

# Permeability Simulation Using PoreSpy and OpenPNM

```
In [9]: import numpy as np
import pandas as pd
import openpnm as op
import porespy as ps
import seaborn as sns
import matplotlib.pyplot as plt
import supplementary_code as sc
from skimage import io, color, img_as_ubyte, morphology
import imageio
np.set_printoptions(precision=4)
np.random.seed(10)
%matplotlib inline
```

In [ ]:

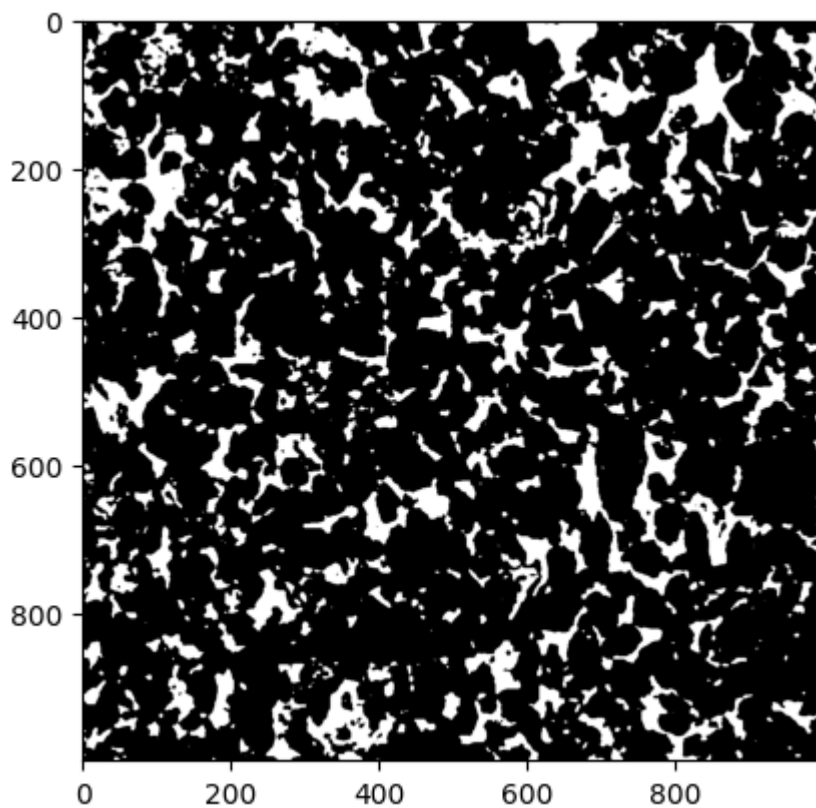
## Loading Binary Image

```
In [10]: Path = "D:/DISSERTATION/CT Data/Berea CT/Berea_2d25um_binary.raw"
```

```
In [11]: resolution = 2.25e-6
name = 'Berea'
# Read input RAW file
raw_file = np.fromfile(Path, dtype=np.uint8)
im = (raw_file.reshape(1000,1000,1000))
```

```
In [12]: im = im == 0
plt.imshow(im[:, :, 23], cmap = 'gray')
```

```
Out[12]: <matplotlib.image.AxesImage at 0x16145df3450>
```



## Porosity, Shape and Dtype

```
In [31]: print(ps.metrics.porosity(im)*100)
print(im.shape)
print(im.dtype)
```

```
21.671533200000002
(1000, 1000, 1000)
bool
```

## Network Extraction PoreSpy Snow2

```
In [33]: ps_network_snow = ps.networks.snow2(im, voxel_size=resolution)
```

```
0it [00:00, ?it/s]
```

```
0it [00:00, ?it/s]
```

```
0it [00:00, ?it/s]
```

```
0it [00:00, ?it/s]
```

```
0it [00:00, ?it/s]
```

```
0it [00:00, ?it/s]
```

```
0it [00:00, ?it/s]
```

```
0it [00:00, ?it/s]
```

```
Extracting pore and throat properties: 0% | 0/126405 [00:00<?, ?it/s]
```

```
In [34]: pn = op.io.network_from_porespy(ps_network_snow.network)
net = ps.networks.label_boundaries(network=pn)
```

```
In [35]: print(pn)
```

```
net : <openpnm.network.Network at 0x1eee739c130>
```

#	Properties	Valid Values
2	throat.conns	205597 / 205597
3	pore.coords	126405 / 126405
4	pore.region_label	126405 / 126405
5	pore.phase	126405 / 126405
6	throat.phases	205597 / 205597
7	pore.region_volume	126405 / 126405
8	pore.equivalent_diameter	126405 / 126405
9	pore.local_peak	126405 / 126405
10	pore.global_peak	126405 / 126405
11	pore.geometric_centroid	126405 / 126405
12	throat.global_peak	205597 / 205597
13	pore.inscribed_diameter	126405 / 126405
14	pore.extended_diameter	126405 / 126405
15	throat.inscribed_diameter	205597 / 205597
16	throat.total_length	205597 / 205597
17	throat.direct_length	205597 / 205597
18	throat.perimeter	205597 / 205597
19	pore.volume	126405 / 126405
20	pore.surface_area	126405 / 126405
21	throat.cross_sectional_area	205597 / 205597
22	throat.equivalent_diameter	205597 / 205597

#	Labels	Assigned Locations
2	pore.all	126405
3	throat.all	205597
4	pore.boundary	9026
5	pore.xmin	1411
6	pore.xmax	1462
7	pore.ymin	1435
8	pore.ymax	1521
9	pore.zmin	1426
10	pore.zmax	1771
11	pore.left	1411
12	pore.right	1462
13	pore.front	1435
14	pore.back	1521
15	pore.top	1426
16	pore.bottom	1771

```
In [ ]:
```

## Check network health

Remove isolated pores or cluster of pores from the network by checking it network health.

```
In [40]: h = op.utils.check_network_health(pn)
print(h)
```

Key	Value
headless_throats	[]
looped_throats	[]
isolated_pores	[]
disconnected_pores	[0, 4, 5, 6, 7, 12, 16, 20, 25, 35, 51, 87, 129, 130, 131, 137, 145, 157, 167, 168, 180, 184, 200, 205, 215, 218, 229, 233, 242, 251, 252, 260, 268, 270, 272, 282, 304, 311, 314, 343, 355, 357, 391, 410, 413, 426, 427, 434, 437, 440, 453, 477, 487, 494, 511, 520, 537, 566, 592, 599, 608, 627, 634, 647, 651, 658, 727, 736, 767, 777, 803, 855, 858, 867, 869, 883, 894, 898, 899, 918, 930, 956, 957, 997, 1007, 1015, 1030, 1039, 1040, 1044, 1064, 1080, 1101, 1117, 1118, 1124, 1135, 1136, 1162, 1166, 1178, 1187, 1244, 1271, 1276, 1289, 1333, 1336, 1343, 1349, 1356, 1388, 1389, 1419, 1426, 1429, 1437, 1445, 1448, 1460, 1471, 1517, 1542, 1544, 1553, 1565, 1582, 1667, 1668, 1680, 1690, 1701, 1703, 1732, 1735, 1737, 1751, 1755, 1776, 1819, 1838, 1843, 1918, 1946, 1947, 1951, 1966, 1978, 2037, 2044, 2109, 2150, 2152, 2172, 2219, 2232, 2257, 2260, 2282, 2292, 2336, 2352, 2382, 2393, 2396, 2455, 2468, 2469, 2473, 2474, 2476, 2480, 2491, 2506, 2560, 2574, 2575, 2580, 2582, 2600, 2646, 2653, 2659, 2751, 2765, 2766, 2862, 2867, 2877, 2886, 2872, 2882, 2812, 2814, 2826, 2824, 2862, 28

```
In [41]: op.topotools.trim(network=pn, pores=h['isolated_pores'])
```

```
In [42]: op.topotools.trim(network=pn, pores=h['disconnected_pores'])
```

```
In [43]: h = op.utils.check_network_health(net)
print(h)
```

Key	Value
headless_throats	[]
looped_throats	[]
isolated_pores	[]
disconnected_pores	[]
duplicate_throats	[]
bidirectional_throats	[]

## Assign geometry

```
In [44]: pn.add_model_collection(op.models.collections.geometry.spheres_and_cylinders)
pn.regenerate_models()
```

## Assign phase

```
In [45]: # water = op.phase.Water(network=pn)
```

```
In [46]: phase = op.phase.Phase(network=pn)
phase['pore.viscosity']=1.0
phase.add_model_collection(op.models.collections.physics.basic)
phase.regenerate_models()
```

```
[14:36:49] WARNING throat.entry_pressure was not run since the following property is
missing: 'throat.surface_tension'
```

```
WARNING throat.diffusive_conductance was not run since the following property is
missing: 'throat.diffusivity'
```

## Apply Stokes Flow

```
In [47]: inlet = pn.pores('left')
outlet = pn.pores('right')
flow = op.algorithms.StokesFlow(network=pn, phase=phase)
flow.set_value_BC(pores=inlet, values=1)
flow.set_value_BC(pores=outlet, values=0)
flow.run()
phase.update(flow.soln)
```

## Calculate effective permeability x - axis

permeability using Darcy's law:

```
In [53]: Q = flow.rate(pores=inlet, mode='group')[0]
A = (1000*1000) * resolution**2
L = 1000 * resolution
Delta_P = 1
mu = 1
K = Q * L * mu / (A * Delta_P) # mu and Delta_P were assumed to be 1.
# K = Q * L / A
print(f'The value of K is: {K/0.98e-12*1000:.2f} mD')
# print(K, "mD")
```

```
[14:37:46] WARNING Attempting to estimate inlet area...will be low
```

```
ERROR Inlet and outlet faces are different area
```

```
WARNING Attempting to estimate domain length...could be low if boundary
not added
```

```
ERROR A unique value of length could not be found
```

The value of K is: 5.28 mD

In [ ]:

In [ ]: