Breeding Management System (BMS)

Overview and potential uses

FACULTY OF AGRICULTURE
& ENVIRONMENT

Angela Pattison
Plant Breeding Institute

THE UNIVERSITY OF SYDNEY

BREEDING MANAGEMENT SYSTEM | WORKBENCH

BROUGHT TO YOU BY:

Generation Challenge Programme

Bioversity International

CIAT

CIMMYT International Maize and Wheat Improvement Center

efficio Technology Services

ICRISAT Science with a human face

INRA SCIENCE & IMPACT

iPlant Collaborative

IRRI

vsn

WAGENINGEN UR

WITH THE GENEROUS FINANCIAL SUPPORT OF:

Bill & Melinda Gates foundation

European Commission

UKaid from the British people

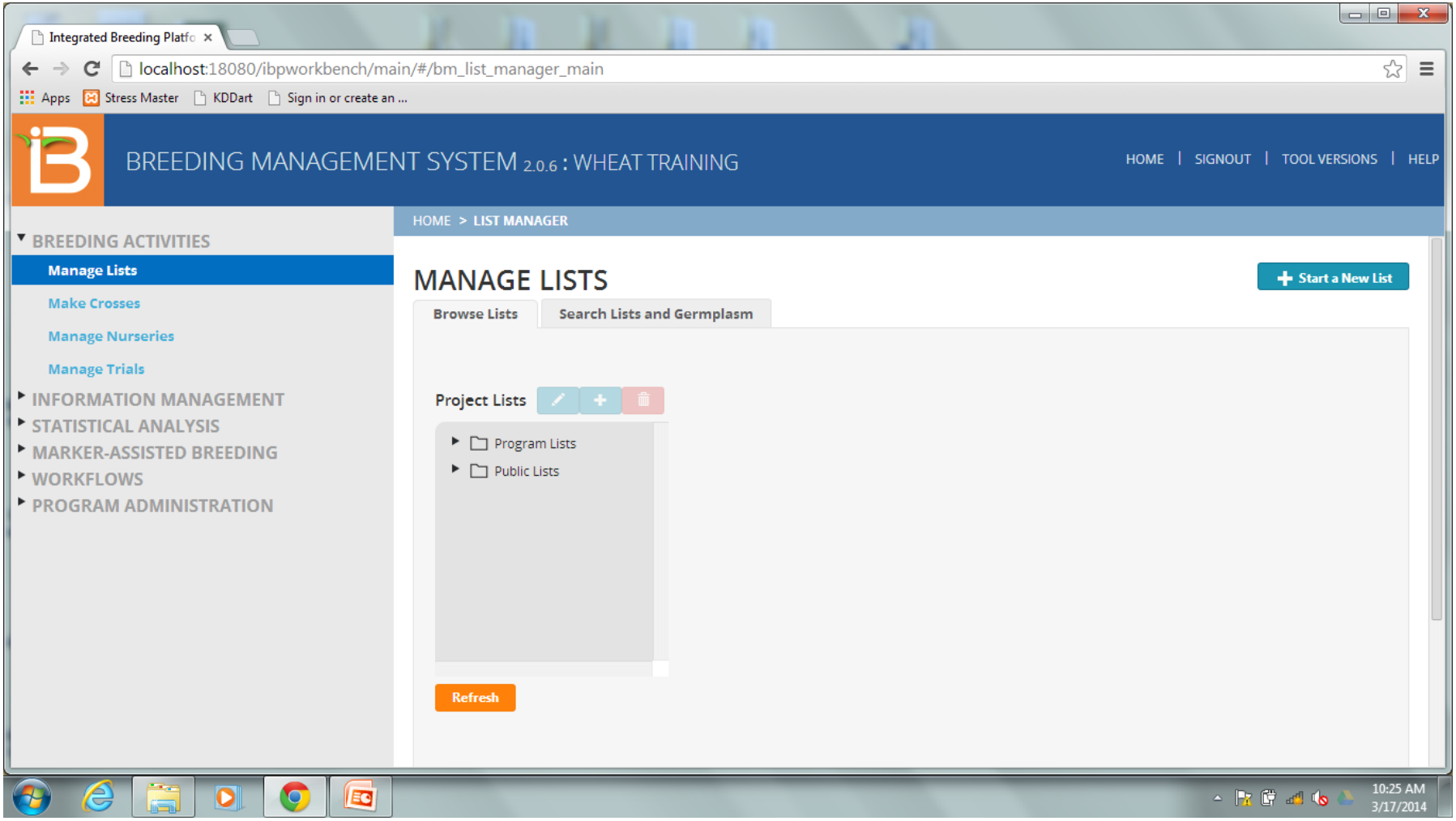
CGIAR Science for a food secure future

Schweizerische Eidgenossenschaft
Confédération suisse
Confederazione Svizzera
Confederaziun svizra

Swiss Agency for Development and Cooperation SDC

Overview

- Bring breeder's tools into a SINGLE PLATFORM
- Integrated with ISIS (pedigrees and trials)
- Integrated with GDMS (genotyping)
- SHARE data
- MULTIPLE CROPS (including wheat, maize, chickpea and sorghum)


Integrated Breeding Platfo
localhost:18080/ibpworkbench/main/#/bm_list_manager_main
Apps
Stress Master
KDDart
Sign in or create an ...
BREEDING MANAGEMENT SYSTEM 2.0.6 : WHEAT TRAINING
HOME | SIGNOUT | TOOL VERSIONS | HELP
BREEDING ACTIVITIES
Manage Lists
Make Crosses
Manage Nurseries
Manage Trials
INFORMATION MANAGEMENT
STATISTICAL ANALYSIS
MARKER-ASSISTED BREEDING
WORKFLOWS
PROGRAM ADMINISTRATION
HOME > LIST MANAGER
MANAGE LISTS
Start a New List
Browse Lists
Search Lists and Germplasm
Project Lists
Program Lists
Public Lists
Refresh
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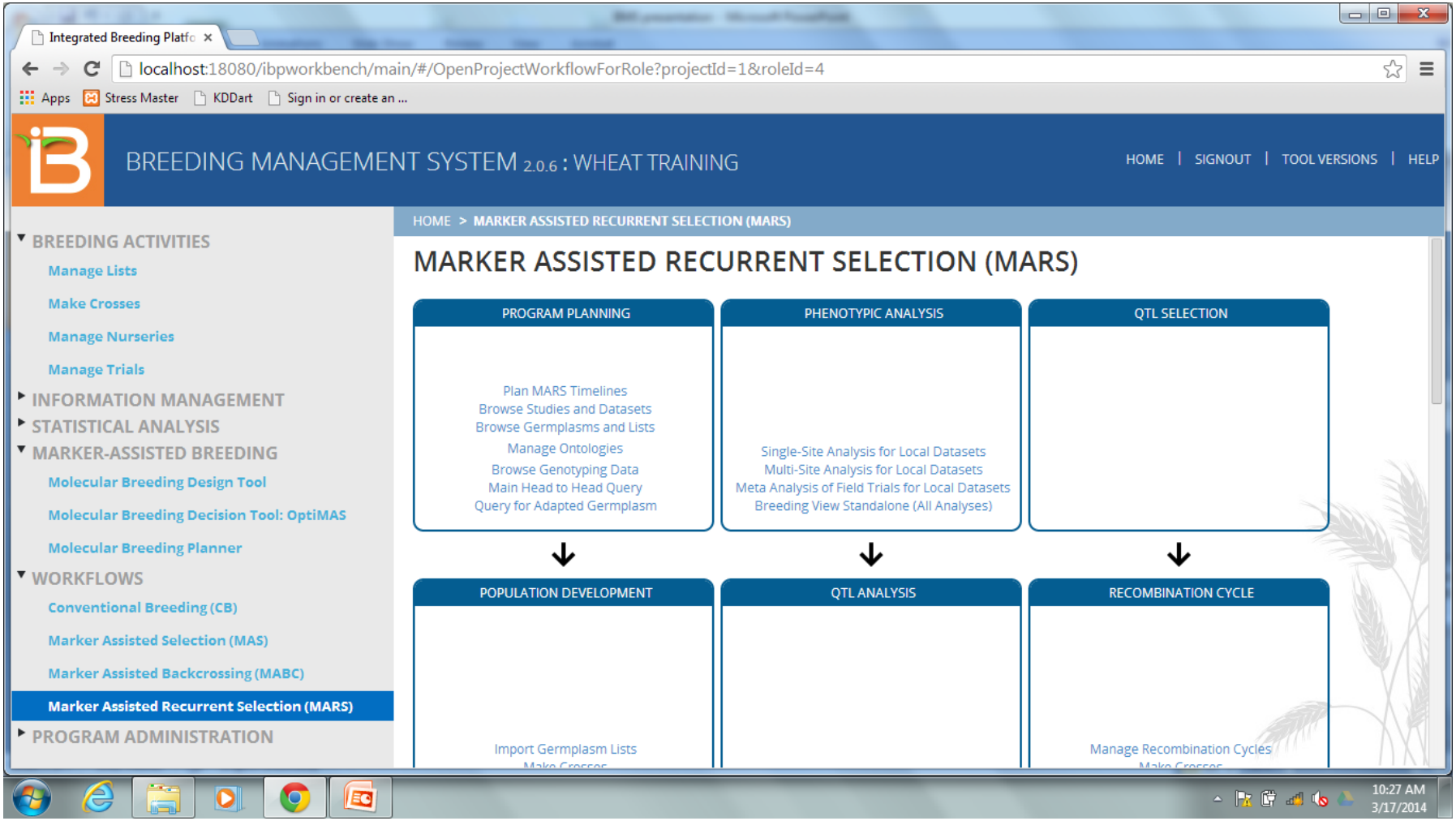
3/17/2014


Integrated Breeding Platfo
localhost:18080/ibpworkbench/main/#/OpenProjectWorkflowForRole?projectId=1&roleId=4
Apps
Stress Master
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Sign in or create an ...
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INFORMATION MANAGEMENT
STATISTICAL ANALYSIS
MARKER-ASSISTED BREEDING
Molecular Breeding Design Tool
Molecular Breeding Decision Tool: OptiMAS
Molecular Breeding Planner
WORKFLOWS
Conventional Breeding (CB)
Marker Assisted Selection (MAS)
Marker Assisted Backcrossing (MABC)
Marker Assisted Recurrent Selection (MARS)
PROGRAM ADMINISTRATION
HOME > MARKER ASSISTED RECURRENT SELECTION (MARS)
MARKER ASSISTED RECURRENT SELECTION (MARS)
PROGRAM PLANNING
Plan MARS Timelines
Browse Studies and Datasets
Browse Germplasms and Lists
Manage Ontologies
Browse Genotyping Data
Main Head to Head Query
Query for Adapted Germplasm
PHENOTYPIC ANALYSIS
Single-Site Analysis for Local Datasets
Multi-Site Analysis for Local Datasets
Meta Analysis of Field Trials for Local Datasets
Breeding View Standalone (All Analyses)
QTL SELECTION
POPULATION DEVELOPMENT
Import Germplasm Lists
QTL ANALYSIS
RECOMBINATION CYCLE
Manage Recombination Cycles
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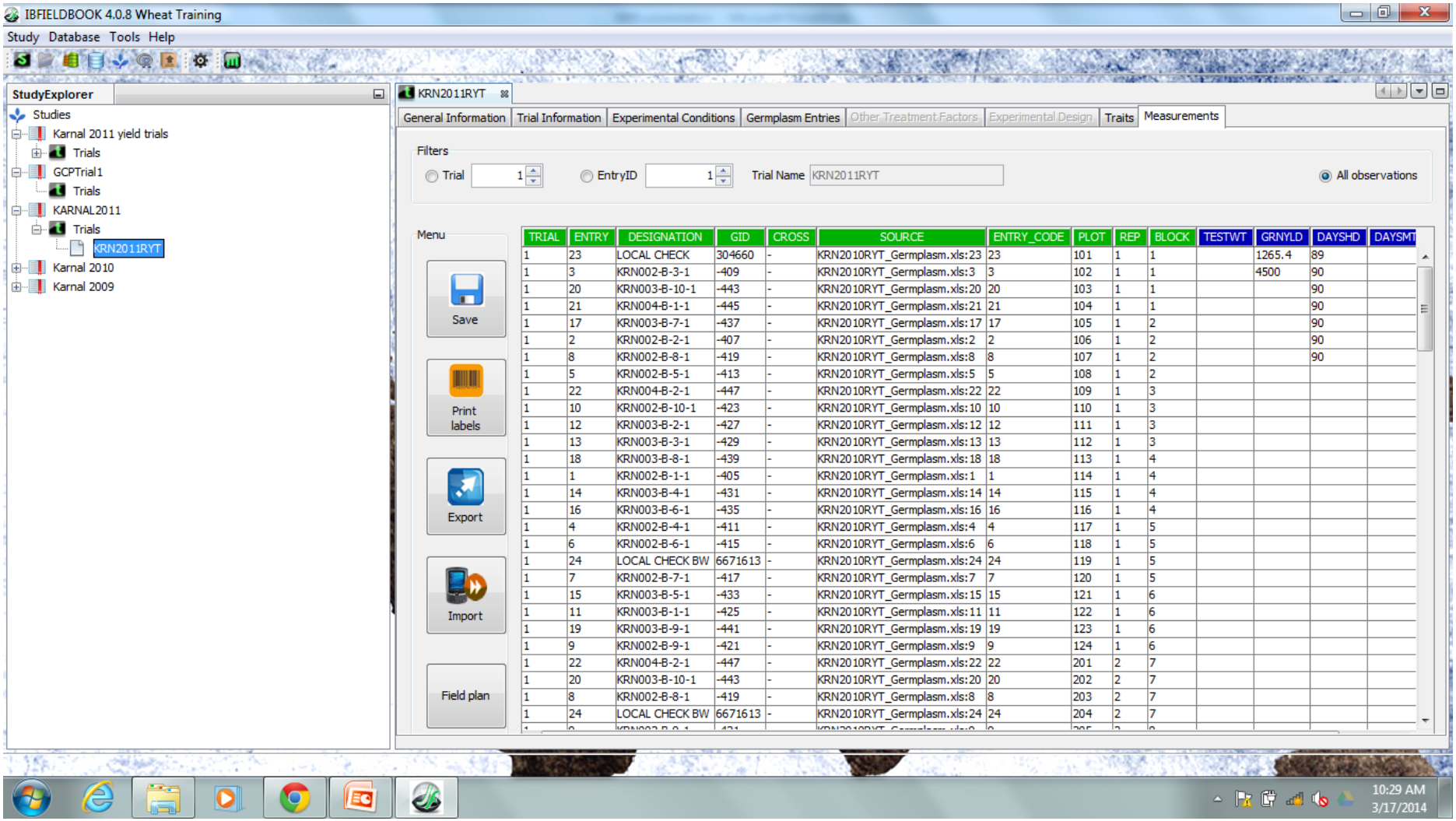
IBFIELDBOOK 4.0.8 Wheat Training
Study Database Tools Help
StudyExplorer
Studies
Karnal 2011 yield trials
Trials
GCPTrial1
Trials
KARNAL2011
Trials
KRN2011RYT
Karnal 2010
Karnal 2009
KRN2011RYT
General Information
Trial Information
Experimental Conditions
Germplasm Entries
Other Treatment Factors
Experimental Design
Traits
Measurements
Filters
Trial
1
EntryID
1
Trial Name
KRN2011RYT
All observations
Menu
Save
Print labels
Export
Import
Field plan
TRIAL ENTRY DESIGNATION GID CROSS SOURCE ENTRY_CODE PLOT REP BLOCK TESTWT GRNYLD DAYSHD DAYSMT
1 23 LOCAL CHECK 304660 - KRN2010RYT_Germplasm.xls:23 23 101 1 1 1265.4 89
1 3 KRN002-B-3-1 -409 - KRN2010RYT_Germplasm.xls:3 3 102 1 1 4500 90
1 20 KRN003-B-10-1 -443 - KRN2010RYT_Germplasm.xls:20 20 103 1 1 90
1 21 KRN004-B-1-1 -445 - KRN2010RYT_Germplasm.xls:21 21 104 1 1 90
1 17 KRN003-B-7-1 -437 - KRN2010RYT_Germplasm.xls:17 17 105 1 2 90
1 2 KRN002-B-2-1 -407 - KRN2010RYT_Germplasm.xls:2 2 106 1 2 90
1 8 KRN002-B-8-1 -419 - KRN2010RYT_Germplasm.xls:8 8 107 1 2 90
1 5 KRN002-B-5-1 -413 - KRN2010RYT_Germplasm.xls:5 5 108 1 2
1 22 KRN004-B-2-1 -447 - KRN2010RYT_Germplasm.xls:22 22 109 1 3
1 10 KRN002-B-10-1 -423 - KRN2010RYT_Germplasm.xls:10 10 110 1 3
1 12 KRN003-B-2-1 -427 - KRN2010RYT_Germplasm.xls:12 12 111 1 3
1 13 KRN003-B-3-1 -429 - KRN2010RYT_Germplasm.xls:13 13 112 1 3
1 18 KRN003-B-8-1 -439 - KRN2010RYT_Germplasm.xls:18 18 113 1 4
1 1 KRN002-B-1-1 -405 - KRN2010RYT_Germplasm.xls:1 1 114 1 4
1 14 KRN003-B-4-1 -431 - KRN2010RYT_Germplasm.xls:14 14 115 1 4
1 16 KRN003-B-6-1 -435 - KRN2010RYT_Germplasm.xls:16 16 116 1 4
1 4 KRN002-B-4-1 -411 - KRN2010RYT_Germplasm.xls:4 4 117 1 5
1 6 KRN002-B-6-1 -415 - KRN2010RYT_Germplasm.xls:6 6 118 1 5
1 24 LOCAL CHECK BW 6671613 - KRN2010RYT_Germplasm.xls:24 24 119 1 5
1 7 KRN002-B-7-1 -417 - KRN2010RYT_Germplasm.xls:7 7 120 1 5
1 15 KRN003-B-5-1 -433 - KRN2010RYT_Germplasm.xls:15 15 121 1 6
1 11 KRN003-B-1-1 -425 - KRN2010RYT_Germplasm.xls:11 11 122 1 6
1 19 KRN003-B-9-1 -441 - KRN2010RYT_Germplasm.xls:19 19 123 1 6
1 9 KRN002-B-9-1 -421 - KRN2010RYT_Germplasm.xls:9 9 124 1 6
1 22 KRN004-B-2-1 -447 - KRN2010RYT_Germplasm.xls:22 22 201 2 7
1 20 KRN003-B-10-1 -443 - KRN2010RYT_Germplasm.xls:20 20 202 2 7
1 8 KRN002-B-8-1 -419 - KRN2010RYT_Germplasm.xls:8 8 203 2 7
1 24 LOCAL CHECK BW 6671613 - KRN2010RYT_Germplasm.xls:24 24 204 2 7
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BMS features: Tools

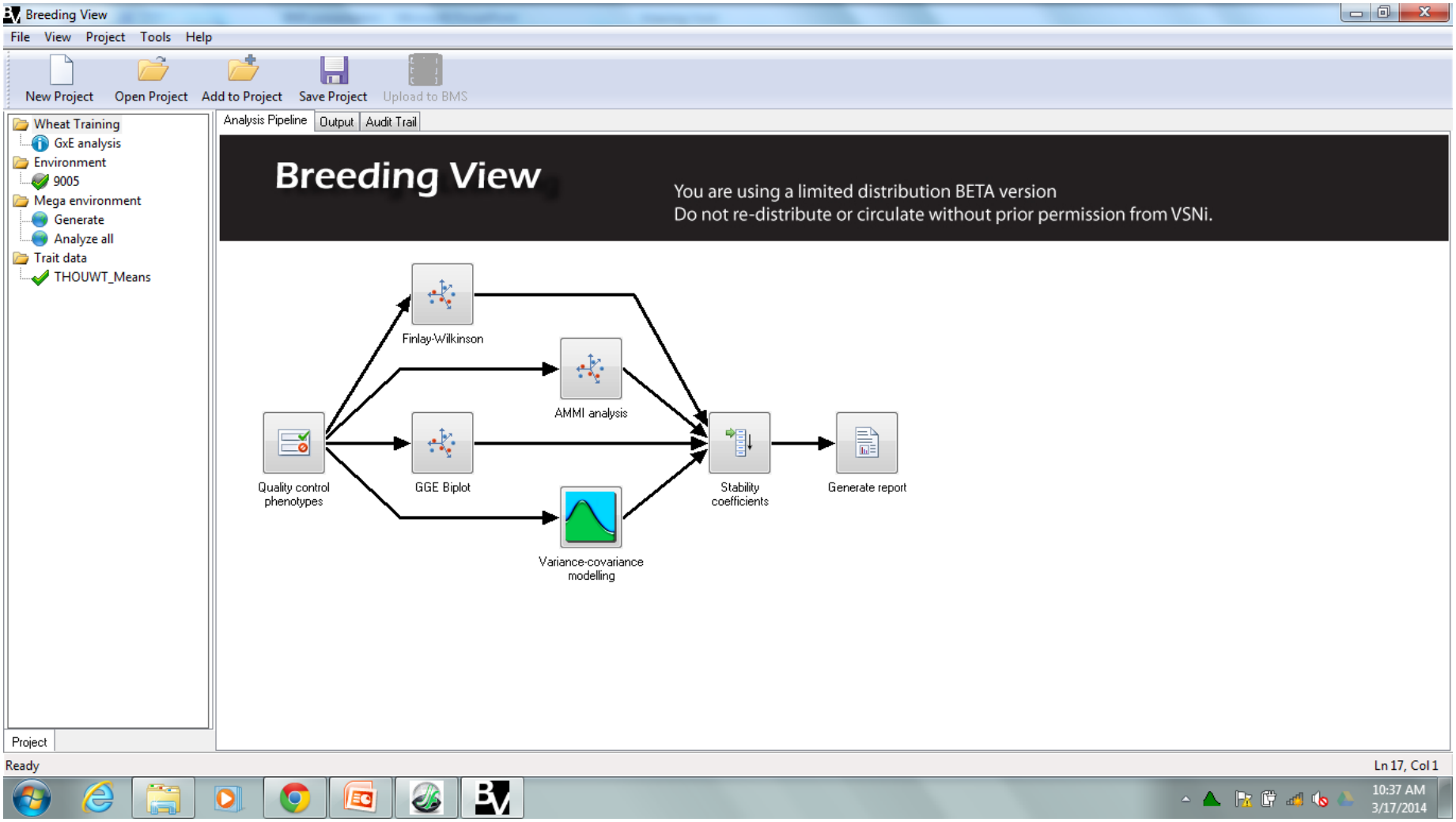
- Breeding manager
  - Create lists
  - Crossing, select progeny
- Nursery/Trial manager
  - Turn lists into trials
  - Enter data
  - Advance selected germplasm

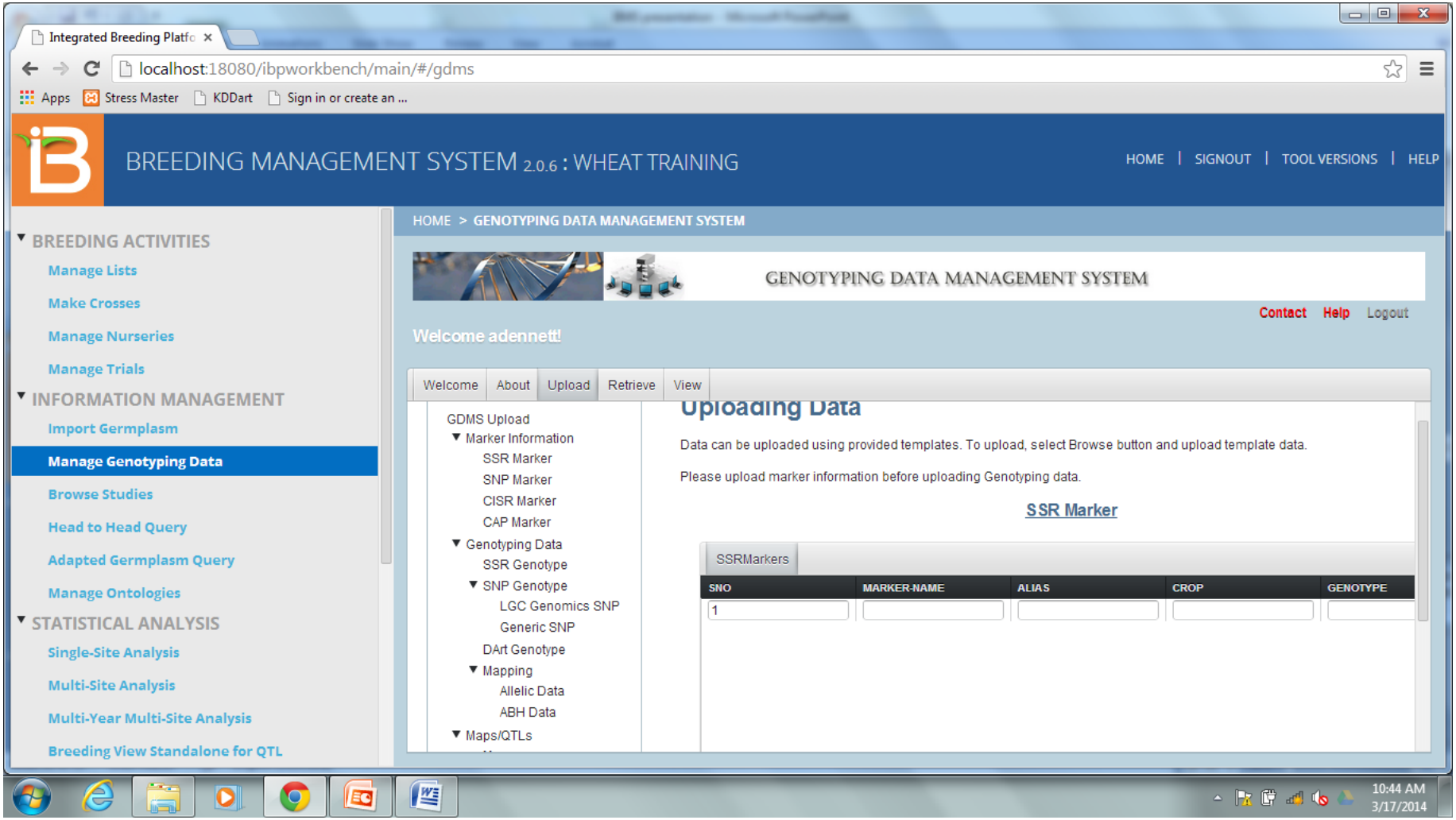
BMS features: Tools

- Statistical analysis (Genstat)
  - Field trials
  - Identify QTLs
- Molecular breeding planner
  - Select germplasm for marker assisted selection
  - Determine optimum population sizes

BMS features: Tools

- Decision support for genotyping
  - OptiMAS
  - Flapjack
  - GDMS
  - Public repository for SNPs, SSRs and DArT


Breeding View
File View Project Tools Help
New Project
Open Project
Add to Project
Save Project
Upload to BMS
Wheat Training
GxE analysis
Environment
9005
Mega environment
Generate
Analyze all
Trait data
THOUWT_Means
Analysis Pipeline
Output
Audit Trail
Breeding View
You are using a limited distribution BETA version
Do not re-distribute or circulate without prior permission from VSNi.
Finlay-Wilkinson
AMMI analysis
Quality control phenotypes
GGE Biplot
Stability coefficients
Generate report
Variance-covariance modelling
Project
Ready
Ln 17, Col 1
10:37 AM
3/17/2014


Integrated Breeding Platfo
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Browse Studies
Head to Head Query
Adapted Germplasm Query
Manage Ontologies
STATISTICAL ANALYSIS
Single-Site Analysis
Multi-Site Analysis
Multi-Year Multi-Site Analysis
Breeding View Standalone for QTL
HOME > GENOTYPING DATA MANAGEMENT SYSTEM
GENOTYPING DATA MANAGEMENT SYSTEM
Contact Help Logout
Welcome adennett!
Welcome About Upload Retrieve View
GDMS Upload
Marker Information
SSR Marker
SNP Marker
CISR Marker
CAP Marker
Genotyping Data
SSR Genotype
SNP Genotype
LGC Genomics SNP
Generic SNP
DArt Genotype
Mapping
Allelic Data
ABH Data
Maps/QTLs
Uploading Data
Data can be uploaded using provided templates. To upload, select Browse button and upload template data.
Please upload marker information before uploading Genotyping data.
SSR Marker
SSRMarkers
SNO
MARKER-NAME
ALIAS
CROP
GENOTYPE
1
10:44 AM
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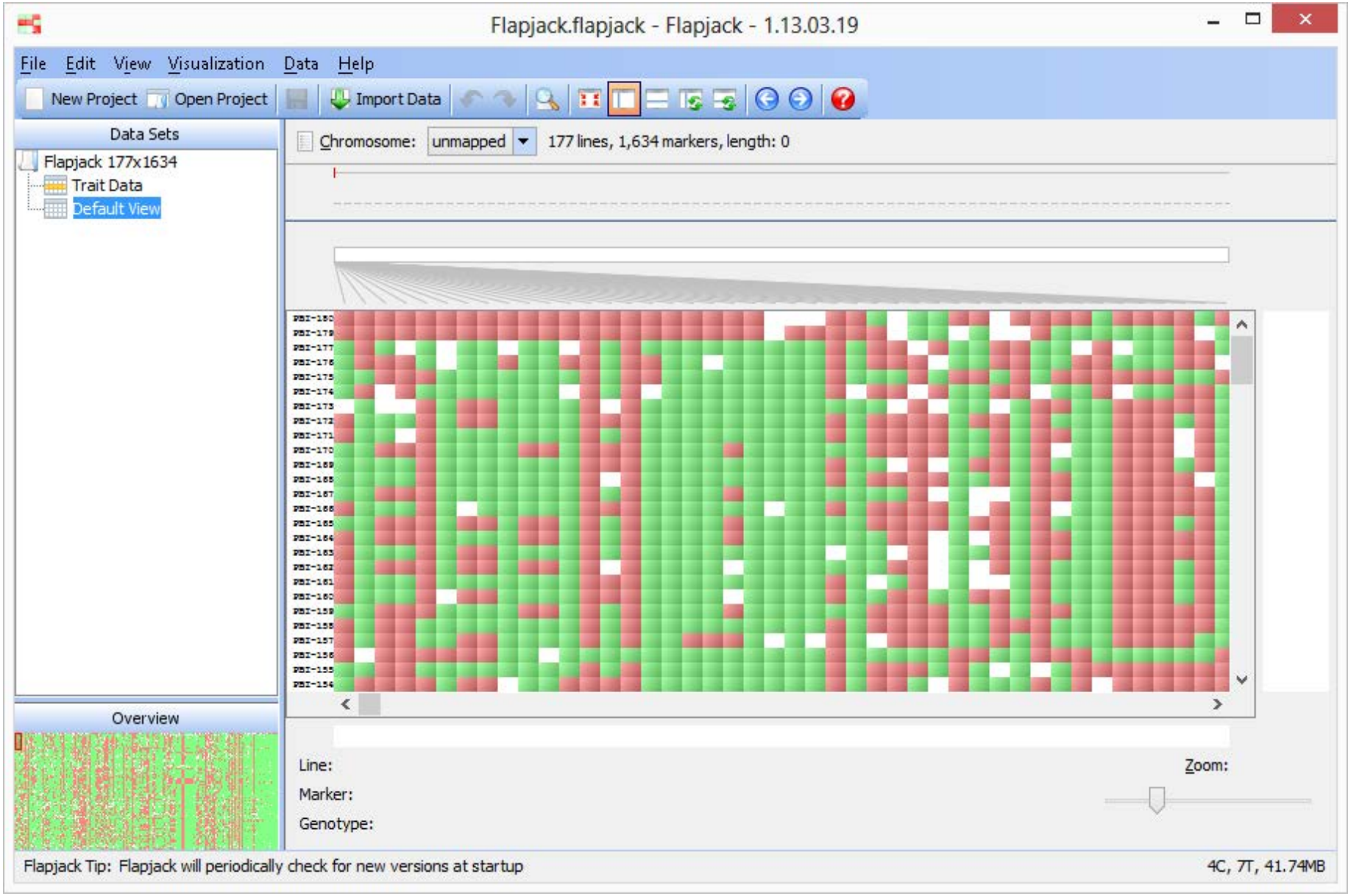
Flapjack.flapjack - Flapjack - 1.13.03.19
File Edit View Visualization Data Help
New Project
Open Project
Import Data
Data Sets
Flapjack 177x1634
Trait Data
Default View
Chromosome:
unmapped
177 lines, 1,634 markers, length: 0
Overview
Line:
Marker:
Genotype:
Zoom:
Flapjack Tip: Flapjack will periodically check for new versions at startup
4C, 7T, 41.74MB

Advantages

- FREE for public institutions
- Excellent USER INTERFACE (and getting better)
- SHARE data worldwide
- CONSISTENCY across organisations (standard ontology)
- ORGANISE the breeding program (ONE version)
- For both genotypic and phenotypic data, the ability to:
  - TRACK and SEARCH
  - access the INTERNATIONAL REPOSITORY
  - INTEGRATE TOOLS for analysis

Disadvantages

- Not in a CLOUD with multi-user access (yet)
- Missing a few FEATURES in searches
- Lots of IMPORTING and EXPORTING
- Multiple COPIES of field data
  - Data is overridden with each new upload
- Can’t create lists from multiple locations (yet)
- Can’t do spatial analysis (yet)

Recommendations

1. Play around during the break
2. Download free onto your own computer
3. WAIT until the next iteration before implementing

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