dclab Documentation

Release 0.14.0

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Contents:

Dclab is a Python library for the post-measurement analysis of real-time deformability cytometry (RT-DC) datasets. This is the documentation of dclab version 0.14.0.

CHAPTER 1

Getting started

1.1 Installation

To install dclab, use one of the following methods:

- **from PyPI:** `pip install dclab[all]`
- **from sources:** `pip install .[all]`

The extra key `[all]` can be omitted if you are not working with the tdms file format or have no need to export to .avi or .fcs files. Then, the basic installation of dclab depends on the Python packages h5py, numpy, and scipy. In addition, dclab contains code from OpenCV (computation of moments) and scikit-image (computation of contours) to reduce the list of dependencies (these libraries are not required by dclab).

If you are working with the outdated tdms file format, you have to specify the extra key `[tdms]`, i.e. `pip install dclab[tdms]` or `pip install .[tdms]`. This will install the additional libraries nptdms and imageio. You may also specify the extra key `[export]`, which will install imageio and fcswrite for .avi and .fcs export. As mentioned above, using `[all]` will install the dependencies for both.

Note that if you are installing from source or if no binary wheel is available for your platform and Python version, Cython will be installed to build the required dclab extensions. If this process fails, please request a binary wheel for your platform (e.g. Windows 64bit) and Python version (e.g. 3.6) by creating a new issue.

1.2 Use cases

If you are a frequent user of RT-DC, you might run into problems that cannot (yet) be addressed with the graphical user interface Shape-Out. Here is a list of use cases that would motivate an installation of dclab.

- You would like to convert old .tdms-based datasets to the new .rtdc file format, because of enhanced speed in Shape-Out and reduced disk usage. What you are looking for is the command line program *dclab-tdms2rtdc* that comes with dclab. It allows to batch-convert multiple measurements at a time. Note that you should keep the original .tdms files backed-up somewhere, because there might be future improvements or bug fixes from which you would like to benefit.

- You would like to apply a simple set of filters (e.g. polygon filters that you exported from within Shape-Out) to every new measurement you take and apply a custom data analysis pipeline to the filtered data. This is a straight-forward Python coding problem with dclab. After reading the basic usage section below, please have a look at the *polygon filter reference*.
- You would like to do advanced statistics or combine your RT-DC analysis with other fancy approaches such as machine-learning. It would be too laborious to do the analysis in Shape-Out, export the data as text files, and then open them in your custom Python script. If your initial analysis step with Shape-Out only involves tasks that can be automated, why not use dclab from the beginning?
- You simulated RT-DC data and plan to import them in Shape-Out for testing. Once you have loaded your data as a numpy array, you can instantiate an `RTDC_Dict` class and then use the `Export` class to create an .rtdc data file.

If you are still unsure about whether to use dclab or not, you might want to look at the *example section*. If you need advice, do not hesitate to create an issue.

1.3 Basic usage

Experimental RT-DC datasets are always loaded with the `new_dataset` method:

```
import numpy as np
import dclab

# .tdms file format
ds = dclab.new_dataset("/path/to/measurement/Online/M1.tdms")
# .rtdc file format
ds = dclab.new_dataset("/path/to/measurement/M2.rtdc")
```

The object returned by *new_dataset* is always an instance of `RTDCBase`. To show all available features, use:

```
print(ds.features)
```

This will list all scalar features (e.g. "area_um" and "deform") and all non-scalar features (e.g. "contour" and "image"). Scalar features can be filtered by editing the configuration of `ds` and calling `ds.apply_filter()`:

```
# register filtering operations
amin, amax = ds["area_um"].min(), ds["area_um"].max()
ds.config["filtering"]["area_um min"] = (amax + amin) / 2
ds.config["filtering"]["area_um max"] = amax
ds.apply_filter()  # this step is important!
```

This will update the binary array `ds.filter.all` which can be used to extract the filtered data:

```
area_um_filtered = ds["area_um"][ds.filter.all]
```

It is also possible to create a hierarchy child of this dataset that only contains the filtered data.

```
ds_child = dclab.new_dataset(ds)
```

The hierarchy child `ds_child` is dynamic, i.e. when the filters in `ds` change, then `ds_child` also changes after calling `ds_child.apply_filter()`.

Non-scalar features do not support fancy indexing (i.e. `ds["image"][ds.filter.all]` will not work. Use a for-loop to extract them.

```
for ii in range(len(ds)):
    image = ds["image"][ii]
    mask = ds["mask"][ii]
    # this is equivalent to ds["bright_avg"][ii]
    bright_avg = np.mean(image[mask])
    print("average brightness of event {}: {:.1f}".format(ii, bright_avg))
```

If you need more information to get started on your particular problem, you might want to check out the *examples section* and the *advanced scripting section*.

CHAPTER 2

Command-line interface

2.1 dclab-condense

Reduce an RT-DC measurement to its scalar-only features. All available ancillary features are computed.

```
usage: dclab-condense [-h] INPUT OUTPUT
```

positional arguments:

- `INPUT` Input path (.tdms or .rtdc file)
- `OUTPUT` Output path (.rtdc file)

2.2 dclab-join

Join two or more RT-DC measurements. This will produce one larger .rtdc file. The meta data of the dataset that was recorded earliest will be used in the output file. Please only join datasets that were recorded in the same measurement run.

```
usage: dclab-join [-h] [-o OUTPUT] [INPUT [INPUT ...]]
```

positional arguments:

- `INPUT` Input paths (.tdms or .rtdc files)

optional arguments:

- `-o, --output` Output path (.rtdc file)

2.3 dclab-tdms2rtdc

Convert RT-DC .tdms files to the hdf5-based .rtdc file format. Note: Do not delete original .tdms files after conversion. The conversion might be incomplete.

```
usage: dclab-tdms2rtdc [-h] [--compute-ancillary-features]
                       [--include-initial-empty-image]
                       TDMS_PATH RTDC_PATH
```

positional arguments:

- `TDMS_PATH` Input path (tdms file or folder containing tdms files)
- `RTDC_PATH` Output path (file or folder), existing data will be overridden

optional arguments:

- `--compute-ancillary-features` *(disabled by default)* Compute features, such as volume or emodulus, that are otherwise computed on-the-fly. Use this if you want to minimize analysis time in e.g. Shape-Out. CAUTION: ancillary feature recipes might be subject to change (e.g. if an error is found in the recipe). Disabling this option maximizes compatibility with future versions and allows to isolate the original data.
- `--include-initial-empty-image` *(disabled by default)* In old versions of Shape-In, the first image was sometimes not stored in the resulting .avi file. In dclab, such images are represented as zero-valued images. Set this option, if you wish to include the first event with empty image data.

2.4 dclab-verify-dataset

Check experimental datasets for completeness. Note that old measurements will most likely fail this verification step. This program is used to enforce data integrity with future implementations of RT-DC recording software (e.g. Shape-In).

```
usage: dclab-verify-dataset [-h] PATH
```

positional arguments:

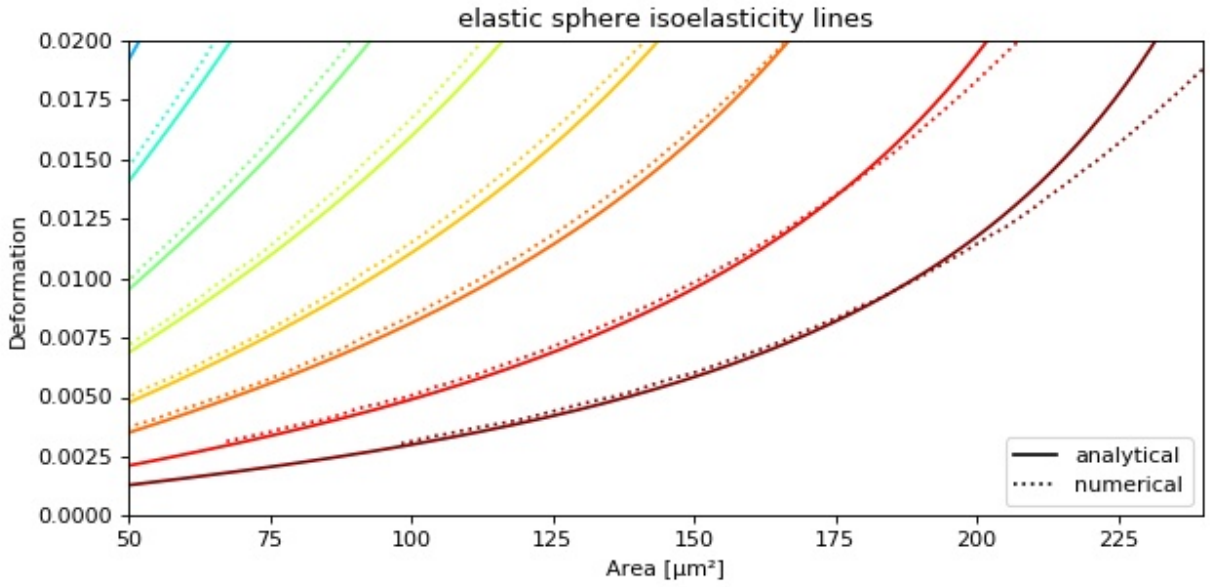
- `PATH` Path to experimental dataset

CHAPTER 3

Examples

3.1 Plotting isoelastics

This example illustrates how to plot dclab isoelastics by reproducing figure 3 (lower left) of [MMM+17].



isoelastics.py

```
import matplotlib.pylab as plt
import matplotlib.lines as mlines
from matplotlib import cm
import numpy as np

```

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```
import dclab

# parameters for isoelastics
kwargs = {"col1": "area_um",  # x-axis
          "col2": "deform",  # y-axis
          "channel_width": 20,  # [um]
          "flow_rate": 0.04,  # [ul/s]
          "viscosity": 15,  # [Pa s]
          "add_px_err": False  # no pixelation error
          }

isos = dclab.isoelastics.get_default()
analy = isos.get(method="analytical", **kwargs)
numer = isos.get(method="numerical", **kwargs)

plt.figure(figsize=(8, 4))
ax = plt.subplot(111, title="elastic sphere isoelasticity lines")
colors = [cm.get_cmap("jet")(x) for x in np.linspace(0, 1, len(analy))]
for aa, nn, cc in zip(analy, numer, colors):
    ax.plot(aa[:, 0], aa[:, 1], color=cc)
    ax.plot(nn[:, 0], nn[:, 1], color=cc, ls=":")

line = mlines.Line2D([], [], color='k', label='analytical')
dotted = mlines.Line2D([], [], color='k', ls=":", label='numerical')
ax.legend(handles=[line, dotted])

ax.set_xlim(50, 240)
ax.set_ylim(0, 0.02)
ax.set_xlabel(dclab.dfn.feature_name2label["area_um"])
ax.set_ylabel(dclab.dfn.feature_name2label["deform"])

plt.tight_layout()
plt.show()
```

CHAPTER 4

Advanced Usage

This section motivates the design of dclab and highlights useful built-in functionalities.

4.1 Notation

When coding with dclab, you should be aware of the following definitions and design principles.

4.1.1 Events

An event comprises all data recorded for the detection of one object (e.g. cell or bead) in an RT-DC measurement.

4.1.2 Features

A feature is a measurement parameter of an RT-DC measurement. For instance, the feature "index" enumerates all recorded events, the feature "deform" contains the deformation values of all events. There are scalar features, i.e. features that assign a single number to an event, and non-scalar features, such as "image" and "contour". The following features are supported by dclab:

scalar features	description [units]
area_cvx	Convex area [px]
area_msd	Measured area [px]
area_ratio	Porosity (convex to measured area ratio)
area_um	Area [µm^2]
aspect	Aspect ratio of bounding box
bright_avg	Brightness average within contour [a.u.]
bright_sd	Brightness SD within contour [a.u.]
circ	Circularity
deform	Deformation

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scalar features	description [units]
emodulus	Young's Modulus [kPa]
fl1_area	FL-1 area of peak [a.u.]
fl1_dist	FL-1 distance between two first peaks [µs]
fl1_max	FL-1 maximum [a.u.]
fl1_max_ctc	FL-1 maximum, crosstalk-corrected [a.u.]
fl1_npeaks	FL-1 number of peaks
fl1_pos	FL-1 position of peak [µs]
fl1_width	FL-1 width [µs]
fl2_area	FL-2 area of peak [a.u.]
fl2_dist	FL-2 distance between two first peaks [µs]
fl2_max	FL-2 maximum [a.u.]
fl2_max_ctc	FL-2 maximum, crosstalk-corrected [a.u.]
fl2_npeaks	FL-2 number of peaks
fl2_pos	FL-2 position of peak [µs]
fl2_width	FL-2 width [µs]
fl3_area	FL-3 area of peak [a.u.]
fl3_dist	FL-3 distance between two first peaks [µs]
fl3_max	FL-3 maximum [a.u.]
fl3_max_ctc	FL-3 maximum, crosstalk-corrected [a.u.]
fl3_npeaks	FL-3 number of peaks
fl3_pos	FL-3 position of peak [µs]
fl3_width	FL-3 width [µs]
frame	Video frame number
g_force	Gravitational force in multiples of g
index	Event index
inert_ratio_cvx	Inertia ratio of convex contour
inert_ratio_prnc	Principal inertia ratio of raw contour
inert_ratio_raw	Inertia ratio of raw contour
nevents	Total number of events in the same image
pc1	Principal component 1
pc2	Principal component 2
pos_x	Position along channel axis [µm]
pos_y	Position lateral in channel [µm]
size_x	Bounding box size x [µm]
size_y	Bounding box size y [µm]
temp	Sample Temperature [°C]
temp_amb	Ambient Temperature [°C]
tilt	Absolute tilt of raw contour
time	Event time [s]
userdef0	User defined 0
userdef1	User defined 1
userdef2	User defined 2
userdef3	User defined 3
userdef4	User defined 4
userdef5	User defined 5
userdef6	User defined 6
userdef7	User defined 7
userdef8	User defined 8
userdef9	User defined 9

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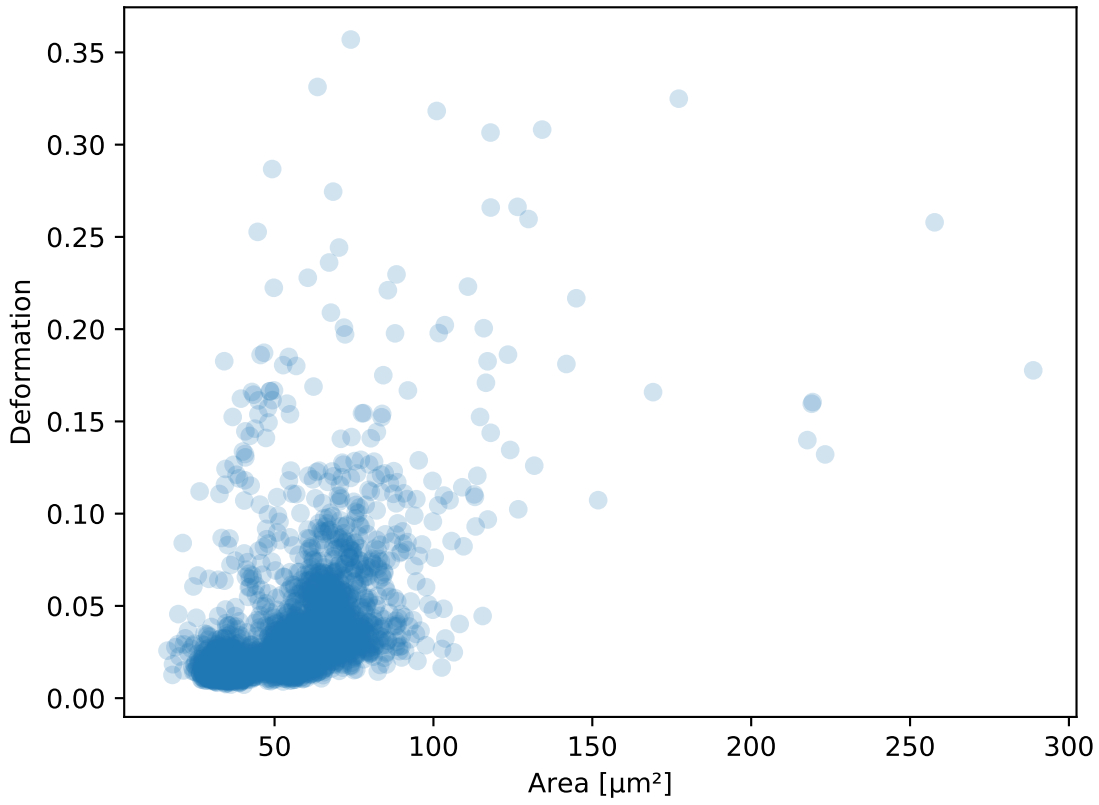
scalar features	description [units]
volume	Volume [µm^3]

non-scalar features	description [units]
contour	Binary event contour image
image	Gray scale event image
mask	Binary region labeling the event in the image
trace	Dictionary of fluorescence traces

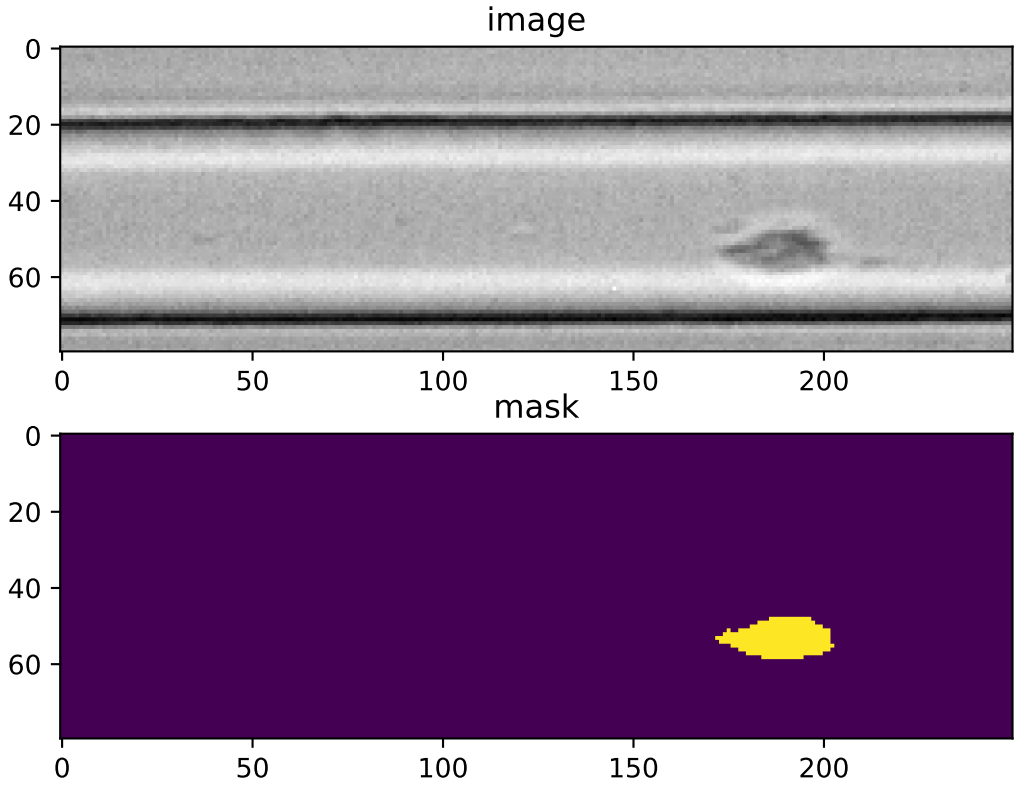
Example: deformation vs. area plot

```
import matplotlib.pylab as plt
import dclab
ds = dclab.new_dataset("data/example.rtdc")
ax = plt.subplot(111)
ax.plot(ds["area_um"], ds["deform"], "o", alpha=.2)
ax.set_xlabel(dclab.dfn.feature_name2label["area_um"])
ax.set_ylabel(dclab.dfn.feature_name2label["deform"])
plt.show()
```



Example: event image plot

```
import matplotlib.pylab as plt
import dclab
ds = dclab.new_dataset("data/example_video.rtdc")
ax1 = plt.subplot(211, title="image")
ax2 = plt.subplot(212, title="mask")
ax1.imshow(ds["image"][6], cmap="gray")
ax2.imshow(ds["mask"][6])
```



4.1.3 Ancillary features

Not all features available in dclab are recorded online during the acquisition of the experimental dataset. Some of the features are computed offline by dclab, such as “volume” or “emodulus”. These ancillary features are computed on-the-fly and are made available seamlessly through the same interface.

4.1.4 Filters

A filter can be used to gate events using features. There are min/max filters and 2D *polygon filters*. The following table defines the main filtering parameters:

filtering	parsed	description [units]
enable filters	*fbool*	Enable filtering
hierarchy parent	str	Hierarchy parent of the dataset
limit events	*fint*	Upper limit for number of filtered events
polygon filters	*fintlist*	Polygon filter indices
remove invalid events	*fbool*	Remove events with inf/nan values

Min/max filters are also defined in the *filters* section:

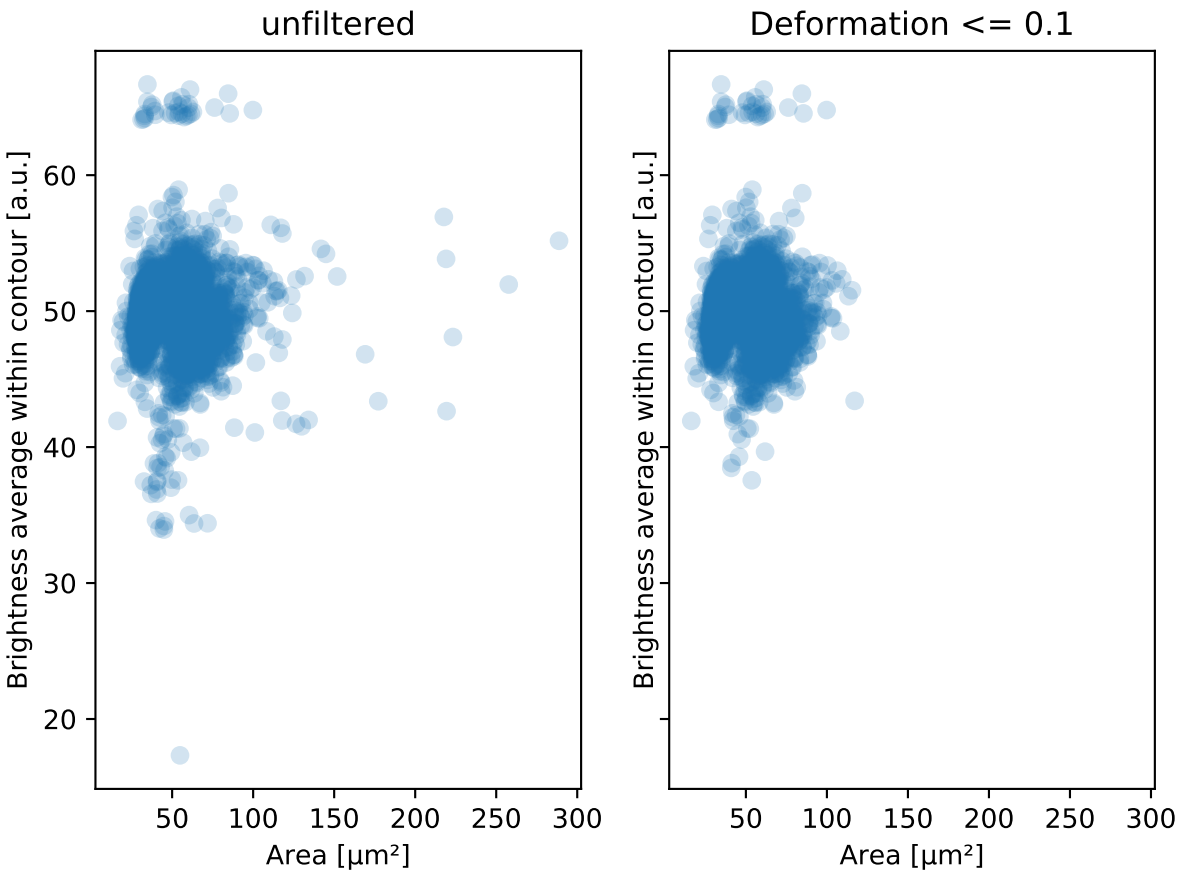
filtering	explanation
area_um min	Exclude events with area [µm^2] below this value
area_um max	Exclude events with area [µm^2] above this value
aspect max	Exclude events with an aspect ratio above this value
...	...

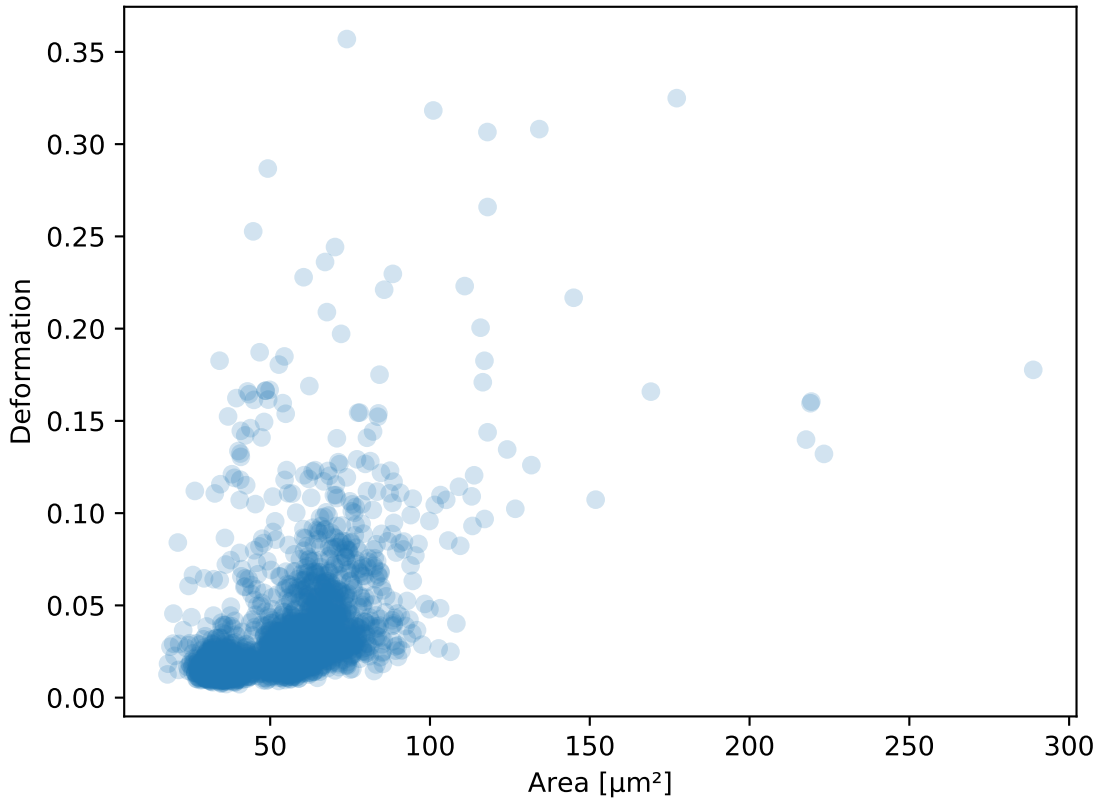
Example: excluding events with large deformation

```
import matplotlib.pylab as plt
import dclab
ds = dclab.new_dataset("data/example.rtdc")

ds.config["filtering"]["deform max"] = .1
ds.apply_filter()
dif = ds.filter.all

f, axes = plt.subplots(1, 2, sharex=True, sharey=True)
axes[0].plot(ds["area_um"], ds["bright_avg"], "o", alpha=.2)
axes[0].set_title("unfiltered")
axes[1].plot(ds["area_um"][dif], ds["bright_avg"][dif], "o", alpha=.2)
axes[1].set_title("Deformation <= 0.1")

for ax in axes:
    ax.set_xlabel(dclab.dfn.feature_name2label["area_um"])
    ax.set_ylabel(dclab.dfn.feature_name2label["bright_avg"])

plt.tight_layout()
plt.show()
```

Example: excluding random events This is useful if you need to have a (sub-)dataset of a specified size. The down-sampling is reproducible (the same points are excluded).

```
import matplotlib.pylab as plt
import dclab
ds = dclab.new_dataset("data/example.rtdc")
ds.config["filtering"]["limit events"] = 4000
ds.apply_filter()
fid = ds.filter.all

ax = plt.subplot(111)
ax.plot(ds["area_um"][fid], ds["deform"][fid], "o", alpha=.2)
ax.set_xlabel(dclab.dfn.feature_name2label["area_um"])
ax.set_ylabel(dclab.dfn.feature_name2label["deform"])
plt.show()
```


unfiltered
Deformation <= 0.1
Brightness average within contour [a.u.]
Area [µm²]
20
30
40
50
60
50
100
150
200
250
300


0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
Deformation
50
100
150
200
250
300
Area [µm²]

4.1.5 Experiment metadata

Every RT-DC measurement has metadata consisting of key-value-pairs. The following are supported:

experiment	parsed	description [units]
date	str	Date of measurement ('YYYY-MM-DD')
event count	fint	Number of recorded events
run index	fint	Index of measurement run
sample	str	Measured sample or user-defined reference
time	str	Start time of measurement ('HH:MM:SS')

fluorescence	parsed	description [units]
bit depth	fint	Trace bit depth
channel 1 name	str	FL1 description
channel 2 name	str	FL2 description
channel 3 name	str	FL3 description
channel count	fint	Number of active channels
channels installed	fint	Number of available channels
laser 1 lambda	float	Laser 1 wavelength [nm]
laser 1 power	float	Laser 1 output power [%]
laser 2 lambda	float	Laser 2 wavelength [nm]
laser 2 power	float	Laser 2 output power [%]
laser 3 lambda	float	Laser 3 wavelength [nm]
laser 3 power	float	Laser 3 output power [%]
laser count	fint	Number of active lasers
lasers installed	fint	Number of available lasers
sample rate	float	Trace sample rate [Hz]
samples per event	fint	Samples per event
signal max	float	Upper voltage detection limit [V]
signal min	float	Lower voltage detection limit [V]
trace median	fint	Rolling median filter size for traces

fmt_tdms	parsed	description [units]
video frame offset	fint	Missing events at beginning of video

imaging	parsed	description [units]
flash device	str	Light source device type (e.g. green LED)
flash duration	float	Light source flash duration [µs]
frame rate	float	Imaging frame rate [Hz]
pixel size	float	Pixel size [µm]
roi position x	float	Image x coordinate on sensor [px]
roi position y	float	Image y coordinate on sensor [px]
roi size x	fint	Image width [px]
roi size y	fint	Image height [px]

online_contour	parsed	description [units]
bin area min	*fint*	Minium pixel area of binary image event
bin kernel	*fint*	Odd ellipse kernel size, binary image morphing
bin threshold	*fint*	Binary threshold for avg-bg-corrected image
image blur	*fint*	Odd sigma for Gaussian blur (21x21 kernel)
no absdiff	*fbool*	Avoid OpenCV 'absdiff' for avg-bg-correction

online_filter	parsed	description [units]
area_ratio max	float	Maximum porosity
area_ratio min	float	Minimum porosity
area_ratio soft limit	*fbool*	Soft limit, porosity
area_um max	float	Maximum area [µm^2]
area_um min	float	Minimum area [µm^2]
area_um soft limit	*fbool*	Soft limit, area [µm^2]
aspect max	float	Maximum aspect ratio of bounding box
aspect min	float	Minimum aspect ratio of bounding box
aspect soft limit	*fbool*	Soft limit, aspect ratio of bbox
deform max	float	Maximum deformation
deform min	float	Minimum deformation
deform soft limit	*fbool*	Soft limit, deformation
fl1_max max	float	Maximum FL-1 maximum [a.u.]
fl1_max min	float	Minimum FL-1 maximum [a.u.]
fl1_max soft limit	*fbool*	Soft limit, FL-1 maximum
fl2_max max	float	Maximum FL-2 maximum [a.u.]
fl2_max min	float	Minimum FL-2 maximum [a.u.]
fl2_max soft limit	*fbool*	Soft limit, FL-2 maximum
fl3_max max	float	Maximum FL-3 maximum [a.u.]
fl3_max min	float	Minimum FL-3 maximum [a.u.]
fl3_max soft limit	*fbool*	Soft limit, FL-3 maximum
size_x max	*fint*	Maximum bounding box size x [µm]
size_x min	*fint*	Minimum bounding box size x [µm]
size_x soft limit	*fbool*	Soft limit, bounding box size x
size_y max	*fint*	Maximum bounding box size y [µm]
size_y min	*fint*	Minimum bounding box size y [µm]
size_y soft limit	*fbool*	Soft limit, bounding box size y
target duration	float	Target measurement duration [min]
target event count	*fint*	Target event count for online gating

setup	parsed	description [units]
channel width	float	Width of microfluidic channel [µm]
chip region	*lcstr*	Imaged chip region (channel or reservoir)
flow rate	float	Flow rate in channel [µL/s]
flow rate sample	float	Sample flow rate [µL/s]
flow rate sheath	float	Sheath flow rate [µL/s]
identifier	str	Unique setup identifier
medium	str	Medium used
module composition	str	Comma-separated list of modules used
software version	str	Acquisition software with version

Example: date and time of a measurement

```
In [1]: import dclab

In [2]: ds = dclab.new_dataset("data/example.rtdc")

In [3]: ds.config["experiment"]["date"], ds.config["experiment"]["time"]
Out[3]: ('2017-07-16', '19:01:36')
```

4.1.6 Analysis metadata

In addition to metadata, dclab also supports a user-defined analysis configuration which is usually part of a specific analysis pipeline and thus not considered to be experimental metadata.

calculation	parsed	description [units]
crosstalk fl12	`float`	Fluorescence crosstalk, channel 1 to 2
crosstalk fl21	`float`	Fluorescence crosstalk, channel 2 to 1
crosstalk fl31	`float`	Fluorescence crosstalk, channel 1 to 3
crosstalk fl31	`float`	Fluorescence crosstalk, channel 3 to 1
crosstalk fl32	`float`	Fluorescence crosstalk, channel 2 to 3
crosstalk fl32	`float`	Fluorescence crosstalk, channel 3 to 1
emodulus medium	`str`	Medium used (e.g. CellCarrierB, water)
emodulus model	*`lcstr`*	Model for computing elastic moduli
emodulus temperature	`float`	Chip temperature [°C]
emodulus viscosity	`float`	Viscosity [Pa*s] if 'medium' unknown

4.2 RT-DC datasets

Knowing and understanding the *RT-DC dataset classes* is an important prerequisite when working with dclab. They are all derived from *`RTDCBase`* which gives access to feature with a dictionary-like interface, facilitates data export and filtering, and comes with several convenience methods that are useful for data visualization. RT-DC datasets can be based on a data file format (*`RTDC_TDMS`* and *`RTDC_HDF5`*), created from user-defined dictionaries (*`RTDC_Dict`*), or derived from other RT-DC datasets (*`RTDC_Hierarchy`*).

4.2.1 Basic usage

The convenience function *`dclab.new_dataset()`* takes care of determining the data file format (tdms or hdf5) and returns the corresponding derived class.

```
In [1]: import dclab

In [2]: ds = dclab.new_dataset("data/example.rtdc")

In [3]: ds.__class__.__name__
Out[3]: 'RTDC_HDF5'
```

Working with other data

It is also possible to load other data into dclab from a dictionary.

```
In [4]: data = dict(deform=np.random.rand(100),
   ...:             area_um=np.random.rand(100))
   ...:

In [5]: ds_dict = dclab.new_dataset(data)

In [6]: ds_dict.__class__.__name__
Out[6]: 'RTDC_Dict'
```

Using filters

Filters are used to mask e.g. debris or doublets from a dataset.

```
# Restrict the deformation to 0.15
In [7]: ds.config["filtering"]["deform max"] = .15

# Manually excluding events using array indices is also possible:
# `ds.filter.manual` is a 1D boolean array of size `len(ds)`
# where `False` values mean that the events are excluded.
In [8]: ds.filter.manual[[0, 400, 345, 1000]] = False

In [9]: ds.apply_filter()

# The boolean array `ds.filter.all` represents the applied filter
# and can be used for indexing.
In [10]: ds["deform"].mean(), ds["deform"][ds.filter.all].mean()
Out[10]: (0.0287258, 0.026486598)
```

Note that `ds.apply_filter()` must be called, otherwise `ds.filter.all` will not be updated.

Creating hierarchies

When applying filtering operations, it is sometimes helpful to use hierarchies for keeping track of the individual filtering steps.

```
In [11]: child = dclab.new_dataset(ds)

In [12]: child.config["filtering"]["area_um max"] = 80

In [13]: grandchild = dclab.new_dataset(child)

In [14]: grandchild.apply_filter()

In [15]: len(ds), len(child), len(grandchild)
Out[15]: (5000, 4933, 4778)

In [16]: ds.filter.all.sum(), child.filter.all.sum(), grandchild.filter.all.sum()
\\\\\\\\\\\\\\\\\\\\\\\\\\\\Out[16]: (4933, 4778, 4778)
```

Note that calling `grandchild.apply_filter()` automatically calls `child.apply_filter()` and `ds.apply_filter()`. Also note that, as expected, the size of each hierarchy child is identical to the sum of the boolean filtering array from its hierarchy parent.

Scripting goodies

Here are a few useful functionalities for scripting with dclab.

```
# unique identifier of the RTDCBase instance (not reproducible)
In [17]: ds.identifier
Out[17]: 'mm-hdf5_f1e7754'

# reproducible hash of the dataset
In [18]: ds.hash
\\\\\\\\\\\\\\\\\\\\\\\\\\\Out[18]: '8ff19f702a236cbf91e13667e144e722'

# dataset format
In [19]: ds.format
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\Out[19]: 'hdf5'

# available features
In [20]: ds.features
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\Out[20]:␣
↪
['area_cvx',
 'area_msd',
 'area_ratio',
 'area_um',
 'aspect',
 'bright_avg',
 'bright_sd',
 'circ',
 'deform',
 'frame',
 'index',
 'inert_ratio_cvx',
 'inert_ratio_raw',
 'nevents',
 'pos_x',
 'pos_y',
 'size_x',
 'size_y',
 'time']

# test feature availability (success)
In [21]: "area_um" in ds
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
↪True

# test feature availability (failure)
In [22]: "image" in ds
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
↪False

# accessing a feature and computing its mean
In [23]: ds["area_um"].mean()
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
↪49.728645

# accessing the measurement configuration
In [24]: ds.config.keys()
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
↪dict_keys(['filtering', 'experiment', 'imaging', 'online_contour', 'set
```

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```
In [25]: ds.config["experiment"]
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
↪
{'date': '2017-07-16',
 'event count': 5000,
 'run index': 1,
 'sample': 'docs-data',
 'time': '19:01:36'}

# determine the identifier of the hierarchy parent
In [26]: child.config["filtering"]["hierarchy parent"]
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
↪'mm-hdf5_f1e7754'
```

4.2.2 Statistics

The *statistics* module comes with a predefined set of methods to compute simple feature statistics.

```
In [27]: import dclab

In [28]: ds = dclab.new_dataset("data/example.rtdc")

In [29]: stats = dclab.statistics.get_statistics(ds,
   ....:                                         features=["deform", "aspect"],
   ....:                                         methods=["Mode", "Mean", "SD"])
   ....:

In [30]: dict(zip(*stats))
Out[30]:
{'Mode Deformation': 0.016635261,
 'Mean Deformation': 0.0287258,
 'SD Deformation': 0.028740086,
 'Mode Aspect ratio of bounding box': 1.1091421916433233,
 'Mean Aspect ratio of bounding box': 1.2719607587337494,
 'SD Aspect ratio of bounding box': 0.2523385371130096}
```

Note that the statistics take into account the applied filters:

```
In [31]: ds.config["filtering"]["deform max"] = .1

In [32]: ds.apply_filter()

In [33]: stats2 = dclab.statistics.get_statistics(ds,
   ....:                                          features=["deform", "aspect"],
   ....:                                          methods=["Mode", "Mean", "SD"])
   ....:

In [34]: dict(zip(*stats2))
Out[34]:
{'Mode Deformation': 0.017006295,
 'Mean Deformation': 0.02476519,
 'SD Deformation': 0.015638638,
 'Mode Aspect ratio of bounding box': 1.1232223188589807,
```

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```
 'Mean Aspect ratio of bounding box': 1.240720618624576,
 'SD Aspect ratio of bounding box': 0.15993707940243287}
```

These are the available statistics methods:

```
In [35]: dclab.statistics.Statistics.available_methods.keys()
Out[35]: dict_keys(['Mean', 'Median', 'Mode', 'SD', 'Events', '%-gated', 'Flow rate'])
```

4.2.3 Export

The *RTDCBase* class has the attribute *RTDCBase.export* which allows to export event data to several data file formats. See *export* for more information.

```
In [36]: ds.export.tsv(path="export_example.tsv",
   ....:               features=["area_um", "deform"],
   ....:               filtered=True,
   ....:               override=True)
   ....:

In [37]: ds.export.hdf5(path="export_example.rtdc",
   ....:                features=["area_um", "aspect", "deform"],
   ....:                filtered=True,
   ....:                override=True)
   ....:
```

Note that data exported as HDF5 files can be loaded with dclab (reproducing the previously computed statistics - without filters).

```
In [38]: ds2 = dclab.new_dataset("export_example.rtdc")

In [39]: ds2["deform"].mean()
Out[39]: 0.02476519
```

4.3 Scatter plots

For data visualization, dclab comes with predefined *kernel density estimators (KDEs)* and an *event downsampling* module. The functionalities of both modules are made available directly via the *RTDCBase* class.

4.3.1 KDE scatter plot

The KDE of the events in a 2D scatter plot can be used to colorize events according to event density using the *RTDCBase.get_kde_scatter* function.

```
import matplotlib.pylab as plt
import dclab
ds = dclab.new_dataset("data/example.rtdc")
kde = ds.get_kde_scatter(xax="area_um", yax="deform")

ax = plt.subplot(111, title="scatter plot with {} events".format(len(kde)))
sc = ax.scatter(ds["area_um"], ds["deform"], c=kde, marker=".")
```

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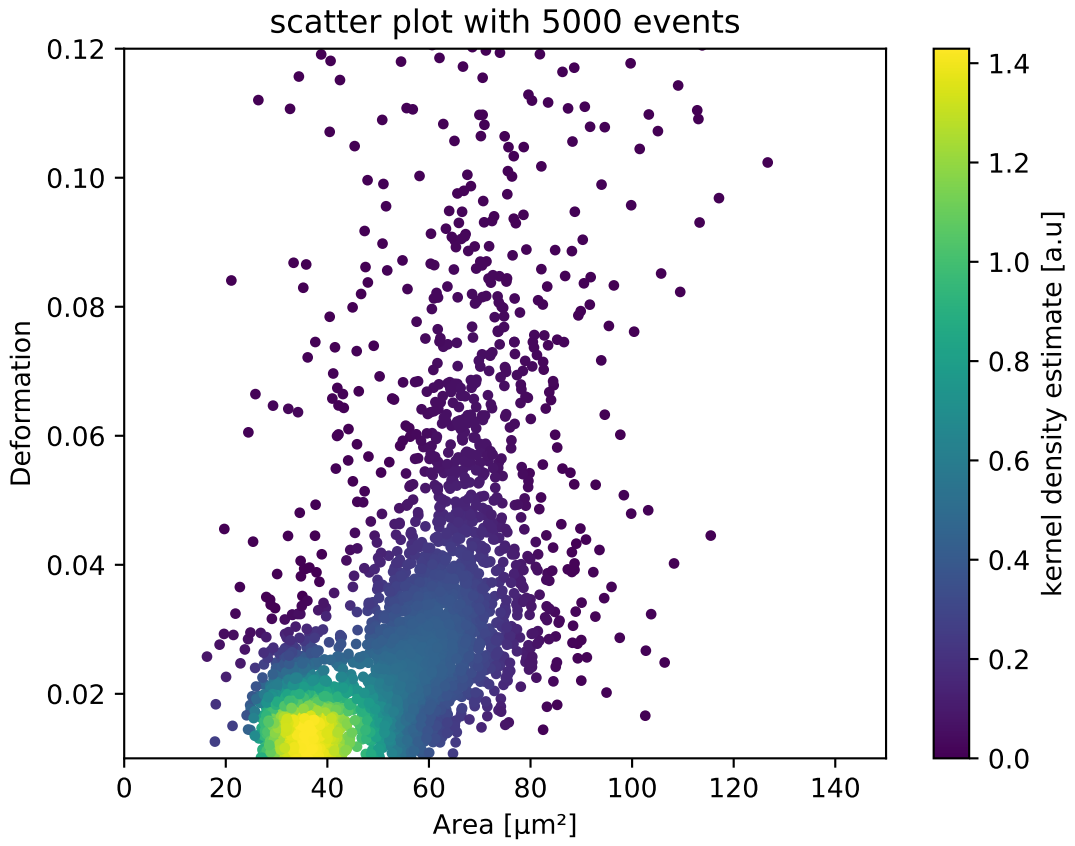
```
ax.set_xlabel(dclab.dfn.feature_name2label["area_um"])
ax.set_ylabel(dclab.dfn.feature_name2label["deform"])
ax.set_xlim(0, 150)
ax.set_ylim(0.01, 0.12)
plt.colorbar(sc, label="kernel density estimate [a.u]")
plt.show()
```



4.3.2 KDE scatter plot with event-density-based downsampling

To reduce the complexity of the plot (e.g. when exporting to scalable vector graphics (.svg)), the plotted events can be downsampled by removing events from high-event-density regions. The number of events plotted is reduced but the resulting visualization is almost indistinguishable from the one above.

```
import matplotlib.pylab as plt
import dclab
ds = dclab.new_dataset("data/example.rtdc")
xsamp, ysamp = ds.get_downsampled_scatter(xax="area_um", yax="deform",␣
↪downsample=2000)
kde = ds.get_kde_scatter(xax="area_um", yax="deform", positions=(xsamp, ysamp))

ax = plt.subplot(111, title="downsampled to {} events".format(len(kde)))
sc = ax.scatter(xsamp, ysamp, c=kde, marker=".")
```

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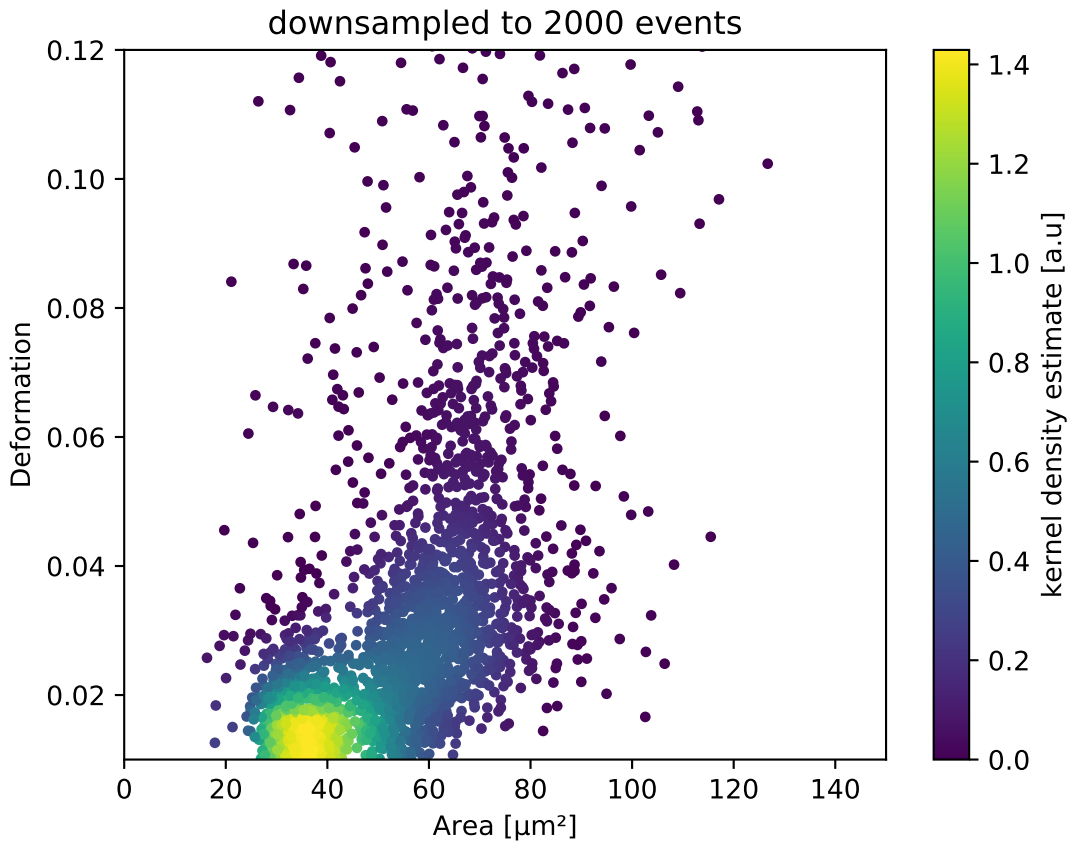
```
ax.set_xlabel(dclab.dfn.feature_name2label["area_um"])
ax.set_ylabel(dclab.dfn.feature_name2label["deform"])
ax.set_xlim(0, 150)
ax.set_ylim(0.01, 0.12)
plt.colorbar(sc, label="kernel density estimate [a.u]")
plt.show()
```



4.3.3 KDE estimate on a log-scale

Frequently, data is visualized on logarithmic scales. If the KDE is computed on a linear scale, then the result will look unaesthetic when plotted on a logarithmic scale. Therefore, the methods *get_downsampled_scatter*, *get_kde_contour*, and *get_kde_scatter* offer the keyword arguments `xscale` and `yscale` which can be set to "log" for prettier plots.

```
import matplotlib.pylab as plt
import dclab
ds = dclab.new_dataset("data/example.rtdc")
kde_lin = ds.get_kde_scatter(xax="area_um", yax="deform", yscale="linear")
kde_log = ds.get_kde_scatter(xax="area_um", yax="deform", yscale="log")

ax1 = plt.subplot(121, title="KDE with linear y-scale")
sc1 = ax1.scatter(ds["area_um"], ds["deform"], c=kde_lin, marker=".")
```

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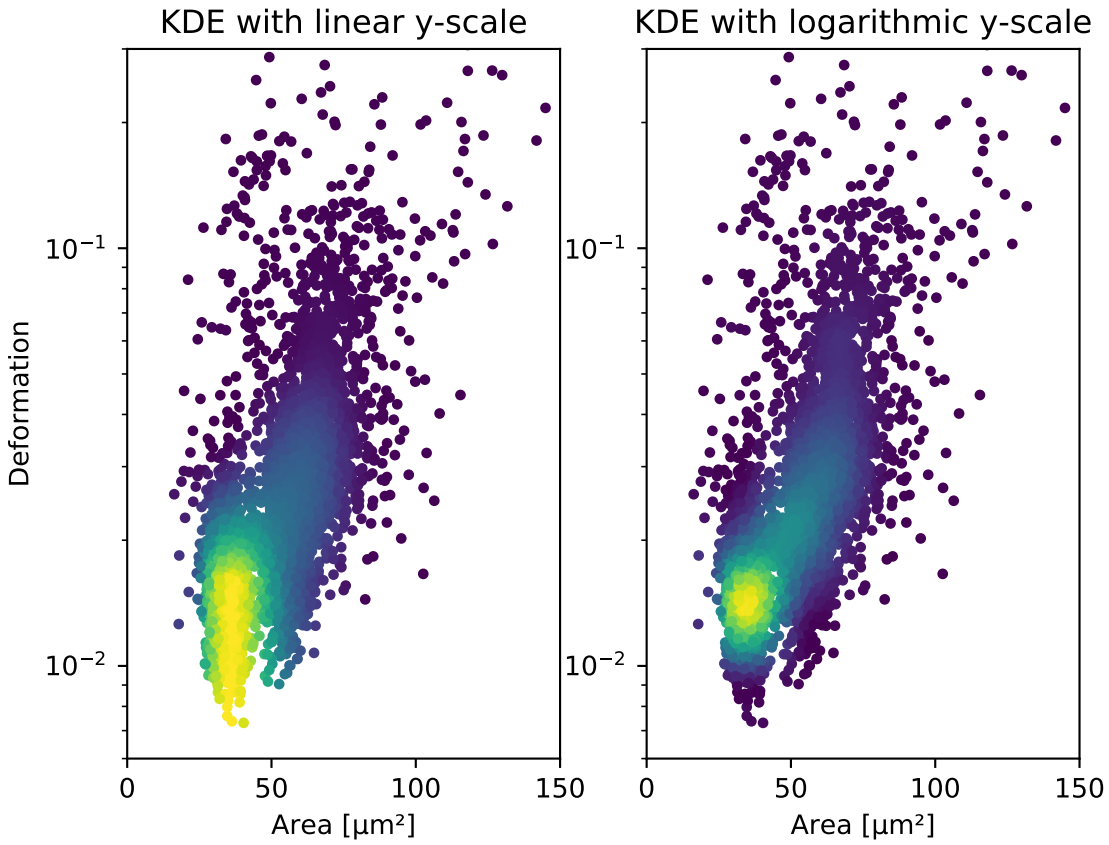
```
ax2 = plt.subplot(122, title="KDE with logarithmic y-scale")
sc2 = ax2.scatter(ds["area_um"], ds["deform"], c=kde_log, marker=".")

ax1.set_ylabel(dclab.dfn.feature_name2label["deform"])
for ax in [ax1, ax2]:
    ax.set_xlabel(dclab.dfn.feature_name2label["area_um"])
    ax.set_xlim(0, 150)
    ax.set_ylim(6e-3, 3e-1)
    ax.set_yscale("log")

plt.show()
```



4.3.4 Isoelasticity lines

In addition, dclab comes with predefined isoelasticity lines that are commonly used to identify events with similar elastic moduli. Isoelasticity lines are available via the *isoelastics* module.

```
import matplotlib.pylab as plt
import dclab
ds = dclab.new_dataset("data/example.rtdc")
kde = ds.get_kde_scatter(xax="area_um", yax="deform")
```

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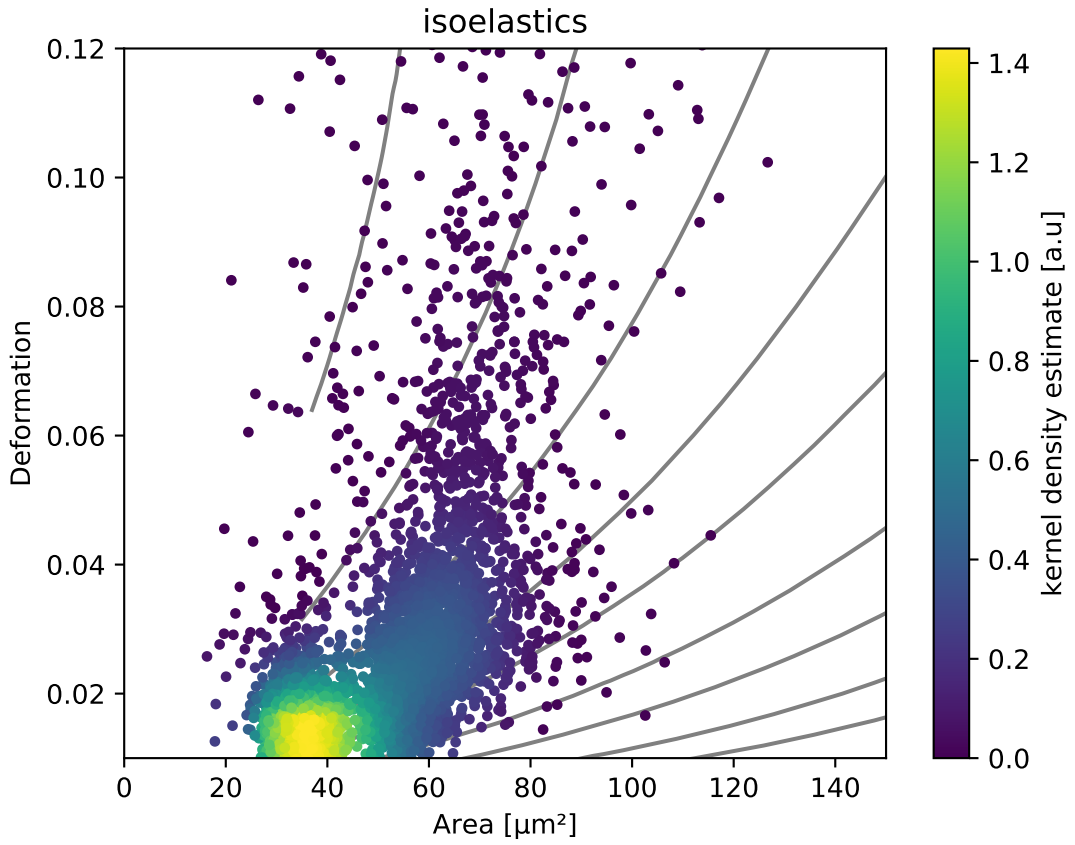
```
isodef = dclab.isoelastics.get_default()
iso = isodef.get_with_rtdcbase(method="numerical",
                               col1="area_um",
                               col2="deform",
                               dataset=ds)

ax = plt.subplot(111, title="isoelastics")
for ss in iso:
    ax.plot(ss[:, 0], ss[:, 1], color="gray", zorder=1)
sc = ax.scatter(ds["area_um"], ds["deform"], c=kde, marker=".", zorder=2)
ax.set_xlabel(dclab.dfn.feature_name2label["area_um"])
ax.set_ylabel(dclab.dfn.feature_name2label["deform"])
ax.set_xlim(0, 150)
ax.set_ylim(0.01, 0.12)
plt.colorbar(sc, label="kernel density estimate [a.u]")
plt.show()
```



4.3.5 Contour plot with percentiles

Contour plots are commonly used to compare the kernel density between measurements. Kernel density estimates (on a grid) for contour plots can be computed with the function *RTDCBase.get_kde_contour*. In addition, it is possible to compute contours at data percentiles using *dclab.kde_contours.get_quantile_levels()*.

```
import matplotlib.pylab as plt
import dclab
ds = dclab.new_dataset("data/example.rtdc")
X, Y, Z = ds.get_kde_contour(xax="area_um", yax="deform")
Z /= Z.max()
quantiles = [.1, .5, .75]
levels = dclab.kde_contours.get_quantile_levels(density=Z,
                                                x=X,
                                                y=Y,
                                                xp=ds["area_um"],
                                                yp=ds["deform"],
                                                q=quantiles,
                                                )

ax = plt.subplot(111, title="contour lines")
sc = ax.scatter(ds["area_um"], ds["deform"], c="lightgray", marker=".", zorder=1)
cn = ax.contour(X, Y, Z,
                levels=levels,
                linestyles=["--", "-", "-"],
                colors=["blue", "blue", "darkblue"],
                linewidths=[2, 2, 3],
                zorder=2)

ax.set_xlabel(dclab.dfn.feature_name2label["area_um"])
ax.set_ylabel(dclab.dfn.feature_name2label["deform"])
ax.set_xlim(0, 150)
ax.set_ylim(0.01, 0.12)
# label contour lines with percentiles
fmt = {}
for l, q in zip(levels, quantiles):
    fmt[l] = "{:.0f}th".format(q*100)
plt.clabel(cn, fmt=fmt)
plt.show()
```

Note that you may compute (and plot) the contour lines directly yourself using the function *dclab.kde_contours.find_contours_level()*.

4.3.6 Polygon filters / Shape-Out

Keep in mind that you can combine your dclab analysis pipeline with Shape-Out. For instance, you can create and export *polygon filters* in Shape-Out and then import them in dclab.

```
import matplotlib.pylab as plt
import dclab
ds = dclab.new_dataset("data/example.rtdc")
kde = ds.get_kde_scatter(xax="area_um", yax="deform")
# load and apply polygon filter from file
pf = dclab.PolygonFilter(filename="data/example.poly")
ds.polygon_filter_add(pf)
ds.apply_filter()
# valid events
val = ds.filter.all

ax = plt.subplot(111, title="polygon filtering")
ax.scatter(ds["area_um"][~val], ds["deform"][~val], c="lightgray", marker=".")
sc = ax.scatter(ds["area_um"][val], ds["deform"][val], c=kde[val], marker=".")
```

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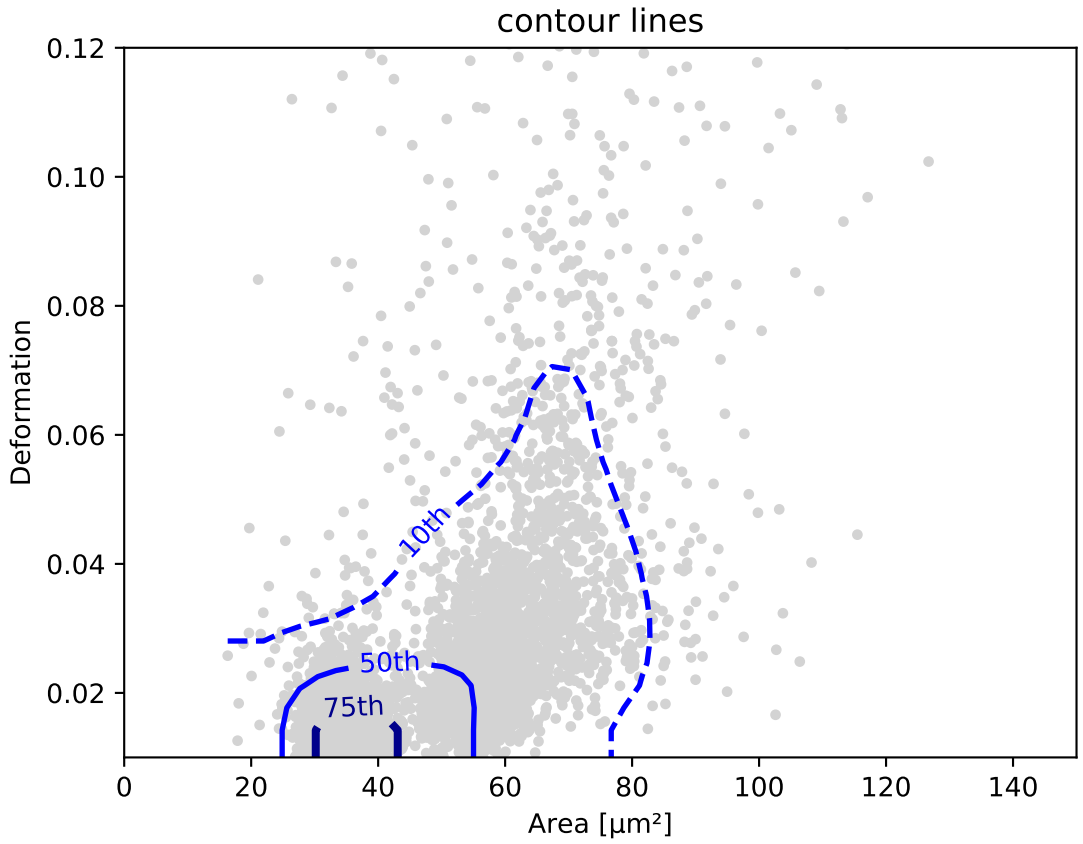
contour lines
0.12
0.10
0.08
0.06
0.04
0.02
Deformation
10th
50th
75th
0
20
40
60
80
100
120
140
Area [µm²]

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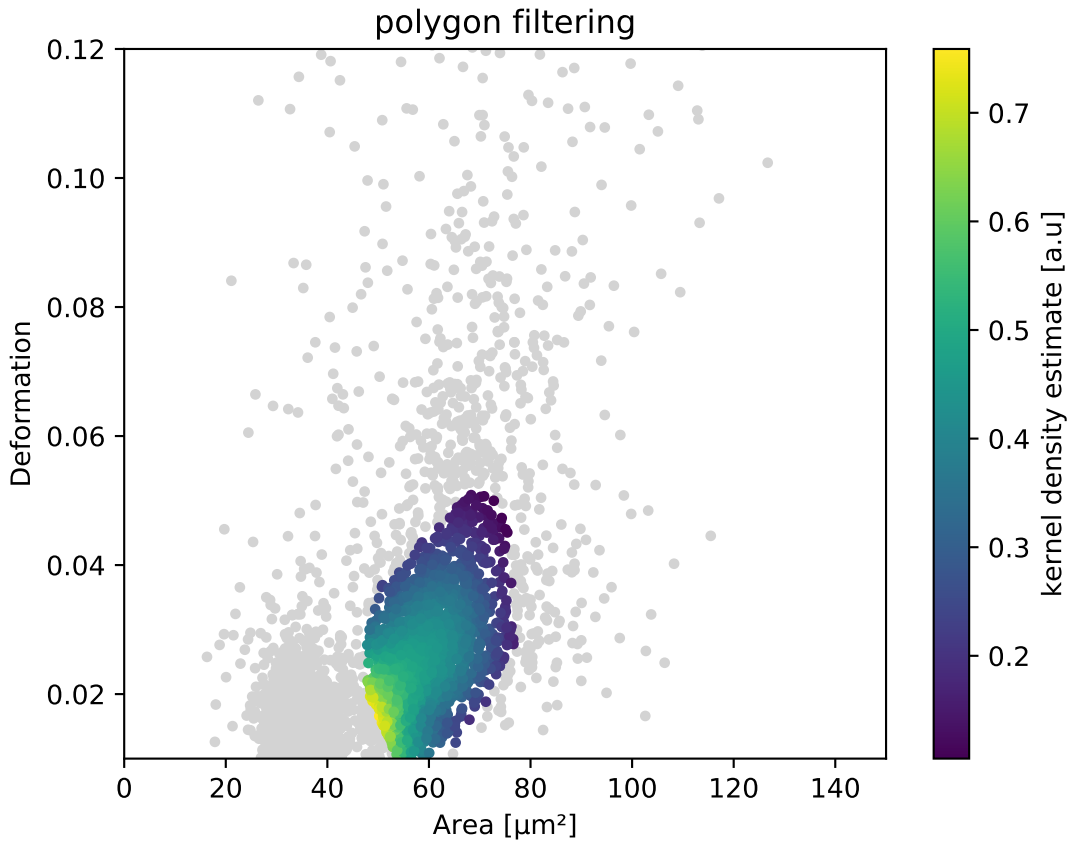
```
ax.set_xlabel(dclab.dfn.feature_name2label["area_um"])
ax.set_ylabel(dclab.dfn.feature_name2label["deform"])
ax.set_xlim(0, 150)
ax.set_ylim(0.01, 0.12)
plt.colorbar(sc, label="kernel density estimate [a.u]")
plt.show()
```



4.4 Fluorescence traces

In RT-FDC, fluorescence data are stored alongside the regular image and scalar features. The fluorescence data consist of the trace data (fluorescence signal over time) and several scalar features (maximum, peak position, peak width, etc.) for each fluorescence channel. The trace data are stored as *raw* and *median-filtered* traces, where *median-filtered* means that the *raw* data is filtered with a rolling median filter.

```
In [1]: import dclab

In [2]: ds = dclab.new_dataset("data/example_traces.rtdc")

# list the available traces in the dataset
In [3]: sorted(ds["trace"].keys())
Out[3]: ['fl1_median', 'fl1_raw', 'fl2_median', 'fl2_raw', 'fl3_median', 'fl3_raw']
```

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```
# show fluorescence meta data
In [4]: ds.config["fluorescence"]
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\Out[4]:␣
↪
{'bit depth': 16,
 'channel 1 name': '525/50',
 'channel 2 name': '593/46',
 'channel 3 name': '700/75',
 'channel count': 3,
 'channels installed': 3,
 'laser 1 lambda': 488.0,
 'laser 1 power': 8.0,
 'laser 3 lambda': 640.0,
 'laser 3 power': 100.0,
 'laser count': 2,
 'lasers installed': 3,
 'sample rate': 312500.0,
 'samples per event': 177,
 'signal max': 1.0,
 'signal min': -1.0,
 'trace median': 0}
```

Please note that the value of `trace median` is zero (no median filter applied), which tells us that the values of the *raw* and *median* trace data are identical. The example dataset is an excerpt from the calibration beads dataset, with a total of three fluorescence channels used.

```
import matplotlib.pylab as plt
import dclab

ds = dclab.new_dataset("data/example_traces.rtdc")
# event index to plot
idx = 8
# measuring time
samples = ds.config["fluorescence"]["samples per event"]
sample_rate = ds.config["fluorescence"]["sample rate"]
t = np.arange(samples) / sample_rate * 1e6

fig, axes = plt.subplots(nrows=3, sharex=True, sharey=True)

# fluorescence traces (colors manually chosen to represent filter set)
axes[0].plot(t, ds["trace"]["fl1_median"][idx], color="#16A422",
             label=ds.config["fluorescence"]["channel 1 name"])
axes[1].plot(t, ds["trace"]["fl2_median"][idx], color="#CE9720",
             label=ds.config["fluorescence"]["channel 2 name"])
axes[2].plot(t, ds["trace"]["fl3_median"][idx], color="#CE2026",
             label=ds.config["fluorescence"]["channel 3 name"])

# detected peak widths
axes[0].axvline(ds["fl1_pos"][idx] + ds["fl1_width"][idx]/2, color="gray")
axes[0].axvline(ds["fl1_pos"][idx] - ds["fl1_width"][idx]/2, color="gray")
axes[1].axvline(ds["fl2_pos"][idx] + ds["fl2_width"][idx]/2, color="gray")
axes[1].axvline(ds["fl2_pos"][idx] - ds["fl2_width"][idx]/2, color="gray")
axes[2].axvline(ds["fl3_pos"][idx] + ds["fl3_width"][idx]/2, color="gray")
axes[2].axvline(ds["fl3_pos"][idx] - ds["fl3_width"][idx]/2, color="gray")
```

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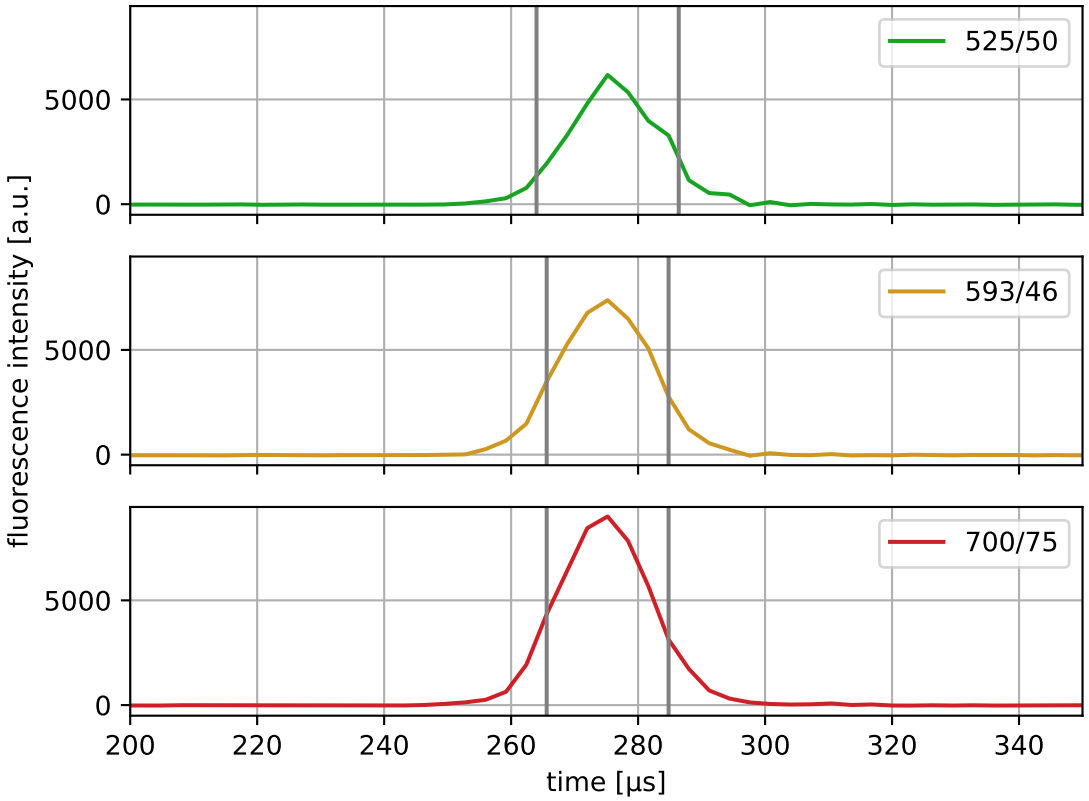
```
# axes labels
axes[1].set_ylabel("fluorescence intensity [a.u.]")
axes[2].set_xlabel("time [µs]")

for ax in axes:
    ax.set_xlim(200, 350)
    ax.grid()
    ax.legend()

plt.show()
```



Please note that the fluorescence traces are stored as integer values and have to be converted to µs using the meta data stored in `ds.config["fluorescence"]`. Also, notice how the scalar features are used for plotting the peak width.

CHAPTER 5

Code reference

5.1 module-level methods

dclab.**new_dataset**(*data*, *identifier=None*)
Initialize a new RT-DC dataset

Parameters

- **data** – can be one of the following:
  - dict
  - .tdms file
  - .rtdc file
  - subclass of *RTDCBase* (will create a hierarchy child)
- **identifier** (*str*) – A unique identifier for this dataset. If set to *None* an identifier is generated.

Returns **dataset** – A new dataset instance

Return type subclass of *dclab.rtdc_dataset.RTDCBase*

5.2 global definitions

These definitionas are used throughout the dclab/Shape-In/Shape-Out ecosystem.

5.2.1 configuration

Valid configuration sections and keys are described in: *Analysis metadata* and *Experiment metadata*.

dclab.dfn.**CFG_ANALYSIS**
User-editable configuration for data analysis.

dclab.dfn.**CFG_METADATA**
Measurement-specific metadata.

dclab.dfn.**config_funcs**
Dictionary of dictionaries containing functions to convert input data to the predefined data type

dclab.dfn.**config_keys**
Dictionary with sections as keys and configuration parameter names as values

dclab.dfn.**config_types**
Dictionary of dictionaries containing the data type of each configuration parameter

5.2.2 features

Features are discussed in more detail in: *Features*.

dclab.dfn.**FEATURES_SCALAR**
Scalar features

dclab.dfn.**FEATURES_NON_SCALAR**
Non-scalar features

dclab.dfn.**feature_names**
List of valid feature names

dclab.dfn.**feature_labels**
List of human-readable labels for each valid feature

dclab.dfn.**feature_name2label**
Dictionary that maps feature names to feature labels

dclab.dfn.**scalar_feature_names**
List of valid scalar feature names

5.2.3 parse functions

dclab.parse_funcs.**fbool**(*value*)
boolean

dclab.parse_funcs.**fint**(*value*)
integer

dclab.parse_funcs.**fintlist**(*alist*)
A list of integers

dclab.parse_funcs.**lcstr**(*astr*)
lower-case string

dclab.parse_funcs.**func_types = {<function fbool>: <class 'bool'>, <function fint>: <class**
maps functions to their expected output types

5.3 RT-DC dataset manipulation

5.3.1 Base class

class dclab.rtdc_dataset.**RTDCBase**(*identifier=None*)
RT-DC measurement base class

Notes

Besides the filter arrays for each data feature, there is a manual boolean filter array `RTDCBase.filter.manual` that can be edited by the user - a boolean value of `False` means that the event is excluded from all computations.

apply_filter (*force=[]*)
Compute the filters for the dataset

get_downsampled_scatter (*xax='area_um'*, *yax='deform'*, *downsample=0*, *xscale='linear'*, *yscale='linear'*, *remove_invalid=False*, *ret_mask=False*)
Downsampling by removing points at dense locations

Parameters

- **xax** (*str*) – Identifier for x axis (e.g. "area_um", "aspect", "deform")
- **yax** (*str*) – Identifier for y axis
- **downsample** (*int*) – Number of points to draw in the down-sampled plot. This number is either
  - **>=1: exactly downsample to this number by randomly adding** or removing points
  - 0 : do not perform downsampling
- **xscale** (*str*) – If set to "log", take the logarithm of the x-values before performing downsampling. This is useful when data are are displayed on a log-scale. Defaults to "linear".
- **yscale** (*str*) – See *xscale*.
- **remove_invalid** (*bool*) – Remove nan and inf values before downsampling; if set to *True*, the actual number of samples returned might be smaller than *downsample* due to infinite or nan values (e.g. due to logarithmic scaling).
- **ret_mask** (*bool*) – If set to *True*, returns a boolean array of length *len(self)* where *True* values identify the filtered data.

Returns

- **xnew, xnew** (1d ndarray of lenght *N*) – Filtered data; *N* is either identical to *downsample* or smaller (if *remove_invalid==True*)
- **mask** (1d boolean array of length *len(RTDCBase)*) – Array for identifying the down-sampled data points

get_kde_contour (*xax='area_um'*, *yax='deform'*, *xacc=None*, *yacc=None*, *kde_type='histogram'*, *kde_kwargs={}*, *xscale='linear'*, *yscale='linear'*)
Evaluate the kernel density estimate for contour plots

Parameters

- **xax** (*str*) – Identifier for X axis (e.g. "area_um", "aspect", "deform")
- **yax** (*str*) – Identifier for Y axis
- **xacc** (*float*) – Contour accuracy in x direction
- **yacc** (*float*) – Contour accuracy in y direction
- **kde_type** (*str*) – The KDE method to use
- **kde_kwargs** (*dict*) – Additional keyword arguments to the KDE method

- **xscale** (*str*) – If set to "log", take the logarithm of the x-values before computing the KDE. This is useful when data are are displayed on a log-scale. Defaults to "linear".
- **yscale** (*str*) – See *xscale*.

Returns **X, Y, Z** – The kernel density Z evaluated on a rectangular grid (X,Y).

Return type coordinates

get_kde_scatter(*xax='area_um'*, *yax='deform'*, *positions=None*, *kde_type='histogram'*, *kde_kwargs={}*, *xscale='linear'*, *yscale='linear'*)

Evaluate the kernel density estimate for scatter plots

Parameters

- **xax** (*str*) – Identifier for X axis (e.g. "area_um", "aspect", "deform")
- **yax** (*str*) – Identifier for Y axis
- **positions** (*list of two 1d ndarrays or ndarray of shape (2, N)*) – The positions where the KDE will be computed. Note that the KDE estimate is computed from the the points that are set in *self.filter.all*.
- **kde_type** (*str*) – The KDE method to use
- **kde_kwargs** (*dict*) – Additional keyword arguments to the KDE method
- **xscale** (*str*) – If set to "log", take the logarithm of the x-values before computing the KDE. This is useful when data are are displayed on a log-scale. Defaults to "linear".
- **yscale** (*str*) – See *xscale*.

Returns **density** – The kernel density evaluated for the filtered data points.

Return type 1d ndarray

polygon_filter_add(*filt*)

Associate a Polygon Filter with this instance

Parameters **filt** (int or instance of *PolygonFilter*) – The polygon filter to add

polygon_filter_rm(*filt*)

Remove a polygon filter from this instance

Parameters **filt** (int or instance of *PolygonFilter*) – The polygon filter to remove

config = None

Configuration of the measurement

export = None

Export functionalities; instance of *dclab.rtdc_dataset.export.Export*.

features

All available features

features_innate

All features excluding ancillary features

filter = None

Filtering functionalities; instance of *dclab.rtdc_dataset.filter.Filter*.

format = None

Dataset format (derived from class name)

hash
Reproducible dataset hash (defined by derived classes)

identifier
Unique (unreproducible) identifier

logs = None
Dictionary of log files. Each log file is a list of strings (one string per line).

title = None
Title of the measurement

5.3.2 Dictionary format

class dclab.rtdc_dataset.**RTDC_Dict**(*ddict*, **args*, ***kwargs*)
Dictionary-based RT-DC dataset

Parameters

- **ddict** (*dict*) – Dictionary with keys from *dclab.definitions.feature_names* (e.g. "area_cvx", "deform", "image") with which the class will be instantiated. The configuration is set to the default configuration of dclab.
- ***args** – Arguments for *RTDCBase*
- ****kwargs** – Keyword arguments for *RTDCBase*

5.3.3 HDF5 (.rtdc) format

class dclab.rtdc_dataset.**RTDC_HDF5**(*h5path*, **args*, ***kwargs*)
HDF5 file format for RT-DC measurements

Parameters

- **h5path** (*str or pathlib.Path*) – Path to a '.tdms' measurement file.
- ***args** – Arguments for *RTDCBase*
- ****kwargs** – Keyword arguments for *RTDCBase*

path
Path to the experimental HDF5 (.rtdc) file

Type pathlib.Path

static parse_config(*h5path*)
Parse the RT-DC configuration of an hdf5 file

dclab.rtdc_dataset.fmt_hdf5.**MIN_DCLAB_EXPORT_VERSION = '0.3.3.dev2'**
rtdc files exported with dclab prior to this version are not supported

5.3.4 Hierarchy format

class dclab.rtdc_dataset.**RTDC_Hierarchy**(*hparent*, **args*, ***kwargs*)
Hierarchy dataset (filtered from RTDCBase)

A few words on hierarchies: The idea is that a subclass of RTDCBase can use the filtered data of another subclass of RTDCBase and interpret these data as unfiltered events. This comes in handy e.g. when the percentage of different subpopulations need to be distinguished without the noise in the original data.

Children in hierarchies always update their data according to the filtered event data from their parent when *apply_filter* is called. This makes it easier to save and load hierarchy children with e.g. Shape-Out and it makes the handling of hierarchies more intuitive (when the parent changes, the child changes as well).

Parameters

- **hparent** (*instance of RTDCBase*) – The hierarchy parent.
- ***args** – Arguments for *RTDCBase*
- ****kwargs** – Keyword arguments for *RTDCBase*

hparent
Hierarchy parent of this instance

Type *RTDCBase*

5.3.5 TDMS format

class dclab.rtdc_dataset.**RTDC_TDMS**(*tdms_path*, **args*, ***kwargs*)
TDMS file format for RT-DC measurements

Parameters

- **tdms_path** (*str or pathlib.Path*) – Path to a '.tdms' measurement file.
- ***args** – Arguments for *RTDCBase*
- ****kwargs** – Keyword arguments for *RTDCBase*

path
Path to the experimental dataset (main .tdms file)

Type pathlib.Path

dclab.rtdc_dataset.fmt_tdms.**get_project_name_from_path**(*path*, *append_mx=False*)
Get the project name from a path.

For a path "/home/peter/hans/HLC12398/online/M1_13.tdms" or For a path "/home/peter/hans/HLC12398/online/data/M1_13.tdms" or without the ".tdms" file, this will return always "HLC12398".

Parameters

- **path** (*str*) – path to tdms file
- **append_mx** (*bool*) – append measurement number, e.g. "M1"

dclab.rtdc_dataset.fmt_tdms.**get_tdms_files**(*directory*)
Recursively find projects based on '.tdms' file endings

Searches the *directory* recursively and return a sorted list of all found '.tdms' project files, except fluorescence data trace files which end with *_traces.tdms*.

5.3.6 config

class dclab.rtdc_dataset.config.**Configuration**(*files=[]*, *cfg={}*)
Configuration class for RT-DC datasets

This class has a dictionary-like interface to access and set configuration values, e.g.

```
cfg = load_from_file("/path/to/config.txt")
# access the channel width
cfg["setup"]["channel width"]
# modify the channel width
cfg["setup"]["channel width"] = 30
```

Parameters

- **files** (*list of files*) – The config files with which to initialize the configuration
- **cfg** (*dict-like*) – The dictionary with which to initialize the configuration

copy()
Return copy of current configuration

keys()
Return the configuration keys (sections)

save(*filename*)
Save the configuration to a file

tostring(*sections=None*)
Convert the configuration to its string representation

The optional argument *sections* allows to export only specific sections of the configuration, i.e. *sections=dclab.dfn.CFG_METADATA* will only export configuration data from the original measurement and no filtering data.

update(*newcfg*)
Update current config with a dictionary

dclab.rtdc_dataset.config.**load_from_file**(*cfg_file*)
Load the configuration from a file

Parameters **cfg_file** (*str*) – Path to configuration file

Returns **cfg** – Dictionary with configuration parameters

Return type CaseInsensitiveDict

5.3.7 export

exception dclab.rtdc_dataset.export.**NoImageWarning**

class dclab.rtdc_dataset.export.**Export**(*rtdc_ds*)
Export functionalities for RT-DC datasets

avi(*path*, *filtered=True*, *override=False*)
Exports filtered event images to an avi file

Parameters

- **path** (*str*) – Path to a .avi file. The ending .avi is added automatically.
- **filtered** (*bool*) – If set to *True*, only the filtered data (index in ds.filter.all) are used.
- **override** (*bool*) – If set to *True*, an existing file `path` will be overridden. If set to *False*, raises *OSError* if `path` exists.

Notes

Raises OSError if current dataset does not contain image data

fcs (*path*, *features*, *filtered=True*, *override=False*)
Export the data of an RT-DC dataset to an .fcs file

Parameters

- **mm** (*instance of dclab.RTDCBase*) – The dataset that will be exported.
- **path** (*str*) – Path to an .fcs file. The ending .fcs is added automatically.
- **features** (*list of str*) – The features in the resulting .fcs file. These are strings that are defined in *dclab.definitions.scalar_feature_names*, e.g. "area_cvx", "deform", "frame", "fl1_max", "aspect".
- **filtered** (*bool*) – If set to *True*, only the filtered data (index in ds.filter.all) are used.
- **override** (*bool*) – If set to *True*, an existing file `path` will be overridden. If set to *False*, raises *OSError* if `path` exists.

Notes

Due to incompatibility with the .fcs file format, all events with NaN-valued features are not exported.

hdf5 (*path*, *features*, *filtered=True*, *override=False*, *compression='gzip'*)
Export the data of the current instance to an HDF5 file

Parameters

- **path** (*str*) – Path to an .rtdc file. The ending .rtdc is added automatically.
- **features** (*list of str*) – The features in the resulting .rtdc file. These are strings that are defined in *dclab.definitions.feature_names*, e.g. "area_cvx", "deform", "frame", "fl1_max", "image".
- **filtered** (*bool*) – If set to *True*, only the filtered data (index in ds.filter.all) are used.
- **override** (*bool*) – If set to *True*, an existing file `path` will be overridden. If set to *False*, raises *OSError* if `path` exists.
- **compression** (*str or None*) – Compression method for "contour", "image", and "trace" data as well as logs; one of [None, "lzf", "gzip", "szip"].

tsv (*path*, *features*, *filtered=True*, *override=False*)
Export the data of the current instance to a .tsv file

Parameters

- **path** (*str*) – Path to a .tsv file. The ending .tsv is added automatically.
- **features** (*list of str*) – The features in the resulting .tsv file. These are strings that are defined in *dclab.definitions.scalar_feature_names*, e.g. "area_cvx", "deform", "frame", "fl1_max", "aspect".
- **filtered** (*bool*) – If set to *True*, only the filtered data (index in ds.filter.all) are used.
- **override** (*bool*) – If set to *True*, an existing file `path` will be overridden. If set to *False*, raises *OSError* if `path` exists.

5.3.8 filter

class dclab.rtdc_dataset.filter.**Filter**(*rtdc_ds*)
Boolean filter arrays for RT-DC measurements

Parameters **rtdc_ds** (*instance of RTDCBase*) – The RT-DC dataset the filter applies to

update(*force=[]*)
Update the filters according to *self.rtdc_ds.config["filtering"]*

Parameters **force** (*list*) – A list of feature names that must be refiltered with min/max values.

Notes

This function is called when *ds.apply_filter* is called.

all = None
All filters combined (see *Filter.update()*); Use this property to filter the features of *dclab.rtdc_dataset.RTDCBase* instances

invalid = None
Invalid (nan/inf) events

manual = None
1D boolean array for manually excluding events; *False* values are excluded.

polygon = None
Polygon filters

rtdc_ds = None
Instance of RTDCBase the filter applies to

5.4 low-level functionalities

5.4.1 downsampling

Content-based downsampling of ndarrays

dclab.downsampling.**downsample_rand**(*a*, *samples*, *remove_invalid=False*, *ret_idx=False*)
Downsampling by randomly removing points

Parameters

- **a** (*1d ndarray*) – The input array to downsample
- **samples** (*int*) – The desired number of samples
- **remove_invalid** (*bool*) – Remove nan and inf values before downsampling
- **ret_idx** (*bool*) – Also return a boolean array that corresponds to the downsampled indices in *a*.

Returns

- **dsa** (1d ndarray of size *samples*) – The pseudo-randomly downsampled array *a*
- **idx** (1d boolean array with same shape as *a*) – Only returned if *ret_idx* is True. A boolean array such that *a[idx] == dsa*

dclab.downsampling.**norm**(*a*, *ref1*, *ref2*)
Normalize *a* with min/max values of *ref1*, using all elements of *ref1* where the *ref1* and *ref2* are not nan or inf

dclab.downsampling.**valid**(*a*, *b*)
Check whether *a* and *b* are not inf or nan

5.4.2 features

dclab.features.contour.**get_contour**(*mask*)
Compute the image contour from a mask

The contour is computed in a very inefficient way using scikit-image and a conversion of float coordinates to pixel coordinates.

Parameters **mask** (*binary ndarray of shape (M,N) or (K,M,N)*) – The mask outlining the pixel positions of the event. If a 3d array is given, then *K* indexes the individual contours.

Returns **cont** – A 2D array that holds the contour of an event (in pixels) e.g. obtained using *mm.contour* where *mm* is an instance of *RTDCBase*. The first and second columns of *cont* correspond to the x- and y-coordinates of the contour.

Return type ndarray or list of K ndarrays of shape (J,2)

dclab.features.bright.**get_bright**(*mask*, *image*, *ret_data='avg*, *sd'*)
Compute avg and/or std of the event brightness

The event brightness is defined by the gray-scale values of the image data within the event mask area.

Parameters

- **mask** (*ndarray or list of ndarrays of shape (M,N) and dtype bool*) – The mask values, True where the event is located in *image*.
- **image** (*ndarray or list of ndarrays of shape (M,N)*) – A 2D array that holds the image in form of grayscale values of an event.
- **ret_data** (*str*) – A comma-separated list of metrices to compute - "avg": compute the average - "sd": compute the standard deviation Selected metrics are returned in alphabetical order.

Returns

- **bright_avg** (*float or ndarray of size N*) – Average image data within the contour
- **bright_std** (*float or ndarray of size N*) – Standard deviation of image data within the contour

dclab.features.emodulus.**get_emodulus**(*area_um*, *deform*, *medium='CellCarrier'*, *channel_width=20.0*, *flow_rate=0.16*, *px_um=0.34*, *temperature=23.0*, *copy=True*)
Compute apparent Young's modulus using a look-up table

Parameters

- **area_um** (*float or ndarray*) – Apparent (2D image) area [µm^2] of the event(s)
- **deform** (*float or ndarray*) – The deformation (1-circularity) of the event(s)
- **medium** (*str or float*) – The medium to compute the viscosity for. If a string in ["CellCarrier", "CellCarrier B"] is given, the viscosity will be computed. If a float is given, this value will be used as the viscosity in mPa*s.

- **channel_width** (*float*) – The channel width [µm]
- **flow_rate** (*float*) – Flow rate [µl/s]
- **px_um** (*float*) – The detector pixel size [µm] used for pixelation correction. Set to zero to disable.
- **temperature** (*float or ndarray*) – Temperature [°C] of the event(s)
- **copy** (*bool*) – Copy input arrays. If set to false, input arrays are overridden.

Returns **elasticity** – Apparent Young's modulus in kPa

Return type float or ndarray

Notes

- The look-up table used was computed with finite elements methods according to [MMM+17].
- The computation of the Young's modulus takes into account corrections for the viscosity (medium, channel width, flow rate, and temperature) [MOG+15] and corrections for pixelation of the area and the deformation which are computed from a (pixelated) image [Her17].

See also:

dclab.features.emodulus_viscosity.get_viscosity() compute viscosity for known media

dclab.features.emodulus_viscosity.**get_viscosity**(*medium='CellCarrier'*, *channel_width=20.0*, *flow_rate=0.16*, *temperature=23.0*)

Returns the viscosity for RT-DC-specific media

Parameters

- **medium** (*str*) – The medium to compute the viscosity for. One of ["CellCarrier", "CellCarrier B", "water"].
- **channel_width** (*float*) – The channel width in µm
- **flow_rate** (*float*) – Flow rate in µl/s
- **temperature** (*float or ndarray*) – Temperature in °C

Returns **viscosity** – Viscosity in mPa*s

Return type float or ndarray

Notes

- CellCarrier and CellCarrier B media are optimized for RT-DC measurements.
- Values for the viscosity of water are computed using equation (15) from [KSW78].

dclab.features.fl_crosstalk.**correct_crosstalk**(*fl1*, *fl2*, *fl3*, *fl_channel*, *ct21=0*, *ct31=0*, *ct12=0*, *ct32=0*, *ct13=0*, *ct23=0*)

Perform crosstalk correction

Parameters

- **fli** (*int, float, or np.ndarray*) – Measured fluorescence signals

- **fl_channel** (*int (1, 2, or 3)*) – The channel number for which the crosstalk-corrected signal should be computed
- **cij** (*float*) – Spill (crosstalk or bleed-through) from channel i to channel j This spill is computed from the fluorescence signal of e.g. single-stained positive control cells; It is defined by the ratio of the fluorescence signals of the two channels, i.e cij = flj / fli.

See also:

get_compensation_matrix() compute the inverse crosstalk matrix

Notes

If there are only two channels (e.g. fl1 and fl2), then the crosstalk to and from the other channel (ct31, ct32, ct13, ct23) should be set to zero.

dclab.features.fl_crosstalk.**get_compensation_matrix**(*ct21*, *ct31*, *ct12*, *ct32*, *ct13*, *ct23*)
Compute crosstalk inversion matrix

The spillover matrix is

| c11 c12 c13 |
| c21 c22 c23 |
| c31 c32 c33 |

The diagonal elements are set to 1, i.e.

ct11 = c22 = c33 = 1

Parameters **cij** (*float*) – Spill from channel i to channel j

Returns **inv** – Compensation matrix (inverted spillover matrix)

Return type np.ndarray

dclab.features.inert_ratio.**get_inert_ratio_cvx**(*cont*)
Compute the inertia ratio of the convex hull of a contour

The inertia ratio is computed from the central second order of moments along x (mu20) and y (mu02) via *sqrt(mu20/mu02)*.

Parameters **cont** (*ndarray or list of ndarrays of shape (N,2)*) – A 2D array that holds the contour of an event (in pixels) e.g. obtained using *mm.contour* where *mm* is an instance of *RTDCBase*. The first and second columns of *cont* correspond to the x- and y-coordinates of the contour.

Returns **inert_ratio_cvx** – The inertia ratio of the contour's convex hull

Return type float or ndarray of size N

Notes

The contour moments mu20 and mu02 are computed the same way they are computed in OpenCV's *moments.cpp*.

See also:

get_inert_ratio_raw() Compute inertia ratio of a raw contour

References

- https://en.wikipedia.org/wiki/Image_moment#Central_moments
- https://github.com/opencv/opencv/blob/f81370232a651bdac5042efe907bcaa50a66c487/modules/imgproc/src/moments.cpp#L93

dclab.features.inert_ratio.**get_inert_ratio_raw**(*cont*)

Compute the inertia ratio of a contour

The inertia ratio is computed from the central second order of moments along x (mu20) and y (mu02) via *sqrt(mu20/mu02)*.

Parameters **cont** (*ndarray or list of ndarrays of shape (N,2)*) – A 2D array that holds the contour of an event (in pixels) e.g. obtained using *mm.contour* where *mm* is an instance of *RTDCBase*. The first and second columns of *cont* correspond to the x- and y-coordinates of the contour.

Returns **inert_ratio_raw** – The inertia ratio of the contour

Return type float or ndarray of size N

Notes

The contour moments mu20 and mu02 are computed the same way they are computed in OpenCV's *moments.cpp*.

See also:

get_inert_ratio_cvx() Compute inertia ratio of the convex hull of a contour

References

- https://en.wikipedia.org/wiki/Image_moment#Central_moments
- https://github.com/opencv/opencv/blob/f81370232a651bdac5042efe907bcaa50a66c487/modules/imgproc/src/moments.cpp#L93

dclab.features.volume.**get_volume**(*cont*, *pos_x*, *pos_y*, *pix*)

Calculate the volume of a polygon revolved around an axis

The volume estimation assumes rotational symmetry. Green's theorem and the Gaussian divergence theorem allow to formulate the volume as a line integral.

Parameters

- **cont** (*ndarray or list of ndarrays of shape (N,2)*) – A 2D array that holds the contour of an event [px] e.g. obtained using *mm.contour* where *mm* is an instance of *RTDCBase*. The first and second columns of *cont* correspond to the x- and y-coordinates of the contour.
- **pos_x** (*float or ndarray of length N*) – The x coordinate(s) of the centroid of the event(s) [µm] e.g. obtained using *mm.pos_x*
- **pos_y** (*float or ndarray of length N*) – The y coordinate(s) of the centroid of the event(s) [µm] e.g. obtained using *mm.pos_y*

- **px_um** (*float*) – The detector pixel size in µm. e.g. obtained using: *mm.config["image"]["pix size"]*

Returns **volume** – volume in um^3

Return type float or ndarray

Notes

The computation of the volume is based on a full rotation of the upper and the lower halves of the contour from which the average is then used.

The volume is computed radially from the the center position given by (*pos_x*, *pos_y*). For sufficiently smooth contours, such as densely sampled ellipses, the center position does not play an important role. For contours that are given on a coarse grid, as is the case for RT-DC, the center position must be given.

References

- Halpern et al. [HWT02], chapter 5, Section 5.4
- This is a translation from a Matlab script by Geoff Olynyk.

5.4.3 isoelastics

Isoelastics management

class dclab.isoelastics.**Isoelastics**(*paths=[]*)

add(*isoel*, *col1*, *col2*, *channel_width*, *flow_rate*, *viscosity*, *method*)

Add isoelastics

Parameters

- **isoel** (*list of ndarrays*) – Each list item resembles one isoelastic line stored as an array of shape (N,3). The last column contains the emodulus data.
- **col1** (*str*) – Name of the first feature of all isoelastics (e.g. isoel[0][:,0])
- **col2** (*str*) – Name of the second feature of all isoelastics (e.g. isoel[0][:,1])
- **channel_width** (*float*) – Channel width in µm
- **flow_rate** (*float*) – Flow rate through the channel in µl/s
- **viscosity** (*float*) – Viscosity of the medium in mPa*s
- **method** (*str*) – The method used to compute the isoelastics (must be one of *VALID_METHODS*).

Notes

The following isoelastics are automatically added for user convenience: - isoelastics with *col1* and *col2* interchanged - isoelastics for circularity if deformation was given

static add_px_err(*isoel*, *col1*, *col2*, *px_um*, *inplace=False*)
Undo pixelation correction

Isoelasticity lines are already corrected for pixelation effects as described in

Mapping of Deformation to Apparent Young's Modulus in Real-Time Deformability Cytometry Christoph Herold, arXiv:1704.00572 [cond-mat.soft] (2017) https://arxiv.org/abs/1704.00572.

If the isoealsticity lines are displayed with deformation data that are not corrected, then the lines must be "un"-corrected, i.e. the pixelation error must be added to the lines to match the experimental data.

Parameters

- **isoel** (*list of 2d ndarrays of shape (N, 3)*) – Each item in the list corresponds to one isoelasticity line. The first column is defined by *col1*, the second by *col2*, and the third column is the emodulus.
- **col2** (*col1,*) – Define the fist to columns of each isoelasticity line. One of ["area_um", "circ", "deform"]
- **px_um** (*float*) – Pixel size [µm]

static check_col12(*col1*, *col2*)

static convert(*isoel*, *col1*, *col2*, *channel_width_in*, *channel_width_out*, *flow_rate_in*, *flow_rate_out*, *viscosity_in*, *viscosity_out*, *inplace=False*)
Convert isoelastics in area_um-deform space

Parameters

- **isoel** (*list of 2d ndarrays of shape (N, 3)*) – Each item in the list corresponds to one isoelasticity line. The first column is defined by *col1*, the second by *col2*, and the third column is the emodulus.
- **col2** (*col1,*) – Define the fist to columns of each isoelasticity line. One of ["area_um", "circ", "deform"]
- **channel_width_in** (*float*) – Original channel width [µm]
- **channel_width_out** (*float*) – Target channel width [µm]
- **flow_rate_in** (*float*) – Original flow rate [µl/s]
- **flow_rate_in** – Target flow rate [µl/s]
- **viscosity_in** (*float*) – Original viscosity [mPa*s]
- **viscosity_out** (*float*) – Target viscosity [mPa*s]

Notes

If only the positions of the isoelastics are of interest and not the value of the elastic modulus, then it is sufficient to supply values for the channel width and set the values for flow rate and viscosity to a constant (e.g. 1).

See also:

dclab.features.emodulus.convert() conversion method used

get(*col1*, *col2*, *method*, *channel_width*, *flow_rate=None*, *viscosity=None*, *add_px_err=False*, *px_um=None*)
Get isoelastics

Parameters

- **col1** (*str*) – Name of the first feature of all isoelastics (e.g. isoel[0][:,0])
- **col2** (*str*) – Name of the second feature of all isoelastics (e.g. isoel[0][:,1])
- **method** (*str*) – The method used to compute the isoelastics (must be one of *VALID_METHODS*).
- **channel_width** (*float*) – Channel width in µm
- **flow_rate** (float or *None*) – Flow rate through the channel in µl/s. If set to *None*, the flow rate of the imported data will be used (only do this if you do not need the correct values for elastic moduli).
- **viscosity** (float or *None*) – Viscosity of the medium in mPa*s. If set to *None*, the flow rate of the imported data will be used (only do this if you do not need the correct values for elastic moduli).
- **add_px_err** (*bool*) – If True, add pixelation errors according to C. Herold (2017), https://arxiv.org/abs/1704.00572
- **px_um** (*float*) – Pixel size [µm], used for pixelation error computation

See also:

dclab.features.emodulus.convert() conversion in-between channel sizes and viscosities

dclab.features.emodulus.corrpix_deform_delta() pixelation error that is applied to the deformation data

get_with_rtdcbase(*col1*, *col2*, *method*, *dataset*, *viscosity=None*, *add_px_err=False*)
Convenience method that extracts the metadata from RTDCBase

Parameters

- **col1** (*str*) – Name of the first feature of all isoelastics (e.g. isoel[0][:,0])
- **col2** (*str*) – Name of the second feature of all isoelastics (e.g. isoel[0][:,1])
- **method** (*str*) – The method used to compute the isoelastics (must be one of *VALID_METHODS*).
- **dataset** (dclab.rtdc_dataset.RTDCBase) – The dataset from which to obtain the metadata.
- **viscosity** (float or *None*) – Viscosity of the medium in mPa*s. If set to *None*, the flow rate of the imported data will be used (only do this if you do not need the correct values for elastic moduli).
- **add_px_err** (*bool*) – If True, add pixelation errors according to C. Herold (2017), https://arxiv.org/abs/1704.00572

load_data(*path*)
Load isoelastics from a text file

The text file is loaded with *numpy.loadtxt* and must have three columns, representing the two data columns and the elastic modulus with units defined in *definitions.py*. The file header must have a section defining meta data of the content like so:

> # [...] # # - column 1: area_um # - column 2: deform # - column 3: emodulus # - channel width [um]: 20 # - flow rate [ul/s]: 0.04 # - viscosity [mPa*s]: 15 # - method: analytical # # [...]

Parameters **path** (*str*) – Path to a isoelastics text file

class dclab.isoelastics.**IsoelasticsDict**

dclab.isoelastics.**get_default**()
Return default isoelasticity lines

5.4.4 kde_contours

dclab.kde_contours.**find_contours_level**(*density*, *x*, *y*, *level*, *closed=False*)
Find iso-valued density contours for a given level value

Parameters

- **density** (*2d ndarray of shape (M, N)*) – Kernel density estimate for which to compute the contours
- **x** (*2d ndarray of shape (M, N) or 1d ndarray of size M*) – X-values corresponding to *density*
- **y** (*2d ndarray of shape (M, N) or 1d ndarray of size M*) – Y-values corresponding to *density*
- **level** (*float between 0 and 1*) – Value along which to find contours in *density* relative to its maximum

Returns **contours** – Contours found for the given level value

Return type list of ndarrays of shape (P, 2)

See also:

skimage.measure.find_contours() Contour finding algorithm used

dclab.kde_contours.**get_quantile_levels**(*density*, *x*, *y*, *xp*, *yp*, *q*, *normalize=True*)
Compute density levels for given quantiles by interpolation

For a given 2D density, compute the density levels at which the resulting contours contain the fraction *1-q* of all data points. E.g. for a measurement of 1000 events, all contours at the level corresponding to a quantile of *q=0.95* (95th percentile) contain 50 events (5%).

Parameters

- **density** (*2d ndarray of shape (M, N)*) – Kernel density estimate for which to compute the contours
- **x** (*2d ndarray of shape (M, N) or 1d ndarray of size M*) – X-values corresponding to *density*
- **y** (*2d ndarray of shape (M, N) or 1d ndarray of size M*) – Y-values corresponding to *density*
- **xp** (*1d ndarray of size D*) – Event x-data from which to compute the quantile
- **yp** (*1d ndarray of size D*) – Event y-data from which to compute the quantile
- **q** (*array_like or float between 0 and 1*) – Quantile along which to find contours in *density* relative to its maximum
- **normalize** (*bool*) – Whether output levels should be normalized to the maximum of *density*

Returns **level** – Contours level corresponding to the given quantile

Return type float

Notes

NaN-values events in *xp* and *yp* are ignored.

5.4.5 kde_methods

Kernel Density Estimation methods

dclab.kde_methods.**bin_num_doane**(*a*)
Compute number of bins based on Doane's formula

dclab.kde_methods.**bin_width_doane**(*a*)
Compute accuracy (bin width) based on Doane's formula

References

- https://en.wikipedia.org/wiki/Histogram#Number_of_bins_and_width
- https://stats.stackexchange.com/questions/55134/doanes-formula-for-histogram-binning

dclab.kde_methods.**get_bad_vals**(*x*, *y*)

dclab.kde_methods.**ignore_nan_inf**(*kde_method*)
Ignores nans and infs from the input data

Invalid positions in the resulting density are set to nan.

dclab.kde_methods.**kde_gauss**(*events_x*, *events_y*, *xout=None*, *yout=None*, **args*, ***kwargs*)
Gaussian Kernel Density Estimation

Parameters

- **events_y** (*events_x,*) – The input points for kernel density estimation. Input is flattened automatically.
- **yout** (*xout,*) – The coordinates at which the KDE should be computed. If set to none, input coordinates are used.

Returns **density** – The KDE for the points in (xout, yout)

Return type ndarray, same shape as *xout*

See also:

scipy.stats.gaussian_kde

Notes

This is a wrapped version that ignores nan and inf values.

dclab.kde_methods.**kde_histogram**(*events_x*, *events_y*, *xout=None*, *yout=None*, **args*, ***kwargs*)
Histogram-based Kernel Density Estimation

Parameters

- **events_y** (*events_x,*) – The input points for kernel density estimation. Input is flattened automatically.
- **yout** (*xout,*) – The coordinates at which the KDE should be computed. If set to none, input coordinates are used.

- **bins** (*tuple (binsx, binsy)*) – The number of bins to use for the histogram.

Returns **density** – The KDE for the points in (xout, yout)

Return type ndarray, same shape as *xout*

See also:

numpy.histogram2d scipy.interpolate.RectBivariateSpline

Notes

This is a wrapped version that ignores nan and inf values.

dclab.kde_methods.**kde_multivariate**(*events_x*, *events_y*, *xout=None*, *yout=None*, **args*, ***kwargs*)

Multivariate Kernel Density Estimation

Parameters

- **events_y** (*events_x,*) – The input points for kernel density estimation. Input is flattened automatically.
- **bw** (*tuple (bwx, bwy) or None*) – The bandwith for kernel density estimation.
- **yout** (*xout,*) – The coordinates at which the KDE should be computed. If set to none, input coordinates are used.

Returns **density** – The KDE for the points in (xout, yout)

Return type ndarray, same shape as *xout*

See also:

statsmodels.nonparametric.kernel_density.KDEMultivariate

Notes

This is a wrapped version that ignores nan and inf values.

dclab.kde_methods.**kde_none**(*events_x*, *events_y*, *xout=None*, *yout=None*)

No Kernel Density Estimation

Parameters

- **events_y** (*events_x,*) – The input points for kernel density estimation. Input is flattened automatically.
- **yout** (*xout,*) – The coordinates at which the KDE should be computed. If set to none, input coordinates are used.

Returns **density** – The KDE for the points in (xout, yout)

Return type ndarray, same shape as *xout*

Notes

This method is a convenience method that always returns ones in the shape that the other methods in this module produce.

5.4.6 polygon_filter

exception dclab.polygon_filter.**FilterIdExistsWarning**

exception dclab.polygon_filter.**PolygonFilterError**

class dclab.polygon_filter.**PolygonFilter**(*axes=None*, *points=None*, *inverted=False*, *name=None*, *filename=None*, *fileid=0*, *unique_id=None*)

An object for filtering RTDC data based on a polygonial area

Parameters

- **axes** (*tuple of str*) – The axes/features on which the polygon is defined. The first axis is the x-axis. Example: ("area_um", "deform").
- **points** (*array-like object of shape (N,2)*) – The N coordinates (x,y) of the polygon. The exact order is important.
- **inverted** (*bool*) – Invert the polygon filter. This parameter is overridden if *filename* is given.
- **name** (*str*) – A name for the polygon (optional).
- **filename** (*str*) – A path to a .poly file as create by this classes' *save* method. If *filename* is given, all other parameters are ignored.
- **fileid** (*int*) – Which filter to import from the file (starting at 0).
- **unique_id** (*int*) – An integer defining the unique id of the new instance.

Notes

The minimal arguments to this class are either *filename* OR (*axes*, *points*). If *filename* is set, all parameters are taken from the given .poly file.

static clear_all_filters()
Remove all filters and reset instance counter

copy(*invert=False*)
Return a copy of the current instance

Parameters **invert** (*bool*) – The copy will be inverted w.r.t. the original

filter(*datax*, *datay*)
Filter a set of datax and datay according to *self.points*

static get_instance_from_id(*unique_id*)
Get an instance of the *PolygonFilter* using a unique id

static import_all(*path*)
Import all polygons from a .poly file.

Returns a list of the imported polygon filters

static instace_exists(*unique_id*)
Determine whether an instance with this unique id exists

static point_in_poly(*p*, *poly*)
Determine whether a point is within a polygon area

Uses the ray casting algorithm.

Parameters

- **p** (*float*) – Coordinates of the point
- **poly** (*array_like of shape (N, 2)*) – Polygon (*PolygonFilter.points*)

Returns **inside** – *True*, if point is inside.

Return type bool

Notes

If *p* lies on a side of the polygon, it is defined as

- "inside" if it is on the top or right
- "outside" if it is on the lower or left

static remove(*unique_id*)
Remove a polygon filter from *PolygonFilter.instances*

save(*polyfile*, *ret_fobj=False*)
Save all data to a text file (appends data if file exists).

Polyfile can be either a path to a file or a file object that was opened with the write "w" parameter. By using the file object, multiple instances of this class can write their data.

If *ret_fobj* is *True*, then the file object will not be closed and returned.

static save_all(*polyfile*)
Save all polygon filters

instances = []

dclab.polygon_filter.**get_polygon_filter_names**()
Get the names of all polygon filters in the order of creation

5.4.7 statistics

Statistics computation for RT-DC dataset instances

exception dclab.statistics.**BadMethodWarning**

class dclab.statistics.**Statistics**(*name*, *method*, *req_feature=False*)
A helper class for computing statistics

All statistical methods are registered in the dictionary *Statistics.available_methods*.

get_feature(*ds*, *feat*)
Return filtered feature data

The features are filtered according to the user-defined filters, using the information in *ds._filter*. In addition, all *nan* and *inf* values are purged.

Parameters

- **ds** (dclab.rtdc_dataset.RTDCBase) – The dataset containing the feature
- **feat** (*str*) – The name of the feature; must be a scalar feature

available_methods = {'%-gated': <dclab.statistics.Statistics object>, 'Events': <dcl

dclab.statistics.**flow_rate**(*ds*)
Return the flow rate of an RT-DC dataset

dclab.statistics.**get_statistics**(*ds*, *methods=None*, *features=None*)
Compute statistics for an RT-DC dataset

Parameters

- **ds** (dclab.rtdc_dataset.RTDCBase) – The dataset for which to compute the statistics.
- **methods** (*list of str or None*) – The methods wih which to compute the statistics. The list of available methods is given with *dclab.statistics.Statistics.available_methods.keys()* If set to *None*, statistics for all methods are computed.
- **features** (*list of str*) – Feature name identifiers are defined in *dclab.definitions.scalar_feature_names*. If set to *None*, statistics for all axes are computed.

Returns

- **header** (*list of str*) – The header (feature + method names) of the computed statistics.
- **values** (*list of float*) – The computed statistics.

dclab.statistics.**mode**(*data*)
Compute an intelligent value for the mode

The most common value in experimental is not very useful if there are a lot of digits after the comma. This method approaches this issue by rounding to bin size that is determined by the Freedman–Diaconis rule.

Parameters **data** (*1d ndarray*) – The data for which the mode should be computed.

Returns **mode** – The mode computed with the Freedman-Diaconis rule.

Return type float

CHAPTER 6

Changelog

List of changes in-between dclab releases.

6.1 version 0.14.0

- feat: new command line script for creating a scalar-feature-only dataset with all available ancillary features "dclab-condense"
- enh: enable scalar feature compression for hdf5 export
- docs: fix doc string for dclab-tdms2rtdc (*–include-initial-empty-image* false shown as "enabled by default")

6.2 version 0.13.0

- feat: allow to obtain a mask representing the filtered data with the *ret_mask* kwarg in *RTDCBase.get_downsampled_scatter*
- feat: allow to force-exclude invalid (inf/nan) events when downsampling using the *remove_invalid* keyword argument
- feat: exclude empty initial images in dclab-tdms2rtdc; they may optionally be included with "–include-initial-empty-image"
- feat: new property *RTDCBase.features_innate* (measuerd feature)
- enh: log which ancillary features were computed in dclab-tdms2rtdc (#65)
- enh: improved tdms meta data import (also affects dclab-tdms2rtdc)
- enh: update channel count and samples per event when writing hdf5 data
- enh: dclab-verify-dataset now recognizes invalid tdms data
- enh: several other improvements when reading tdms data

- enh: group meta data in log files (dclab-tdms2rtdc and dclab-join)
- fix: correctly handle hdf5 export when the image or contour columns have incorrect sizes (affects dclab-tdms2rtdc)
- fix: ignore empty configuration values when loading tdms data
- fix: image/contour files were searched recursively instead of only in the directory of the tdms file
- fix: check for precence of "time" feature before using it to correct measurement date and time
- fix: ancillary feature computation for brightness had wrong dependency coded (contour instead of mask)
- fix: ancillary feature computation when contour data is involved lead to error, because *LazyContourList* did not implement *identifier* (see #61)
- ref: remove NoContourDataWarning for tdms file format
- tests: improve dataset checks (#64)

6.3 version 0.12.0

- feat: add command line script for joining measurements "dclab-join" (#57)
- feat: make log files available as *RTDCBase.logs*
- feat: include log data in "dclab-join" and "dclab-tdms2rtdc"
- fix: *features* property for tdms file format falsely contains the keys "contour", "image", "mask", and "trace" when they are actually not available.
- enh: support loading TDMS data using the 'with' statement
- docs: add example for joining measurements
- docs: other minor improvements
- setup: add Python 3.7 wheels for Windows (#62)
- setup: remove Python 2 wheels for macOS

6.4 version 0.11.1

- docs: add example for fluorescence trace visualization
- docs: restructure advanced usage section
- ref: make dclab in principle compatible with imageio>=2.5.0; Dependencies are pinned due to segfaults during testing
- setup: make tdms format support and data export dependency optional; To get the previous behavior, use *pip install dclab[all]*

6.5 version 0.11.0

- feat: compute contours lazily (#61)

6.6 version 0.10.5

- setup: migrate to PEP 517 (pyproject.toml)

6.7 version 0.10.4

- enh: ignore defective feature "aspect" from Shape-In 2.0.6 and 2.0.7
- enh: support loading HDF5 data using the 'with' statement (e.g. *with dclab.new_dataset(rtdc_path) as ds:*)

6.8 version 0.10.3

- fix: add numpy build dependency (setup_requires)

6.9 version 0.10.2

- fix: HDF5-export did not re-enumerate "index" feature

6.10 version 0.10.1

- fix: support nan-valued events when computing quantile levels in submodule *kde_contours*

6.11 version 0.10.0

- BREAKING CHANGE: Change np.meshgrid indexing in *RTDCBase.get_kde_contour* from "xy" to "ij"
- feat: new submodule *kde_contours* for computing kernel density contour lines at specific data percentiles (#60)
- fix: range for contour KDE computation did not always contain end value (*RTDCBase.get_kde_contour*)
- fix: *positions* keyword argument in *RTDCBase.get_kde_scatter* was not correctly scaled in the logarithmic case
- ref: cleanup and document PolygonFilter.point_in_poly
- ref: move skimage code to separate submodule "external"
- ref: drop dependency on statsmodels and move relevant code to submodule "external"

6.12 version 0.9.1

- fix: all-zero features were treated as non-existent due to relic from pre-0.3.3 era
- fix: correct extraction of start time from tdms format (1h offset from local time and measurement duration offset)
- fix: correct extraction of module composition from tdms format (replace "+" with ",")
- enh: add configuration key mapping for tdms format to simplify conversion to hdf5 format (see `fmt_tdms.naming`)

- enh: do not add laser info for unused lasers for tdms format
- enh: dclab-verify-dataset checks for image attribute dtype
- enh: include original software version when exporting to rtdc format

6.13 version 0.9.0

- feat: add new feature: gravitational force, temperature, and ambient temperature
- ref: remove unused *has_key* function in *rtdc_dataset.config.CaseInsensitiveDict*
- setup: require numpy>=1.10.0 because of *equal_nan* argument in *allclose*

6.14 version 0.8.0

- fix: usage of "xor" (^) instead of "or" (|) in statistics
- feat: support *remove_invalid=False* in downsampling.downsample_rand (#27)
- feat: add keyword arguments *xscale* and *yscale* to improve data visualization in *RTDCBase.get_downsampled_scatter*, *RTDCBase.get_kde_contour*, and *RTDCBase.get_kde_scatter* (#55)
- enh: make downsampling code more transparent
- BREAKING CHANGE: low-level downsampling methods refactored
  - downsampling.downsample_grid: removed keyword argument *remove_invalid*, because setting it to *False* makes no sense in this context
  - downsampling.downsample_rand: changed default value of *remove_invalid* to *False*, because this is more objective
  - rename keyword argument *retidx* to *ret_idx*
  - these changes do not affect any other higher level functionalities in *dclab.rtdc_dataset* or in Shape-Out

6.15 version 0.7.0

- feat: add new ancillary feature: principal inertia ratio (#46)
- feat: add new ancillary feature: absolute tilt (#53)
- feat: add computation of viscosity for water (#52)

6.16 version 0.6.3

- fix: channel width not correctly identified for old tdms files

6.17 version 0.6.2

- ci: automate release to PyPI with appveyor and travis-ci

6.18 version 0.6.0

- fix: image export as .avi did not have option to use unfiltered data
- fix: avoid a few unicode gotchas
- feat: use Doane's formula for kernel density estimator defaults (#42)
- docs: usage examples, advanced scripting, and code reference update (#49)

6.19 version 0.5.2

- Migrate from os.path to pathlib (#50)
- fmt_hdf5: Add run index to title

6.20 version 0.5.1

- Setup: add dependencies for statsmodels
- Tests: filter known warnings
- fmt_hdf5: import unknown keys such that "dclab-verify-dataset" can complain about them

6.21 version 0.5.0

- BREAKING CHANGES:
  - definitions.feature_names now contains non-scalar features (inlcuding "image", "contour", "mask", and "trace"). To test for scalar features, use definitions.scalar_feature_names.
  - features bright_* are computed from mask instead of from contour
- Bugfixes:
  - write correct event count in exported hdf5 data files
  - improve implementation of video file handling in fmt_tdms
- add new non-scalar feature "mask" (#48)
- removed configuration key [online_contour]: "bin margin" (#47)
- minor improvements for the tdms file format

6.22 version 0.4.0

- Bugfix: CLI "dclab-tdms2rtdc" did not work for single tdms files (#45)
- update configuration keys:
  - added new keys for [fluorescence]
  - added [setup]: "identifier"
  - removed [imaging]: "exposure time", "flash current"

  - removed [setup]: “temperature”, “viscosity”
- renamed feature “ncells” to “nevents”

6.23 version 0.3.3

- ref: do not import missing features as zeros in fmt_tdms
- CLI:
  - add tdms-to-rtdc converter “dclab-tdms2rtdc” (#36)
  - improve “dclab-verify-dataset” user experience
- Bugfixes:
  - “limit events” filtering must be integer not boolean (#41)
  - Support opening tdms files with capitalized “userDef” column names
  - OSError when trying to open files from repository root

6.24 version 0.3.2

- CLI: add rudimentary dataset checker “dclab-verify-dataset” (#37)
- Add logic to compute parent/root/child event indices of RTDC_Hierarchy
  - Hierarchy children now support contour, image, and traces
  - Hierarchy children now support and remember manual filters (#22)
- Update emodulus look-up table with larger values for deformation
- Implement pixel size correction for emodulus computation
- Allow to add pixelation error to isoelastics (*add_px_err=True*) (#28)
- Bugfixes:
  - Pixel size not read from tdms-based measurements
  - Young’s modulus computation wrong due to faulty FEM simulations (#39)

6.25 version 0.3.1

- Remove all-zero dummy columns from dict format
- Implement hdf5-based RT-DC data reader (#32)
- Implement hdf5-based RT-DC data writer (#33)
- Bugfixes:
  - Automatically fix inverted box filters
  - RTDC_TDMS trace data contained empty arrays when no trace data was present (trace key should not have been accessible)
  - Not possible to get isoelastics for circularity

6.26 version 0.3.0

- New fluorescence crosstalk correction feature recipe (#35)
- New ancillary features “fl1_max_ctc”, “fl2_max_ctc”, “fl3_max_ctc” (#35)
- Add priority for multiple ancillary features with same name
- Bugfixes:
  - Configuration key values were not hashed for ancillary features
- Code cleanup:
  - Refactoring: Put ancillary columns into a new folder module
  - Refactoring: Use the term “feature” consistently
  - Unify trace handling in dclab (#30)
  - Add functions to convert input config data

6.27 version 0.2.9

- Bugfixes:
  - Regression when loading configuration strings containing quotes
  - Parameters missing when loading ShapeIn 2.0.1 tdms data

6.28 version 0.2.8

- Refactor configuration class to support new format (#26)

6.29 version 0.2.7

- New submodule and classes for managing isoelastics
- New ancillary columns “inert_ratio_raw” and “inert_ratio_cvx”
- Bugfixes:
  - Typo when finding contour data files (tdms file format)
- Rrefactoring:
  - “features” submodule with basic methods for ancillary columns

6.30 version 0.2.6

- Return event images as gray scale (#17)
- Bugfixes:
  - Shrink ancillary column size if it exceeds dataset size

  - Generate random RTDCBase.identifier (do not use RTDCBase.hash) to fix problem with identical identifiers for hierarchy children
  - Correctly determine contour data files (tdms file format)
  - Allow contour data indices larger than uint8

6.31 version 0.2.5

- Add ancillary columns “bright_avg” and “bright_sd” (#18, #19)
- Standardize attributes of RTDCBase subclasses (#12)
- Refactoring:
  - New column names and removal of redundant column identifiers (#16)
  - Minor improvements towards PEP8 (e.g. #15)
  - New class for handling filters (#13)
- Bugfixes:
  - Hierarchy child computed all ancillary columns of parent upon checking availability of a column

6.32 version 0.2.4

- Replace OpenCV with imageio
- Add (ancilliary) computation of volume (#11)
- Add convenience methods for *Configuration*
- Refactoring (#8):
  - Separate classes for .tdms, dict-based, and hierarchy datasets
  - Introduce “_events” attribute for stored data
  - Data columns (including image, trace, contour) are accessed via keys instead of attributes.
  - Make space for new hdf5-based file format
  - Introduce ancilliary columns that are computed on-the-fly (new “_ancilliaries” attribute and “ancilliary_columns.py”)

6.33 version 0.2.3

- Add look-up table for elastic modulus (#7)
- Add filtering option “remove invalid events” to remove nan/inf
- Support nan and inf in data analysis
- Improve downsampling performance
- Refactor downsampling methods (#6)

6.34 version 0.2.2

- Add new histogram-based kernel density estimator (#2)
- Refactoring:
  - Configuration fully handled by RTDC_DataSet module (#5)
  - Simplify video export function (#4)
  - Removed "Plotting" configuration key
  - Removed .cfg configuration files

6.35 version 0.2.1

- Support npTDMS 0.9.0
- Add AVI-Export function
- Add lazy submodule for event trace data and rename *RTDC_DataSet.traces* to *RTDC_DataSet.trace*
- Add "Event index" column

6.36 version 0.2.0

- Compute sensible default configuration parameters for KDE estimation and contour plotting
- Speed-up handling of contour text files
- Add support for "User Defined" column in tdms files

6.37 version 0.1.9

- Implement hierarchical instantiation of RTDC_DataSet
- Bugfix: Prevent instances of PolygonFilter that have same id
- Load InertiaRatio and InertiaRatioRaw from tdms files

6.38 version 0.1.8

- Allow to instantiate RTDC_DataSet without a tdms file
- Add statistics submodule
- Bugfixes:
  - Faulty hashing strategy in *RTDC_DataSet.GetDownSampledScatter*
- Code cleanup (renamed methods, cleaned structure)
- Corrections/additions in definitions (fRT-DC)

6.39 version 0.1.7

- Added channel: distance between to first fl. peaks
- Added fluorescence channels: peak position, peak area, number of peaks
- Allow to disable KDE computation
- Add filter array for manual (user-defined) filtering
- Add config parameters for log axis scaling
- Add channels: bounding box x- and y-size
- Bugfixes:
  - cached.py did not handle *None*
  - Limiting number of events caused integer/bool error

6.40 version 0.1.6

- Added *RTDC_DataSet.ExportTSV* for data export
- Bugfixes:
  - Correct determination of video file in RTDCDataSet
  - Fix multivariate KDE computation
  - Contour accuracy for Defo overridden by that of Circ

6.41 version 0.1.5

- Fix regressions with filtering. https://github.com/ZELLMECHANIK-DRESDEN/ShapeOut/issues/43
- Ignore empty columns in .tdms files (#1)
- Moved RTDC_DataSet and PolygonFilter classes to separate files
- Introduce more transparent caching - improves speed in some cases

6.42 version 0.1.4

- Added support for 3-channel fluorescence data (FL-1..3 max/width)

6.43 version 0.1.3

- Fixed minor polygon filter problems.
- Fix a couple of Shape-Out-related issues:
  - https://github.com/ZELLMECHANIK-DRESDEN/ShapeOut/issues/17
  - https://github.com/ZELLMECHANIK-DRESDEN/ShapeOut/issues/20

  - https://github.com/ZELLMECHANIK-DRESDEN/ShapeOut/issues/37
  - https://github.com/ZELLMECHANIK-DRESDEN/ShapeOut/issues/38

6.44 version 0.1.2

- Add support for limiting amount of data points analyzed with the configuration keyword "Limit Events"
- Comments refer to "events" instead of "points" from now on

6.45 version

CHAPTER 7

Bilbliography

CHAPTER 8

Imprint/Impressum

8.1 Imprint and disclaimer

For more information, please refer to the imprint and disclaimer (Impressum und Haftungsausschluss) at https://www.zellmechanik.com/Imprint.html.

8.2 Privacy policy

This documentation is hosted on https://readthedocs.org/ whose privacy policy applies.

CHAPTER 9

Indices and tables

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Bibliography

[HWT02] David Halpern, Howard B. Wilson, and Louis H. Turcotte. Gauss integration with geometric property applications. In *Advanced Mathematics and Mechanics Applications Using MATLAB, Third Edition*. Chapman & Hall, sep 2002. doi:10.1201/9781420035445.ch5.

[Her17] Christoph Herold. Mapping of Deformation to Apparent Young's Modulus in Real-Time Deformability Cytometry. *ArXiv e-prints 1704.00572 [cond-mat.soft]*, 2017. arXiv:1704.00572v1.

[KSW78] Joseph Kestin, Mordechai Sokolov, and William A. Wakeham. Viscosity of liquid water in the range -8\hspace 0.167em°C to 150\hspace 0.167em°C. *Journal of Physical and Chemical Reference Data*, 7(3):941–948, jul 1978. doi:10.1063/1.555581.

[MOG+15] Alexander Mietke, Oliver Otto, Salvatore Girardo, Philipp Rosendahl, Anna Taubenberger, Stefan Golfier, Elke Ulbricht, Sebastian Aland, Jochen Guck, and Elisabeth Fischer-Friedrich. Extracting Cell Stiffness from Real-Time Deformability Cytometry: Theory and Experiment. *Biophysical Journal*, 109(10):2023–2036, nov 2015. doi:10.1016/j.bpj.2015.09.006.

[MMM+17] M. Mokbel, D. Mokbel, A. Mietke, N. Träber, S. Girardo, O. Otto, J. Guck, and S. Aland. Numerical Simulation of Real-Time Deformability Cytometry To Extract Cell Mechanical Properties. *ACS Biomaterials Science & Engineering*, 3(11):2962–2973, jan 2017. doi:10.1021/acsbiomaterials.6b00558.

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