Genetic Data Analysis in Tree Breeding Workshop (May 16-20, 2011)

Organized by
Cooperative Tree Improvement Program
North Carolina State University, Raleigh, USA

Instructors and their specialties
Dr. Fikret Isik, Quantitative genetics, tree breeding
Dr. Ross Whetten, Molecular genetics, tree breeding
Dr. Christian Maltecca, Quantitative genetics, animal breeding

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Conifer Translational Genomics Network (CTGN)

Workshop Outline

We will cover analysis of genetic data (phenotypic data as well as DNA markers) in tree breeding. The workshop will be taught at an intermediate level. The major topics will include: 1) BLUP of breeding values, 2) Spatial analysis of progeny tests, 3) Pedigree construction using markers, 4) Genome-wide selection methods using DNA markers. We plan to use ASReml, SAS or R, CERVUS, and GS3 for analyzing data. Familiarity with CERVUS and GS3 is not required, but some familiarity with ASReml syntax will be expected. The participants are expected to have some understanding of mixed models.

Location: North Carolina State University, Raleigh, North Carolina, USA

The tentative outline of the course is as follows:
May 16: Some theory of mixed models, ASReml basics, and options
May 17: BLUP of breeding values, provenance-progeny data, half-sibs, full-sibs, clones
May 18: Spatial analysis, and prediction of breeding values
May 19: Construction of pedigree from markers and G-BLUP
May 20: Marker-trait associations and genome-wide selection methods

Workshop registration Cost: $500 (our best estimate)
We plan to have two lecture-exercise cycles in the morning and two in the afternoon. Each cycle will be a 30-minute lecture and 60-minute exercise. You may bring your own data to work on. Number of participants will be limited to 20. CERVUS and GS3 are freely available. ASReml can be downloaded and used for one month free of charge.

See the website for updates and registration:
http://www.treeimprovement.org/public/events/genetic-data-analysis-tree-breeding-workshop/genetic-data-analysis-tree-breeding