Setting up Neo4j/PostgreSQL Database

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1 Introduction

1.1 Neo4j

In progress.

1.2 PostgreSQL

In progress.

2 Prerequisites

2.1 Conda environment

- 1. Install Conda
- 2. Clone GitHub repository:

git clone https://github.com/BackofenLab/protein-graph-database.git
cd protein-graph-database/

3. Create a conda environment:

make **env**

4. Activate the conda environment:

conda activate pgdb

2.2 Install neo4j & apoc library

• Mac OS Installation:

brew install neo4j

- Install Apoc
- Move Apoc.jar into the neo4j plugins folder
- Add permissions to the neo4j.conf:

```
dbms.security.procedures.whitelist=apoc.export.*
apoc.import.file.use_neo4j_config=false
apoc.export.file.enabled=true
```

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2.3 Install postgreSQL

• Mac OS Installation:

```
brew install postgresql
```

• Start the postgresql database:

```
brew services start postgresql
```

• Create superuser postgres if not exists:

```
createuser postgres -s
```

3 Load STRING data onto PostgreSQL

- 1. First we need to download our STRING Database subsets:
 - STRING_Mouse.zip
 - STRING Human.zip
- 2. Creating an empty PostgreSQL database "string":

```
psql -U postgres -c "DROP_DATABASE_string;"
psql -U postgres -c "CREATE_DATABASE_string;"
```

3. Loading dump & schema(mouse) onto the "string" database:

```
psql -U postgres string < dump.schema.psql
psql -U postgres string < dump.mouse.psql
```

4 Build a Graph Database (PostegreSQL -> Neo4j)

To build now our database in neo4j we have to setup both databases

1. Starting the neo4j database:

```
neo4j start
```

2. Build the graph databse with build_graph_db.py:

```
python build_graph_db.py --credentials tests/credentials.test.yml
--species_name "mus_musculus"
--combined_score_threshold 750
```

Arguments for build_graph_db.py:

```
--credentials CREDENTIALS
                        Path to the credentials YAML file that will be used
                        (default: credentials.yml)
--species_name SPECIES_NAME
                        Species name (default: Homo sapiens)
--protein_list PROTEIN_LIST
                        Path to the file containing protein Ensembl IDs
                        (default: None)
--combined_score_threshold COMBINED_SCORE_THRESHOLD
                        Threshold above which the associations between
                        proteins will be considered (default: None)
--skip_actions SKIP_ACTIONS
                        Do not add protein – protein actions to the resulting
                        graph database (default: True)
--skip_drugs SKIP_DRUGS
                        Do not add drugs to the resulting graph database
                        (default: False)
--skip_compounds SKIP_COMPOUNDS
                        Do not add compounds to the resulting graph database
                        (default: False)
--skip_diseases SKIP_DISEASES
                        Do not add diseases to the resulting graph database
                        (default: False)
--keep_old_database KEEP_OLD_DATABASE
                        Do not overwrite the existing Neo4j graph database
                        (default: False)
```