
Bio2BEL HSDN Documentation

Release 0.0.2-dev

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Converts the human symptoms-disease network produced by Zhou and Himmelstein to BEL.

Manager for Bio2BEL HSDN.

```
class bio2bel_hsdn.manager.Manager(*args, **kwargs)
```

Disease-symptom associations.

```
count_diseases()
```

Count the diseases in the database.

Return type `int`

```
count_relations()
```

Count the number of relations in the database.

Return type `int`

```
count_symptoms()
```

Count the symptoms in the database.

Return type `int`

```
static is_populated()
```

Check if the Bio2BEL HSDN database is populated.

Return type `bool`

```
populate()
```

Populate the Bio2BEL HSDN database.

Return type `None`

```
summarize()
```

Summarize the contents of the Bio2BEL HSDN database.

Return type `Mapping[str, int]`

```
to_bel()
```

Convert the HSDN to BEL.

Return type `BELGraph`

SQLAlchemy models for Bio2BEL HSDN.

```
class bio2bel_hsdn.models.Base(**kwargs)
```

The most base type

BIO2BEL_HSDN

Default connection at None

using Bio2BEL v0.2.1

```
bio2bel_hsdn [OPTIONS] COMMAND [ARGS]...
```

Options

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

1.1 bel

Manage BEL.

```
bio2bel_hsdn bel [OPTIONS] COMMAND [ARGS]...
```

1.1.1 upload

Upload BEL to network store.

```
bio2bel_hsdn bel upload [OPTIONS]
```

Options

-c, --connection <connection>

1.1.2 write

Write as BEL Script.

```
bio2bel_hsdn bel write [OPTIONS]
```

Options

-o, --output <output>

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