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# **dclab Documentation**

***Release 0.23.0***

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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 0.23.0.





### 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If you are working with the outdated `tdms` file format, you have to specify the extra key `[tdms]`, i.e. `pip install dclab[tdms]` or `pip install .[tdms]`.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*.



---

## Command-line interface

---

### 2.1 dclab-compress

Create a compressed version of an .rtdc file. This can be used for saving disk space. The data generated during an experiment is usually not compressed.

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

**required arguments:**

- INPUT Input path (.rtdc file)
- OUTPUT Output path (.rtdc file)

### 2.2 dclab-condense

Reduce an RT-DC measurement to its scalar-only features (i.e. without *contour*, *image*, *mask*, or *trace*). All available ancillary features are computed.

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

**required arguments:**

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

### 2.3 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 ...]]
```

**required arguments:**

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

## 2.4 dclab-repack

Repack an .rtdc file. The difference to dclab-compress is that no logs are added. Other logs can optionally be stripped away. Repacking also gets rid of old clutter data (e.g. previous metadata stored in the HDF5 file).

```
usage: dclab-repack [-h] [--strip-logs] INPUT OUTPUT
```

**required arguments:**

- INPUT Input path (.rtdc file)
- OUTPUT Output path (.rtdc file)

**optional arguments:**

- `--strip-logs` (*disabled by default*) Do not copy any logs to the output file.

## 2.5 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
```

**required 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.

## 2.6 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
```

### required arguments:

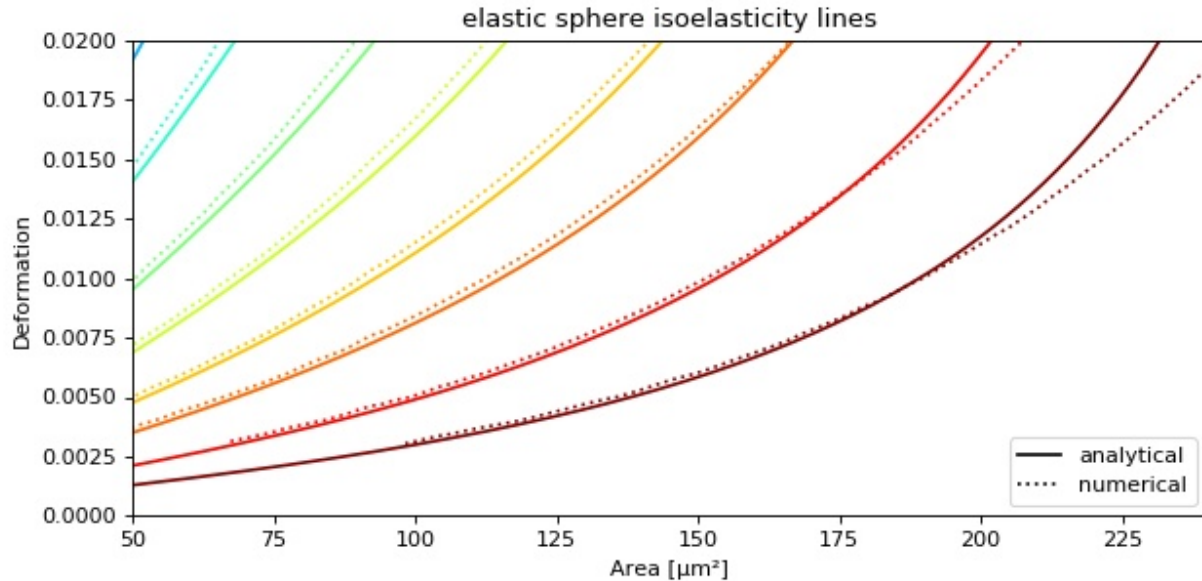
- `PATH` Path to experimental dataset





### 3.1 Plotting isoelastics

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



isoelastics.py

```
1 import matplotlib.pyplot as plt
2 import matplotlib.lines as mlines
3 from matplotlib import cm
4 import numpy as np
5
```

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```

6 import dclab
7
8 # parameters for isoelastics
9 kwargs = {"col1": "area_um", # x-axis
10           "col2": "deform", # y-axis
11           "channel_width": 20, # [um]
12           "flow_rate": 0.04, # [ul/s]
13           "viscosity": 15, # [mPa s]
14           "add_px_err": False # no pixelation error
15           }
16
17 isos = dclab.isoelastics.get_default()
18 analy = isos.get(method="analytical", **kwargs)
19 numer = isos.get(method="numerical", **kwargs)
20
21 plt.figure(figsize=(8, 4))
22 ax = plt.subplot(111, title="elastic sphere isoelasticity lines")
23 colors = [cm.get_cmap("jet")(x) for x in np.linspace(0, 1, len(analy))]
24 for aa, nn, cc in zip(analy, numer, colors):
25     ax.plot(aa[:, 0], aa[:, 1], color=cc)
26     ax.plot(nn[:, 0], nn[:, 1], color=cc, ls=":")
27
28 line = mlines.Line2D([], [], color='k', label='analytical')
29 dotted = mlines.Line2D([], [], color='k', ls=":", label='numerical')
30 ax.legend(handles=[line, dotted])
31
32 ax.set_xlim(50, 240)
33 ax.set_ylim(0, 0.02)
34 ax.set_xlabel(dclab.dfn.feature_name2label["area_um"])
35 ax.set_ylabel(dclab.dfn.feature_name2label["deform"])
36
37 plt.tight_layout()
38 plt.show()

```

## 3.2 Dataset overview plot

This example demonstrates basic data visualization with dclab and matplotlib. To run this script, download the reference dataset *calibration\_beads.rtdc* [RHMG19] and place it in the same directory.

You will find more examples in the *advanced usage* section of this documentation.

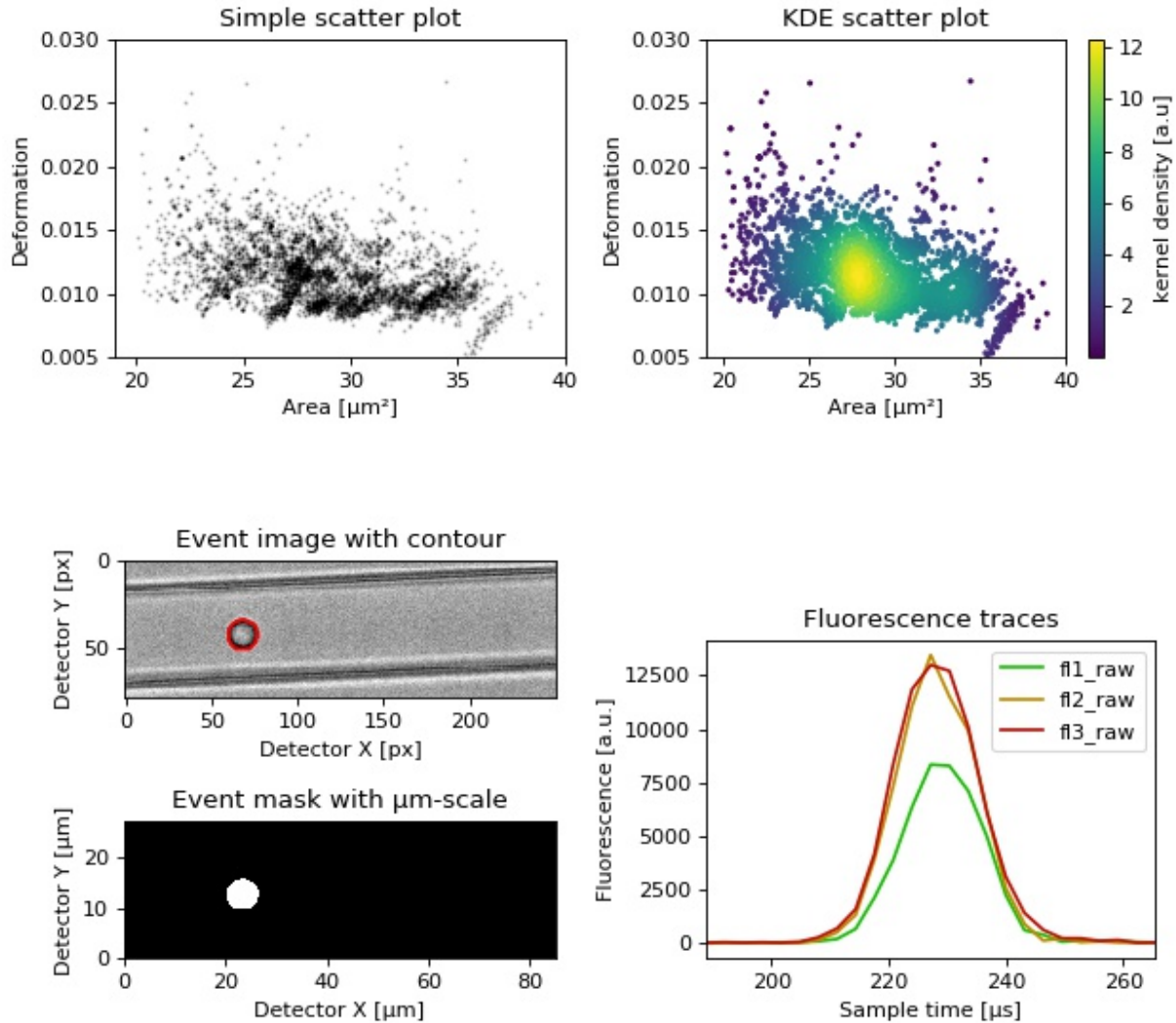
overview\_plot.py

```

1 import matplotlib.pyplot as plt
2 import numpy as np
3
4 import dclab
5
6 # Dataset to display
7 DATASET_PATH = "calibration_beads.rtdc"
8 # Features for scatter plot
9 SCATTER_X = "area_um"
10 SCATTER_Y = "deform"
11 # Event index to display
12 EVENT_INDEX = 100

```

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```

13
14 xlabel = dclab.dfn.feature_name2label[SCATTER_X]
15 ylabel = dclab.dfn.feature_name2label[SCATTER_Y]
16
17 ds = dclab.new_dataset(DATASET_PATH)
18
19 fig = plt.figure(figsize=(8, 7))
20
21
22 ax1 = plt.subplot(221, title="Simple scatter plot")
23 ax1.plot(ds[SCATTER_X], ds[SCATTER_Y], "o", color="k", alpha=.2, ms=1)
24 ax1.set_xlabel(xlabel)
25 ax1.set_ylabel(ylabel)
26 ax1.set_xlim(19, 40)
27 ax1.set_ylim(0.005, 0.03)
28
29 ax2 = plt.subplot(222, title="KDE scatter plot")
30 sc = ax2.scatter(ds[SCATTER_X], ds[SCATTER_Y],
31                 c=ds.get_kde_scatter(xax=SCATTER_X,
32                                     yax=SCATTER_Y,
33                                     kde_type="multivariate"),
34                 s=3)
35 plt.colorbar(sc, label="kernel density [a.u]", ax=ax2)
36 ax2.set_xlabel(xlabel)
37 ax2.set_ylabel(ylabel)
38 ax2.set_xlim(19, 40)
39 ax2.set_ylim(0.005, 0.03)
40
41 ax3 = plt.subplot(425, title="Event image with contour")
42 ax3.imshow(ds["image"][EVENT_INDEX], cmap="gray")
43 ax3.plot(ds["contour"][EVENT_INDEX][:, 0],
44         ds["contour"][EVENT_INDEX][:, 1],
45         c="r")
46 ax3.set_xlabel("Detector X [px]")
47 ax3.set_ylabel("Detector Y [px]")
48
49 ax4 = plt.subplot(427, title="Event mask with  $\mu\text{m}$ -scale")
50 pxsize = ds.config["imaging"]["pixel size"]
51 ax4.imshow(ds["mask"][EVENT_INDEX],
52           extent=[0, ds["mask"].shape[2] * pxsize,
53                  0, ds["mask"].shape[1] * pxsize],
54           cmap="gray")
55 ax4.set_xlabel("Detector X [ $\mu\text{m}$ ]")
56 ax4.set_ylabel("Detector Y [ $\mu\text{m}$ ]")
57
58 ax5 = plt.subplot(224, title="Fluorescence traces")
59 flsamples = ds.config["fluorescence"]["samples per event"]
60 flrate = ds.config["fluorescence"]["sample rate"]
61 fltime = np.arange(flsamples) / flrate * 1e6
62 # here we plot "f1?_raw"; you may also plot "f1?_med"
63 ax5.plot(fltime, ds["trace"]["f11_raw"][EVENT_INDEX],
64         c="#15BF00", label="f11_raw")
65 ax5.plot(fltime, ds["trace"]["f12_raw"][EVENT_INDEX],
66         c="#BF8A00", label="f12_raw")
67 ax5.plot(fltime, ds["trace"]["f13_raw"][EVENT_INDEX],
68         c="#BF0C00", label="f13_raw")
69 ax5.legend()

```

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```
70 ax5.set_xlim(ds["fll_pos"][EVENT_INDEX] - 2*ds["fll_width"][EVENT_INDEX],  
71             ds["fll_pos"][EVENT_INDEX] + 2*ds["fll_width"][EVENT_INDEX])  
72 ax5.set_xlabel("Event time [μs]")  
73 ax5.set_ylabel("Fluorescence [a.u.]")  
74  
75 plt.tight_layout()  
76  
77 plt.show()
```



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 [ $\mu\text{m}^2$ ]
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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Table 1 – continued from previous page

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 [ $\mu$ s]
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 [ $\mu$ s]
fl1_width	FL-1 width [ $\mu$ s]
fl2_area	FL-2 area of peak [a.u.]
fl2_dist	FL-2 distance between two first peaks [ $\mu$ s]
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 [ $\mu$ s]
fl2_width	FL-2 width [ $\mu$ s]
fl3_area	FL-3 area of peak [a.u.]
fl3_dist	FL-3 distance between two first peaks [ $\mu$ s]
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 [ $\mu$ s]
fl3_width	FL-3 width [ $\mu$ s]
frame	Video frame number
g_force	Gravitational force in multiples of g
index	Event index (Dataset)
index_online	Event index (Online)
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 [ $\mu$ m]
pos_y	Position lateral in channel [ $\mu$ m]
size_x	Bounding box size x [ $\mu$ m]
size_y	Bounding box size y [ $\mu$ m]
temp	Chip temperature [ $^{\circ}$ C]
temp_amb	Ambient temperature [ $^{\circ}$ 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

Continued on next page



Table 1 – continued from previous page

scalar features	description [units]
userdef9	User defined 9
volume	Volume [ $\mu\text{m}^3$ ]

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

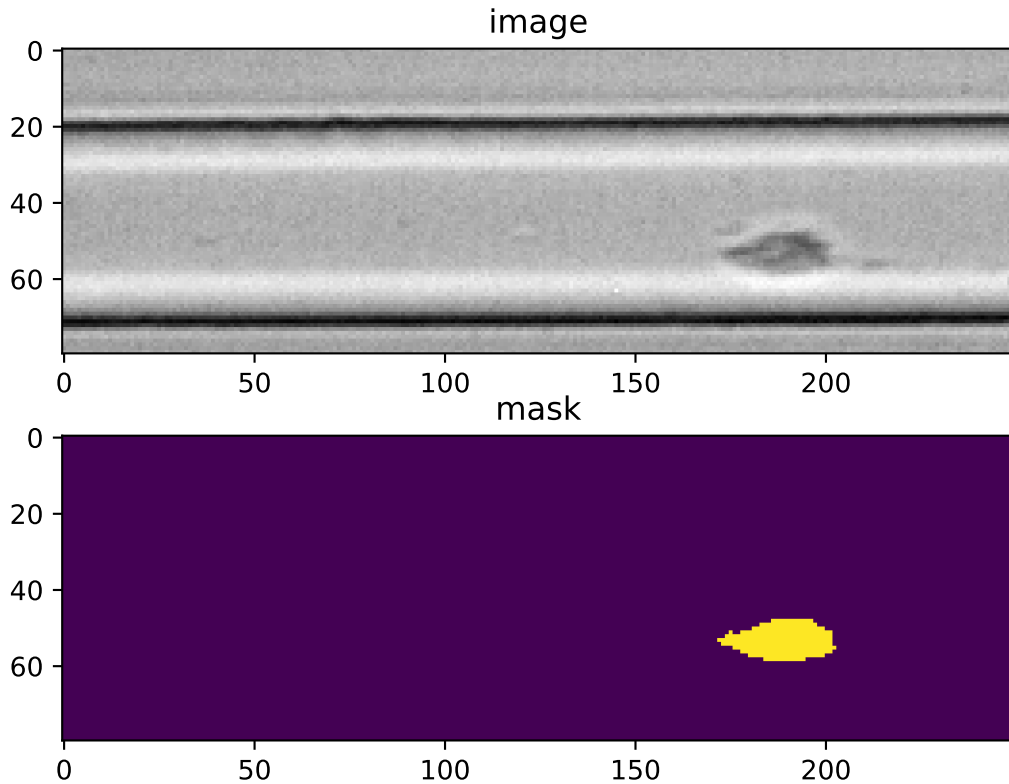
**Example:** deformation vs. area plot

```
import matplotlib.pyplot 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.pyplot 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	<i>fbool</i>	Enable filtering
hierarchy parent	<i>str</i>	Hierarchy parent of the dataset
limit events	<i>fint</i>	Upper limit for number of filtered events
polygon filters	<i>fintlist</i>	Polygon filter indices
remove invalid events	<i>fbool</i>	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 [ $\mu\text{m}^2$ ] below this value
area_um max	Exclude events with area [ $\mu\text{m}^2$ ] above this value
aspect max	Exclude events with an aspect ratio above this value
...	...

**Example:** excluding events with large deformation

```
import matplotlib.pyplot 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"])

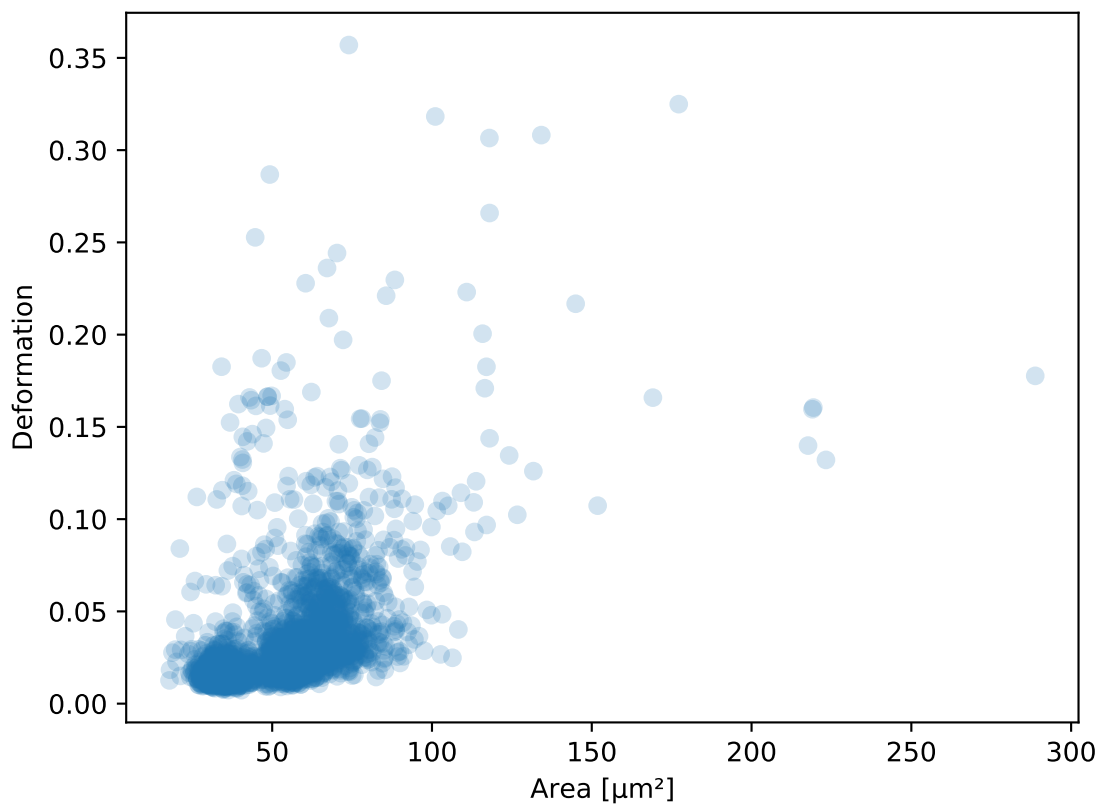
plt.tight_layout()
plt.show()
```

**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.pyplot 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()
```





## 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	<i>str</i>	Date of measurement ('YYYY-MM-DD')
event count	<i>fint</i>	Number of recorded events
run index	<i>fint</i>	Index of measurement run
sample	<i>str</i>	Measured sample or user-defined reference
time	<i>str</i>	Start time of measurement ('HH:MM:SS[.S]')

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

fmt_tdms	parsed	description [units]
video frame offset	<i>fint</i>	Missing events at beginning of video

imaging	parsed	description [units]
flash device	<i>str</i>	Light source device type
flash duration	<i>float</i>	Light source flash duration [ $\mu$ s]
frame rate	<i>float</i>	Imaging frame rate [Hz]
pixel size	<i>float</i>	Pixel size [ $\mu$ m]
roi position x	<i>float</i>	Image x coordinate on sensor [px]
roi position y	<i>float</i>	Image y coordinate on sensor [px]
roi size x	<i>fint</i>	Image width [px]
roi size y	<i>fint</i>	Image height [px]

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

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

setup	parsed	description [units]
channel width	<i>float</i>	Width of microfluidic channel [ $\mu\text{m}$ ]
chip region	<i>lcstr</i>	Imaged chip region (channel or reservoir)
flow rate	<i>float</i>	Flow rate in channel [ $\mu\text{L/s}$ ]
flow rate sample	<i>float</i>	Sample flow rate [ $\mu\text{L/s}$ ]
flow rate sheath	<i>float</i>	Sheath flow rate [ $\mu\text{L/s}$ ]
identifier	<i>str</i>	Unique setup identifier
medium	<i>str</i>	Medium used
module composition	<i>str</i>	Comma-separated list of modules used
software version	<i>str</i>	Acquisition software with version
temperature	<i>float</i>	Mean chip temperature [ $^{\circ}\text{C}$ ]

**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 f12	float	Fluorescence crosstalk, channel 1 to 2
crosstalk f13	float	Fluorescence crosstalk, channel 1 to 3
crosstalk f21	float	Fluorescence crosstalk, channel 2 to 1
crosstalk f23	float	Fluorescence crosstalk, channel 2 to 3
crosstalk f31	float	Fluorescence crosstalk, channel 3 to 1
crosstalk f32	float	Fluorescence crosstalk, channel 3 to 2
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_3cb9f7d'

# 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
Out[21]: True

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

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

# accessing the measurement configuration
In [24]: ds.config.keys()
Out[24]: dict_keys(['filtering', 'experiment', 'imaging', 'online_contour', 'setup'])

In [25]: ds.config["experiment"]
Out[25]:
{'date': '2017-07-16',
```

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```
'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"]
Out[26]: 'mm-hdf5_3cb9f7d'
```

## 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,
'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

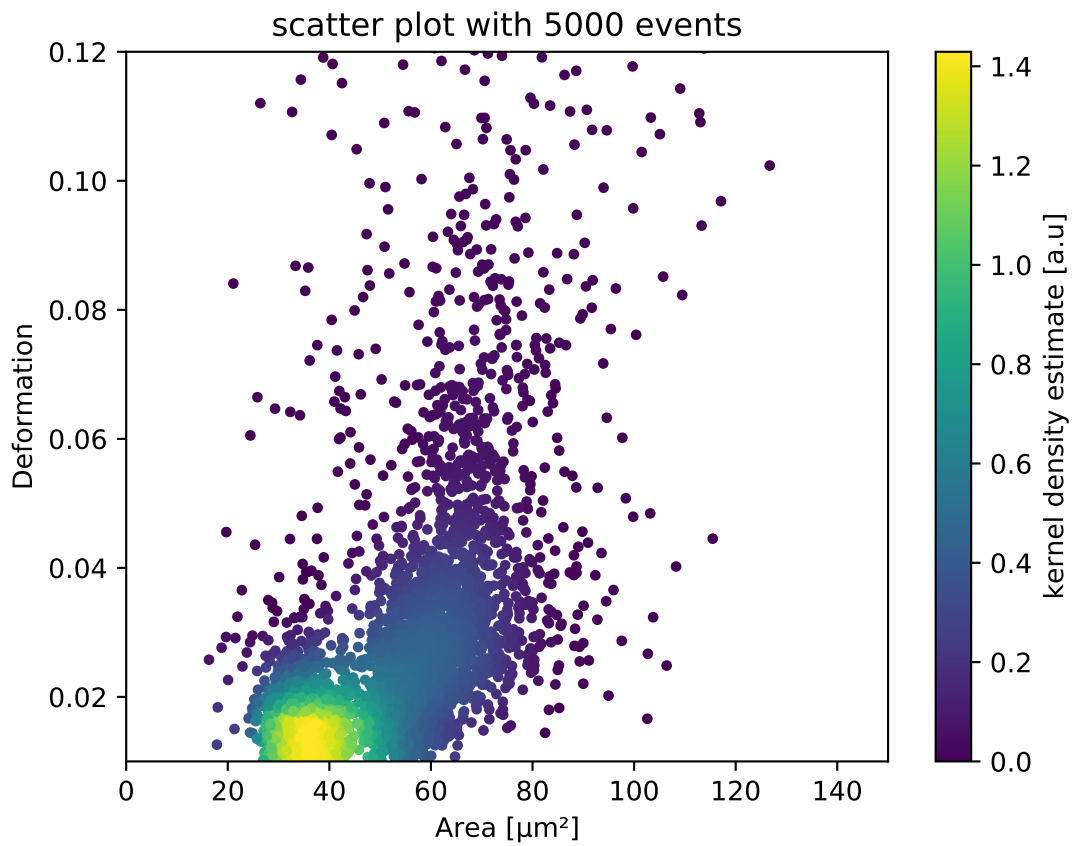
The KDE of the events in a 2D scatter plot can be used to colorize events according to event density using the `RTDCBase.get_kde_scatter` function.

```
import matplotlib.pyplot 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=".")
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

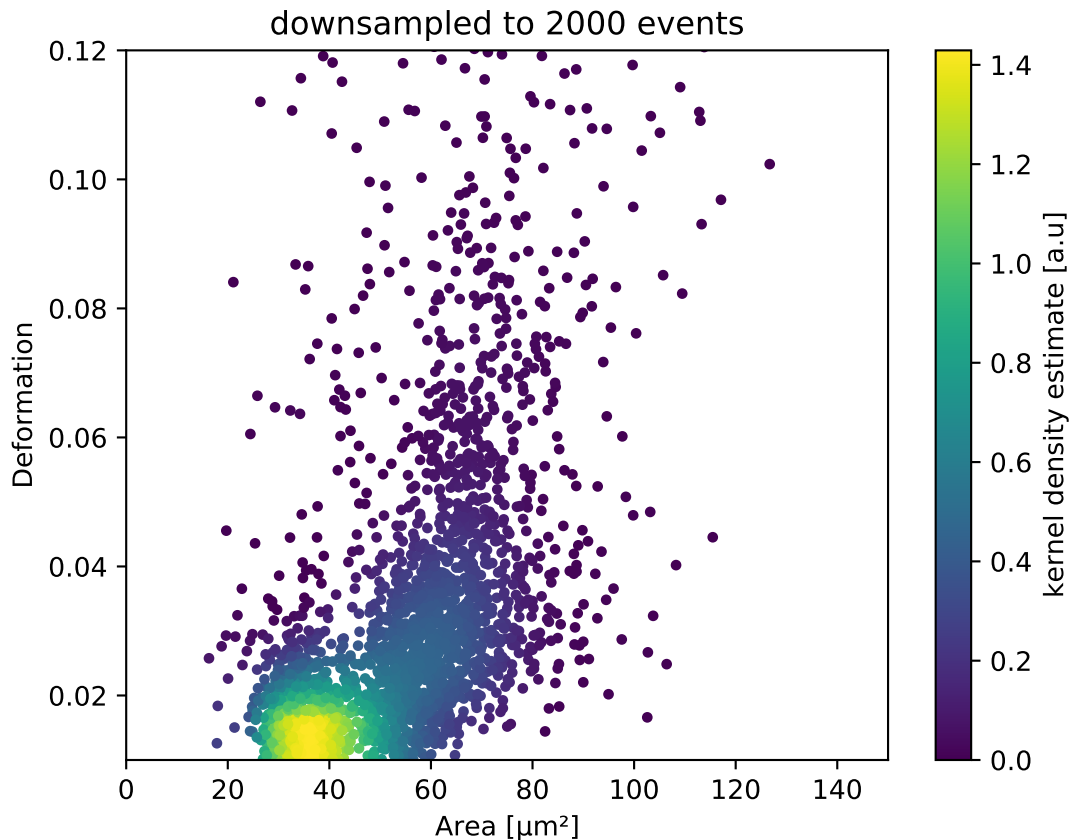
To reduce the complexity of the plot (e.g. when exporting to scalable vector graphics (.svg)), the plotted events can be downsampled by removing events from high-event-density regions. The number of events plotted is reduced but the



resulting visualization is almost indistinguishable from the one above.

```
import matplotlib.pyplot 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=".")
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.pyplot 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=".")

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

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

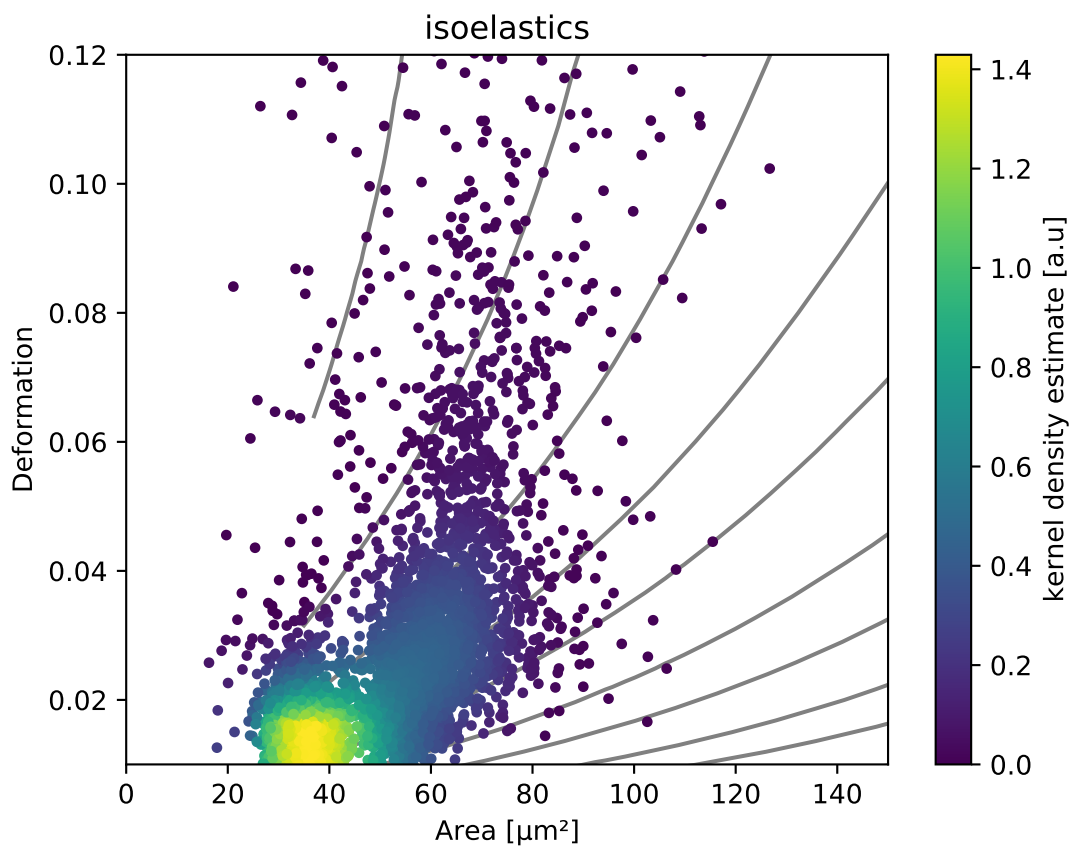
Contour plots are commonly used to compare the kernel density between measurements. Kernel density estimates (on a grid) for contour plots can be computed with the function *RTDCBase.get\_kde\_contour*. In addition, it is possible to compute contours at data percentiles using *dclab.kde\_contours.get\_quantile\_levels()*.

```
import matplotlib.pyplot 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)
```

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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)
# 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.pyplot as plt
import dclab
ds = dclab.new_dataset("data/example.rtdc")

```

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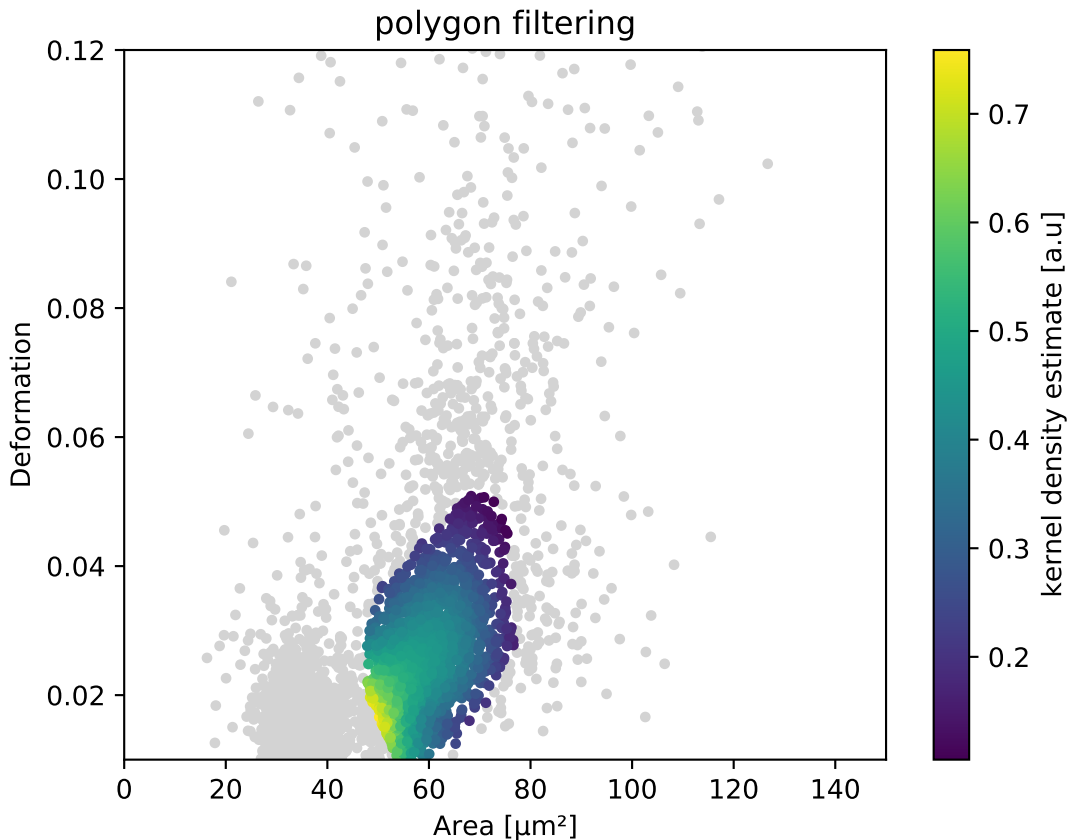
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```

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=".")
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']

# 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.pyplot 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
```

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```

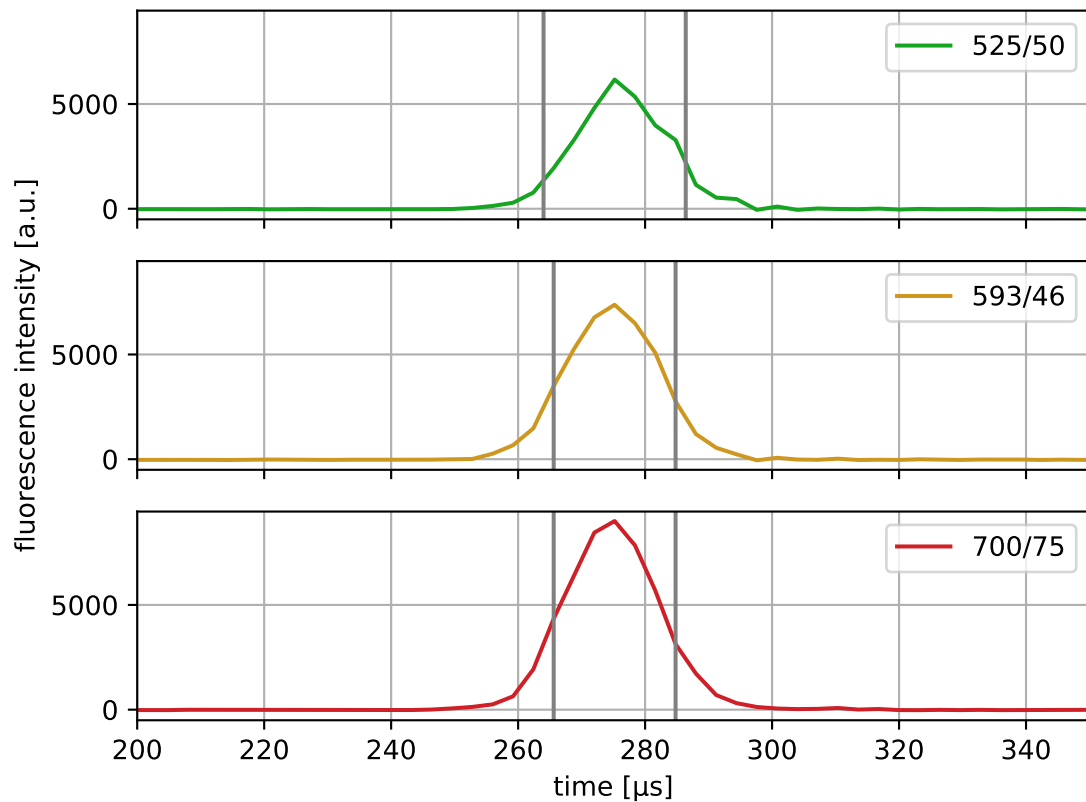
axes[0].axvline(ds["fl1_pos"][idx] + ds["fl1_width"][idx]/2, color="gray")
axes[0].axvline(ds["fl1_pos"][idx] - ds["fl1_width"][idx]/2, color="gray")
axes[1].axvline(ds["fl2_pos"][idx] + ds["fl2_width"][idx]/2, color="gray")
axes[1].axvline(ds["fl2_pos"][idx] - ds["fl2_width"][idx]/2, color="gray")
axes[2].axvline(ds["fl3_pos"][idx]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

# 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  $\mu\text{s}$  using the meta data stored in `ds.config["fluorescence"]`. Also, notice how the scalar features are used for plotting the peak width.

## 4.5 Young's modulus computation

The computation of the Young's modulus uses a look-up table that was derived from finite elements methods according to [MMM+17]. The computation 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].

Since the Young's modulus is model-dependent, it is not made available right away as an *ancillary feature* (in contrast to e.g. event volume or average event brightness).

```
In [1]: import dclab

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

# "False", because we have not set any additional information.
In [3]: "emodulus" in ds
Out[3]: False
```

Additional information is required. There are three scenarios:

- A) The viscosity/Young's modulus is computed individually from the chip temperature for **each** event. Required information:
  - The *temp* feature which holds the chip temperature of each event
  - The configuration key [calculation]: 'emodulus medium'
  - The configuration key [calculation]: 'emodulus model'
- B) Set a global viscosity. Use this if you have measured the viscosity of your medium (and know all there is to know about shear thinning [Her17]). Required information:
  - The configuration key [calculation]: 'emodulus model'
  - The configuration key [calculation]: 'emodulus viscosity'
- C) Compute the Young's modulus using the viscosities of known media.
  - The configuration key [calculation]: 'emodulus medium'
  - The configuration key [calculation]: 'emodulus model'
  - The configuration key [calculation]: 'emodulus temperature'

Note that if 'emodulus temperature' is given, then this temperature is used, even if the *temp* feature exists (scenario A).

The key 'emodulus model' currently (2019) only supports the value 'elastic sphere'. The key 'emodulus medium' must be one of the supported media defined in `dclab.features.emodulus_viscosity.KNOWN_MEDIA` and can be taken from [setup]: 'medium'. The key 'emodulus temperature' is the mean chip temperature and could possibly be available in [setup]: 'temperature'.

```
import matplotlib.pyplot as plt

import dclab

ds = dclab.new_dataset("data/example.rtdc")

# Add additional information. We cannot go for (A), because this example
# does not have the temperature feature (`"temp" not in ds`). We go for
# (C), because the beads were measured in a known medium.
```

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```

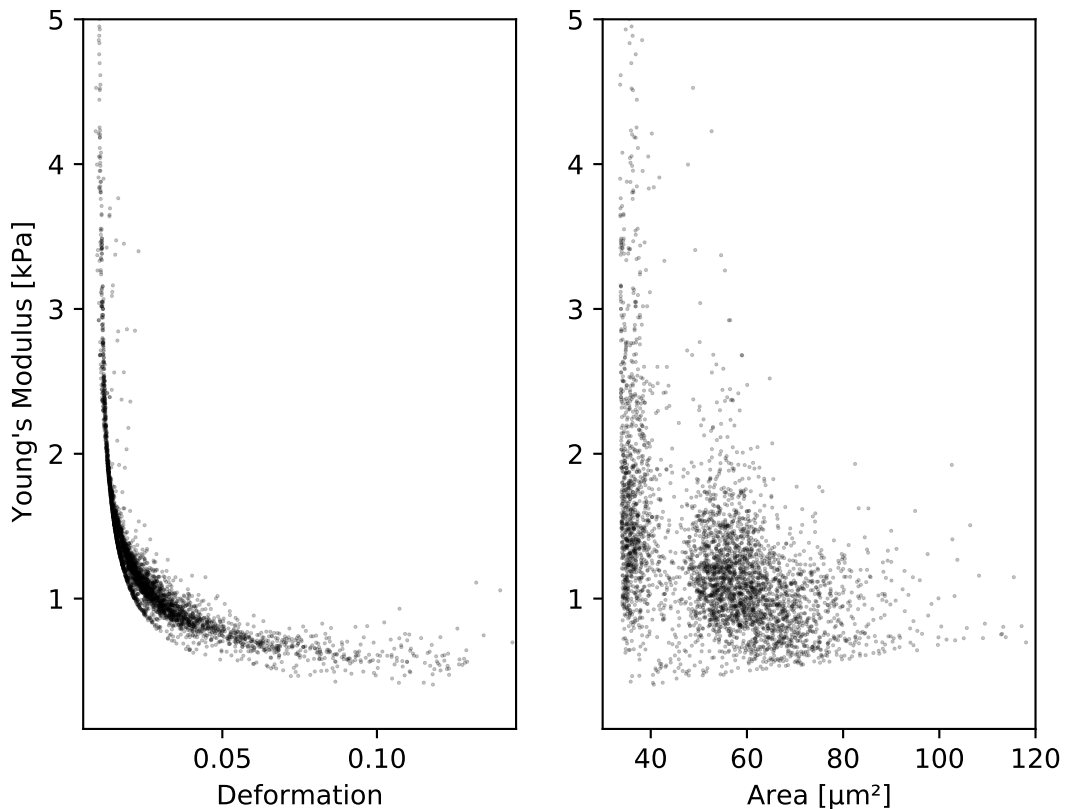
ds.config["calculation"]["emodulus medium"] = ds.config["setup"]["medium"]
ds.config["calculation"]["emodulus model"] = "elastic sphere"
ds.config["calculation"]["emodulus temperature"] = 23.0 # a guess

# Plot a few features
ax1 = plt.subplot(121)
ax1.plot(ds["deform"], ds["emodulus"], ".", color="k", markersize=1, alpha=.3)
ax1.set_ylim(0.1, 5)
ax1.set_xlim(0.005, 0.145)
ax1.set_xlabel(dclab.dfn.feature_name2label["deform"])
ax1.set_ylabel(dclab.dfn.feature_name2label["emodulus"])

ax2 = plt.subplot(122)
ax2.plot(ds["area_um"], ds["emodulus"], ".", color="k", markersize=1, alpha=.3)
ax2.set_ylim(0.1, 5)
ax2.set_xlim(30, 120)
ax2.set_xlabel(dclab.dfn.feature_name2label["area_um"])

plt.show()

```



## 4.6 Accessing DCOR data

The [deformability cytometry open repository \(DCOR\)](#) allows you to upload and access RT-DC datasets online (internet connection required). The advantage is that you can access parts of the dataset (e.g. just two features) without downloading the entire data file (which includes image, contour, and traces information).

### 4.6.1 Public data

When you would previously download an entire dataset and do

```
import dclab
ds = dclab.new_dataset("/path/to/Downloads/calibration_beads.rtdc")
```

you can now skip the download and use the identifier (id) of a DCOR resource like so:

```
import dclab
ds = dclab.new_dataset("fb719fb2-bd9f-817a-7d70-f4002af916f0")
```

To determine the DCOR resource id, go to <https://dcor.mpl.mpg.de>, find the resource you are interested in, scroll down to the bottom, and copy the value from the **id** (not *package id* or *revision id*) field in (*Additional Information*). The DCOR format is documented in *DCOR (online) format*.

### 4.6.2 Private data

If you want to access private data, you need to pass your personal API Key:

```
import dclab
ds = dclab.new_dataset("fb719fb2-bd9f-817a-7d70-f4002af916f0",
                       api_key="XXXX-YYYY-ZZZZ")
```

You can find your API Key in the left panel of your profile page when logged in at <https://dcor.mpl.mpg.de>.

Alternatively, you can also set the API Key globally using

```
import dclab
from dclab.rtdc_dataset.fmt_dcor import APIHandler
APIHandler.add_api_key("XXXX-YYYY-ZZZZ")
ds = dclab.new_dataset("fb719fb2-bd9f-817a-7d70-f4002af916f0")
```



## 5.1 module-level methods

`dclab.new_dataset` (*data*, *identifier=None*, *\*\*kwargs*)

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)
  - DCOR resource URL
- **identifier** (*str*) – A unique identifier for this dataset. If set to *None* an identifier is generated.
- **kwargs** (*dict*) – Additional parameters passed to the *RTDCBase* subclass

**Returns** **dataset** – A new dataset instance

**Return type** subclass of `dclab.rtdc_dataset.RTDCBase`

## 5.2 global definitions

These definitions 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 'int'>, <function fintlist>: <class 'list'>, <function lcstr>: <class 'str'>}`  
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 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, ynew** (1d ndarray of length *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 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 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

**static get\_kde\_spacing** (*a*, *scale*=‘linear’, *method*=<function bin\_width\_doane>,  
*method\_kw*={}, *feat*=‘undefined’, *ret\_scaled*=False)  
Convenience function for computing the contour spacing

#### Parameters

- **a** (*ndarray*) – feature data
- **scale** (*str*) – how the data should be scaled (“log” or “linear”)
- **method** (*callable*) – KDE method to use (see *kde\_methods* submodule)
- **method\_kw** (*dict*) – keyword arguments to *method*
- **feat** (*str*) – feature name for debugging
- **ret\_scale** (*bool*) – whether or not to return the scaled array of *a*

**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

**reset\_filter** ()

Reset the current filter

**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

**features\_loaded**

All features including ancillary that have been computed

## Notes

Features that are computationally cheap to compute are always included. They are defined in *dclab.rtdc\_dataset.ancillaries.FEATURES\_RAPID*.

**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 DCOR (online) format

**class** *dclab.rtdc\_dataset.RTDC\_DCOR* (*url*, *use\_ssl=None*, *host='dcor.mpl.mpg.de'*, *api\_key=""*,  
\**args*, \*\**kwargs*)

Wrap around the DCOR API

### Parameters

- **url** (*str*) – Full URL or resource identifier; valid values are
  - <https://dcor.mpl.mpg.de/api/3/action/dcserv?id=b1404eb5-f661-4920-be79-5ff4e85915d5>
  - [dcor.mpl.mpg.de/api/3/action/dcserv?id=b1404eb5-f661-4920-be79-5ff4e85915d5](https://dcor.mpl.mpg.de/api/3/action/dcserv?id=b1404eb5-f661-4920-be79-5ff4e85915d5)

- b1404eb5-f661-4920-be79-5ff4e85915d5
- **use\_ssl** (*bool*) – Set this to False to disable SSL (should only be used for testing). Defaults to None (does not force SSL if the URL starts with “<http://>”).
- **host** (*str*) – The host machine (used if the host is not given in *url*)
- **api\_key** (*str*) – API key to access private resources
- **\*args** – Arguments for *RTDCBase*
- **\*\*kwargs** – Keyword arguments for *RTDCBase*

**path**

Full URL to the DCOR resource

Type *str*

**static get\_full\_url** (*url*, *use\_ssl*, *host*)

Return the full URL to a DCOR resource

**Parameters**

- **url** (*str*) – Full URL or resource identifier; valid values are
  - <https://dcor.mpl.mpg.de/api/3/action/dcserv?id=caab96f6-df12-4299-aa2e-089e390aafd5>
  - [dcor.mpl.mpg.de/api/3/action/dcserv?id=caab96f6-df12-4299-aa2e-089e390aafd5](https://dcor.mpl.mpg.de/api/3/action/dcserv?id=caab96f6-df12-4299-aa2e-089e390aafd5)
  - [caab96f6-df12-4299-aa2e-089e390aafd5](https://dcor.mpl.mpg.de/api/3/action/dcserv?id=caab96f6-df12-4299-aa2e-089e390aafd5)
- **use\_ssl** (*bool*) – Set this to False to disable SSL (should only be used for testing). Defaults to None (does not force SSL if the URL starts with “<http://>”).
- **host** (*str*) – Use this host if it is not specified in *url*

**hash**

Hash value based on file name and content

**class** `dclab.rtdc_dataset.fmt_dcor.APIHandler` (*url*, *api\_key*=’’)

Handles the DCOR api with caching for simple queries

**classmethod** **add\_api\_key** (*api\_key*)

Add an API Key to the base class

When accessing the DCOR API, all available API Keys are used to access a resource (trial and error).

**api\_keys** = []

DCOR API Keys in the current session

**cache\_queries** = ['metadata', 'size', 'feature\_list', 'valid']

these are cached to minimize network usage

### 5.3.3 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*

### 5.3.4 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 `can_open` (*h5path*)

Check whether a given file is in the .rtdc file format

#### static `parse_config` (*h5path*)

Parse the RT-DC configuration of an hdf5 file

#### hash

Hash value based on file name and content

`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

### 5.3.5 Hierarchy format

**class** `dclab.rtdc_dataset.RTDC_Hierarchy` (*hparent*, *apply\_filter=True*, \*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
- **apply\_filter** (*bool*) – Whether to apply the filter during instantiation; If set to *False*, *apply\_filter* must be called manually.
- **\*args** – Arguments for *RTDCBase*
- **\*\*kwargs** – Keyword arguments for *RTDCBase*

#### hparent

Hierarchy parent of this instance

Type *RTDCBase*

### 5.3.6 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*.

### 5.3.7 config

**class** `dclab.rtdc_dataset.config.Configuration` (*files=[]*, *cfg={}*, *disable\_checks=False*)  
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
- **disable\_checks** (*bool*) – Set this to True if you want to avoid checking against section and key names defined in *dclab.definitions* using *verify\_section\_key()*. This avoids excess warning messages when loading data from configuration files not generated by dclab.



**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** ConfigurationDict

### 5.3.8 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, meta\_data={}, 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”.
- **meta\_data** (*dict*) – User-defined, optional key-value pairs that are stored in the primary TEXT segment of the FCS file; the version of dclab is stored there by default
- **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, meta\_data={'dclab version': '0.23.0'}, 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”.
- **meta\_data** (*dict*) – User-defined, optional key-value pairs that are stored at the beginning of the tsv file - one key-value pair is stored per line which starts with a hash. The version of dclab is stored there by default.
- **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.

### 5.3.9 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

**reset** ()

Reset all filters

**update** (`rtdc_ds`, `force=[]`)

Update the filters according to `rtdc_ds.config["filtering"]`

**Parameters**

- **rtdc\_ds** (`dclab.rtdc_dataset.core.RTDCBase`) – The measurement to which the filter is applied
- **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.

## 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

### image-based

`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 metrics 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.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 ( $\mu_{20}$ ) and y ( $\mu_{02}$ ) via  $\sqrt{\mu_{20}/\mu_{02}}$ .

**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://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://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  $\mu\text{m}^3$

**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 Olynky.

## emodulus

Computation of apparent Young’s modulus for RT-DC measurements

**exception** `dclab.features.emodulus.KnowWhatYouAreDoingWarning`

`dclab.features.emodulus.convert` (*area\_um, deform, channel\_width\_in, channel\_width\_out, emodulus=None, flow\_rate\_in=None, flow\_rate\_out=None, viscosity\_in=None, viscosity\_out=None, inplace=False*)

convert area-deformation-emodulus triplet

The conversion formula is described in [MOG+15].

### Parameters

- **area\_um** (*ndarray*) – Convex cell area [μm<sup>2</sup>]
- **deform** (*ndarray*) – Deformation
- **channel\_width\_in** (*float*) – Original channel width [μm]
- **channel\_width\_out** (*float*) – Target channel width [μm]
- **emodulus** (*ndarray*) – Young’s Modulus [kPa]
- **flow\_rate\_in** (*float*) – Original flow rate [μl/s]
- **flow\_rate\_out** (*float*) – Target flow rate [μl/s]

- **viscosity\_in** (*float*) – Original viscosity [mPa\*s]
- **viscosity\_out** (*float or ndarray*) – Target viscosity [mPa\*s]; This can be an array
- **inplace** (*bool*) – If True, override input arrays with corrected data

#### Returns

- **area\_um\_corr** (*ndarray*) – Corrected cell area [ $\mu\text{m}^2$ ]
- **deform\_corr** (*ndarray*) – Deformation (a copy if *inplace* is False)
- **emodulus\_corr** (*ndarray*) – Corrected emodulus [kPa]; only returned if *emodulus* is given.

#### Notes

If only *area\_um*, *deform*, *channel\_width\_in* and *channel\_width\_out* are given, then only the area is corrected and returned together with the original deform. If all other arguments are not set to None, the emodulus is corrected and returned as well.

`dclab.features.emodulus.corrpix_deform_delta` (*area\_um, px\_um=0.34*)

Deformation correction term for pixelation effects

The contour in RT-DC measurements is computed on a pixelated grid. Due to sampling problems, the measured deformation is overestimated and must be corrected.

The correction formula is described in [Her17].

#### Parameters

- **area\_um** (*float or ndarray*) – Apparent (2D image) area in  $\mu\text{m}^2$  of the event(s)
- **px\_um** (*float*) – The detector pixel size in  $\mu\text{m}$ .
- **inplace** (*bool*) – Change the deformation values in-place

**Returns** **deform\_delta** – Error of the deformation of the event(s) that must be subtracted from *deform*. `deform_corr = deform - deform_delta`

**Return type** *float or ndarray*

`dclab.features.emodulus.extrapolate_emodulus` (*lut, area\_um, deform, emod, deform\_norm, deform\_thresh=0.05, inplace=True*)

Use spline interpolation to fill in nan-values

When points (*area\_um*, *deform*) are outside the convex hull of the *lut*, then `scipy.interpolate.griddata()` returns nan-values.

With this function, some of these nan-values are extrapolated using `scipy.interpolate.SmoothBivariateSpline`. The supported extrapolation values are currently limited to those where the deformation is above 0.05.

A warning will be issued, because this is not really recommended.

#### Parameters

- **lut** (*ndarray of shape (N, 3)*) – The normalized (!! see `normalize()`) LUT (first axis is points, second axis enumerates *area\_um*, *deform*, and *emodulus*)
- **area\_um** (*ndarray of size N*) – The normalized *area\_um* (corresponding to `lut[:, 0]`)

- **deform** (*ndarray of size N*) – The normalized deform (corresponding to *lut[:, 1]*)
- **emod** (*ndarray of size N*) – The emodulus (corresponding to *lut[:, 2]*); If *emod* does not contain nan-values, there is nothing to do here.
- **deform\_norm** (*float*) – The normalization value used to normalize *lut[:, 1]* and *deform*.
- **deform\_thresh** (*float*) – Not the entire LUT is used for bivariate spline interpolation. Only the points where *lut[:, 1] > deform\_thresh/deform\_norm* are used. This is necessary, because for small deformations, the LUT has an extreme slope that kills any meaningful spline interpolation.

```
dclab.features.emodulus.get_emodulus(area_um, deform, medium='CellCarrier',
                                     channel_width=20.0, flow_rate=0.16, px_um=0.34, temper-
                                     ature=23.0, extrapolate=False, copy=True)
```

Compute apparent Young's modulus using a look-up table

#### Parameters

- **area\_um** (*float or ndarray*) – Apparent (2D image) area [ $\mu\text{m}^2$ ] 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 is given, the viscosity is computed. If a float is given, this value is used as the viscosity in  $\text{mPa}\cdot\text{s}$  (Note that *temperature* must be set to *None* in this case).
- **channel\_width** (*float*) – The channel width [ $\mu\text{m}$ ]
- **flow\_rate** (*float*) – Flow rate [ $\mu\text{l/s}$ ]
- **px\_um** (*float*) – The detector pixel size [ $\mu\text{m}$ ] used for pixelation correction. Set to zero to disable.
- **temperature** (*float, ndarray, or None*) – Temperature [ $^{\circ}\text{C}$ ] of the event(s)
- **extrapolate** (*bool*) – Perform extrapolation using *extrapolate\_emodulus()*. This is discouraged!
- **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.normalize(data, dmax)
Perform normalization in-place for interpolation
```



Note that `scipy.interpolate.griddata()` has a *rescale* option which rescales the data onto the unit cube. For some reason this does not work well with LUT data, so we just normalize it by dividing by the maximum value.

```
dclab.features.emodulus.INACCURATE_SPLINE_EXTRAPOLATION = False
```

Set this to True to globally enable spline extrapolation when the *area\_um/deform* data are outside of a LUT.

This is discouraged and a *KnowWhatYouAreDoingWarning* warning will be issued.

Viscosity computation for various media

**exception** `dclab.features.emodulus_viscosity.TemperatureOutOfRangeWarning`

```
dclab.features.emodulus_viscosity.get_viscosity(medium='CellCarrier',      chan-
                                                nel_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; Valid values are defined in *KNOWN\_MEDIA*.
- **channel\_width** (*float*) – The channel width in  $\mu\text{m}$
- **flow\_rate** (*float*) – Flow rate in  $\mu\text{l/s}$
- **temperature** (*float or ndarray*) – Temperature in  $^{\circ}\text{C}$

**Returns** *viscosity* – Viscosity in  $\text{mPa}\cdot\text{s}$

**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].
- A *TemperatureOutOfRangeWarning* is issued if the input temperature range exceeds the temperature ranges given by [Her17] and [KSW78].

```
dclab.features.emodulus_viscosity.KNOWN_MEDIA = ['CellCarrier', 'CellCarrierB', 'water']
```

Media for which computation of viscosity is defined

## fluorescence

```
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

- **fl\_i** (*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  $c_{ij} = f_{lj} / f_{li}$ .

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`

## 5.4.3 isoelastics

Isoelastics management

**exception** `dclab.isoelastics.IsoelasticsEmodulusMeaninglessWarning`

**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  $\mu\text{m}$
- **flow\_rate** (*float*) – Flow rate through the channel in  $\mu\text{l/s}$
- **viscosity** (*float*) – Viscosity of the medium in  $\text{mPa}\cdot\text{s}$
- **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 isoelasticity 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 first 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 first 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\_out** (*float*) – 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  $\mu\text{m}$
- **flow\_rate** (float or *None*) – Flow rate through the channel in  $\mu\text{l/s}$ . 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  $\text{mPa}\cdot\text{s}$ . 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 [ $\mu\text{m}$ ], 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, *None*, or *False*) – Viscosity of the medium in  $\text{mPa}\cdot\text{s}$ . If set to *None*, the viscosity is computed from the meta data (medium, flow rate, channel width, temperature) in the [setup] config section. If this is not possible, the flow rate of the imported data is used and a warning will be issued.
- **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(s) corresponding to the given quantile

**Return type** np.ndarray or 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 contour spacing based on Doane's formula

### References

- [https://en.wikipedia.org/wiki/Histogram#Number\\_of\\_bins\\_and\\_width](https://en.wikipedia.org/wiki/Histogram#Number_of_bins_and_width)
- <https://stats.stackexchange.com/questions/55134/doanes-formula-for-histogram-binning>

### Notes

Doane's formula is actually designed for histograms. This function is kept here for backwards-compatibility reasons. It is highly recommended to use *bin\_width\_percentile()* instead.

dclab.kde\_methods.**bin\_width\_percentile** (*a*)

Compute contour spacing based on data percentiles

The 10th and the 90th percentile of the input data are taken. The spacing then computes to the difference between those two percentiles divided by 23.

### Notes

The Freedman–Diaconis rule uses the interquartile range and normalizes to the third root of len(a). Such things do not work very well for RT-DC data, because len(a) is huge. Here we use just the top and bottom 10th percentiles with a fixed normalization.

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* (*bw\_x*, *bw\_y*) or *None*) – The bandwidth 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 polygonal 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

**static unique\_id\_exists** (*pid*)

Whether or not a filter with this unique id exists

**hash**

Hash of *axes*, *points*, and *inverted*

```
instances = []  
points  
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.all*. 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': <dclab.statistics.Statistics object>}

`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 with 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`



List of changes in-between dclab releases.

### 6.1 version 0.23.0

- feat: enable emodulus extrapolation for *area\_um/deform* values outside of the given LUT.

### 6.2 version 0.22.7

- enh: dclab-verify-dataset now also checks whether the sheath and sample flow rates add up to the channel flow rate
- ref: Configuration does not anymore load unknown meta data keyword arguments, but ignores them. This implies that dclab-verify-dataset will not anymore check them actively. Instead, any warning issued when opening a file is added to the list of cues.
- setup: bump nptdms to 0.23.0

### 6.3 version 0.22.6

- fix: data export to HDF5 did not work when the “frame rate” is not given in the configuration

### 6.4 version 0.22.5

- enh: add checks for valid keys in the Configuration dictionary of a dataset *RTDCBase().config*; unknown keys will issue an *UnknownConfigurationKeyWarning* (#58)
- ref: moved *rtdc\_dataset.fmt\_hdf5.UnknownKeyWarning* to *rtdc\_dataset.config.UnknownConfigurationKeyWarning*

- ref: renamed *rtdc\_dataset.config.CaseInsensitiveDict* to *rtdc\_dataset.config.ConfigurationDict* and added option to check new keys

## 6.5 version 0.22.4

- fix: disable computation of Young's modulus for reservoir measurements (#75)
- enh: new keyword argument *req\_func* for *AncillaryFeature* to define additional logic for checking whether a feature is available for a given instance of *RTDCBase*.

## 6.6 version 0.22.3

- enh: add *data* property to ICues (and use it when checking for compression)

## 6.7 version 0.22.2

- fix: when computing the contour from the mask image, always use the longest contour - critical when the mask image contains artefacts
- fix: minor issue with dclab-verify-dataset when nptdms was not installed and an exception occurred
- enh: dclab-verify-dataset shows some info on data compression

## 6.8 version 0.22.1

- enh: remember working API Key
- docs: document DCOR format

## 6.9 version 0.22.0

- feat: implement DCOR client
- enh: improved .rtdc file format detection (with wrong extension)

## 6.10 version 0.21.2

- enh: dclab-verify-dataset now also checks HDF5 "mask" feature attributes
- setup: bump h5py to 2.10.0 (need *<object>.attrs.get\_id*)

## 6.11 version 0.21.1

- fix: correct type of HDF5 image attributes for "mask" feature

## 6.12 version 0.21.0

- feat: implement new CLI dclab-repack
- fix: don't write "logs" group to HDF5 files if there aren't any
- fix: support HDF5 files that have no "logs" group
- docs: fix docstring of dclab-join

## 6.13 version 0.20.8

- fix: regression where old .tmds data could not be opened if they did not contain the "area\_msd" feature
- fix: convert bytes logs to string in fmt\_hdf5
- enh: support len(ds.logs) for fmt\_hdf5
- enh: replace "info" by "build" in CLI job info

## 6.14 version 0.20.7

- fix: ensure file extension is .rtdc in dclab-join
- fix: correct "frame" and "index\_online" features when exporting to hdf5
- enh: allow to set metadata dictionary in dclab.cli.join

## 6.15 version 0.20.6

- fix: typo in contour check resulted in small tolerance

## 6.16 version 0.20.5

- fix: be more trustful when it comes to contour data in the tdms file format; instead of raising errors, issue warnings (#72)

## 6.17 version 0.20.4

- ref: move integrity checks to new class check.IntegrityChecker
- docs: document remaining dictionaries in dclab.dfn

## 6.18 version 0.20.3

- docs: fix bad anchors

## 6.19 version 0.20.2

- ref: using temperature values outside the range for viscosity computation now issues a warning instead of raising an error; warnings were added for the CellCarrier buffers
- fix: handle number detection correctly in `get_emodulus`

## 6.20 version 0.20.1

- fix: always return an array when computing the KDE
- ref: make accessible static function `RTDCBase.get_kde_spacing`

## 6.21 version 0.20.0

- feat: compute elastic modulus from “temp” feature (#51)
- enh: computing isoelastics from datasets can use [setup]: “temperature” to compute the viscosity/emodulus (#51)
- enh: define new meta data key [setup]: “temperature”
- docs: add an advanced section on Young’s modulus computation (#51)

## 6.22 version 0.19.1

- fix: hierarchy children did not pass *force* argument to hierarchy parent when *apply\_filter* is called
- fix: revert histogram2d “density” argument to “normed” to support numpy 1.10 (Shape-Out 1)
- fix: implement unambiguous `RTDCBase.__repr__`

## 6.23 version 0.19.0

- feat: added better contour spacing computation based on percentiles (`dclab.kde_methods.bin_width_percentile`)
- feat: add feature “index\_online” which may be missing values (#71)
- feat: implement `__getstate__` and `__setstate__` for polygon filters
- fix: write UTF-8 BOM when exporting to .tsv
- enh: add check whether `unique_id` exists in `PolygonFilter`

## 6.24 version 0.18.0

- fix: correctly handle filtering when features are removed from a dataset
- ref: move `dclab.rtdc_dataset.util` to `dclab.util`



- ref: minor cleanup in computation of viscosity (support lower-case *medum* values, add *dclab.features.emodulus\_viscosity.KNOWN\_MEDIA*)
- ref: cleanup *dclab.rtdc\_dataset.filter* (use logical operators, correctly display nan-warning messages, keep track of polygon filters, add consistency checks, improve readability)

## 6.25 version 0.17.1

- maintenance release

## 6.26 version 0.17.0

- feat: add command line script for compressing HDF5 (.rtdc) data “dclab-compress”
- enh: record warnings under “/log” for all command line scripts
- enh: set gzip data compression for all command line scripts

## 6.27 version 0.16.1

- fix: circumvent UnicodeDecodeErrors which occurred in frozen macOS binaries that use dclab
- enh: support subsecond accuracy in the the configuration key [experiment] time (e.g. “HH:MM:SS.SSS” instead of “HH:MM:SS”)
- enh: store the correct, relative measurement time in *dclab-join* (#63)

## 6.28 version 0.16.0

- fix: *RTDCBase.downsample\_scatter* with *ret\_mask=True* did not return boolean array of *len(RTDCBase)* as indicated in the docs
- ref: remove *RTDCBase.\_plot\_filter*, which was confusing anyway
- ref: deprecate usage of *RTDCBase.\_filter*

## 6.29 version 0.15.0

- feat: add method *RTDCBase.reset\_filter*
- feat: implement *RTDCBase.features\_loaded*
- feat: allow to instantiate *RTDC\_Hierarchy* without initially applying the filter
- fix: non-scalar columns of *RTDC\_Hierarchy* did not implement *len()*
- docs: add an example script dedicated to data plotting
- ref: remove circular references between *Filter* and *RTDCBase*

## 6.30 version 0.14.8

- fix: Ignore feature “trace” when the trace folder exists but is empty (HDF5 format)
- fix: If no contour can be found, raise an error before other ancillary features produce cryptic errors

## 6.31 version 0.14.7

- enh: allow to add meta data when exporting to .fcs or .tsv (dclab version is saved by default)
- setup: bump fcswrite from 0.4.1 to 0.5.0

## 6.32 version 0.14.6

- fix: improved handling of tdms trace data (split trace with fixed samples per event to avoid ValueError when exporting to hdf5)
- fix: transposed roi size x/y config value when exporting to hdf5

## 6.33 version 0.14.5

- cli: write warning messages to logs in tdms2rtdc
- ref: increase verbosity of warning messages

## 6.34 version 0.14.4

- fix: discard trace data when “samples per event” has multiple values for tdms data
- fix: prefer image shape over config keywords when determining the shape of the event mask and check the shape in dclab-verify-dataset
- fix: avoid ContourIndexingError by also searching the neighboring (+2/-2) events when the contour frame number does not match (#67)

## 6.35 version 0.14.3

- enh: explicitly check contour data when testing whether to include the first event in tdms2rtdc

## 6.36 version 0.14.2

- ref: convert said ValueError to ContourIndexingError

## 6.37 version 0.14.1

- fix: ValueError when verifying contour frame index due to comparison of float with int

## 6.38 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* falsely shown as “enabled by default”)

## 6.39 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* (measured 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 presence 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)

## 6.40 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

## 6.41 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]*

## 6.42 version 0.11.0

- feat: compute contours lazily (#61)

## 6.43 version 0.10.5

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

## 6.44 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:*)

## 6.45 version 0.10.3

- fix: add numpy build dependency (setup\_requires)

## 6.46 version 0.10.2

- fix: HDF5-export did not re-enumerate “index” feature

## 6.47 version 0.10.1

- fix: support nan-valued events when computing quantile levels in submodule *kde\_contours*

## 6.48 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”

## 6.49 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 rtcd format

## 6.50 version 0.9.0

- feat: add new feature: gravitational force, temperature, and ambient temperature
- ref: remove unused *has\_key* function in *rtcd\_dataset.config.CaseInsensitiveDict*
- setup: require numpy>=1.10.0 because of *equal\_nan* argument in *allclose*

## 6.51 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*

## 6.52 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)

## 6.53 version 0.6.3

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

## 6.54 version 0.6.2

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

## 6.55 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)

## 6.56 version 0.5.2

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

## 6.57 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

## 6.58 version 0.5.0

- BREAKING CHANGES:
  - `definitions.feature_names` now contains non-scalar features (including “`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

## 6.59 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`”

## 6.60 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

## 6.61 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)

## 6.62 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



## 6.63 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

## 6.64 version 0.2.9

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

## 6.65 version 0.2.8

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

## 6.66 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)
- Refactoring:
  - “features” submodule with basic methods for ancillary columns

## 6.67 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`

## 6.68 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

## 6.69 version 0.2.4

- Replace OpenCV with `imageio`
- Add (ancillary) 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 ancillary columns that are computed on-the-fly (new “`_ancillaries`” attribute and “`ancillary_columns.py`”)

## 6.70 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)

## 6.71 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

## 6.72 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

## 6.73 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

## 6.74 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

## 6.75 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)

## 6.76 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

## 6.77 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*

## 6.78 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

## 6.79 version 0.1.4

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

## 6.80 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/ZELLMCHANIK-DRESDEN/ShapeOut/issues/37>
- <https://github.com/ZELLMCHANIK-DRESDEN/ShapeOut/issues/38>

## 6.81 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



## CHAPTER 7

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### Bibliography

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#### 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>.

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## CHAPTER 9

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### Indices and tables

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