GeWare 2.0 - On the way to a virtual repository

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- Generic approach to manage experiment annotations and import clinical data using annotation templates and controlled vocabularies
- Hybrid integration of web data using SRS
- Closed loop analysis workflow: Use of chip and gene/clone groups for easy and iterative analysis execution
- Data analysis by R BioCondutor (reuse of existing analysis software)

Content

What's GeWare
Requirements
GeWare 2.0 Approach
System Architecture
Kernel and Module Concepts
Conclusion & Future Work
Thesis Topics

New Requirements

- Requirements born by upcoming very (!) large scale projects and clinical trials
- **New** experimental data types generated by new high-throughput array techniques, e.g., tiling ~ exon ~ snp arrays
- **New** chip producers, e.g., Illumina
- Integration of **third party** data management solutions, e.g. BC|SNPMax
- Generic exchange of clinical data, e.g., by using XML
- Need for a **generic** approach to store all types of object groups
- User-right-management: rights per user on data and function

New Requirements cont.

- Flexible analysis integration (upload and execution of R analysis scripts)
- Move of (long running) analysis jobs to dedicated analysis servers
- Storage and return (on demand) of RData objects for every analysis
- Flexible analysis annotation (use of ontologies?)
- **Versioned integration** of web-data
- Web-GUI using Web 2.0 techniques
- Fat client on desktop (e.g., Rich Client)

GeWare 2.0

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  - own warehouse (ext. DB schema of GeWare 1.0)
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- **Generic** source access layer
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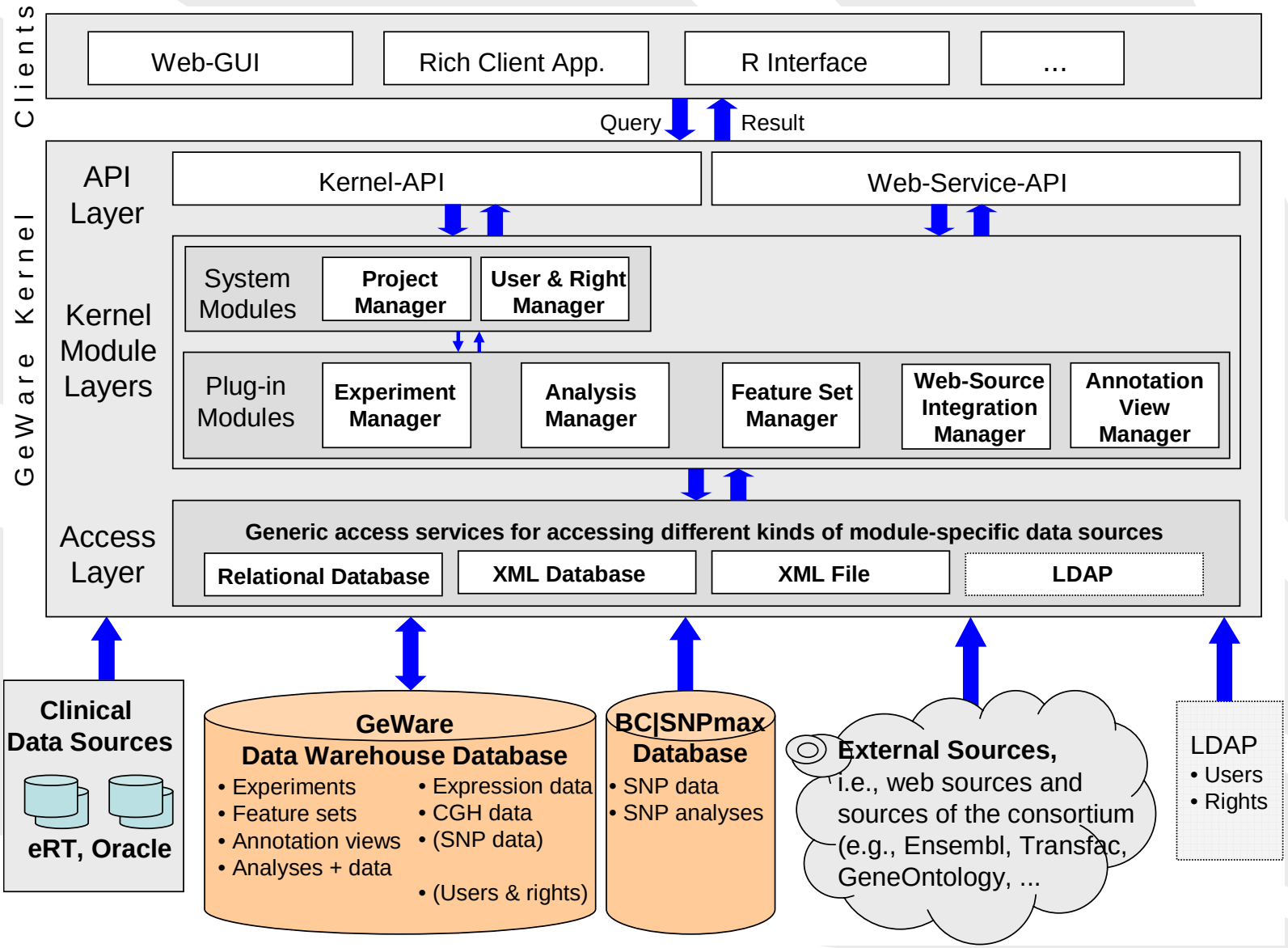
  - portability
- **Modularization**: Kernel and task-specific modules
  - system vs. plug-in modules
  - flexible module development (integrate a new or replace an existing module) by using a defined abstract module interface

System Architecture



Generic Source Access Layer

- Initialization by a set of data source connections
- Transparent data source access by kernel and modules
- Connection pooling for fast and parallel access
  - Problem: Which modules can store / retrieve data from which data source?
  - Solution: source-specific metadata

source-metadata(source id, module name, schema version)

- Mount (and unmount) data sources on system's runtime
- Further problems:
  - Uniqueness of object identifiers
  - Selection of insert source

Uniqueness of Object Identifiers

- Problem: No unique object identifiers when multiple sources are used for same type of data
- Solution: Encoding and decoding of source-specific object identifiers

$$f : \mathbb{N} \times \mathbb{N} \rightarrow \mathbb{N}$$

$$f(id_{Src\,k-Obj}, k) = id_{Sys-Obj} = id_{Src\,k-Obj} * c + k$$

$k \in \mathbb{N} :=$ unique source identifier

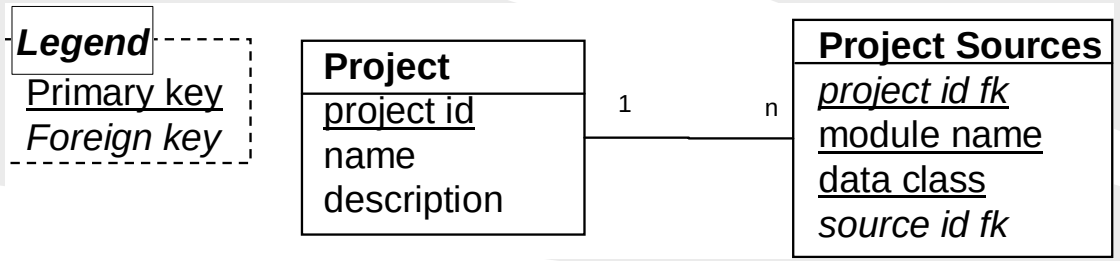
$c = 10^e, e \in \mathbb{N}, e > 0 (e.g., c = 1000)$

$$f^{-1}_{Src}(id_{Sys-Obj}) = k = id_{Sys-Obj} \mod c$$

$$f^{-1}_{Obj}(id_{Sys-Obj}, k) = id_{Src\,k-Obj} = (id_{Sys-Obj} - k)/c$$

Project Manager

- Project
  - typically, singular (planned) process for a specified time
  - in GeWare: Container for storing every type of data; project semantics keeps in user's responsibility
- Problem: Selection of an insert source
- Solution:
  - Association of each project and module with a singluar data source as selection for insert operation
  - read, update and delete for all other data sources



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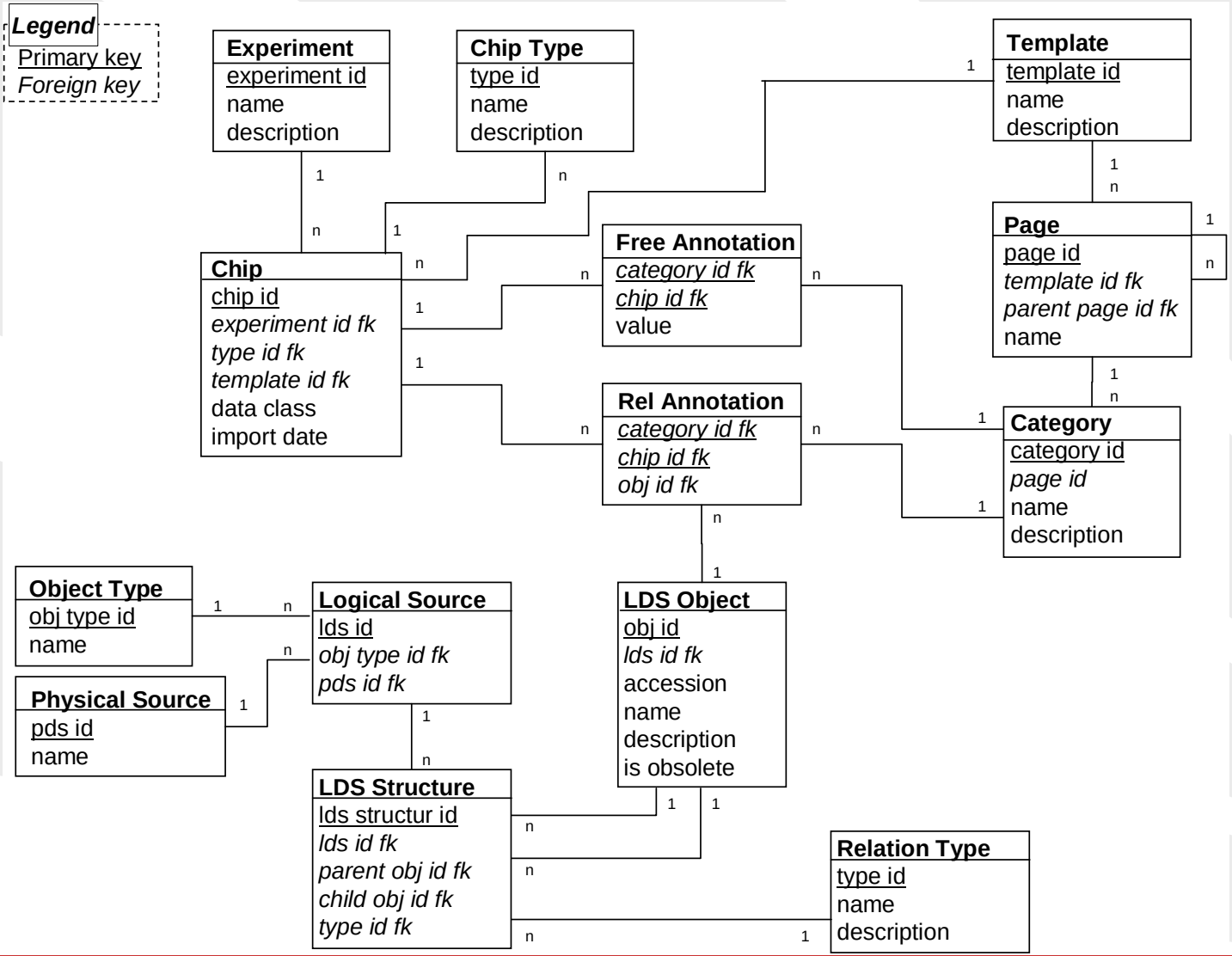
- Input values
  - manual input
  - selected **ontology** concepts (no flat vocabularies)

Experiment Manager cont.

Module-specific Database Schema Portion



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- Methods for
  - retrieval and im-/export
  - set manipulation, e.g., union, intersect, diff, majority

Feature Set Manager cont.

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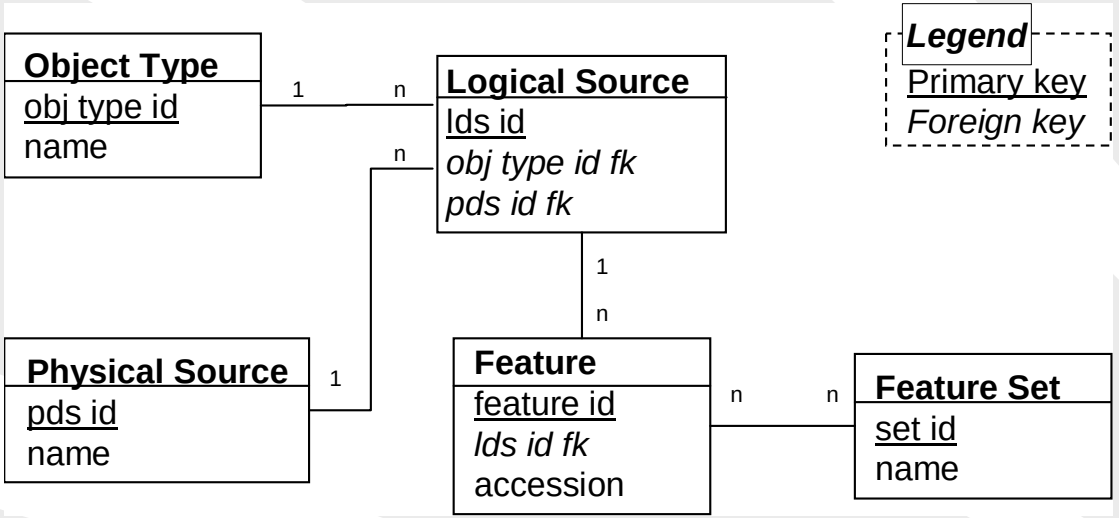

Annotation View Manager

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Primary object

Annotation (set of describing attributes)

Probe Set ID	Gene Title	Gene Symbol	go biological process term	go molecular function term	go cellular component term	Pathway
1000_at	mitogen-activated protein kinase 3	MAPK3	protein amino acid phosphorylation protein amino acid phosphorylation cell cycle	nucleotide binding protein kinase activity protein serine/threonine kinase activity MAP kinase activity MAP kinase activity protein binding ATP binding		MAPK_Cascade S1P_Signaling TGF_Beta_Signaling_Pathway

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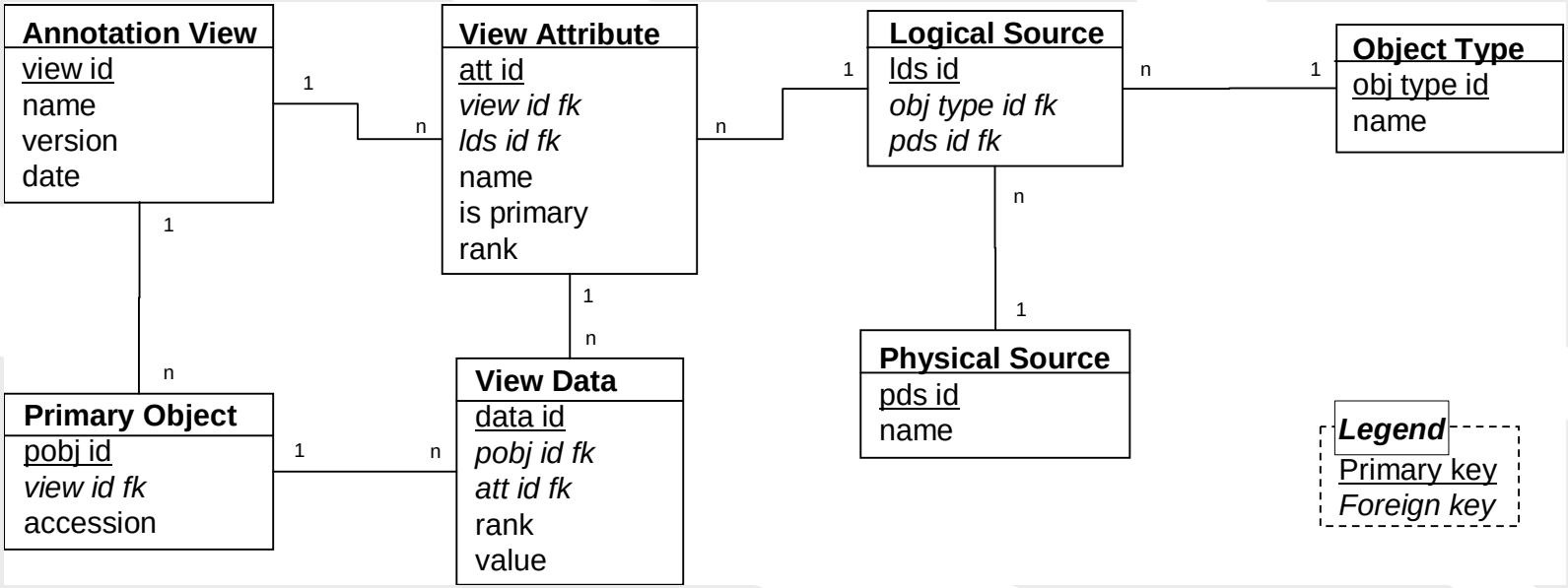

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- Problems:
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- Solution (First Approach)
  - versioning: physical source name = source name + version
  - view generation: new method genView() in BioFuice

$$view = genView(M_1, \ldots, M_n, A_{s_i})$$

where it exists a compositional path from mapping M_1 to M_n and set of attributes A_{s_i} from sources $s_i \in (domain(M_j) \in \{M_1, \ldots, M_n\} | range(M_j) \in \{M_1, \ldots, M_n\})$

Conclusion & Future Work

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- Current state: Concept and implementation of system architecture, kernel and most modules
- Future work
  - Need to implement: Experiment & Web-Source Integration Manager
  - Need a detailed concept for analysis handling, monitoring, distribution (e.g., by using available Grid infrastructure), and annotation

Topics for Diploma/Master/Bachelor Thesis

- Web-GUI (re-)design
- Rich client application
- Application allowing to configure the clinical data exchange
- Analysis management and distribution

GeWare-Coders-Club

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”Gehirnsturm am Freitagabend”

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