```
Useful-python-for-medical-physics (/github/robmarkcole/Useful-python-for-medical-physics/tree/master)

/ Experiments in ipython notebooks (/github/robmarkcole/Useful-python-for-medical-physics/tree/master/Experiments in ipython notebooks)

/ Omnipro (/github/robmarkcole/Useful-python-for-medical-physics/tree/master/Experiments in ipython notebooks/Omnipro)
```

Loading omnipro data (/github/robmarkcole/Useful-python-for-medical-physics/tree/master/Experiments in ipython notebooks/Omnipro/Loading omnipro data)

http://chrisalbon.com/python/pandas\_dataframe\_load\_xls.html (http://chrisalbon.com/python/pandas\_dataframe\_load\_xls.html)

PDD & Profil Data exported from omnipro.

Step by step Scan:

- 60mm to -0.5mm depth: 0.5mm step size, 15mm/s speed, 1s meas time,
- 350mm to 50mm depth: 2mm step size, 15 or 20mm/s speed, 0.5s meas time

Resample the deep dose profile to 1mm and join the two plots together.

OMNIPRO - if multiple tables are selected for export, x,y,z coordinate info is lost and data is sampled at 1mm. Export traces individually to keep coordinate data, e.g. if higher at higher or lower sample than 1mm.

```
In [1]:
```

```
%matplotlib inline
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import os
from scipy import interpolate
```

```
In [1]:
print('yo')
yo
```

In [3]:

```
os.listdir()
Out[3]:
```

```
['.ipynb_checkpoints',
  'archive',
  'data',
  'files.txt',
  'Omnipro data ANALYSIS v1 5-1-2017.ipynb',
  'Omnipro data load v2 3-1-2017.ipynb']
```

In [4]:

```
# whats in the data folder
data = os.listdir('data/')
data # returns a list of the contents of data folder
```

```
Out[4]:
```

```
['6MV 100FSD PROFILE (PDD JUNE - RAW).csv',
  'LA6(2015) 6MV 100FSD PDD microDiamond_ALL- RC edit.csv',
  'Microdiamond_6MV_raw_RC_from_June.xlsx']
```

#### Plot raw data

Note: normalised to PDD max = 100%

```
In [5]:
```

```
data_path = 'data/' + data[2] # load zeroth file in data
print(data_path)
HL_data = pd.ExcelFile(data_path)
```

 ${\tt data/Microdiamond\_6MV\_raw\_RC\_from\_June.xlsx}$ 

```
In [6]:
```

```
HL_data.sheet_names
Out[6]:
```

```
['High', 'Low']
```

```
In [7]:
```

```
High_df = HL_data.parse('High', index_col=0) # # is reading in the whole file ,
Low_df = HL_data.parse('Low', index_col=0)
```

#### In [8]:

```
High_df.max()
```

#### Out[8]:

Dose\_pct 100.07 dtype: float64

```
In [9]:

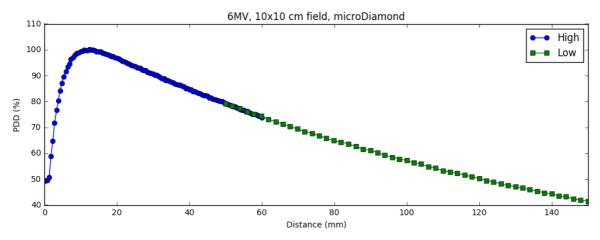
fig_width = 12
fig_height = 4
plt.figure(figsize=(fig_width,fig_height))

plt.plot(High_df, label='High', marker='o')
plt.plot(Low_df, label='Low', marker='s')

plt.xlim(0, 150)
plt.ylim(40, 110)
plt.ylim(40, 110)
plt.title('6MV, 10x10 cm field, microDiamond')
plt.ylabel('PDD (%)')
plt.xlabel('Distance (mm)')
plt.legend()
```

#### Out[9]:

<matplotlib.legend.Legend at 0xad6a170>



### In [10]:

```
High_low_concat = pd.concat([High_df, Low_df], axis=0).sort_index().dropna() # join the two arrays, drop the NAN
x = High_low_concat.index.values
y = High_low_concat['Dose_pct'].values
f = interpolate.interp1d(x, y) # returns an interpolate function
```

```
In [11]:
```

```
xnew = np.arange(0, 349)
ynew = f(xnew)  # use interpolation function returned by `interp1d`

fig_width = 12
fig_height = 6
plt.figure(figsize=(fig_width,fig_height))

plt.plot(xnew, ynew, color='red', marker='x', markersize = 20, label='interpolated', linestyle='')

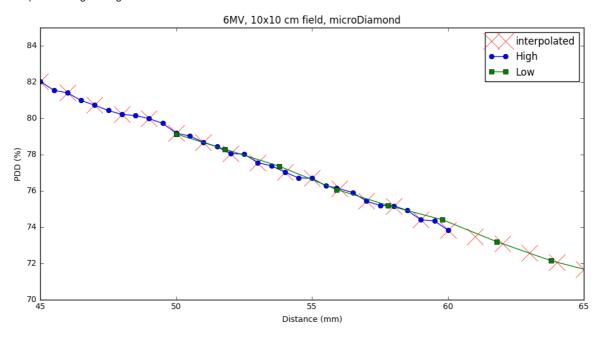
plt.plot(High_df, label='High', marker='o')

plt.plot(Low_df, label='Low', marker='s')
plt.xlim(45, 65)
plt.ylim(70, 85)

plt.title('6MV, 10x10 cm field, microDiamond')
plt.ylabel('PDD (%)')
plt.xlabel('Distance (mm)')
plt.legend()
```

#### Out[11]:

<matplotlib.legend.Legend at 0xae27910>



# Plot all PDD data

Note this is the data that was processed by james, PDD normalised to 100% at 5 cm.

```
In [12]:
```

```
load_csv = 'LA6(2015) 6MV 100FSD PDD microDiamond_ALL- RC edit.csv' # edited scan type, makes multi-index work data_path = 'data/' + load_csv # data[1] # hard code for fail safe
```

#### In [13]

```
PDD = pd.read_table(data_path, sep= ",", index_col=0, header=[1,4], skiprows=[5,6]); # comma for csv
```

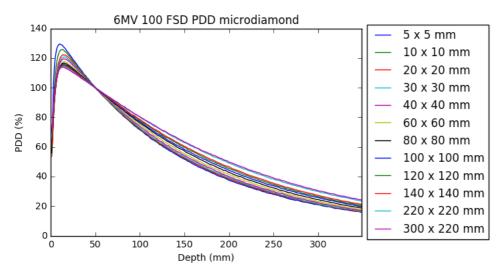
#### In [14]:

```
In [15]:
```

```
ax = PDD['Joined'].plot()
ax.set_xlabel('Depth (mm)')
ax.set_ylabel('PDD (%)')
ax.legend(loc='center left', bbox_to_anchor=(1, 0.5));
plt.title('6MV 100 FSD PDD microdiamond')
```

Out[15]:

<matplotlib.text.Text at 0xae5f370>



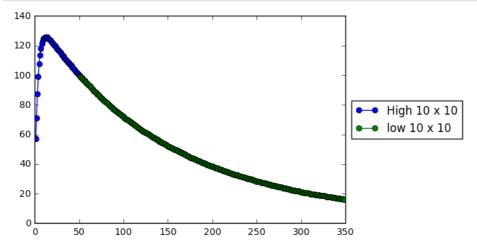
## Analyse omnipro 10x10 cm PDD data

#### In [16]:

```
fig_width = 12
fig_height = 4

high10 = PDD['High']['10 x 10 mm']
low10 = PDD['Low']['10 x 10 mm']

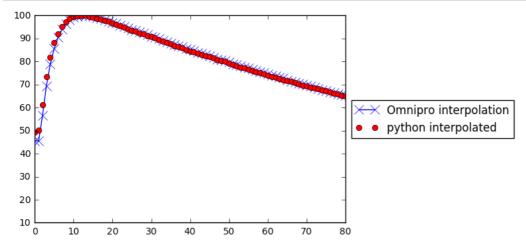
plt.plot(high10, label = 'High 10 x 10', marker='o')
plt.plot(low10, label = 'low 10 x 10', marker='o')
plt.legend(loc='center left', bbox_to_anchor=(1, 0.5));
xmin=30
xmax=70
#pLt.xLim( xmin, xmax )
```



Recreate the RESAMPLED trace. Concat the two differently sampled data, sort on index, then interpolate on linear spacing

```
In [17]:
```

```
joined10 = PDD['Joined']['10 x 10 mm']
plt.plot(100*joined10/joined10.max(), color='blue', marker='x', markersize = 10, label = 'Omnipro interpolation'); # Jamses resample
plt.plot(xnew, 100*ynew/ynew.max(), color='red', marker='o', label='python interpolated', linestyle='')
plt.xlim( 0,80 )
#plt.ylim( [90,110] )
plt.legend(loc='center left', bbox_to_anchor=(1, 0.5));
```



## Now profile data

#### In [18]:

```
# pd.read_table('6MV 100FSD PROFILE (PDD JUNE - RAW).csv', sep= ",").ix[:8] # see raw header
```

### In [20]:

```
PROFILE = pd.read_table('data/6MV 100FSD PROFILE (PDD JUNE - RAW).csv', sep= ",", index_col=0, header=[1,4,5], skiprows=[6]); # commc PROFILE.head()
```

## Out[20]:

Scan Type:	Crossline			Inline		
Fieldsize:	60 x 60 mm			60 x 60 mm		
Depth:	15.0 mm	100.0 mm	350.0 mm	15.0 mm	100.0 mm	350.0 mm
Coordinate [mm]:						
-90	NaN	NaN	1.3	NaN	NaN	1.3
-89	NaN	NaN	1.2	NaN	NaN	1.3
-88	NaN	NaN	1.2	NaN	NaN	1.2
-87	NaN	NaN	1.2	NaN	NaN	1.3
-86	NaN	NaN	1.4	NaN	NaN	1.3