

Integrating ICIS with IRRISTAT and PediTree

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Integrating IRRISTAT with ICIS

- ICIS manages data but it needs analysis tool to extract information from it. IRRISTAT is a package developed at IRRI for statistical analysis.
- IRRISTAT is a computer program for basic statistical analysis of experimental data.
- It has been developed primarily for the analysis of data from agricultural field trials, but many of the features can be used for analysis of data from other sources.

Main Modules of IRRISTAT

- Descriptive statistics and Scatterplot Graphics
- Balanced analysis of variance
- Unbalanced analysis (generalized linear models)
- Linear Mixed Models
- Combined analysis of variance
- REML analysis
- Analysis of repeated measures
- Regression and correlation analysis
- Single-site analysis for variety trials
- Spatial Analysis
- Genotype \times environment interaction analysis
- Pattern Analysis
- Quantitative trait loci analysis
- Graphics
- Utilities for randomization and layout, and orthogonal polynomial

Strategies for integration

- Creates an Excel file compatible with IRRISTAT from an ICIS Workbook Study through a macro command

	A	B	C	D	E	F	G	H
1	plot	entry	block	rep	basin	row	column	yield
2	1.0	49.0	1.0	1.0	1.0	1.0	1.0	4.4
3	2.0	173.0	1.0	1.0	1.0	1.0	2.0	14.4
4	3.0	76.0	1.0	1.0	1.0	1.0	3.0	7.0
5	4.0	166.0	1.0	1.0	1.0	1.0	4.0	9.6
6	5.0	178.0	1.0	1.0	1.0	1.0	5.0	3.5
7	6.0	117.0	1.0	1.0	1.0	1.0	6.0	7.8
8	7.0	105.0	1.0	1.0	1.0	1.0	7.0	7.2
9	8.0	1.0	1.0	1.0	1.0	1.0	8.0	5.7
10	9.0	175.0	1.0	1.0	1.0	1.0	9.0	6.4
11	10.0	180.0	1.0	1.0	1.0	1.0	10.0	8.0
12	11.0	119.0	1.0	1.0	1.0	1.0	11.0	6.8
13	12.0	120.0	1.0	1.0	1.0	1.0	12.0	25.4
14	13.0	207.0	1.0	1.0	1.0	1.0	13.0	
15	14.0	77.0	2.0	1.0	1.0	1.0	14.0	6.3
16	15.0	176.0	2.0	1.0	1.0	1.0	15.0	11.1
17	16.0	26.0	2.0	1.0	1.0	1.0	16.0	6.1
18	17.0	184.0	2.0	1.0	1.0	1.0	17.0	8.7
19	18.0	83.0	2.0	1.0	1.0	1.0	18.0	12.4
20	19.0	15.0	2.0	1.0	1.0	1.0	19.0	23.3
21	20.0	66.0	2.0	1.0	1.0	1.0	20.0	11.2
22	21.0	145.0	2.0	1.0	1.0	1.0	21.0	13.2
23	22.0	63.0	2.0	1.0	1.0	1.0	22.0	10.2
24	23.0	150.0	2.0	1.0	1.0	1.0	23.0	4.6
25	24.0	60.0	2.0	1.0	1.0	1.0	24.0	16.3
26	25.0	37.0	2.0	1.0	1.0	1.0	25.0	4.2
27	26.0	1.0	2.0	1.0	1.0	1.0	26.0	16.7
28	27.0	165.0	3.0	1.0	1.0	1.0	27.0	6.6
29	28.0	52.0	3.0	1.0	1.0	1.0	28.0	9.0
30	29.0	50.0	3.0	1.0	1.0	1.0	29.0	2.1
31	30.0	88.0	3.0	1.0	1.0	1.0	30.0	9.3
32	31.0	45.0	3.0	1.0	1.0	1.0	31.0	4.2
33	32.0	95.0	3.0	1.0	1.0	1.0	32.0	7.3
34	33.0	187.0	3.0	1.0	1.0	1.0	33.0	6.1
35	34.0	92.0	3.0	1.0	1.0	1.0	34.0	11.5

	A
1	V001 PLOT
2	V002 ENTRY
3	V003 BLOCK
4	V004 REP
5	V005 BASIN
6	V006 ROW
7	V007 COLUMN
8	V008 GY G/M G/M
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Strategies for integration

- Creates a Sys file from ICIS Workbook Study which is readily used by IRRISTAT using a macro
Issue: IRRISTAT uses a particular module for creating the SYS file. How easily can it be called from Excel?
- Add a procedure in IRRISTAT to read and write to an ICIS Workbook.
Issue: This will require modification in IRRISTAT

PediTree

- possible visualization tool for ICIS data

- ICIS manages pedigree data but they are better visualized in a tree-shaped representation. PediTree creates a tree-shaped representation of pedigree information. Moreover, trait can be linked, displayed with the pedigree tree.

PediTree

- Similar to ICOP and IDEND applications which were previously incorporated with ICIS on its previous versions.

The screenshot displays the Peditree software interface. The main window is titled "Peditree" and contains several panels:

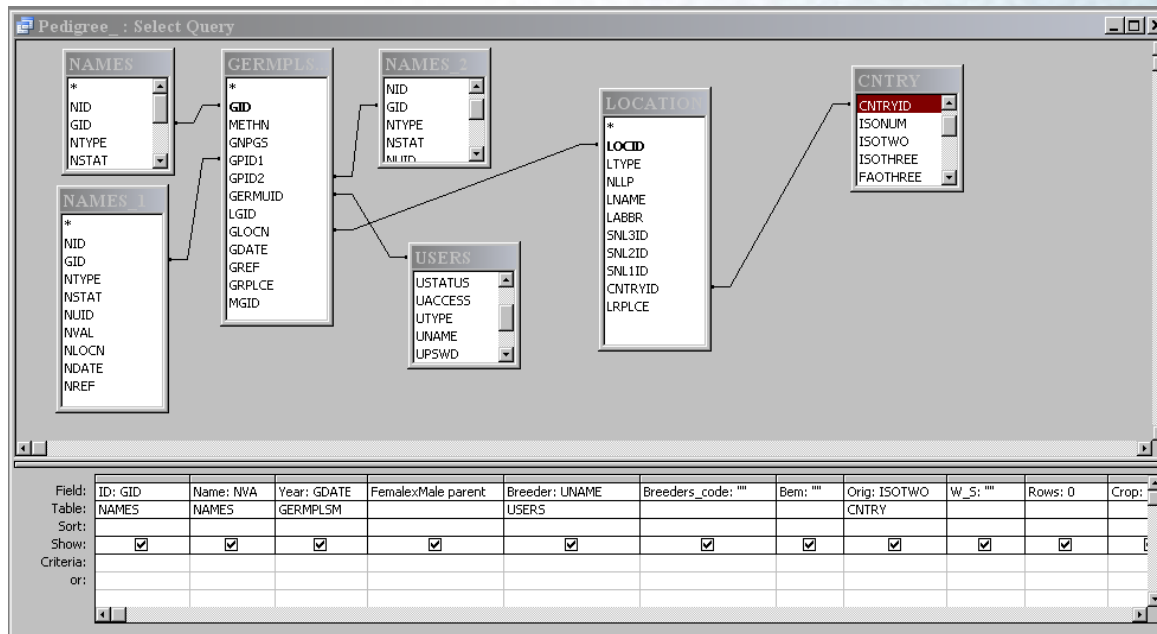
- lookup >>**: A search bar containing the text "PETA".
- Name**: A list of genotypes including "NMS 4*2/T (N) 1", "INDIAN SANDOW//BBS 873/TN 1", "IR 8//81 B 25//DAWN", "PETA*2/T (N) 1", "IR 8*2/3//IR 8//CP SLD//NMS 4", "TKM 6*2/T (N) 1", "CI 9524//CR 24", and "IR 8*3//IR 8*2//WAGWAG".
- Tree Control**: Buttons for "Compare", "Image options", and "Save text".
- Compare entries**: Two input fields for "genotype name" and a "< Compare >" button.
- alphabetically sorted pedigree members**: A list containing "DEE GEO WOO GEN", "IR 8-CROSS", and "PETA".
- Pedigree-Tree**: A hierarchical tree view showing the relationships between genotypes. The root node is "MILYANG 40//IR 8//RAMTALASI (0) L:1 #:2 IBC: 0.000". It branches into "MILYANG 40" and "IR 8//RAMTALASI". "MILYANG 40" further branches into "IR 64-CROSS (19850000) L:1 #:2 IBC: 0.000" and "IR 8-CROSS (19680000) L:1 #:2 IBC: 0.000". "IR 64-CROSS" branches into "GAM PAI-15" and "TAICHUNG NATIVE 1". "IR 8-CROSS" branches into "PETA" and "DEE GEO WOO GEN".
- Status Bar**: Displays "2 genotypes in this progeny tree - 1 generations deep", "Inbreeding Coefficient: 0.000", and "DEE GEO WOO GEN".

PediTree ...

- It is programmed in Delphi and runs under MS Windows environment with data stored in a MS Access table named Pedigree.
- It uses an external pedigree drawing routine PediGraph
- It has a lookup of a complete pedigree tree structure based on genotype name and year of release/development
- It can estimate coefficient of parentage based on the method described by Falconer and Mackay (1996)
- It can also display as a tree the pedigree where the cultivar of interest appears a progenitors.
- It can link trait data within the pedigree tree through another database Traits with key field Cultivar.

Strategies for integration

- Creates a table Pedigree through a query which retrieves information from the GMS database



Strategies for integration

- Select a List of Entries and retrieve all related germplasms into a PEDIGREE table.

Using Retriever, retrieve the traits of interest into TRAITS table with CULTIVAR as primary field

Issues in integration

- It can only use an Access database
- The database should be named rasped.mdb
- The creation of the tree is based on genotype names. Duplicate names are resolved through year of release/development
- It slows down with IRIS ~ 300,000 crosses