Bio4j: the bioinformatics data platform

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What is Bio4j?

Bio4j is a bioinformatics graph-based data platform integrating the most representative open data sources around protein information

Data sources

- UniProt KB (SwissProt + Trembl)
- Gene Ontology (GO)
- UniRef (50,90,100)
- RefSeq
- NCBI Taxonomy
- Expasy Enzyme DB

Data as a service

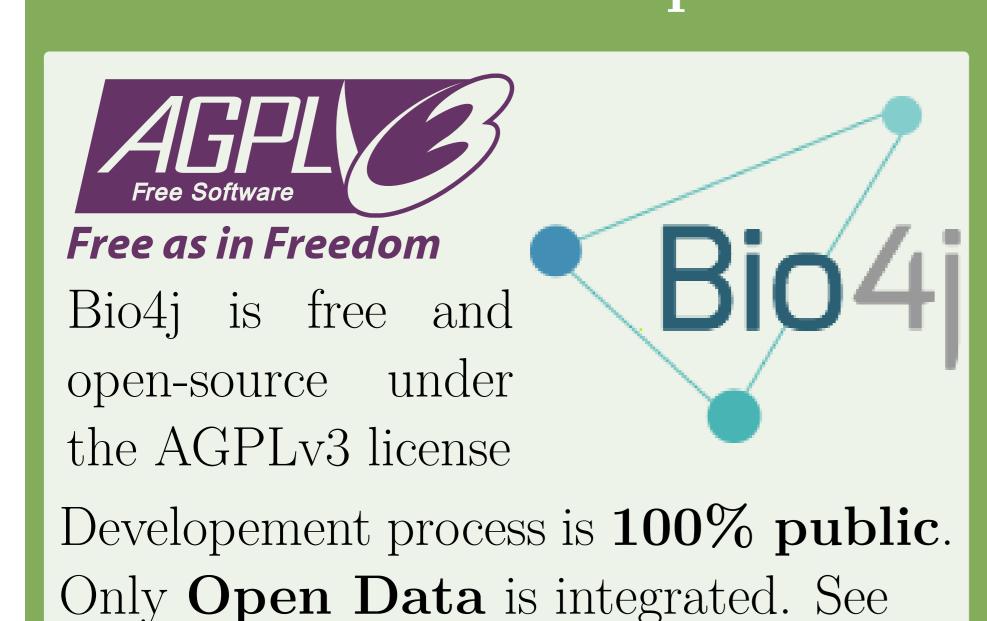
- Data distribution
- Scalability
- Cost-effectiveness



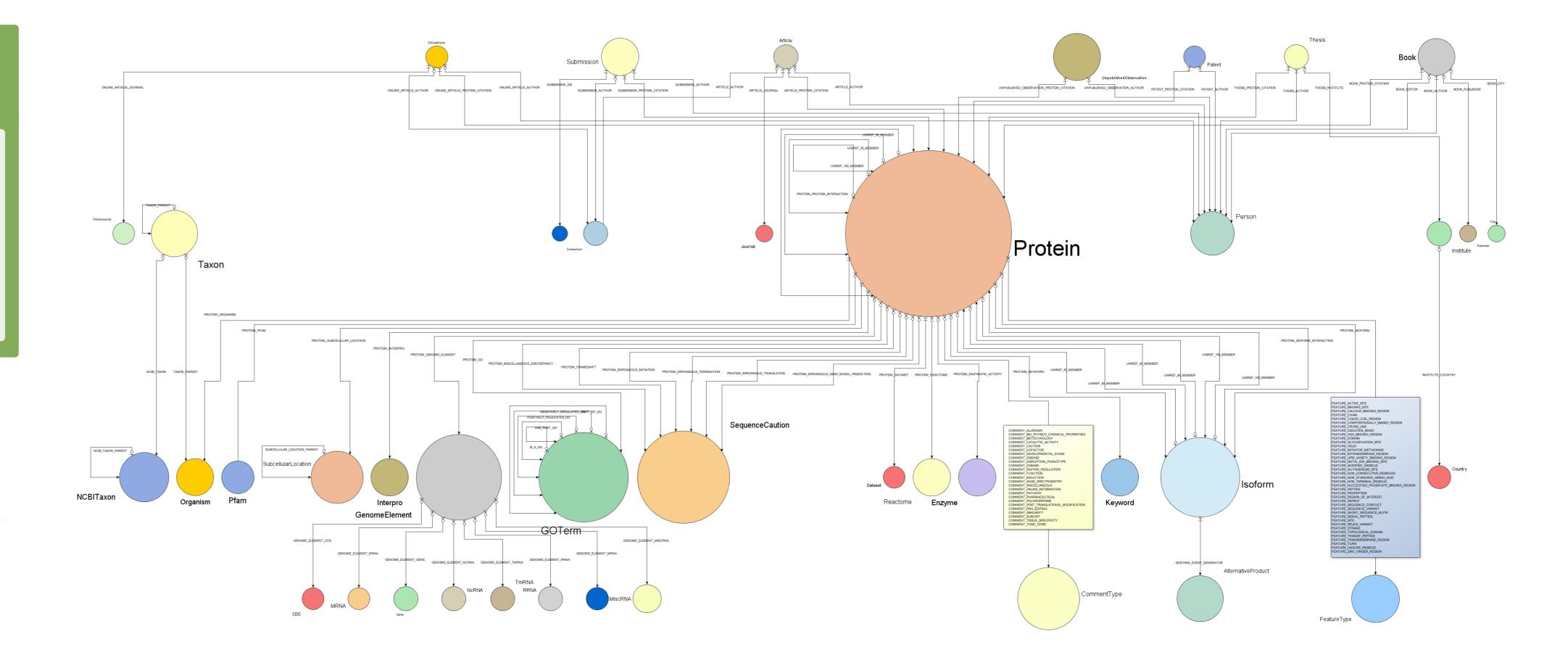
Graph databases

- Data is stored in a way that semantically represents its own structure
- Incorporating new data is easy \Rightarrow it's scalable
- Vertex-centric (local) indexes allow to overcome the supernode problem

It's free and open!



bio4j.com



Bio4j domain model

Bio4j database has a well-defined domain model and all nodes and relationships comply with this abstract model.

- 10^9 edges of ~ 150 types
- 2×10^8 nodes of ~ 40 types
- 6×10^8 properties

Different layers of Bio4j

Different graph topologies at the storage level, same domain model in the client's code.

- Abstract domain model with precise typing.
- Universal *Blueprints* implementation.
- Technology-specific versions:
 - Neo4j DB
- TitanDB
- DynamoDB (WIP)

Use cases

- Era7 Bioinformatics:
 - **BG7** genome annotation
 - Metapasta metagenomics analysis
 - Comparative genomics, network analysis, genome assembly
- Ohio State University:
- Integration and analysis of Chip-seq data
- Modeling genomic information and gene regulatory networks
- Berkeley Phylogenomics Group:
- Graph database for Big Data challenges in genomics developed on top of Bio4j

Flexible module system

Statika helps to manage dependencies between modules and simplifies import and deployment in the cloud.

The importing process is *modular* and *customizable* allowing you to import just the data you are interested in.

Some technical details

- Java + Scala source code
- Statika-based module system
- **SBT** for building sources and automated tests & release
- Git + Github: versioning, docs, collaboration, coordination

Acknowledgments

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