

In this tutorial, we extended JSNMF to analyze single-cell multi-omics data with more than two modalities measured from the same single cell. A scNMT-seq dataset generated from the developing mouse embryo, where gene expression, chromatin accessibility and methylation were profiled simultaneously in the same cell

```
addpath(genpath(' ../data'))
addpath(' ../codes')
addpath(' ../external')
```

Load three modalities scNMT-seq data

```
load('genebody.mat')
X1 = rna; X2 = acc; X3 = met;

load('stage_lineage.mat')
[label_name, I] = sort(stage_lineage_2);
label_name = strrep(label_name, '_', '\_');
num_clu = length(unique(label_name));

tag = unique(label_name);
tag = cellstr(tag);
[~, label] = ismember(label_name, tag);

[alpha, gamma, Inits] = pa_sel(X1, X2, X3, num_clu);
[~,~,~,H1,H2,H3,S,iter,objs] = jsnmf_3mod(X1,X2,X3,alpha,gamma,Inits);
```

```
iteration starts!
number of iteration:10  obj:16161948.1468
number of iteration:20  obj:15936813.377
number of iteration:30  obj:15870628.7942
number of iteration:40  obj:15839232.4395
number of iteration:50  obj:15820792.2577
number of iteration:60  obj:15808549.3579
number of iteration:70  obj:15799735.1604
number of iteration:80  obj:15793012.4302
number of iteration:90  obj:15787667.1533
number of iteration:100 obj:15783283.6795
number of iteration:110 obj:15779601.2306
number of iteration:120 obj:15776447.356
number of iteration:130 obj:15773703.6129
number of iteration:140 obj:15771286.3463
number of iteration:150 obj:15769134.138
number of iteration:160 obj:15767200.5378
number of iteration:170 obj:15765449.8243
converged!
```

```
%% Visualization with UMAP
addpath(' ../umapFileExchange/umap')
addpath(' ../umapFileExchange/util')

term = '.';
colors = generateColors(max(length(unique(label_name))),length(unique(term)));

D_jsnmf = 1-S; D_jsnmf = D_jsnmf-diag(diag(D_jsnmf));
```

```
[reduction_jsnmf, ~, ~, ~]=run_umap(D_jsnmf,'metric','precomputed','min_dist',0.38,'n_neighbors'
```

Can not reach host ":80 because ": Connection refused: connect

Can not reach host "cgworkspace.cytogenie.org:80 because ": 杓櫛櫛櫛尤富鏈哄稀瑙 f 濫鏃墮 氫父鍑虹幫鑽勹殊鏃墮枝璇 紕

Can not reach host "drive.google.com:80 because ": connect timed out

Can not reach host "54.39.2.45:80 because ": connect timed out

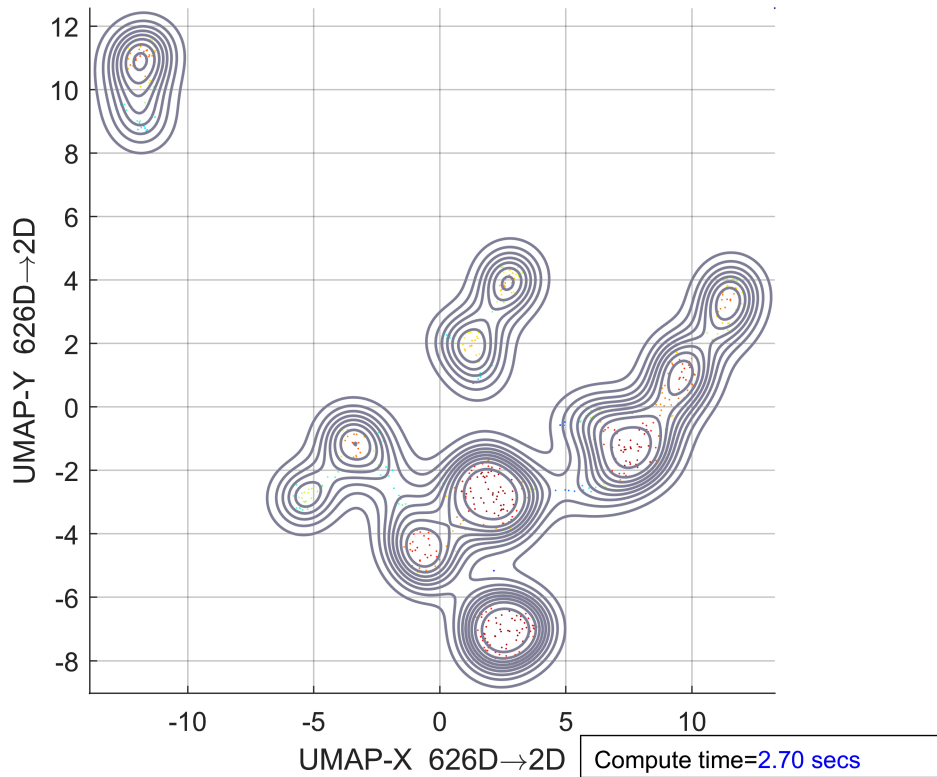
Parallelizing UMAP with MATLAB's 16 assigned logical cores for nn_descent_tasks, sgd_tasks

Running basic (ub) reduction, v2.1.3

(ub=basic, us=supervised, ubt=template, ust=supervised template)

警告: Start point not provided, choosing random start point.

UMAP(method=MEX, n_neighbors=6, n_components=2, metric='precomputed', n_epochs=[], learning_rate=1, init=spectral, n



UMAP reduction finished (cost 2.71 secs)

Finished basic (ub) reduction

```
reduction_jsnmf = reduction_jsnmf(I,:);
gscatter(reduction_jsnmf(:,1),reduction_jsnmf(:,2),label_name,colors,[],6);
set(gca,'xtick',[],'ytick',[]);
title('JSNMF')

legend('Location','westoutside','Box','off','FontSize',9.5);
legendmarkeradjust(16)
legend('boxoff')
```

JSNMF

Warning: 更新 Legend 时出错。

通过 uifigure 函数创建的图窗不支持该功能。有关详细信息，请参阅 App 设计工

- E4.5_Epiblast
- E5.5_Epiblast
- E6.5_Epiblast
- E6.5_Mesoderm
- E6.5_Primitive_Streak
- E7.5_Ectoderm
- E7.5_Endoderm
- E7.5_Mesoderm

