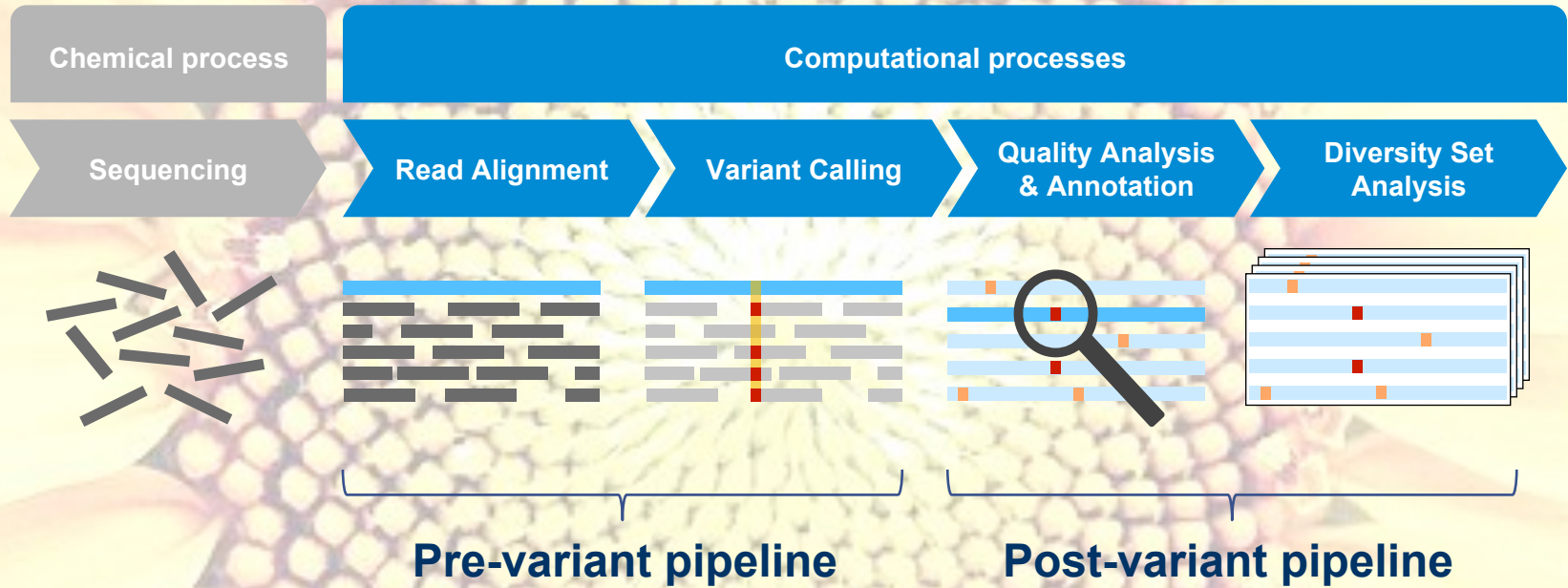
$\approx 10Tb$



SAP HANA® Solution
Redefines In-memory Computing

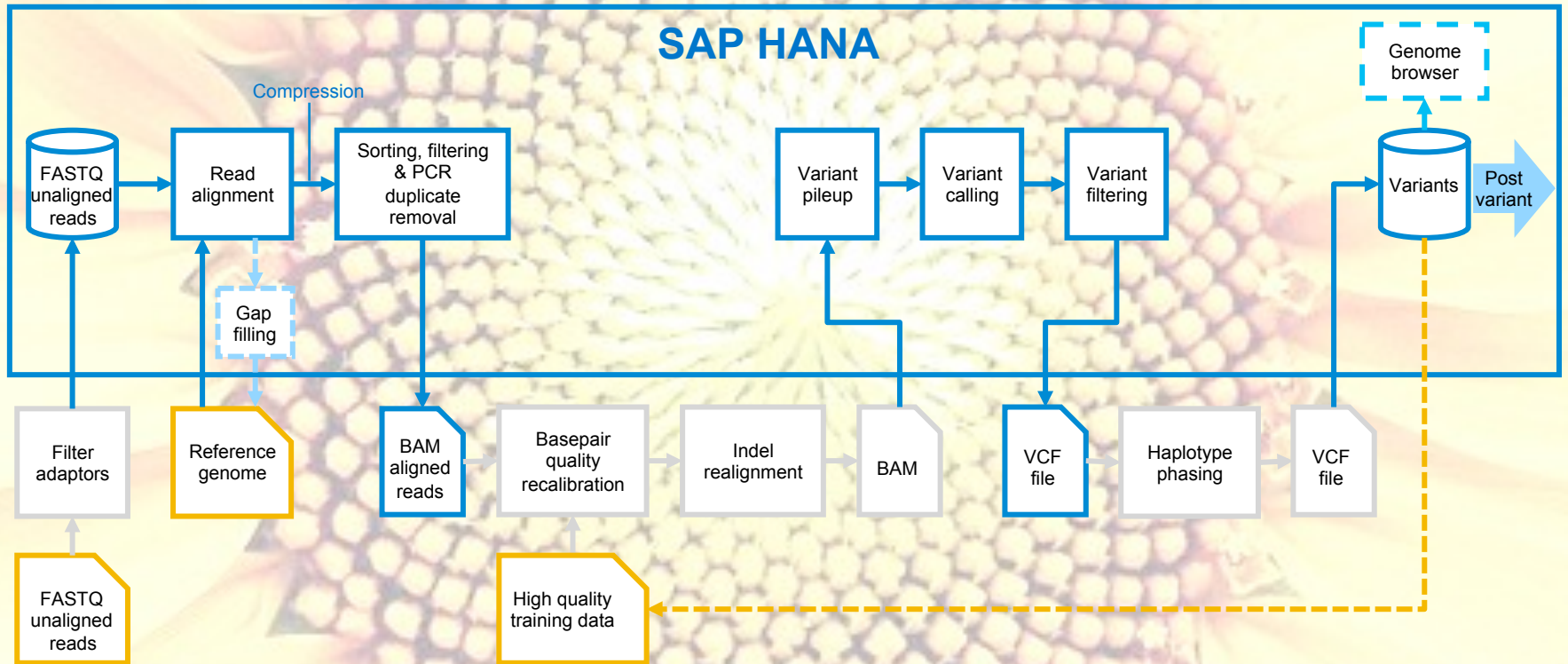


Overview genomics analysis process

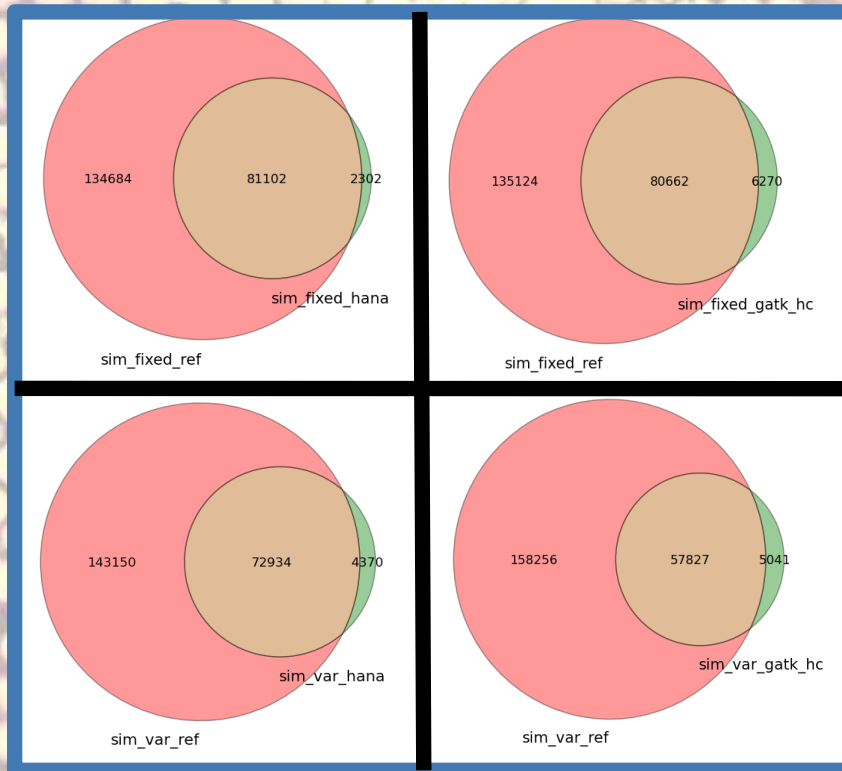


Pre-variant pipeline

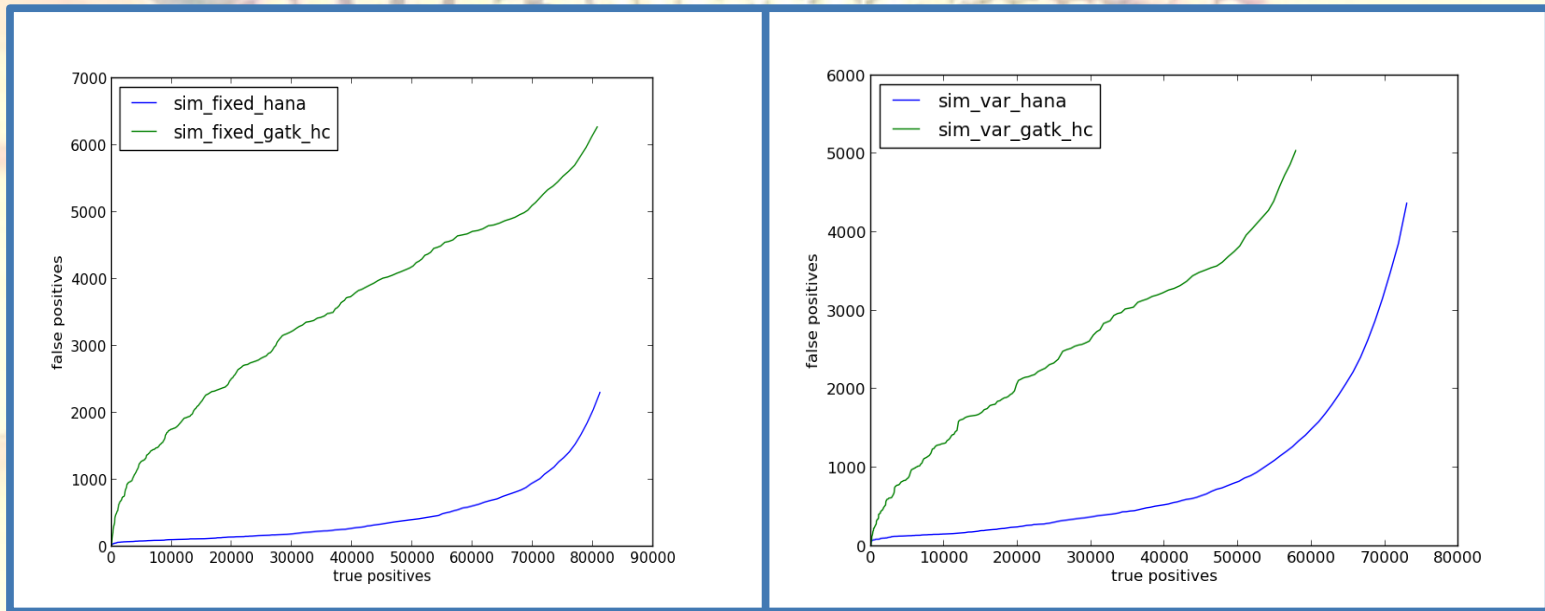
— Existing SAP Assets — UBC Assets — 3rd party assets - - - Not part of regular pipeline



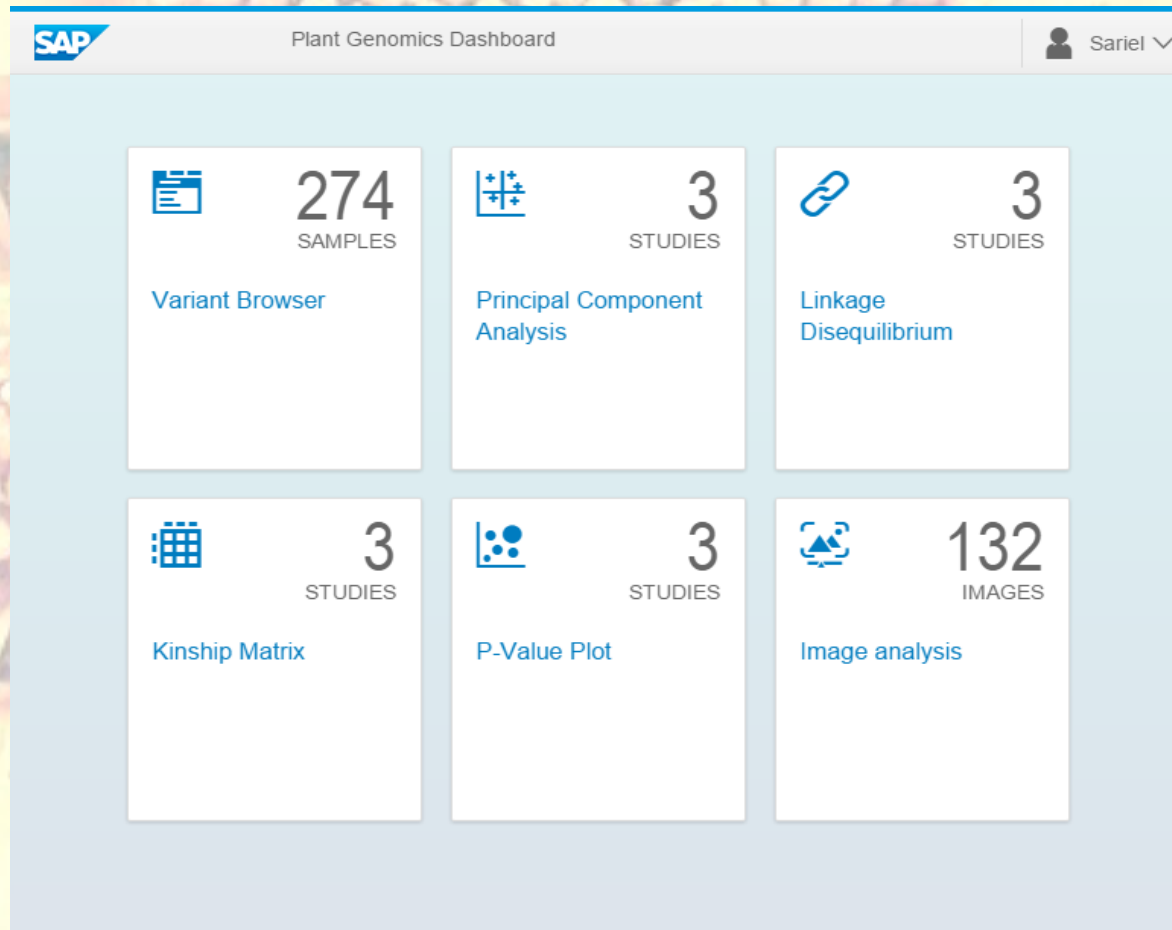
Benchmarking: SAP vs. GATK



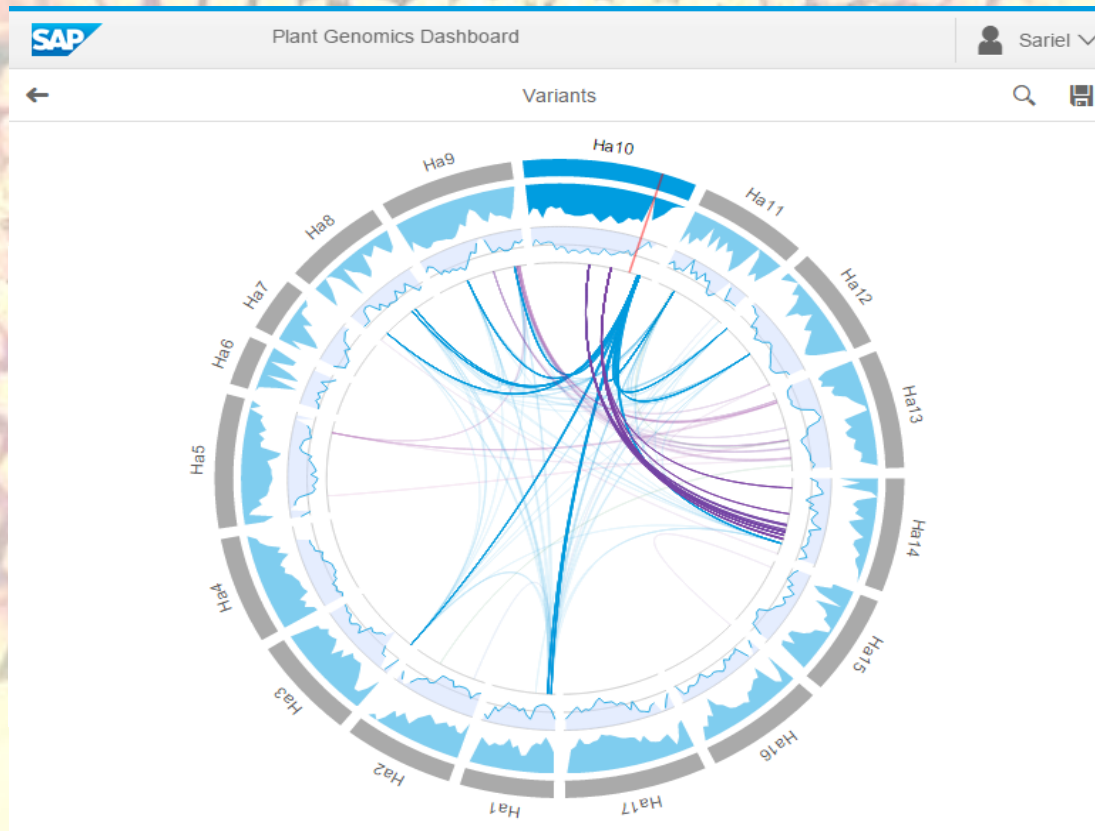
Benchmarking: SAP vs. GATK



Plant genomics application



High quality SNPs: 72,305,390
After filtering (MAF = 10%; NA<30%): 4,129,575



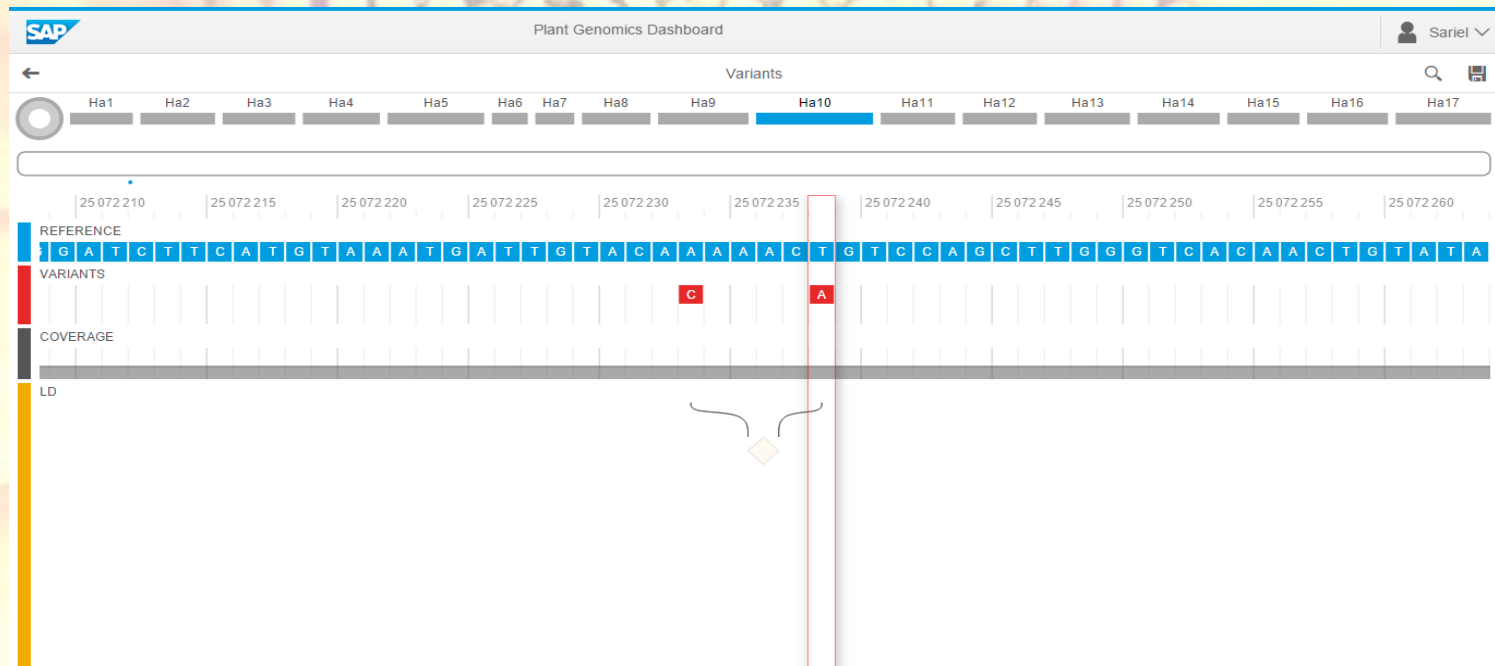
Chromosome Ha10



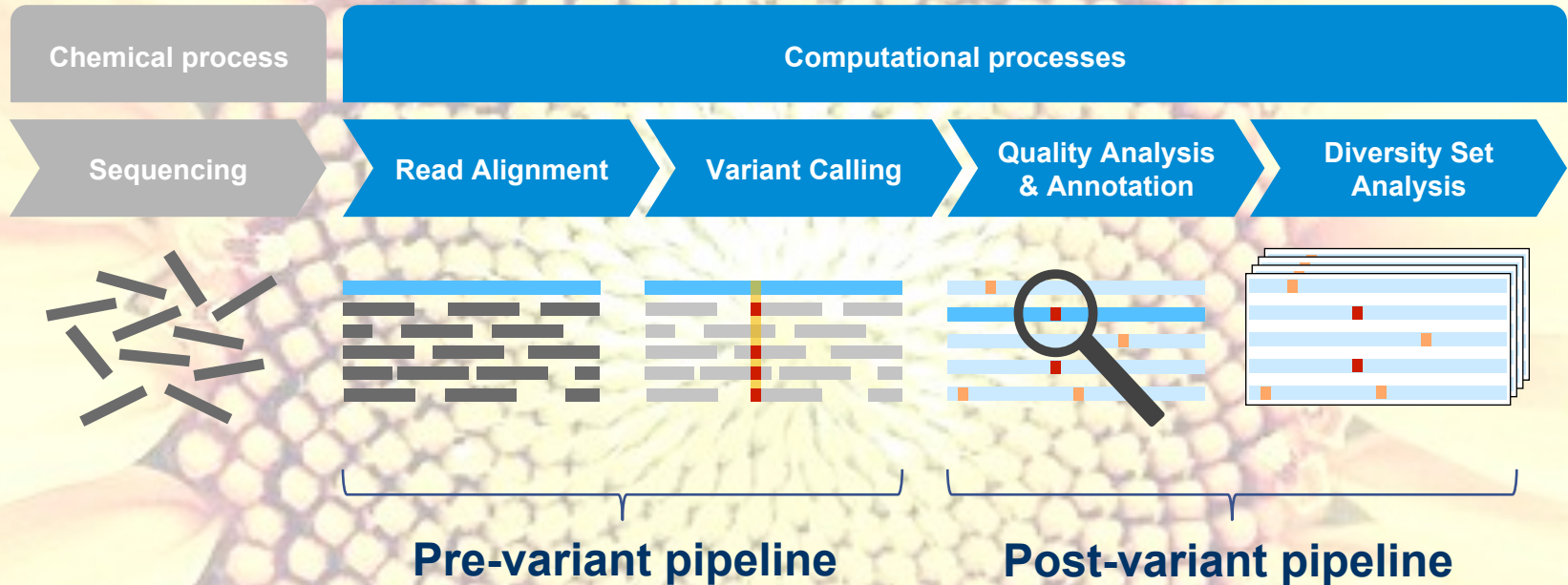
Chromosome Ha10



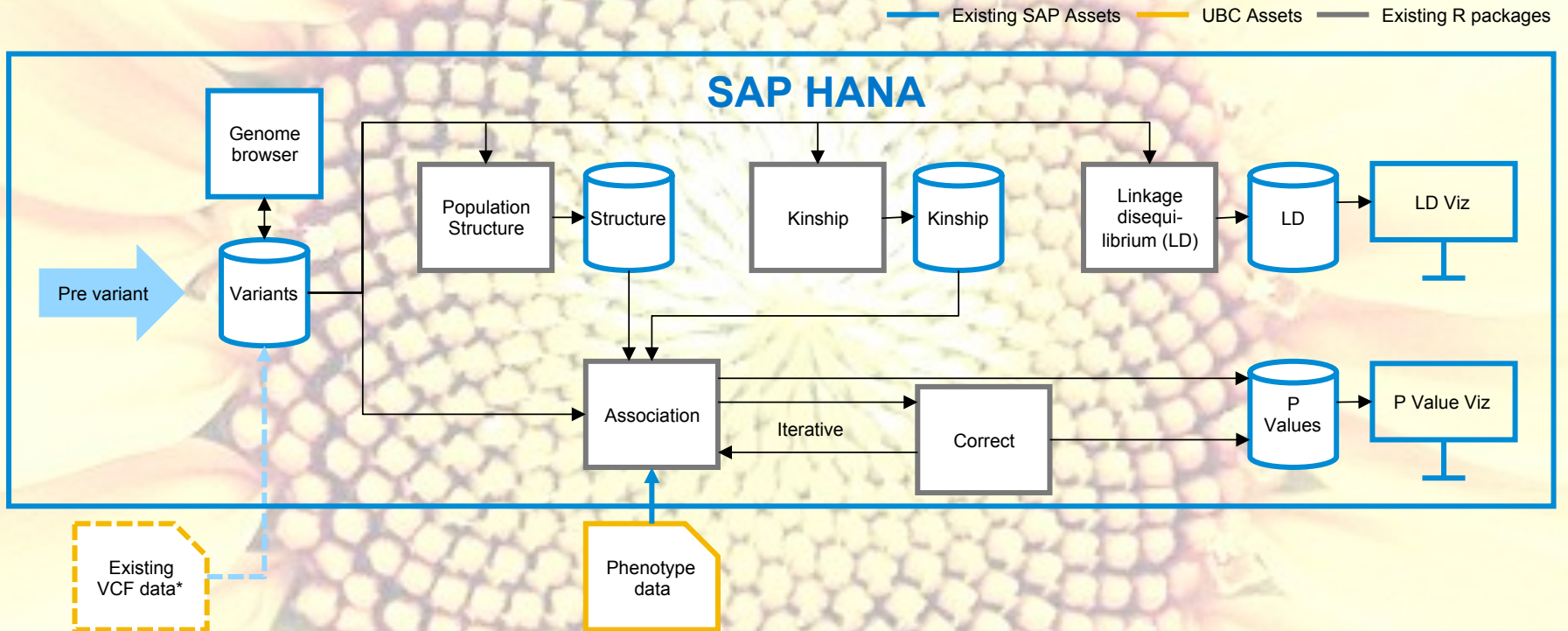
Chromosome Ha10



Overview genomics analysis process



Post-variant pipeline



Downey mildew resistance in sunflower

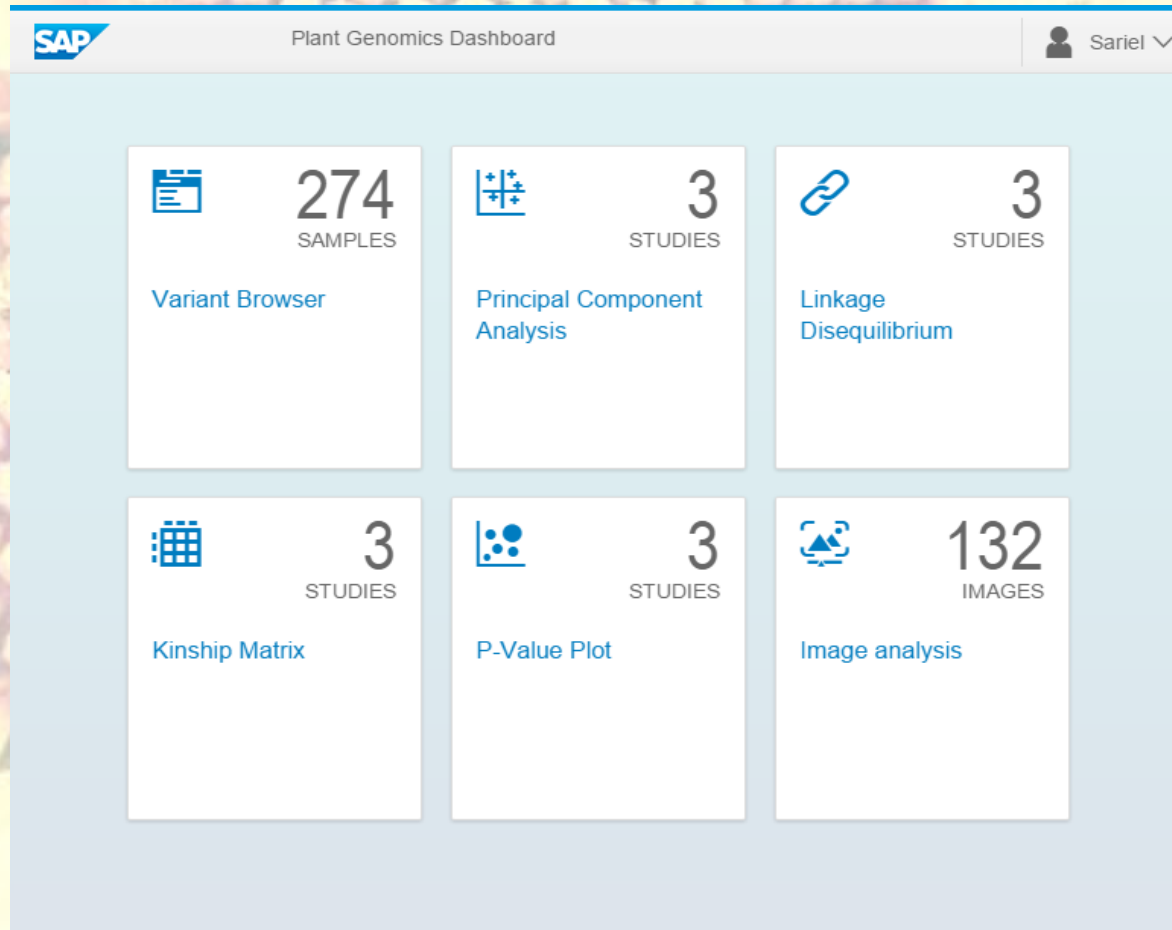
Natalia Bercovich



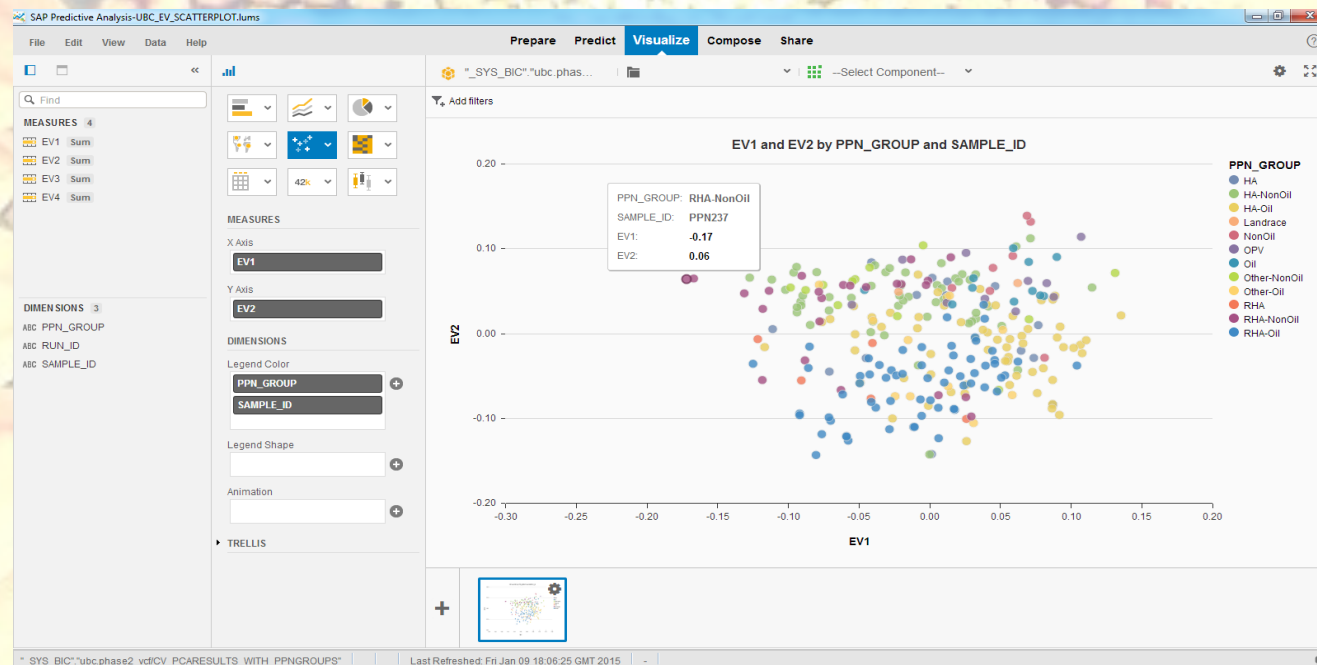
- Presence of spores in cotyledons
- Presence of spores in leaves
- Spores density in cotyledons

$$\left(\prod_{i=1}^n t_i \right)^{\frac{1}{n}} = \sqrt[3]{pC \times dC \times pL}$$

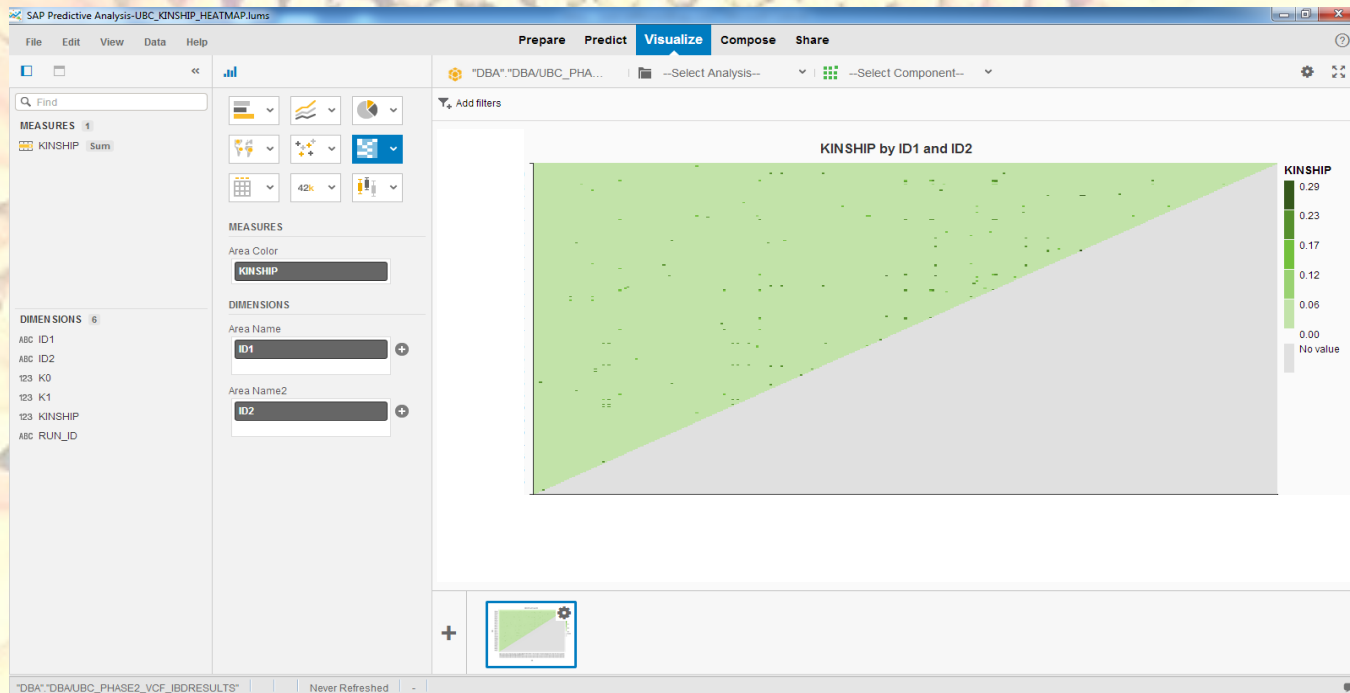
Plant genomics application



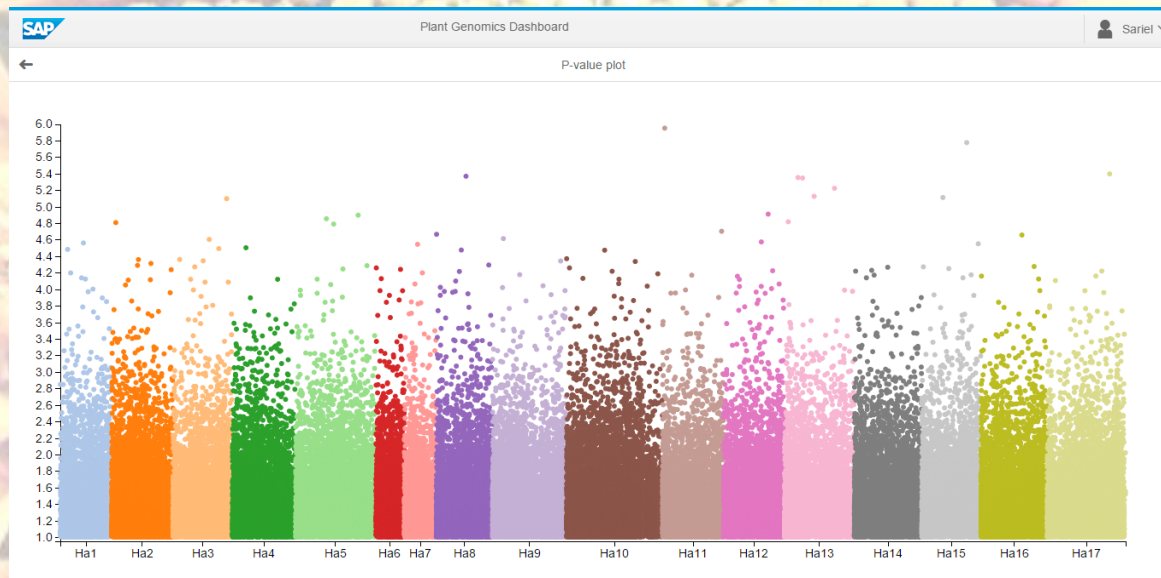
Population structure based on 1.5M SNPs



Kinship matrix based on 1.5M SNPs

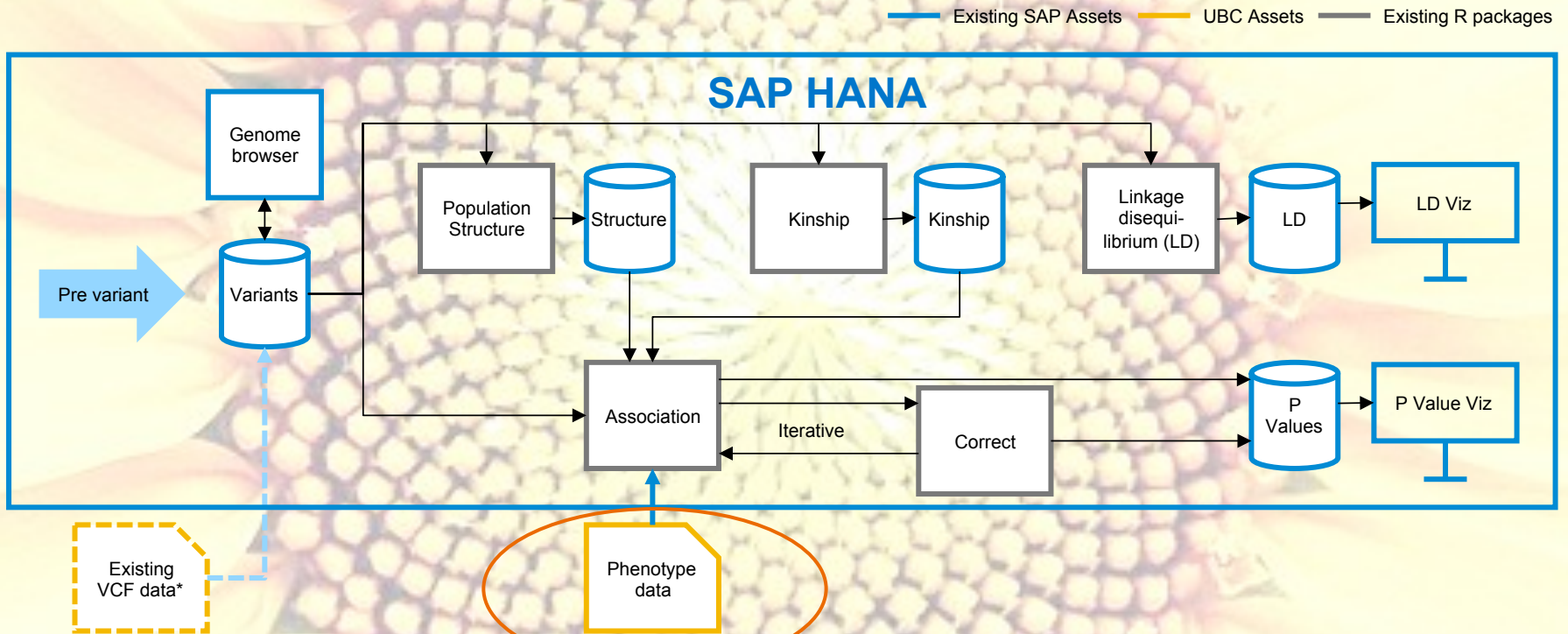


Association mapping of Downey mildew resistance in sunflower



Filtering at any stringency using Bonferroni, BH-FDR, SimpleM

Post-variant pipeline

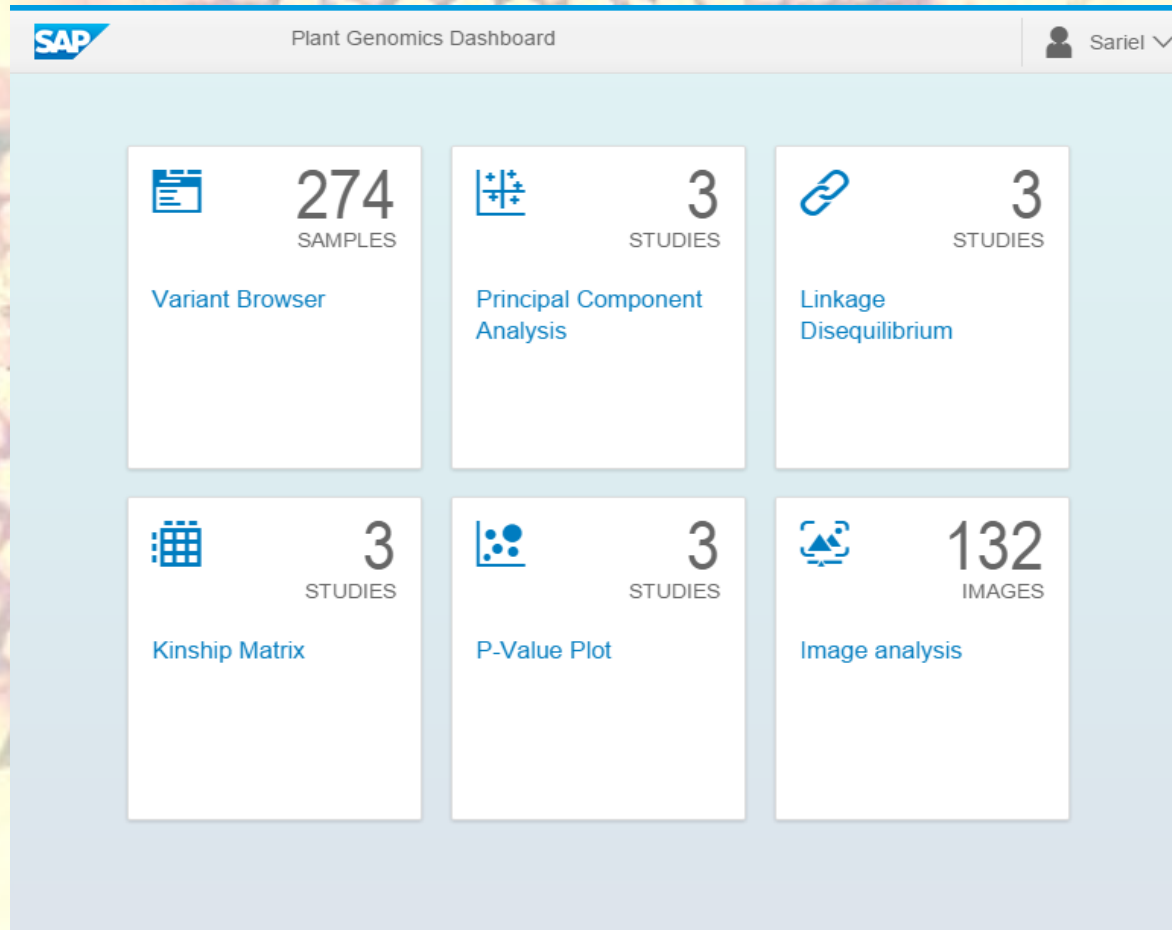


Jerusalem artichoke variation

Dan Bock and Michael Kantar



Plant genomics application



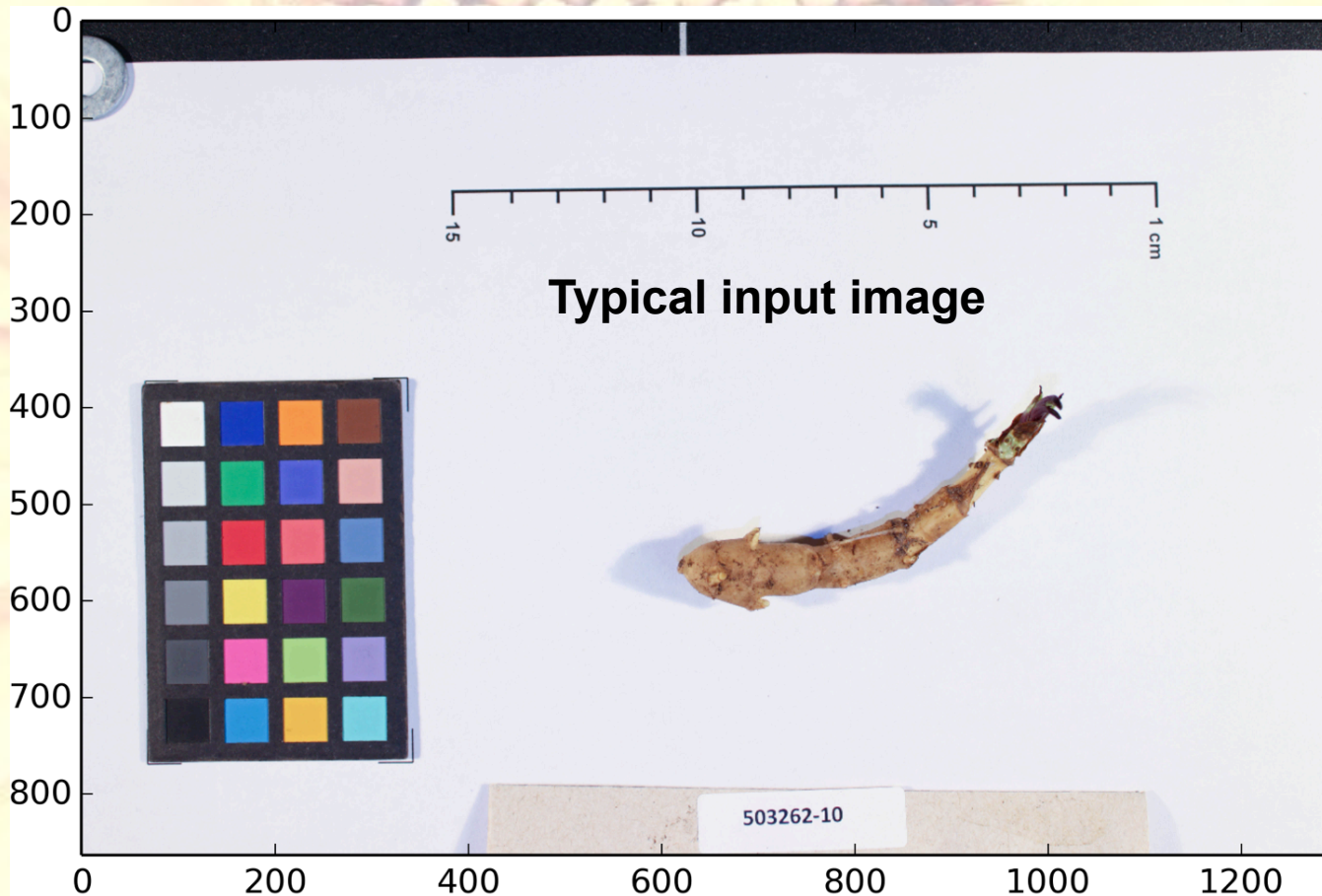
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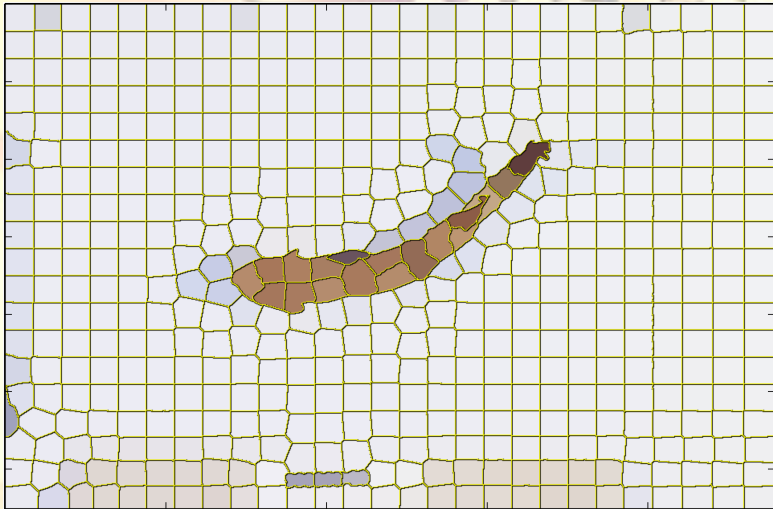
Lab Preview

Phenotype analysis for plant genomics

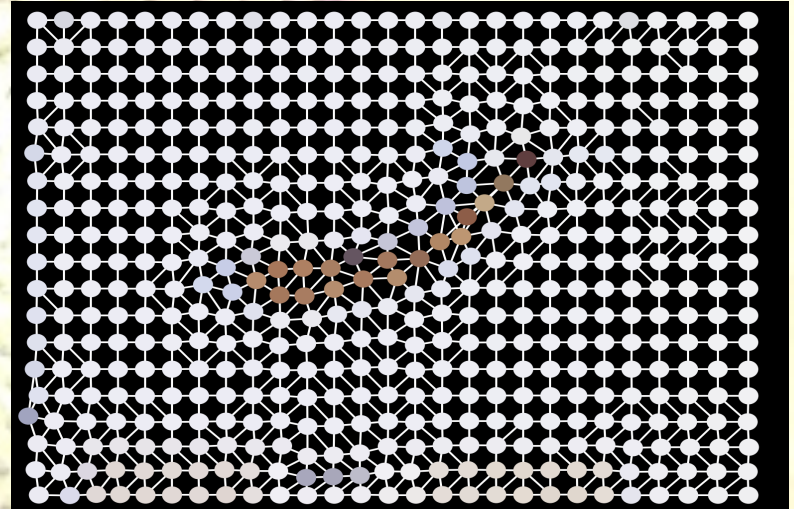


Lab Preview

Image processing algorithms



Superpixel pre-segmentation for data reduction



Graph-based representation of superpixels for segmentation by graph clustering

Lab Preview

Image processing algorithms


Extraction of most representative colors by color space clustering













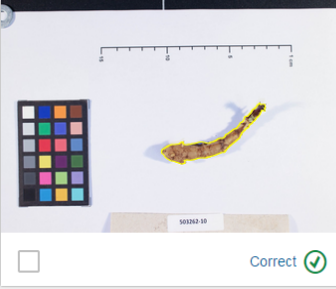
Lab Preview

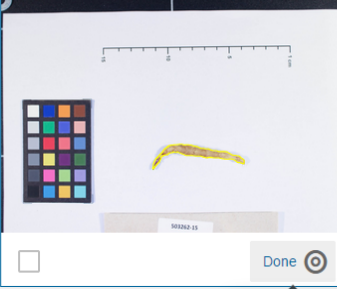
Image processing algorithms

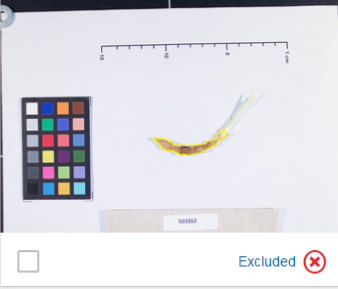
Accession 503262 - 503279
Jerusalem Artichoke (Helianthus Tuberosus)

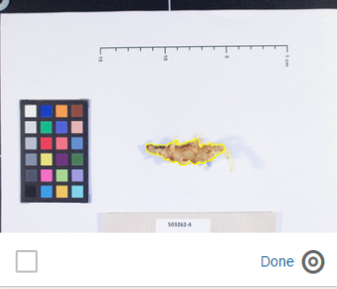
Image Analyzer 

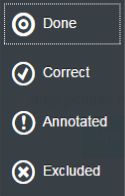
         


 Correct ✓


 Done 🎯


 Excluded ✖

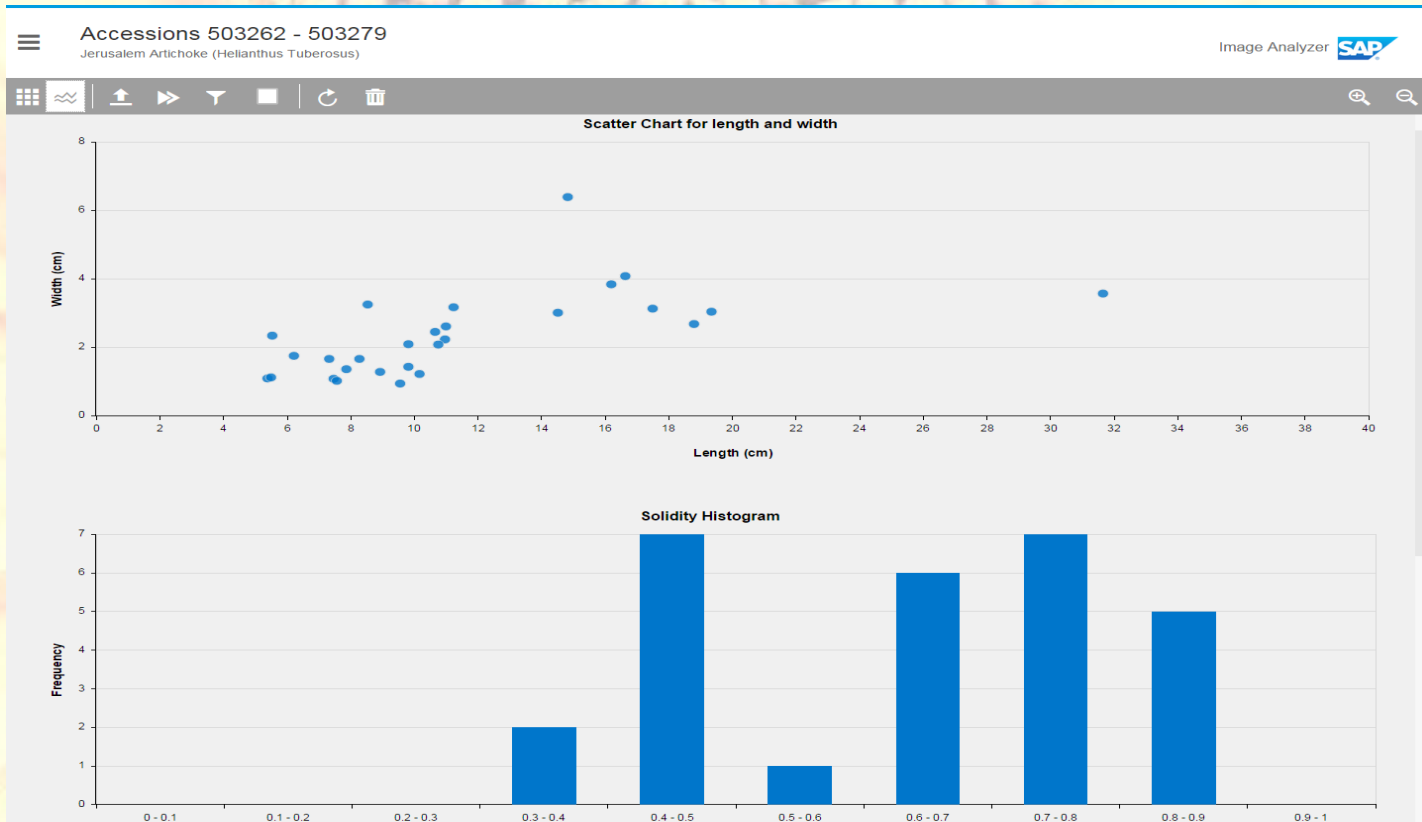

 Done 🎯



here or press
ad

Lab Preview

Image processing algorithms



Lab Preview

What's next?

- **Finish alignments (2-3 weeks)**
- **Process alignments (2-3 weeks)**
- **Variant calling (10-14 days)**
- **Phasing, imputation and correction**
- **Association mapping (meta-analysis)**
- **Structural and copy number variation**
- **Diversity, differentiation, selection**



Thanks!

Emanuel Ziegler

Loren Rieseberg

Mark Heffernan

Christian Bock

Greg Baute

Timo Kubach

Natalia Bercovich

Markus Noga

Dan Bock

Michael Kantar

Thomas Holst

Marco Todesco

David Blumenthal-Barby

Jenifer Mandel