
Bio2BEL ADEPTUS Documentation

Release 0.0.2-dev

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Aug 13, 2019

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Bio2BEL ADEPTUS.

Manager for Bio2BEL ADEPTUS.

class `bio2bel_adeptus.manager.Manager` (*args, **kwargs)

Disease-specific differential gene expression.

count_diseases ()

Count the number of diseases.

Return type `int`

count_relations ()

Count the number of disease-differential expressed gene relations.

Return type `int`

count_rnas ()

Count the number of RNAs.

Return type `int`

static is_populated ()

Check if the Bio2BEL ADEPTUS database is populated.

Return type `bool`

populate ()

Populate the Bio2BEL ADEPTUS database.

Return type `None`

summarize ()

Summarize the contents of the Bio2BEL ADEPTUS database.

Return type `Mapping[str, int]`

to_bel ()

Output ADEPTUS as a BEL graph.

Return type `BELGraph`

SQLAlchemy models for Bio2BEL ADEPTUS.

class `bio2bel_adeptus.models.Base` (**kwargs)

The most base type

BIO2BEL_ADEPTUS

Default connection at None

using Bio2BEL v0.2.1

```
bio2bel_adeptus [OPTIONS] COMMAND [ARGS]...
```

Options

-c, --connection <connection>
Defaults to None

1.1 bel

Manage BEL.

```
bio2bel_adeptus bel [OPTIONS] COMMAND [ARGS]...
```

1.1.1 upload

Upload BEL to network store.

```
bio2bel_adeptus bel upload [OPTIONS]
```

Options

-c, --connection <connection>

1.1.2 write

Write as BEL Script.

```
bio2bel_adeptus bel write [OPTIONS]
```

Options

-o, --output <output>

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