
```
class CanDI.candi.candi.Cancer (disease, subtype=None, gender=None, source=None,  
                                all_except=False)
```

```
Bases: CanDI.structures.entity.Entity
```

Collects all data from cell lines of a specific disease or subtype.

```
property get_name
```

```
mutation_matrix (subset=None)
```

Returns binary n by m dataframe with DepMap_IDs as rows and gene symbols as columns.

Note: If the nth row and mth column is equal to 0 the nth gene is not mutated in the mth cell line. If the nth row and mth column is equal to 1 the nth gene is mutated in the mth cell line.

Parameters **subset** – str or list, optional Specific gene or list of genes for which to generate a mutation matrix

Returns pandas.core.frame.DataFrame

```
class CanDI.candi.candi.CellLine (cellline)
```

```
Bases: CanDI.structures.entity.Entity
```

Contains methods for gather data for a specific cell line. Can be instantiated by DepMap_ID (preferred) or name (in all caps).

```
property get_name
```

```
class CanDI.candi.candi.CellLineCluster (lines, all_except=False)
```

```
Bases: CanDI.structures.entity.Entity
```

Functions the same as a *Cancer* object, but has predefined set of cell lines defined by user.

```
property get_name
```

```
mutation_matrix (subset=None)
```

Returns binary n by m dataframe with DepMap_IDs as rows and gene symbols as columns.

Note: If the nth row and mth column is equal to 0 the nth gene is not mutated in the mth cell line. If the nth row and mth column is equal to 1 the nth gene is mutated in the mth cell line.

Parameters **subset** – str or list, optional Specific gene or list of genes for which to generate a mutation matrix

Returns pandas.core.frame.DataFrame

```
class CanDI.candi.candi.Gene (name, by='symbol')
```

```
Bases: CanDI.structures.entity.Entity
```

Class used for gathering information on a single gene. Instantiated by gene name (preferred) or ENTREZ ID. Note: Not all genes have been assigned entrez ids and gene names are inconsistent across sources. If something doesn't show up, try alternate names.

```
property get_name
```

```
class CanDI.candi.candi.GeneCluster (genes, name=None)
```

```
Bases: CanDI.structures.entity.Entity
```

Functions the same as Organelle, except the genes are predetermined by the user.

```
class CanDI.candi.candi.Organelle (organelle, min_conf=3)
```

```
    Bases: CanDI.structures.entity.Entity
```

Organelle class is a group of genes defined by their subcellular location. It is instantiated by providing a specific organelle. During instantiation candi will subset the locations dataset by the user provided organelle.

```
    property get_name
```

```
class CanDI.candi.candi.SubsetHandler
```

```
    Bases: object
```

SubsetHandler gets subsets from various datasets. It provides the logic for determining how to query various datasets. Automates finding what type of argument the user provided.

```
    static get_cancer_ids (cancer, subtype=None)
```

```
    static get_many (arg, dat)
```

```
    static get_one (arg, df)
```

```
    static get_organelle_genes (organelle, conf=6)
```

```
    handle_string (arg, dat)
```

```
    handle_tuple (arg, dat)
```