# Bio4j: bigger, faster, leaner

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Bio4j

ohnosequences!

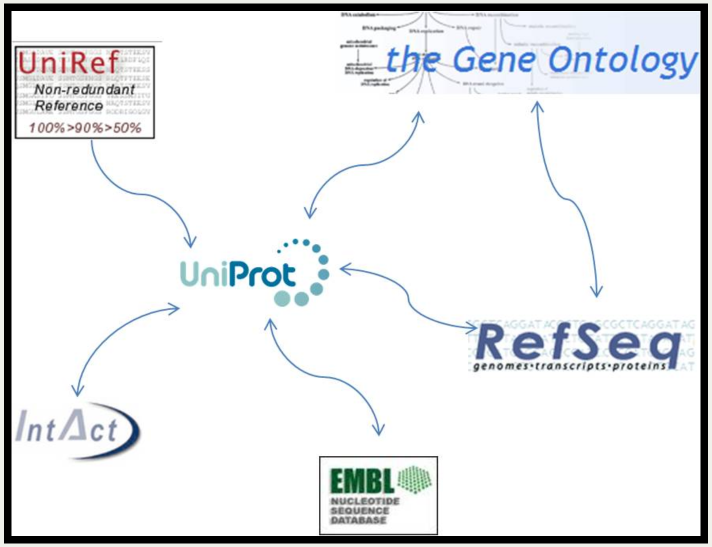
Era7 bioinformatics

# Introduction

# 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*

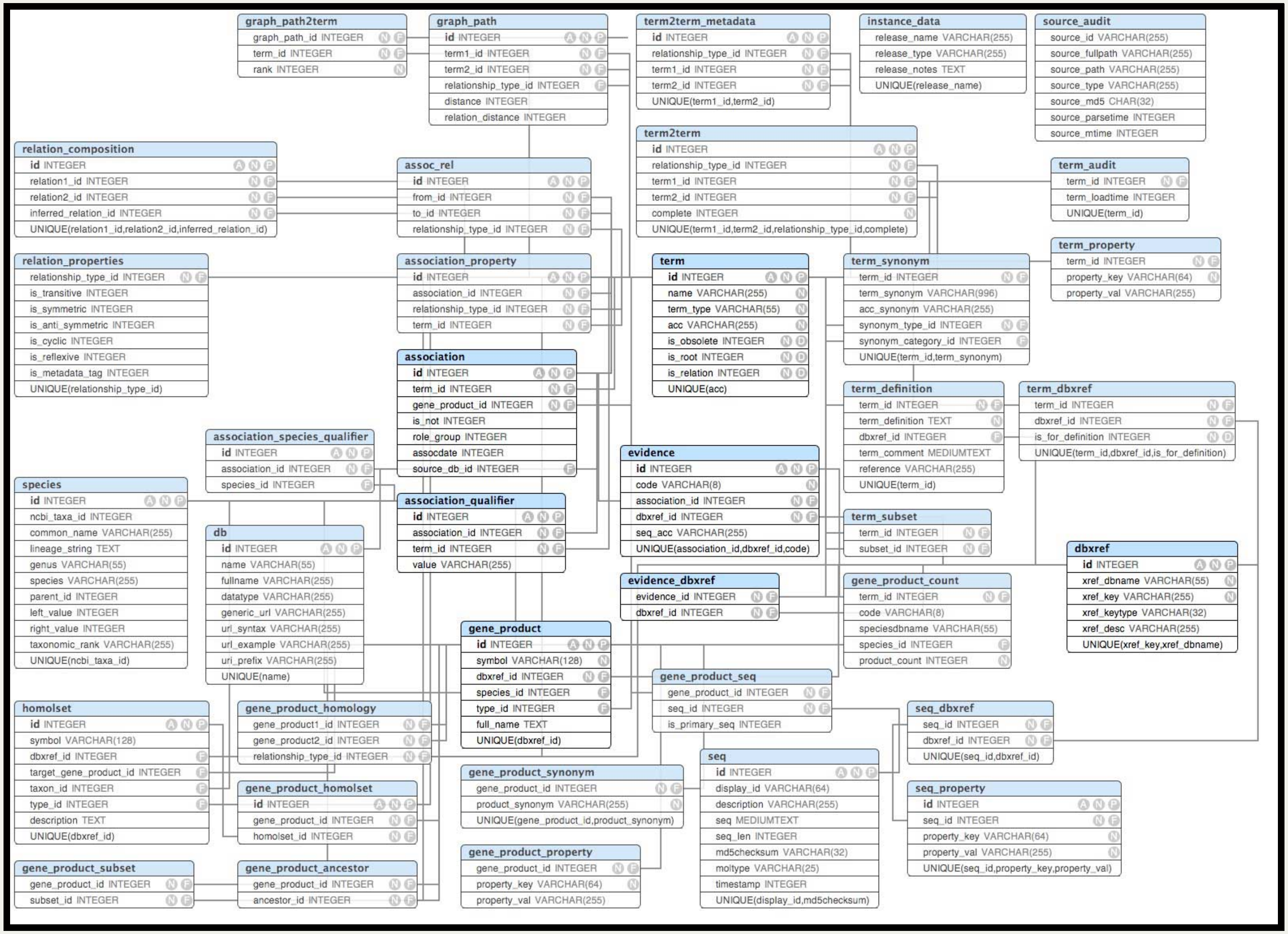
# It’s open!

- Code is under the **AGPLv3** license
- Only **Open Data** is integrated
- Implementation & release process is **100% public** and totally transparent

# Biology & Databases today

- Highly **interconnected overlapping** knowledge
- spread over **different data sources**
- maintained in the **Relational Databases**
  or sometimes even just as plain **CSV files**

That might be fine for simple scenarios
but as the **amount** and **diversity** of data grows,
**domain models** become *crazily complicated!*



**graph_path2term**
graph_path_id INTEGER N F
term_id INTEGER N F
rank INTEGER N

**graph_path**
id INTEGER A N P
term1_id INTEGER N F
term2_id INTEGER N F
relationship_type_id INTEGER F
distance INTEGER
relation_distance INTEGER

**term2term_metadata**
id INTEGER A N P
relationship_type_id INTEGER N F
term1_id INTEGER N F
term2_id INTEGER N F
UNIQUE(term1_id,term2_id)

**instance_data**
release_name VARCHAR(255)
release_type VARCHAR(255)
release_notes TEXT
UNIQUE(release_name)

**source_audit**
source_id VARCHAR(255)
source_fullpath VARCHAR(255)
source_path VARCHAR(255)
source_type VARCHAR(255)
source_md5 CHAR(32)
source_parsetime INTEGER
source_mtime INTEGER

**relation_composition**
id INTEGER A N P
relation1_id INTEGER N F
relation2_id INTEGER N F
inferred_relation_id INTEGER N F
UNIQUE(relation1_id,relation2_id,inferred_relation_id)

**assoc_rel**
id INTEGER A N P
from_id INTEGER N F
to_id INTEGER N F
relationship_type_id INTEGER N F

**term2term**
id INTEGER A N P
relationship_type_id INTEGER N F
term1_id INTEGER N F
term2_id INTEGER N F
complete INTEGER N
UNIQUE(term1_id,term2_id,relationship_type_id,complete)

**term_audit**
term_id INTEGER N F
term_loadtime INTEGER
UNIQUE(term_id)

**term_property**
term_id INTEGER N F
property_key VARCHAR(64) N
property_val VARCHAR(255)

**relation_properties**
relationship_type_id INTEGER N F
is_transitive INTEGER
is_symmetric INTEGER
is_anti_symmetric INTEGER
is_cyclic INTEGER
is_reflexive INTEGER
is_metadata_tag INTEGER
UNIQUE(relationship_type_id)

**association_property**
id INTEGER A N P
association_id INTEGER N F
relationship_type_id INTEGER N F
term_id INTEGER N F

**term**
id INTEGER A N P
name VARCHAR(255) N
term_type VARCHAR(55) N
acc VARCHAR(255) N
is_obsolete INTEGER N D
is_root INTEGER N D
is_relation INTEGER N D
UNIQUE(acc)

**term_synonym**
term_id INTEGER N F
term_synonym VARCHAR(996)
acc_synonym VARCHAR(255)
synonym_type_id INTEGER N F
synonym_category_id INTEGER F
UNIQUE(term_id,term_synonym)

**association**
id INTEGER A N P
term_id INTEGER N F
gene_product_id INTEGER N F
is_not INTEGER
role_group INTEGER
assocdate INTEGER
source_db_id INTEGER F

**term_definition**
term_id INTEGER N F
term_definition TEXT N
dbxref_id INTEGER F
term_comment MEDIUMTEXT
reference VARCHAR(255)
UNIQUE(term_id)

**term_dbxref**
term_id INTEGER N F
dbxref_id INTEGER N F
is_for_definition INTEGER N D
UNIQUE(term_id,dbxref_id,is_for_definition)

**association_species_qualifier**
id INTEGER A N P
association_id INTEGER N F
species_id INTEGER F

**evidence**
id INTEGER A N P
code VARCHAR(8) N
association_id INTEGER N F
dbxref_id INTEGER N F
seq_acc VARCHAR(255)
UNIQUE(association_id,dbxref_id,code)

**species**
id INTEGER A N P
ncbi_taxa_id INTEGER
common_name VARCHAR(255)
lineage_string TEXT
genus VARCHAR(55)
species VARCHAR(255)
parent_id INTEGER
left_value INTEGER
right_value INTEGER
taxonomic_rank VARCHAR(255)
UNIQUE(ncbi_taxa_id)

**association_qualifier**
id INTEGER A N P
association_id INTEGER N F
term_id INTEGER N F
value VARCHAR(255)

**term_subset**
term_id INTEGER N F
subset_id INTEGER N F

**db**
id INTEGER A N P
name VARCHAR(55)
fullname VARCHAR(255)
datatype VARCHAR(255)
generic_url VARCHAR(255)
url_syntax VARCHAR(255)
url_example VARCHAR(255)
uri_prefix VARCHAR(255)
UNIQUE(name)

**dbxref**
id INTEGER A N P
xref_dbname VARCHAR(55) N
xref_key VARCHAR(255) N
xref_keytype VARCHAR(32)
xref_desc VARCHAR(255)
UNIQUE(xref_key,xref_dbname)

**evidence_dbxref**
evidence_id INTEGER N F
dbxref_id INTEGER N F

**gene_product_count**
term_id INTEGER N F
code VARCHAR(8)
speciesdbname VARCHAR(55)
species_id INTEGER F
product_count INTEGER N

**gene_product**
id INTEGER A N P
symbol VARCHAR(128) N
dbxref_id INTEGER N F
species_id INTEGER F
type_id INTEGER F
full_name TEXT
UNIQUE(dbxref_id)

**gene_product_seq**
gene_product_id INTEGER N F
seq_id INTEGER N F
is_primary_seq INTEGER

**homolset**
id INTEGER A N P
symbol VARCHAR(128)
dbxref_id INTEGER F
target_gene_product_id INTEGER F
taxon_id INTEGER F
type_id INTEGER F
description TEXT
UNIQUE(dbxref_id)

**gene_product_homology**
gene_product1_id INTEGER N F
gene_product2_id INTEGER N F
relationship_type_id INTEGER N F

**seq_dbxref**
seq_id INTEGER N F
dbxref_id INTEGER N F
UNIQUE(seq_id,dbxref_id)

**seq**
id INTEGER A N P
display_id VARCHAR(64)
description VARCHAR(255)
seq MEDIUMTEXT
seq_len INTEGER
md5checksum VARCHAR(32)
moltype VARCHAR(25)
timestamp INTEGER
UNIQUE(display_id,md5checksum)

**gene_product_synonym**
gene_product_id INTEGER N F
product_synonym VARCHAR(255) N
UNIQUE(gene_product_id,product_synonym)

**gene_product_homolset**
id INTEGER A N P
gene_product_id INTEGER N F
homolset_id INTEGER N F

**seq_property**
id INTEGER A N P
seq_id INTEGER N F
property_key VARCHAR(64) N
property_val VARCHAR(255) N
UNIQUE(seq_id,property_key,property_val)

**gene_product_property**
gene_product_id INTEGER N F
property_key VARCHAR(64) N
property_val VARCHAR(255)

**gene_product_subset**
gene_product_id INTEGER N F
subset_id INTEGER N F

**gene_product_ancestor**
gene_product_id INTEGER N F
ancestor_id INTEGER N F

*Doesn't look very compelling right?*

# Relational model

With relational paradigm the double implication

**Entity** $\Leftrightarrow$ **Table**

doesn’t go both ways, which implies

- **auxiliary tables**
- **artificial IDs**
- dealing with **raw tables**
  (in spite of entity-relationship diagrams)

**Integrating** new knowledge becomes **difficult**

# Biology $\neq$ Table

- **Life** in general and **biology** in particular are probably not 100% like a graph…
- but one thing is sure: they ***are not a set of tables!***

# Why 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)* indices allow to overcome the supernode problem

# Why in the cloud?

amazon web services™

## Data as a service

- Services interoperability
- Data distribution
- Backup and storage
- Scalability
- Cost-effectiveness

# Bio4j

=

Bio Data

+

Graph Databases

+

The Cloud

# Details about Bio4j

# How it all started

- Need for **massive access** to *Gene Ontology* annotations
- **BG7** bacterial genome annotation system
- Need for massive direct access to **protein information**

# More and more data!

- As *other* data sources were becoming a *bottleneck* they were integrated into Bio4j
- First it was Uniprot KB, then Uniref, …
- And **we didn’t stop yet!**

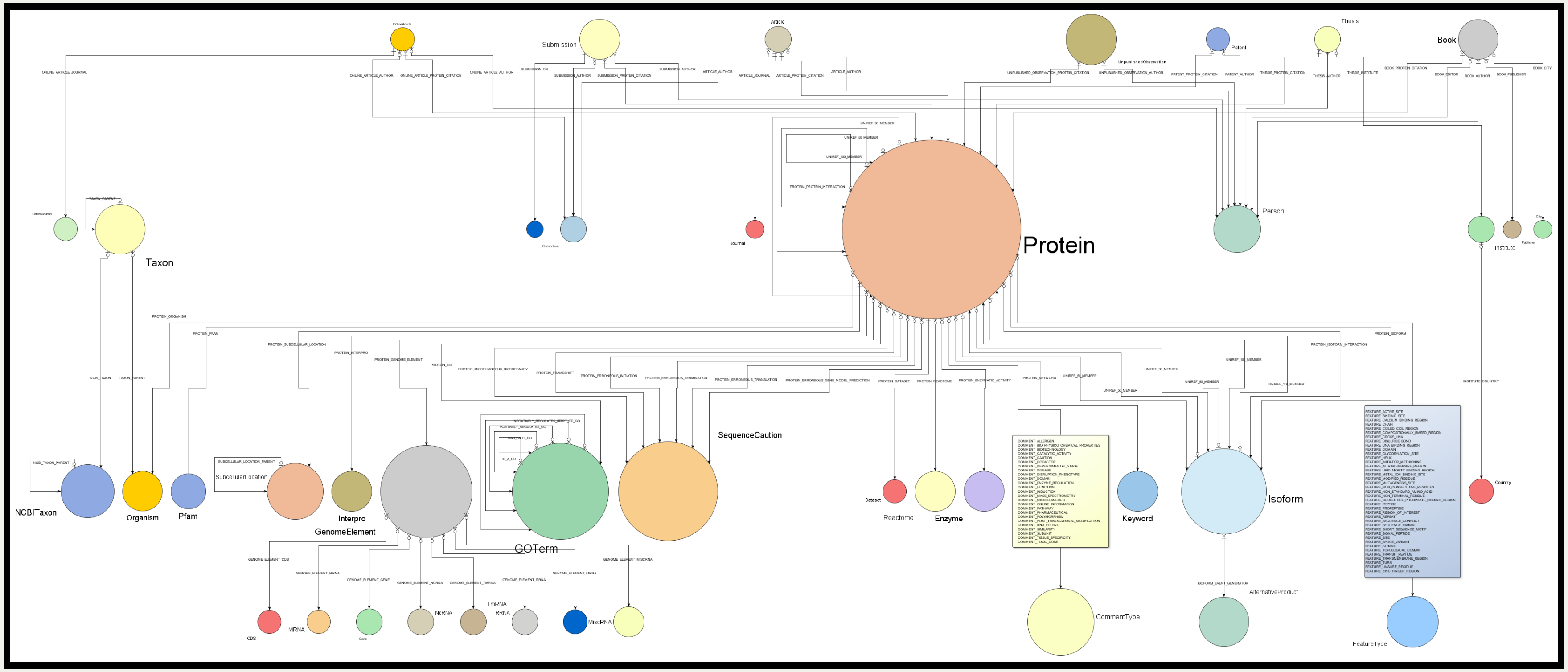
# Different layers of Bio4j

1. Abstract **domain model** with precise typing
2. Universal Blueprints implementation
3. **Technology-specific** versions:
   - Neo4j
   - Titan (WIP)
   - OrientDB (planned)

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

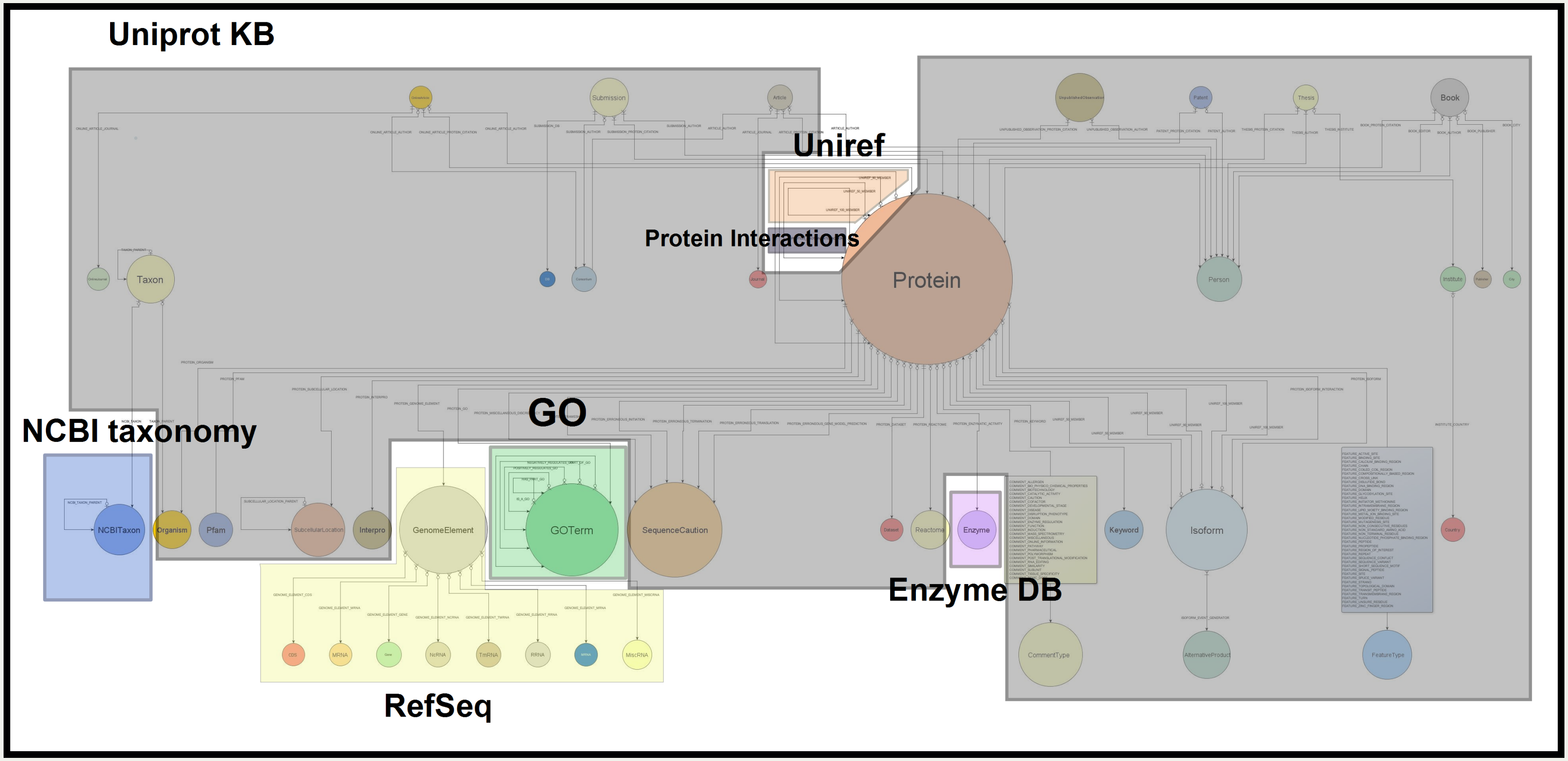
# Bio4j domain model

- $10^9$ edges of **150 types**
- $2 \times 10^8$ nodes of **40 types**
- $6 \times 10^8$ properties



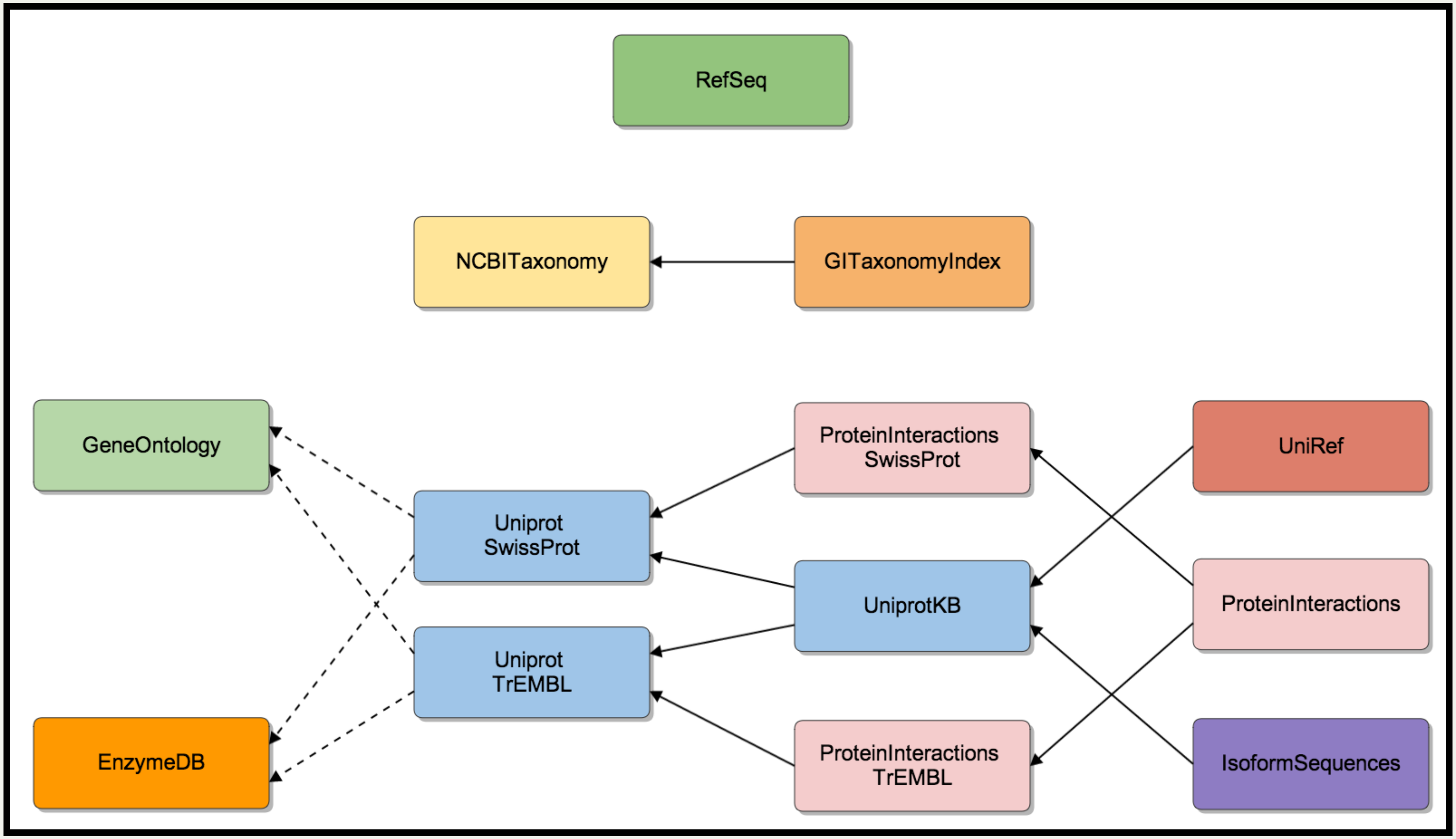
# Bio4j structure

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



# Bio4j module system

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



# Under the hood

# How we use Bio4j in Era7

- **BG7** genome annotation
- **MG7** metagenomics analysis
- Comparative genomics, network analysis, genome assembly, …

# How others use Bio4j

## 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**

# How we develop Bio4j

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

# Who's doing Bio4j

Ohnosequences!

Era7 bioinformatics R&D group

| | |
|---|---|
| **Pablo Pareja** | project leader & main developer |
| **Eduardo Pareja-Tobes** | technology & architecture |
| **Raquel Tobes** | bio data integration |
| **Marina Manrique** | bio data integration |
| **Alexey Alekhin** | module system developer |
| **Evdokim Kovach** | developer |

# Contacts

- @bio4j **Twitter** for news
- bio4j **Github** org for the development process
- bio4j-user **Google group** for the user feedback
- bio4j **Linkedin**

bio4j.com

# Thank you for attention!

*The source and the latest version of these slides can be found at*

`github.com/ohnosequences/IWBBIO-2014`