
pyFishManager Documentation

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pyFishManager is a simple Python based fish stock manager useful for managing fish stocks in biological laboratories. It consists of two main classes, namely

- `database`,
- `line`.

The `line` class contains information about a certain line in your fish facility, the `database` module provides a data structure for handling `line` classes. Moreover, it has the following features

- Easy-to-use minimal GUI based on PyQT4
- Input of previously existing stock-lists from CSV files
- CSV I/O
- Pickle I/O
- Warning systems about critical lines

I have tried to keep the documentation short but clear. If it unclear, don't hesitate to mail.

1.1 pyfishmanager.database module

class `pyfishmanager.database.database` (*name*)

Bases: `object`

Main database class. Basically stores a list of lines objects and provides methods for printout/filtering and manipulating line objects

checkNumberOfLineEntries ()

defaultDict ()

Creates default dictionary for stock list I/O.

Returns Dictionary translating from stocklist to database.

Return type dict

extractLineProperty (*r*, *prop*)

Extracts a single property from list of lines.

Parameters

- **r** (*list*) – List of lines.
- **prop** (*int*) – property to be extracted.

Returns List of values of property of all lines.

Return type list

filterDead (*r*)

Filters out dead lines.

Parameters **r** (*list*) – List of lines.

Returns Filtered list.

Return type list

filterNotGenotyped (*r*)

Filters out non-genotyped lines.

Parameters **r** (*list*) – List of lines.

Returns Filtered list.

Return type list

getAllContainGenotype (*genotype*)

Returns all lines that contains given genotype.

Parameters **genotype** (*str*) – Genotype that is looked for.

Returns List of lines containing genotype.

Return type list

getAllGenotypes ()

Returns all different genotypes in the database.

Returns List of genotypes.

Return type list

getAllOfGenotype (*genotype*)

Returns all lines that have exactly given genotype.

Parameters **genotype** (*str*) – Genotype that is looked for.

Returns List of lines having genotype.

Return type list

getDatabaseStats (*onlyGenotyped=True*)

Computes statistics of database.

Keyword Arguments **onlyGenotyped** (*bool*) – Only check genotyped lines.

Returns statistics per line.

Return type dict

getNumberOfFishesOfGenotype (*genotype, onlyGenotyped=True*)

Returns number of fishes of given genotype.

Parameters **genotype** (*str*) – Genotype of fish line

Keyword Arguments **onlyGenotyped** (*bool*) – Only check genotyped lines.

Returns Number of fish.

Return type int

getNumberOfLineEntries (*line*)

makeCSVHeader ()

Checks line object properties of first line and uses them to build a header.

Returns Header

Return type list

printCriticalLines (*onlyGenotyped=True, nCrit=60*)

Prints all critical fish lines as table.

Keyword Arguments

- **onlyGenotyped** (*bool*) – Only check genotyped lines.
- **nCrit** (*int*) – Number of fish that is considered to be critical.

printDatabase ()

Prints out complete database in tabular form.

printDatabaseStats (*onlyGenotyped=True*)

Prints statistics of database as table.

Keyword Arguments `onlyGenotyped` (*bool*) – Only check genotyped lines.

readStockList (*fn*)

Reads in stock list from csv file

Parameters `fn` (*str*) – Filename of stock list.

Returns List of lines in stock list.

Return type list

readStockListHeader (*fn, irow=0, delimiter=';', quotechar='|'*)

Reads in header of stock list.

Parameters `fn` (*str*) – Filename of stock list.

Keyword Arguments

- `irow` (*int*) – Row of header
- `delimiter` (*str*) – Delimiter that is used in csv sheet.
- `quotechar` (*str*) – Quotechar that is used in csv sheet.

Returns Header.

Return type list

saveToCSV (*fn=None, delimiter=', '*)

Saves database to csv file.

Keyword Arguments

- `fn` (*str*) – filename
- `delimiter` (*str*) – Delimiter used in csv file

Returns True if success, False else

Return type bool

saveToPickle (*fn=None*)

Saves database to pickle file.

Keyword Arguments `fn` (*str*) – filename

Returns True

Return type bool

updateAllLineAttr (*attr, prop, lines=None*)

Updates attribute in list of lines. If lines is not given, will set attribute for all lines.

Parameters

- `attr` (*str*) – Attribute to be set
- `prop` (*any*) – Value to be set

Keyword Arguments `lines` (*list*) – List of lines.

Returns List of updates lines.

Return type list

writeLinesToCSV (*csvFile*)

Write all lines to csv file.

Parameters `csvFile` (*file*) – csv file object

Returns the csv file object

Return type file

1.2 pyfishmanager.line module

class `pyfishmanager.line.line` (*Id, genotype=None, mutation=None, chromosome=None, dateOfBirth=None, fatherId=None, motherId=None, fatherGenotype=None, motherGenotype=None, nFish=None, nMales=None, nFemales=None, nTanks=None, tankType=None, genotypedComment=None, comments=None*)

Bases: object

adjustDataTypes ()

adjustDateOfBirth (*sep='/', mode='dmy'*)

assignInt (*n*)

assignListDataType (*l, sep=',', dtype=<type 'int'>*)

getDay (*d, mode*)

getMonth (*d, mode*)

getYear (*d, mode*)

hasGenotype (*genotype*)

isDead ()

isDoubleMutant ()

isGenotyped ()

isSingleMutant ()

isWildType ()

printLine ()

readFromArray (*arr, header, dic, silent=True*)

Reads in array and assigns value using header that is then translated by dict.

Parameters

- **arr** (*list*) – Array from reading stock list.
- **header** (*list*) – header of stock list.
- **dic** (*dict*) – Dictionary of stock list.

Keyword Arguments **silent** (*bool*) – Show warning messages?

renameGenotype (*oldGenotype, newGenotype*)

1.3 pyfishmanager.manager module

`pyfishmanager.manager.main` ()

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