

The 17th Webinar for Quantitative Genetics Tools for Mapping Trait Variation to Mechanisms, Therapeutics, and Interventions

Identifying sample mix-ups in eQTL data

Friday, June 11th, 2021
10am PDT/ 11am MDT/ 12pm CDT/ 1pm EDT

Presented by:

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There is no fee associated with this webinar, but users are asked to register to receive the Zoom link and password.

Registration: http://bit.ly/osga_2021-06-11



Goals of this webinar:

Sample mix-ups interfere with our ability to detect genotype-phenotype associations. However, the presence of numerous eQTL with strong effects provides the opportunity to not just identify sample mix-ups, but also to correct them.

- To illustrate methods for identifying sample duplicates and errors in sex annotations
- To illustrate methods for identifying sample mix-ups in DNA and RNA samples from experimental cross data

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