profile_demo_rise

November 21, 2023

[1]:
```
"""
N.B.: Jupyter notebook compatible with RISE and pytest -nblab.
Can be executed as a regular notebook, as a presentation, a test, or converted␣
 ↪to html slides.

These are the only things that are added to a conventional notebook:

* RISE settings are edited in notebook metadata and override system-wide␣
 ↪settings in ~/.jupyter/nbconfig/rise.json
Refer to https://rise.readthedocs.io/en/stable/customize.html for usage and␣
 ↪details.

Run from jupyter menu bar to obtain a live presentation, or generate html with:

     jupyter nbconvert --to slides profile_demo_rise.ipynb

* nblab uses cell directives (es. # NBVAL_IGNORE_OUTPUT) to define how to␣
 ↪handle output changes.
Refer to https://nbval.readthedocs.io/en/latest/#Skipping-certain-output-types
for usage and details.

You may want to run this test with:

    py.test --nbval  profile_demo_rise.ipynb

if option `--sanitize-with nbval.cfg` is added, a file containing replacement␣
 ↪of regular expression can be
used for a finer control of check (e.g. to ignore results that are expected to␣
 ↪differ or exceptions that are expected
to happen).

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Vincenzo Cotroneo 2021/08/14

To use as template for .ipynb demos

""";
```

[2]:
```
# Has duplicated part in P(2) rofile_class_tutorial  (which have addition).and
# and also Profile_class_test(3) (minimal version entirely contained in (2)).

# here detailed merge and resample tests
```

[3]:
```
# Da Profile_class_test
# NBVAL_IGNORE_OUTPUT

%reset
%load_ext autoreload
%autoreload 2
```

```
Nothing done.
```

[4]:
```
import matplotlib.pyplot as plt
import numpy as np
import os

from dataIO.span import span
from dataIO.fn_add_subfix import fn_add_subfix

from IPython.display import display
from plotting.backends import maximize
```

[5]:
```
pwd
```

[5]:
```
'c:\\Users\\kovor\\Documents\\python\\pyXTel\\source\\pyProfile\\test'
```

[6]:
```
np
```

[6]:
```
<module 'numpy' from 'c:\\Users\\kovor\\anaconda3\\lib\\site-
packages\\numpy\\__init__.py'>
```

1 Profile class

1.1 New class implementation (2020/06/25)

Test new implementation of class from profile methods to objects, in analogy to what is done with pySurf. Here we test and document.

[7]:
```
import sys
```

The main class is `Profile`, representing a set of x,y data with related information and operations.

[8]:
```
from pyProfile.profile_class import Profile
```

[9]:
```
from pyProfile.profile import make_signal
```

Can be defined in the most trivial way from x and y:

```
P = Profile(x, y, units=['mm','nm'], name='profile_1')
```

It is generally easy to write a routine to read its own format and return a Profile object.

Helper function `make_signal` (see Appendix or `make_signal?` for details) can be used to generate a (sinusoid-based) test profile.

I can use Python introspection to get info on each function:

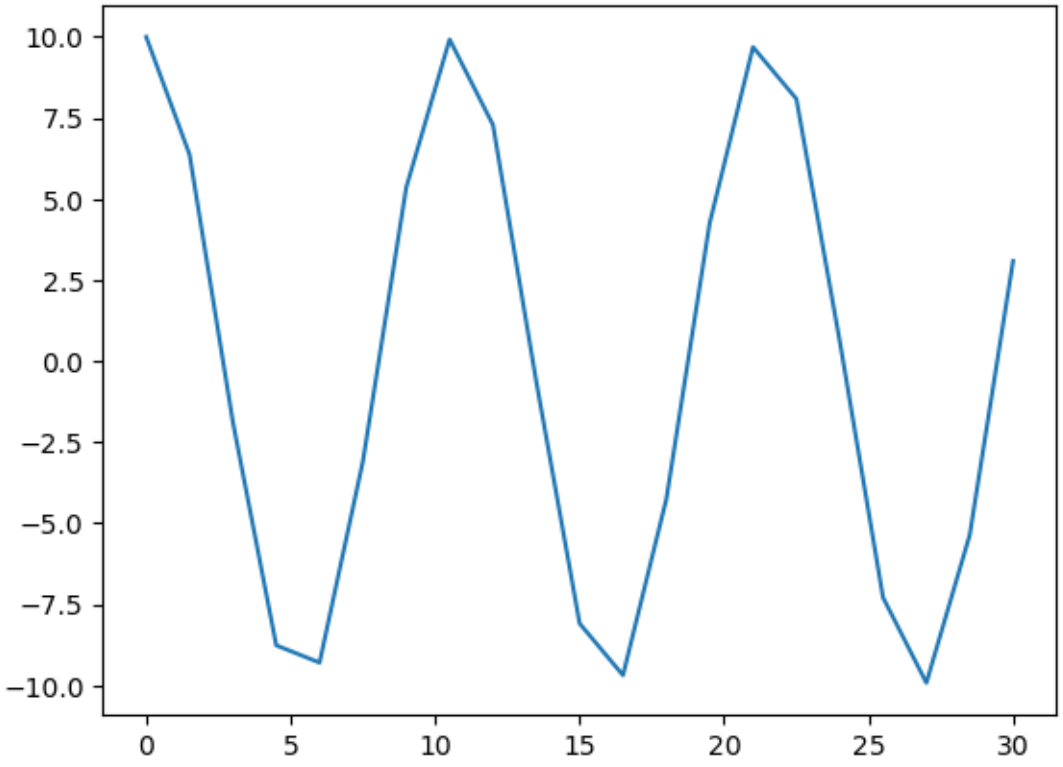
[9]:
```
make_signal?
```

```
Signature:
make_signal(
    amp,
    x=None,
    L=None,
    N=None,
    nwaves=None,
    phase=0,
    ystartend=(0,
0),
    noise=0.0,
    minus_one=False,
)
Docstring:
Build a signal of length L and number of points N, as a sum of a cosinusoid, a
line and a noise. minus_one remove last point (just a convenience e.g. for a
periodic profile), note that in
this case the returned x corresponds to values returned by
np.arange e .linspace, however it needs to be called with N+1
points, so the last one can be excluded and N points returned,
keeping intervals consistent (this might change in future versions).
Signal is generated on `x` if this is provided.
Otherwise it is generated on length `L` (can be range).
Phase adds a phase in radians (the armonic component of signal is defined as
`amp*np.sin(2*np.pi*x/L*nwaves+phase)`).

VC 2020/09/11 added option for L as range and x on which to generate signal.
2020/07/17 make signal a cosine (it was a sine), because more consistent with
real part of imaginary number.
VC 2020/06/27 horrible interface with args, replace with kwargs with defaults.
Added phase.
OLD CODE NEEDS TO be UPDATED! TODO: file search
File:
```

```
c:\users\kovor\documents\python\pyxtel\source\pyprofile\profile.py
Type:       function
```

[10]:
```
# use helper function to create x and y:
x,y = make_signal(amp=10.,L=30.,N=21,nwaves=2.8,ystartend=(0,0),noise=0)

# plot them with usual matplotlib commands:
plt.plot(x,y)
```

[10]:
```
[<matplotlib.lines.Line2D at 0x1fe8e19f700>]
```



This is how a Profile object can be defined:

[11]:
```
P = Profile(x,y,units=['mm','nm'],name='profile_1')
```

[12]:
```
P.std()
```

[12]:
```
7.044127837632114
```

As well, `x` and `y` can be retrieved either as `P.x` and `P.y`, or with `x,y = P()`

[13]:
```
P()
```

[13]:
```
(array([ 0. ,  1.5,  3. ,  4.5,  6. ,  7.5,  9. , 10.5, 12. , 13.5, 15. ,
        16.5, 18. , 19.5, 21. , 22.5, 24. , 25.5, 27. , 28.5, 30. ]),
 array([10.        ,  6.3742399 , -1.87381315, -8.7630668 , -9.29776486,
        -3.09016994,  5.35826795,  9.92114701,  7.28968627, -0.6279052 ,
        -8.09016994, -9.68583161, -4.25779292,  4.25779292,  9.68583161,
         8.09016994,  0.6279052 , -7.28968627, -9.92114701, -5.35826795,
         3.09016994]))
```

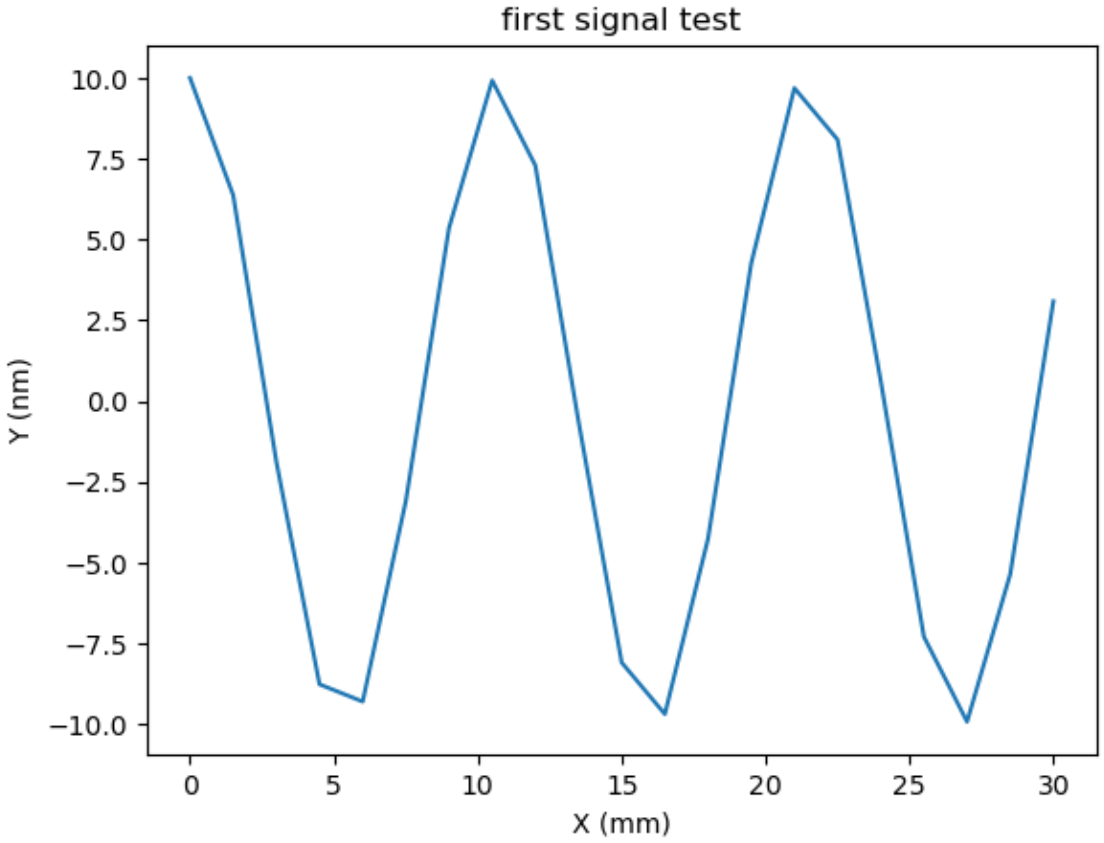
[14]:
```
P.x
```

[14]:
```
array([ 0. ,  1.5,  3. ,  4.5,  6. ,  7.5,  9. , 10.5, 12. , 13.5, 15. ,
       16.5, 18. , 19.5, 21. , 22.5, 24. , 25.5, 27. , 28.5, 30. ])
```

Plotting is standard python plotting (`matplotlib`), accept same arguments and manipulation.

[15]:
```
P.plot()
plt.title('first signal test')
```

[15]:
```
Text(0.5, 1.0, 'first signal test')
```



[16]:
```
#TODO: test remove_nan_ends.
#TODO: test register_profile.
```

2 Profile methods and functions

2.1 Algebraic operations

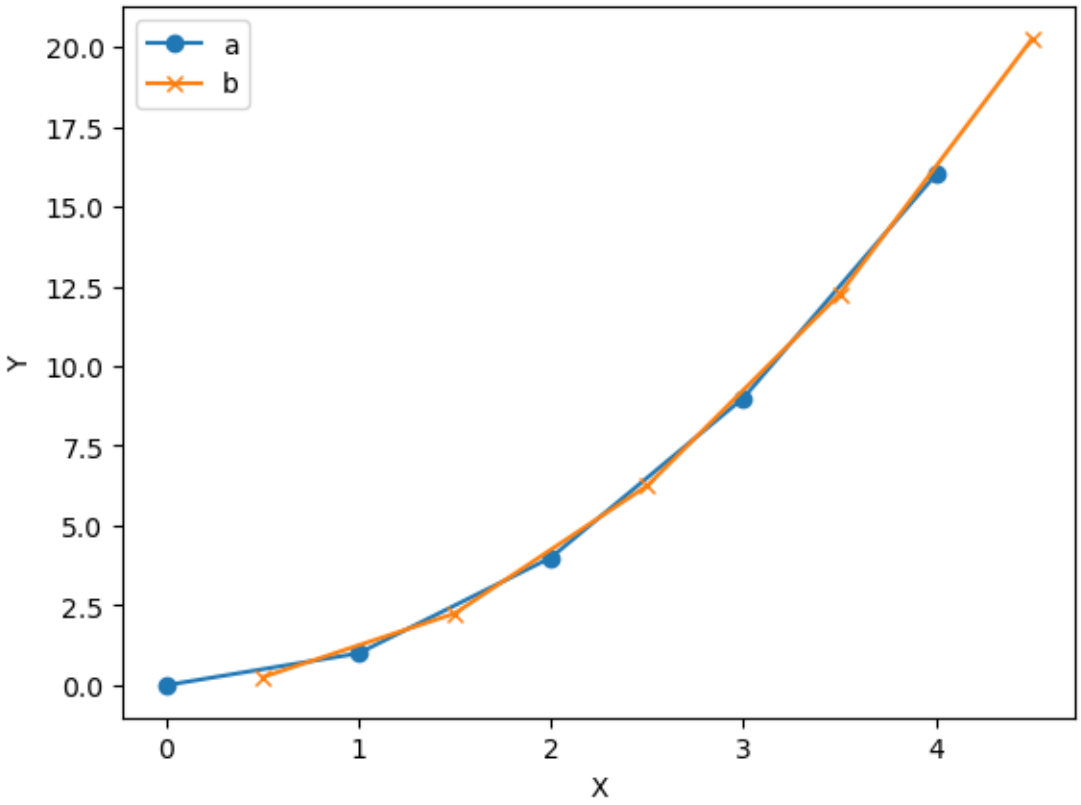
We build different test profiles.

Create two similar quadratic profiles `a` and `b` with different x values:

BEWARE: units in algebraic operations are not verified, usually the ones from first term are used for result, this may change in future.

[24]:
```
# Make different test profiles:

x0 = np.arange(5)

a = Profile(x0,x0**2)
a.plot(marker='o',ls='-',label = 'a')

b =  Profile(x0+0.5,(x0+0.5)**2)
b.plot(marker='x',ls='-',label = 'b')

plt.legend(loc=0)
```

[24]:
```
<matplotlib.legend.Legend at 0x1fe8e860dc0>
```

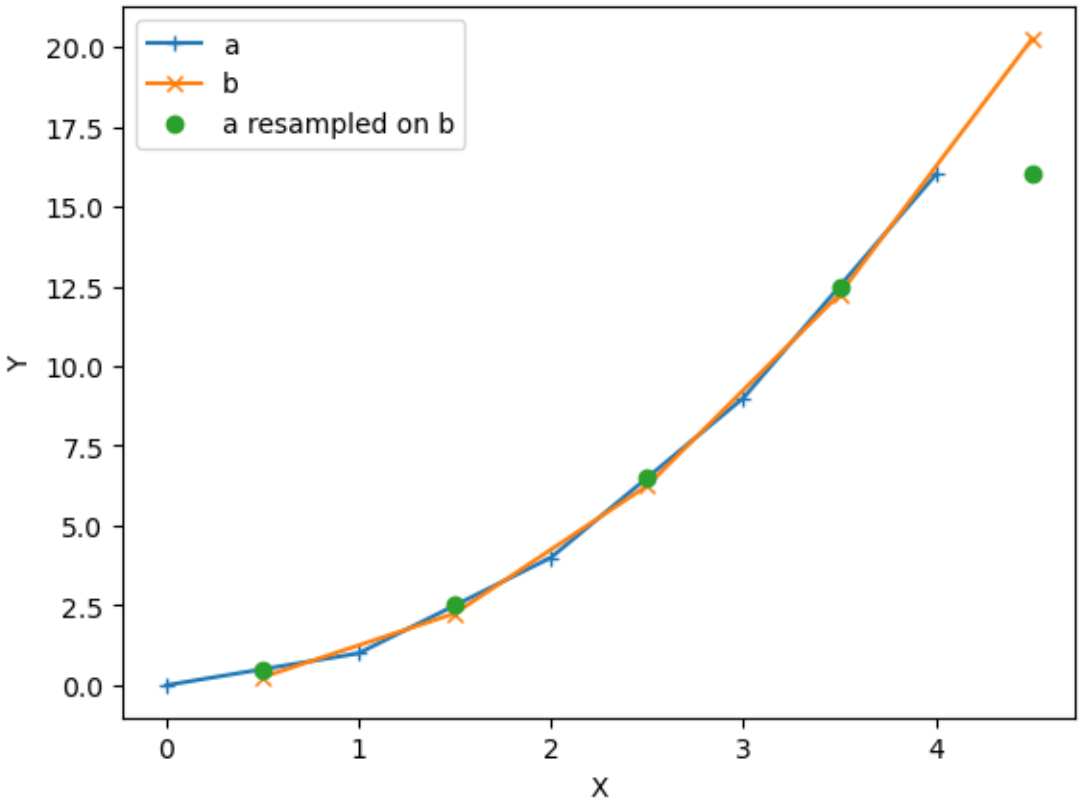


Algebraic operations can be performed on `Profile` objects.

Resampling can be directly accessed by `resample` method, but there is usually no need to perform, because it is automatically handled by algebraic operations (resample on first by default,):

[25]:
```
# plot interpolation old, note that a can be resampled (extrapolated)
# beyond its edges, but its values are determined by `np.interpol` options␣
↪which by default replicate edge value.
c = a.resample(b,trim=False)

a.plot(marker='+',ls='-',label = 'a')
b.plot(marker='x',ls='-',label = 'b')
c.plot(marker='o',ls='',label='a resampled on b')

plt.legend(loc=0)
```

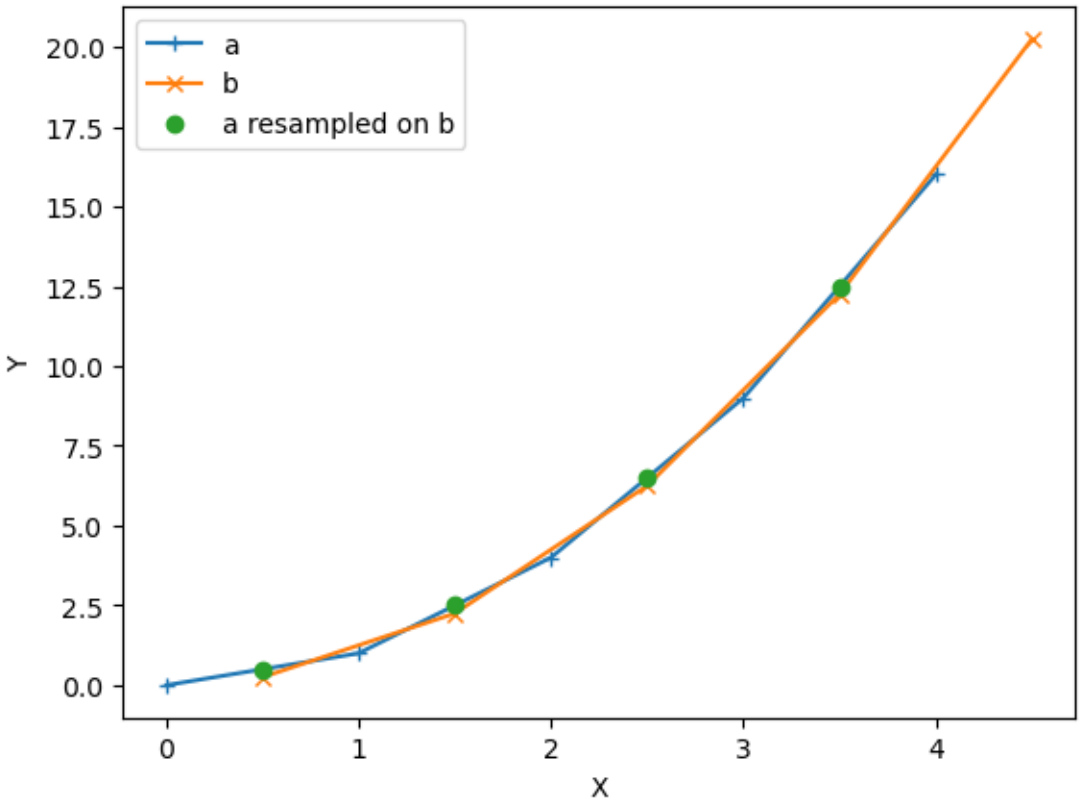
[25]:
```
<matplotlib.legend.Legend at 0x1fe8e936f70>
```



[26]:
```
# plot interpolation,
# in new function, trim defaults to True, cannot sum yc + yb
c = a.resample(b)

print(a())
print(b())
print(c())

a.plot(marker='+',ls='-',label = 'a')
b.plot(marker='x',ls='-',label = 'b')
c.plot(marker='o',ls='',label='a resampled on b')

plt.legend(loc=0)
```

```
(array([0., 1., 2., 3., 4.]), array([ 0.,  1.,  4.,  9., 16.]))
(array([0.5, 1.5, 2.5, 3.5, 4.5]), array([ 0.25,  2.25,  6.25, 12.25, 20.25]))
(array([0.5, 1.5, 2.5, 3.5]), array([ 0.5,  2.5,  6.5, 12.5]))
```

[26]: `<matplotlib.legend.Legend at 0x1fe8e936f40>`

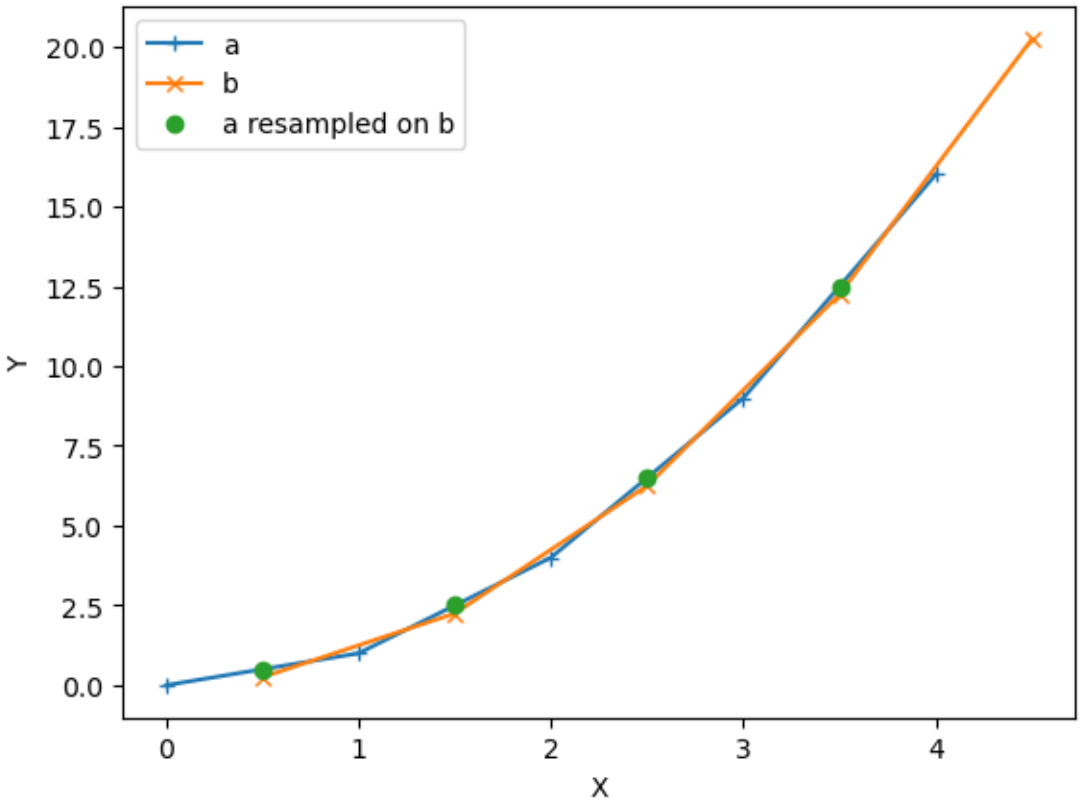


Here some examples of algebraic operations on different `x`:

[27]:
```
c = a.resample(b,trim=True)
print(a())
print(b())
print(c())
#print(a+b)
a.plot(marker='+',ls='-',label = 'a')
b.plot(marker='x',ls='-',label = 'b')
c.plot(marker='o',ls='',label='a resampled on b')
plt.legend()
```

```
(array([0., 1., 2., 3., 4.]), array([ 0.,  1.,  4.,  9., 16.]))
(array([0.5, 1.5, 2.5, 3.5, 4.5]), array([ 0.25,  2.25,  6.25, 12.25, 20.25]))
(array([0.5, 1.5, 2.5, 3.5]), array([ 0.5,  2.5,  6.5, 12.5]))
```

[27]:
```
<matplotlib.legend.Legend at 0x1fe8e116610>
```

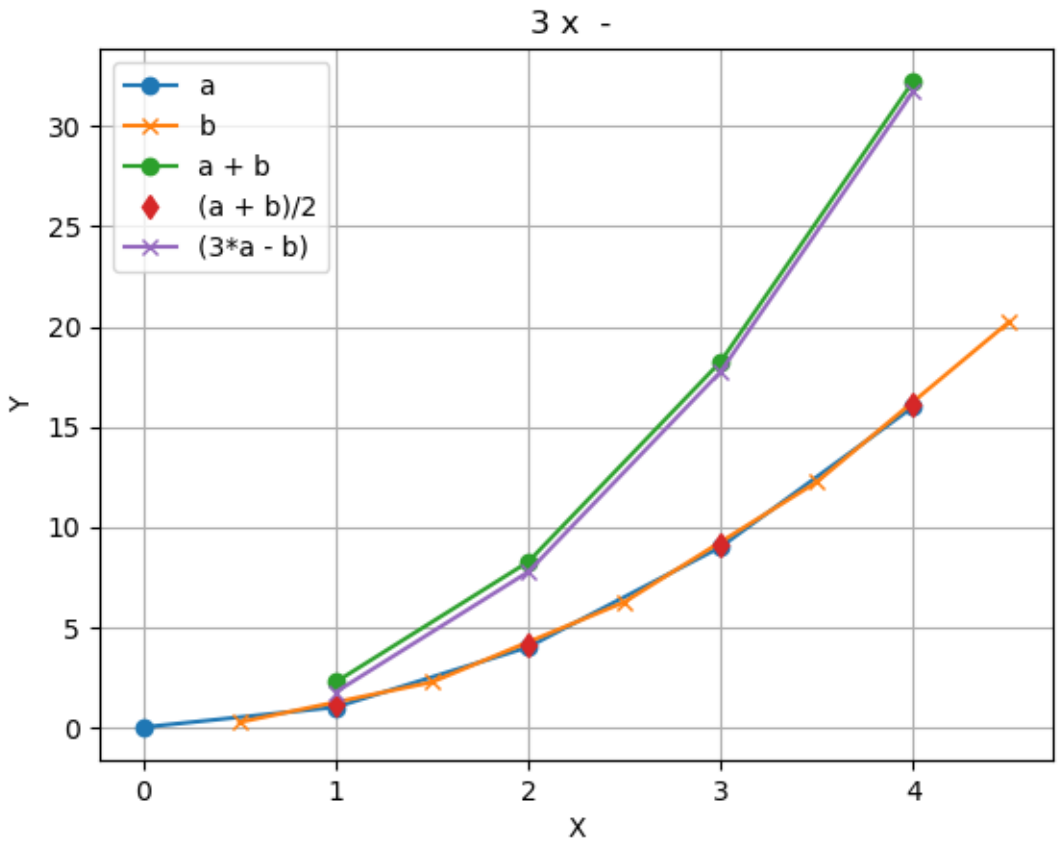


[28]:
```
a+b
```

[28]: <.Profile " + " at 0x1fe8ea7f460>

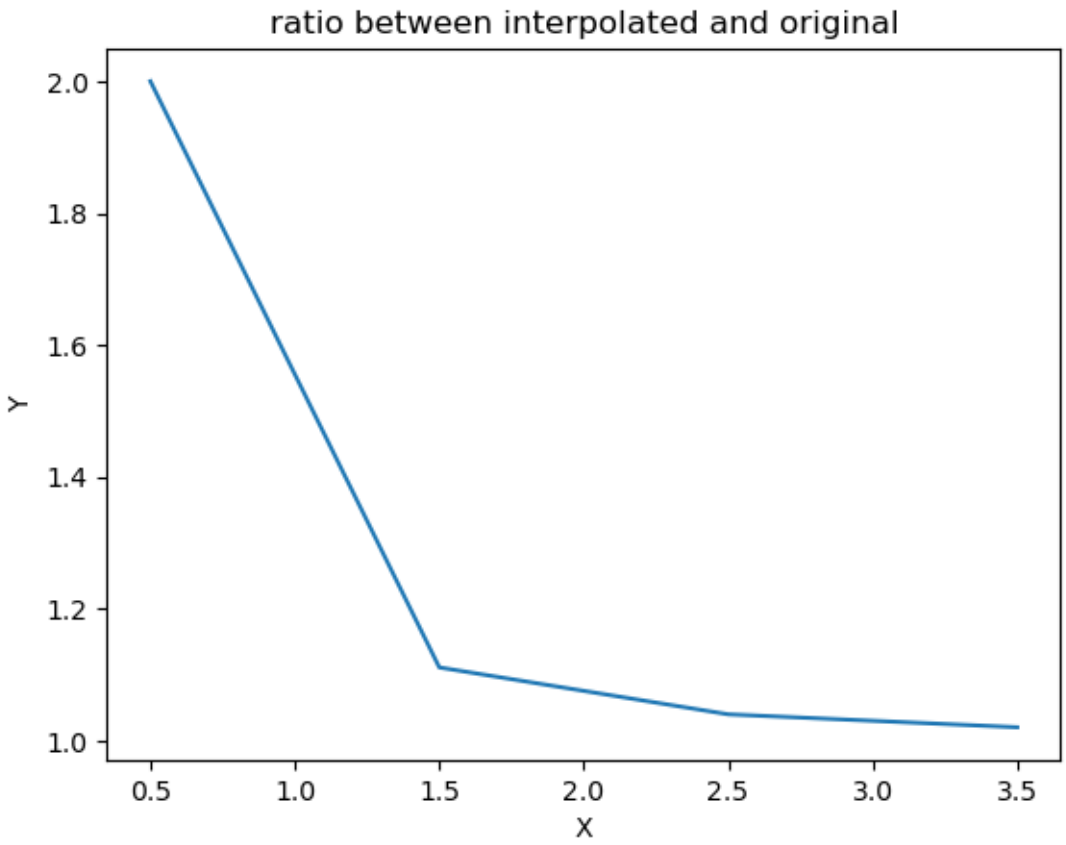
[29]:
```
# test algebraic operations:
a.plot(marker='o',ls='-', label = 'a')
b.plot(marker='x',ls='-', label = 'b')
(a+b).plot(label = 'a + b',marker='o')
((a+b)/2).plot(label = '(a + b)/2',marker='d',ls='')
(3*a-b).plot(label = '(3*a - b)',marker='x',ls='-')
plt.grid()
plt.legend(loc=0)
```

[29]: <matplotlib.legend.Legend at 0x1fe8ebe6c40>



[30]:
```
#(a/b).plot(label='a/b')
#(b/a).plot(label='b/a')
(c/b).plot()
plt.title('ratio between interpolated and original')
```

[30]: Text(0.5, 1.0, 'ratio between interpolated and original')



2.2 Test of `merge` and `resample` functions

merger for Elettra data Prototype for a generic (n-region) reader and merger, then reimplemented in `processa_enscan.py`:

2.2.1 Environment setup

[10]:
```
dirresult = 'tests'
os.makedirs(dirresult, exist_ok=True)
infolder = r'input_data\Elettra_20221107'
```

[11]:
```
from pyProfile.profile import merge_profiles, merge_profile, test_merge_profile
from pyProfile.profile import test_merge_init, test_merge_init_plot
from pyProfile.profile import resample_profile, test_resample_profile
from pyProfile.profile import test_resample_trim, test_merge_mode

from pyProfile.profile import crop_profile, sum_profiles

from dataIO.span import span
```

[12]:
```
# see updated version in processa_enescan
def mergen(files, ranges = None, binned = False):
    """Read n files representing 4 energetic regions,
    merge them according to hardcoded energies.
    The number of files is determined by the ranges passed, which are n-1.
    In this version a couple of merged files is passed, rather than a ratio,
    so they can be analysed separately, or divided outside of the function.
    (the previous version returned merged profile with ratio detector/monitor.
    The ``calib`` parameter was removed in this version, you can obtain the same
    effect dividing result[1]/result[0]*calib, where calib is a calibration␣
 ↪Profile
    (monitor/direct beam vs energy)."""

    a = [read_enscan(f,) for f in files]  #each file gives a couple detector/
 ↪monitor
    a = [bb/aa for aa, bb in a]   #normalize each file

    ## start looping and merging
    m = a[0]
    for aa,ss in zip(a[1:],r):
        m=m.merge(aa,ranges=ss, binned = binned)

    return m
```

[13]:
```
r = [[[0,170],[0,259]],    # these couples of ranges are passed to each␣
 ↪iteration of a
       [[0,260],[0,439]],    # two-profile merge, represent the x intevals to␣
 ↪merge
       [[0,440],[0,1000]]]   # it must include 0 because the first profile is␣
 ↪always the
                             # total of previous merges.

r = [[0,170],[0,259],[0,439],[0,1000]]

files = [os.path.join(infolder,f) for f in
        ['file(1)_Region 1__0164.txt',
        'file(1)_Region 2__0164.txt',
        'file(1)_Region 3__0164.txt',
        'file(1)_Region 4__0164.txt']]

#from processa_enescan import mergen
```

[14]:
```
# test merge_profies: manual merge

def read_enscan(file1,xcol=1):
    #fromo processa_enescan
    """return monitor and diode as Profile object."""
```

```
    with open(file1,'r',encoding='ISO-8859-1') as ff:
        f = ff.readlines()
        first = [i for i,l in enumerate(f) if  ('___________' in l) ][-1]+2
        p1m = Profile(*np.genfromtxt(file1,usecols=[xcol,5],
            delimiter='',unpack=1,skip_header=first,encoding='ISO-8859-1'),
            name='dir mon',units=['eV','']).sort()
        p1d = Profile(*np.genfromtxt(file1,usecols=[xcol,6],
            delimiter='',unpack=1,skip_header=first,encoding='ISO-8859-1'),
            name='dir dio',units=['eV','']).sort()

    return p1m, p1d

#load a:
a = [read_enscan(f) for f in files]  #each file gives a couple detector/monitor
a = [bb/aa for aa, bb in a]   #normalize each file
```

[15]:
```
# set initial data for both merge_profiles and merge_profile from real data
profiles = [a[0](),a[1]()]
x1,y1 = a[0]()
x2,y2 = a[1]()
```

2.3 Development of multiple merges

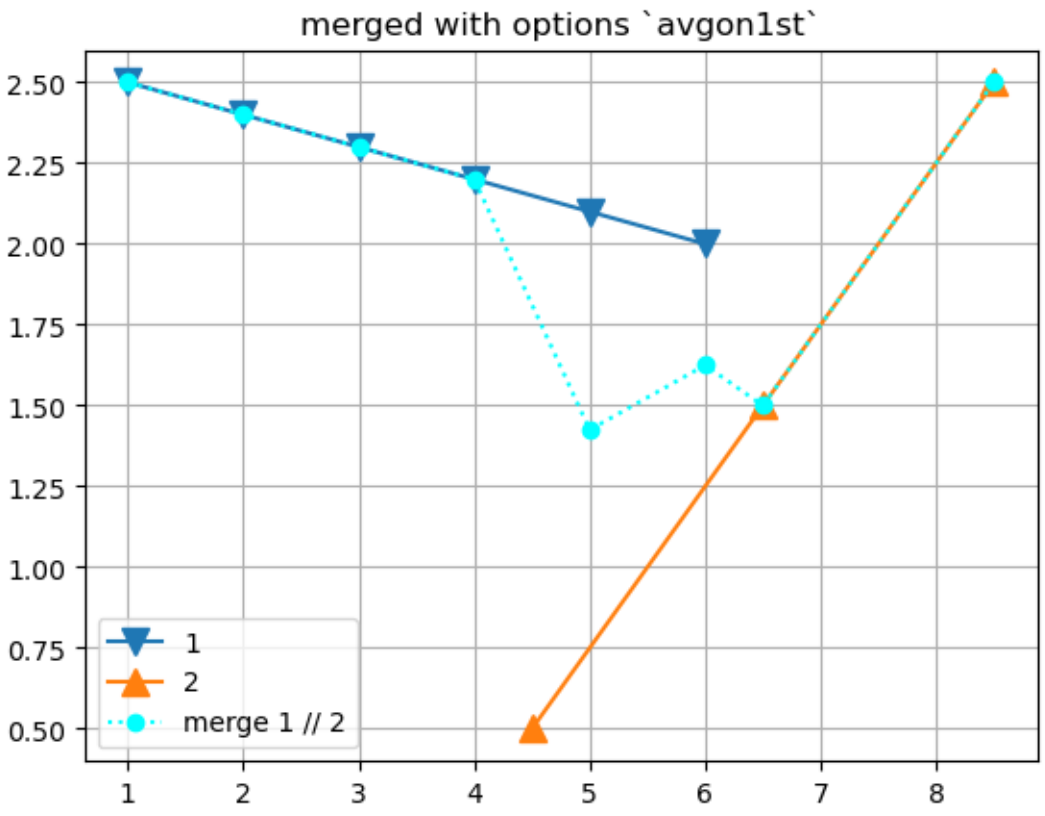
2.3.1 This can be done with `merge_profile` (merge only two profiles)

Works well with all options. Test of resample and sum works well here:

[24]:
```
x1,y1,x2,y2 = test_merge_init(set=3)
```

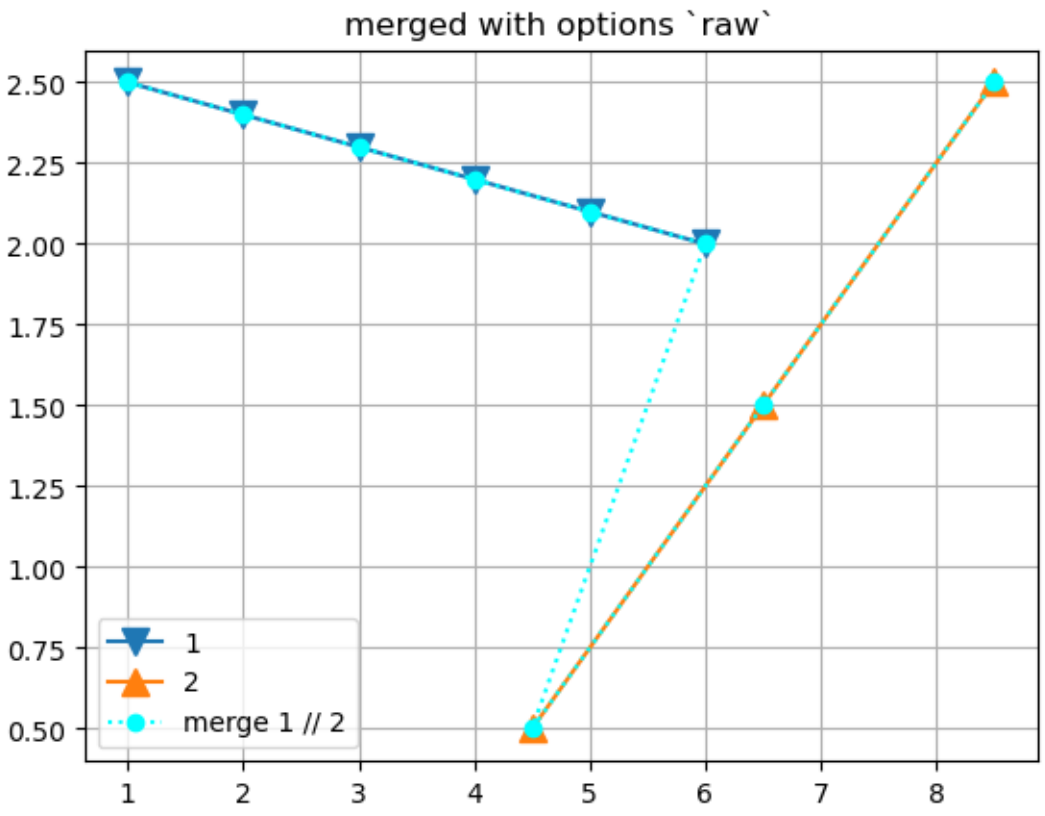
[25]:
```
# This tests a single mode:

m4 = test_merge_profile(x1,y1,x2,y2,mode='avgon1st')
print(m4)
```

```
6 4.5 False
6 5 False
(array([1. , 2. , 3. , 4. , 5. , 6. , 6.5, 8.5]), array([2.5  , 2.4  , 2.3  ,
2.2  , 1.425, 1.625, 1.5  , 2.5  ]))
```

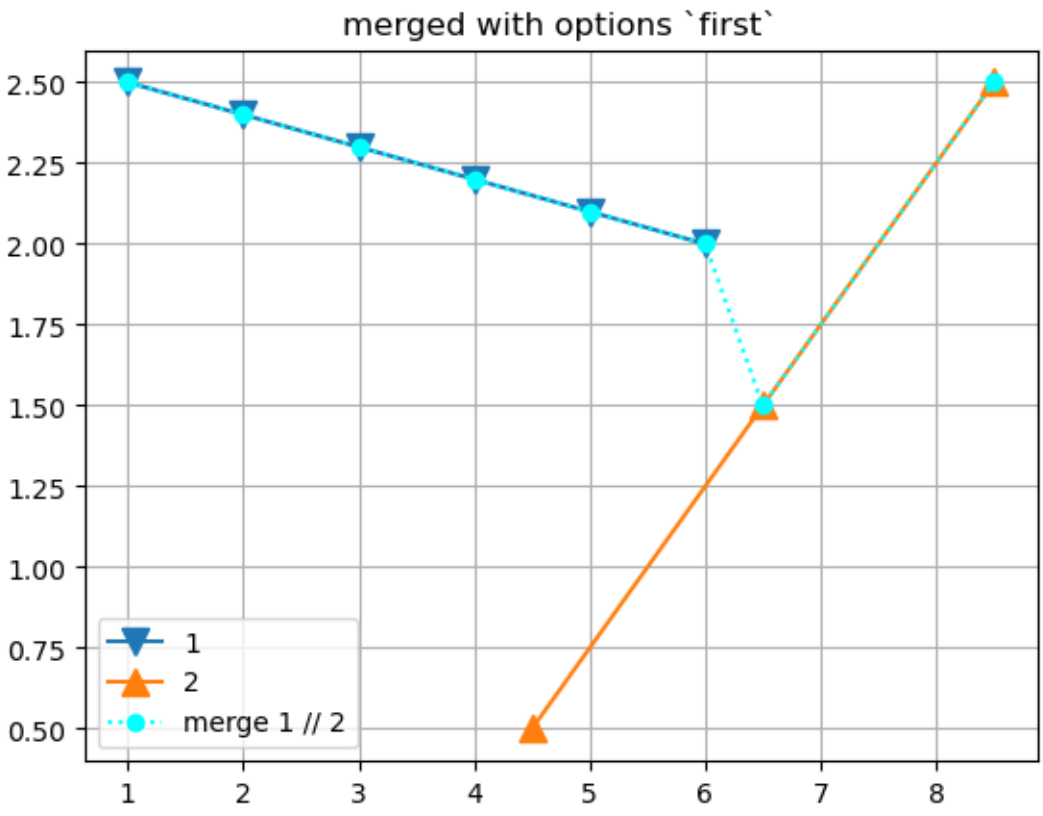


[26]:
```
test_merge_mode(x1,y1,x2,y2)
```

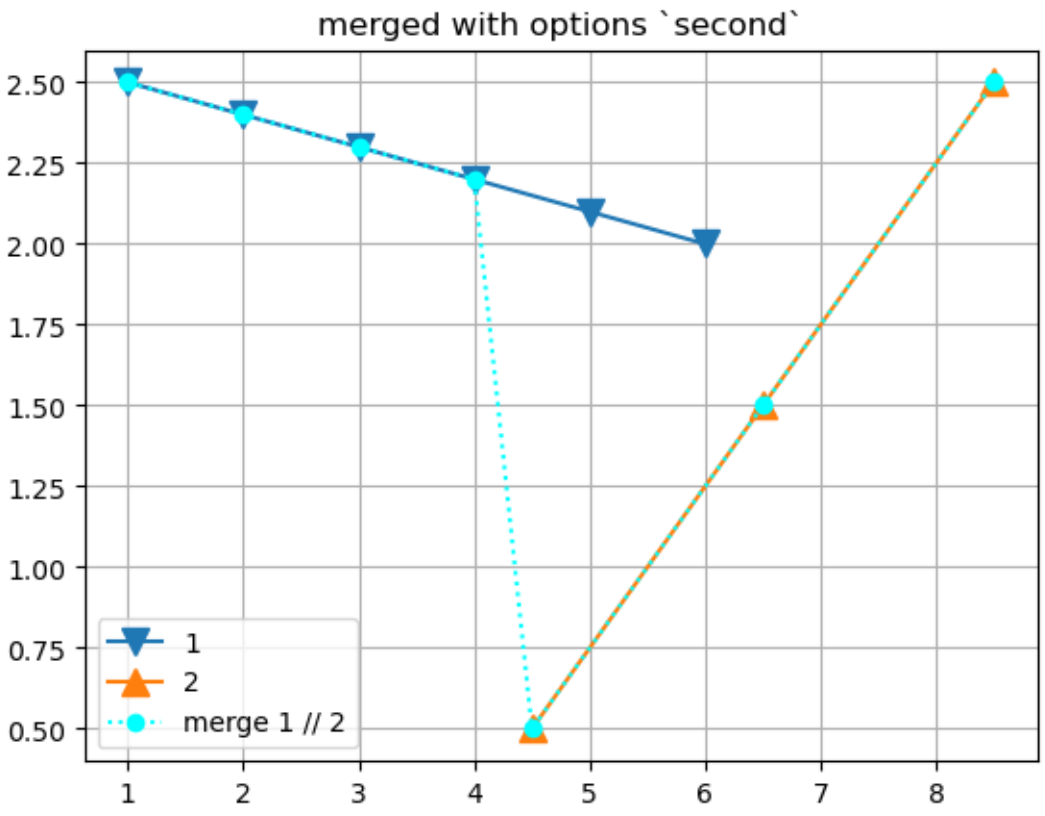
```
6 4.5 False
6 4.5 False
(array([1. , 2. , 3. , 4. , 5. , 6. , 6.5, 8.5]), array([2.5, 2.4, 2.3, 2.2,
2.1, 2. , 1.5, 2.5]))
6 4.5 False
(array([1. , 2. , 3. , 4. , 4.5, 6.5, 8.5]), array([2.5, 2.4, 2.3, 2.2, 0.5,
1.5, 2.5]))
6 4.5 False
6 5 False
(array([1. , 2. , 3. , 4. , 5. , 6. , 6.5, 8.5]), array([2.5  , 2.4  , 2.3  ,
2.2  , 1.425, 1.625, 1.5  , 2.5  ]))
```



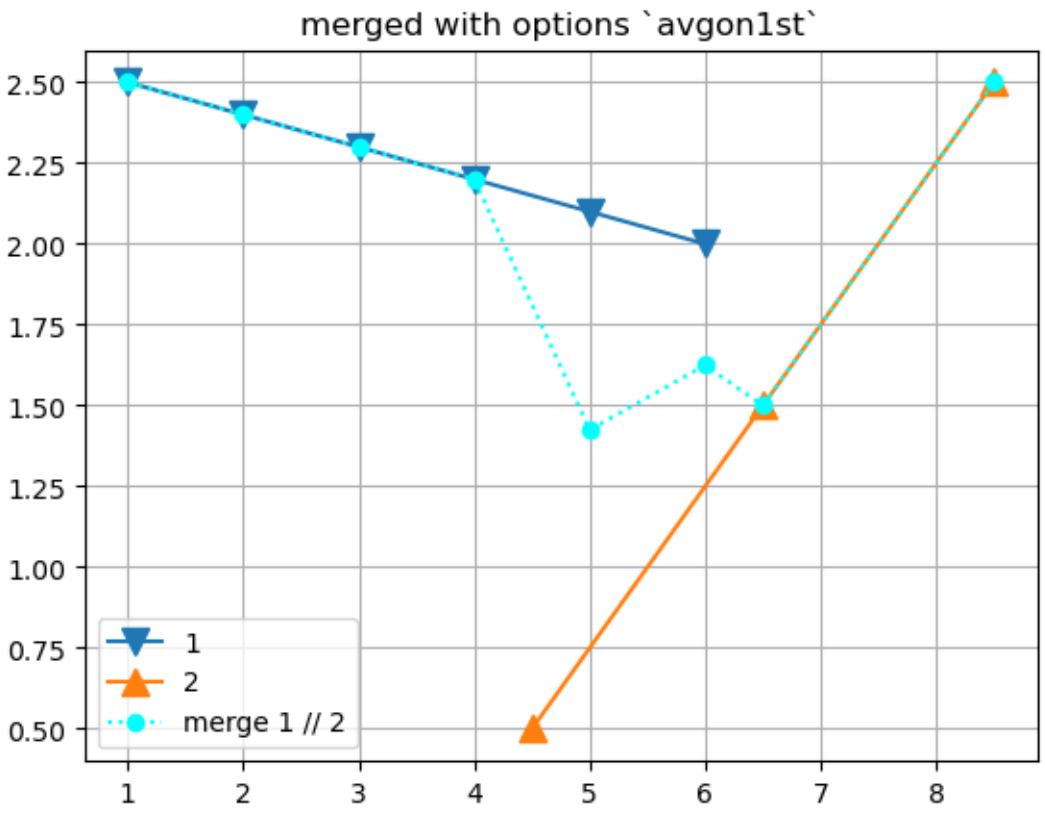

```
<Figure size 640x480 with 0 Axes>
```




```
<Figure size 640x480 with 0 Axes>
```




```
<Figure size 640x480 with 0 Axes>
```



2.3.2 Reimplementation of merge_profiles

Debug of `merge_profiles` old version

[105]:
```
# This reproduces the first part of the function, used if binning is not used.
# gives xtot and ytot as lists of vectors.
# They will be stacked before return.

ranges = None
removezero = False

if ranges is None:
    ranges = np.repeat([[None],[None]],
                       len(profiles),axis=1).T

xtot,ytot,bins,xvals,yvals = [] , [], [], [], []

for ran,pr in zip(ranges,profiles):
    if ran is not None:
        #print(d)
        x,y = pr
        if removezero:
```

```
            if x[0] == 0:  # this is for PSD
                x=x[1:]
                y=y[1:]
        xx,yy = crop_profile(x,y,ran)
        #plot_psd(xx,yy,label=lab,units=['um','um','nm'])
        xtot.append(xx)
        ytot.append(yy)
```

[106]:
```
for x,y in zip(xtot,ytot): print(len(x),len(y))
```

```
5 5
6 6
```

[107]:
```
# now reproduce the second part, preparing and running loop
pmin = [a.min() for a in xtot]   #xtot and ytot are now lists of profiles
igroup = np.argsort(pmin)
igroup
```

[107]:
```
array([0, 1], dtype=int64)
```

[108]:
```
print(xtot)
print(xvals)
for x,y in zip(xtot,ytot): print(len(x),len(y))
```

```
[array([100.000933, 119.996453, 139.993429, 159.994105, 179.995658]),
array([170.005221, 189.989255, 209.993582, 229.995753, 250.008344,
       269.998138])]
[]
5 5
6 6
```

[109]:
```
#print(xtot,ytot)
merge_profile(xtot[0],ytot[0],xtot[1],ytot[1])
```

[109]:
```
(array([100.000933, 119.996453, 139.993429, 159.994105, 179.995658,
        189.989255, 209.993582, 229.995753, 250.008344, 269.998138]),
 array([51.03133799, 30.02642307, 30.19383133, 33.52539943, 36.83041337,
        42.22760291, 47.51014816, 52.74996293, 60.51004572, 61.22432716]))
```

[110]:
```
# at the end they are stacked
xtot=np.hstack(xtot)
ytot=np.hstack(ytot)
#xvals=np.hstack(xvals)
#yvals=np.hstack(yvals)
#xbins = np.hstack(bins)
```

This is an example of a problematic case of merging:

[ ]:
```
# TODO: simplify to a more immediate example, update to last Elettra functions␣
↪(run03)

xblocks = [
    np.array([100.000197, 119.997119, 139.990071, 159.995605, 180.006148, 200.
↪004466]), np.array([170.006025, 189.992488, 209.994727, 230.002501, 250.
↪003368, 270.007416,
        289.983999, 310.012652]),
    np.array([259.999258, 279.998319, 300.003284, 319.984708, 340.013181, 359.
↪990443,
        380.02042, 399.984509, 420.008402, 440.006061, 459.975749, 480.017338]),
    np.array([440.012712, 459.976969, 480.009518, 500.007687, 519.981063, 540.
↪018112,
        560.006537, 579.993575, 600.023119, 619.974386, 640.019435, 659.991401,
        679.98877, 699.999849, 720.034351, 740.006997, 759.970621, 779.971205,
        800.035201, 820.001015, 840.006276, 859.979971, 879.986153, 899.994386,
        920.021177, 940.018302, 960.014845, 979.995367, 1000.01037])
    ]

yblocks = [
    np.array([0.01742948, 0.032655  , 0.03085043, 0.02779778, 0.02435627,
    0.15982401]),
    np.array([0.02821546, 0.0214196 , 0.01885777, 0.01703009, 0.01467265,
    0.01482432, 0.08721571, 0.08040641]),
    np.array([0.0128626 , 0.01649427, 1.66675707, 0.30323858, 0.23641212,
    0.20698373, 0.18030195, 0.1552664 , 0.14823087, 0.11937488,
        0.10714445, 0.02015584]),
    np.array([0.1105932 , 0.10031411, 0.09541419, 0.08685909, 0.07906037,
    0.07683974, 0.07843662, 0.07246274, 0.06789404, 0.06453243,
    0.06165937, 0.058863  , 0.05573335, 0.05271368, 0.04999151,
    0.04724698, 0.04429059, 0.04126784, 0.03791348, 0.03468448,
    0.03163833, 0.02879261, 0.02607514, 0.02360885, 0.02138706,
    0.01944354, 0.0178    , 0.01639909, 0.0152415 ])
    ]

merge_block(xblocks, yblocks)
```

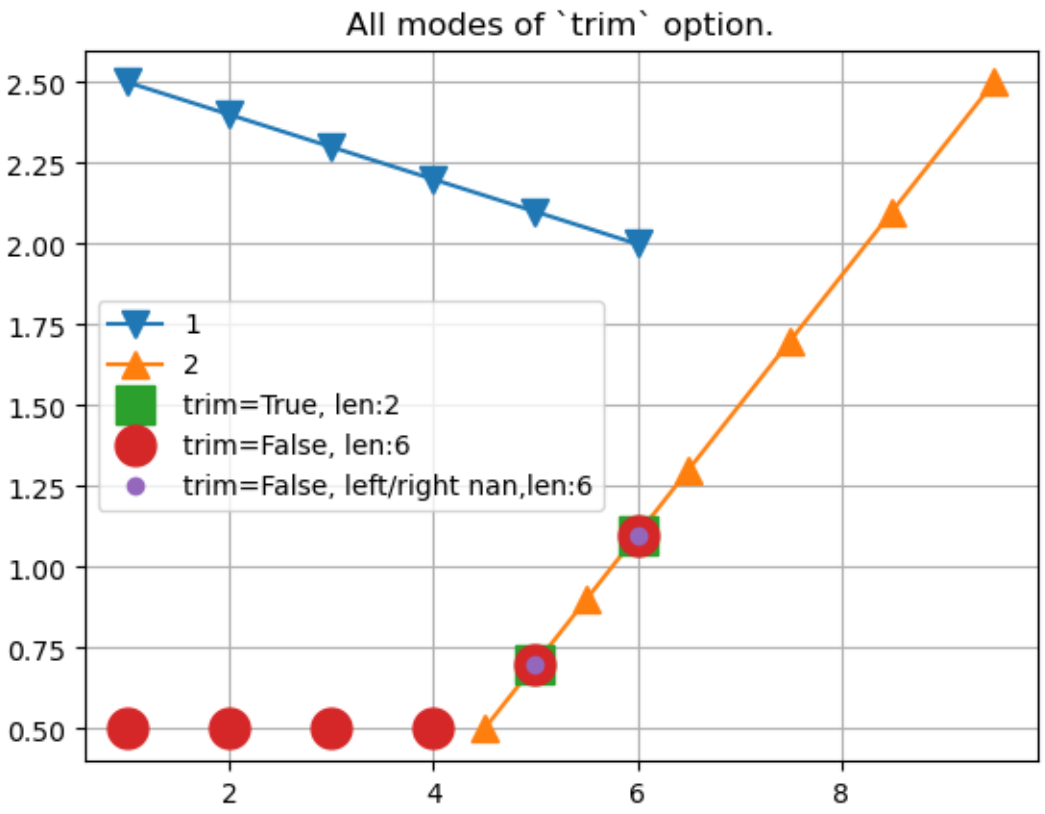
2.4 Test for profile merge and resample

2.5 Test `resample`

[111]:
```
%matplotlib inline
```

[112]:
```
x1,y1,x2,y2 = test_merge_init()
```

[113]:
```
test_resample_trim (x1,y1,x2,y2)
```



Debug of resample

[114]:
```
# resample x1 on x2
# works on interp and crop

yy2 = np.interp(x2,x1,y1)

print('x1',x1,y1)
print('x2',x2,y2)
print('resampled:',x2,yy2)
print(crop_profile(x2,yy2,span(x1)))
```

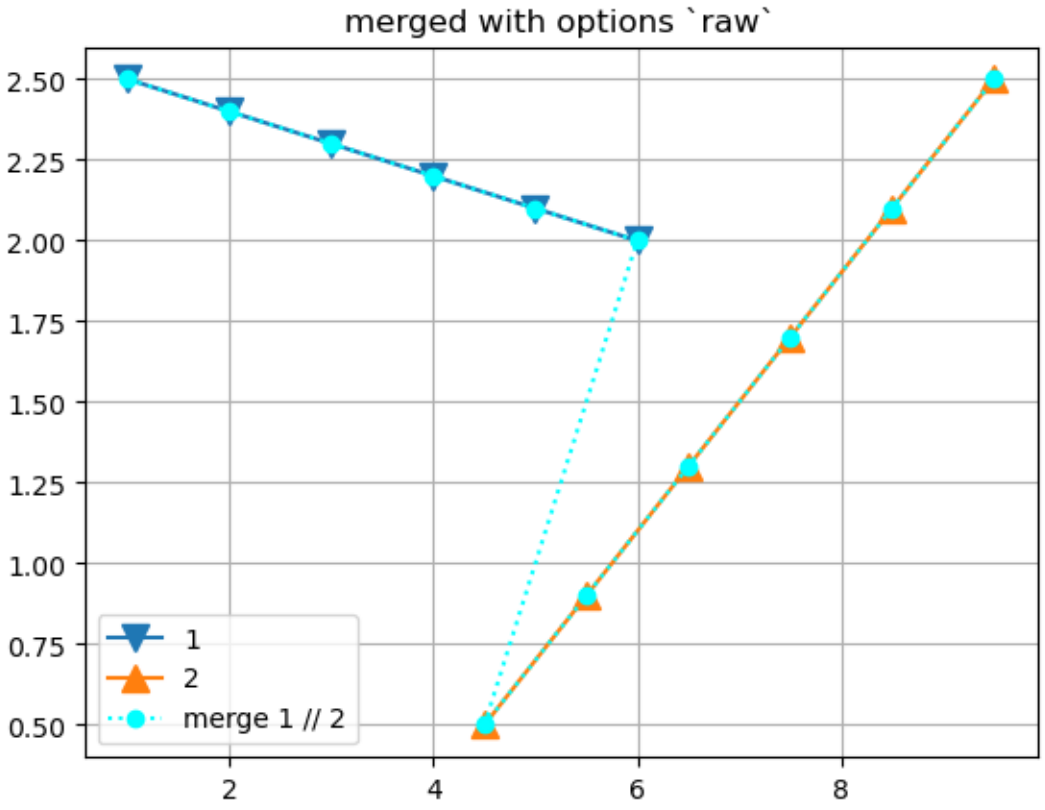
```
x1 [1 2 3 4 5 6] [2.5 2.4 2.3 2.2 2.1 2. ]
x2 [4.5 5.5 6.5 7.5 8.5 9.5] [0.5 0.9 1.3 1.7 2.1 2.5]
resampled: [4.5 5.5 6.5 7.5 8.5 9.5] [2.15 2.05 2.   2.   2.   2.  ]
(array([4.5, 5.5]), array([2.15, 2.05]))
```

2.5.1 Test of merge

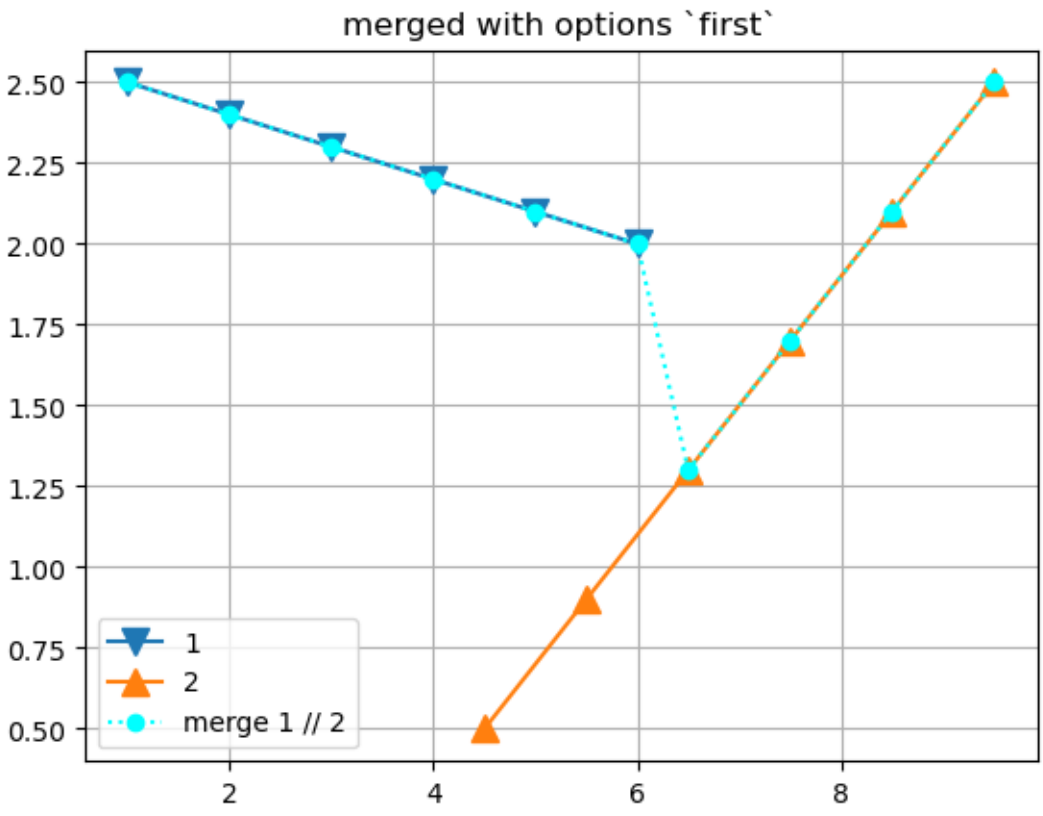
[115]:
```
test_merge_mode (x1,y1,x2,y2)
```

```
(array([1. , 2. , 3. , 4. , 5. , 6. , 6.5, 7.5, 8.5, 9.5]), array([2.5, 2.4,
```

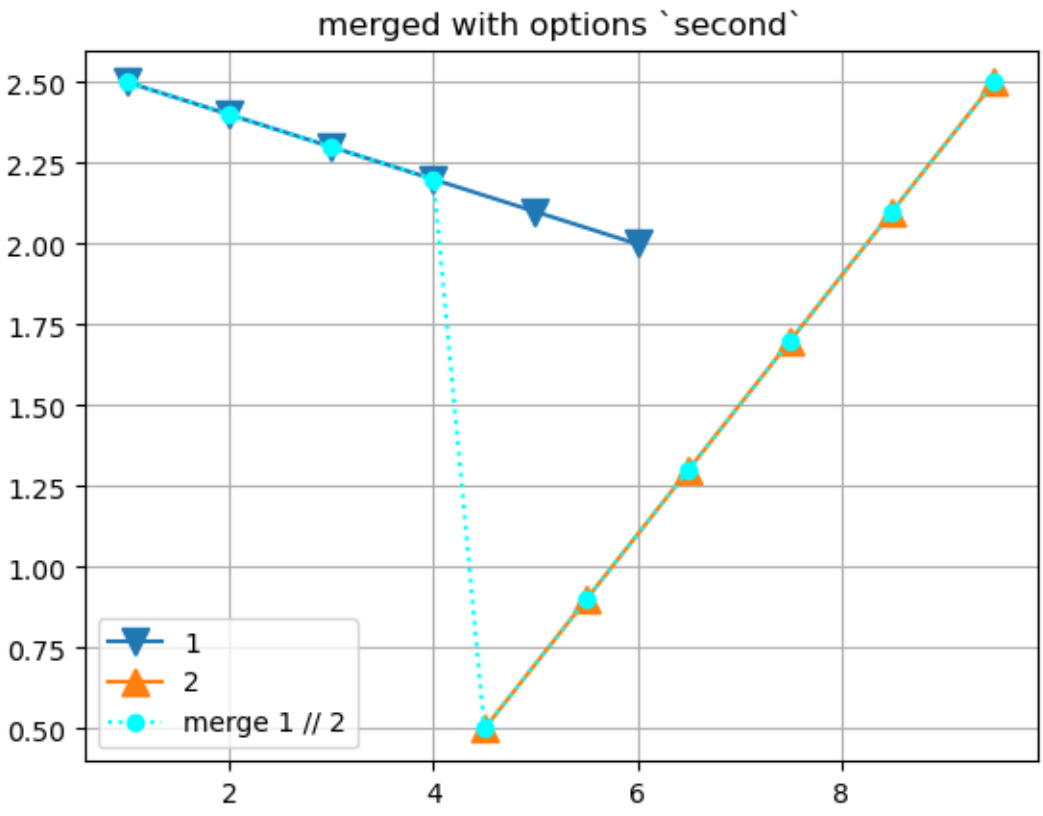
```
2.3, 2.2, 2.1, 2. , 1.3, 1.7, 2.1, 2.5]))
(array([1. , 2. , 3. , 4. , 4.5, 5.5, 6.5, 7.5, 8.5, 9.5]), array([2.5, 2.4,
2.3, 2.2, 0.5, 0.9, 1.3, 1.7, 2.1, 2.5]))
(array([1. , 2. , 3. , 4. , 5. , 6. , 6.5, 7.5, 8.5, 9.5]), array([2.5 , 2.4 ,
2.3 , 2.2 , 1.4 , 1.55, 1.3 , 1.7 , 2.1 , 2.5 ]))
```



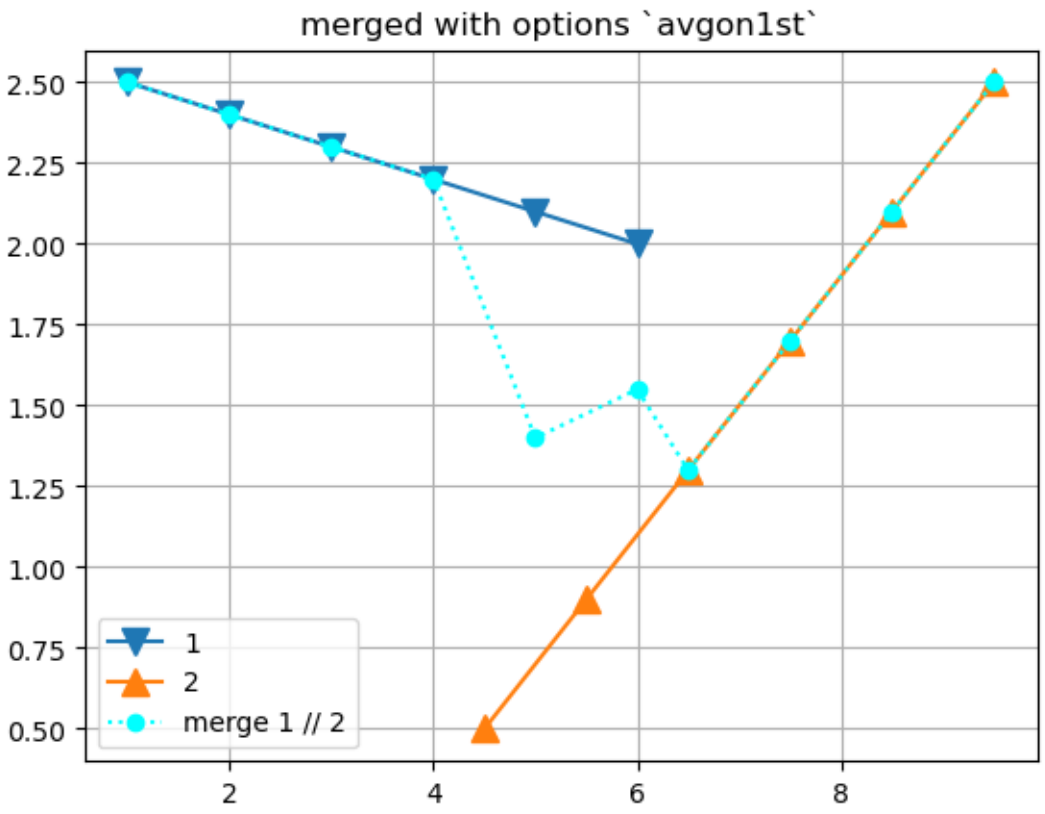

```
<Figure size 640x480 with 0 Axes>
```




```
<Figure size 640x480 with 0 Axes>
```



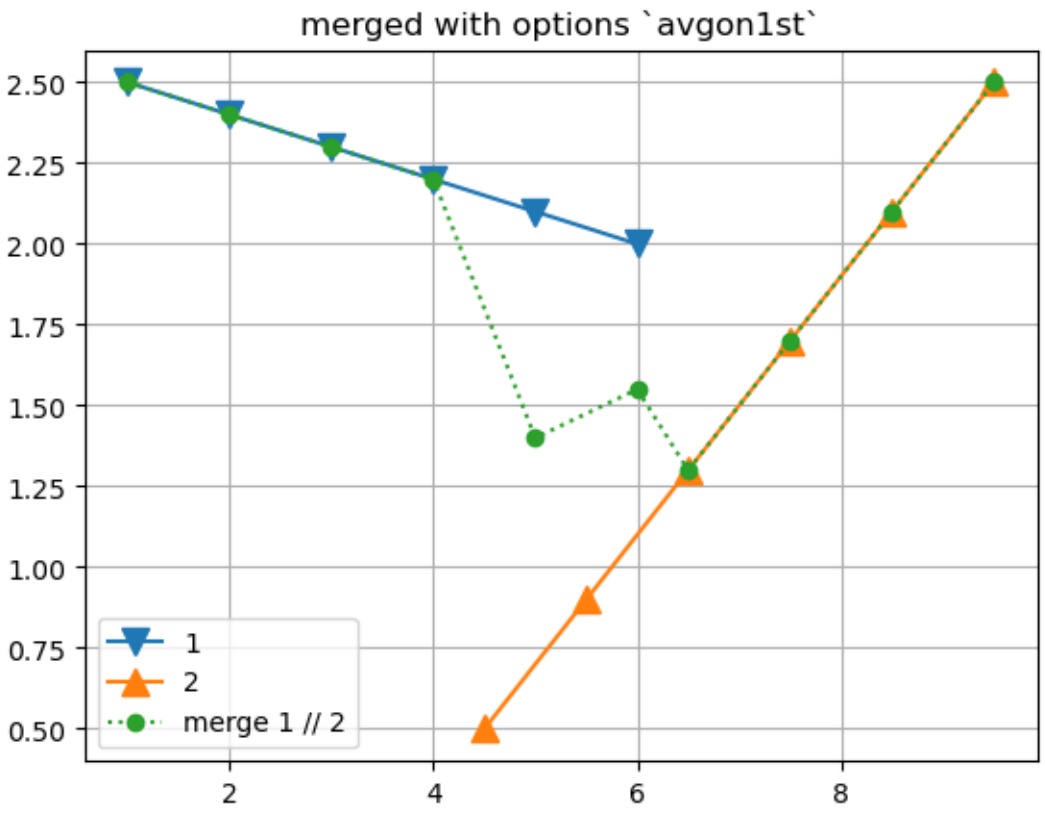

```
<Figure size 640x480 with 0 Axes>
```



Debug of `merge_profile` Works well with all options. Test of resample and sum works well here:

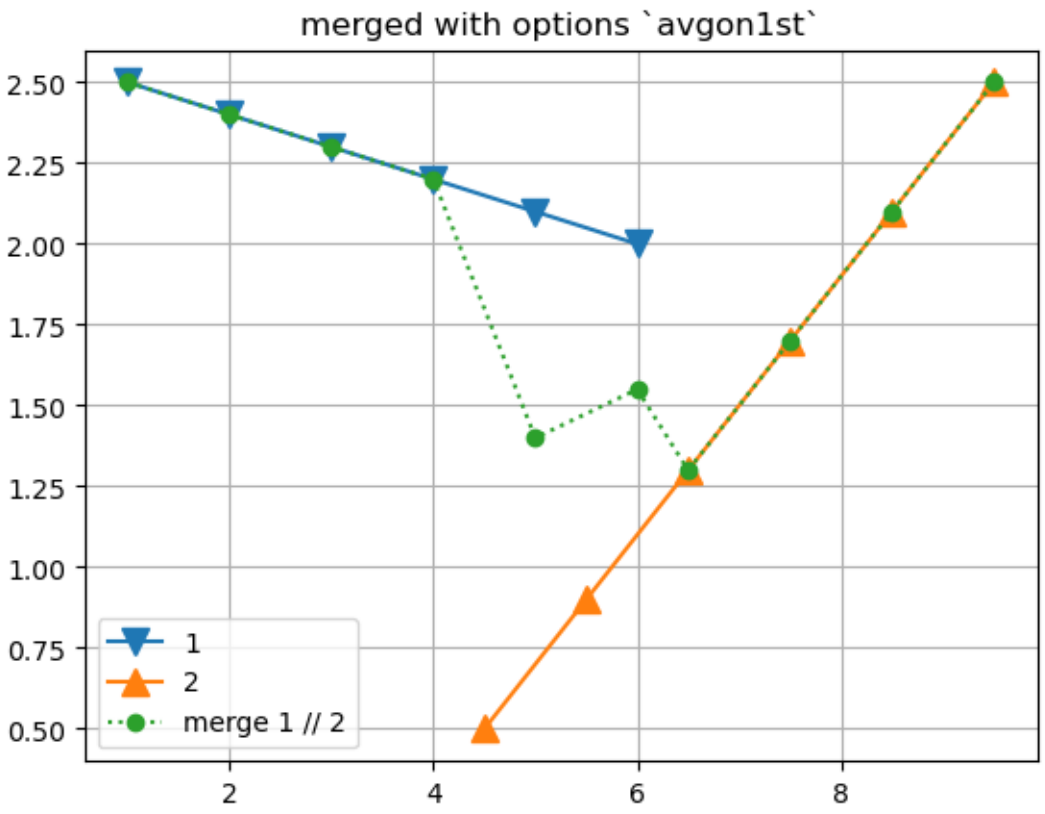
[ ]:
```
# This tests a single mode:

m4 = test_merge_profile(x1,y1,x2,y2,mode='avgon1st')
print(m4)
```

```
(array([1. , 2. , 3. , 4. , 5. , 6. , 6.5, 7.5, 8.5, 9.5]), array([2.5 , 2.4 ,
2.3 , 2.2 , 1.4 , 1.55, 1.3 , 1.7 , 2.1 , 2.5 ]))
```



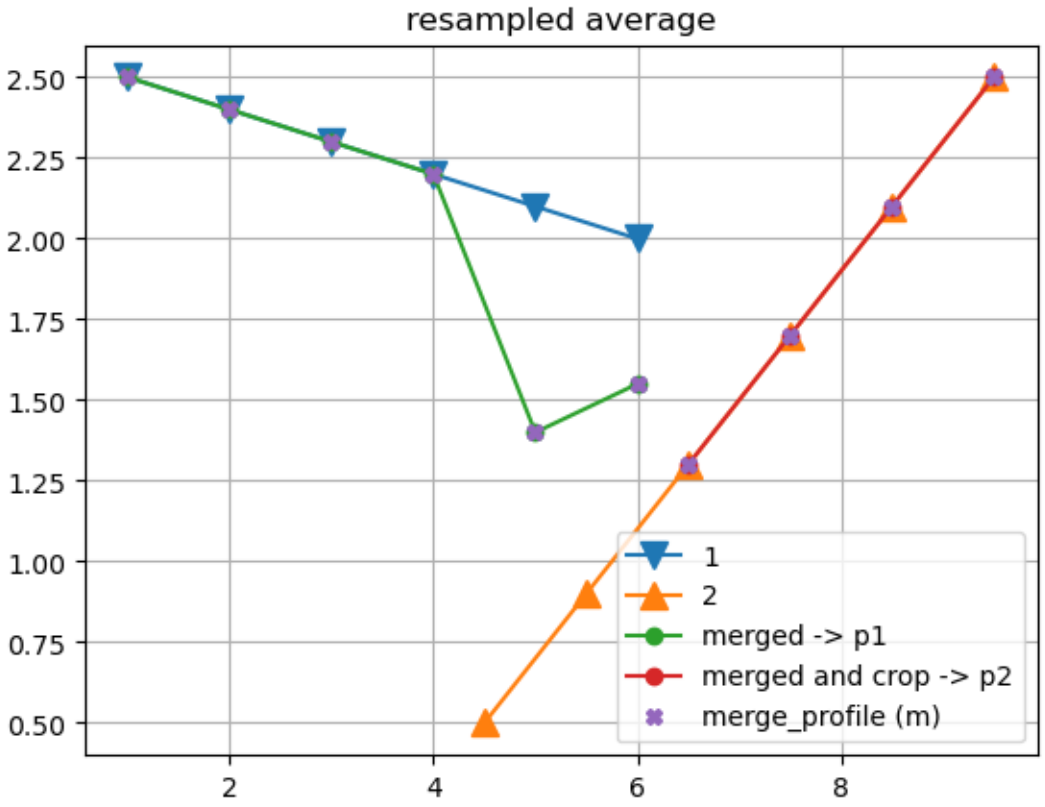
[ ]:
```
# this is the internal call:

test_merge_init_plot(x1,y1,x2,y2)
m = merge_profile(x1,y1,x2,y2,mode='avgon1st')

plt.plot(*m,marker='o',ls=':',label = 'merge 1 // 2')
plt.grid()
plt.legend()
plt.title("merged with options `%s`"%mode)
```

```
Text(0.5, 1.0, 'merged with options `avgon1st`')
```



[ ]:
```
# which is internally handled as

# Internally implements a workaround that is:
xx2,yy2  = resample_profile(x2,y2,x1) # p2 resampled on p1, can have fewer␣
 ↪points than p1
xx1,yy1 = resample_profile(x1,y1,xx2) # gives points of x1 on overlap.

test_merge_init_plot(x1,y1,x2,y2)

# in merge_profile
# beware, variable names were changed to not alter p1 and p2
xx2, yy2 = sum_profiles(x1,y1,x2, y2)
yy2 = yy2/2
x1_,y1_ = merge_profile(x1,y1,xx2,yy2,mode = 'second') #joins x1,y1 below␣
 ↪overlapping region with interpolated points on overlapped region
xr,yr = crop_profile(x2,y2,[max(x1_),None])  # second segment is points of␣
 ↪x2,y2 above overlapping

# plot
plt.plot(x1_,y1_,'o-',label='merged -> p1')
```

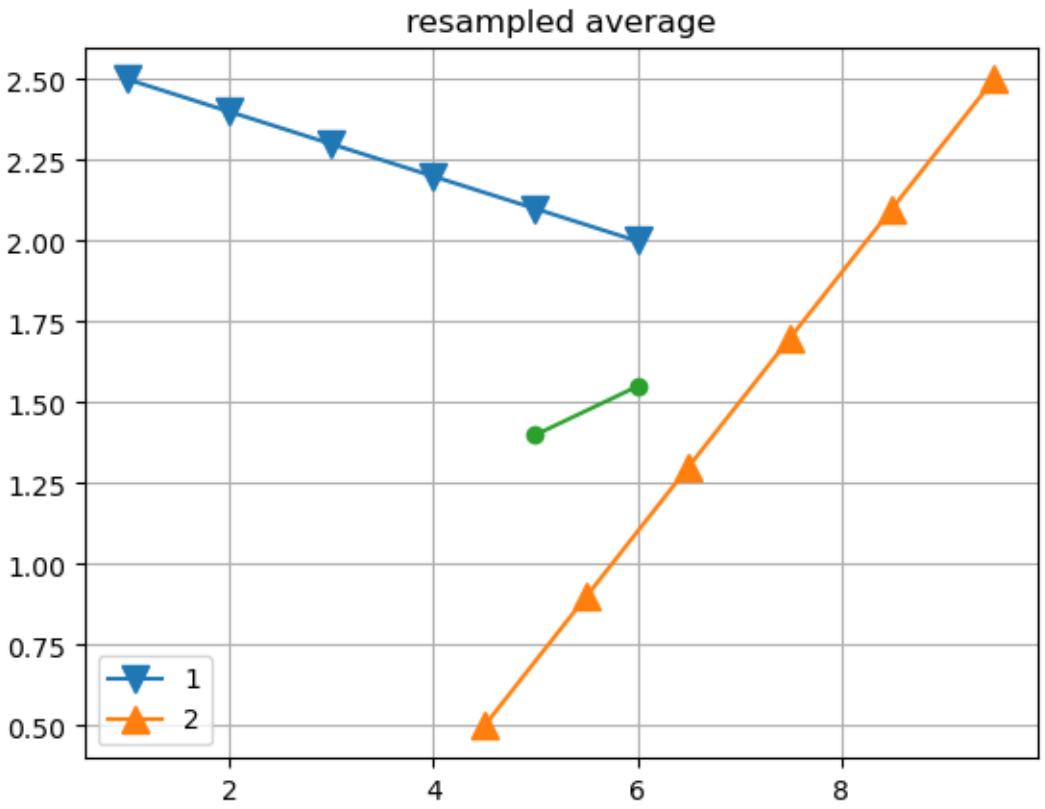
```
plt.plot(xr,yr,'o-',label='merged and crop -> p2')
plt.plot(*m,'X',label='merge_profile (m)')
plt.grid()
plt.legend()
plt.title('resampled average')

plt.show() #make figure appear before print
print('1:',x1,y1)
print('2:',x2,y2)
print('resampled:',xr,yr)
```




```
1: [1 2 3 4 5 6] [2.5 2.4 2.3 2.2 2.1 2. ]
2: [4.5 5.5 6.5 7.5 8.5 9.5] [0.5 0.9 1.3 1.7 2.1 2.5]
resampled: [6.5 7.5 8.5 9.5] [1.3 1.7 2.1 2.5]
```

[ ]:
```
# resample and sum don't work if y1 is not also trimmed.

# This is embedded in `profile` algebraic operations, but to use them you need
#   to use e.g. `sum_profiles` instead of operating of components.
# Internally implements a workaround that is:
```

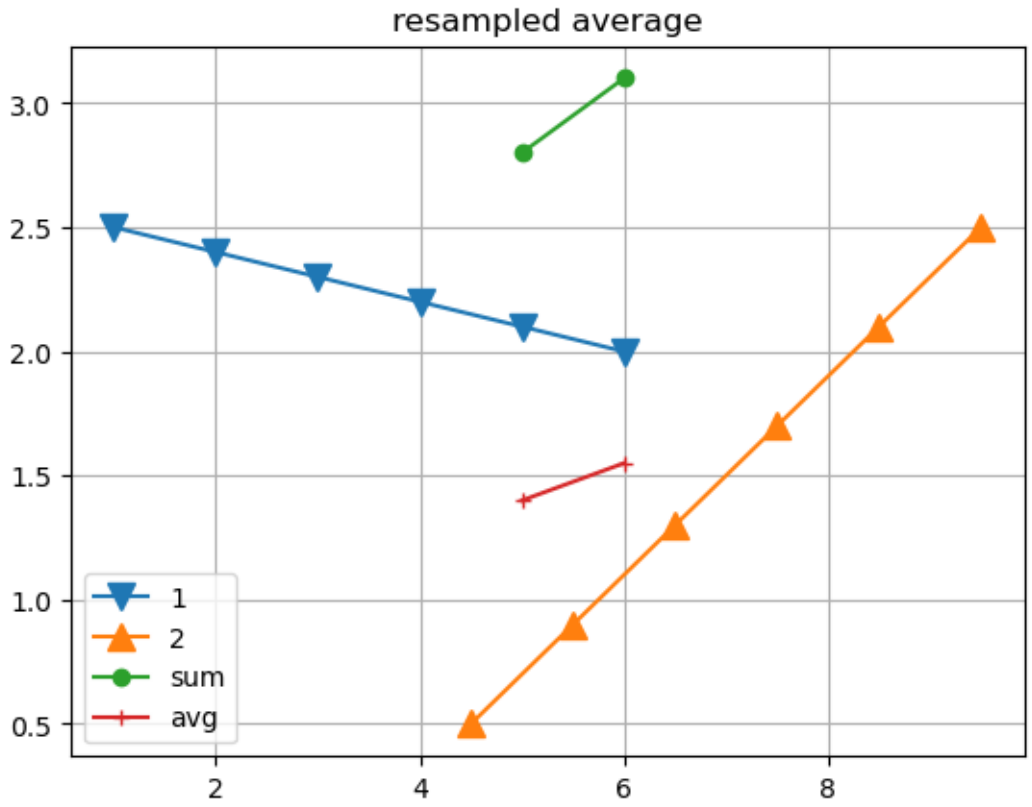
```
xx2,yy2  = resample_profile(x2,y2,x1) # p2 resampled on p1, can have fewer␣
 ↪points than p1
xx1,yy1 = resample_profile(x1,y1,xx2) # gives points of x1 on overlap.

xr = xx1
yr = (yy1 + yy2)/2
#yy2 = (yy1 + yy2)/2

test_merge_init_plot(x1,y1,x2,y2)
plt.plot(xr,yr,'o-')
plt.grid()
plt.legend()
plt.title('resampled average')

plt.show() #make figure appear before print
print('1:',x1,y1)
print('2:',x2,y2)
print('resampled:',xr,yr)
```




```
1: [1 2 3 4 5 6] [2.5 2.4 2.3 2.2 2.1 2. ]
2: [4.5 5.5 6.5 7.5 8.5 9.5] [0.5 0.9 1.3 1.7 2.1 2.5]
```

```
resampled: [5 6] [1.4  1.55]
```

[ ]:
```
# this is how internally works in sum

xr , yr =  sum_profiles (x1,y1,x2,y2)
yr2 =yr/2

test_merge_init_plot(x1,y1,x2,y2)
plt.plot(xr,yr,'o-',label='sum')
plt.plot(xr,yr2,'+-',label='avg')
plt.grid()
plt.legend()
plt.title('resampled average')

plt.show() #make figure appear before print
print('1:',x1,y1)
print('2:',x2,y2)
print('resampled:',xr,yr)
```




```
1: [1 2 3 4 5 6] [2.5 2.4 2.3 2.2 2.1 2. ]
2: [4.5 5.5 6.5 7.5 8.5 9.5] [0.5 0.9 1.3 1.7 2.1 2.5]
resampled: [5 6] [2.8 3.1]
```

[ ]:
```
print('1:',x1,y1)
print('2:',x2,y2)
print('resampled:',xr,yr)
```

```
1: [1 2 3 4 5 6] [2.5 2.4 2.3 2.2 2.1 2. ]
2: [4.5 5.5 6.5 7.5 8.5 9.5] [0.5 0.9 1.3 1.7 2.1 2.5]
resampled: [5 6] [2.8 3.1]
```

[ ]:
```
xx2,yy2 = resample_profile(x2,y2,x1,y1) #Trim True by default
xx1,yy1 = resample_profile(xx2,yy2,x1,y1)  # gives coordinates on overlap
yy2 = (yy1 + yy2)/2

# x1,y1 = merge_profile(x1,y1,xx2,yy2,mode = 'second')
# x2,y2 = crop_profile(x2,y2,[max(x1),None])

# this is the implemented version, note the use of `open`:
x1,y1 = merge_profile(x1,y1,xx2,yy2,mode = 'second') #joins x1,y1 below␣
 ↪overlapping region with interpolated points on overlapped region
x2,y2 = crop_profile(x2,y2,[max(x1),None], open = True)  # second segment is␣
 ↪points of x2,y2 above overlapping
```

[ ]:
```
x1,y1,x2,y2 = test_merge_init() # reinitialize data for the tests above
```

Different data set and Offset

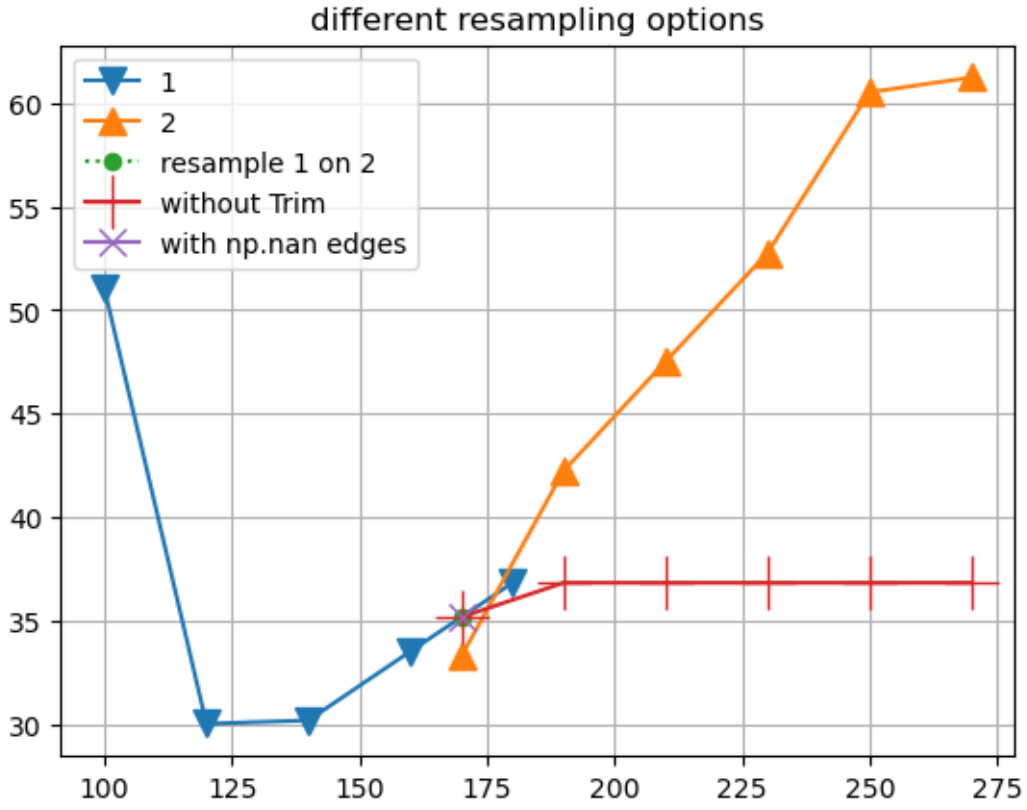
[ ]:
```
from pyProfile.profile import test_resample_profile
```

[ ]:
```
# modifies x1 and x2
# repeat with merge_profiles
plt.figure()
x1,y1 = a[0]()
x2,y2 = a[1]()
mode = 'avgon1st'

m = test_resample_profile(x1,y1,x2,y2,trim=True) #default
m2 = resample_profile(x1,y1,x2,y2,trim=False)
m3 = resample_profile(x1,y1,x2,y2,trim=False,left=np.nan,right=np.nan)


plt.plot(*m2,label='without Trim',marker='+',ms=20)
plt.plot(*m3,label='with np.nan edges',marker='x',ms=10)

plt.title('different resampling options')
plt.legend()

for v in [m,m2,m3]: print('npoints:',len(v[0]))
```

```
npoints: 1
npoints: 6
```

```
npoints: 6
```

```
<Figure size 640x480 with 0 Axes>
```



2.5.2 Development of `merge_profiles`

[ ]:
```
## N.B. TBD later, this belongs to Plist
```

This shows how merging works without defined intervals. Overlapping is simply not handled. It is up to the user to trim the arrays beforehand to correct for overlapping. `binned` option accounts for overlapping but is not functionning at the moment:

[ ]:
```
merge_profiles([a[0](),a[1]()])
```

[ ]:
```
# result: it is creating different length x and y
# when binning is selected. This is because bins as array in binned_statistics
# includes both left and right extreme. Select center point of each interval.
# make option to set bin centers.

m = a[0].merge(a[1])
m2 = a[0].merge(a[1],binned=True)
```

```
P = Plist(a[:2])
P.plot()
m.plot(marker='o',ls=':')
plt.legend()
#plt.xlim([150,200])
```

[ ]:
```
# repeat with merge_profiles

plt.plot(*a[0](),label = '1')
plt.plot(*a[1](),label = '2')
m = merge_profiles([a[0](),a[1]()])

plt.plot(*m,marker='o',ls=':',label = 'merged 1//2')
plt.legend()
#plt.xlim([150,200])
plt.title('merge a list of 2 couples x,y with profile.merge_profiles')
```

[ ]:
```
# repeat adding binned test

plt.plot(*a[0](),label = '1',lw=5,color='yellow')
plt.plot(*a[1](),label = '2',lw=5,color='orange')
m = merge_profiles([a[0](),a[1]()])
mb = merge_profiles([a[0](),a[1]()], binned = True)

plt.plot(*m,marker='o',ls=':',color='green',label = 'merged 1//2')
plt.plot(*mb,marker='+',ms = 20,color = 'blue',ls=None,label = 'merged 1//2')
plt.legend()
#plt.xlim([150,200])
plt.title('merge a list of 2 couples x,y with profile.merge_profiles')
```

Development of binning

[ ]:
```
mb = merge_profiles([a[0](),a[1]()], binned = True)
for m in mb:print (len(m))
```

```
---------------------------------------------------------------------------

ValueError                                Traceback (most recent call last)

~\AppData\Local\Temp\ipykernel_14364\922337808.py in <cell line: 1>()

----> 1 mb = merge_profiles([a[0](),a[1]()], binned = True)

      2 for m in mb:print (len(m))
```

```
c:\users\kovor\documents\python\pyxtel\source\pyProfile\profile.py in␣
 ↪merge_profiles(profiles, ranges, binned, removezero, mode)

    712     yvals=np.hstack(yvals)

    713     xbins = (xvals[:1]+xvals[1:])/2 #np.hstack(bins)

--> 714     ybins = binned_statistic(xtot,ytot,bins=xbins,statistic='mean') [0]

    715     ###

    716     if mode == 'raw':  #include all points, sorted by value



c:\Users\kovor\anaconda3\lib\site-packages\scipy\stats\_binned_statistic.py in␣
 ↪binned_statistic(x, values, statistic, bins, range)

    181             range = [range]

    182

--> 183     medians, edges, binnumbers = binned_statistic_dd(

    184         [x], values, statistic, bins, range)

    185



c:\Users\kovor\anaconda3\lib\site-packages\scipy\stats\_binned_statistic.py in␣
 ↪binned_statistic_dd(sample, values, statistic, bins, range, expand_binnumbers␣
 ↪binned_statistic_result)

    569     if binned_statistic_result is None:

    570         nbin, edges, dedges = _bin_edges(sample, bins, range)

--> 571         binnumbers = _bin_numbers(sample, nbin, edges, dedges)

    572     else:

    573         edges = binned_statistic_result.bin_edges
```

```
c:\Users\kovor\anaconda3\lib\site-packages\scipy\stats\_binned_statistic.py in␣
 ↪_bin_numbers(sample, nbin, edges, dedges)

    749         dedges_min = dedges[i].min()

    750         if dedges_min == 0:

--> 751             raise ValueError('The smallest edge difference is␣
 ↪numerically 0.')

    752         decimal = int(-np.log10(dedges_min)) + 6

    753         # Find which points are on the rightmost edge.



ValueError: The smallest edge difference is numerically 0.
```

[ ]:
```
mb
```

```
---------------------------------------------------------------------------

NameError                                 Traceback (most recent call last)

~\AppData\Local\Temp\ipykernel_14364\1239492857.py in <cell line: 1>()

----> 1 mb



NameError: name 'mb' is not defined
```

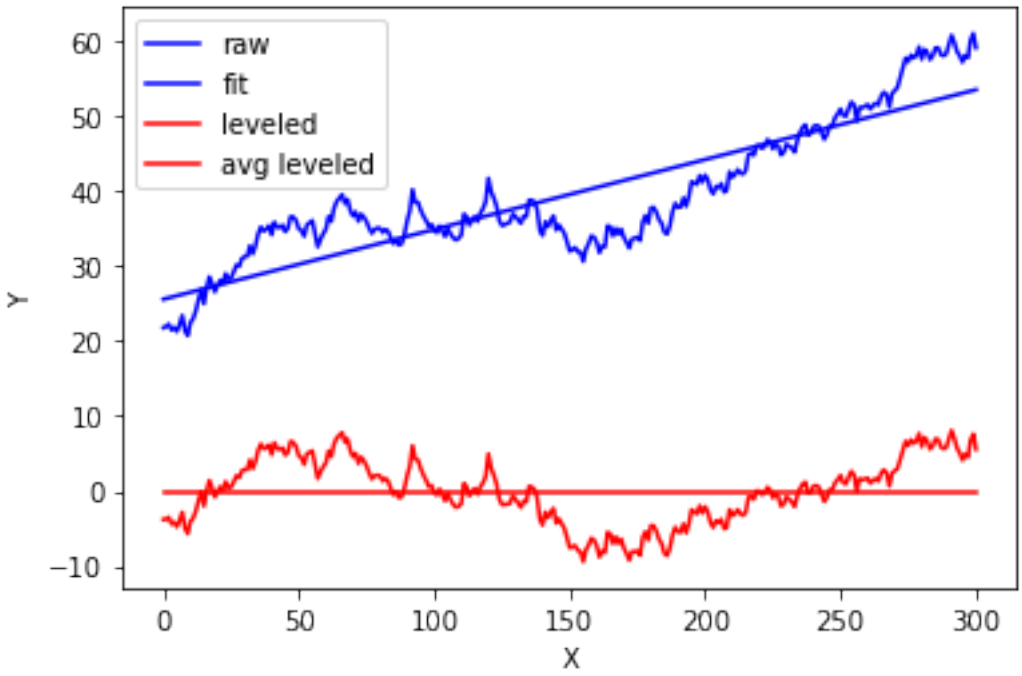
2.6 Leveling

[ ]:
```
# riproduce esempio di matlab da:
# https://it.mathworks.com/help/matlab/data_analysis/detrending-data.html
#
#

fn = r'input_data\matlab-normaldata.dat'
```

[ ]:
```
y = np.genfromtxt(fn)
p=Profile(np.arange(len(y)),y)
p.plot(color='b',label = 'raw')
(p-p.level()).plot(color='b',label = 'fit')
```

```
p.level().plot(color='r',label = 'leveled')
plt.plot(p.x,p.y*0+p.level().y.mean(),color='r',label = 'avg leveled')
plt.legend()
```

```
<matplotlib.legend.Legend at 0x2f9e5743438>
```



2.6.1 Outliers filtering

TBD

[ ]:
```
a=0
```

[ ]:
```
a = 1
```

[ ]:
```
print(a)
```

```
1
```

[ ]:

[ ]:

[ ]: