Applications of the Breeding Management System (BMS)

Project planning

BMS Workbench: Main screen that gives an overview of all projects and their contents. Users can directly access and browse specific projects, create new projects, administer programme members, breeding locations and methods and the templates used in breeding processes.

Breeding Planner: Lists all molecular breeding programmes within an open project. Three distinct programmes can be considered: MARS, MABC and MAS for gene pyramiding. View/edit breeding parameters; visualize a breeding scheme flowchart; and select current stage/generation of breeding programmes.

Integrated Breeding FieldBook

List Manager: Create and save new germplasm lists by drawing from existing lists and germplasm in the public and programme crop databases. View many germplasm properties during list creation, initially concentrating on pedigree or passport and seed inventory information.

Crossing Manager: Allows the user to specify planned crosses or realized crosses in a simple way, and ensure that pedigrees are tracked correctly. Create new lists of germplasm based on crosses and save these lists to the programme database; manually specify parent lists and crosses or upload a nursery template file to create crossing lists. Option to export as spreadsheet files (.xls).

Nursery Manager: Facilitates population development by interacting with the List Manager and ontologies to produce nursery books and labels for seed packets and nursery plots, so that populations can be grown, characterised, selected and advanced. Also interacts with the seed inventory to record available seed stocks. Specify and lay-out check entries, and collect data and selection decisions to produce new lists of germplasm for the next generation.

Trial Manager: Helps design trials for the evaluation of germplasm. Merge a list of germplasm entries with a set of traits to be observed and get randomised field lay-outs for one or more trial environments. The trait list and trial structure can be inherited form a 'template' trial or any previously conducted trial. New traits can be added to a trial and planting, plot and harvest labels can be designed and printed. Basic set of trial designs are supported: randomised complete block designs (RCBD), incomplete block designs and row and column designs.

Electronic data capture: The IB FieldBook lets the user develop field maps and labels with barcodes to assist planting, with functionality to export templates and data for data collection and statistical analysis in a variety of formats. Data collection functionality is supported for electronic tablets and other handheld devices.

Molecular Analysis

Genotypic Data Management System (GDMS): The BMS provides the means to store and access low level fingerprinting data ('000s) and any marker trait association information for breeding traits (QTL data and diagnostic markers); data that can be used as an aid for decisions required in day to day breeding activities e.g., parental and progeny selection. Data can easily be retrieved, visualized and manipulated in various ways including the easy creation of genotyping orders.
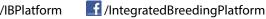
ISMU:	The Integrated SNP Mining and Utilization (ISMU) Pipeline is a Graphical User Interface (GUI)-based software application that is used to perform SNP discovery and developing genotyping assays (version 1.0), and to facilitate the conduct of Genomic Selection (version 2.0). ISMU v1.0 provides capabilities for filtering raw sequence data, alignment and SNP prediction, and to generate standard formats required in developing assays for called SNPs (KASP and Golden Gate). ISMU v2.0 lets users undertake Genomic Selection without having much knowledge of programming and technical expertise. It supplies several popular R and FORTRAN scripts (Ridge Regression Best Linear Unbiased Predictor (RR-BLUP), Kinship Gauss, Bayesian Ridge Regression, Bayesian LASSO, BayesA, BayesB, BayesCπ and Random Forest) to quickly process large datasets. Users will also find modules to check quality and different features of marker datasets, such as percentage of missing data, minor allele frequency (MAF) and polymorphism information content (PIC).

Data Analysis

Breeding View:	Breeding View, a statistical analysis application, can perform phenotypic data analyses and identify quantitative trait loci (QTL). Phenotypic analysis with Breeding View is integrated with the programme database – meaning that selected project data will automatically import into Breeding View from the Workbench, and Breeding View results files can be saved directly to the programme database. Breeding View can also be launched as a standalone application for the identification of QTL and analysis of data imported from external sources. It is a state-of-the-art solution, with batch mode functionality, designed to efficiently analyse multiple phenotypic datasets in one run of a pipeline, and quickly view results. Select from four analytical pipelines: Single-Site Analysis; Multi-Site Analysis; Multi-Year Multi-Site Analysis; Breeding View Standalone for QTL.

Breeding Decision Support

Molecular Breeding Design Tool (MBDT):	The Molecular Breeding Design Tool can be used to design ideotypes based on QTL target regions (foreground markers) and to recover recurrent parent genome (background markers) in backcross breeding applications. The graphical display facilitates the comparison of germplasm based on genotype. Graphical display assists with: selection of donor and recurrent parents; assignment of foreground markers associated with QTL; assignment of background markers to recover recurrent parent genome; design of a target genotype (ideotype). Additional functionality lets the user determine the minimum number of individuals that need to be genotyped in each BC generation to recover at least one double homozygote for the markers flanking target QTL at the end of the programme, and identify polymorphic makers between any two accessions.
OptiMAS:	OptiMAS follows three steps to aid marker-assisted selection: prediction, selection, intermating. It predicts crossing strategies that optimize the likelihood of assembling favourable alleles into a target genotype. Molecular markers in the vicinity of favourable parental QTL are used to trace the movement of QTL between generations. OptiMAS uses genotype data to predict the probability of allele transmission in different MAS schemes and mating designs (intercrossing, selfing, backcrossing, double haploids, RIL), allowing some generations to be considered without the need to genotype. Selection and crossing strategies are based on expected progeny genotypes. OptiMAS supports decision-making associated with the marker-assisted breeding plan generated by the Breeding Planner. It is a standalone application that can be launched from the BMS Workbench or from a desktop icon. It has a graphical user interface, but can also operate from command line.

SERVICES, COMMUNITIES AND SUPPORT

In addition to in-house support services addressing technical and logistical needs in the adoption of these technologies, the Integrated Breeding Platform (IBP) provides access to contracted external partners that offer registered users genotyping, sequencing and other services at concessionary rates. A complete list of breeding services providers is available on the IBP portal at https://www.integratedbreeding.net/34/breeding-services. Registered users also have access to complementary resources for their crop breeding programmes through the IBP web portal, including genetic resources, SNP and SSR markers and genotypic databases for molecular breeding, as well as training opportunities in molecular breeding, data management and statistical analysis. IBP staff are available to answer queries and suggestions posted on the blogs and forums of the Crop Community pages (https://www.integratedbreeding.net/233/communities), where researchers and breeders can also share experiences, best practices and improved varieties with the larger community.