UNIVERSIDADE DE AVEIRO

COEUS: “Semantic Web in a Box”

http://bioinformatics.ua.pt/coeus

In this tutorial you will learn:

- What is COEUS
- How to create a new COEUS instance
  - From GitHub download to web deployment
- How to integrate data from heterogeneous *omics sources
  - Exploring integration connectors
- How to use COEUS API to access aggregated data
  - Build new rich web information systems using the API
  - Access the SPARQL and LinkedData interfaces

Outline

1 Workshop Setup

1.1 Requirements

- Application Server
  - Tomcat (.war deployment release, recommended)
    - https://github.com/bioinformatics-ua/COEUS/releases/download/2.1/coeus.war
  - Java environment with IDE, Maven, Tomcat (for developer release)
    - https://github.com/bioinformatics-ua/COEUS/
- Database
  - MySQL
    - Sample data: http://bioinformatics.ua.pt/coeus/hummer.sql

1.2 Get ready

To start this tutorial, you must configure your Tomcat application server authentication first. COEUS uses the Tomcat manager application (installed by default on "/manager"), which needs you to define the authentication realm. This is done by simple adding a line on the tomcat-users.xml file of your Tomcat server: `<user name="admin" password="admin123" roles="manager-gui, manager-script" />`

To start, just deploy your COEUS instance to the application server. By default, it should be available at `http://localhost:8080/coeus/`.

Once it's online, you're ready to go!

2 News Reader

In this first example, we will build a simple news aggregator. The goal is to collect, merge and query news from multiple websites. This example highlights the workflow for creating new COEUS seeds.

Requirements Analysis

1. Identify data sources for integration
2. Draft internal seed model

Implementation

1. Setup COEUS seed
2. Create internal configuration
3. Build knowledge base

Test

1. Query data
2. Test APIs

Use (not covered in this tutorial)

- Use APIs to build client-side applications

2.1 Requirements Analysis

This News Reader will integrate sports news from four distinct sources. For each news outlet, we need to identify the required RSS feed:

- **Reuters**: http://feeds.reuters.com/reuters/sportsNews
- **BBC**: http://feeds.bbci.co.uk/sport/0/rss.xml
- **Marca**: http://estaticos.marca.com/rss/portada.xml
- **A Bola**: http://www.abola.pt/rss/index.aspx

Next, we need to create a semantic model to accommodate our news data. This model is mapped to COEUS' internal model, and defines the hierarchical structure organising our knowledge. For this scenario, we will draft a very simple model, with just one **entity** and one **concept** for each news source. This way, a single news entry matches a single **item** in the knowledge base (thus, belonging to a single **concept**). The final structure is the following:

- **Entity**: News
  - **Concept**: Reuters
  - **Concept**: BBC
  - **Concept**: Marca
  - **Concept**: A Bola

At this stage, we also identify what data we need to save for each news entry. We will not create a custom ontology to store these data, we will reuse existing ontologies/predicates:

- **dc:identifier**: entry id
- **dc:title**: entry title
- **dc:description**: entry text
- **rdfs:seeAlso**: entry link to original news
- **dc:date**: entry publication date

2.2 Implementation/Configuration

There isn't any actual implementation to setup the backend for new COEUS seeds. Everything can be configured and managed from the seed setup web interface. This is where the fun starts: launch COEUS and start configuring your seed.

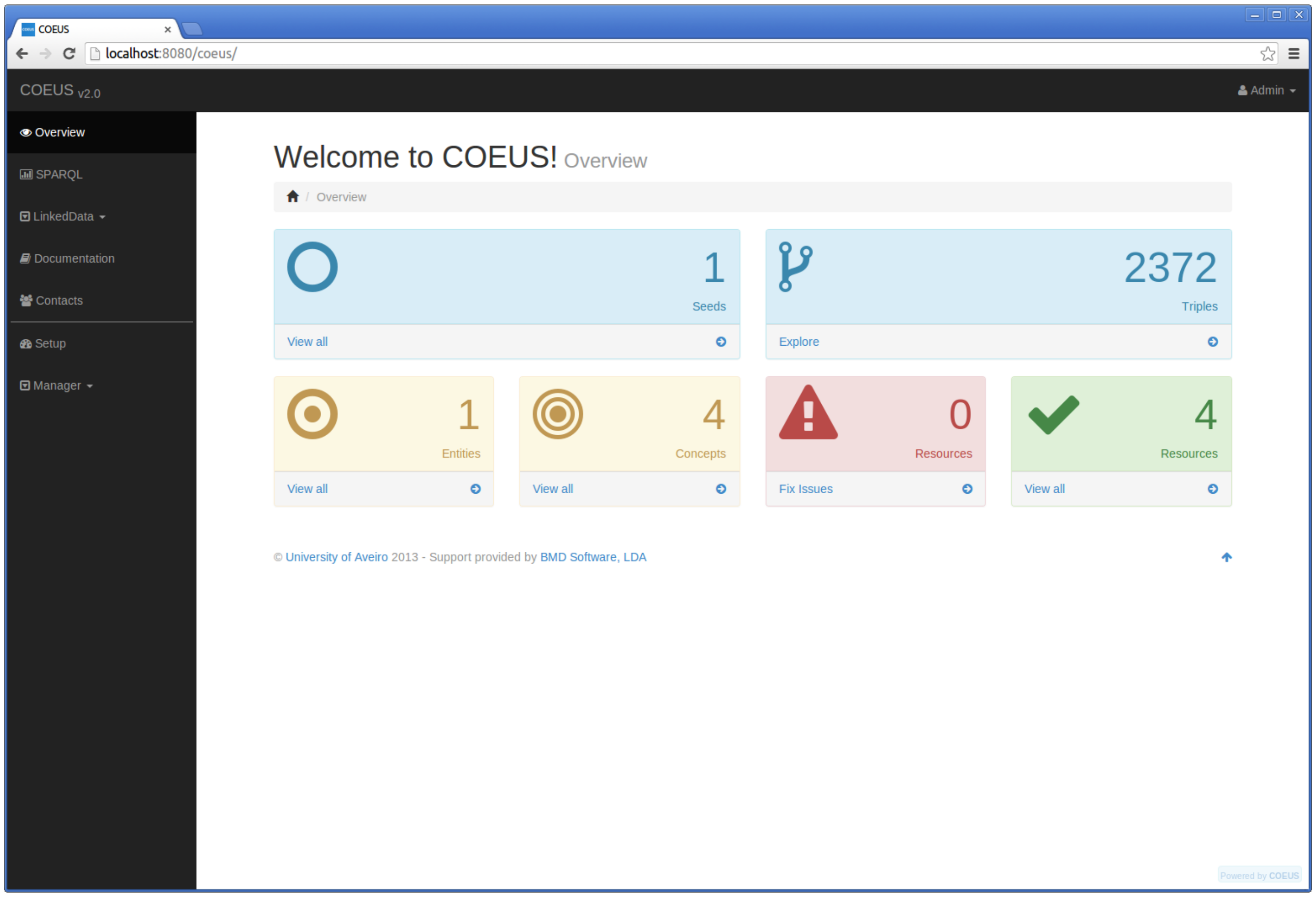
2.2.1 Setting up the environment

Notes

- COEUS seeds are organised in environments
- Environments define server properties
  - MySQL connection
  - Public/private LinkedData configuration
  - Model
  - Prefix list
  - ...
- Usage
  - Configure multiple setups in a single machine
  - Setup “development”, “test” and “production” environments

2.2.1.1 Launch COEUS web app

- Go to `/coeus` on your browser of choice

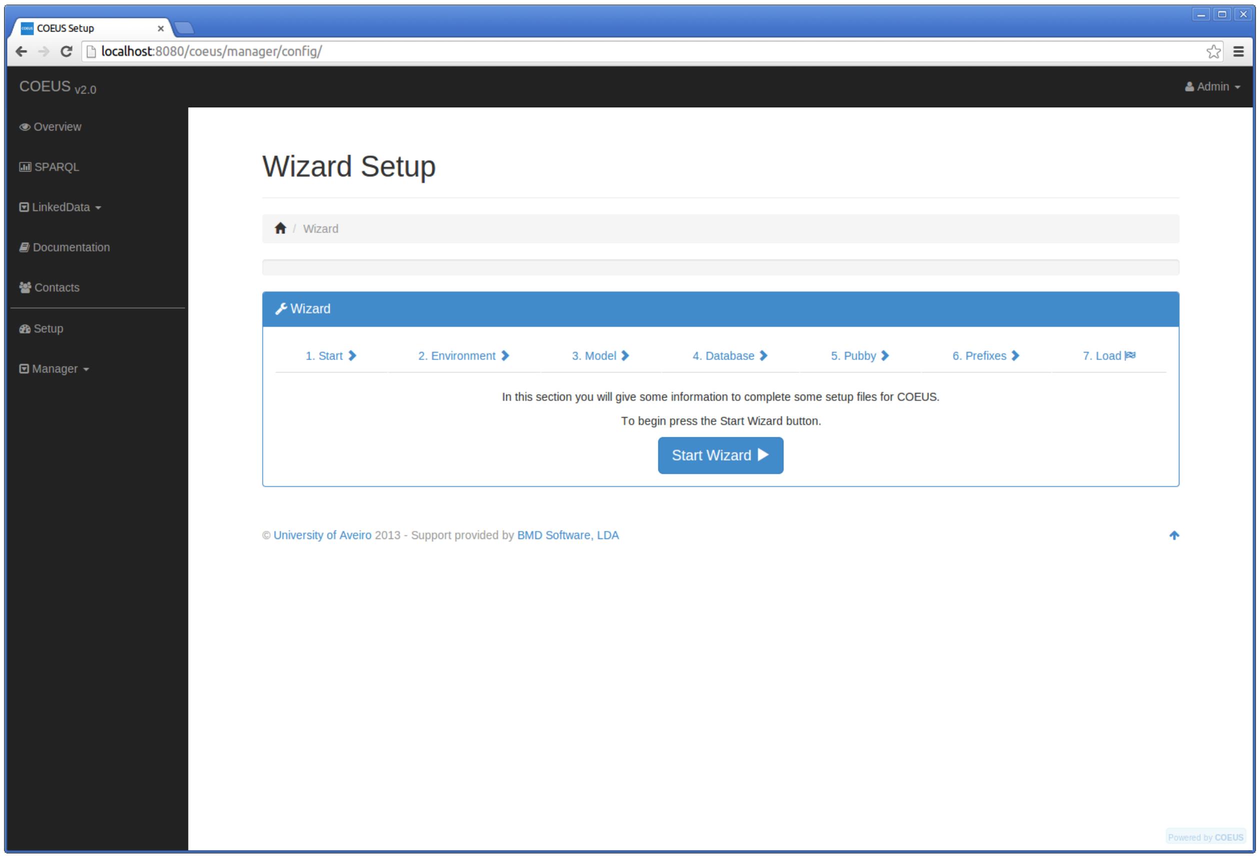


2.2.1.2 Go to setup page

- Click the `Setup` link in the left menu bar
  - If authentication is enabled use your tomcat credentials.

If it is the first time running COEUS' setup, the *Configuration Wizard* will be displayed automatically.

1. Press the ***Start Wizard*** button to begin.



In this section you will give some information to complete some setup files for COEUS.

To begin press the Start Wizard button.

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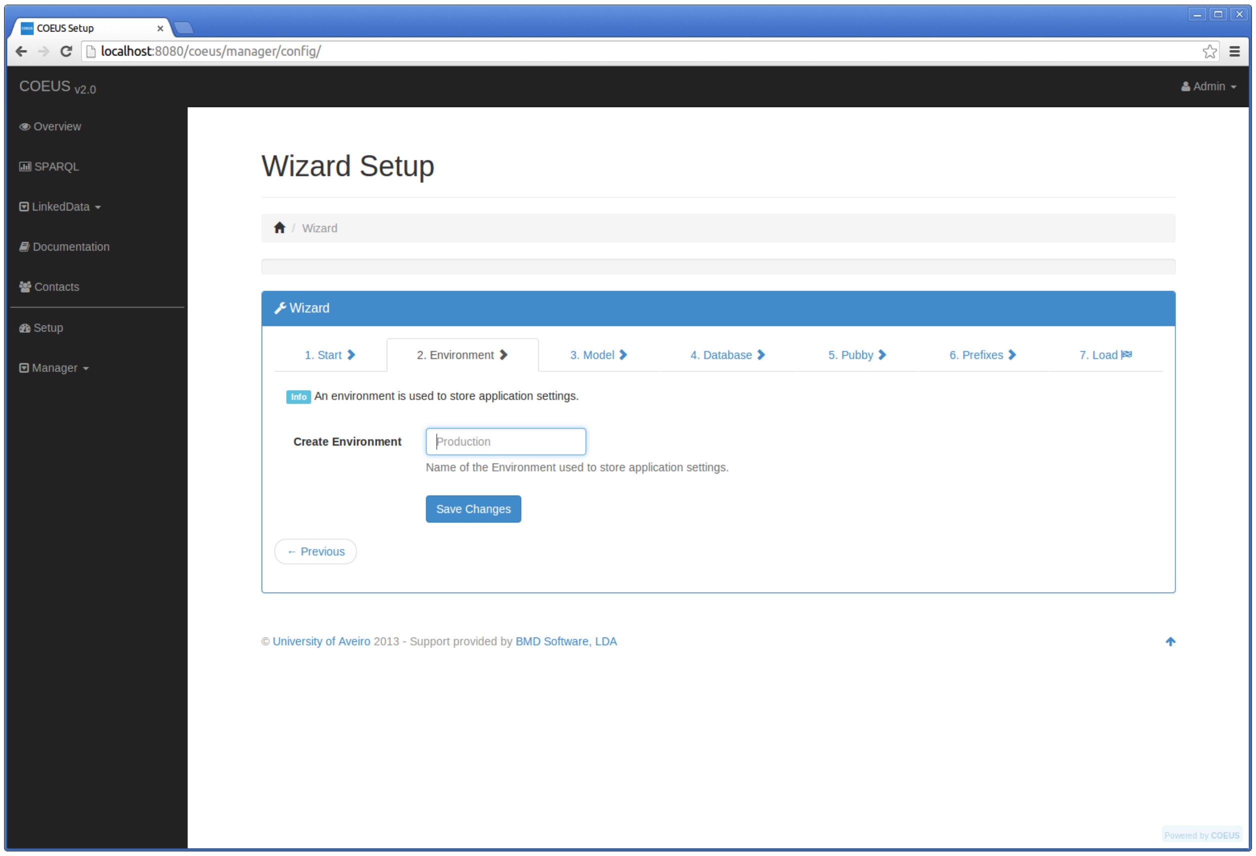
2.2.1.3 Environment Configuration

2. Set the environment name. For instance, "tutorial".



Wizard Setup

Info An environment is used to store application settings.

Create Environment: Production

Name of the Environment used to store application settings.

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Save the changes and press *Next*.

2.2.1.4 Model Setup

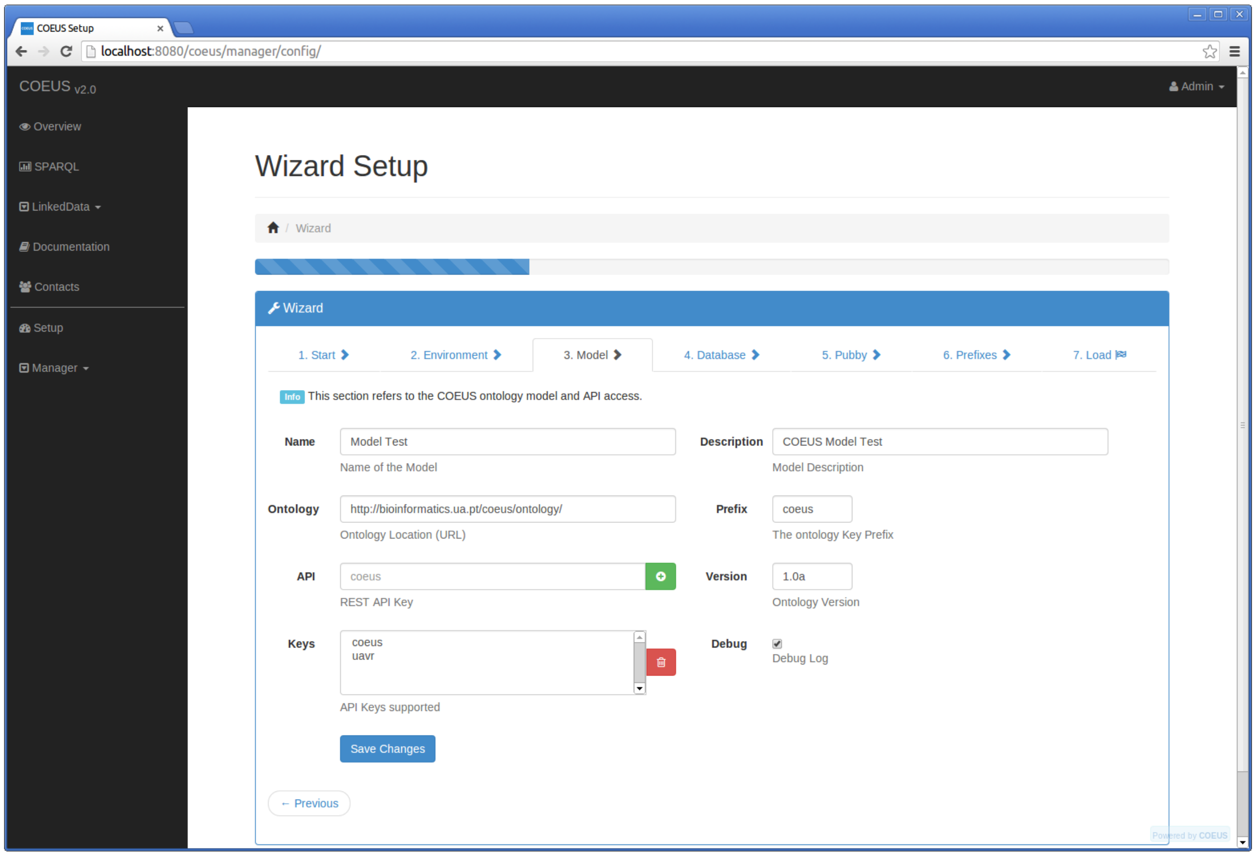
Notes

Each COEUS environment has an internal model. Besides the integration structure, the model has several properties:

- *Name*: The model name
- *Ontology*: External ontology URL, if used
- *Description*: The model description
- *Key Prefix*: The base semantic prefix to store the data
- *API Key*: List of API keys for usage in client applications (delimited by |)

- *Version*: Model version
- *Debug*: Debug mode generates a verbose server output

3. No changes are required for the *News Reader* example. Feel free to update it according to your setup (change the name or the API keys).



Info This section refers to the COEUS ontology model and API access.

Name	Model Test Name of the Model	Description	COEUS Model Test Model Description
Ontology	http://bioinformatics.ua.pt/coeus/ontology/ Ontology Location (URL)	Prefix	coeus The ontology Key Prefix
API	coeus REST API Key	Version	1.0a Ontology Version
Keys	coeus uavr API Keys supported	Debug	✓ Debug Log

Save the changes and press *Next*.

2.2.1.5 Database Setup

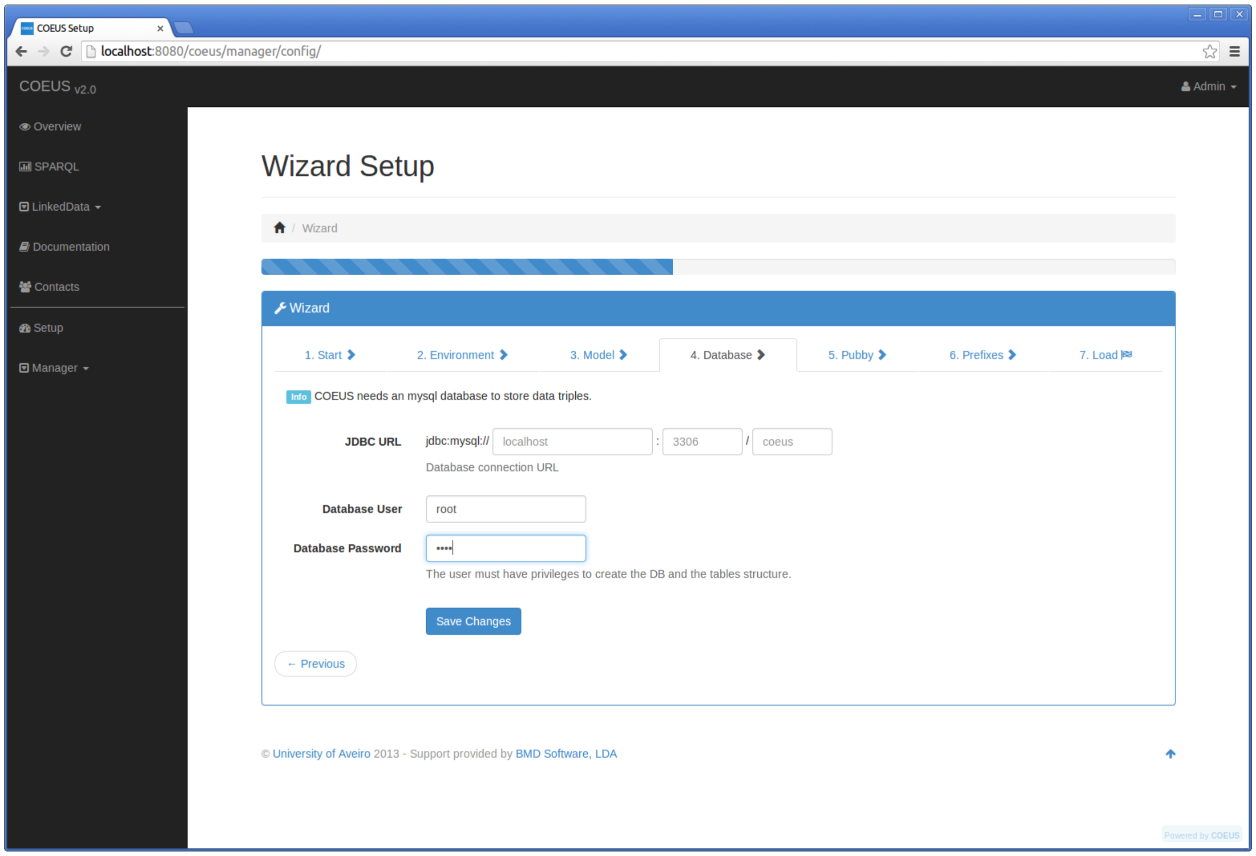
Notes

- COEUS requires a MySQL database
  - with a user with root privileges or other similar to create the DB and tables structure.
- Used to
  - Support Jena triplestore
  - Store temporary configuration properties

– Extend client-side applications

4. Configure the connections properties of the environment database. If you don't have MySQL installed, you can use the following details:

- *Host*: `localhost`
- *Port*: `3306`
- *Database*: `tutorial_xyz` (change *xyz* to any other word...)
- *User*: `tutorial`
- *Password*: `coeus`



Info COEUS needs an mysql database to store data triples.

JDBC URL jdbc:mysql:// localhost : 3306 / coeus
Database connection URL

Database User: root

Database Password: ••••

The user must have privileges to create the DB and the tables structure.

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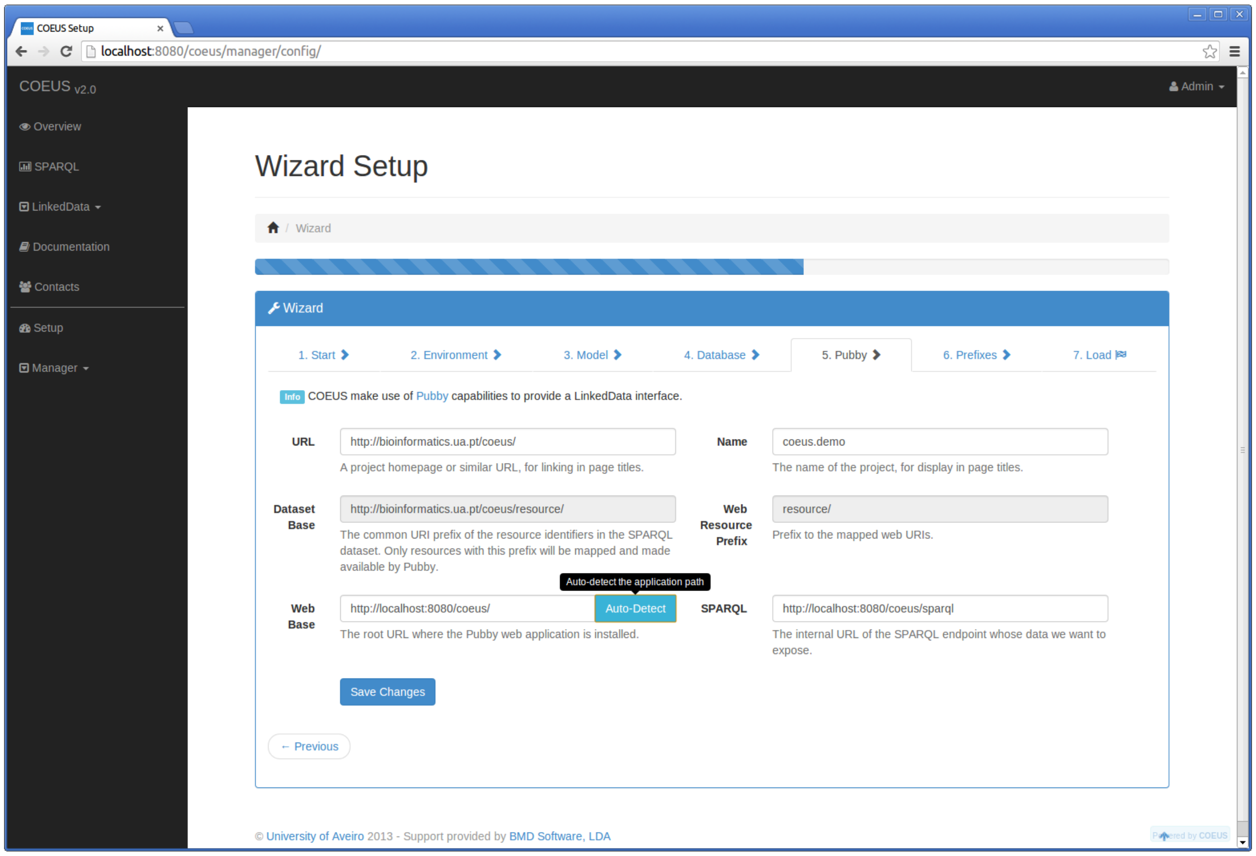
Save the changes and press *Next*.

2.2.1.6 Pubby Setup

Pubby manages the LinkedData publishing interfaces. On the Pubby configuration screen you can define seed-specific properties to be used by the Pubby engine, such as the project homepage, the SPARQL endpoint address or the base knowledge base URI.

5. For now, we can leave the Pubby setup with the default values by only clicking on the auto-detect button that ensures that your app has the correct location.



Wizard Setup

Info COEUS make use of Pubby capabilities to provide a LinkedData interface.

URL	http://bioinformatics.ua.pt/coeus/ A project homepage or similar URL, for linking in page titles.	Name	coeus.demo The name of the project, for display in page titles.
Dataset Base	http://bioinformatics.ua.pt/coeus/resource/ The common URI prefix of the resource identifiers in the SPARQL dataset. Only resources with this prefix will be mapped and made available by Pubby.	Web Resource Prefix	resource/ Prefix to the mapped web URIs.
Web Base	http://localhost:8080/coeus/ The root URL where the Pubby web application is installed.	SPARQL	http://localhost:8080/coeus/sparql The internal URL of the SPARQL endpoint whose data we want to expose.

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Save the changes and press *Next*.

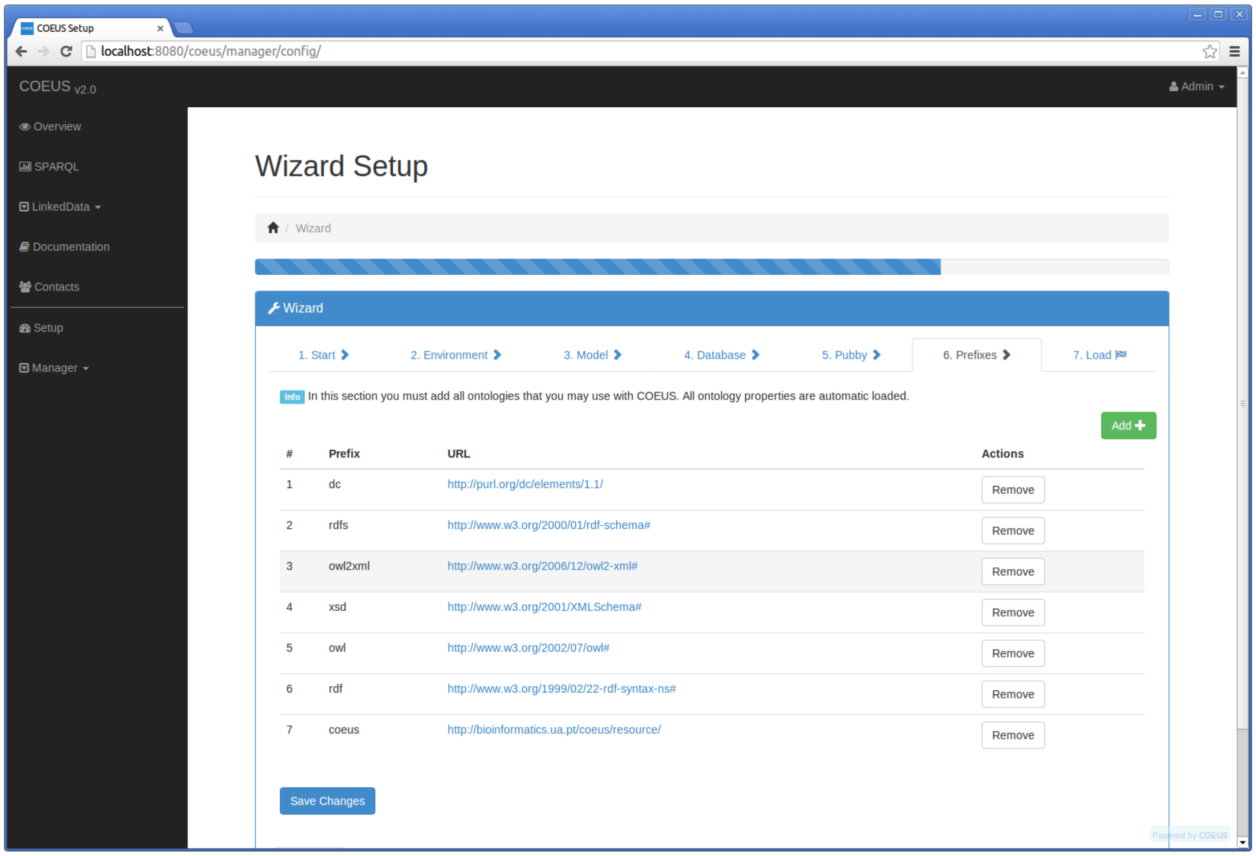
2.2.1.7 Prefix Setup

Notes

For improved performance, COEUS includes an internal semantic name resolution engine. This tools translates long-form URIs into short-form strings and vice-versa. For instance, `http://www.w3.org/1999/02/22-rdf-syntax-ns#label` to `rdf:label`. These prefixes are prepoluted on the COEUS engine. Hence, in this step, you have to include any external ontology that will be used in the COEUS environment.

6. If not available, add the following schema to the prefix list.

- *Prefix*: `dc`
- *URI*: http://purl.org/dc/elements/1.1/



Info In this section you must add all ontologies that you may use with COEUS. All ontology properties are automatic loaded.

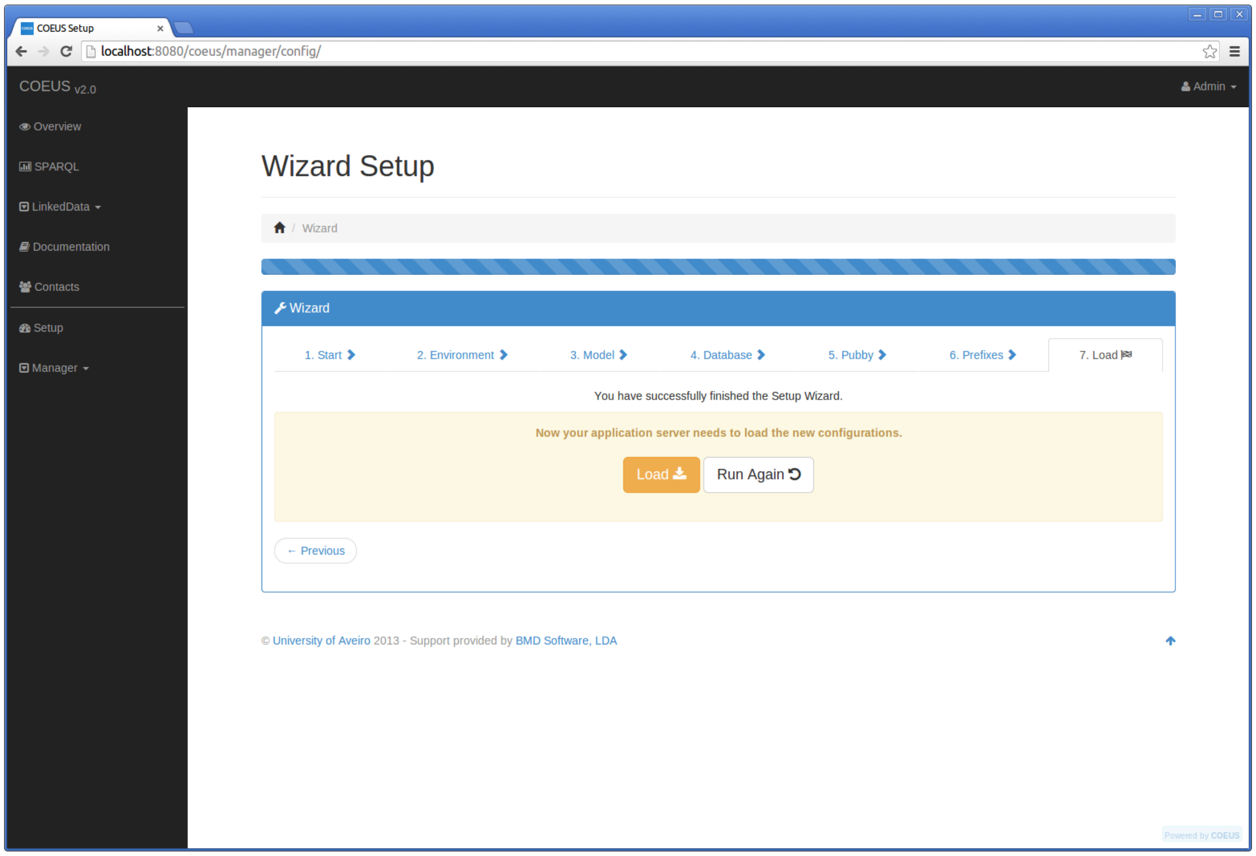
#	Prefix	URL	Actions
1	dc	http://purl.org/dc/elements/1.1/	Remove
2	rdfs	http://www.w3.org/2000/01/rdf-schema#	Remove
3	owl2xml	http://www.w3.org/2006/12/owl2-xml#	Remove
4	xsd	http://www.w3.org/2001/XMLSchema#	Remove
5	owl	http://www.w3.org/2002/07/owl#	Remove
6	rdf	http://www.w3.org/1999/02/22-rdf-syntax-ns#	Remove
7	coeus	http://bioinformatics.ua.pt/coeus/resource/	Remove

Save the changes and press *Next*.

2.2.1.8 Finish Environment Setup

If all went well, pressing the *Load* button will load the new settings to start using COEUS.

7. Press the *Load* button and wait a few seconds. After success response you must click on “Start with COEUS” button.



You have successfully finished the Setup Wizard.

Now your application server needs to load the new configurations.

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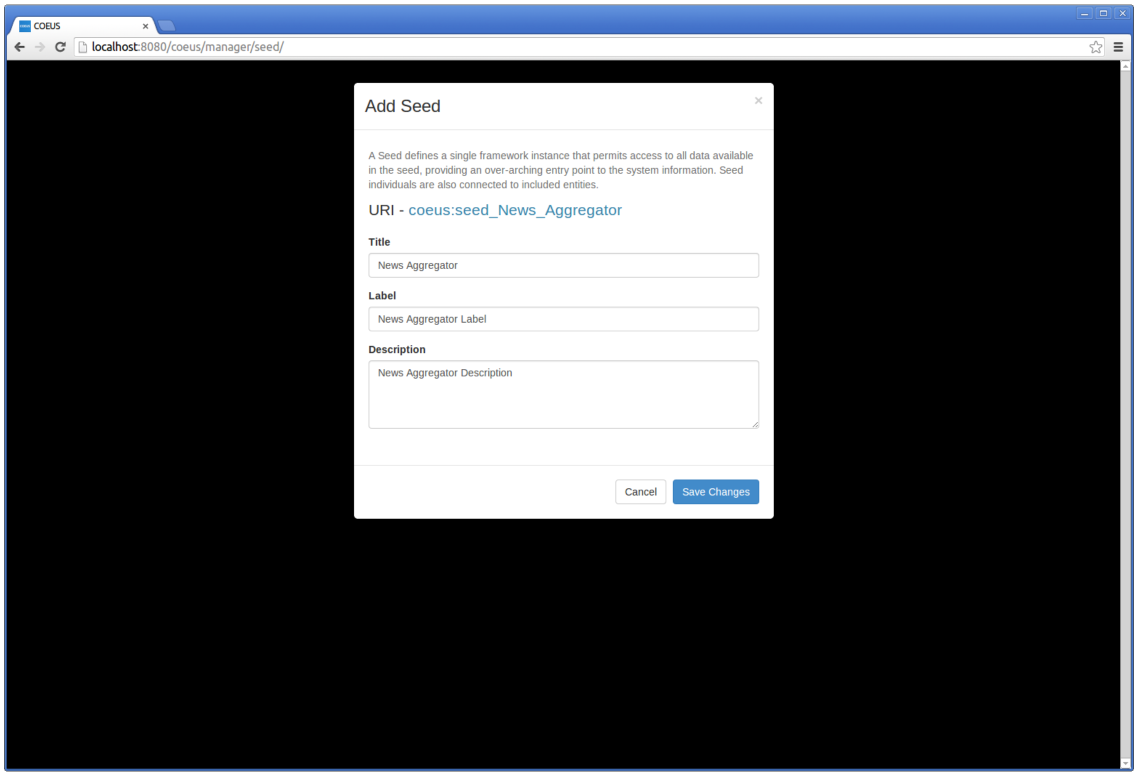
2.2.2 Configuring your first seed

- On the COEUS homepage, press the left *Setup* link.
  - In this screen you can manage all the COEUS seeds under a specific environment.

1. Press the *Add Seed* button. On the seed configuration form, set the Seed title, label and a description. The new seed will appear on the seed-listing interface.



A Seed defines a single framework instance that permits access to all data available in the seed, providing an over-arching entry point to the system information. Seed individuals are also connected to included entities.

URI - coeus:seed_News_Aggregator

Title: News Aggregator

Label: News Aggregator Label

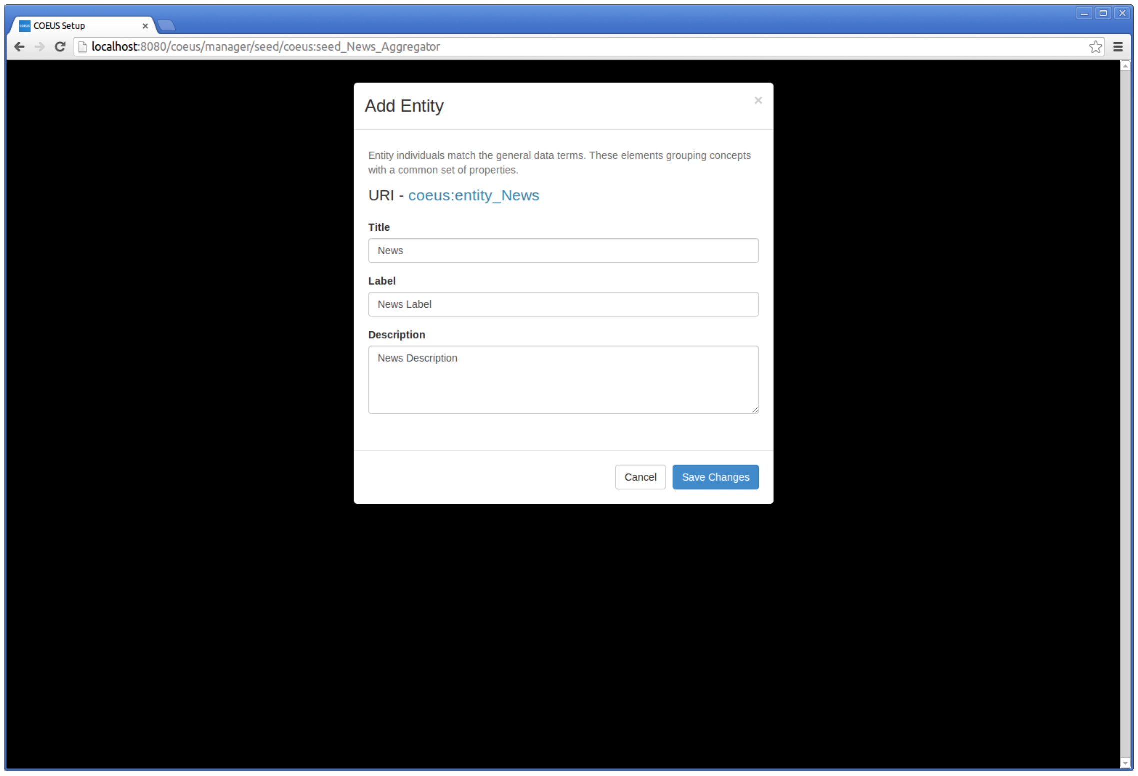
Description: News Aggregator Description

2. To start configuring the internal data structure, press the *Choose* button on the new seed. COEUS will display the Seed dashboard.
   - The seed dashboard provides a general overview of the entire seed content. The structure tree display the entire hierarchical structure configured in the seed. The action toolbox provides direct access buttons to the most common seed actions.

2.2.3 Adding the News Entity

With the environment and seed already configured, we can transpose our integration setup, from the requirements analysis to the actual seed.

- On the seed dashboard, press the *Add Entity* button.
  - Fill in the required details, Title, Label and Description, and save the changes.


COEUS Setup
localhost:8080/coeus/manager/seed/coeus:seed_News_Aggregator

Add Entity

Entity individuals match the general data terms. These elements grouping concepts with a common set of properties.

URI - coeus:entity_News

Title: News

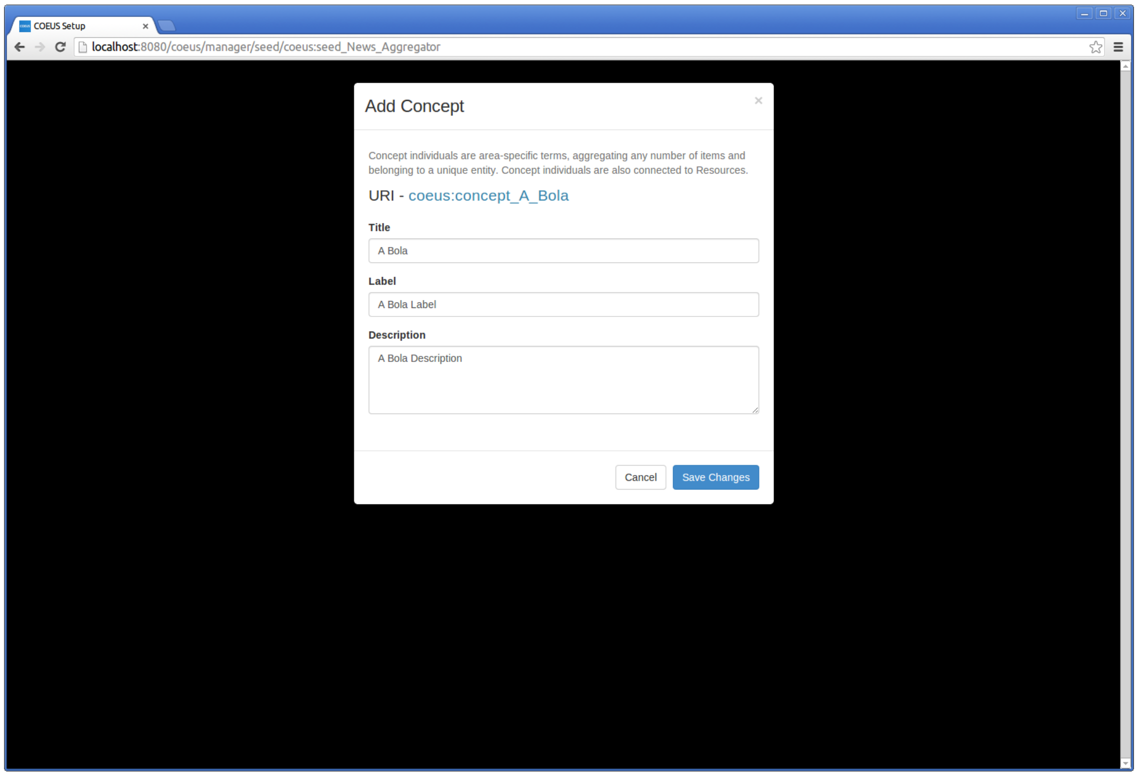
Label: News Label

Description: News Description

2.2.4 Adding the news Concepts

New concepts can be added directly from the seed dashboard knowledge base tree, from the entities list or from the concept list.

- We need to create a new concept for each news outlet.
- Press the *Concept +* button and fill in the required details in the displayed modal box (Title, Label and Description).
  - Repeat for the tree remaining news outlets.


COEUS Setup
localhost:8080/coeus/manager/seed/coeus:seed_News_Aggregator
Cancel
Save Changes

Add Concept

Concept individuals are area-specific terms, aggregating any number of items and belonging to a unique entity. Concept individuals are also connected to Resources.

URI - coeus:concept_A_Bola

Title: A Bola

Label: A Bola Label

Description: A Bola Description

2.2.5 Configuring Resources

Notes

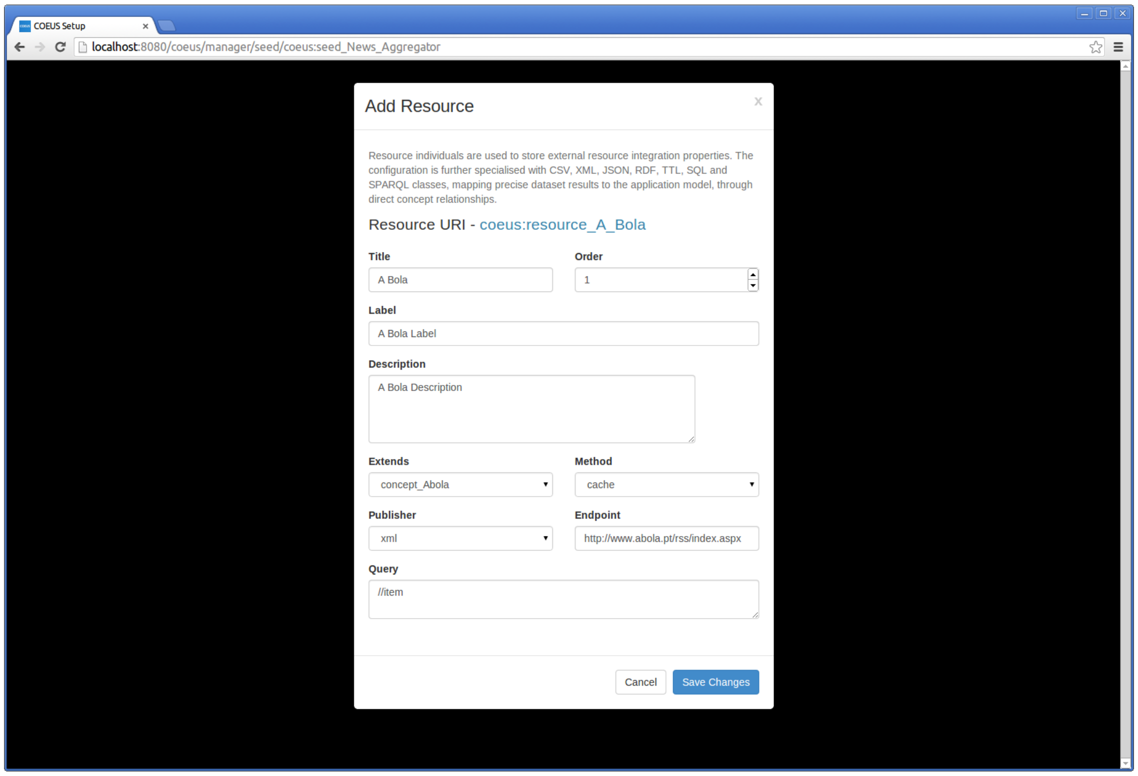
- Resources are related to Concepts
    - **Many-to-One**: *one* resource has *one* concept, *one* concept can have many *resources*
- Resources store the metadata configuring the **ETL** being performed for each Concept
- Examples
    - Endpoint `coeus:endpoint`
        - **CSV**: http://bioinformatics.ua.pt/coeus/list.csv
        - **SQL**: jdbc:mysql://localhost:3306/?user=&password=
    - Query `coeus:query`
        - **SQL**: SELECT * FROM genes;
        - **XML**: //entry

We need to define the resource integration properties for each of the four Concepts:

- Select a Concept from the list
- Press the *Resource +* button to display the new Resource modal
- Fill in the resource metadata
    - Title, Label and Comment: matching the given news outlet
    - `Order`: the integration order for this resource (irrelevant for this example)
    - `Extends`: when using an integration graph the Concept data extraction requires data from other Concept (previously loaded)
    - `Method`: the type of data integration being performed, select *cache* to copy all data to the COEUS knowledge base
    - `Publisher`: the resource data format, select *XML*

– `Endpoint`: resource URI, insert each news item respective RSS/Atom URL

– `Query`: the base query that will provide the integration list, insert *//item*


COEUS Setup

localhost:8080/coeus/manager/seed/coeus:seed_News_Aggregator

Add Resource

Resource individuals are used to store external resource integration properties. The configuration is further specialised with CSV, XML, JSON, RDF, TTL, SQL and SPARQL classes, mapping precise dataset results to the application model, through direct concept relationships.

Resource URI - coeus:resource_A_Bola

Title: A Bola

Order: 1

Label: A Bola Label

Description: A Bola Description

Extends: concept_Abola

Method: cache

Publisher: xml

Endpoint: http://www.abola.pt/rss/index.aspx

Query: //item

In this simple News Reader example, the process is similar to all concepts and resources. With all resources introduces, we must specify their selectors to finish the configuration.

2.2.6 Configuring Selectors

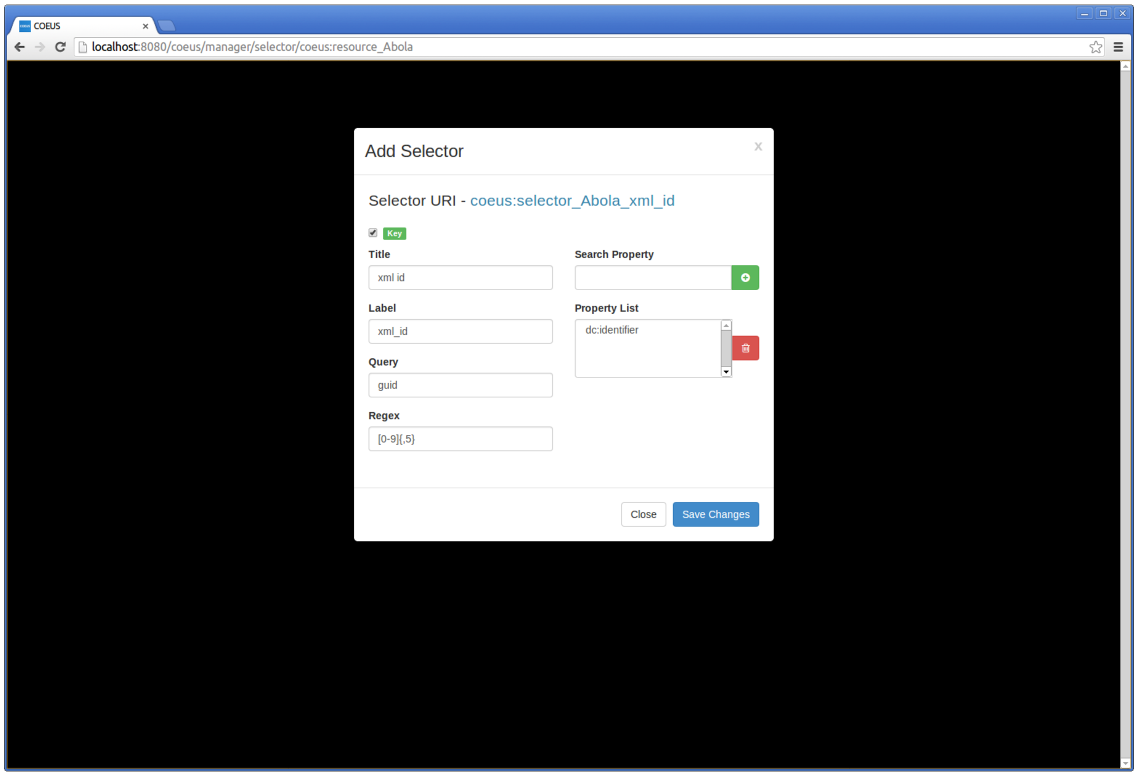
Notes

- Selectors specify the mapping between predicates and the extraction being performed
  - Applied to the Resource output list
- Examples
  - **CSV**, column number
    - dc:identifier, 0 (matches column zero)
  - **XML**, XPath query
    - dc:title, //title
  - **JSON**, JSONPath query
    - dc:description, entry.description
  - **SQL**, column name
    - dc:identifier, “id” (matches “id” column from SELECT)
  - **SPARQL**, variable name
    - dc:description, d (matches ?d variable)

On the resources listing interface, press the *Configuration* button to setup the selectors.

- Press the *New* button to add a selector
- Let's start with the news identifier selector
  - `Key`: Select this checkbox to use this selector as the identity generator for the new Items being generated
  - `Query`: the selector query to extract data from the resource list, in this case use the XPath *guid*
  - `Regex`: an optional regular expression to filter or validate values, use *[0-9]{5,}*

- `Property`: selectors can import data for one or multiple semantic predicates, add *dc:identifier* to the list (use the `Search Property` input to search and press *Enter* to add to the list)



Selector URI - coeus:selector_Abola_xml_id

Title: xml id
Label: xml_id
Query: guid
Regex: [0-9]{,5}
Search Property:
Property List: dc:identifier

- Fill in the remaining selectors
  - **dc:title**: entry title - `title`
  - **dc:description**: entry text - `description`
  - **rdfs:seeAlso**: entry link to original news - `link`
  - **dc:date**: entry publication date - `pubDate`

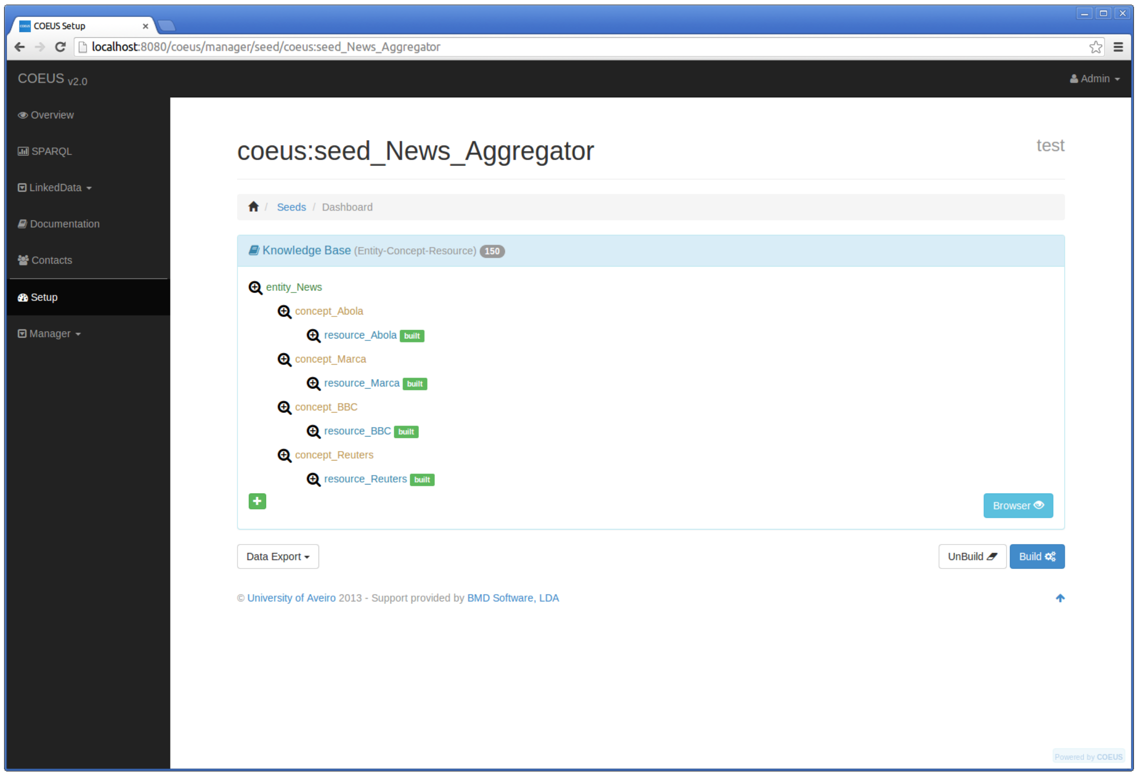
2.2.6.1 Reusing Selectors

Since we are working with similar data sources (i.e., using the same configurations), we do not need to define new selectors for each Resource. We can reuse existing selectors, making the integration process much simpler.

- On the Resource configuration interface, press the "Existing +" button to associate a previously configured selector with the resource.

2.2.7 Building the knowledge base

With all the entities, concepts, resources and selectors configured, you can go back to the seed dashboard. The seed structure tree, should list a single entity (News), with four concepts each with its own resource (BBC, Reuters, Marca and A Bola).



If you are using an IDE, view the server output to check what's happening behind the scenes:

- Traverse Resources list
  - Check dependencies
    - Concept Extends
  - Process Resource data
    - Apply Resource query
  - Process selectors
    - Apply selectors' queries
    - Build axioms with properties

2.3 Testing

With the knowledge base built, COEUS provides multiple methods to access the aggregated dataset. In this first example, we will just use the SPARQL endpoint to performs simple queries.

2.3.1 List all news items

```
PREFIX coeus:   <http://bioinformatics.ua.pt/coeus/resource/>
PREFIX dc:   <http://purl.org/dc/elements/1.1/>

SELECT ?item ?title ?description {
    ?item a coeus:Item .
    ?item dc:title ?title .
    ?item dc:description ?description .
    ?item dc:date ?date
}
```

2.3.2 List all news items with specific outlet

```
PREFIX coeus:   <http://bioinformatics.ua.pt/coeus/resource/>
PREFIX dc:   <http://purl.org/dc/elements/1.1/>

SELECT ?item ?title ?description {
    ?item a coeus:Item .
    ?item dc:title ?title .
    ?item dc:description ?description .
    ?item dc:date ?date .
    ?item coeus:hasConcept coeus:concept_BBC
}
```

2.3.3 List all news items ordered by date

```
PREFIX coeus:   <http://bioinformatics.ua.pt/coeus/resource/>
PREFIX dc:   <http://purl.org/dc/elements/1.1/>

SELECT ?date ?item ?title ?description {
    ?item a coeus:Item .
    ?item dc:title ?title .
    ?item dc:description ?description .
    ?item dc:date ?date
} ORDER BY DESC(?date)
```

3 Proteomics Knowledge Base

With second example we aim to build a proteomics knowledge base, aggregating miscellaneous data for associated with proteins. This scenario is more complex than the first one, as we will integrate and combine data from distinct heterogeneous resources.

The Proteomics KB will feature a mashup of data from HGNC, UniProt, InterPro, and OMIM. We will adopt the same workflow for this tutorial: (1) requirements analysis, (2) configuration & building, (3) testing.

3.1 Requirements Analysis

The first step is to think about a shared model to organize these data. There are lots of distinct solutions, we are proposing only one that fits COEUS' internal model. This model is a subset of the one used in Diseasecard.

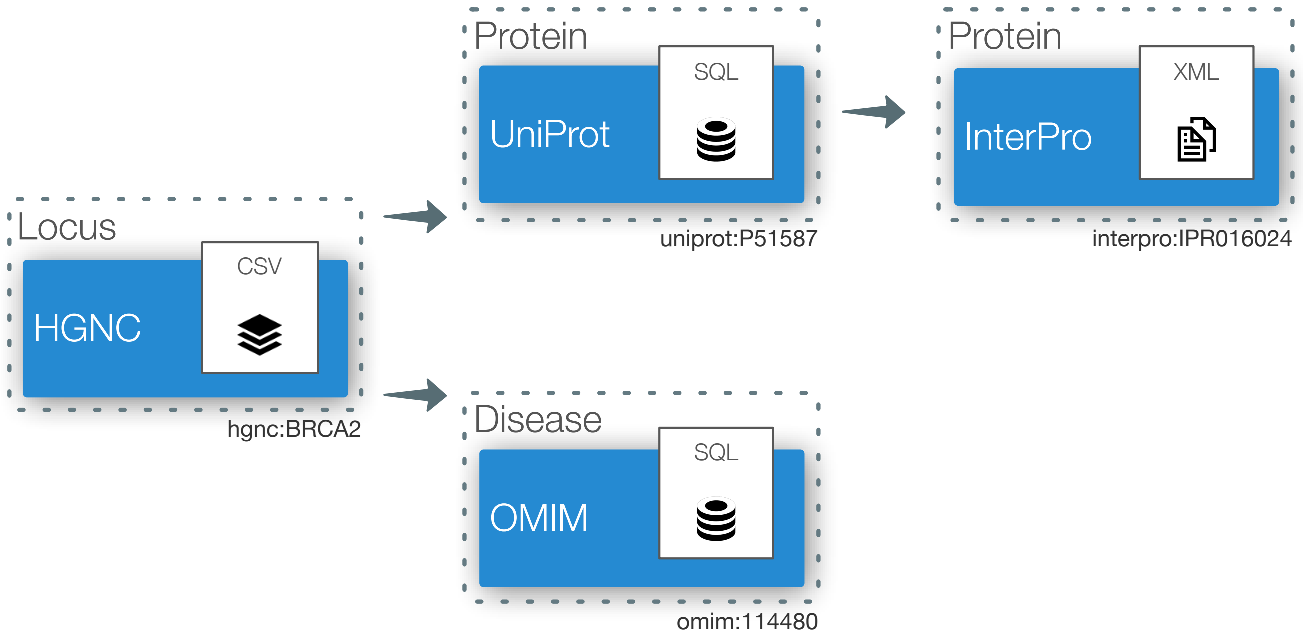
- **Entity**: Gene
  - **Concept**: HGNC
- **Entity**: Protein
  - **Concept**: UniProt
  - **Concept**: InterPro
- **Entity**: Disease
  - **Concept**: OMIM

To simplify this model, we will focus on loading unique identifiers for each data source (**dc:identifier**).

More important than just importing data, we need to establish new relationship. Hence, data will be loaded from our own "dependency graph". This graph can take many shapes and distinct structures. The following data-loading map relates the data from the multiple sources being integrated, which will result in a new semantic network in the proteomics knowledge base.

- **HGNC** (starting seed, loaded from file, *CSV*)

- **UniProt** (matches from UniProt query, *SQL*)
    - **InterPro** (from individual UniProt entries, *XML*)
- **OMIM** (from OMIM genemap, *SQL*)
    - **Orphanet** (from OrphaData, *SQL*)



Further details regarding the resources and selectors configurations for each Concept are described in the **Configuring Resources & Selectors** activity.

3.2 Configuration

COEUS allows multiple seeds in a single environment. As such, the Proteomics KB will be a new seed within the already set environment. (If you have not setup the COEUS environment with the News Reader example, go back and do the initial configuration tasks.)

3.2.1 Creating the Proteomics KB Seed

- Go back to the seeds list and create the new *Proteomics* seed.

3.2.2 Adding Entities & Concepts

- Replicate the seed organisation obtained in the requirements analysis using the COEUS GUI.

- All steps were covered in the News Reader example.

3.2.3 Configuring Resources & Selectors

In this more complex scenario, the integration is based on a dependency graph: to discover information about a certain concept, we need details (in this case, identifiers) of a concept that was previously loaded. Hence, on the resource configuration tasks, some resources extend concepts beyond their original pair.

3.2.3.1 HGNC

HGNC data is easily obtained in CSV format from the GeneNames website. The download can be customized to feature multiple columns, including gene symbol, names, chromosome locations or reference sequence identifiers, among others. For instance, the following CSV file includes the approved gene symbol, HGNC identifier and name:

- http://www.genenames.org/cgi-bin/hgnc_downloads.../

To reduce the tutorial server load, a smaller listing will be used.

3.2.3.1.1 Resource

- Add a new Resource to the HGNC Concept
  - `Order`: 1 *(this is the starting point)*
  - `Extends`: Concept HGNC *(has no dependencies)*
  - `Method`: cache *(copy everything)*
  - `Publisher`: CSV
  - `Endpoint`: http://bioinformatics.ua.pt/diseasecard/hgnc.csv
  - `CSV Starting Line`: 0 *(no headers)*

3.2.3.1.2 Selectors

For HGNC data, we will extract the gene symbol as the identifier and the gene name as a simple description. Hence, we need two distinct selectors.

- Id
  - `Query`: 1 *(column number 1)*

- `Property`: dc:identifier

- Name
  - `Query`: 2 *(column number 2)*
  - `Property`: dc:description

3.2.3.2 UniProt

According to the Proteomics Knowledge Base graph, UniProt entries will be obtained based on the HGNC concept items. This has three main consequences for the UniProt Resource:

- it must be loaded after the HGNC resource (higher `order` property)
- it must extend the HGNC resource (to use the loaded identifiers)
- it must use a template endpoint URI or query to use the HGNC identifiers (apply the keyword `#replace#`with the gene symbol)

3.2.3.2.1 Resource

- Add a new Resource to the UniProt Concept
  - `Order`: 2 *(higher than HGNC)*
  - `Extends`: Concept HGNC *(the dependency)*
  - `Method`: cache *(copy everything)*
  - `Publisher`: SQL
  - `Host`: localhost
  - `Port`: 3306
  - `Database`: hummer
  - `Login/Password`: tutorial / coeus
  - `Query`: SELECT uniprot FROM uniprot WHERE hgnc = '#replace#';

3.2.3.2.2Selectors

For UniProt data, we will extract the identifier.

- Id
  - `Query`: uniprot *(the SQL SELECT column name)*
  - `Property`: dc:identifier

COEUS doesn't just copy data into its knowledge base. You can configure a model to add properties to items that are already in the triplestore. To show this, we will import the UniProt items name. COEUS will use the dependency concept identifier to perform the query/endpoint composition.

3.2.3.2.3Resource

- Add a new Resource to complete the Uniprot Concept
  - `Order`: 3 *(higher than UniProt)*
  - `Extends`: Concept UniProt *(the dependency)*
  - `Method`: complete *(add statements)*
  - `Publisher`: SQL
  - `Host`: localhost
  - `Port`: 3306
  - `Database`: hummer
  - `Login/Password`: tutorial / coeus
  - `Query`: SELECT name FROM uniprot WHERE uniprot = '#replace#';

3.2.3.2.4Selectors

- Name
  - `Query`: name
  - `Property`: dc:title

3.2.3.3 InterPro

InterPro items are also discovered through UniProt. In this case, we will use UniProt entries' XML to extract InterPro identifiers.

3.2.3.3.1 Resource

- Add a new Resource to the InterPro Concept
  - `Order`: 3 *(higher than UniProt)*
  - `Extends`: Concept UniProt *(the dependency)*
  - `Method`: cache *(copy everything)*
  - `Publisher`: XML
  - `Endpoint`: http://uniprot.org/uniprot/#replace#.xml
  - `Query`: //entry

3.2.3.3.2 Selectors

For InterPro data, we will only extract the identifier.

- Id
  - `Query (XPath)`: //dbReference[@type='InterPro']/@id
  - `Property`: dc:identifier

3.2.3.4 OMIM

OMIM items are obtained from an external database mapping in HUMMER, based on HGNC gene symbols.

3.2.3.4.1 Resource

- Add a new Resource to the OMIM Concept
  - `Order`: 2 *(higher than HGNC)*
  - `Extends`: Concept HGNC *(the dependency)*
  - `Method`: cache *(copy everything)*
  - `Publisher`: SQL
  - `Host`: localhost
  - `Port`: 3306
  - `Database`: hummer
  - `Login/Password`: tutorial / coeus
  - `Query`: SELECT omim FROM omim WHERE hgnc = '#replace#';

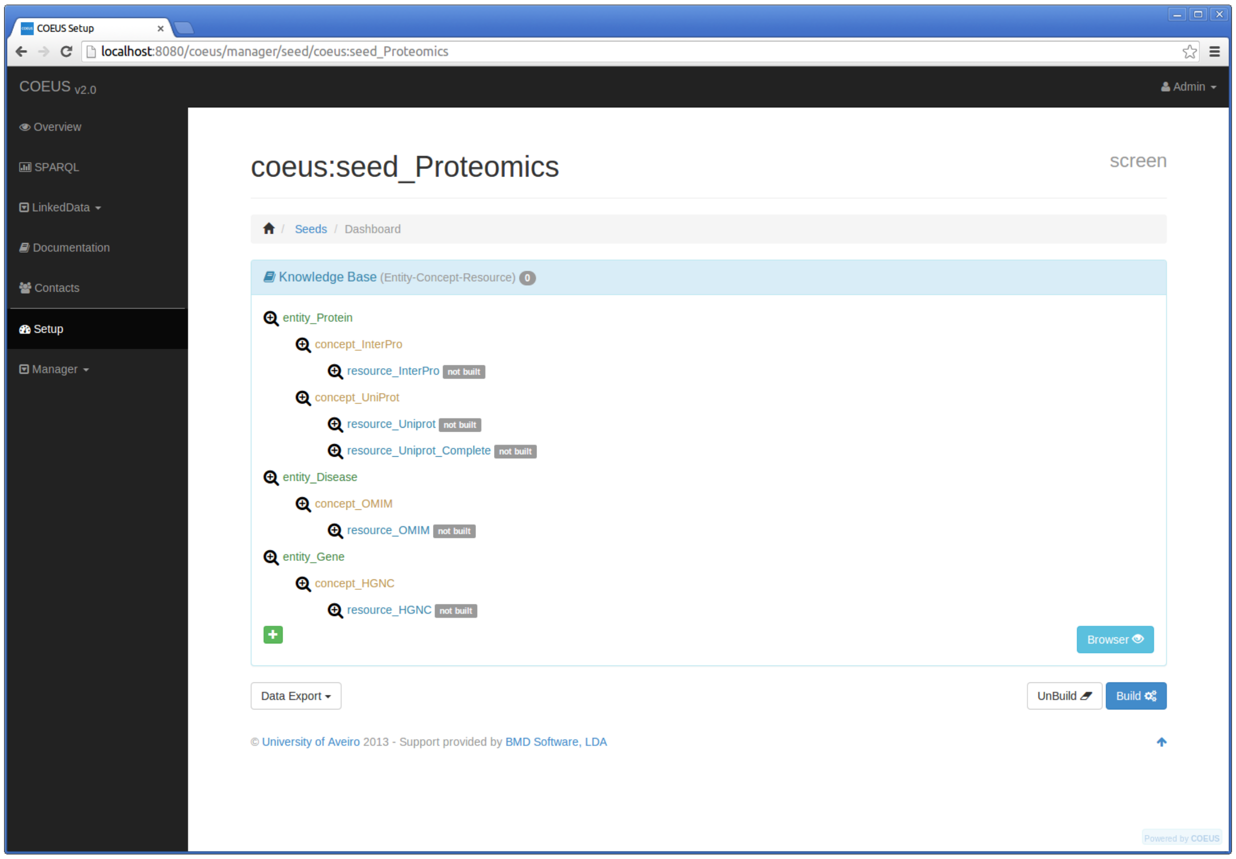
3.2.3.4.2 Selectors

For OMIM data, we will only extract the identifier.

- Id
  - `Query`: omim
  - `Property`: dc:identifier

3.2.4 Building the knowledge base

As previously, the final step is to integrate the data. Go to the seed dashboard and make sure the knowledge base structure matches what was obtained in the requirements analysis. To start the integration process you must click on *Build* button.



Testing

With the knowledge base built, COEUS provides multiple methods to access the aggregated dataset.

3.2.5 List all UniProt individuals

```
PREFIX coeus: <http://bioinformatics.ua.pt/coeus/resource/>
PREFIX dc: <http://purl.org/dc/elements/1.1/>

SELECT * {
    ?uniprot coeus:hasConcept coeus:concept_Uniprot .
    ?uniprot dc:identifier ?id
}
```

3.2.6 List protein info for BRCA2

```
PREFIX coeus: <http://bioinformatics.ua.pt/coeus/resource/>
PREFIX dc: <http://purl.org/dc/elements/1.1/>

SELECT ?name ?uniprot ?interpro {
        ?g dc:description ?name .
        ?g dc:identifier "BRCA2" .
        ?g coeus:isAssociatedTo ?up .
        ?up coeus:hasConcept coeus:concept_Uniprot .
        ?up dc:identifier ?uniprot .
        ?up coeus:isAssociatedTo ?ip .
        ?ip coeus:hasConcept coeus:concept_InterPro .
        ?ip dc:identifier ?interpro
        }
```

3.2.7 List protein info for all genes (where available)

```
PREFIX coeus: <http://bioinformatics.ua.pt/coeus/resource/>
PREFIX dc: <http://purl.org/dc/elements/1.1/>

SELECT ?id ?name ?uniprot ?interpro {
        ?g dc:description ?name .
        ?g dc:identifier ?id .
        ?g coeus:isAssociatedTo ?up .
        ?up coeus:hasConcept coeus:concept_Uniprot .
        ?up dc:identifier ?uniprot .
        ?up coeus:isAssociatedTo ?ip .
        ?ip coeus:hasConcept coeus:concept_InterPro .
        ?ip dc:identifier ?interpro
        }
```

3.3 LinkedData browsing

- Go to: http://localhost:8080/coeus/resource/seed_Proteomics

4 Overview

4.1 Model

- Seed – Entity – Concept – Item
    - Resource – Selector

Notes

- Internal structure
- Can accommodate multiple data models

4.2 Integration

- Multiple entry points (connectors)
    - CSV
    - XML
    - JSON (not covered)
    - SQL
    - SPARQL (not covered)
    - LinkedData (not covered)
    - RDF (not covered)
- Flexible
    - Map to any ontology
    - Create complex axioms

4.3 API

- Multiple access points
  - SPARQL
  - LinkedData
  - Java
  - Javascript
  - “REST”
  - Ruby gem (gem install coeus)
  - Python package (pip install coeus, by Luís Bastião)
- Flexible
  - “Anything” can be used for client-side development

4.4 Documentation

Full information for everything covered (and not covered) available online at http://bioinformatics.ua.pt/coeus/documentation/.

5 Feedback

Your feedback is highly appreciated; please submit your opinions on the form at http://goo.gl/gcphs3.