

Please RSVP here

Genotyping Lunch and Learn

UF ICBR Gene Expression and Genotyping Core

December 1st, 12:00 pm-1:00 pm, CGRC 451

Array-based genotyping provides high-quality genotype data cost-effectively across large sample sets. The UF ICBR Gene Expression and Genotyping Core uses the Applied Biosystems Axiom workflow, automated liquid handling, and the GeneTitan Instrument to give UF investigators local access to array-based genotyping.

TOPICS

- Axiom workflow, sample requirements, throughput, and turnaround
- Catalog arrays for plant, animal, and human applications
- Custom array design for species or marker sets not covered by existing content
- Axiom Analysis Suite and ICBR Bioinformatics support for downstream analysis
- Study planning and grant proposal considerations

WHO SHOULD ATTEND

Principal investigators, postdocs, graduate students, and lab staff working in GWAS, marker-assisted selection, population genetics, breeding, pharmacogenomics, cancer genomics, or other studies that need reliable genotypes across many samples.

Q&A follows

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