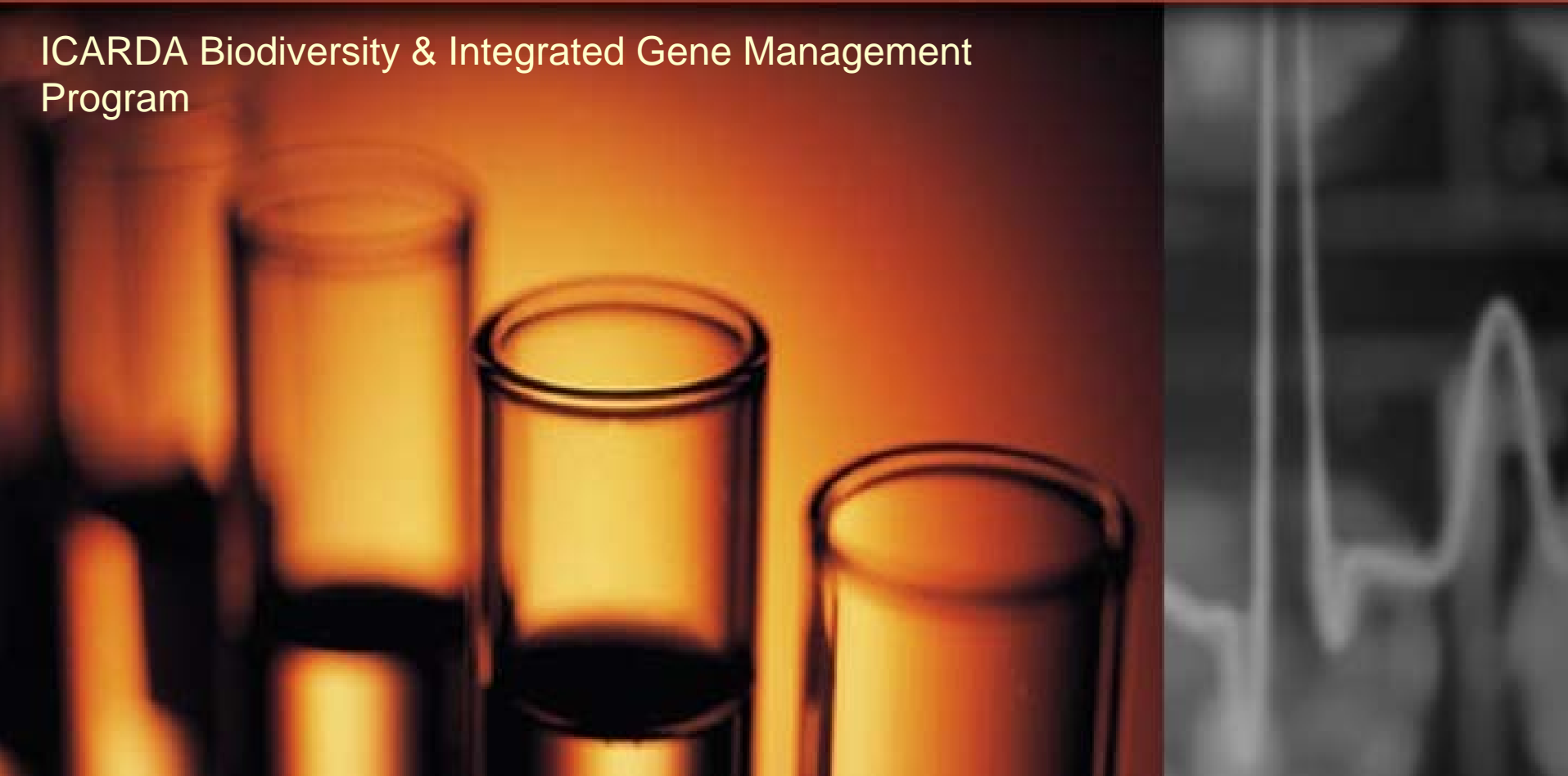




ICARDA Generation Genomics Laboratory Information Management System (LIMS) and Gene Management System (GeMS)

ICARDA Biodiversity & Integrated Gene Management
Program



ICARDA Generation Genomics Laboratory Information Management System (LIMS) and Gene Management System (GeMS)

- **What is ICARDA Generation Genomics “LIMS and GeMS”?**
- **What is the relation between LIMS & ICIS?**
- **What “LIMS and GeMS” can do?**
 - **How can “LIMS and GeMS” help the end users?**
- **How does LIMS work?**
 - **What about the security system?**
- **What are our achievements? (Where are we now?)**
- **What are our next steps? (What’s next?)**
- **Difficulties and solutions!**

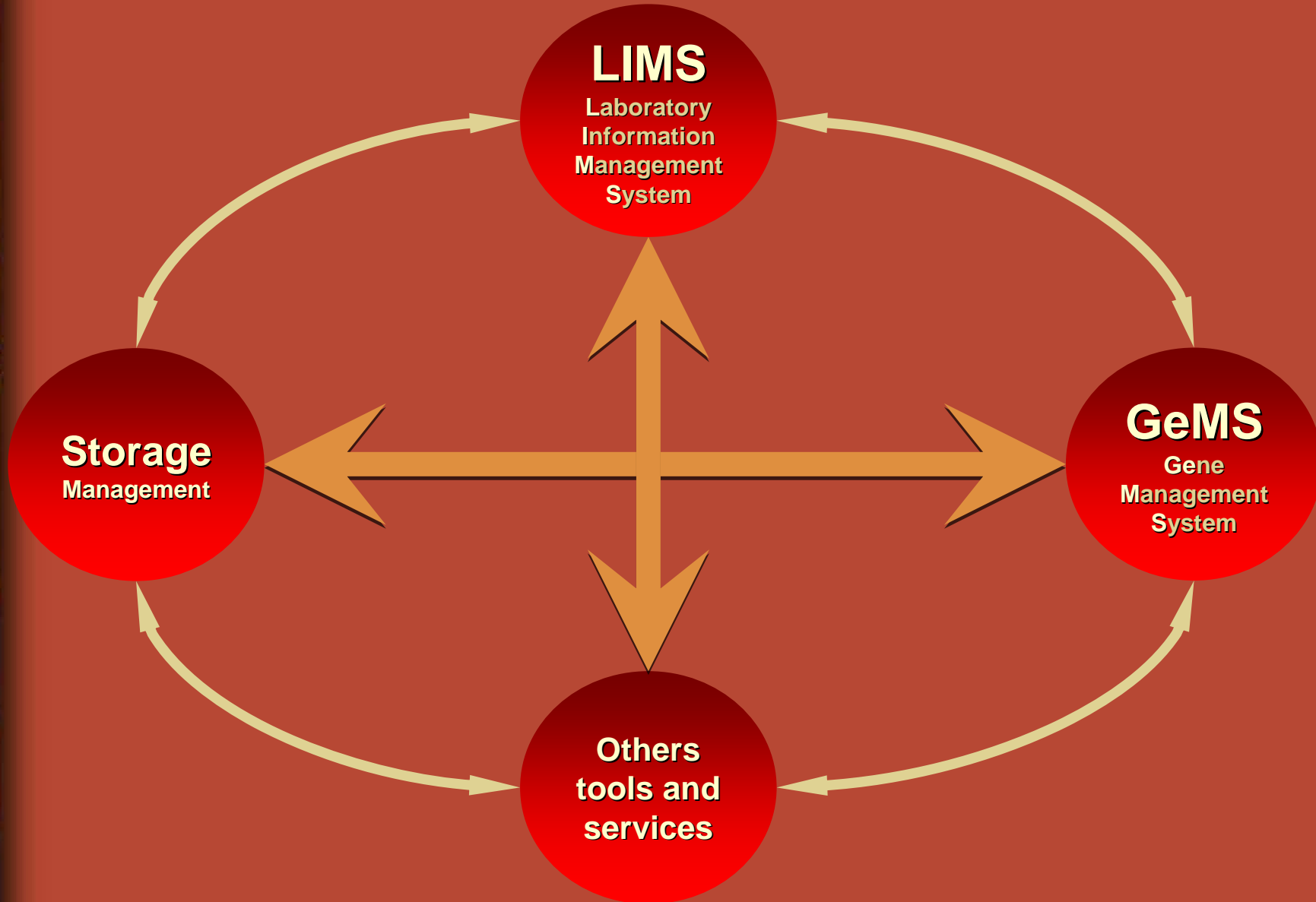


What is ICARDA Generation Genomics "LIMS and GeMS"?

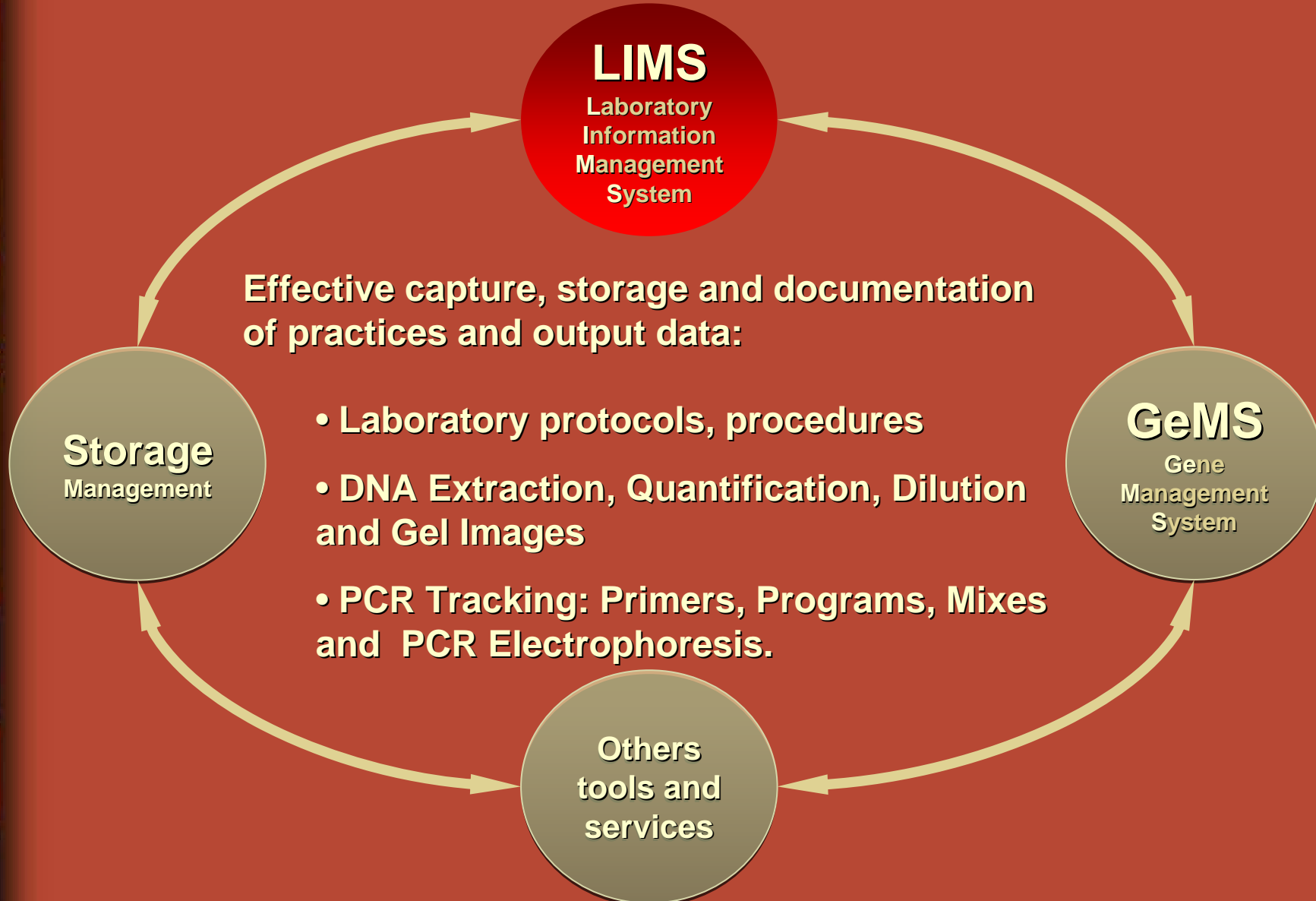


Tool to store, organize and analyze data.

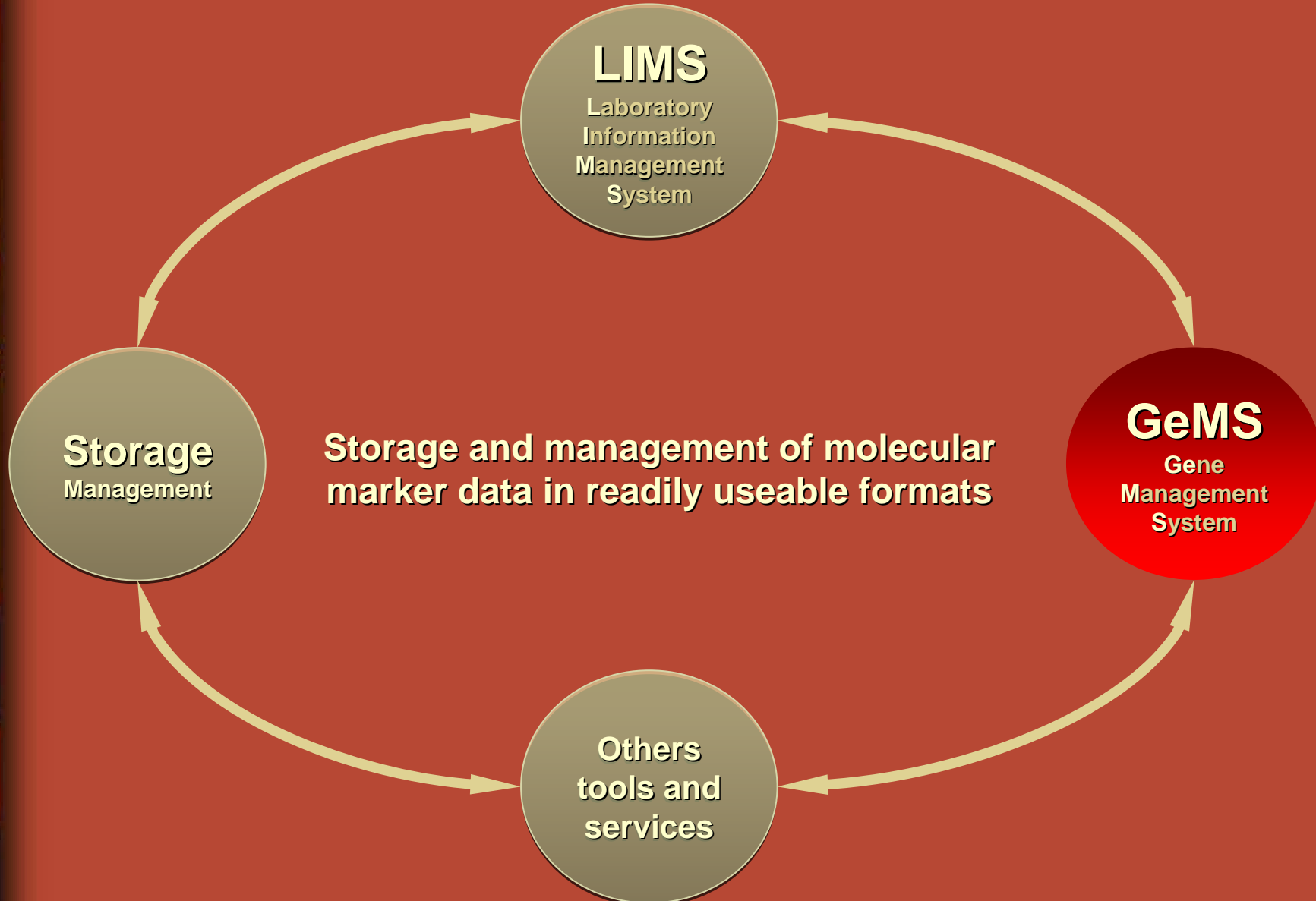
What is ICARDA Generation Genomics "LIMS and GeMS"?



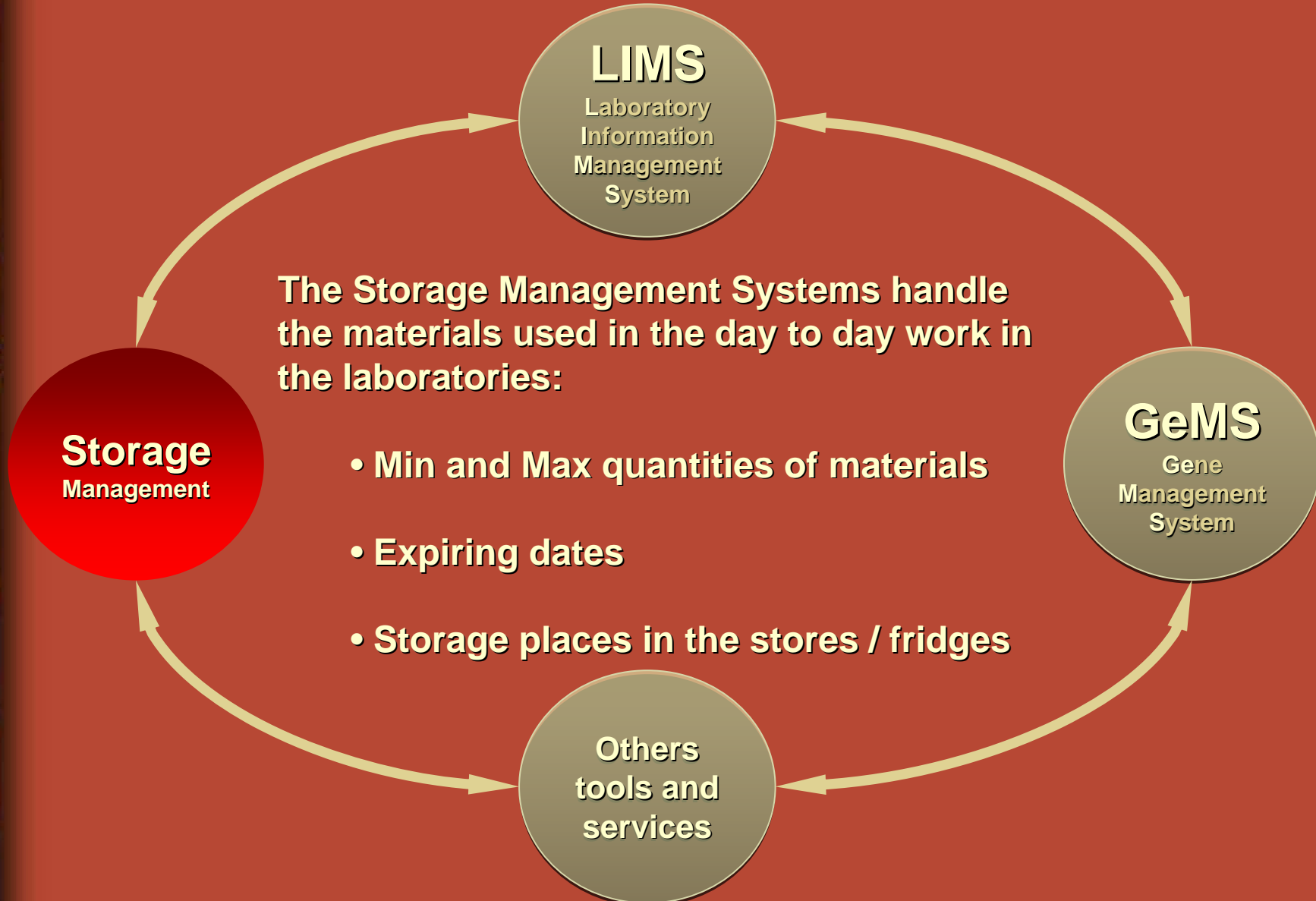
What is ICARDA Generation Genomics "LIMS and GeMS"?



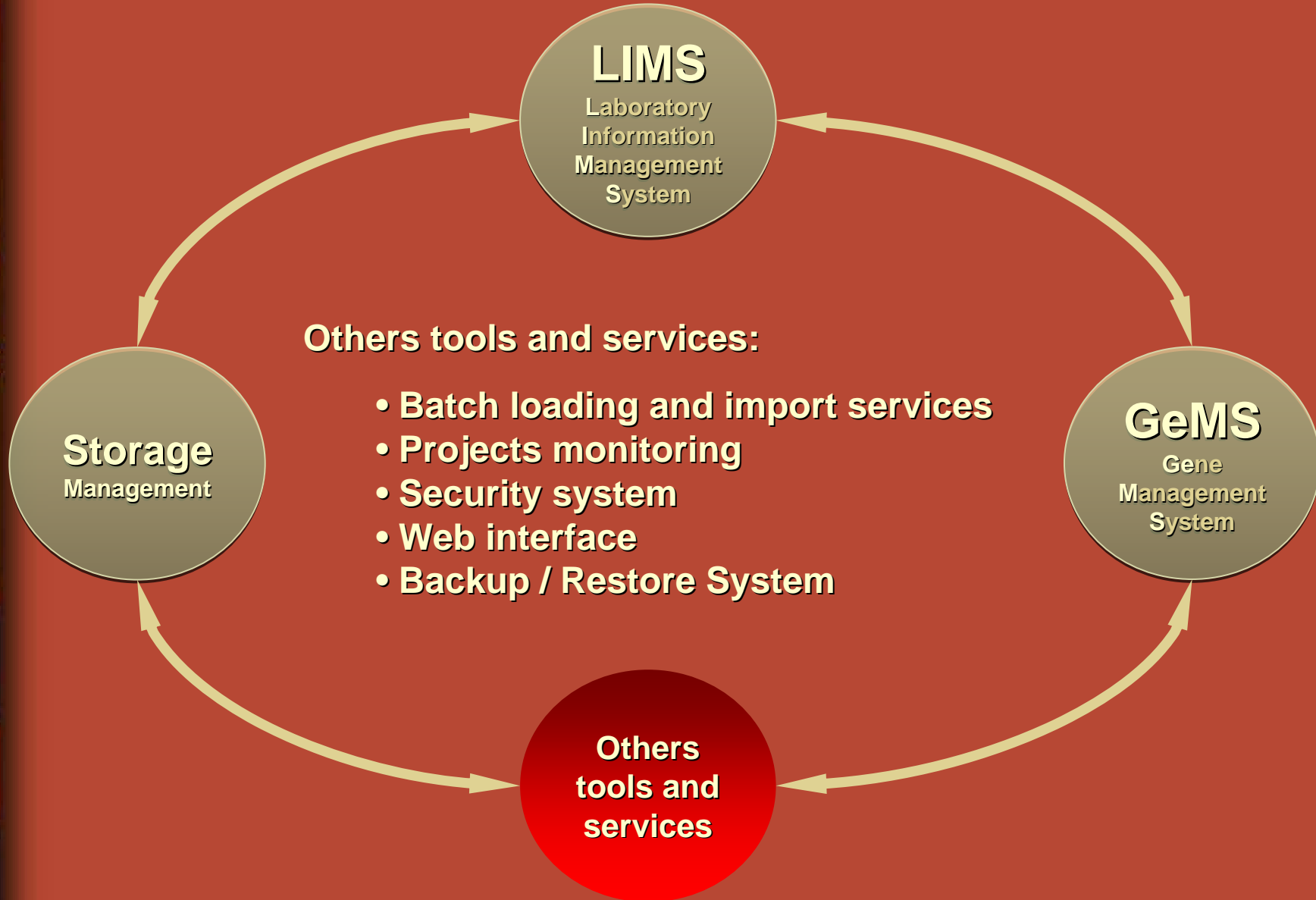
What is ICARDA Generation Genomics "LIMS and GeMS"?



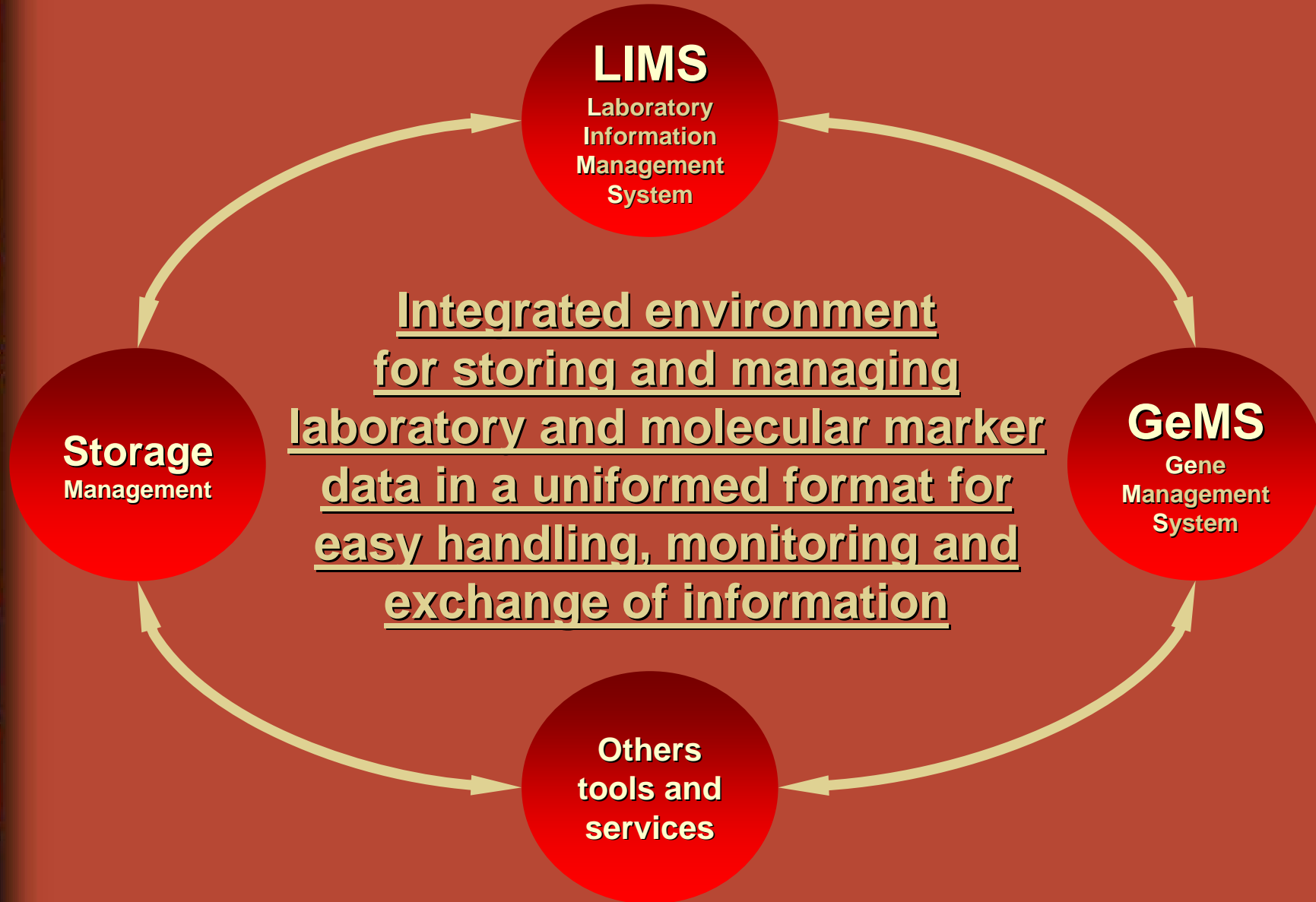
What is ICARDA Generation Genomics "LIMS and GeMS"?



What is ICARDA Generation Genomics "LIMS and GeMS"?



What is ICARDA Generation Genomics "LIMS and GeMS"?



What are Generation GLIMS And GeMS Inputs & Outputs?



What are Generation GLIMS And GeMS Inputs & Outputs?

Inputs

- Germplasm
- DNA Extraction
- DNA Dilution

Storage Management

LIMS

- DNA Quantification
- DNA Dilution
- PCR Tracking
- Plates Management
- Electrophoresis
- Security System

Outputs

- Project monitoring
- Stock monitoring
- Gel Images
- Elec. Images
- Genotypic Data.

XML



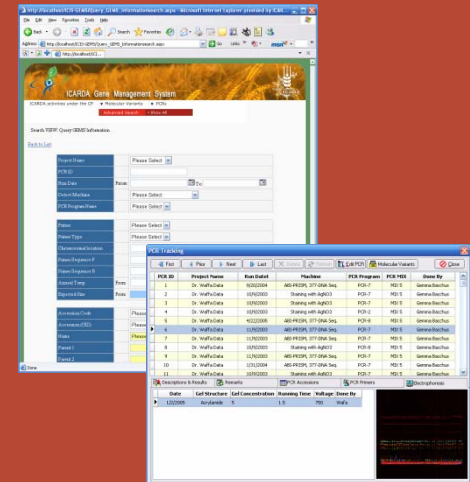
Markers

Extraction
Protocols

PCR
Programs

PCR Mix

PCR
machines



What is the relation between LIMS & ICIS?



What is the relation between LIMS & ICIS?

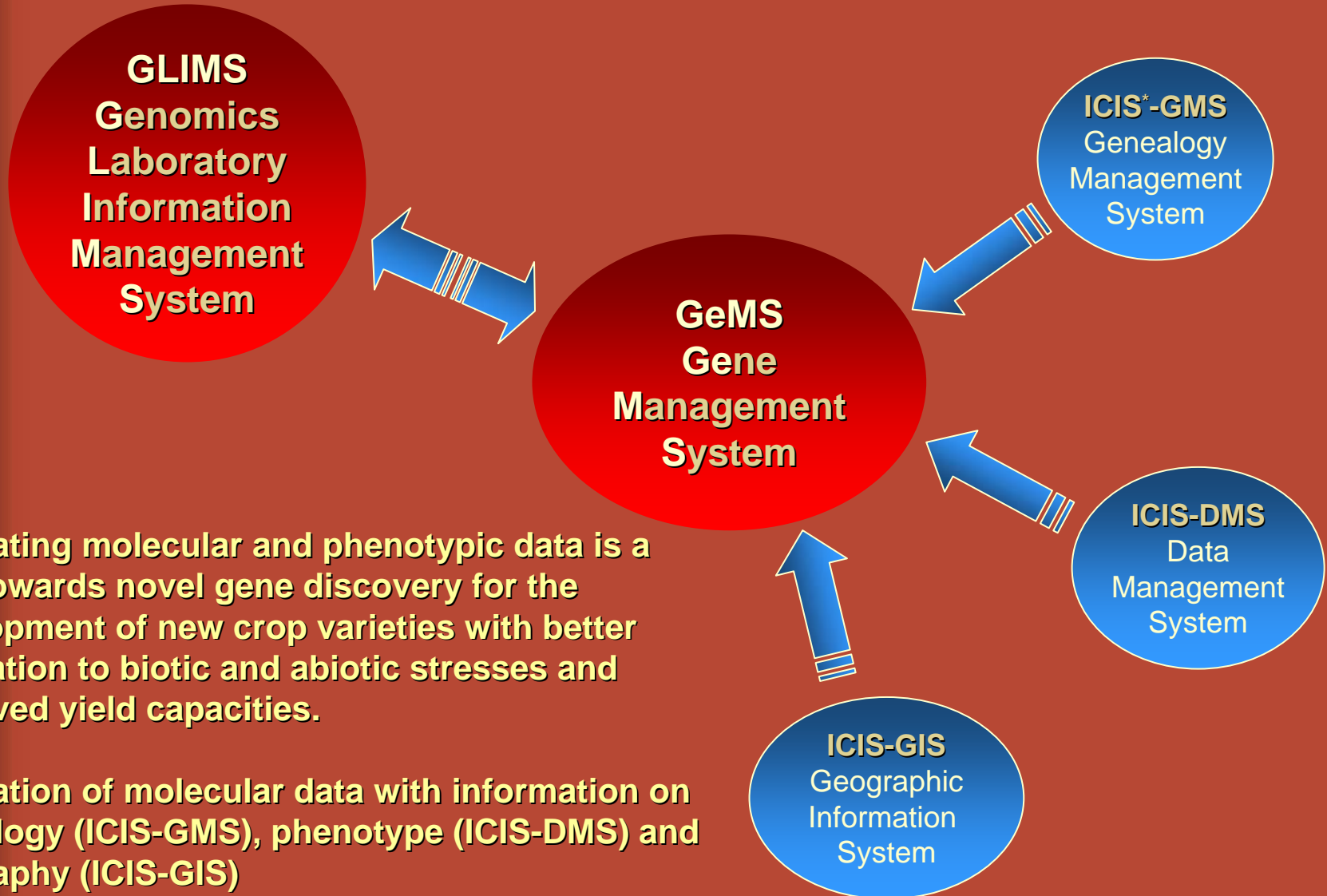
- **Genealogy (ICIS-GMS)**
- **Phenotype (ICIS-DMS)**
- **Geography (ICIS-GIS)**

ICIS*-GMS
Genealogy
Management
System

ICIS-DMS
Data
Management
System

ICIS-GIS
Geographic
Information
System

What is the relation between LIMS & ICIS?



Integrating molecular and phenotypic data is a step towards novel gene discovery for the development of new crop varieties with better adaptation to biotic and abiotic stresses and improved yield capacities.

Integration of molecular data with information on genealogy (ICIS-GMS), phenotype (ICIS-DMS) and geography (ICIS-GIS)

What can “LIMS and GeMS” do?

Some examples of different functions in ICARDA Generation Genomics LIMS and GeMS:

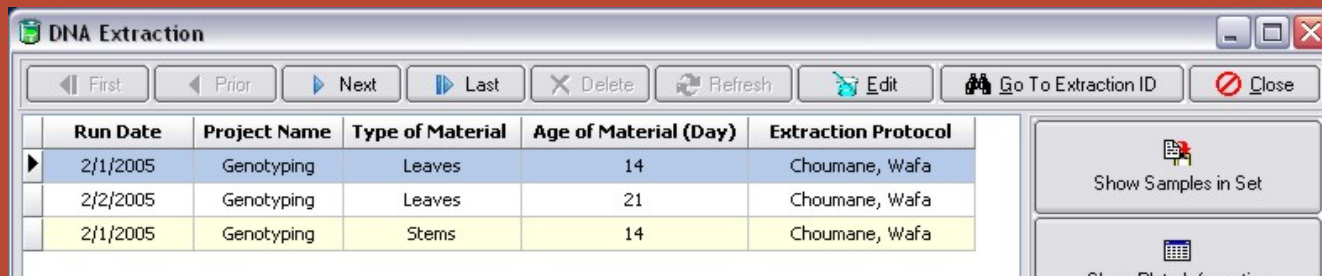


- Manage the information of DNA extraction
- Manage and Track PCR information
- My workspace
- Batch loading and import services
- Search depending on a range of different parameters
- The Web interface
- e-notification system (Storage Management)

Can I manage the information of the DNA extraction?



Can I manage the information of the DNA extraction?



The screenshot shows the 'DNA Extraction' software window. At the top, there are navigation buttons: First, Prior, Next, Last, Delete, Refresh, Edit, Go To Extraction ID, and Close. Below the buttons is a table with columns: Run Date, Project Name, Type of Material, Age of Material (Day), and Extraction Protocol. The table contains three rows of data. To the right of the table are two buttons: 'Show Samples in Set' and 'Show Plate Information'.

Run Date	Project Name	Type of Material	Age of Material (Day)	Extraction Protocol
2/1/2005	Genotyping	Leaves	14	Choumane, Wafa
2/2/2005	Genotyping	Leaves	21	Choumane, Wafa
2/1/2005	Genotyping	Stems	14	Choumane, Wafa



The screenshot shows the 'Plates Management - Dilution' software window. At the top, there are input fields for 'Final volume: 100' and 'Final Concentration: 10'. Below these are three dropdown menus: 'DNA Quantity (ul)', 'Dilution water (ul)', and 'Stock Concentration (ng/ul)'. To the right is a Close button. The main area is a grid with 8 rows (A-H) and 16 columns. Each cell in the grid contains a pair of values, such as '0.3 99.8' or '4000.000', representing DNA quantity and dilution water respectively for each well.

	DNA Quantity (ul)		Dilution water (ul)		Stock Concentration (ng/ul)										
A	0.3 99.8	0.1 99.929	0.2 99.8	0.1 99.9	0.1 99.9	0.1 99.9	0.5 99.5	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9
B	0.2 99.8	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.2 99.8	0.1 99.9	0.2 99.8	0.2 99.8	1.0 99.0	0.1 99.0
C	0.1 99.9	0.5 99.5	0.1 99.9	0.3 99.7	0.1 99.9	0.3 99.8	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9
D	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9
E	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.3 99.8	0.1 99.9
F	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.3 99.7	0.1 99.9	0.2 99.8	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9
G	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 100.0	0.1 99.9	0.1 99.9	0.1 99.9	0.3 99.8	0.1 99.9	0.2 99.8	0.1 99.9	0.2 99.8	0.1 99.9
H	0.1 99.9	0.1 99.9	0.5 99.5	0.1 99.9	1.0 99.0	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.1 99.9	0.2 99.8

- Add 2/3 volume of cold 2-propanol and cover with parafilm. Mix gently to precipitate the nucleic acids. Incubate in freezer for 30min.
- Centrifuge at 4000 rpm for 5 min.

DNA Extraction: Protocols, quantification, gel images, accession information, DNA dilutions (calculated by the program based on stem and final DNA concentrations)

Can I manage and track PCR information?



Can I manage and track PCR information?

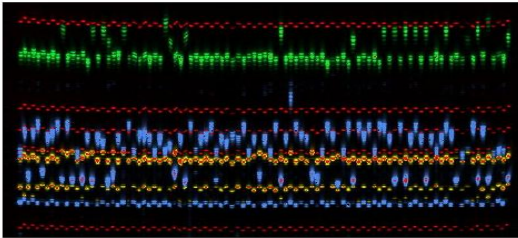
PCR Tracking

First Prior Next Last Refresh Edit PCR Molecular Variants Close

PCR ID	Project Name	Run Datet	Machine	Done By
63	CP Genotyping Lentil	8/23/2006	ABI-PRISM, 377-DNA Seq.	Hamwieh,
64	CP Genotyping Lentil	8/23/2006	ABI-PRISM, 377-DNA Seq.	Hamwieh,
65	CP Genotyping Lentil	8/23/2006	ABI-PRISM, 377-DNA Seq.	Hamwieh,
66	CP Genotyping Lentil	8/23/2006	ABI-PRISM, 377-DNA Seq.	Hamwieh,
40	CP Genotyping Barley	8/7/2006	ABI-PRISM, 377-DNA Seq.	Choumane,
41	CP Genotyping Barley	8/7/2006	ABI-PRISM, 377-DNA Seq.	Choumane,
42	CP Genotyping Barley	8/7/2006	ABI-PRISM, 377-DNA Seq.	Choumane,
43	CP Genotyping Barley	8/7/2006	ABI-PRISM, 377-DNA Seq.	Choumane,
2	Genotyping barley (Demo Data)	3/17/2006	Staining with AgNO3	Bacchus,
3	Genotyping barley (Demo Data)	5/21/2006	Staining with AgNO3	Bacchus,

Descriptions & Results Remarks PCR Accessions PCR Primers Electrophoresis

Primers Name	Color	Mix	Program
Scssr15864	Fam / Blue	MIX	PCR
Scssr02748	Vic / Green	MIX	PCR
Scssr25691	Ned /	MIX	PCR



Primer information

Primer Name: **Scssr15864** Color: **Fam / Blue**
 Primer Type: **SSR** Primer Origin:
 Chromosomal Location: **7H**
 Primer Sequence F: **GCATAAACGGGTGTAAGAGC**
 Primer Sequence R: **CATCCAGTTCAGAGGATAGAGC**
 Expected Size (bp):
 Length (F): **20** Length (R): **22**
 Anneal Temp.: **58**

Mix information

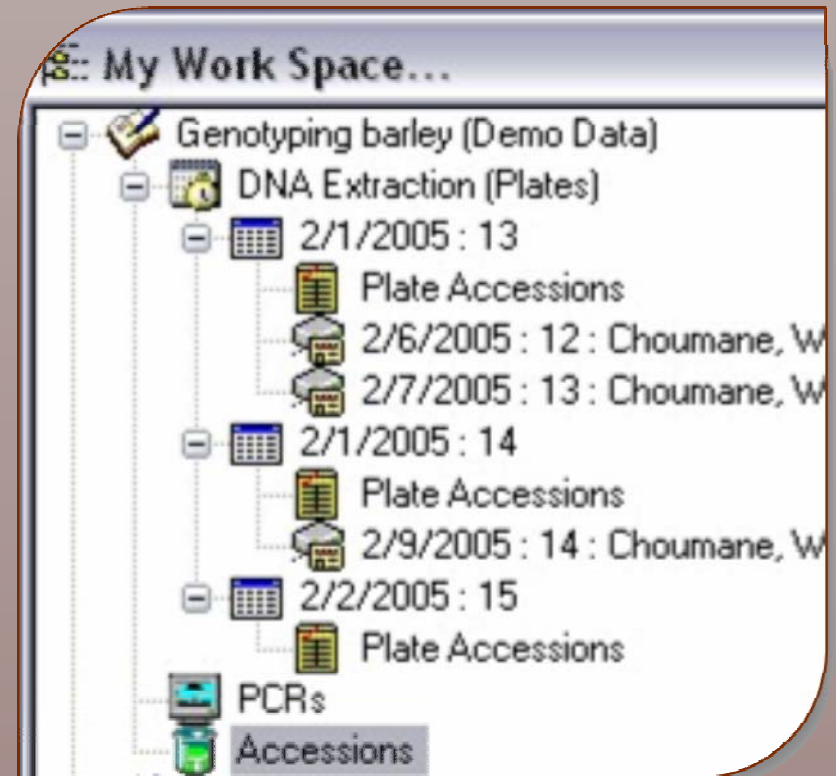
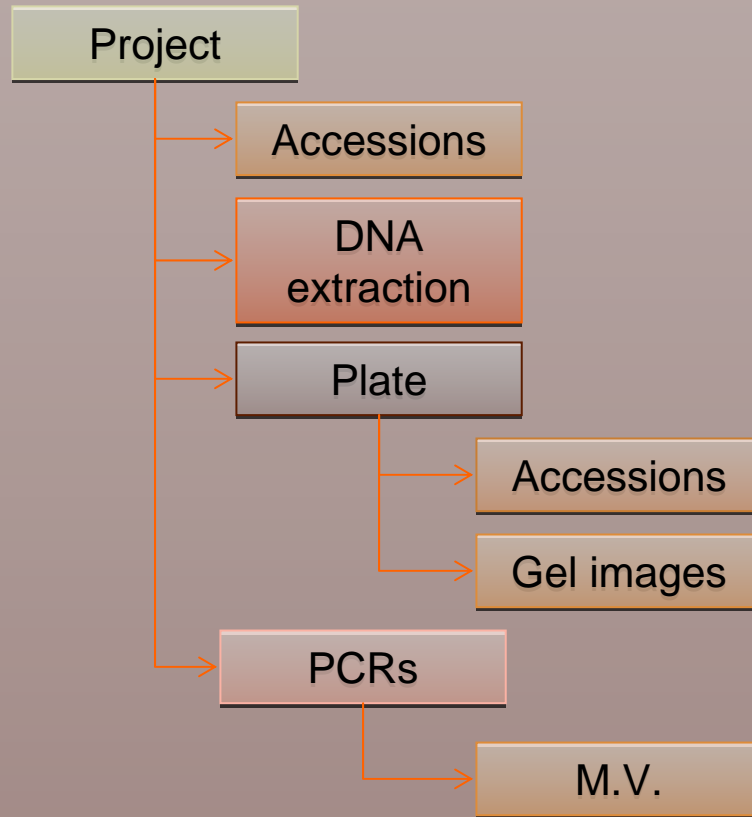
Program information

PCR Tracking: Managing the information of accessions, primers, programs, mixes and PCR conditions

What is my workspace?



What is my workspace?



My Work Space: A clear interface for information management: project information, accessions, DNA extraction (plates), gel images, PCR's and molecular variants

What is my workspace?

ICARDA Generation LIMS and GEMS

File DNA Extraction PCR Tracking Gene Management System Additional Information Storage Management Links Window About

My Work Space...

IG No.	Optical density (260)	Optical density (280)	Dilution Factor	Estimated DNA Concentration	Ratio	Tax Name	Accession Code	Project Acces
16898	0.80	0.90	200	8.0000	0.8889	Hordeum vu 1		1
16925	1.90	2.00	200	19.0000	0.9500	Hordeum vu 2		2
17554	1.10	1.20	200	11.0000	0.9167	Hordeum vu 75		75
17561	0.50	0.30	200	5.0000	1.6667	Hordeum vu 76		76
17566	1.00	1.10	200	10.0000	0.9091	Hordeum vu 77		77
17568	0.60	0.20	200	6.0000	3.0000	Hordeum vu 78		78
17579	1.10	1.50	200	11.0000	0.7333	Hordeum vu 79		79
17586	0.70	0.10	200	7.0000	7.0000	Hordeum vu 80		80
17596	1.20	1.25	200	12.0000	0.9600	Hordeum vu 81		81
17604	0.90	0.20	200	9.0000	4.5000	Hordeum vu 82		82
17611	1.30	1.30	200	13.0000	1.0000	Hordeum vu 83		83
17627	0.70	0.30	200	7.0000	2.3333	Hordeum vu 84		84
17628	1.40	1.40	200	14.0000	1.0000	Hordeum vu 85		85
17631	0.60	0.40	200	6.0000	1.5000	Hordeum vu 86		86

My Work Space...

Run Date (m/d/yyyy) Extraction ID Done By Project Name
 2/1/2005 13 Choumane, Wafa Genotyping barley (Demo Data)

Extraction Protocol Type of Materials Age of Material (Day)
 Legumes and pathogenic fungi Leaves 14

Extraction Protocol Details

1. Grind 0.3g of dry sample tissue (2g for fresh tissue) in 10ml of preheated (60C) 2X CTAB buffer. Transfer the fluid to a 50-ml Erlenmeyer flask.
2. Incubate in a shaking water bath (60C) for 30min.
3. Add 6.5 ml of chloroform:isoamylalcohol (24:1), and mix gently but thoroughly for 10min.
4. Transfer carefully to a corex tube and centrifuge at 4000rpm (1900g) for 15 min.

Remarks

2.0.1.4153

My Work Space: A clear interface for information management: project information, accessions, DNA extraction (plates), gel images, PCRs and molecular variants

Does LIMS have Batch loading and import services?




Does LIMS have Batch loading and import services?

Molecular Variants PCR ID. : 43

Lane No.	Accession Code	GID No.	Primer	MV Type	Molecular Weight	Allele No.	Quality	Amount
45	24		Scssr02748	Allele	143.22	144	200	1
27	21		Scssr02748	Allele	143.68	144	200	1
15	19		Scssr02748	Allele	143.93	144	200	1
21	20			Allele	143.94	144	200	1
65	258			Allele	144.39	144	200	1
39	23			Allele	144.44	144	200	1
30	398			Allele	145.08	144	200	1
9	18			Allele	145.23	144	200	1
27	235			Allele	145.28	144	200	1
80	180							1
37	515							1
15	233							1
90	310							1
57	26							1
68	275							1
51	25							1
78	308							1
4	475							1
20	564							1
28	581							1
22	613							1

Import ICARDA Dataset

1- Select data file:  C:\Documents and Settings\Hsimo\My Documents\VCIS-GEMS\VCIS-GEMS CD\Data

2- Select Crop Name: Lentil



3- Select Project Name: CP Genotyping Lentil

4- Select PCR:

- 52: 8/23/2006 : Hamwiah, Aladdin
- 53: 8/23/2006 : Hamwiah, Aladdin
- 54: 8/23/2006 : Hamwiah, Aladdin
- 55: 8/23/2006 : Hamwiah, Aladdin
- 56: 8/23/2006 : Hamwiah, Aladdin
- 57: 8/23/2006 : Hamwiah, Aladdin
- 58: 8/23/2006 : Hamwiah, Aladdin
- 59: 8/23/2006 : Hamwiah, Aladdin
- 60: 8/23/2006 : Hamwiah, Aladdin


5- Quality: 200
If the Quality measure is provided with the data then please provide details of the scale. This will depend on the genotyping software used. For example the LI-COR software provides a value from 0 to 100 or 200 if quality of the data is checked manually.

6- Loading: 0%



 Start Loading  Close

Batch Loading

1- Select machine name: ABI Sequencer 377

2- Select data file:  C:\Documents and Settings\Hsimo\My Documents\VCIS-GEMS\VCIS-GEMS CD\VCIS-GEMS

3- Loading: 0%

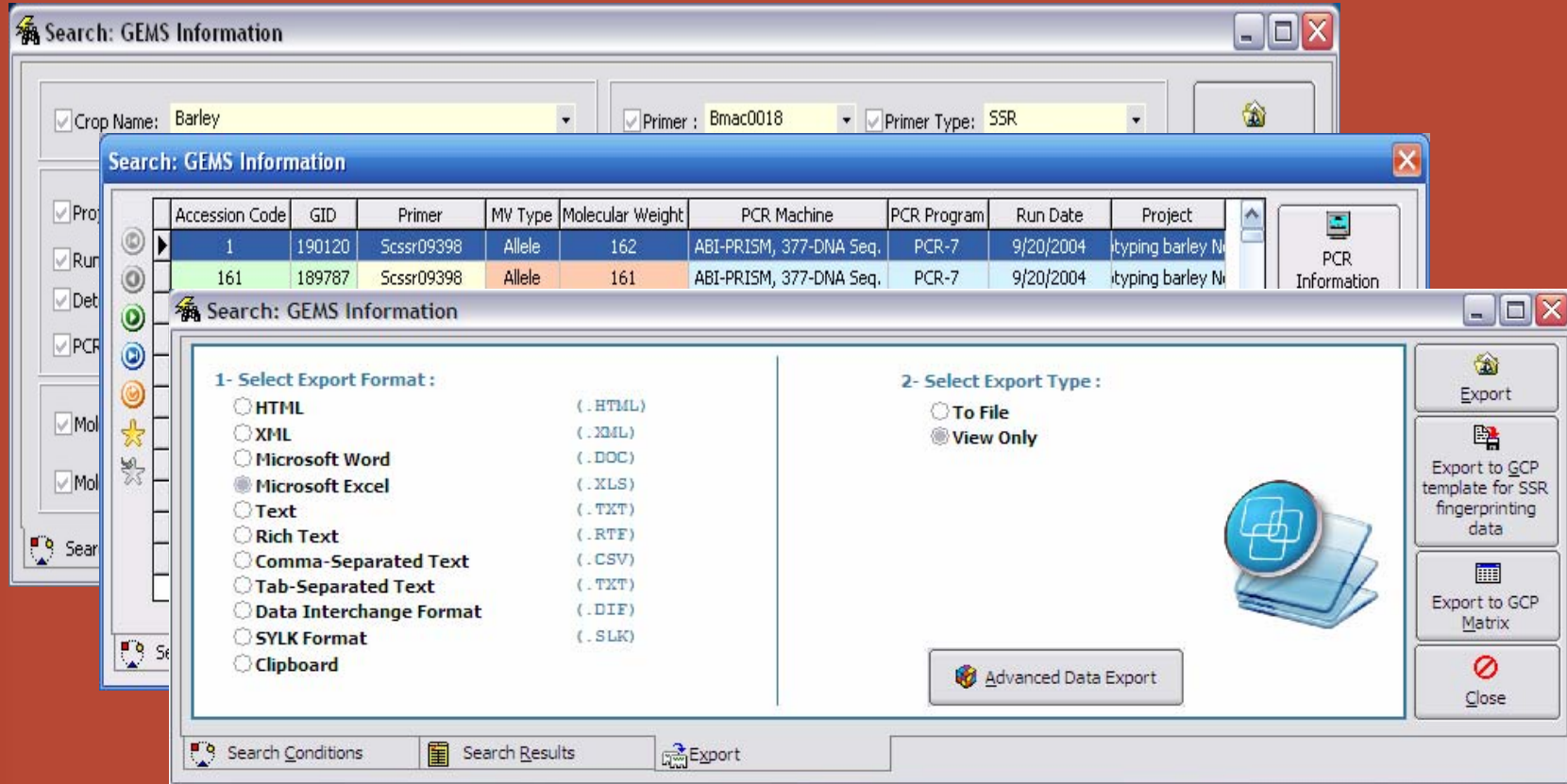
 Start Loading  Close

Batch loading and import services: The batch input program saves time and secures high accuracy for data entry by importing the information directly from the sequencer or excel files.

Can I search depending on a range of different parameters?



Can I search depending on a range of different parameters?



The screenshot displays the GeMS software interface. The top window, titled "Search: GEMS Information", shows search criteria: Crop Name: Barley, Primer: Bmac0018, and Primer Type: SSR. Below this, a table displays search results for two entries:

Accession Code	GID	Primer	MV Type	Molecular Weight	PCR Machine	PCR Program	Run Date	Project
1	190120	Scssr09398	Allele	162	ABI-PRISM, 377-DNA Seq.	PCR-7	9/20/2004	typing barley M
161	189787	Scssr09398	Allele	161	ABI-PRISM, 377-DNA Seq.	PCR-7	9/20/2004	typing barley M

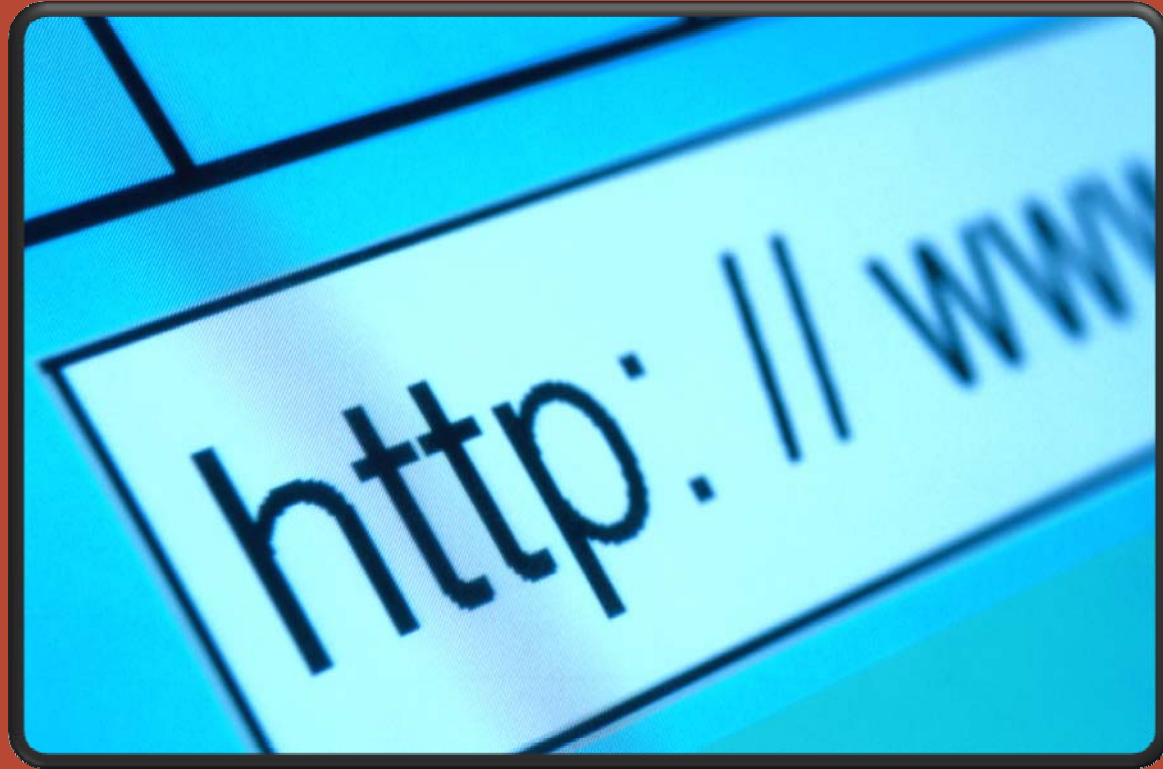
An "Export" dialog box is open in the foreground, titled "Search: GEMS Information". It contains two sections:

- 1- Select Export Format :**
 - HTML (.HTML)
 - XML (.XML)
 - Microsoft Word (.DOC)
 - Microsoft Excel (.XLS)
 - Text (.TXT)
 - Rich Text (.RTF)
 - Comma-Separated Text (.CSV)
 - Tab-Separated Text (.TXT)
 - Data Interchange Format (.DIF)
 - SYLK Format (.SLK)
 - Clipboard
- 2- Select Export Type :**
 - To File
 - View Only

Buttons for "Export", "Advanced Data Export", "Export to GCP template for SSR fingerprinting data", "Export to GCP Matrix", and "Close" are visible on the right side of the dialog box.

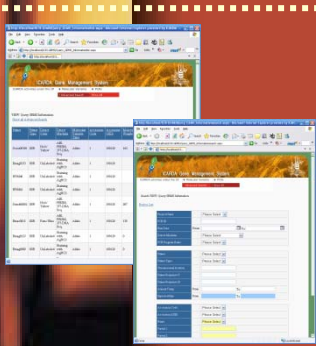
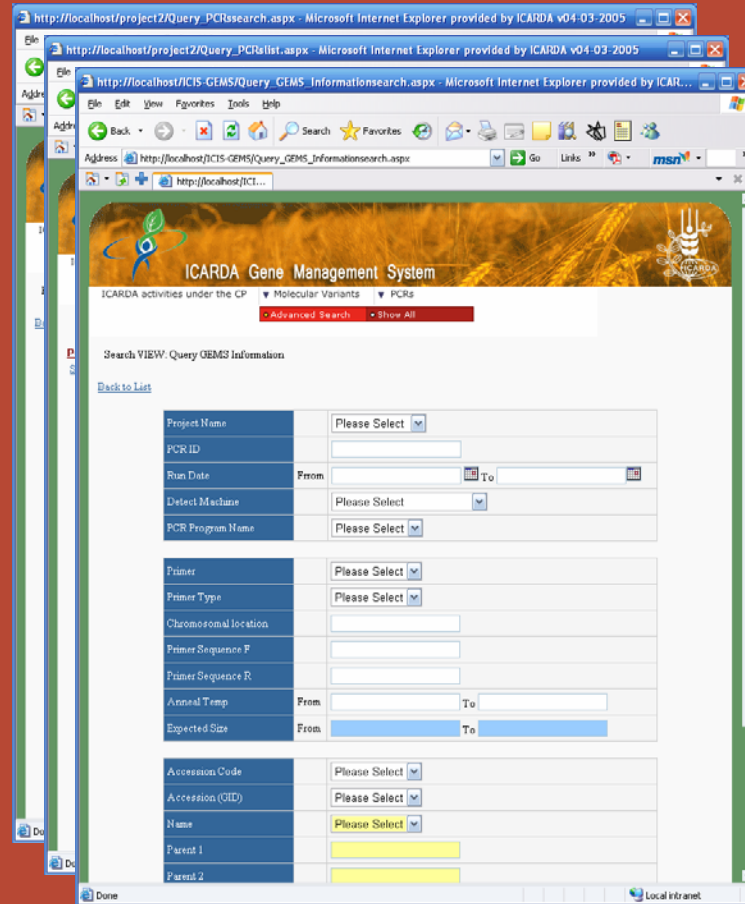
Search, browse and share: GeMS allows to search for a range of different parameters, to display the search results and export them in different formats (eg. HTML, XML, MS Word, MS Excel, Text, GCP format ... etc)

What is the web interface?

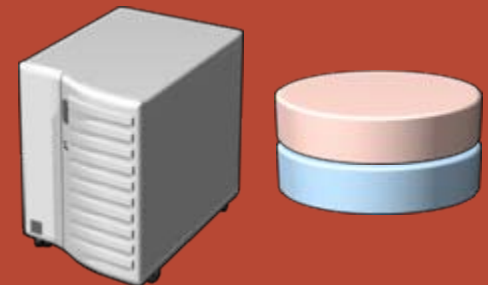


What is the web interface?

The Intranet / internet users can access the ICARDA genes' information from any computer without a special program, they only need an internet browser.



Web Clients



WEB Application

e-notification system (Storage Management)

The Storage Management Systems handle the materials used in the day to day work in the laboratories:

- Min and Max quantities of materials
- Expiring dates
- Storage places in the stores / fridges

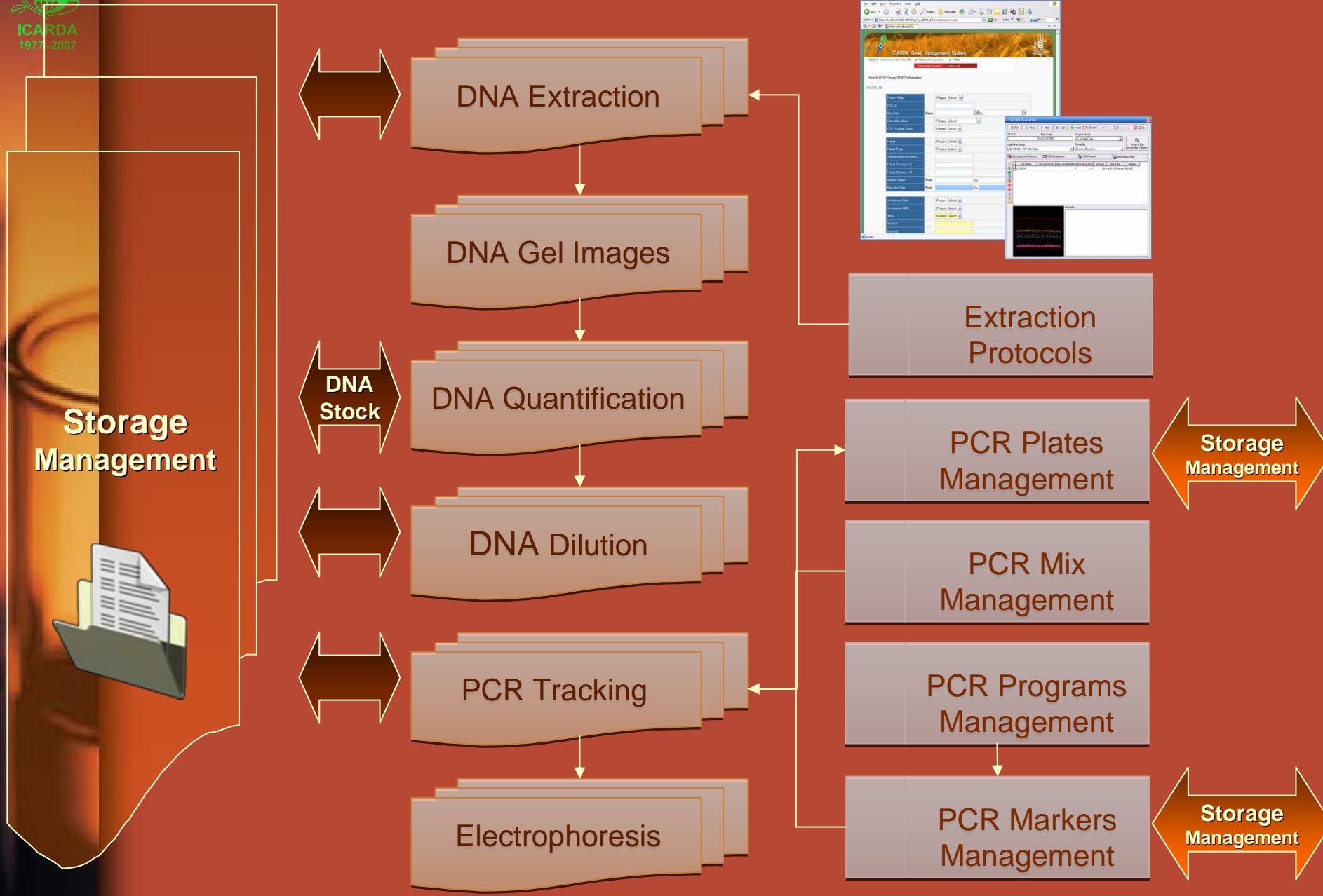
e-notification system sends an e-mail to stores' administrators when any user registers a new store request



Flow of Work Processes



Flow of Work Processes



Accessions

**Electrophoresis
Images**

Primers

GMS

**Gene
Management
System**

MV Types
(Allele, Morph, Nucleotide,
Fragment ... etc)

Molecular Variants

PCR Tracking

**Detect
Machines**

**PCR Mix
Information**

**PCR Program
Information**

PCR Tracking

PCR ID	Project Name	Run Date	Machine	PCR Program	PCR MIX	Done By
1	Dr. Waifa Data	9/20/2004	ABI-PRISM, 377-DNA Seq.	PCR-7	MIX 5	Genina Bacchus
2	Dr. Waifa Data	10/9/2003	Staining with AgtV03	PCR-7	MIX 5	Genina Bacchus
3	Dr. Waifa Data	10/9/2003	Staining with AgtV03	PCR-7	MIX 5	Genina Bacchus
4	Dr. Waifa Data	10/9/2003	Staining with AgtV03	PCR-2	MIX 6	Genina Bacchus
5	Dr. Waifa Data	4/22/2005	ABI-PRISM, 377-DNA Seq.	PCR-8	MIX 5	Genina Bacchus
6	Dr. Waifa Data	11/9/2003	ABI-PRISM, 377-DNA Seq.	PCR-7	MIX 5	Genina Bacchus
7	Dr. Waifa Data	11/9/2003	ABI-PRISM, 377-DNA Seq.	PCR-7	MIX 5	Genina Bacchus
8	Dr. Waifa Data	10/9/2003	Staining with AgtV03	PCR-8	MIX 5	Genina Bacchus
9	Dr. Waifa Data	11/9/2003	ABI-PRISM, 377-DNA Seq.	PCR-7	MIX 5	Genina Bacchus
10	Dr. Waifa Data	1/31/2004	ABI-PRISM, 377-DNA Seq.	PCR-7	MIX 5	Genina Bacchus
11	Dr. Waifa Data	10/9/2003	Staining with AgtV03	PCR-7	MIX 5	Genina Bacchus

Primer Information

Primer Name: 19762 (L1Label)

Primer Type: SSR

Chromosomal Location: 3P1

Primer Sequence F: TCGGACCAAGGAG

Primer Sequence R: AGCTAGCCAGAG

Expected Size (bp): 251

Length: 18

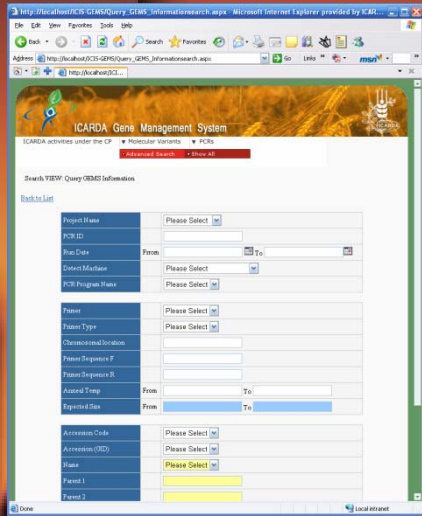
Anneal Temp.: 58

ICARDA Gene Management System

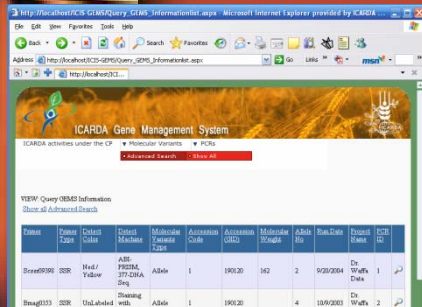
ICARDA Gene Management System

ICARDA Gene Management System

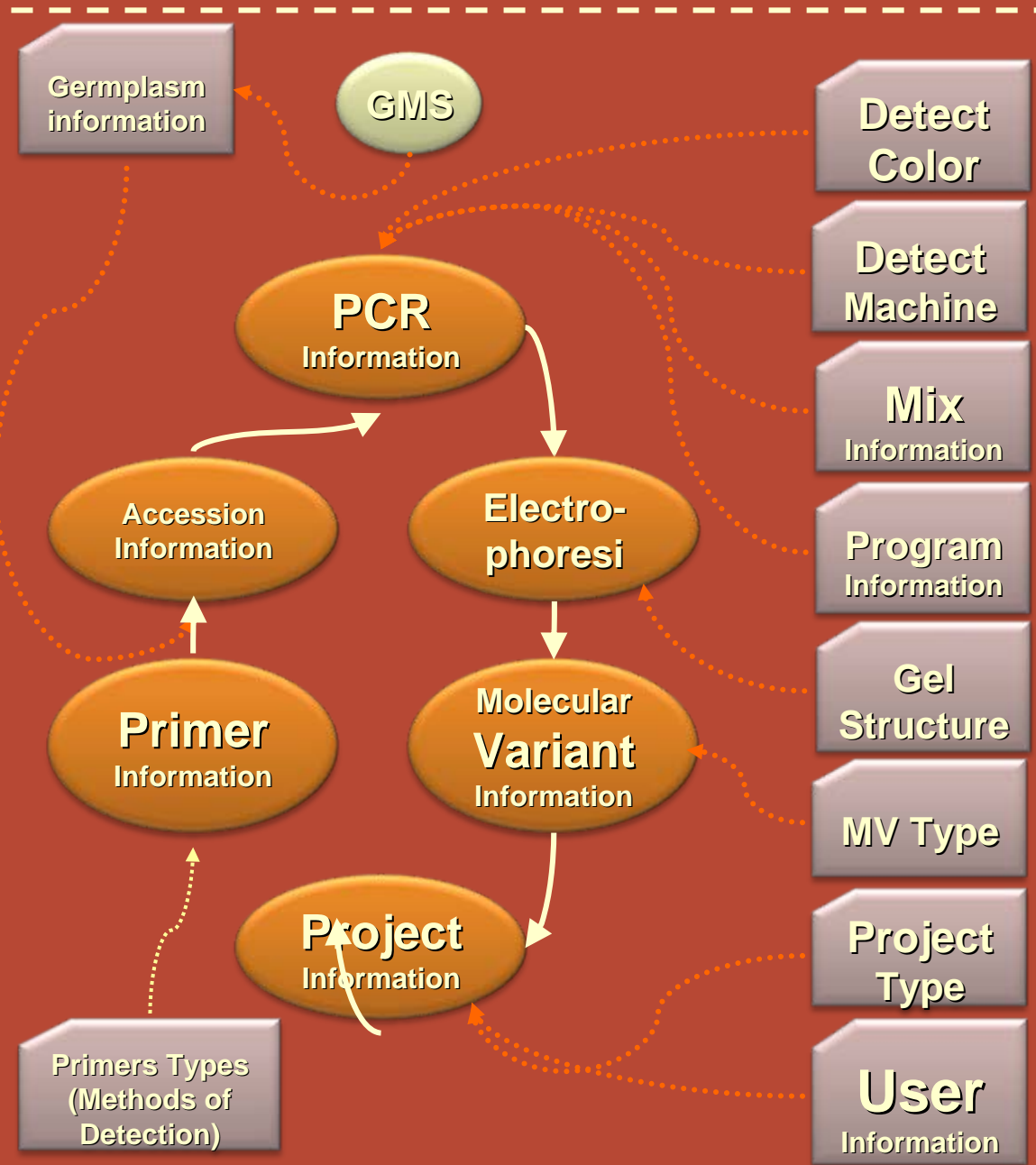
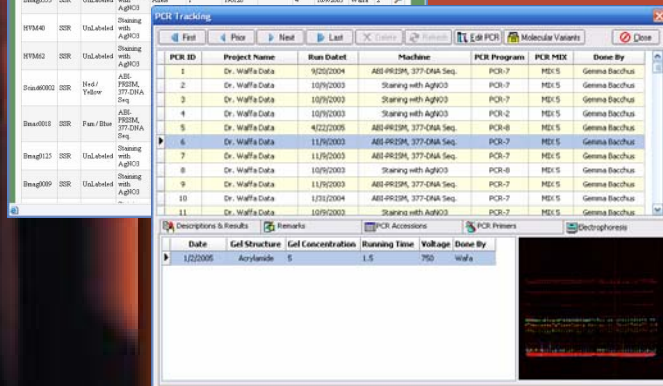
ICARDA Gene Management System...



Request



Response



How can "LIMS and GeMS" help the end users?



How can "LIMS and GeMS" help the end users?

Who are the expected users of "LIMS and GeMS"?



How can "LIMS and GeMS" help the end users?

Who are the expected users of "LIMS and GeMS"?

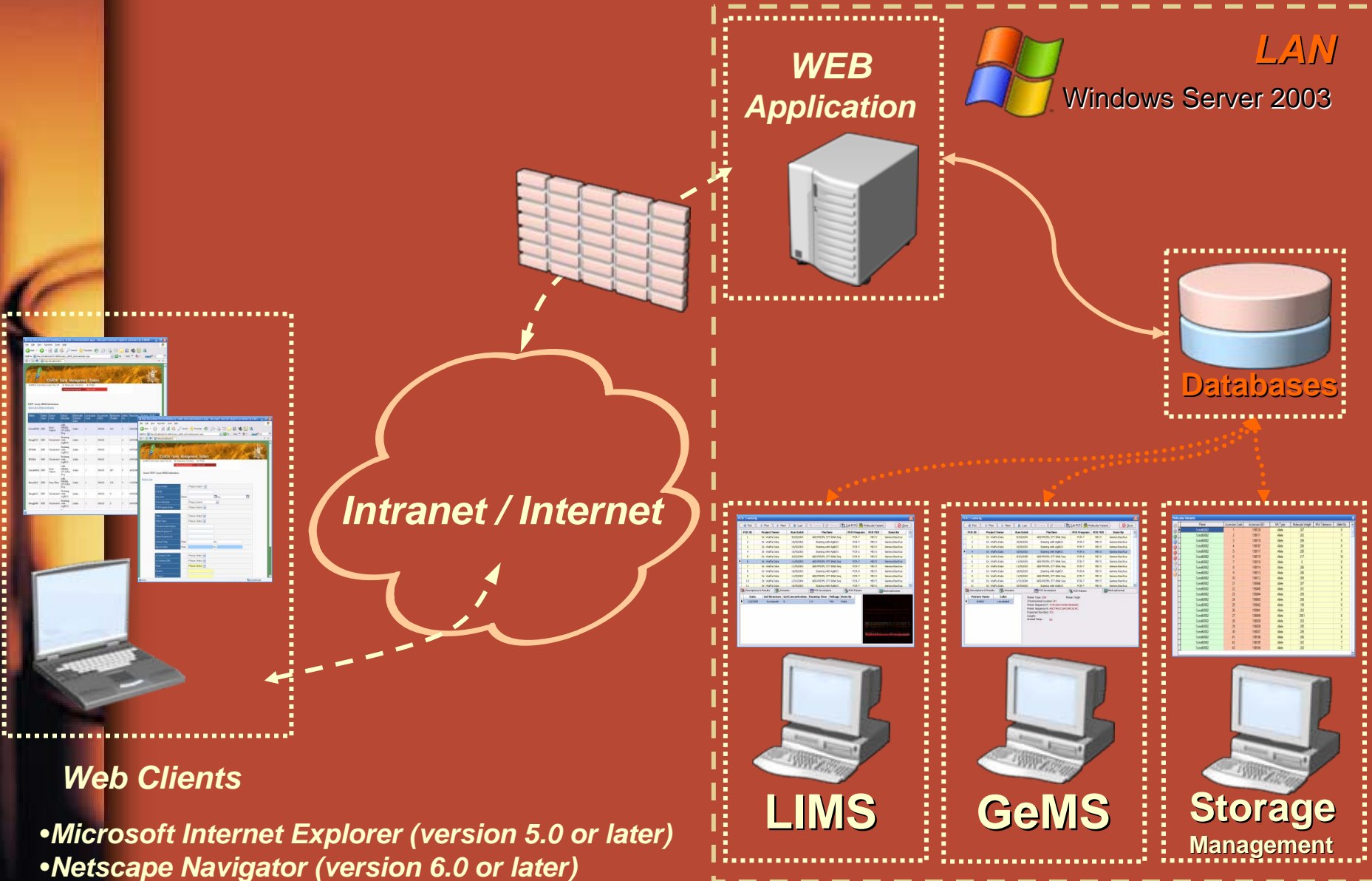
- Technicians: they enter the data of the daily work (plates information, DNA extraction, quantification, dilution, etc).
- Researchers (professional users): they analyze, evaluate, import, export data, etc.



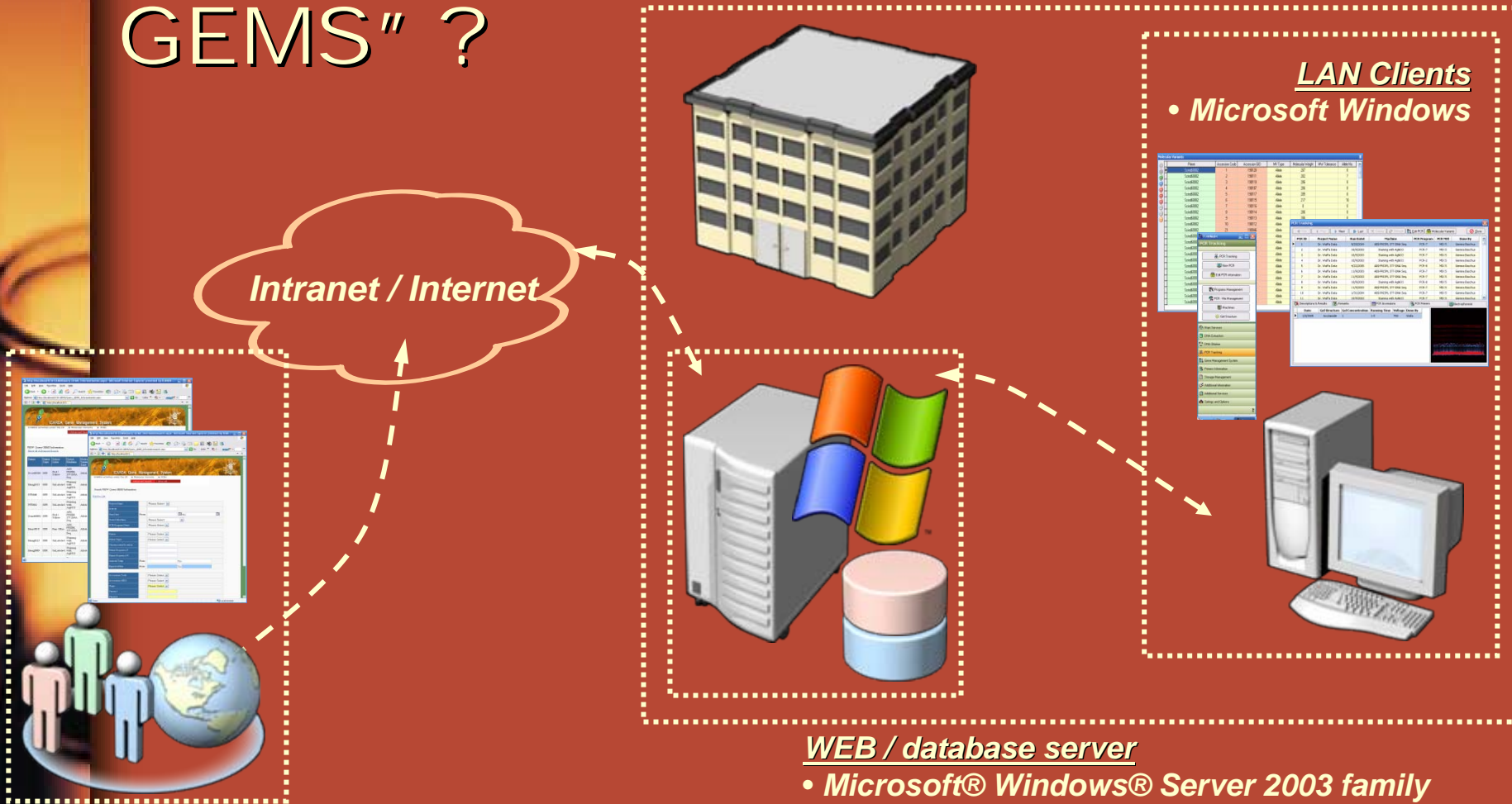
How can “LIMS and GeMS” help Researchers and Technicians (the end users)?

- Collect and Link data generated during work steps, perform documentation, calculations and review results using integrated database...
- Supervise the lab process, react to bottlenecks in workflow and ensure regulatory demands.
- Follow up on progress, review results and print out reports and other documentation (perhaps even historically).

How does LIMS work?



What do I need in order to run ICARDA Generation "LIMS & GEMS" ?



Web Clients:

- *Microsoft Internet Explorer (version 5.0 or later)*
- *Netscape Navigator (version 6.0 or later)*

WEB / database server

- *Microsoft® Windows® Server 2003 family*
- *Microsoft Internet Information Services*
- *.NET Framework 1.0/1.1.*
- *Microsoft Data Access Components*

What about security issues



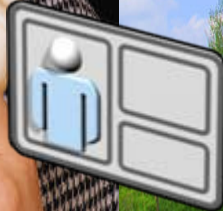
There are three levels of security access in “LIMS & GEMS” :

Administrators: Users who have these accounts are responsible for managing the data (Add/ Modify/ Delete). These accounts have all permissions on the system.

Users: All users can browse and search data. Users can only modify their own data but not the data entered by someone else.

Guests: This account is read only. This means users with guest Privileges can only browse and search.

How does the security system work?



Local Network

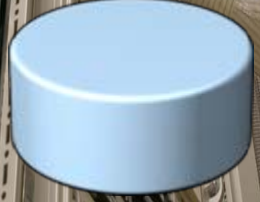
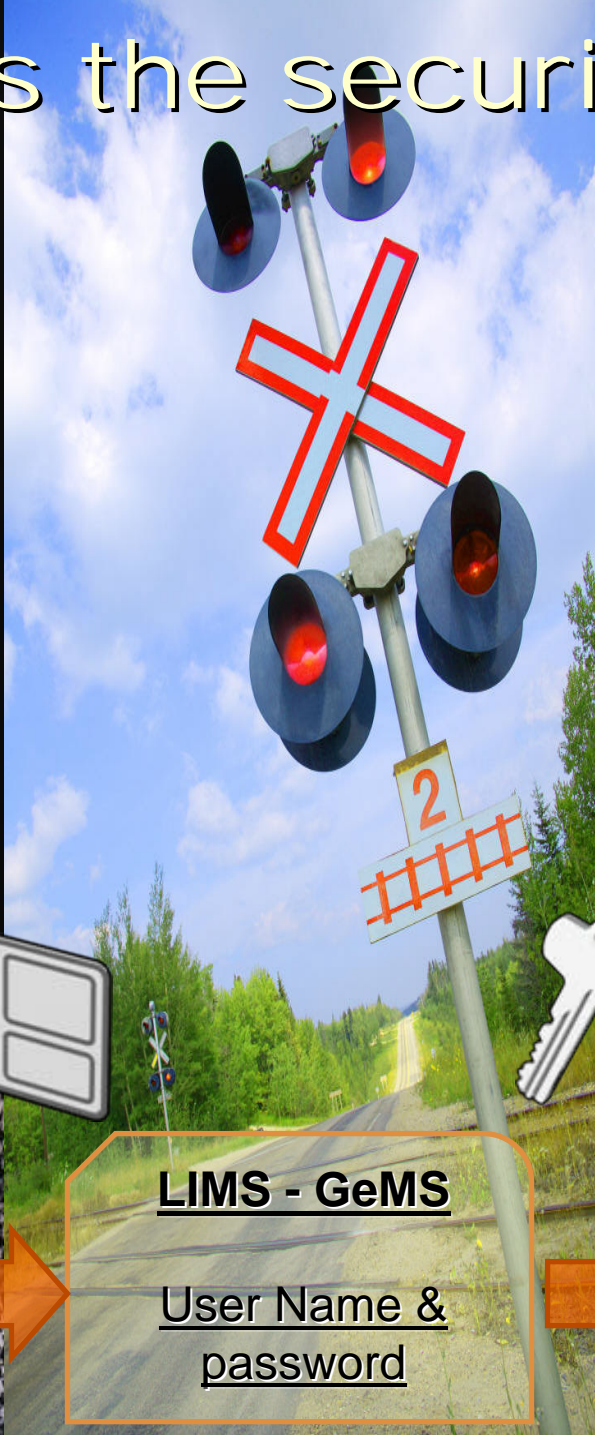
User Name & password

LIMS - GeMS

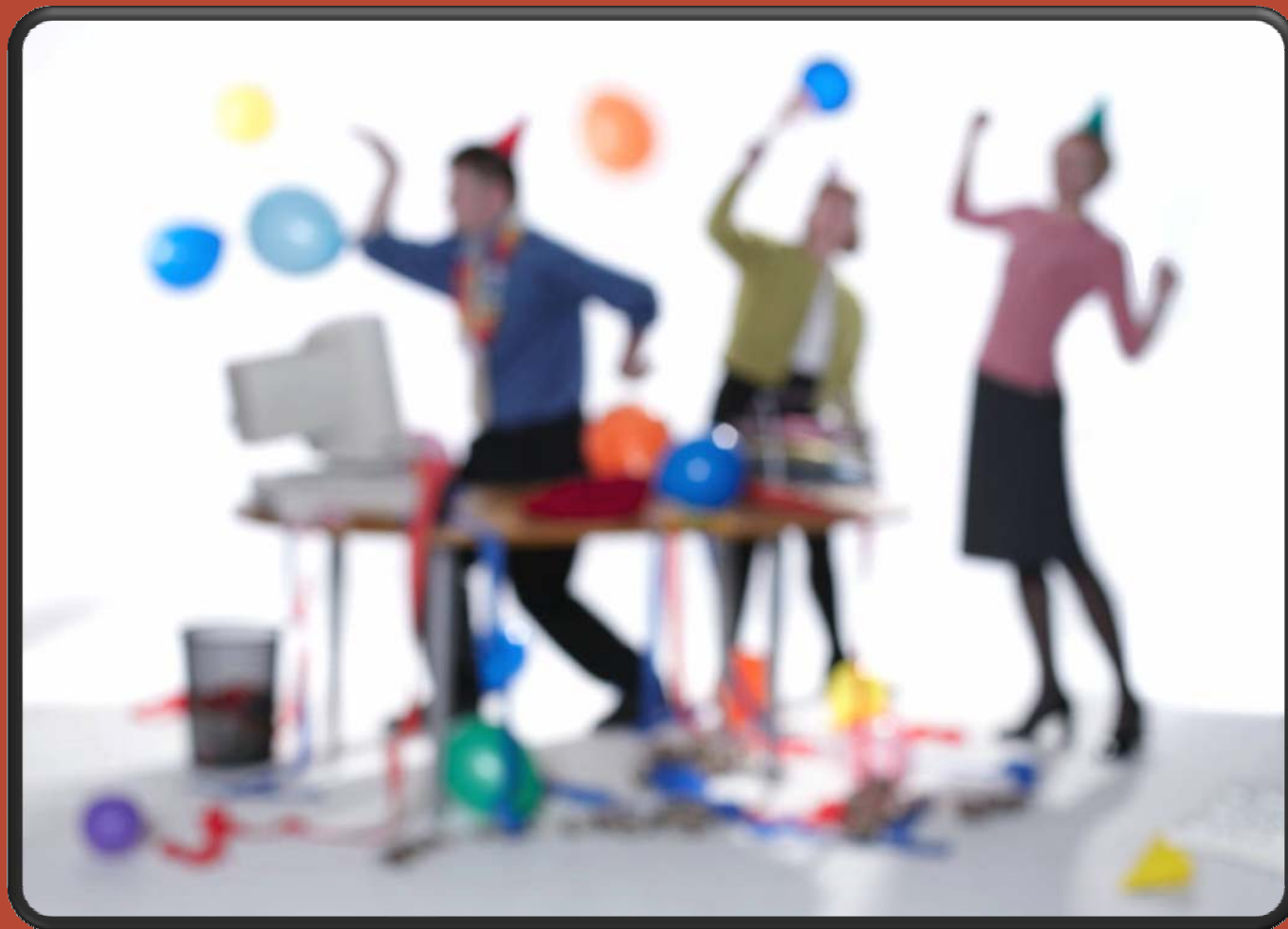
User Name & password

Microsoft SQL Server

User Name & password



What are our achievements?



What are our achievements?

- Uploading information on primers, accessions and genotype data of the commissioned genotyping projects (GCP) in barley, lentil and chickpea carried out at ICARDA
- Uploading ICARDA lab procedures into GLIMS
- Add support GCP dataset template for SSR fingerprinting data.
- A new export service in ICARDA Generation Genomic GeMS to create the Molecular Variants information as a Matrix
- Now our Genomic LIMS and GeMS can handle accessions information depending on many IDs (like IG, ICC ... etc), it stores ICIS GID as the default identifier for Accessions...

What are our next steps? (What's next?)

- **Visualisation tools: statistics graphs and reports...**
- **Output for immediate use in different analysis programs (Darwin, NTSYS, Tassel, Structure, PopGen, Arlequin)**
- **Developing a database for storing results of QTL analyses and association mapping for integrating data across different populations and studies**
- **Developing an interface for retrieving data from ICIS-DMS (phenotype data), ICIS-GMS (genealogy) and ICIS-GIS**
- **Microsatellite finder and primer designer: fully integrated with ICARDA GLIMS & GeMS**

Visualisation tools: statistics graphs and reports...



Why Microsoft SQL Server 2005 Express?



Why Microsoft SQL Server 2005 Express?

- Database Size: 4 GB
- Online System Changes: Includes Hot Add Memory, dedicated administrative connection, and other online operations.
- Auto Tuning: Automatically tunes database for optimal performance
- Serviceability Enhancements: Dynamic management views and reporting enhancements.
- Full-text Search
- Advanced Auditing, Authentication, and Authorization
- Data Encryption and Key Management: Built-in data encryption for advanced data security.

Why Microsoft SQL Server 2005 Express?

- Native XML: Includes XML indexing and full-text XML search (Native XML data can be stored, queried, and indexed in a SQL Server).
- User-defined Types: Extend the server with your own custom data types.
- Transact-SQL (T-SQL) Enhancements: Includes exception handling, recursive queries, support for new data types, error handling, recursive query capabilities, relational operator PIVOT, APPLY, ROW_NUMBER and other row ranking functions, and more.
- Integration with Microsoft Update
- SQL Server Management Studio Express : Easy-to-use graphical management tool.
- SQL Analytical Functions and Star Query Optimization

Why Microsoft SQL Server 2005 Express?

- Native Support for Web Services: With SQL Server 2005 developers can develop Web services in the database tier, making SQL Server a hypertext transfer protocol (HTTP) listener and providing a new type of data access capability for Web services-centric applications.

Why Microsoft SQL Server 2005 Express?

- Visual Studio Integration: Tight integration with Microsoft Visual Studio and the .NET Framework streamlines development and debugging of data-driven applications. Developers can build database objects, such as stored procedures, using any .NET language and can seamlessly debug across .NET and Transact-SQL (TSQL) languages.

Why Microsoft SQL Server 2005 Express?

ICARDA Generation Genomics
“LIMS and GeMS”

Microsoft Office

Microsoft Office
SharePoint
Portal Server 2003

Third Party
Apps

Microsoft
SQL Server 2005 Express

Reporting Services

Analysis Services

Notification Services

Data Transformation Services

Replication Services

Relational Database

Management
Tools

Microsoft
Windows Server 2003

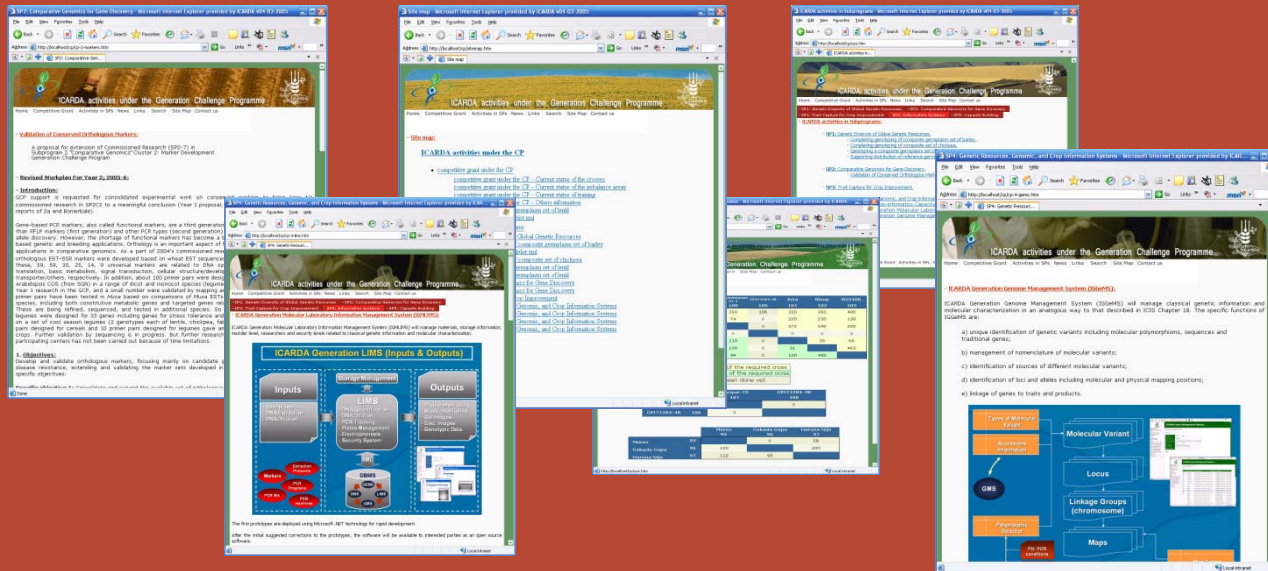
Why ADO.NET?



Why ADO.NET?

- The standard way to access data in .NET
- Familiar to most .NET developers
- Data Providers do the dirty work
- Developer has maximum control / flexibility
- Ease of switching data providers makes phased migration easier
- Very low cost
- Updating Data more efficiently (Faster, Easier transactions and Better caching strategies)
- Better caching strategies

Where can I get more information?



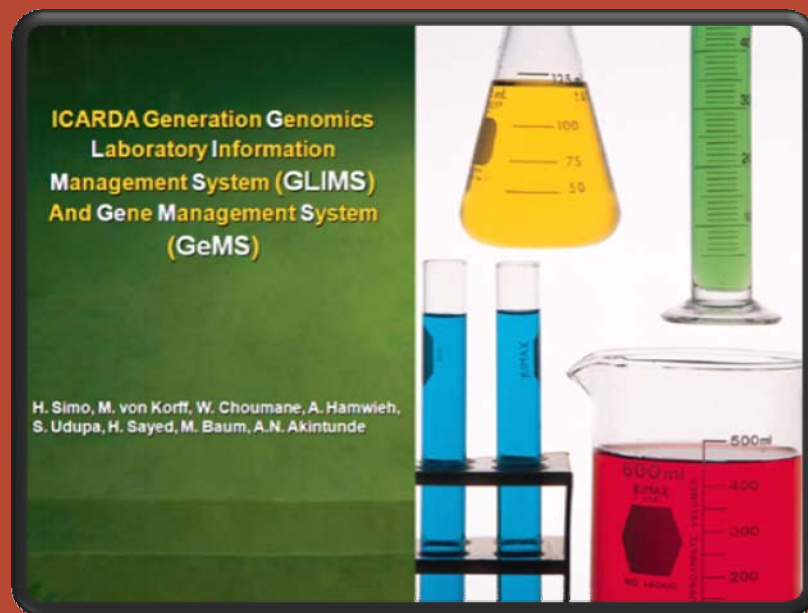
The web pages of ICARDA activities under the CP:
<http://www.icarda.org/generationcp/>

This website provides information and details about ICARDA's activities under Generation Challenge Program, you can find the latest information, news, progress reports And full contact information of ICARDA Generation Challenge Program Team work.

Where can I get more information?

More information and details available on:

<http://www.icarda.org/GenerationCP/igglimsgems/>



ICARDA Generation Genomic LIMS & GeMS

Introduction:

With the large amount of molecular data generated through the commissioned research of the Generation Challenge Program (GCP), it becomes imperative to provide tools to the researchers to store, organize and analyze the data and thus support decisions by stakeholders. Integrating molecular and phenotypic data is a step towards novel gene discovery for the development of new crop varieties with better adaptation to biotic and a biotic stresses and improved yield capacities.

Objectives:

- Integrated environment for Genomic LIMS, GeMS and Storage Management
- Output for immediate use in different analysis programs (Darwin, NTSYS, Tassel, Structure, PopGen, Arlequin)
- Effective capture, storage and documentation of laboratory protocols, procedures, practices and output data (Genomic LIMS)
- Storage and management of molecular marker data in readily useable formats (GeMS)
- Integration of molecular data with information on genealogy (ICIS-GMS), phenotype (ICIS-DMS) and geography (ICIS-GIS)
- Creation of a searchable WEB based user friendly interface to enhance allele mining
- User-friendly program for storing and managing laboratory procedures and molecular marker data in an uniform format for easy exchange of information

Laboratory Management System (LIMS) at ICARDA:

The International Centre for Agricultural Research in Dry Areas (ICARDA) is one of the leading centre among the Consultative Group on International Agricultural Research (CGIAR) that has taken the bull by the horn by the development of a user friendly Laboratory Management System specifically to target the protocol, processes and materials in a Molecular Laboratory setting, thanks to the support of the Generation Challenge Program on "Cultivating Plant Diversity for the Resource poor"

The software includes:

1. Storage management modules (for materials used in the laboratory)
2. Laboratory Information Management Modules
 - i. Germplasm
 - ii. DNA Protocols, extractions, dilutions, quantification
 - iii. PCR machines, programs, mixes, & tracking
 - iv. Plates Management, Electrophoresis
 - v. Security System
3. Genomic Management Modules (Windows and WEB applications)
 - i. Project monitoring
 - ii. Stock monitoring
 - iii. Gel & Electrophoresis images
 - iv. Genotypic data

Genomic Management Systems (GeMS) at ICARDA:

The GeMS seamlessly integrates with the LIMS and indeed the lines between the two is very thin because the information collected and managed by the LIMS is what the GEMS exposes at three different levels, first at the level of an administrator of the database, then at the level of a particular technician/researcher in the laboratory generating the information and lastly at the level of a guest that may only browse the information in the database for information. This user may have read only access to the information contained in the database.

Information could be searched based on exposed list of criteria which includes the list under LIMS above.

What next?

- Integrated user environment for linking genomic data to ICIS-DMS (phenotype data), ICIS-GMS (genealogy) and ICIS-GIS
- Developing a database for storing results of QTL analyses and association mapping for integrating data across different populations and studies
- Microsatellite finder and primer designer: fully integrated with ICARDA Genomic LIMS & GeMS

ICARDA Generation Genomic LIMS & GeMS Downloads:

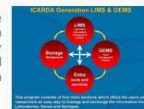
- [Brochure](#)
- [Introduction](#)
- [Read me](#)
- [System Specification](#)
- [User Manual](#)
- [Install Package and MS SQL Server Database files](#)



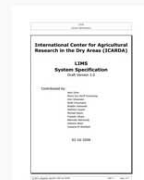
GLIMS & GeMS Brochure



Introduction



Read me



System Specification



User Manual