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# **platelib Documentation**

***Release 0.1.4-alpha***

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## INTRODUCTION

### 1.1 Summary

platelib is an attempt to make common tasks when working with kinetic platereader, especially amyloid aggregation, data easy and compatible with Python.

### 1.2 Disclaimer

The state of this repository is one of very early development, the code is not elegant, there most likely are bugs so **Use with caution!**

### 1.3 Read the docs

A brief overview is given below, for more detailed information see the docs directory and subfolders, or even better have a look at the source :)



## INSTALLATION

### 2.1 Prerequisites

- `python`
- `pip`
- `git` (optional)

### 2.2 Download

Either download the [source distribution](#) directly or use:

```
git https://github.com/edager/platelib
```

### 2.3 Install

Go to directory where the platelib source file is (`platelib/dist/` if `git` was used) and run the following in the terminal:

```
pip install platelib-X.X.tar.gz
```

Where `X.X` should be replaced by the version that was downloaded.

### 2.4 Upgrade

Go to directory where the platelib source file is (`platelib/dist/` if `git` was used) and run the following in the terminal:

```
pip install --upgrade platelib-X.X.tar.gz
```

Where `X.X` should be replaced by the version that was downloaded.

### 2.5 Uninstall

Simply go to the terminal and run:

```
pip uninstall platelib
```



## SUPPORT

- **For questions related to usage:**
  - [Stack Overflow](#) using the tags `python` and `matplotlib`
- **For questions related to bugs or enhancements:**
  - [GitHub](#) using the issue system



## 4.1 Reading in data

The main functionality of `platelib` is the `read_plate` function that allows for reading in platereader data from kinetic experiments into a common framework namely into the `Plate_data` class.

If an equal number of replicates per sample were prepared this can be specified (default is 3):

```
p = read_plate('path/to/file', replicates=5)
```

It can be specified which direction the replicates were loaded onto the plate where 'hori' (horizontal) means towards increasing numbers and 'vert' is towards increasing letters (default is 'hori'):

```
p = read_plate('path/to/file', rep_direction='vert')
```

**NOTE that the replicates have to be next to each other!**

Alternatively it can be specified which wells contains replicates:

```
p = read_plate('path/to/file', named_samples=[['B03', 'D07'], ['B02', 'E06', 'G12']])
```

Data from Tecan platereaders can be read in as (default is 'bmg'):

```
p = read_plate('path/to/file', platereader='tecan')
```

**NOTE that this functionality has not been fully tested yet!**

As well as from BMG platereaders either where the data has prior been transposed `True` such that well data are in column format or in row format `False` (default is `True`):

```
p = read_plate('path/to/file', transposed=False)
```

Note that it's automatically detected if several measurements (*e.g.*) were made per time-point (see [Accessing data](#))

The time unit can also be specified which as either 'seconds', 'minutes', 'hours', or 'days' will carry along into indexes if exported and to unit of x-axis if plotted (default is 'hours'):

```
p = read_plate('path/to/file', time_unit='days')
```

## 4.2 Accessing data

The `Plate_data` class allows for different ways of accessing the data

Through index:

```
p[1]
```

Through index slice:

```
p[:3]
```

Through well name:

```
p['B02']
```

Through list of well names:

```
p[['B02', 'C03', 'D04']]
```

Retrieved as a pandas.DataFrame with wellnames as column names and time points as index:

```
df = Plate_data.to_a_dataframe()
```

Or as a (C)omma (S)eperated (V)aribles file with the first line being (time unit + ) well names and the first column are the time points:

```
Plate_data.to_a_csv('path/to/file.csv')
```

## 4.3 Plotting data

The data is plotted according to replicates, and subtitles can be added (default is *None*):

```
p.plot(titles=['condition 1', 'conditions 2'])
```

It can be specified whether all plots should have its own y-axis, whether all plots should have the same (default is *True*):

```
p.plot(sharey='False')
```

If several measurements were made per time-point it can be specified whether all measurements should be plotted or not (default is *True*):

```
p.plot(plot_multi='False')
```

## 5.1 platelib package

### 5.1.1 Submodules

#### 5.1.2 platelib.fitfun module

```
platelib.fitfun.exp_rise(t, a, b, k)
platelib.fitfun.fit_fun(func, df, bounds=([0, 0, 0, 0], [1, 50, 10, 65]))
class platelib.fitfun.fit_plate(data, replicates=3, rep_direction='hori', multi_chrom=1)
    Bases: platelib.plateread.Plate_data
platelib.fitfun.gauss(x, amp, cen, sigma)
    basic gaussian
platelib.fitfun.gauss_dataset(params, i, x)
    calc gaussian from params for data set i using simple, hardwired naming convention
platelib.fitfun.linear(t, a, b)
platelib.fitfun.objective(params, x, data)
    calculate total residual for fits to several data sets held in a 2-D array, and modeled by Gaussian functions
platelib.fitfun.quadratic(t, a, b, c)
platelib.fitfun.sigmoid(x, y0, L, k, x_half)
platelib.fitfun.sigmoidal_auto(t, a, b, k)
```

#### 5.1.3 platelib.plateread module

```
class platelib.plateread.Plate_data(data, replicates=3, rep_direction='hori',
                                     multi_chrom=1)
    Class for containing data from a platereader assay.
```

##### Parameters

- **data** – A pandas DataFrame with time points as index and wells as columns
- **replicates** – Positive integer of replicates, assuming equal number of replicates of all samples

```
plot(titles=None, sharey=True, plot_multi=True)
    Plots the number the number of sample i.e. replicates/wells in the data set.
```

### Parameters

- **titles** – List-like object of subtitles
- **sharey** – Boolean, default is True, where all y-axis limits will be identical. If False y-axis limits per plot are given by matplotlib defaults.
- **plot\_multi** – Boolean, default is False, is several different measurements are present, only plot the first one. If False plots all of the values.

**to\_a\_csv** (*path, one\_per\_multi\_c=False*)

Returns the data as a pandas dataframe with times as indexes

### Parameters

- **path** – String of path to store output
- **one\_per\_multi\_c** – Boolean, if ‘True’ one measurement per dataframe will be exported otherwise all will be exported in one file.

**to\_a\_dataframe** (*one\_per\_multi\_c=False*)

Returns the data as a list of pandas dataframe(s) with times as indexes

**Parameters one\_per\_multi\_c** – Boolean, if ‘True’ one measurement per dataframe will be exported otherwise all will be exported in one dataframe.

`platelib.plateread.read_plate` (*filename, replicates=3, rep\_direction='hori', time\_unit='hours', named\_samples=[], platereader='bmg', transposed=True*)

Reads in data from a CSV file from a BMG or Tecan platereader and returns a platedata object.

### Parameters

- **filename** – Path to filename as a string
- **replicates** – The number of replicates per sample, expects a positive integer.
- **rep\_direction** – The directions replicates is in. Only ‘hori’ and ‘vert’ are accepted directions, ‘hori’ if replicates are going from left to right ‘vert’ from replicates going from top to bottom.
- **time\_unit** – The time unit one would like to have, accepted values are: ‘seconds’, ‘minutes’, ‘hours’, ‘days’
- **platereader** – The plate reader used to collect the data. Only ‘bmg’ and ‘tecan’ are accepted platereaders
- **transposed** – Whether the wells are in column (True) or row format (False).

`platelib.plateread.read_tecan` (*filename*)

Reads in untransposed data from a tecan platereader and returns a pandas DataFrame object.

**Parameters filename** – Path to filename as a string

`platelib.plateread.read_transposed_bmg` (*filename*)

Reads in transposed data from a BMG platereader and returns a pandas DataFrame object.

**Parameters filename** – Path to filename as a string

`platelib.plateread.read_untransposed_bmg` (*filename*)

Reads in untransposed data from a BMG platereader and returns a pandas DataFrame object.

**Parameters filename** – Path to filename as a string

`platelib.plateread.search_start` (*filename*)

Find start of data region and returns the line number by finding the line that starts with “Well”.

**Parameters filename** – Path to filename as a string

`platelib.plateread.vert_order(cols, reps)`

Helper function to reorder data if vertical replicates were made.

#### Parameters

- **cols** – List-like object of columns names (wells) all assumed to have the form ‘A12’.
- **reps** – List of positive integer number of replicates.

### 5.1.4 Module contents





## CONTRIBUTE

Contributions are more than welcome, please raise an issue on the [github](#) page highlighting the bug/extension/compatibilities before doing a pull request.

### 6.1 More tools

Apart from the tools listed in [Installation](#) the following is needed:

- Unix-like system
- [git](#)
- [pandoc](#)

### 6.2 Building

You have made some wicked cool changes to the source code or the documentation that you want to share with the world, awesome!

Now there's just a few steps before they can be incorporated into the platelib master branch

#### 6.2.1 Changing the version number

The versioning scheme of platelib should be done in reasonable accordance with the so called [Semantic versioning](#) where X.Y.Z should be read as MAJOR.MINOR.PATCH.

The version number has to be changed in the two files `setup.py` and `docs/source/conf.py`

#### 6.2.2 Create new source distribution

Go to the docs folder and run:

```
./full_make.sh
```

If no errors occurred it can be uploaded to your local branch and a pull request can be made.

## 6.3 Planned improvements

This is as much a wish-list as literally planned improvements:

- Plotting
  - Plotting of data from several plates in some sensible way.
- Fitting
  - Local fitting of traces in plate
  - Global fitting of traces in plate
- Statistical analysis
  - Goodness-of-fit
  - Variance along traces, among replicates, and between conditions
- Python 3.X compatibility
- PyPI availability

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