

# building

January 20, 2023

## 1 Prepare and export stream files with f3ast

This notebook aims to give an overview of possible functionalities of the `f3ast` package, with probably only parts of it relevant to your specific structure/problem. Mix and match to your heart's delight :-)

### 1.1 Import packages and define microscope settings

```
[1]: import f3ast
import numpy as np

[2]: # settings can be loaded from a specified json file (given by file_path="...")
settings = f3ast.load_settings()

# or settings can be defined manually in a dictionary:
settings = {}
settings['structure'] = { \
    'pitch': 3, # in nm
    'fill': False
}
settings['stream_builder'] = { \
    'addressable_pixels': [65536, 56576],
    'max_dwt': 5, # in ms
    'cutoff_time': 0.01, # in md, for faster exporting: remove dwells_
    ↪below cutoff time
    'screen_width': 10.2e3, # in nm, horizontal screen width / field of_
    ↪view
    'scanning_order': 'serpentine' # 'serpentine' or 'serial', scanning_
    ↪order between slices
}
settings['dd_model'] = { \
    'single_pixel_width': 50 # pixel size for thermal resistance
}
```

## 1.2 Import and modify stl structure

```
[3]: file_path = 'FunktyBall.stl'
struct = f3ast.Structure.from_file(file_path, **settings["structure"])

# rotate: specify axis and angle in degrees
# this is for example useful if FEBID growth is done with a tilted SEM sample
↳stage
rotation_axis, rotation_angle = (0,0,1), 45.
struct.rotate( rotation_axis, rotation_angle )

# In some cases (e.g. Helios 600) , stream files appear mirrored on the SEM
↳screen
# compared to the orientation of the initial stl structure.
# If precise orientation of the structure (e.g. with respect to the GIS) is
↳important,
# a mirror operation can be applied: mirror plane can be x, y, or z
struct.mirror( mirror_plane='x' )

struct.centre() # centers xy to zero and sets minimum z value to zero
struct.rescale(3) # scale the structure 3x

# interactive plot for inspection
struct.show()
```

```
[3]: <IPython.core.display.HTML object>
```

## 1.3 Define the growth model

For the two main growth models - RRL (reaction-rate limited growth) with constant dwell time in height, and DD (desorption-dominated growth), for which the dwell time are modified taking into account increasing thermal resistance with structure length and height.

```
[4]: GRO = 50e-3 # in um/s, base growth rate
k = 1. # in 1/nm?, thermal conductivity
sigma = 4.4 # in nm, dwell size

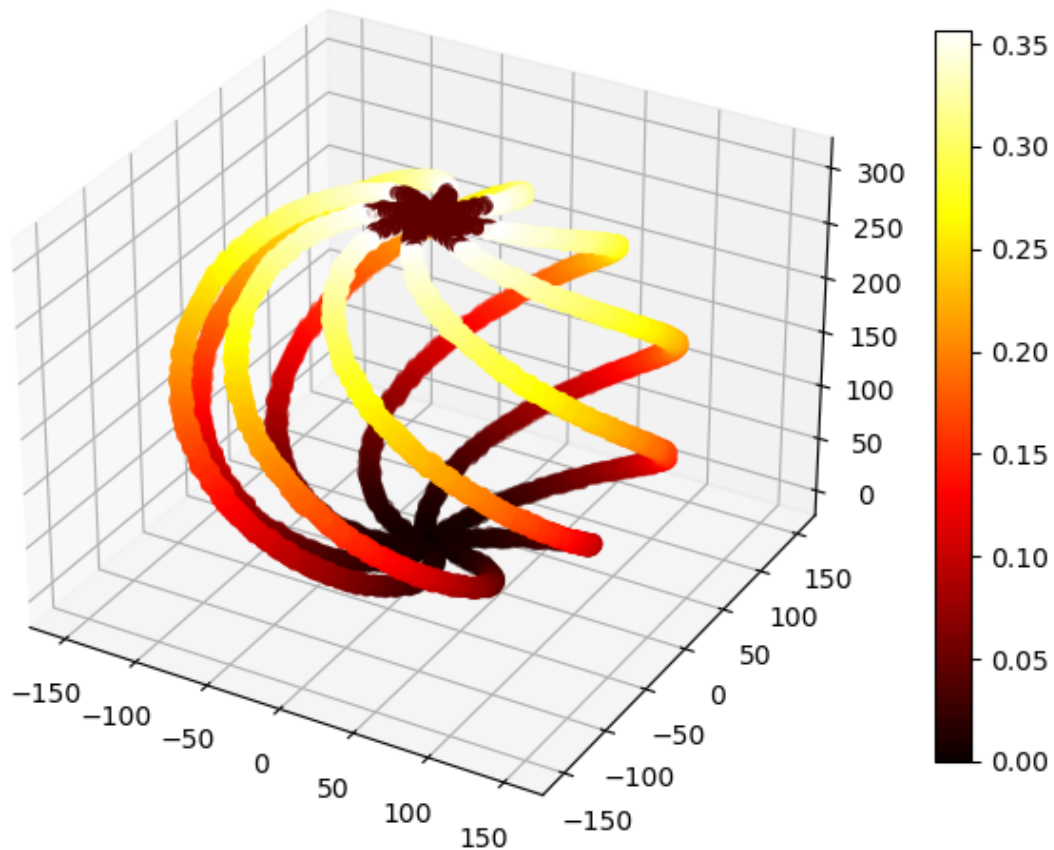
# simple model, without thermal correction
%time model = f3ast.RRLModel(struct, GRO, sigma)

# with correction due to thermal conductivity
%time model = f3ast.DDModel(struct, GRO, k, sigma, **settings['dd_model'])
```

```
CPU times: total: 0 ns
Wall time: 0 ns
Slicing...
Sliced
CPU times: total: 17 s
```

Wall time: 7.76 s

```
[5]: # plot thermal resistance for a check
# if there are discontinuities a z-dependent model for the dwell time might be
    ↪ better (see below)
ax = struct.plot_slices(c=np.concatenate(model.resistance), cmap='hot')
```



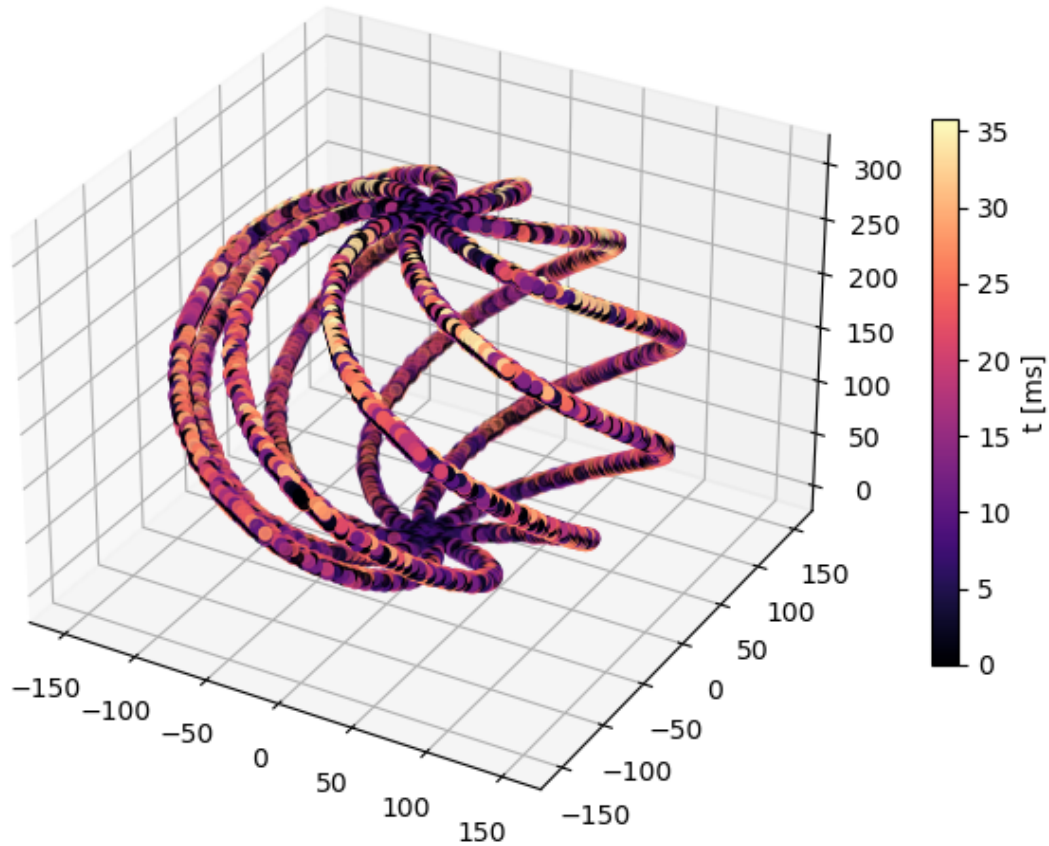
#### 1.4 Solve for dwells and inspect

```
[6]: %time stream_builder, dwell_solver = f3ast.StreamBuilder.from_model(model,
    ↪ **settings['stream_builder'])
dwell_solver.print_total_time()

# inspect dwells
ax, sc = dwell_solver.show_solution()
```

Solving for dwells...  
Solved

CPU times: total: 266 ms  
Wall time: 5.84 s  
Total stream time: 0:01:53.843431



## 1.5 Export stream files

Depending on the interface of the SEM/dual beam you are working with, the visible name of the stream file might be very short (e.g., 18 characters only for the Helios 600). In this case, it makes sense to keep a short filename, and/or put the most important pieces of information of the pattern into the beginning.

It can be helpful to also add the total writing time for an exported stream at the end, see example below how to create a descriptive filename from patterning parameters.

```
[7]: # get stream
      strm = stream_builder.get_stream()

      # export with simple name
      out_filename = 'stream_test'
```

```

strm.write(f'{out_filename}.str')

# this is an example on how to build a descriptive filename
# e.g. with growth rate GRO in nm/s, and total writing time in seconds
total_time = f'{strm.get_time().seconds}.{strm.get_time().microseconds/1e5:.
    ↪0f}s'
out_filename = f'stream_test-GR{GRO*1e3:.0f}-{total_time}'
print(out_filename)

```

stream\_test-GR50-113.8s

```

[8]: #the stream can be loaded back if the stream_builder object is still defined:
#strm.from_file(f'{save_path}.str')

```

## 1.6 Load stream files and inspect

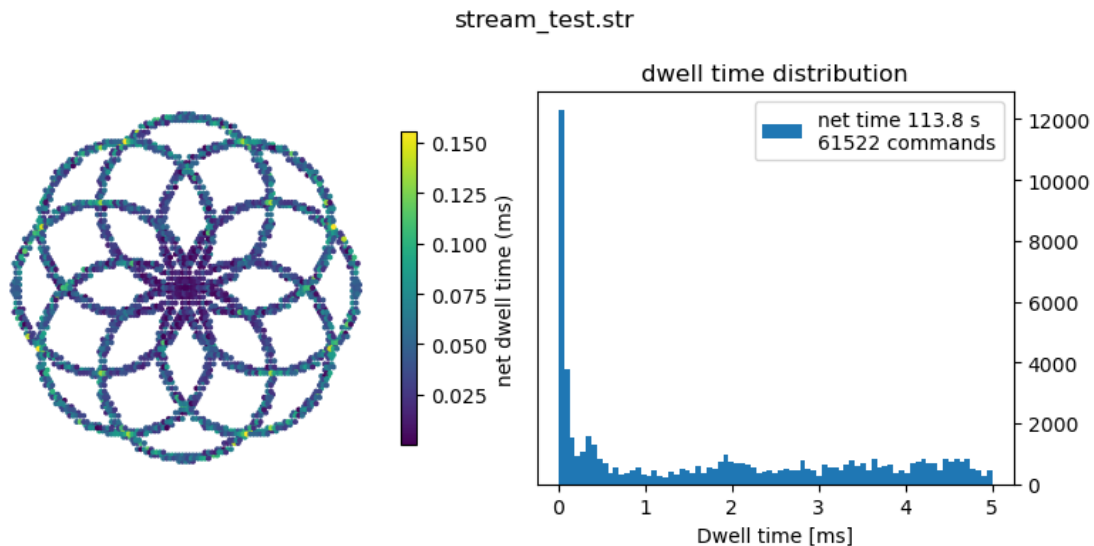
The functions `read_stream_file` allow to read stream files, and `plot_stream_file` plots both the spatial  $xy$  distribution of dwells as well as shows the histogram of dwell times of the generated pattern.

```

[9]: #from f3ast.stream_analysis import read_stream_file
from f3ast.stream_analysis import plot_stream_file

out_filename = 'stream_test'
plot_stream_file( f'{out_filename}.str', savefig=False )

```



## 1.7 Save models

f3ast also allows to save a stream builder object for later use. This is particularly useful for large structures to be treated with the DDModel, as the calculation of thermal correction/connectivity scales non-linearly with the size of the bounding box of the structure.

```
[10]: # save
save_path = 'stream_test'
f3ast.save_build(save_path, dwell_solver, stream_builder)

# retrieve
load_path = f'{save_path}.pickle'
dwell_solver, stream_builder = f3ast.load_build(load_path)
```

## 1.8 Exponential dwell time correction in $z$

Sometimes the DDModel does not work well, e.g., if the stl structure has disconnected segments – in this case the above plot of the thermal resistance would feature discontinuities in  $z$ . For this case, the following model, based on doubling of the dwell time with height, can give better growth results.

The correct doubling length needs to be determined experimentally, e.g., by tracking how the pitch of a nominally periodic structure varies with growth height.

```
[11]: from f3ast.stream_builder import stream_exp_correction_with_z

# settings are mandatory to be defined
GR0 = 50e-3 # in um/s, base growth rate (at bottom)
doubling_length = 1000. # innm, doubling length of dwell time
sigma = 4.2 # in nm, deposit size

%time stream_builder, dwell_solver = stream_exp_correction_with_z(struct,
↪ settings, GR0=GR0, doubling_length=doubling_length, sigma=sigma)

# export and inspection is the same as for the examples above
```

Solving for dwells...

Solved

CPU times: total: 125 ms

Wall time: 1.36 s

```
[ ]:
```