

# **PRACTICAL DATA ANALYSIS TOOLS FOR TREE BREEDERS**

## **OBJECTIVES OF THE COURSE**

The course will enable participants to analyse data that is typically encountered in a tree improvement program. The course will cover a wide array of topics including (but not limited to) elementary trial design, Analysis of Variance, heritability estimates, genetic correlations, repeatabilities, selection using BL(U)P indices, genetic gains prediction as well as interpretation of results.

Course participants will gain both the theoretical background and practical exposure to data analysis. There will be a strong emphasis on practical analysis of field data. The course will not go into great theoretical depth and will focus on simple, practical models. Different situations will be covered including progeny and provenance trials, pure species and hybrids, families and clones.

Participants are encouraged to bring their own data for analysis. A workshop will be held on the last day where participants can discuss and analyse their own data.

Participants will receive a manual in English for future reference.

## **WHO SHOULD ATTEND?**

All tree breeders/forest geneticists who want to acquire or improve their skills in basic tree improvement data analysis. Participants should have a working knowledge of genetics and mathematics/statistics.

The course will be presented in English.

## **COURSE CONTENT**

- Elementary trial design  
Issues such as optimal plot size, choice of trial design (e.g. for provenance trials vs. progeny trials) and randomization will be discussed. Focus will be on the most basic designs.
- Data capture and data editing. Various practical editing methods will be explored.
- Correction for fixed effects
- Standardization of data
- Analysis of Variance (ANOVA)
- Calculation of heritability based on ANOVA.
- Calculation of genetic correlations based on ANOVA.  
Correlations such as age-age, trait-trait and site-site will be discussed and calculated based on ANOVA.

- Calculation of genotype-by-environment (GEI) interaction.
- Repeatability using ANOVA outputs.
  - Selection index. BL(U)P for forward, backward and clonal selection. The focus will be on the application of the Matgen BLP programme.
  - Genetic gains prediction. The focus will be on the G-assist programme.

## **PROGRAMMES**

Participants will be introduced to the following programmes:

- SAS
- Matgen, a BLP package for unbalanced index selection in tree breeding
- G-assist, a deterministic tool for genetic gains prediction

Free copies of the programmes Matgen and G-assist will be available for use during the course. Should the participants wish to use the packages after the course, they will be able to purchase these programmes at a 20% discount on the standard prices:

## **ENQUIRIES**

For more information, please contact the course coordinator between 08h00 and 16h00 (Central African time).

*E-mail:* courses@csir.co.za (Subject: Data analysis)

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