01_thresholding

June 29, 2018

1 Local Thresholding

In this notebook, I extract orbits for a signle chromosome in all 4 cell lines, using a different method of thresholding. In order to do this, I slide a kernel of size k through each pixel and check if it has a particular property. If the property is satisified, then the pixel is set to 1, otherwise it is set to 0. The two properties that I experiment with are *maximum thresholding* and *normal thresholding*. 1. **Maximum Thresholding**: in max thresholding, if the pixel is the maximum of its neighbors with respect to the kernel, then it is set.

```
def local_threshold(mat, k=1, method='max', t=1):
    mat2 = np.zeros_like(mat)
    n, m = mat.shape
    if isinstance(k, tuple):
        k1, k2 = k
    else:
        k1 = k2 = k
    for i in range(k1, n-k1):
        for j in range(k, m-k2):
            if method == 'max':
                condition = mat[i, j] == np.max(mat[i-k1:i+k1, j-k2:j+k2])
            elif method=='normal':
                temp = mat[i-k1:i+k1, j-k2:j+k2]
                condition = mat[i, j] >= np.mean(temp) + t * np.std(temp)
            elif method = 'max_linear':
                condition = mat[i, j] == np.max(mat[i, j-k1:j+k2])
            if condition:
                mat2[i, j] = 1
    return mat2
```

2. **Normal Thresholding**: in normal thresholding, if the pixel is larger that the average of the neighbors then it is set.

```
In [1]: import numpy as np
        import cv2
        from library.utility import *
        import matplotlib.pyplot as plt
        from iced import normalization
```

```
from iced import filter
from sets import Set
import os
%load_ext autoreload
%autoreload 2
%pylab inline
```

```
Populating the interactive namespace from numpy and matplotlib


/home/bzr0014/git/watson/virt/local/lib/python2.7/site-packages/IPython/core/magics/pylab.py:161
`%matplotlib` prevents importing * from pylab and numpy
  "\n`%matplotlib` prevents importing * from pylab and numpy"
```

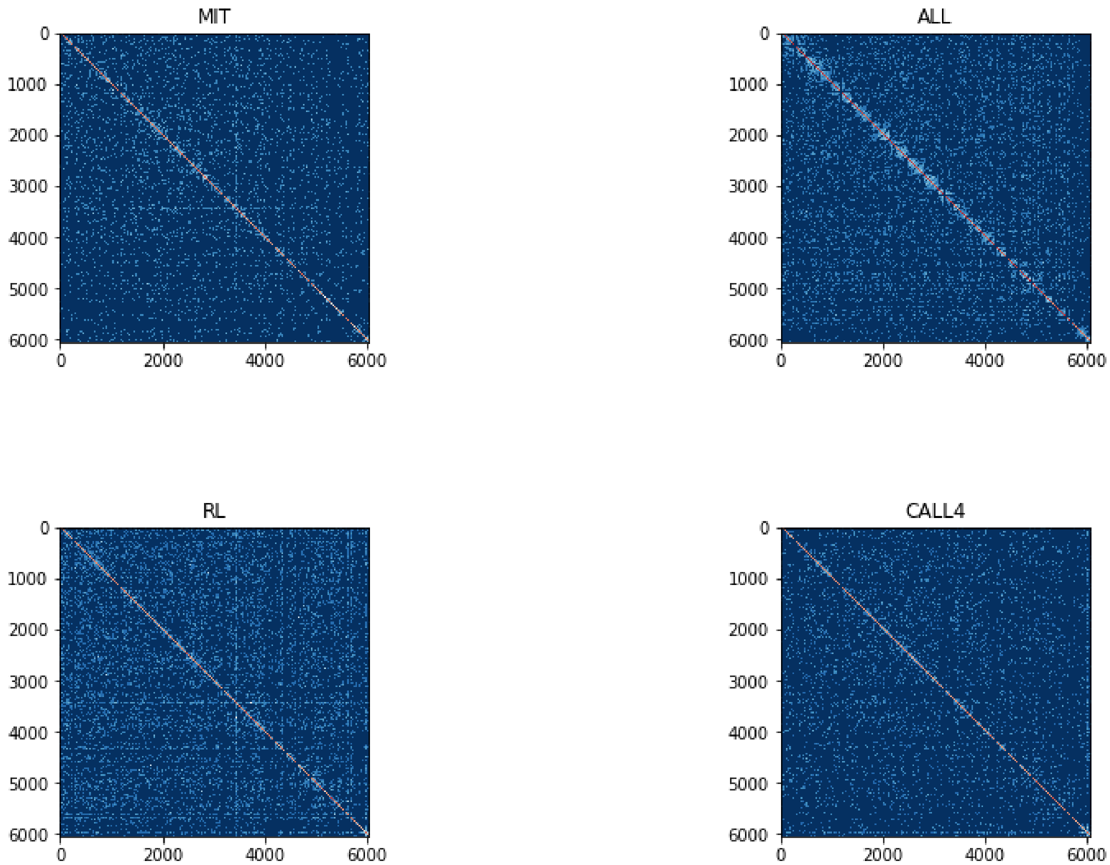
2 Loading Data

The first step is to load the raw Hi-C contact maps. We have already extracted all inter- and intra-chromosomal contact maps and compiled them into as single large numpy array format.

```
In [2]: pylab.rcParams['figure.figsize'] = (15, 9)

        lengths_low_res = np.load('../numpy_data/length_low_res.npy')
        mit_full  = (np.load('../numpy_data/mit_low_res.npy'))
        all_full  = (np.load('../numpy_data/all_low_res.npy'))
        rl_full  = (np.load('../numpy_data/rl_low_res.npy'))
        call4_full  = (np.load('../numpy_data/call4_low_res.npy'))
        data = {}
        showImages([mit_full , all_full , rl_full , call4_full ], rows=2, titles=['MIT', 'ALL',
```

```
Number of rows and columns: 2, 2
(4, 4)
```

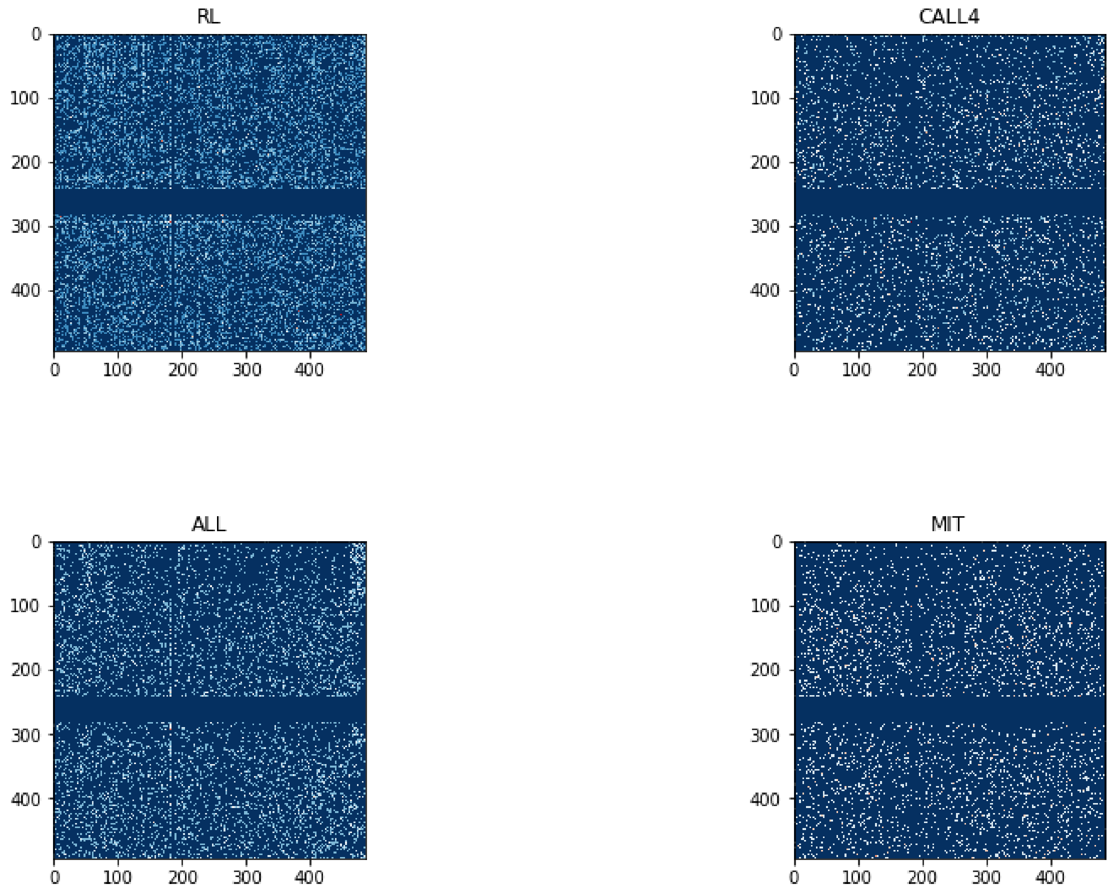


3 Selecting a inter-/intra-chromosomal contact map

You can chang chr1 and chr2 variables based on the contact map you want to investigate.

```
In [3]: chr1 = 1
        chr2 = 2
        data['MIT']          = get_contact_map(mit_full         , lengths_low_res, chr1, chr2)
        data['ALL']          = get_contact_map(all_full         , lengths_low_res, chr1, chr2)
        data['RL']           = get_contact_map(rl_full          , lengths_low_res, chr1, chr2)
        data['CALL4']        = get_contact_map(call4_full       , lengths_low_res, chr1, chr2)
        showImages(data, rows = 2, titles=['MIT', 'ALL', 'RL', 'CALL4'])
```

```
Number of rows and columns: 2, 2
(4, 4)
```



3.1 Cleaning Data

As can be observed above, there are several rows and columns that simply don't contain any data and are all zeros, in the following code we clean the matrices to remove these zero rows and columns since they will cause problems in future analysis.

In [4]:
```
#There are some blank rows and columns in the matrix. let's remove them.
blankRows0, blankCols0 = getBlankRowsAndColumns(data['MIT'])
blankRows1, blankCols1 = getBlankRowsAndColumns(data['ALL'])
blankRows2, blankCols2 = getBlankRowsAndColumns(data['RL'])
blankRows3, blankCols3 = getBlankRowsAndColumns(data['CALL4'])
blankRows = Set([])
blankCols = Set([])
blankRows.update(blankRows0)
blankRows.update(blankRows1)
blankRows.update(blankRows2)
blankRows.update(blankRows3)
blankCols.update(blankCols0)
blankCols.update(blankCols1)
```

```
blankCols.update(blankCols2)
blankCols.update(blankCols3)
data['MIT'] = removeRowsAndColumns(data['MIT'], blankRows, blankCols)
data['ALL'] = removeRowsAndColumns(data['ALL'], blankRows, blankCols)
data['RL'] = removeRowsAndColumns(data['RL'], blankRows, blankCols)
data['CALL4'] = removeRowsAndColumns(data['CALL4'], blankRows, blankCols)
n1, m1 = data['MIT'].shape
n2, m2 = data['RL'].shape
n3, m3 = data['ALL'].shape
n4, m4 = data['CALL4'].shape
```

```
('size of old matrix:', (495, 486))
('size of new matrix:', (454, 479))
('size of old matrix:', (495, 486))
('size of new matrix:', (454, 479))
('size of old matrix:', (495, 486))
('size of new matrix:', (454, 479))
('size of old matrix:', (495, 486))
('size of new matrix:', (454, 479))
```

3.1.1 Comparing CALL4 with RL low-resolution data:

Feel free to change D1 and D2 to pick any data from set of "'['MIT', 'ALL', 'RL', 'CALL4']"".

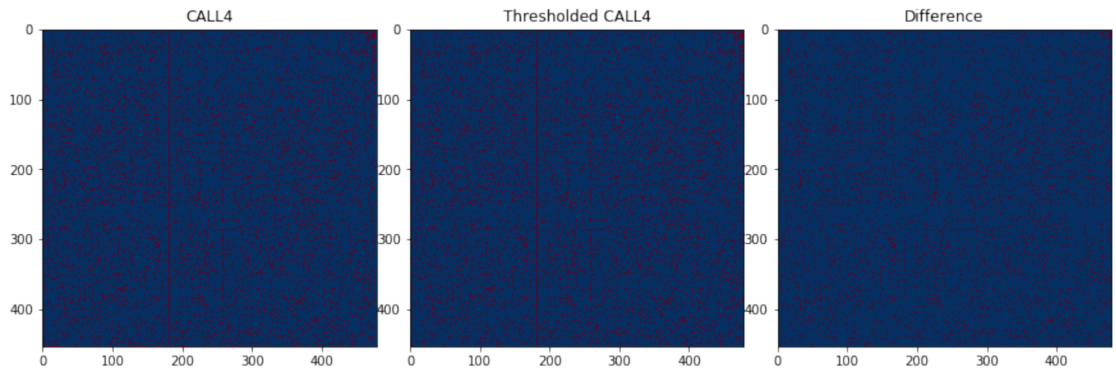
```
In [6]: D1 = 'CALL4'
        D2 = 'RL'
        pylab.rcParams['figure.figsize'] = (15, 20)
        # Size of the kernel
        k = (2, 2, 2, 2)
        # can be either 'max' for setting the maximum value in each kernel to 1 and the rest to
        # or 'normal' for setting all values above mean + t * std withing the kernel to 1 and
        # the rest to 0
        method = 'normal'
        # in case of normal thresholding, t is the coefficient
        # of the standard deviation; that is, n each kernel iteration K
        # if K[i, j] > mean(K) + t * std(K), then it is set to 1.
        t = 0
        params = None
        symmetric= chr1==chr2
        D1_os = local_threshold(((data[D1]+1+1e-5)), k = k, method=method, t = t, params=params,
        D2_os = local_threshold(((data[D2]+1+1e-5)), k = k, method=method, t = t, params=params,
        n1, m1 = D1_os.shape
        n2, m2 = D2_os.shape
        n = np.min([n1, n2])
        m = np.min([m1, m2])
        D1_os = D1_os[:n, :m]
        D1_data = data[D1][:n, :m]
```

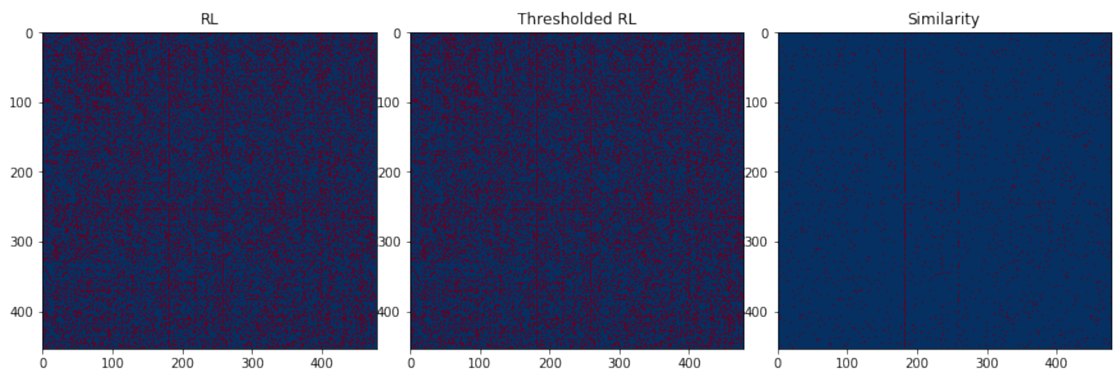
```
        D2_os = D2_os[:n, :m]
        D2_data = data[D2][:n, :m]
        a = ((D1_os * D1_data) > 0) * 1
        b = ((D2_os * D2_data) > 0) * 1
```

```
(2, 2, 2, 2)
(2, 2, 2, 2)
```

```
In [8]: images = [ D1_os, a, (a-b) > 0, D2_os,  b, a * b ]
        titles = [D1, 'Thresholded %s'%D1, 'Difference', D2, 'Thresholded %s'%D2, 'Similarity']
        showImages(images, 2, titles=titles)
```

```
Number of rows and columns: 2, 3
(6, 6)
```


CALL4
Thresholded CALL4
Difference
0
100
200
300
400


RL
Thresholded RL
Similarity
0
100
200
300
400