

# BIAS

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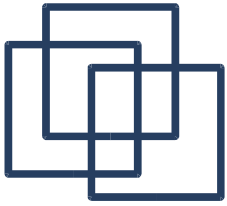
## Bioinformatics Integrated Application Software

BOSC 2004

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McGill Centre for Bioinformatics

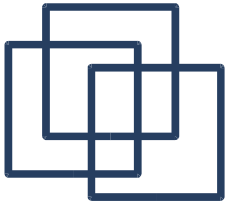
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# Outline

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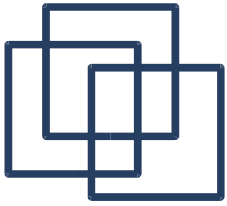
- Motivation
- Requirements
- Object-relational system
- Libraries
- Modules



# Motivation

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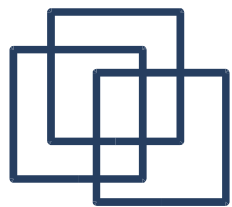
- Systems Biology / Integrative Bioinformatics
  - Development platform
  - Integration
    - data
      - Structural, sequences, interactions, ...
    - Algorithms and statistics
      - pipelining existing algorithms
      - developing new algorithms
      - Large-scale computations (machine learning, data mining)
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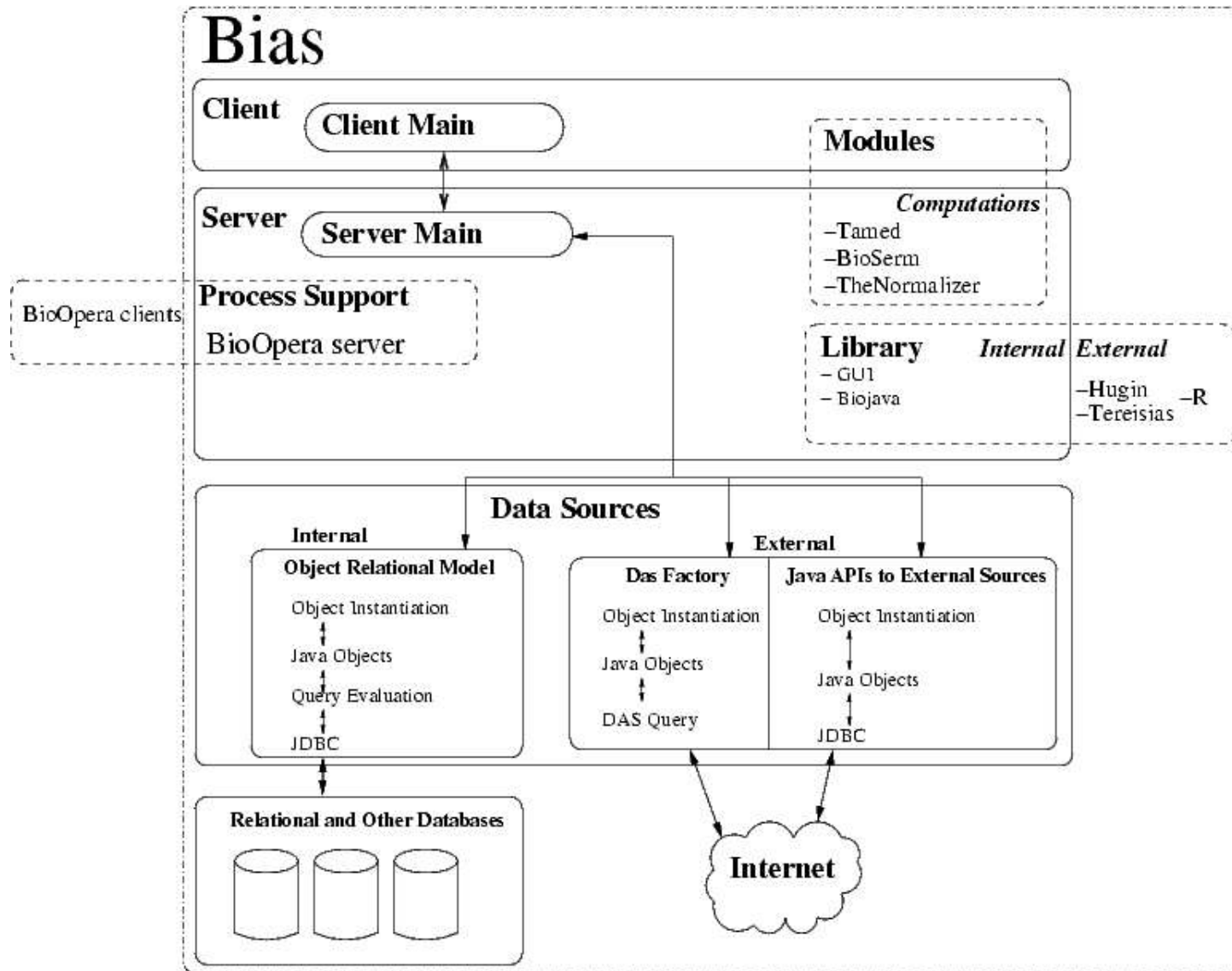
# Requirements

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- Central consistent data repository
  - Databases
- Easy to create prototypes
  - Java
- Useable by non-experts
  - GUI library



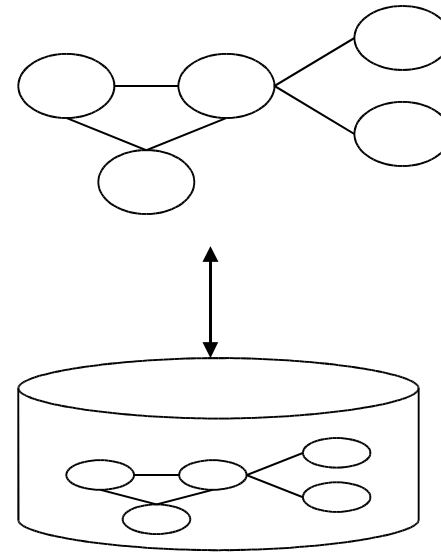
# Bias infrastructure

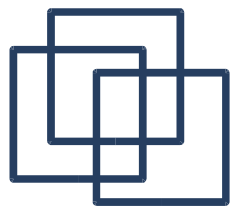


# Object-oriented database

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- Save objects “as-is” in the database.
- Very flexible
- Too flexible?

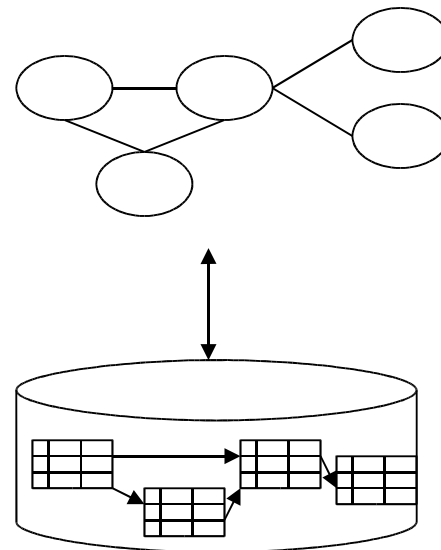


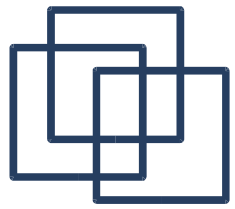


# Relational databases

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- Force to respect predefined schema and relationships.
- Structure helps to optimize queries, ensure consistency.
- Too much restrictive?



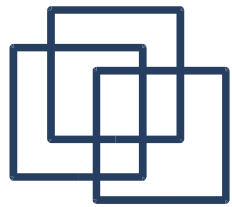


# Object-Relational database

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- Relational database:
  - + Mature and well established
  - Requires a lot of database-specific access code
- Object-oriented databases:
  - + Intuitive with Object-Oriented languages
  - More difficult to maintain.
- Object-Relational:
  - Object-based, backed by a relational database





# Using Apache's OJB system

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- Using the ODMG standard
- Query

```
gene = Gene.getGeneByName("YAL001C");
```

or

```
gene = yeast.genes.get("YAL001C");
```

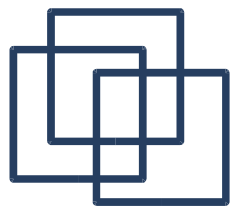
- Store new objects

```
new Gene("YAL001C", yeast, sync);
```

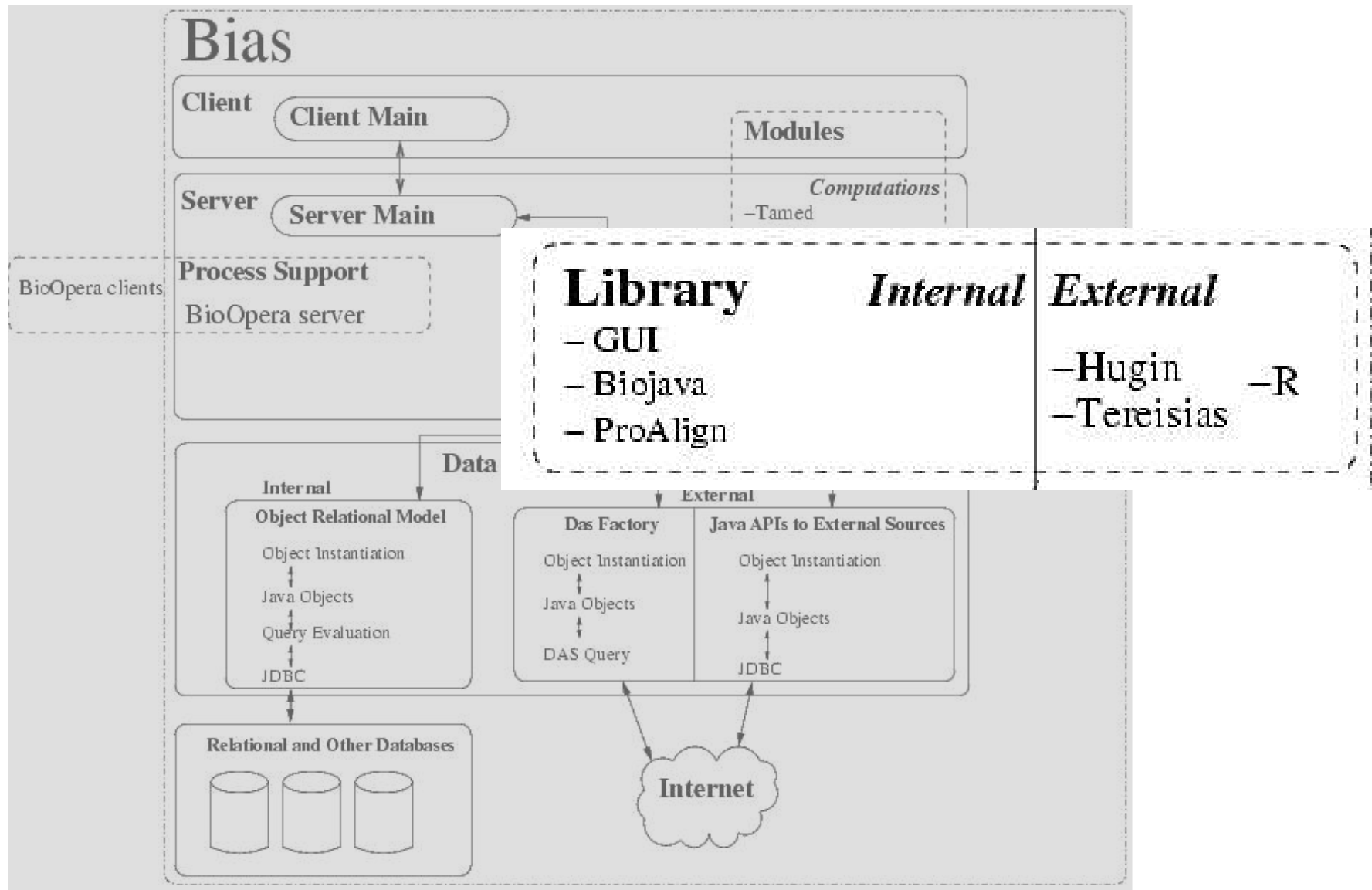
- Update

```
gene.setName("TFC3");
```

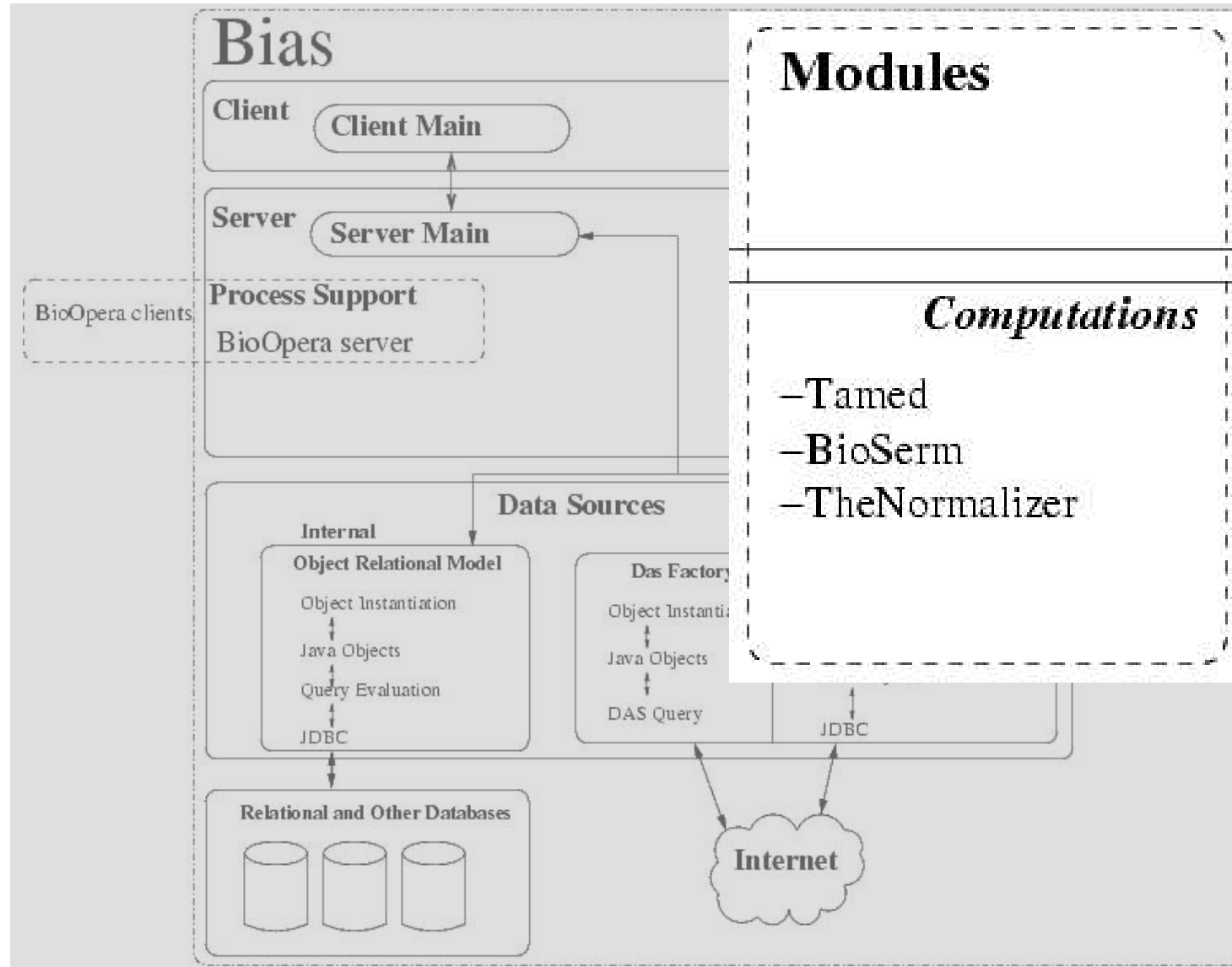
```
gene.sync();
```



# Bias infrastructure (library)



# Bias infrastructure (modules)





# Acknowledgements

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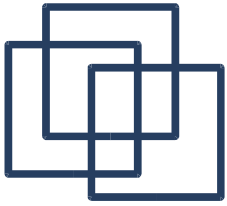
***Proteomics***

Michelle Scott

Sara Calafell

Funding:





# URL

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**<http://www.mbc.mcgill.ca/~bias/>**