

Rice Gene Machine Information Management System (RGMIMS)

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Introduction to RGMIMS

- **A product of the collaboration between CSIRO Plant Industry Rice Functional Genomics Project and CSIRO Mathematical and Information Sciences.**
- **A Laboratory Information Management System (LIMS) for plant functional genomics, particularly rice mutagenesis.**
 - Helps biologists, lab managers and technicians manage the high volume of data generated by large-scale, high-throughput rice insertional experiments.
- **Comprises software and laboratory processes**
 - Currently operational in a wet-laboratory
- **The system components are**
 - A Web based desktop system integrated with barcode devices and sequence preprocessing software
 - Palm device applications for the “mobile worker” for activities including phenotyping, harvesting....
 - Web-pages with dynamic, up-to-date and consolidated information on mutant lines



Introduction to RGMIMS

- **Modular system implemented incrementally**
- **CSIRO is looking for opportunities to collaborate to continue the development of RGMIMS as a generic LIMS to increase its rate of adoption and impact.**
 - Initially developed for the Rice Gene Machine Project at CSIRO and their external collaborators, keeping in mind its possible applications in other areas.
 - Developed with financial support from NSW Agricultural Genomics Center, which ends in June 2006.



The Benefits of RGMIMS as Perceived By The Users

- **Designed with biologists' requirements in mind.**
- **Better data integration and management.**
- **Generally the UI is easy to use, unambiguous and intuitive and facilitates high-volume data entry.**
- **Enforces data quality and consistency through in-built error-checking based on lab procedures.**
- **Makes information accessible.**
- **Provides a “single source of truth” through centralised data storage.**
- **Provides specimen traceability and barcode tracking.**
- **Integrates experimental data with external data sources, including**
 - **Ontologies - Plant Ontology's Anatomical and Development Stage Ontologie; Gramene's Trait and Environment Ontologies**
 - **NCBI's Species Taxonomy**



RGMIMS Software Development Features

- **Develop software modules and functionality based on the model of the laboratory's workflow and the model of laboratory requirements**
- **Develop modules iteratively and incrementally and focusing first on user determined high priority use cases / functionality**
- **Model laboratory object (concepts/entities) and their relations**
- **Evolutionary approach to a working system – begin with prototype GUI to validate requirements & to reduce risk of rework. Rework can delay the project considerably. However there is still the potential for rework once the users start using the system extensively.**
- **Produce business process workflows, - workflow integrated with system functionality.**
- **Conduct unit, system and acceptance testing to ensure quality software and software passes acceptance criteria.**
- **Incremental conversion of legacy data.**



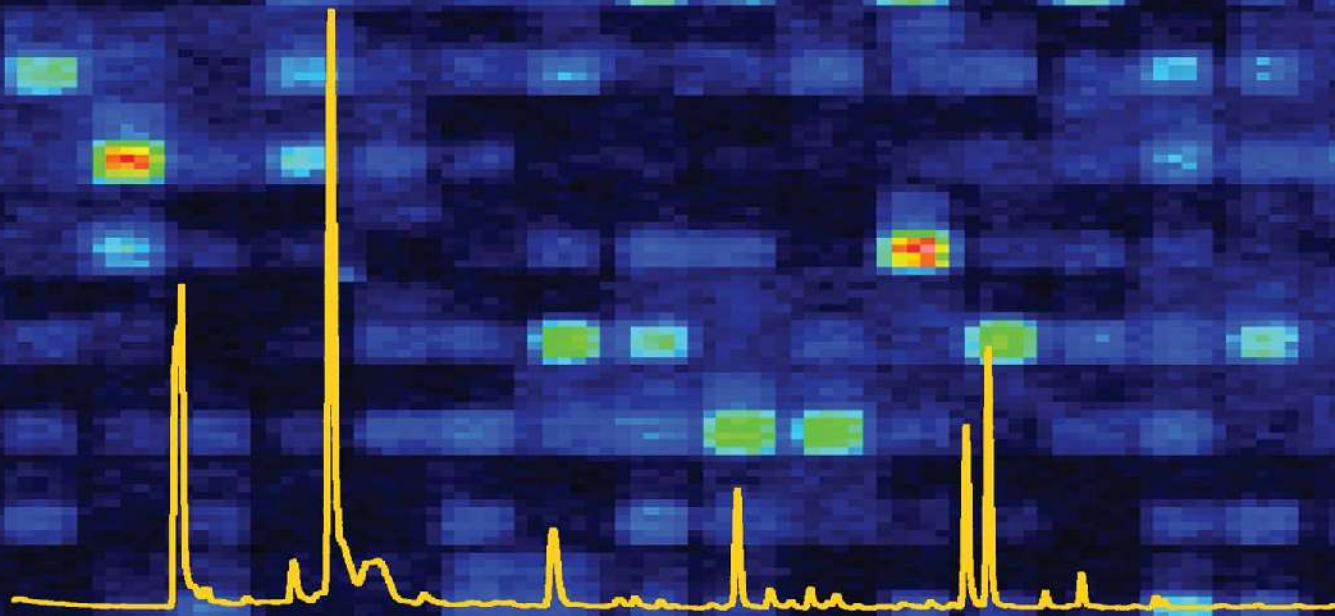
Features of Software Development

- **Development environment**

- Complex and rich system functionality.
- Development team –
 - 1 full time staff performing multiple roles of project manager, software developer and business analyst
 - A team of domain experts (research scientists, lab manager and technicians).
- Development tools - Apache Tomcat 5; SQLServer 2000; Ant build; Java 1.5; Java Help 2.0 to build online help; Design Patterns; CVS; JBuilder



Online Demo



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www.pi.csiro.au/fgrttpub

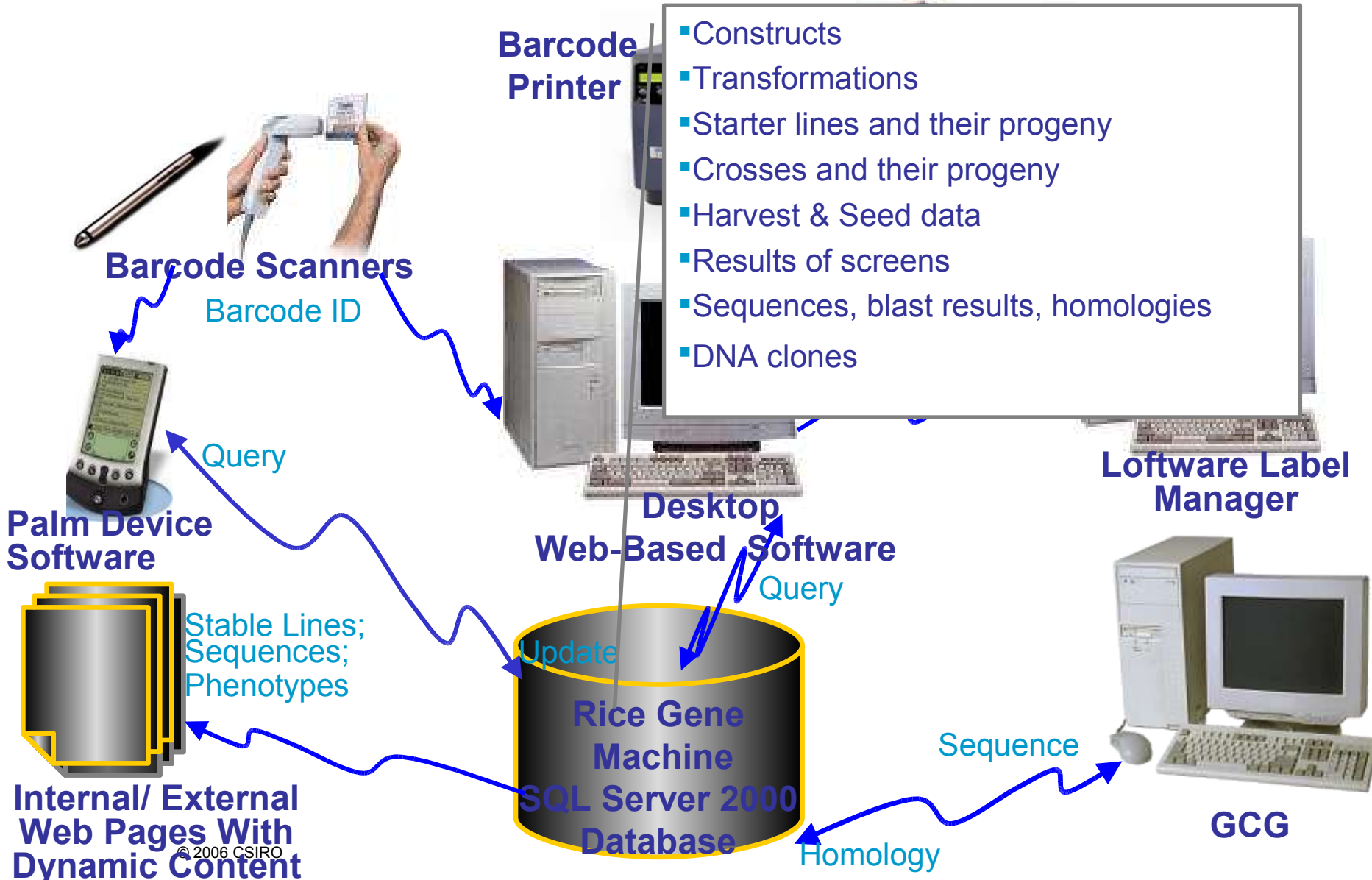
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(CSIRO Mathematical and Information Sciences)
www.cmis.csiro.au/bhi

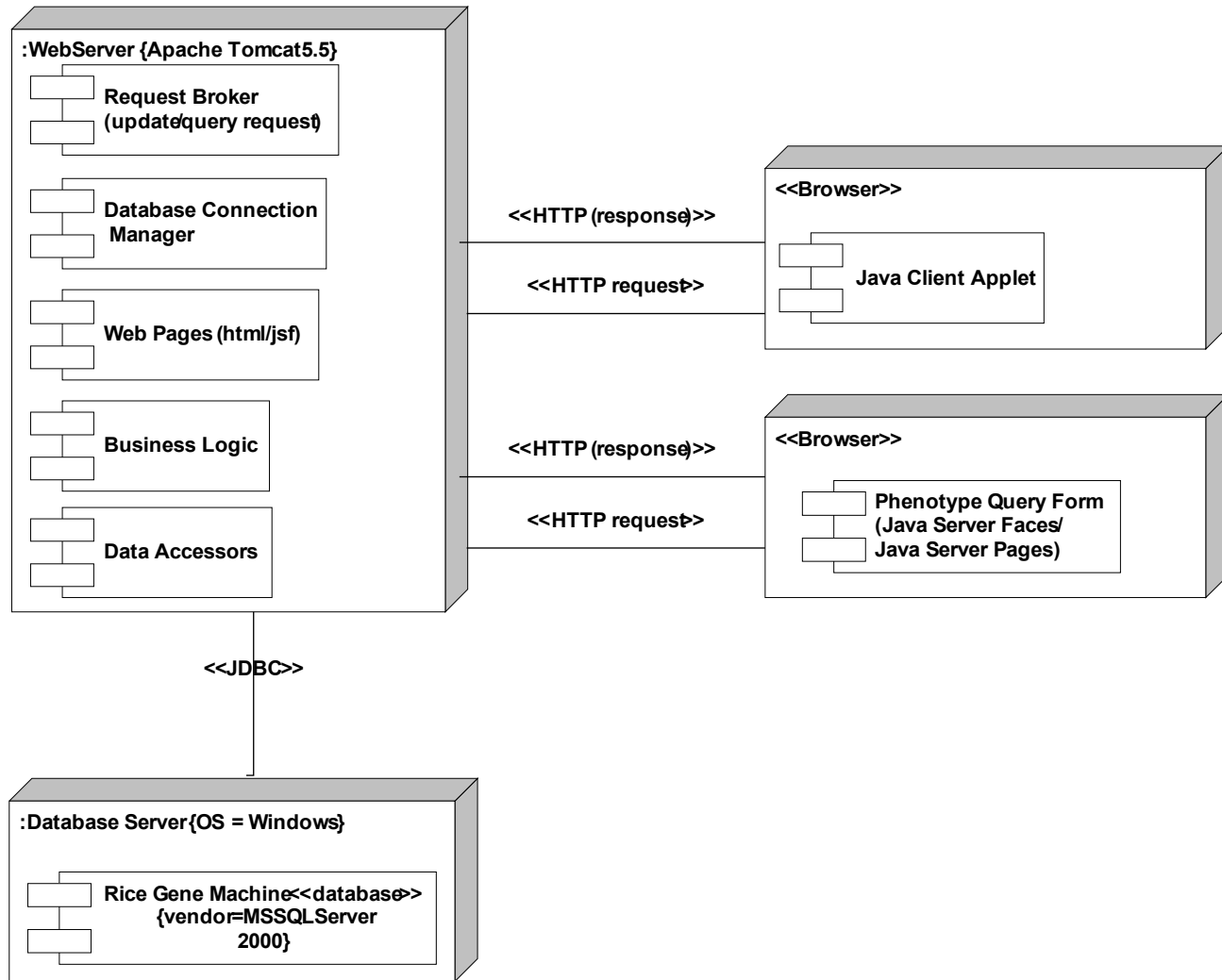
Components of a phenotypic observation

- Trait (e.g., dry root weight) → • Trait Ontology
- OR
- Chemical expression pattern (e.g., from GUS/GFP) → • Presence (+) / Absence (-)
- Observed value → • Free text (qualitative values)
- Images → • Numbers (quantitative values) with associated measurement unit
- Date/time of observation → • Links to image files
- In a particular anatomy (e.g., shoot) → • Capture date/time of observation
- At a particular Development/Growth Stage (e.g., Seedling) → • Anatomy Ontology
- In certain Environmental Conditions (e.g., 50°C heat treated; 3.5g agar) → • Development Ontology
- For an study initiated by XXXXX → • Environment Ontology
- Environment Profile
- Experiment

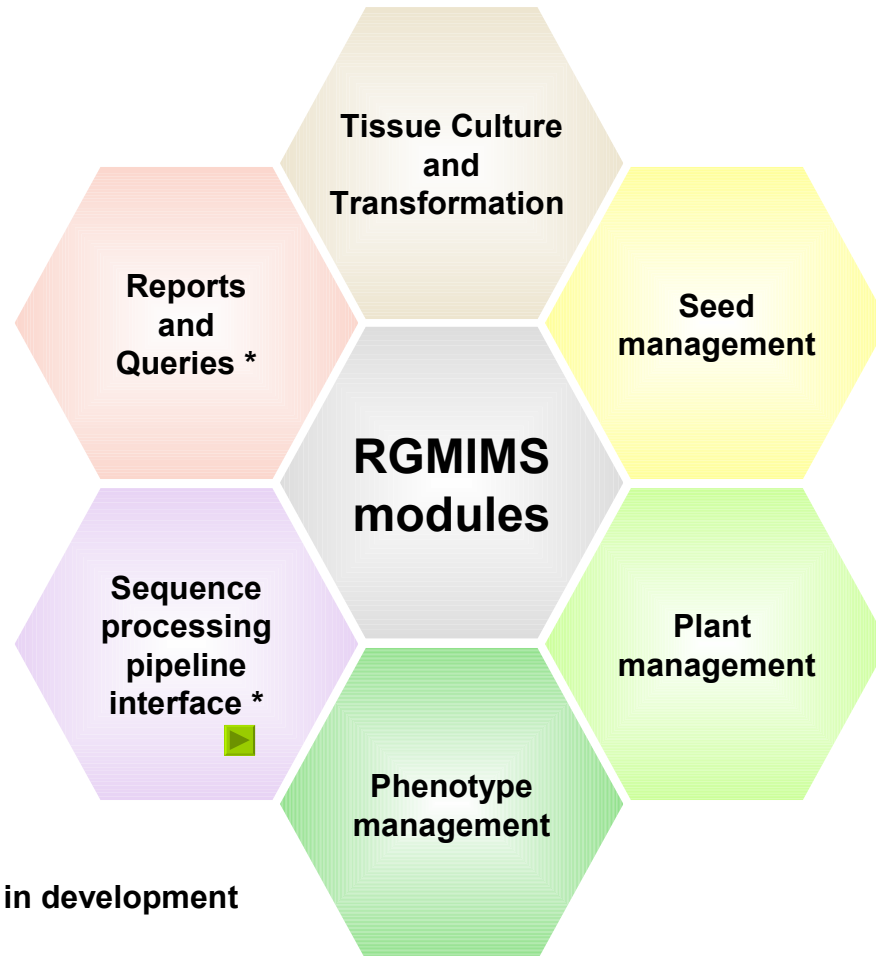
RGMIMS Architecture Components



RGMIMS Hardware and Software Deployment Configuration

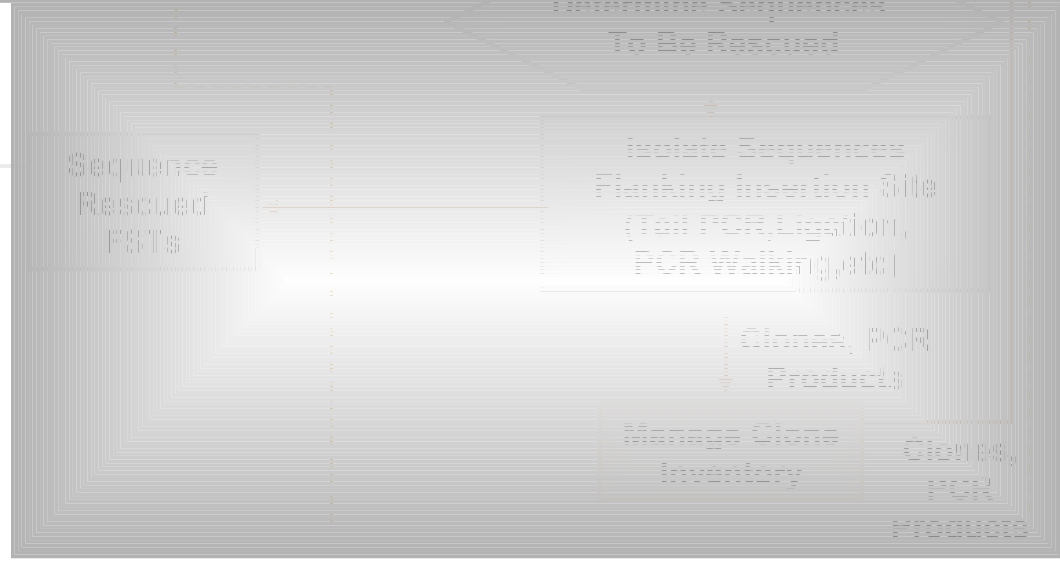
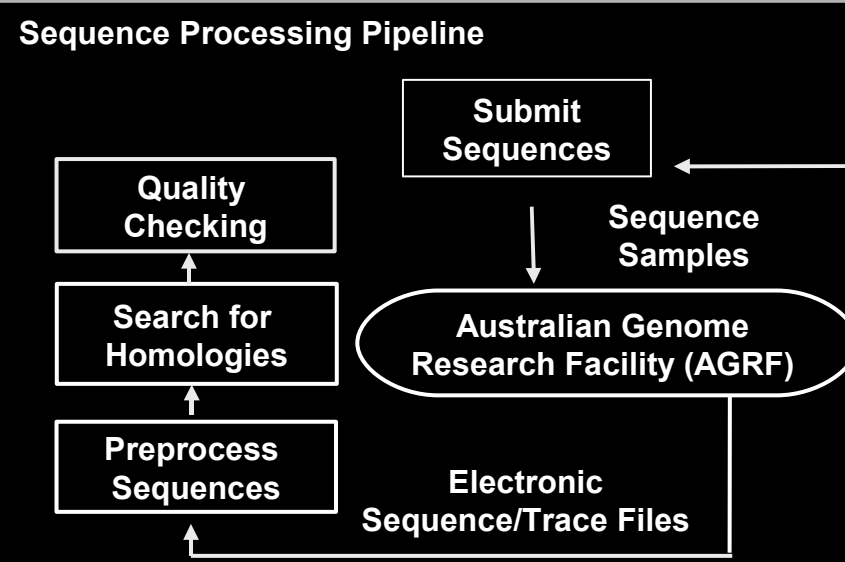


RGMIMS Modules

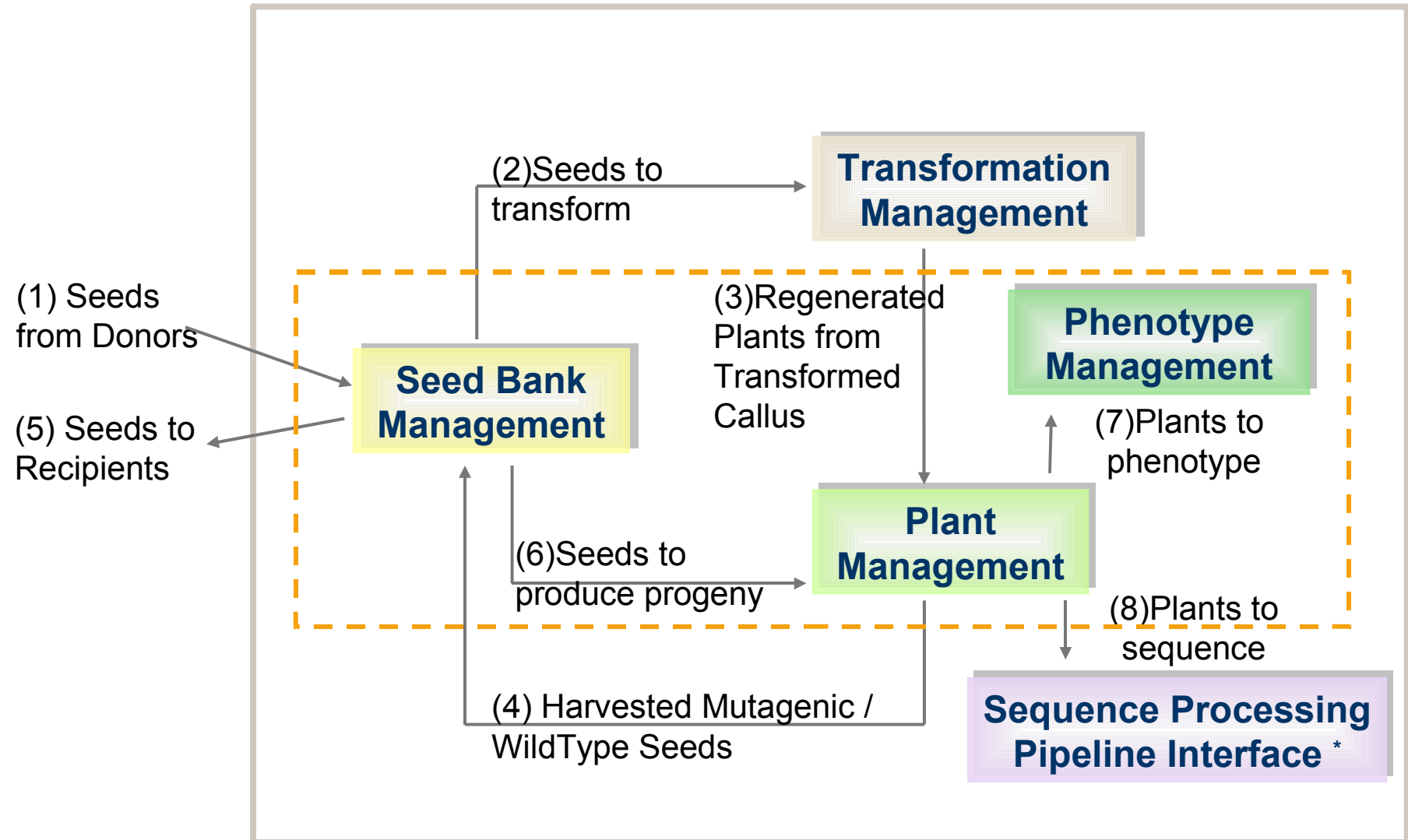




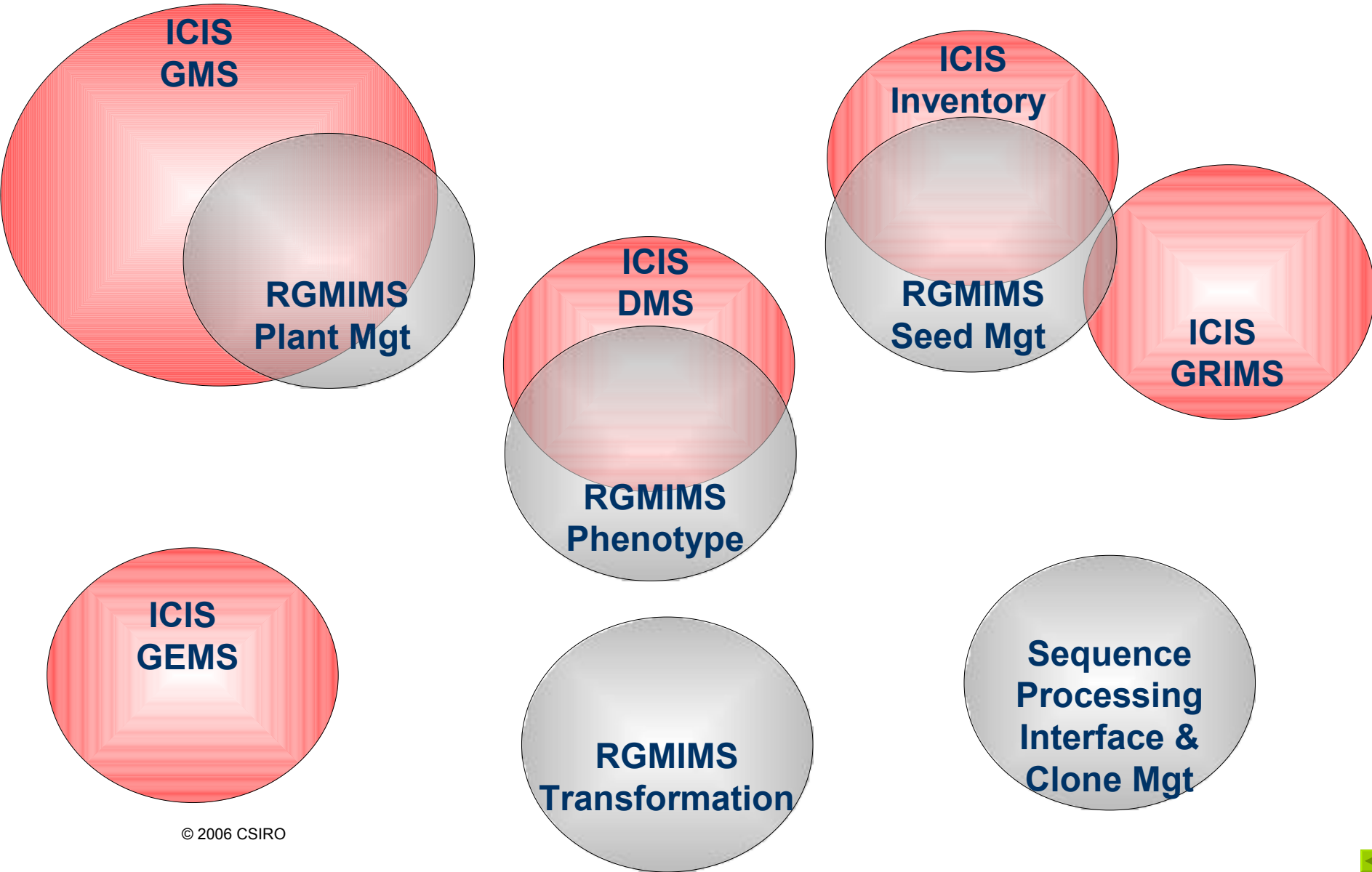
RGMIMS Interface To Sequence Processing Pipeline Flow (TBD)



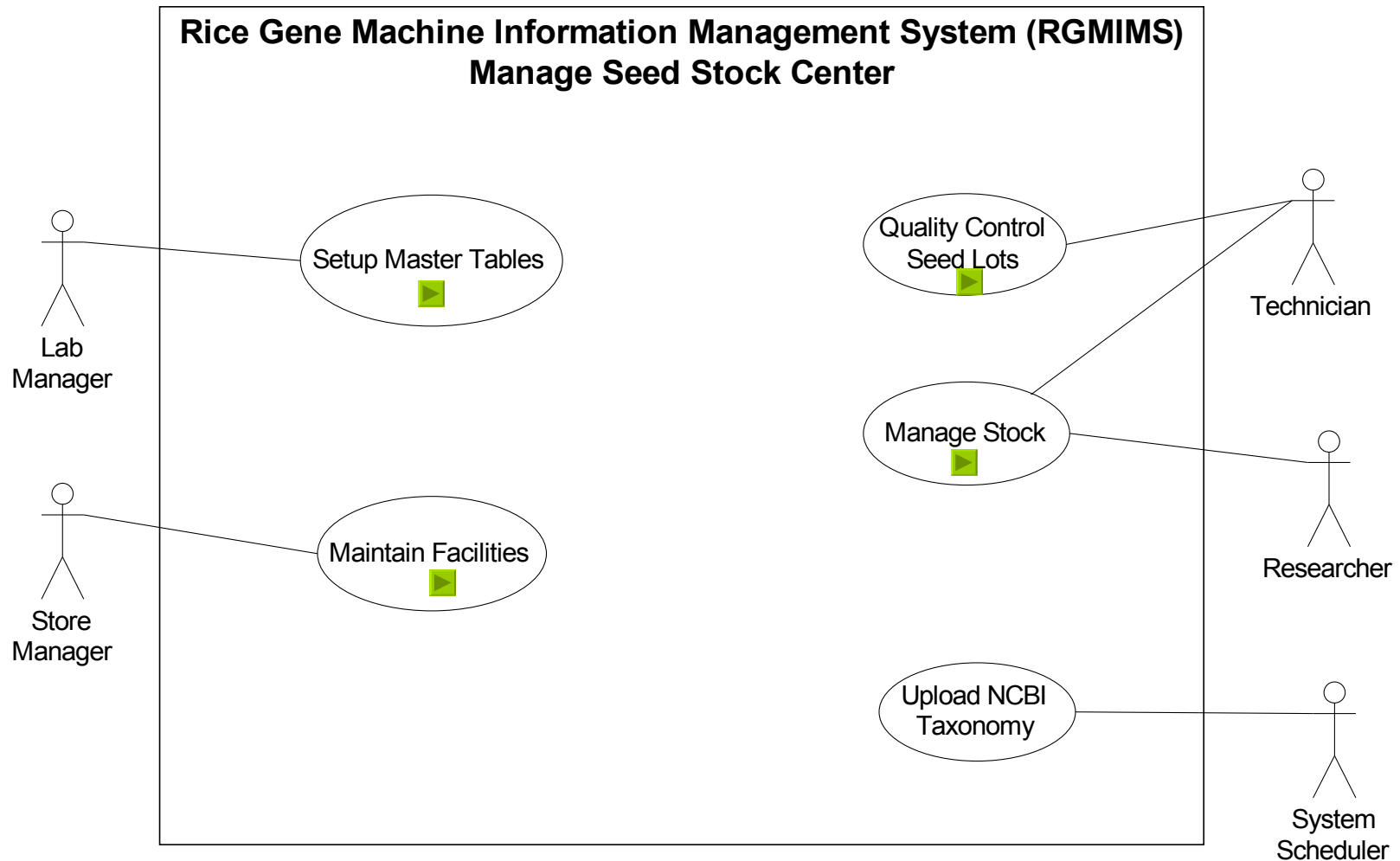
Interaction of RGMIMS Modules In The Lab



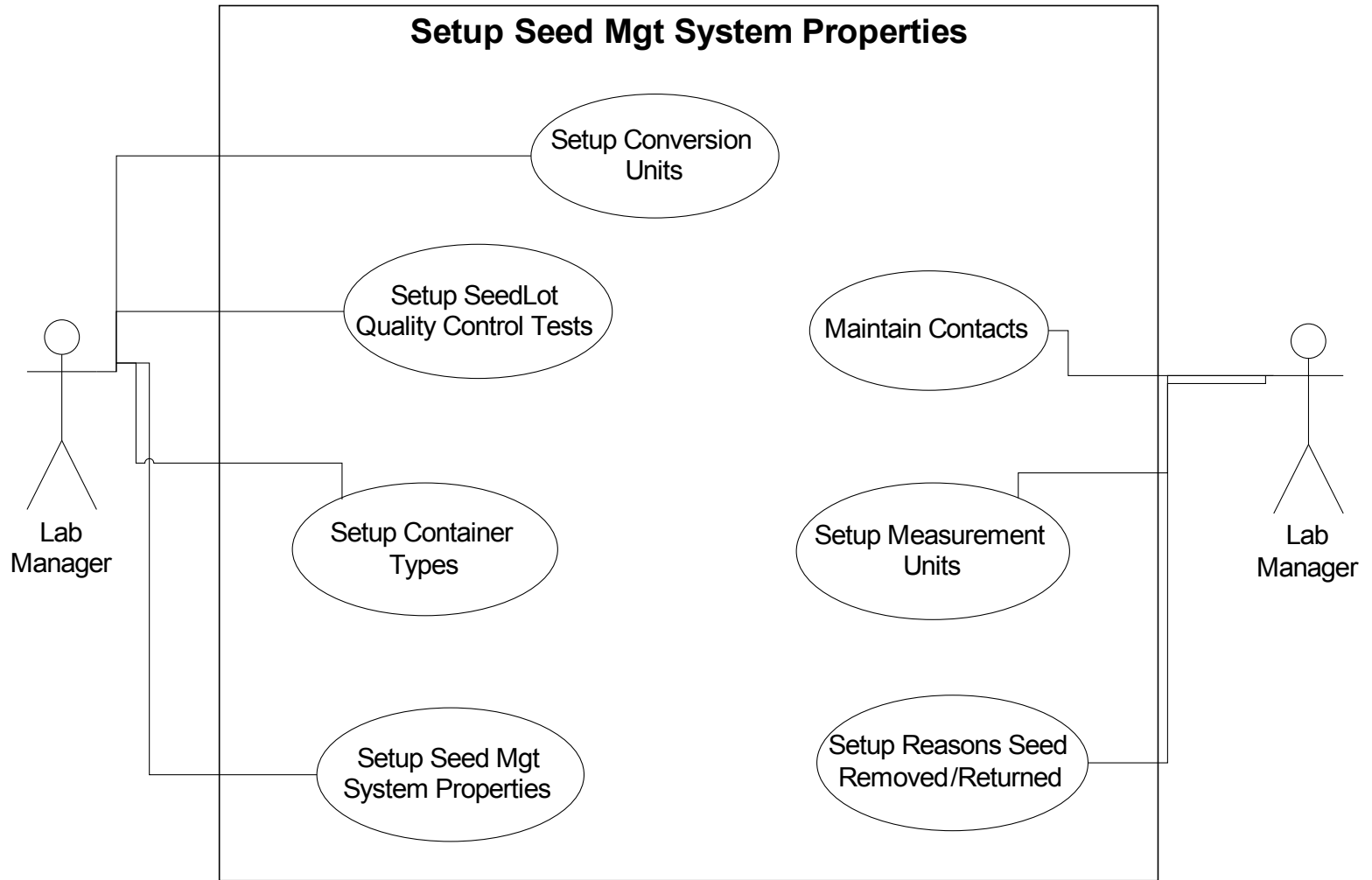
RGMIMS Modules in the Context of ICIS Modules



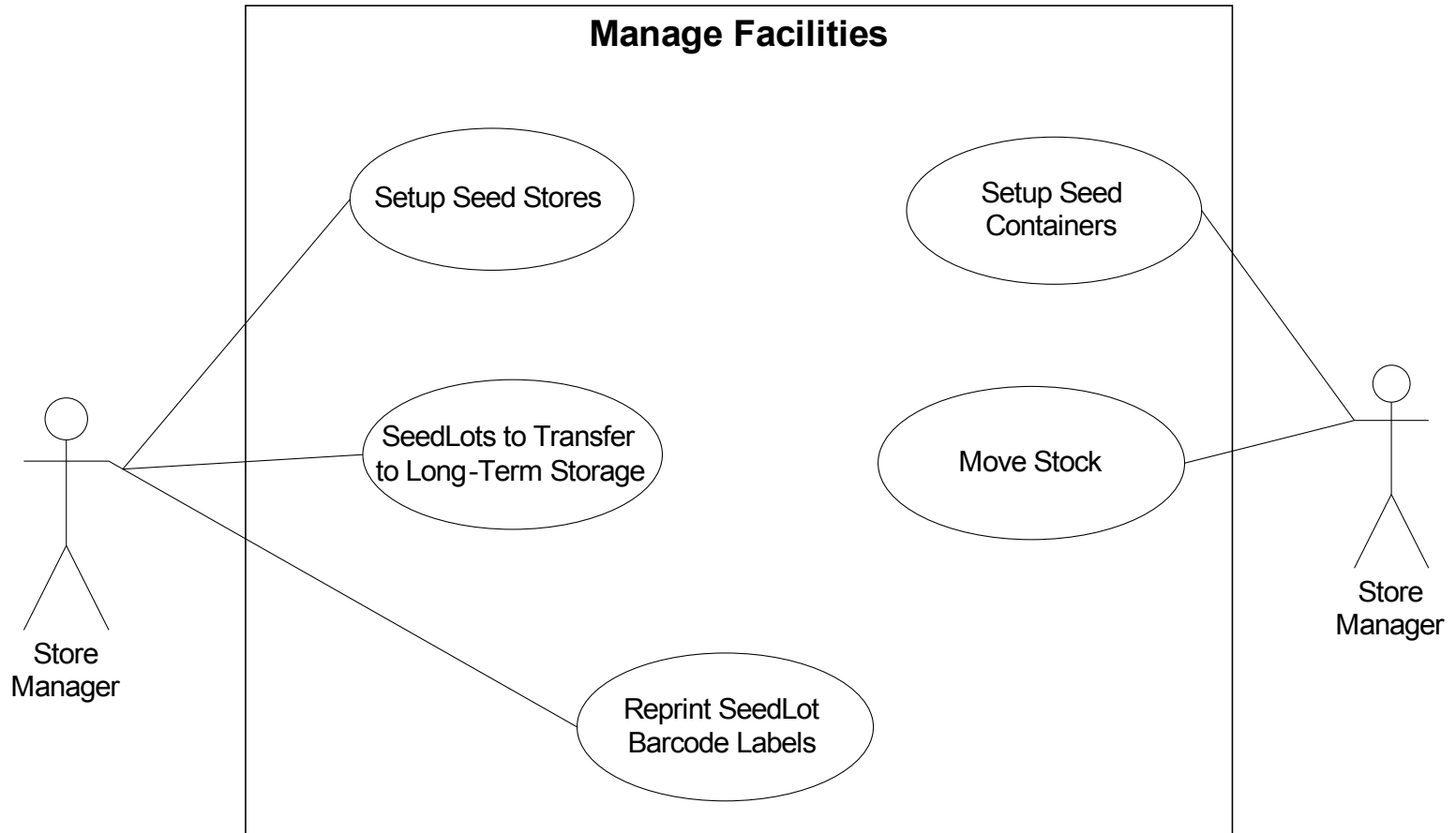
Seed Mgt Use Case



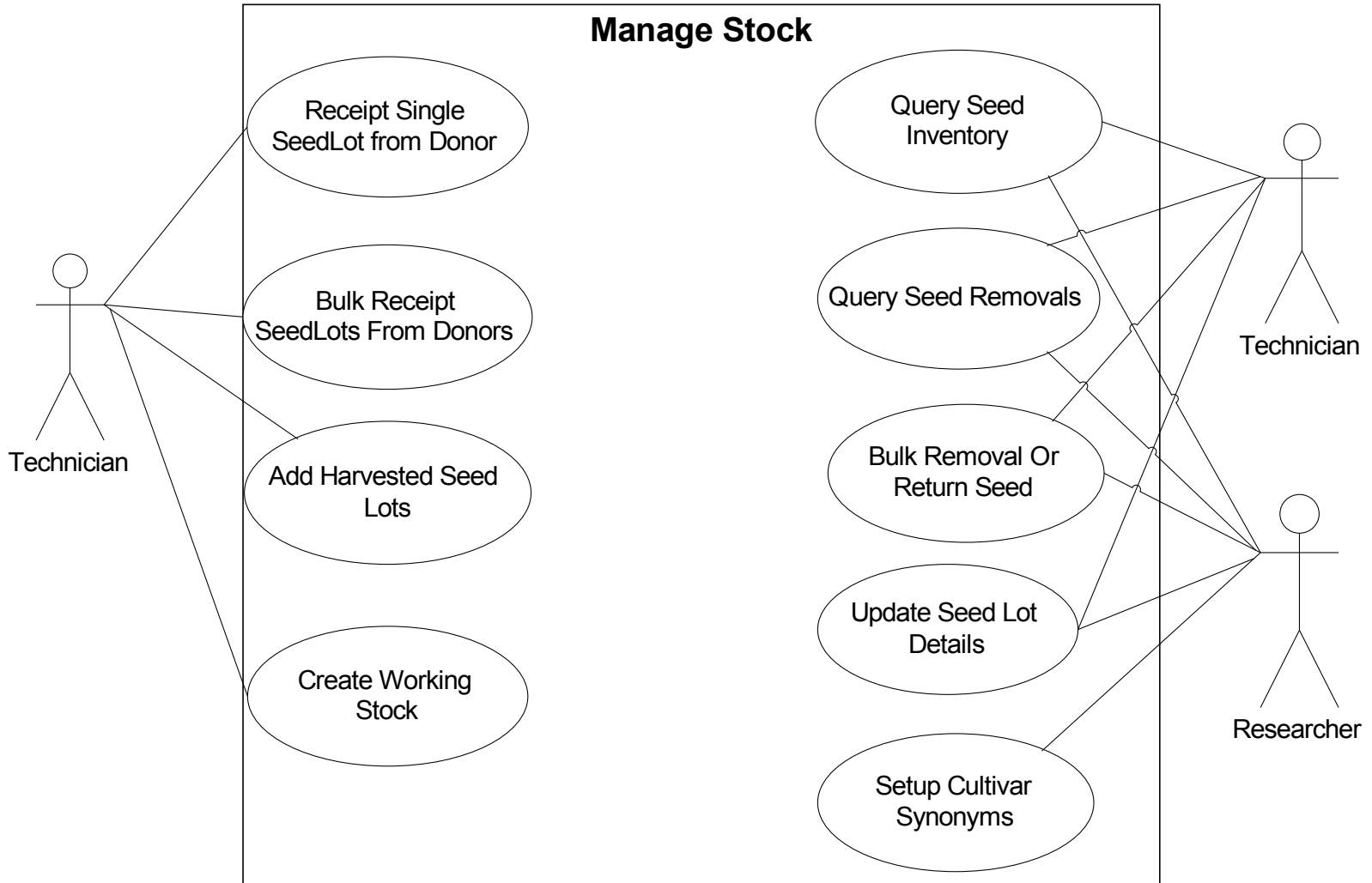
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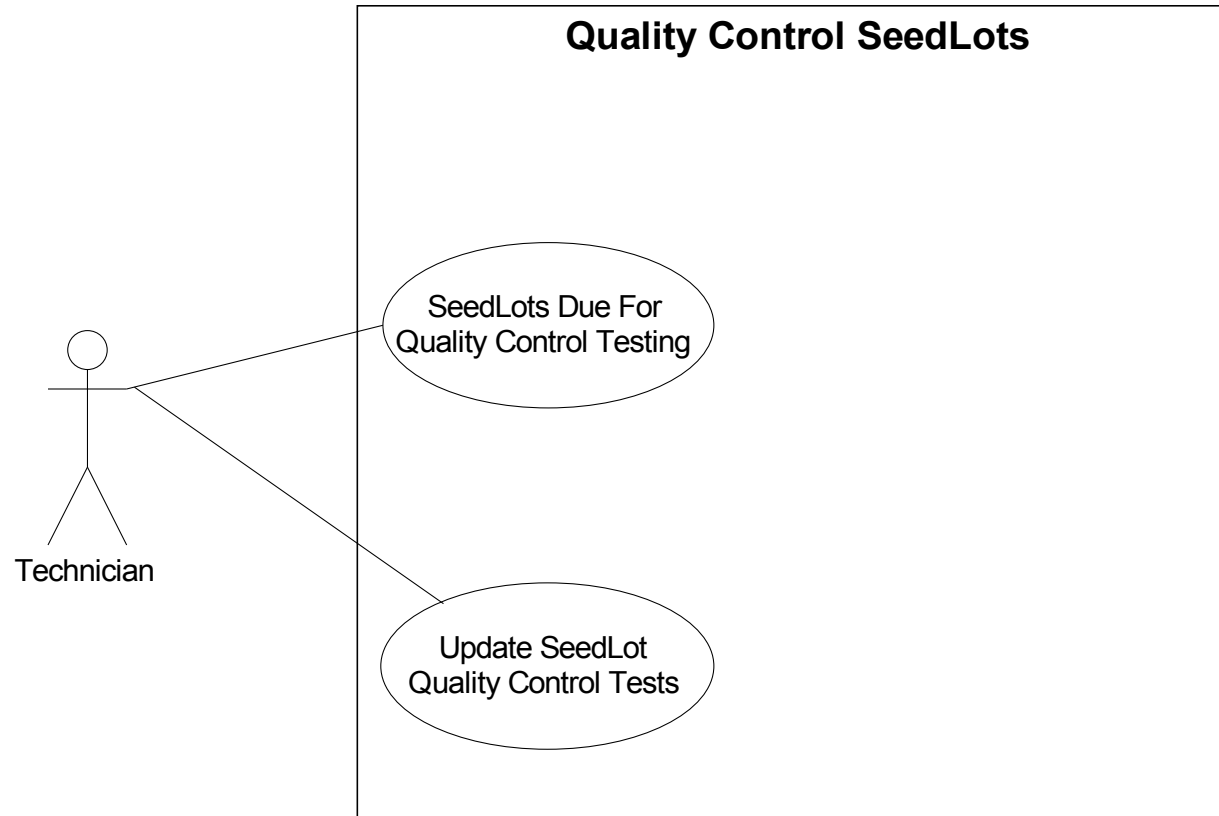
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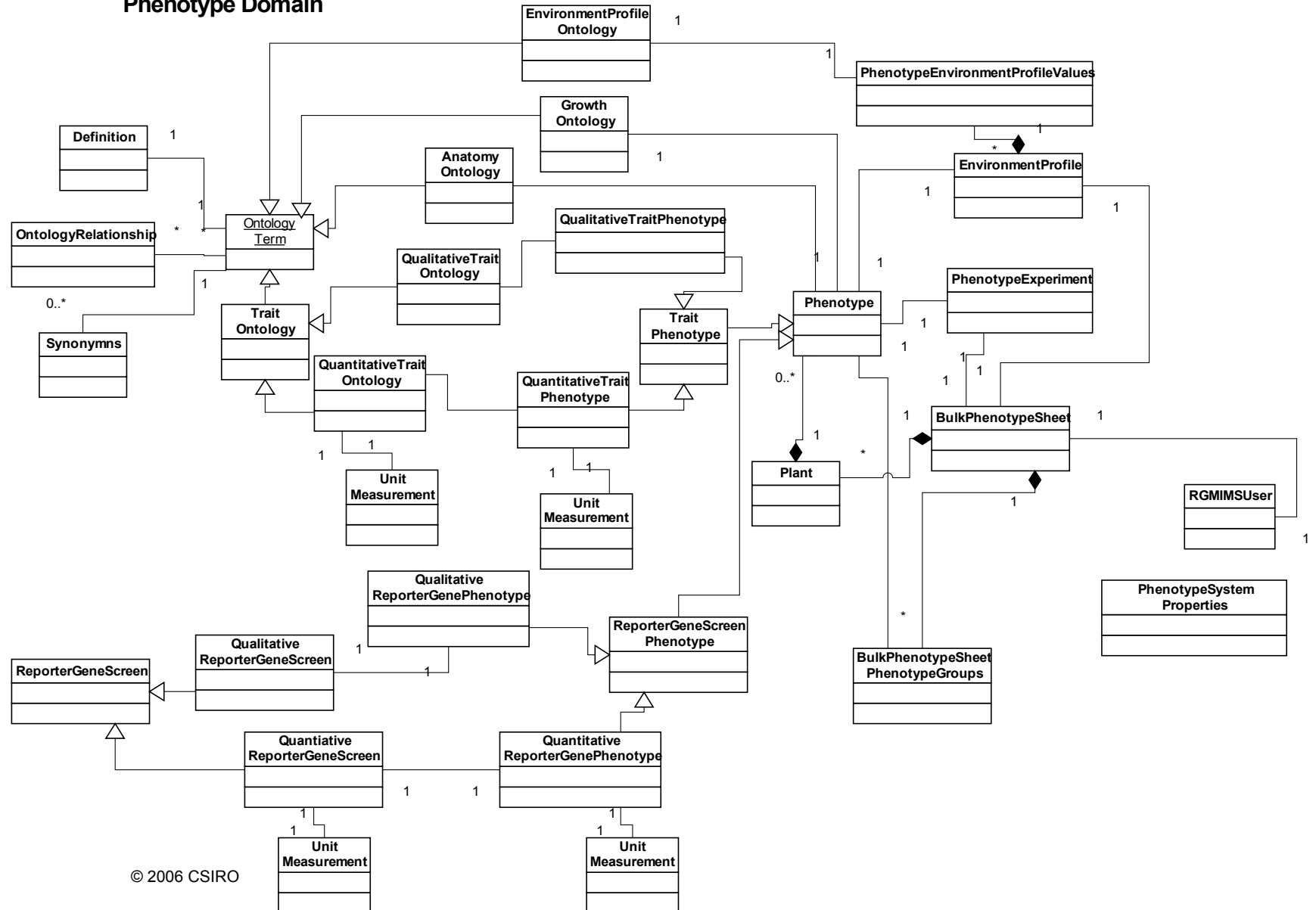
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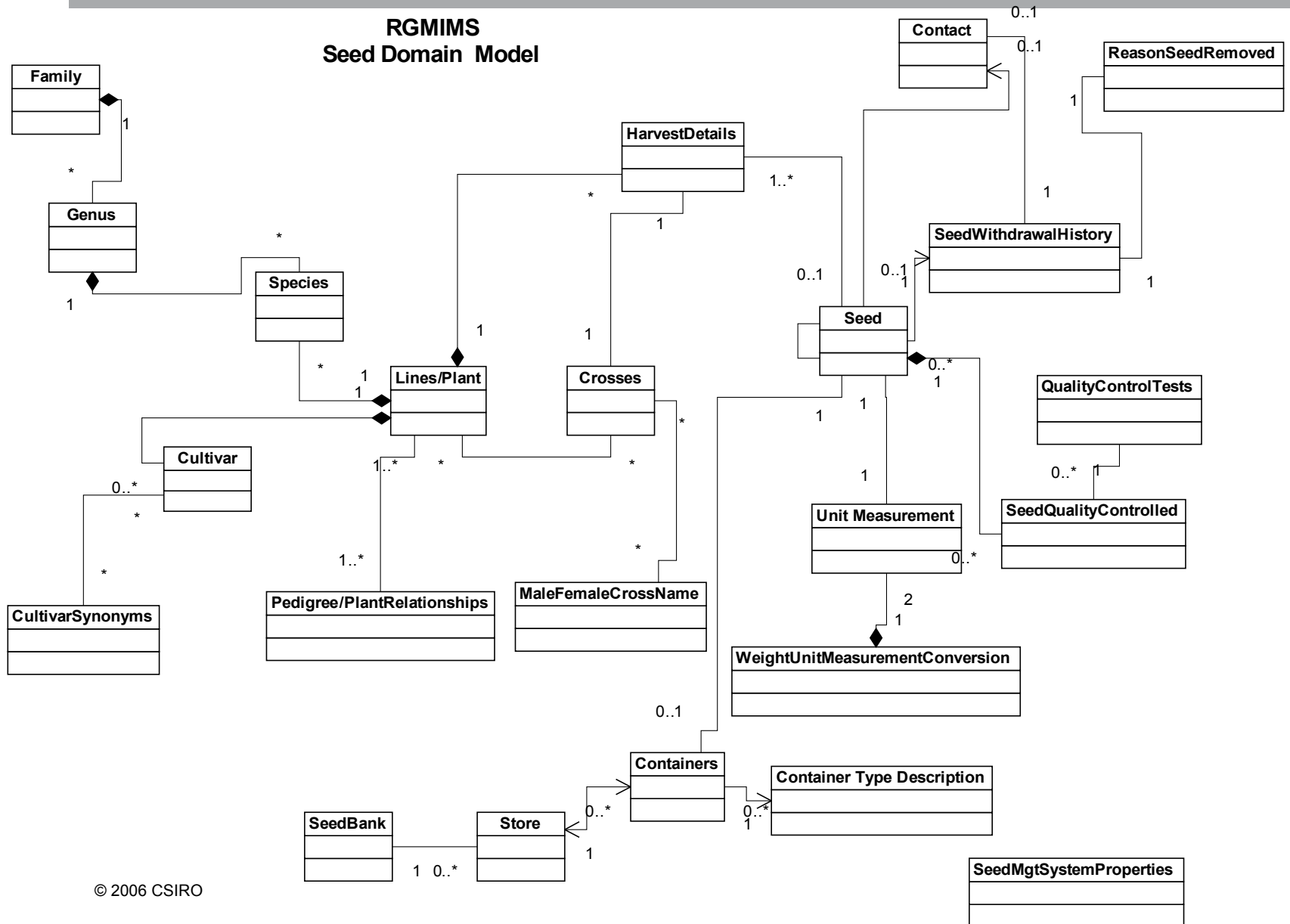
Domain Models

Phenotype Domain

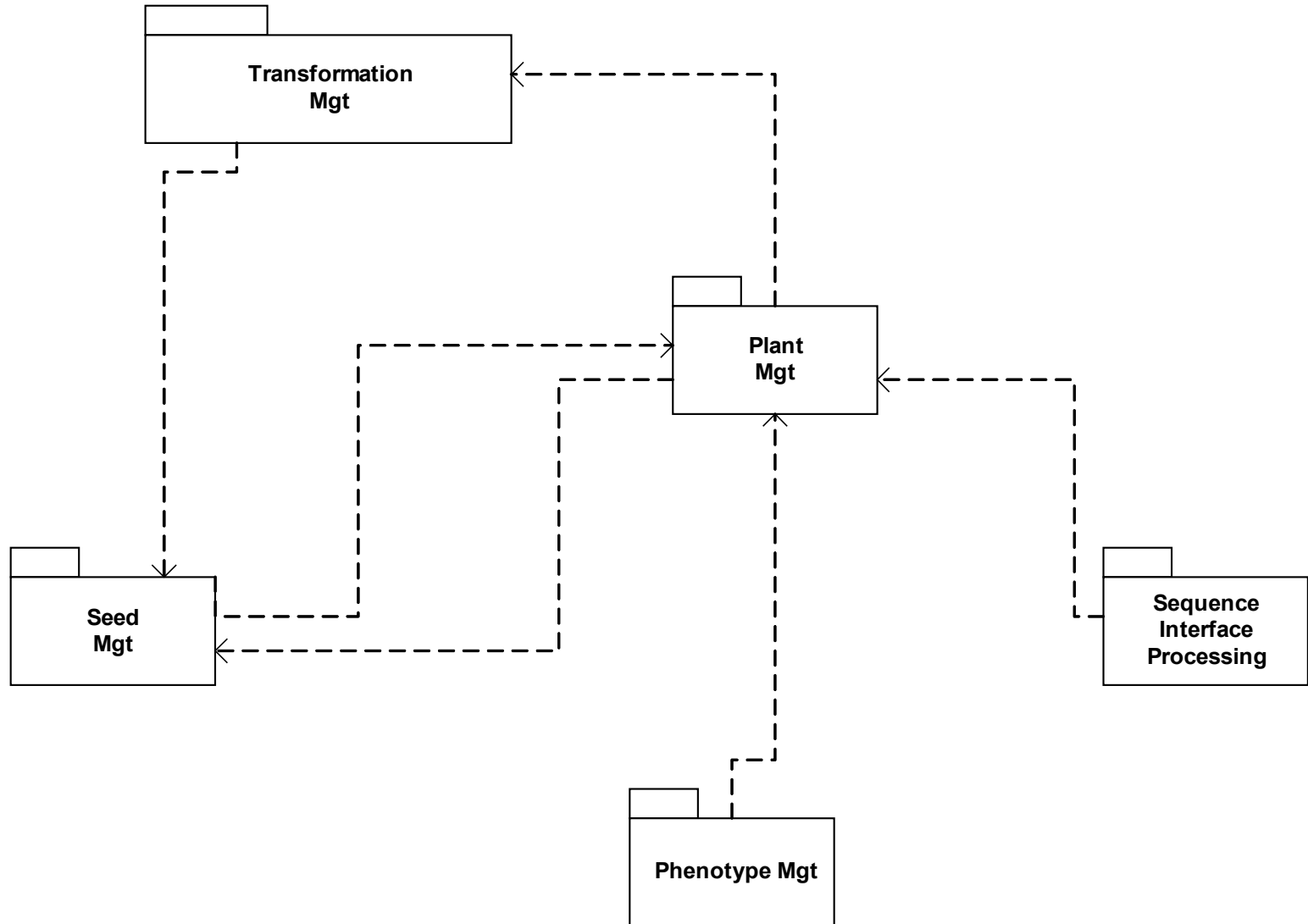


Domain Model

**RGMIMS
Seed Domain Model**



Use Case Package Diagrams - Dependency





Seed Mgt Module Class Package Diagram (A Model for other modules)

