sle_notebook_B_cells_T6_notebook_result_LN_1630363103

August 31, 2021

[2]:
```
# preparing the dataset based on the SLEDAI score and LDA

import pandas as pd
import os
import re
import copy
import time
import numpy as np
import pickle
folder ='B_cells'
trt = 'T6'
file = os.path.join('../SLE_long_list', folder,folder+'_'+trt+'_A_LN.csv')

df = pd.read_csv(file)
df1 = df.copy(deep=True)
df1=df1.loc[(df['score'] != 100.0)]

df3=df1.loc[(df['LN']==1)]
df4=df1.loc[(df['LN']==0)]


df5=pd.concat([df3,df4]).reset_index(drop=True)

print('dataset \n')
print(df5)
```

```
dataset

                        fcs_file  score  LDA   LN
0   20_317_A_T6_CD19+ B cells.fcs   28.0  0.0  1.0
1   22_325_A_T6_CD19+ B cells.fcs   18.0  0.0  1.0
2   24_327_A_T6_CD19+ B cells.fcs   16.0  0.0  1.0
3   24_329_A_T6_CD19+ B cells.fcs   15.0  0.0  1.0
4   26_323_A_T6_CD19+ B cells.fcs   18.0  0.0  1.0
5   28_330_A_T6_CD19+ B cells.fcs   24.0  0.0  1.0
6   29_336_A_T6_CD19+ B cells.fcs   25.0  0.0  1.0
7   11_307_A_T6_CD19+ B cells.fcs    7.0  0.0  0.0
```

```
8   12_306_A_T6_CD19+ B cells.fcs   12.0  0.0  0.0
9   13_308_A_T6_CD19+ B cells.fcs    7.0  0.0  0.0
10  19_316_A_T6_CD19+ B cells.fcs    4.0  0.0  0.0
11   1_302_A_T6_CD19+ B cells.fcs    6.0  0.0  0.0
12  21_319_A_T6_CD19+ B cells.fcs   17.0  0.0  0.0
13  21_321_A_T6_CD19+ B cells.fcs   24.0  0.0  0.0
14  22_322_A_T6_CD19+ B cells.fcs   13.0  0.0  0.0
15  23_326_A_T6_CD19+ B cells.fcs    9.0  0.0  0.0
16  27_328_A_T6_CD19+ B cells.fcs   18.0  0.0  0.0
17   2_303_A_T6_CD19+ B cells.fcs    3.0  0.0  0.0
18   3_305_A_T6_CD19+ B cells.fcs   19.0  0.0  0.0
19   4_309_A_T6_CD19+ B cells.fcs   19.0  0.0  0.0
20   7_310_A_T6_CD19+ B cells.fcs    6.0  0.0  0.0
21   8_311_A_T6_CD19+ B cells.fcs   10.0  0.0  0.0
```

[6]:

```python
file1 = os.path.join('../SLE_long_list', folder,folder+'_'+trt+'_LN_binary.csv')
df5.to_csv(file1,index=False)
#curr_time = int(time.time())
folder_suffix='notebook_result_LN_'+ '1630363103'#str(curr_time)
nfold=5
if trt=='T0':
    marker_file='surface_markers.csv'
else:
    marker_file='signal_markers.csv'
```

[3]:

```python
# running CellCNN analysis
from sle_long import run_analysis
final_result, final_result_acc, train_sample_fold, train_phenotype_fold,␣
 ↪valid_sample_fold, valid_phenotype_fold, patient_dict, OUTDIR,␣
 ↪markers=run_analysis(folder,folder_suffix,nfold,marker_file, trt)
```

```
markers

['145Nd_IFNg', '147Sm_IL1a', '148Nd_IL17a', '157Gd_IL1RA', '158Gd_MIP1b',
'159Tb_PTEN', '160Gd_IL8', '164Dy_IL6', '166Er_TNFa', '169Tm_IL1b',
'170Er_MCP1', '171Yb_IL12p40', '175Lu_IFNa-EQ', '176Yb_IL23p19']

 csv file… ../SLE_long_list/B_cells/B_cells_T6_LN_binary.csv

 training data

 training ids ['336', '329', '326', '302', '305', '317', '311', '322', '325',
'310', '328', '316', '330', '309']

 training phenotypes [[1], [1], [0], [0], [0], [1], [0], [0], [1], [0], [0],
[0], [1], [0]]

 training fcs files [['29_336_A_T6_CD19+ B cells.fcs'], ['24_329_A_T6_CD19+ B
```

```
cells.fcs'], ['23_326_A_T6_CD19+ B cells.fcs'], ['1_302_A_T6_CD19+ B
cells.fcs'], ['3_305_A_T6_CD19+ B cells.fcs'], ['20_317_A_T6_CD19+ B
cells.fcs'], ['8_311_A_T6_CD19+ B cells.fcs'], ['22_322_A_T6_CD19+ B
cells.fcs'], ['22_325_A_T6_CD19+ B cells.fcs'], ['7_310_A_T6_CD19+ B
cells.fcs'], ['27_328_A_T6_CD19+ B cells.fcs'], ['19_316_A_T6_CD19+ B
cells.fcs'], ['28_330_A_T6_CD19+ B cells.fcs'], ['4_309_A_T6_CD19+ B
cells.fcs']]

 validation data

 validation ids ['327', '307', '303', '323', '321', '308', '319', '306']

 validation phenotypes [[1], [0], [0], [1], [0], [0], [0], [0]]

 validation  fcs files [['24_327_A_T6_CD19+ B cells.fcs'], ['11_307_A_T6_CD19+ B
cells.fcs'], ['2_303_A_T6_CD19+ B cells.fcs'], ['26_323_A_T6_CD19+ B
cells.fcs'], ['21_321_A_T6_CD19+ B cells.fcs'], ['13_308_A_T6_CD19+ B
cells.fcs'], ['21_319_A_T6_CD19+ B cells.fcs'], ['12_306_A_T6_CD19+ B
cells.fcs']]
63/63 [==============================] - 0s 2ms/step - loss: 0.6331 - accuracy:
0.6678
Best validation accuracy 0.6678356528282166
63/63 [==============================] - 0s 2ms/step - loss: 0.5773 - accuracy:
0.7575
Best validation accuracy 0.757515013217926
63/63 [==============================] - 0s 2ms/step - loss: 0.5904 - accuracy:
0.7720
Best validation accuracy 0.7720440626144409
63/63 [==============================] - 0s 1ms/step - loss: 0.6450 - accuracy:
0.8176
Best validation accuracy 0.8176352977752686
63/63 [==============================] - 0s 2ms/step - loss: 0.4555 - accuracy:
0.7976
Best validation accuracy 0.797595202922821
63/63 [==============================] - 0s 2ms/step - loss: 0.5286 - accuracy:
0.7971
Best validation accuracy 0.7970941662788391
63/63 [==============================] - 0s 3ms/step - loss: 0.5168 - accuracy:
0.7535
Best validation accuracy 0.7535070180892944
63/63 [==============================] - 0s 1ms/step - loss: 0.5843 - accuracy:
0.7961
Best validation accuracy 0.7960922122001648
63/63 [==============================] - 0s 3ms/step - loss: 0.5451 - accuracy:
0.8211
Best validation accuracy 0.8211422562599182
63/63 [==============================] - 0s 4ms/step - loss: 0.4508 - accuracy:
0.8121
```

```
Best validation accuracy 0.8121242523193359
63/63 [==============================] - 0s 1ms/step - loss: 0.6216 - accuracy:
0.7224
Best validation accuracy 0.7224448919296265
63/63 [==============================] - 0s 3ms/step - loss: 0.5185 - accuracy:
0.7650
Best validation accuracy 0.7650300860404968
63/63 [==============================] - 0s 3ms/step - loss: 0.5466 - accuracy:
0.7886
Best validation accuracy 0.788577139377594
63/63 [==============================] - 0s 1ms/step - loss: 0.5531 - accuracy:
0.8091
Best validation accuracy 0.8091182112693787
63/63 [==============================] - 0s 1ms/step - loss: 0.5427 - accuracy:
0.8332
Best validation accuracy 0.8331663608551025
63/63 [==============================] - 0s 3ms/step - loss: 0.5377 - accuracy:
0.7680
Best validation accuracy 0.7680360674858093
63/63 [==============================] - 0s 2ms/step - loss: 0.5213 - accuracy:
0.7585
Best validation accuracy 0.7585170269012451
63/63 [==============================] - 0s 3ms/step - loss: 0.5176 - accuracy:
0.8287
Best validation accuracy 0.828657329082489
63/63 [==============================] - 0s 3ms/step - loss: 0.5713 - accuracy:
0.7891
Best validation accuracy 0.7890781760215759
63/63 [==============================] - 0s 2ms/step - loss: 0.4552 - accuracy:
0.8307
Best validation accuracy 0.8306612968444824

 training data

 training ids ['328', '309', '302', '311', '305', '326', '317', '319', '322',
'330', '327', '306', '325', '316']

 training phenotypes [[0], [0], [0], [0], [0], [0], [1], [0], [0], [1], [1],
[0], [1], [0]]

 training fcs files [['27_328_A_T6_CD19+ B cells.fcs'], ['4_309_A_T6_CD19+ B
cells.fcs'], ['1_302_A_T6_CD19+ B cells.fcs'], ['8_311_A_T6_CD19+ B cells.fcs'],
['3_305_A_T6_CD19+ B cells.fcs'], ['23_326_A_T6_CD19+ B cells.fcs'],
['20_317_A_T6_CD19+ B cells.fcs'], ['21_319_A_T6_CD19+ B cells.fcs'],
['22_322_A_T6_CD19+ B cells.fcs'], ['28_330_A_T6_CD19+ B cells.fcs'],
['24_327_A_T6_CD19+ B cells.fcs'], ['12_306_A_T6_CD19+ B cells.fcs'],
['22_325_A_T6_CD19+ B cells.fcs'], ['19_316_A_T6_CD19+ B cells.fcs']]
```

```
 validation data

 validation ids ['321', '329', '303', '336', '308', '310', '307', '323']

 validation phenotypes [[0], [1], [0], [1], [0], [0], [0], [1]]

 validation  fcs files [['21_321_A_T6_CD19+ B cells.fcs'], ['24_329_A_T6_CD19+ B
cells.fcs'], ['2_303_A_T6_CD19+ B cells.fcs'], ['29_336_A_T6_CD19+ B
cells.fcs'], ['13_308_A_T6_CD19+ B cells.fcs'], ['7_310_A_T6_CD19+ B
cells.fcs'], ['11_307_A_T6_CD19+ B cells.fcs'], ['26_323_A_T6_CD19+ B
cells.fcs']]
63/63 [==============================] - 0s 3ms/step - loss: 0.5144 - accuracy:
0.7779
Best validation accuracy 0.7778889536857605
63/63 [==============================] - 0s 3ms/step - loss: 0.5278 - accuracy:
0.7314
Best validation accuracy 0.7313656806945801
63/63 [==============================] - 0s 2ms/step - loss: 0.5306 - accuracy:
0.7714
Best validation accuracy 0.771385669708252
63/63 [==============================] - 0s 3ms/step - loss: 0.4081 - accuracy:
0.8389
Best validation accuracy 0.838919460773468
63/63 [==============================] - 0s 2ms/step - loss: 0.3212 - accuracy:
0.8279
Best validation accuracy 0.8279139399528503
63/63 [==============================] - 0s 3ms/step - loss: 0.4917 - accuracy:
0.7849
Best validation accuracy 0.7848924398422241
63/63 [==============================] - 0s 2ms/step - loss: 0.5073 - accuracy:
0.7339
Best validation accuracy 0.7338669300079346
63/63 [==============================] - 0s 1ms/step - loss: 0.5874 - accuracy:
0.7399
Best validation accuracy 0.7398699522018433
63/63 [==============================] - 0s 3ms/step - loss: 0.3820 - accuracy:
0.8724
Best validation accuracy 0.8724362254142761
63/63 [==============================] - 0s 2ms/step - loss: 0.3155 - accuracy:
0.8279
Best validation accuracy 0.8279139399528503
63/63 [==============================] - 0s 4ms/step - loss: 0.5285 - accuracy:
0.7539
Best validation accuracy 0.7538769245147705
63/63 [==============================] - 0s 3ms/step - loss: 0.4862 - accuracy:
0.7674
Best validation accuracy 0.7673836946487427
63/63 [==============================] - 0s 4ms/step - loss: 0.4980 - accuracy:
```

```
0.7304
Best validation accuracy 0.7303651571273804
63/63 [==============================] - 0s 1ms/step - loss: 0.5180 - accuracy:
0.8429
Best validation accuracy 0.8429214358329773
63/63 [==============================] - 0s 2ms/step - loss: 0.3170 - accuracy:
0.8224
Best validation accuracy 0.8224111795425415
63/63 [==============================] - 0s 1ms/step - loss: 0.5322 - accuracy:
0.7784
Best validation accuracy 0.7783892154693604
63/63 [==============================] - 0s 3ms/step - loss: 0.5121 - accuracy:
0.7464
Best validation accuracy 0.746373176574707
63/63 [==============================] - 0s 3ms/step - loss: 0.5123 - accuracy:
0.7094
Best validation accuracy 0.7093546986579895
63/63 [==============================] - 0s 2ms/step - loss: 0.4491 - accuracy:
0.8909
Best validation accuracy 0.8909454941749573
63/63 [==============================] - 0s 4ms/step - loss: 0.3027 - accuracy:
0.8259
Best validation accuracy 0.8259129524230957

 training data

 training ids ['323', '311', '303', '326', '308', '310', '302', '330', '317',
'327', '328', '329', '319', '336']

 training phenotypes [[1], [0], [0], [0], [0], [0], [0], [1], [1], [1], [0],
[1], [0], [1]]

 training fcs files [['26_323_A_T6_CD19+ B cells.fcs'], ['8_311_A_T6_CD19+ B
cells.fcs'], ['2_303_A_T6_CD19+ B cells.fcs'], ['23_326_A_T6_CD19+ B
cells.fcs'], ['13_308_A_T6_CD19+ B cells.fcs'], ['7_310_A_T6_CD19+ B
cells.fcs'], ['1_302_A_T6_CD19+ B cells.fcs'], ['28_330_A_T6_CD19+ B
cells.fcs'], ['20_317_A_T6_CD19+ B cells.fcs'], ['24_327_A_T6_CD19+ B
cells.fcs'], ['27_328_A_T6_CD19+ B cells.fcs'], ['24_329_A_T6_CD19+ B
cells.fcs'], ['21_319_A_T6_CD19+ B cells.fcs'], ['29_336_A_T6_CD19+ B
cells.fcs']]

 validation data

 validation ids ['322', '307', '321', '325', '305', '316', '309', '306']

 validation phenotypes [[0], [0], [0], [1], [0], [0], [0], [0]]

 validation  fcs files [['22_322_A_T6_CD19+ B cells.fcs'], ['11_307_A_T6_CD19+ B
```

```
cells.fcs'], ['21_321_A_T6_CD19+ B cells.fcs'], ['22_325_A_T6_CD19+ B
cells.fcs'], ['3_305_A_T6_CD19+ B cells.fcs'], ['19_316_A_T6_CD19+ B
cells.fcs'], ['4_309_A_T6_CD19+ B cells.fcs'], ['12_306_A_T6_CD19+ B
cells.fcs']]
63/63 [==============================] - 0s 2ms/step - loss: 0.6330 - accuracy:
0.5617
Best validation accuracy 0.5616850256919861
63/63 [==============================] - 0s 4ms/step - loss: 0.6560 - accuracy:
0.5070
Best validation accuracy 0.5070210695266724
63/63 [==============================] - 0s 4ms/step - loss: 0.6730 - accuracy:
0.4047
Best validation accuracy 0.4047141373157501
63/63 [==============================] - 0s 4ms/step - loss: 0.6801 - accuracy:
0.3435
Best validation accuracy 0.3435305953025818
63/63 [==============================] - 0s 3ms/step - loss: 0.6515 - accuracy:
0.4027
Best validation accuracy 0.40270811319351196
63/63 [==============================] - 0s 1ms/step - loss: 0.5637 - accuracy:
0.6805
Best validation accuracy 0.6805416345596313
63/63 [==============================] - 0s 3ms/step - loss: 0.6795 - accuracy:
0.5426
Best validation accuracy 0.5426278710365295
63/63 [==============================] - 0s 5ms/step - loss: 0.6745 - accuracy:
0.3962
Best validation accuracy 0.39618855714797974
63/63 [==============================] - 0s 3ms/step - loss: 0.6747 - accuracy:
0.3786
Best validation accuracy 0.3786359131336212
63/63 [==============================] - 0s 3ms/step - loss: 0.6547 - accuracy:
0.4198
Best validation accuracy 0.41975927352905273
63/63 [==============================] - 0s 1ms/step - loss: 0.6266 - accuracy:
0.5346
Best validation accuracy 0.5346038341522217
63/63 [==============================] - 0s 2ms/step - loss: 0.6458 - accuracy:
0.4870
Best validation accuracy 0.48696088790893555
63/63 [==============================] - 0s 3ms/step - loss: 0.6937 - accuracy:
0.3806
Best validation accuracy 0.3806419372558594
63/63 [==============================] - 0s 2ms/step - loss: 0.6479 - accuracy:
0.3771
Best validation accuracy 0.3771314024925232
63/63 [==============================] - 0s 3ms/step - loss: 0.6532 - accuracy:
0.3676
```

```
Best validation accuracy 0.36760279536247253
63/63 [==============================] - 0s 3ms/step - loss: 0.6687 - accuracy:
0.5246
Best validation accuracy 0.5245737433433533
63/63 [==============================] - 0s 3ms/step - loss: 0.6784 - accuracy:
0.4980
Best validation accuracy 0.49799397587776184
63/63 [==============================] - 0s 3ms/step - loss: 0.6784 - accuracy:
0.4178
Best validation accuracy 0.4177532494068146
63/63 [==============================] - 0s 3ms/step - loss: 0.6709 - accuracy:
0.3681
Best validation accuracy 0.36810430884361267
63/63 [==============================] - 0s 2ms/step - loss: 0.6578 - accuracy:
0.3676
Best validation accuracy 0.36760279536247253

 training data

 training ids ['306', '311', '317', '328', '303', '308', '319', '323', '327',
'329', '321', '316', '326', '325']

 training phenotypes [[0], [0], [1], [0], [0], [0], [0], [1], [1], [1], [0],
[0], [0], [1]]

 training fcs files [['12_306_A_T6_CD19+ B cells.fcs'], ['8_311_A_T6_CD19+ B
cells.fcs'], ['20_317_A_T6_CD19+ B cells.fcs'], ['27_328_A_T6_CD19+ B
cells.fcs'], ['2_303_A_T6_CD19+ B cells.fcs'], ['13_308_A_T6_CD19+ B
cells.fcs'], ['21_319_A_T6_CD19+ B cells.fcs'], ['26_323_A_T6_CD19+ B
cells.fcs'], ['24_327_A_T6_CD19+ B cells.fcs'], ['24_329_A_T6_CD19+ B
cells.fcs'], ['21_321_A_T6_CD19+ B cells.fcs'], ['19_316_A_T6_CD19+ B
cells.fcs'], ['23_326_A_T6_CD19+ B cells.fcs'], ['22_325_A_T6_CD19+ B
cells.fcs']]

 validation data

 validation ids ['305', '302', '336', '310', '322', '330', '307', '309']

 validation phenotypes [[0], [0], [1], [0], [0], [1], [0], [0]]

 validation  fcs files [['3_305_A_T6_CD19+ B cells.fcs'], ['1_302_A_T6_CD19+ B
cells.fcs'], ['29_336_A_T6_CD19+ B cells.fcs'], ['7_310_A_T6_CD19+ B
cells.fcs'], ['22_322_A_T6_CD19+ B cells.fcs'], ['28_330_A_T6_CD19+ B
cells.fcs'], ['11_307_A_T6_CD19+ B cells.fcs'], ['4_309_A_T6_CD19+ B
cells.fcs']]
63/63 [==============================] - 0s 2ms/step - loss: 0.5375 - accuracy:
0.6448
Best validation accuracy 0.6447895765304565
```

```
63/63 [==============================] - 0s 2ms/step - loss: 0.5275 - accuracy:
0.6393
Best validation accuracy 0.6392785310745239
63/63 [==============================] - 0s 2ms/step - loss: 0.5306 - accuracy:
0.6157
Best validation accuracy 0.6157314777374268
63/63 [==============================] - 0s 3ms/step - loss: 0.5061 - accuracy:
0.6799
Best validation accuracy 0.6798596978187561
63/63 [==============================] - 0s 4ms/step - loss: 0.4143 - accuracy:
0.7951
Best validation accuracy 0.7950901985168457
63/63 [==============================] - 0s 3ms/step - loss: 0.5503 - accuracy:
0.6152
Best validation accuracy 0.6152304410934448
63/63 [==============================] - 0s 2ms/step - loss: 0.5671 - accuracy:
0.5631
Best validation accuracy 0.563126266002655
63/63 [==============================] - 0s 2ms/step - loss: 0.6069 - accuracy:
0.4945
Best validation accuracy 0.49448898434638977
63/63 [==============================] - 0s 2ms/step - loss: 0.4775 - accuracy:
0.7435
Best validation accuracy 0.7434870004653931
63/63 [==============================] - 0s 1ms/step - loss: 0.5028 - accuracy:
0.7936
Best validation accuracy 0.7935871481895447
63/63 [==============================] - 0s 2ms/step - loss: 0.5272 - accuracy:
0.7084
Best validation accuracy 0.7084168195724487
63/63 [==============================] - 0s 2ms/step - loss: 0.5253 - accuracy:
0.6593
Best validation accuracy 0.6593186259269714
63/63 [==============================] - 0s 2ms/step - loss: 0.5786 - accuracy:
0.5797
Best validation accuracy 0.5796593427658081
63/63 [==============================] - 0s 2ms/step - loss: 0.5680 - accuracy:
0.8517
Best validation accuracy 0.851703405380249
63/63 [==============================] - 0s 2ms/step - loss: 0.4348 - accuracy:
0.7751
Best validation accuracy 0.7750501036643982
63/63 [==============================] - 0s 3ms/step - loss: 0.5640 - accuracy:
0.6288
Best validation accuracy 0.6287575364112854
63/63 [==============================] - 0s 2ms/step - loss: 0.5182 - accuracy:
0.6558
Best validation accuracy 0.655811607837677
```

```
63/63 [==============================] - 0s 2ms/step - loss: 0.5437 - accuracy:
0.6037
Best validation accuracy 0.6037074327468872
63/63 [==============================] - 0s 3ms/step - loss: 0.5949 - accuracy:
0.5361
Best validation accuracy 0.5360721349716187
63/63 [==============================] - 0s 3ms/step - loss: 0.4022 - accuracy:
0.7816
Best validation accuracy 0.7815631031990051
```

[4]:

```python
import pickle
import numpy as np

if final_result_acc:

    import operator
    max_fold = max(final_result_acc.items(), key=operator.itemgetter(1))[0]
    results = final_result[max_fold]

    print('best model validation accuracy is {}'.
 ↪format(final_result_acc[max_fold]))

    # save samples

    pickle.dump(train_sample_fold[max_fold], open(OUTDIR+'/model/train_samples.
 ↪p','wb'))
    pickle.dump(valid_sample_fold[max_fold], open(OUTDIR+'/model/valid_samples.
 ↪p','wb'))
    pickle.dump(train_phenotype_fold[max_fold], open(OUTDIR+'/model/
 ↪train_phenotypes.p','wb'))
    pickle.dump(valid_phenotype_fold[max_fold], open(OUTDIR+'/model/
 ↪valid_phenotypes.p','wb'))

    #save results

    pickle.dump(results, open(OUTDIR+'/model/results.p','wb'))

    samples = train_sample_fold[max_fold] + valid_sample_fold[max_fold]
    phenotypes = np.hstack([train_phenotype_fold[max_fold],␣
 ↪valid_phenotype_fold[max_fold]])
    patients  = patient_dict[max_fold]

    pickle.dump(patients, open(OUTDIR+'/model/patients.p','wb'))
    pickle.dump(samples, open(OUTDIR+'/model/samples.p','wb'))
    pickle.dump(phenotypes, open(OUTDIR+'/model/phenotypes.p','wb'))
    pickle.dump(results, open(OUTDIR+'/model/results.p','wb'))
```

```
else:

    print('no suitable model is found')
```

```
best model validation accuracy is 0.8909454941749573
```

[7]:

```
OUTDIR = '../SLE_long_results/'+folder+'_'+trt+'_'+folder_suffix
patients=pickle.load(open(OUTDIR+'/model/patients.p','rb'))
samples=pickle.load(open(OUTDIR+'/model/samples.p','rb'))
phenotypes=pickle.load(open(OUTDIR+'/model/phenotypes.p','rb'))
results=pickle.load(open(OUTDIR+'/model/results.p','rb'))
marker_csv = '../metadata/'+marker_file
marker_info = np.array(pd.read_csv(marker_csv, sep=',').columns)
markers = list(marker_info)
```

[8]:

```
from plotting import plot_results
print('generating the plots...')
percentile=98
filter_idx=plot_results(results, samples, phenotypes,
                        markers, OUTDIR, patients, percentile,␣
 ↪filter_response_thres=0,
                        filter_diff_thres=0.
 ↪2,regression=True,group_a='LN(0)',group_b='LN(1)')
```

```
generating the plots…
number of measured markers 14
keep_idx [0]
performing z-transformation
umap for subset of the data…
shape (x_for_umap,x) 100000 246652
UMAP is computed
marker lables ['145Nd_IFNg', '147Sm_IL1a', '148Nd_IL17a', '157Gd_IL1RA',
'158Gd_MIP1b', '159Tb_PTEN', '160Gd_IL8', '164Dy_IL6', '166Er_TNFa',
'169Tm_IL1b', '170Er_MCP1', '171Yb_IL12p40', '175Lu_IFNa-EQ', '176Yb_IL23p19']
threhsold  1.4580836395263248
2D maps are generated..
ncols 14
marker values for the selected cells are plotted in the UMAP
box plots and histograms are being generated
plotting marker distribution
marker distribution is generated …
box plots and histograms generated
```

[10]:

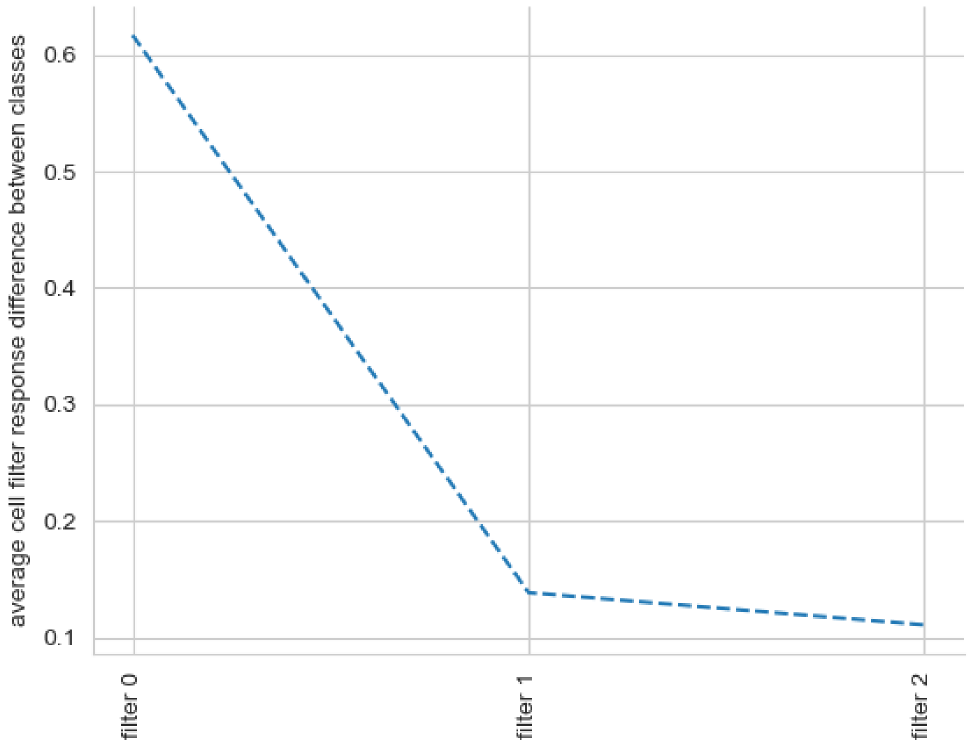
```
from IPython.display import Image
fig_path = '../SLE_long_results/'+folder+'_'+trt+'_'+ folder_suffix
```

[11]:

```
file='filter_response_differences.png'
print('filter_response_differences')
Image(fig_path+'/'+file, width=600, height=350)
```

```
filter_response_differences
```

[11]:

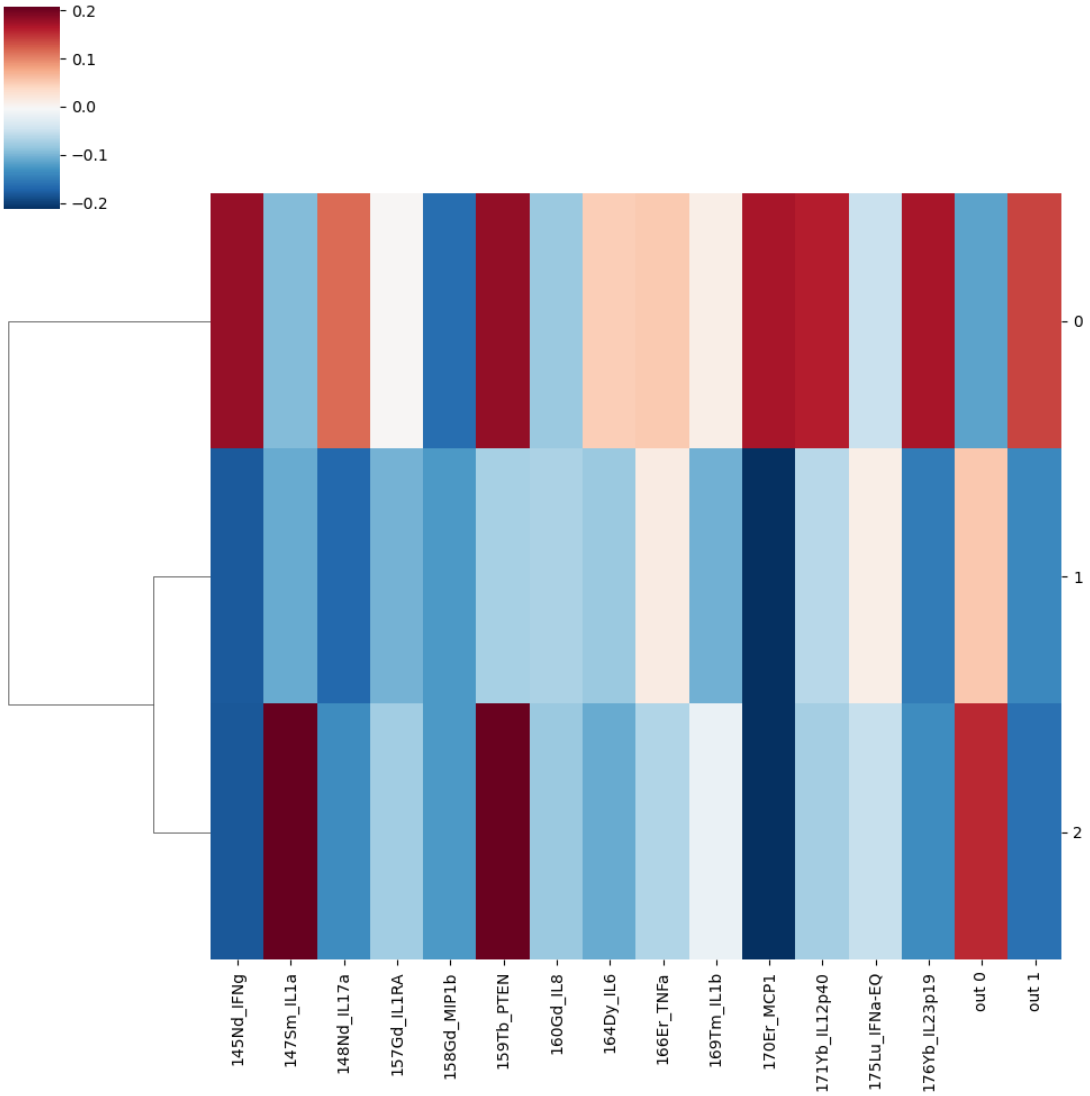


[12]:

```
file='consensus_filter_weights.png'
print('consensus_filter_weights')
Image(fig_path+'/'+file, width=600, height=350)
```

```
consensus_filter_weights
```

[12]:

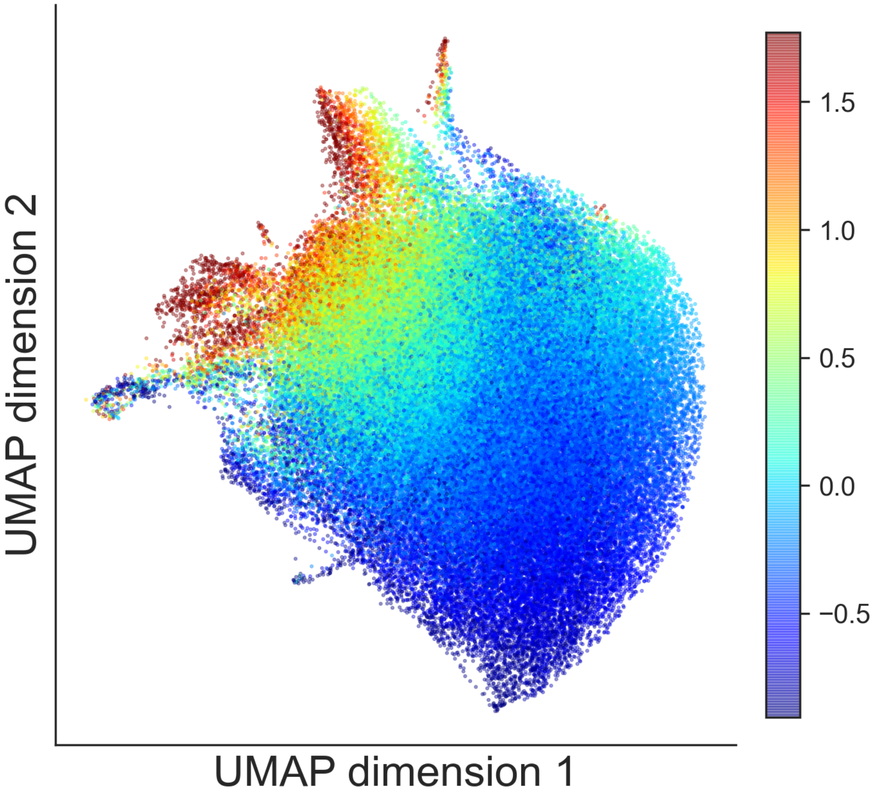


[13]:

```
print('umap of cell response filter 0')
Image(fig_path+'/'+'umap_cell_response_filter_0.png',width=600, height=350)
```

```
umap of cell response filter 0
```

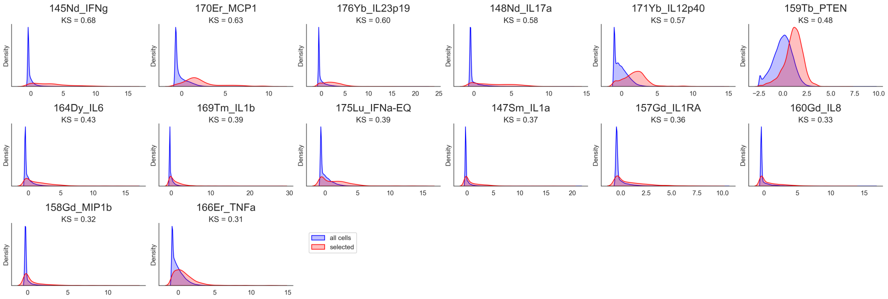
[13]:



```
[14]: print('selected population distribution for filter 0')
      Image(fig_path+'/'+'selected_population_distribution_filter_0.png')
```

```
selected population distribution for filter 0
```

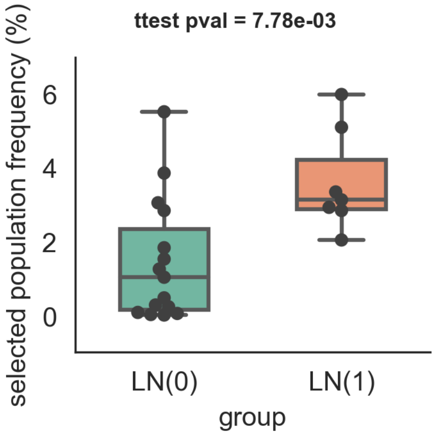
[14]:



```
[15]: print('selected population frequencies for filter 0')
      Image(fig_path+'/'+'selected_population_frequencies_filter_0.png',width=600,␣
       ↪height=350)
```

```
selected population frequencies for filter 0
```

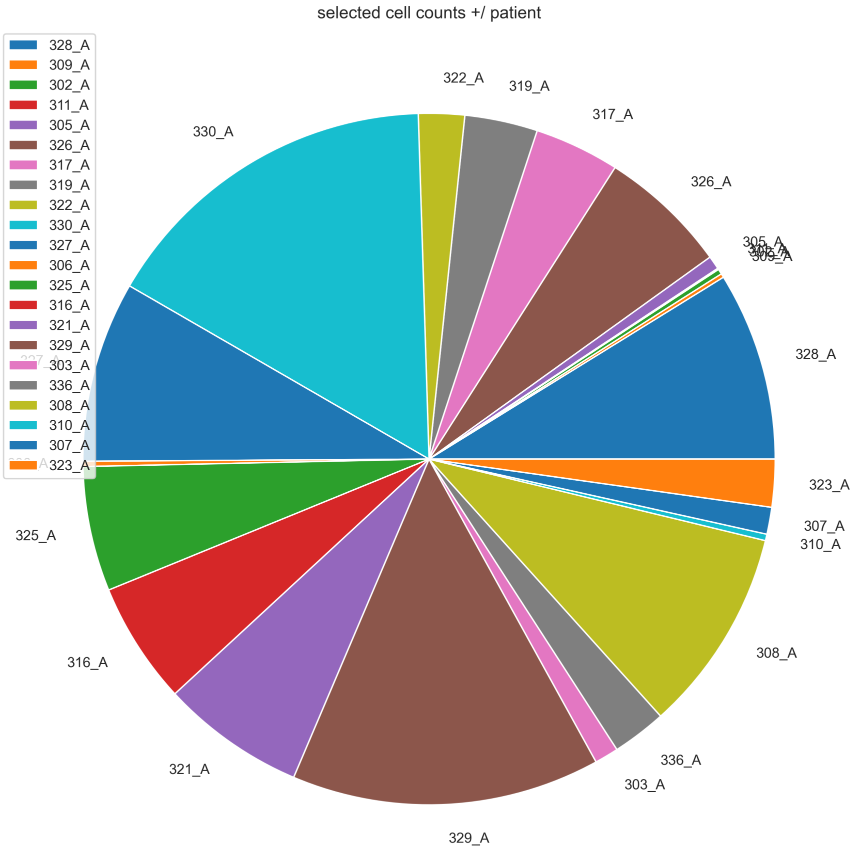
```
[15]:
```



```
[16]: print('selected cell counts per patients 0')
      Image(fig_path+'/'+'selected_cells_per_patient_0.png',width=600, height=350)
```

```
selected cell counts per patients 0
```

```
[16]:
```


selected cell counts +/ patient
328_A
309_A
302_A
311_A
305_A
326_A
317_A
319_A
322_A
330_A
327_A
306_A
325_A
316_A
321_A
329_A
303_A
336_A
308_A
310_A
307_A
323_A
322_A
319_A
317_A
330_A
326_A
305_A
309_A
328_A
323_A
307_A
310_A
325_A
308_A
316_A
336_A
303_A
321_A
329_A

[ ]: