In-silico perturbation

Material

NCBI dataset: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE90546

Paper Adamson B, Norman TM, Jost M, Cho MY et al. A Multiplexed Single-Cell CRISPR Screening Platform Enables Systematic Dissection of the Unfolded Protein Response. Cell 2016 Dec 15;167(7):1867-1882.e21. PMID: 27984733

Methods

Training Process

All Catagory
{'3x_neg_ctrl_pMJ144-1',
'3x_neg_ctrl_pMJ144-2',
'ATF6_IRE1_pMJ152',
'ATF6_PERK_IRE1_pMJ158',
'ATF6_PERK_pMJ150',
'ATF6_only_pMJ145',
'IRE1_only_pMJ148',
'PERK_IRE1_pMJ154',
'PERK_only_pMJ146'}

Training Dataset
{'3x_neg_ctrl_pMJ144-1',

'ATF6_only_pMJ145',
'IRE1_only_pMJ148',
'PERK_only_pMJ146'}

Test Dataset
{'ATF6_IRE1_pMJ152',

'ATF6_PERK_pMJ150',
'PERK_IRE1_pMJ154',}

process the dataset

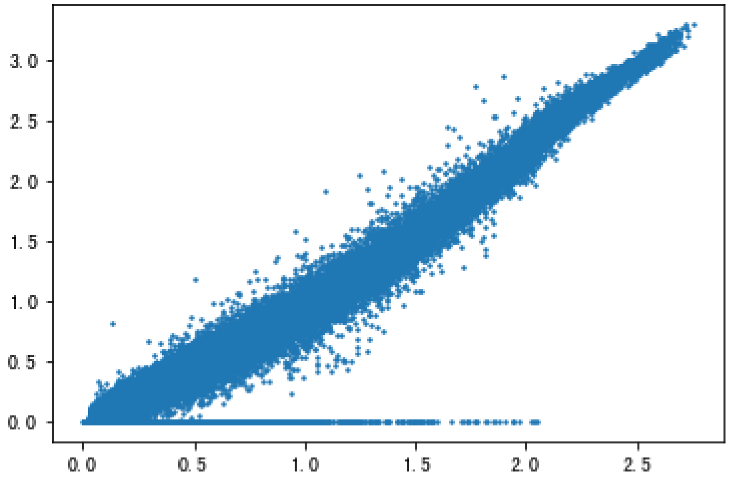
Use the mean value of each type of cell type

```
test_z_genes = np.array([np.mean(adata[adata.obs['cell_type'].str.startswith('3x_neg_ctrl_pMJ144
np.mean(adata[adata.obs['cell_type'].str.startswith('ATF6_only_pMJ145') ,:].X,axis=0),
np.mean(adata[adata.obs['cell_type'].str.startswith('IRE1_only_pMJ148') ,:].X,axis=0),
np.mean(adata[adata.obs['cell_type'].str.startswith('PERK_only_pMJ146') ,:].X,axis=0)
])
test_z =  np.array([np.mean(adata[adata.obs['cell_type'].str.startswith('3x_neg_ctrl_pMJ144-1')
np.mean(adata[adata.obs['cell_type'].str.startswith('ATF6_only_pMJ145') ,tfs_pmbc].X,axis=0),
np.mean(adata[adata.obs['cell_type'].str.startswith('IRE1_only_pMJ148') ,tfs_pmbc].X,axis=0),
np.mean(adata[adata.obs['cell_type'].str.startswith('PERK_only_pMJ146') ,tfs_pmbc].X,axis=0)
])
```

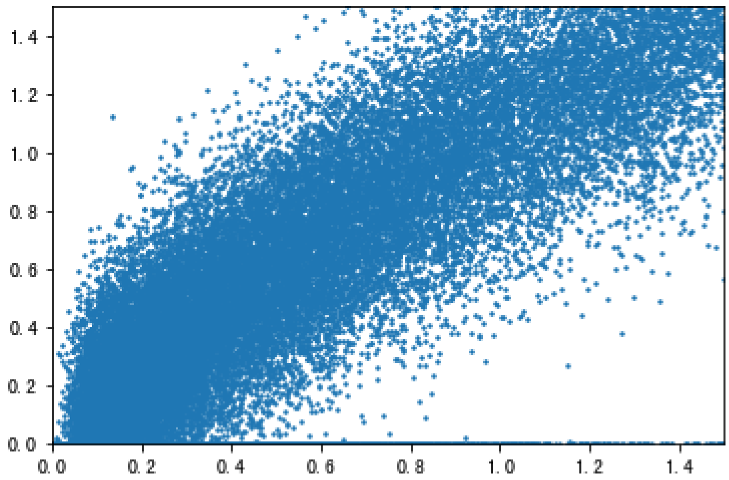
Result

Training dataset Visualization

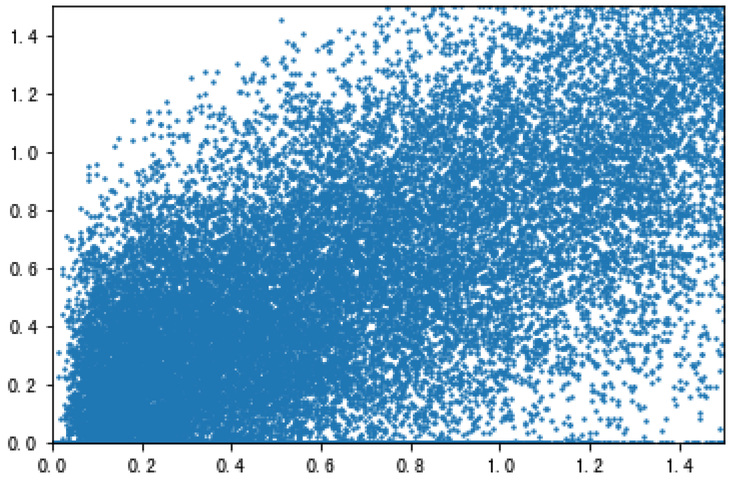
reconstruction plot



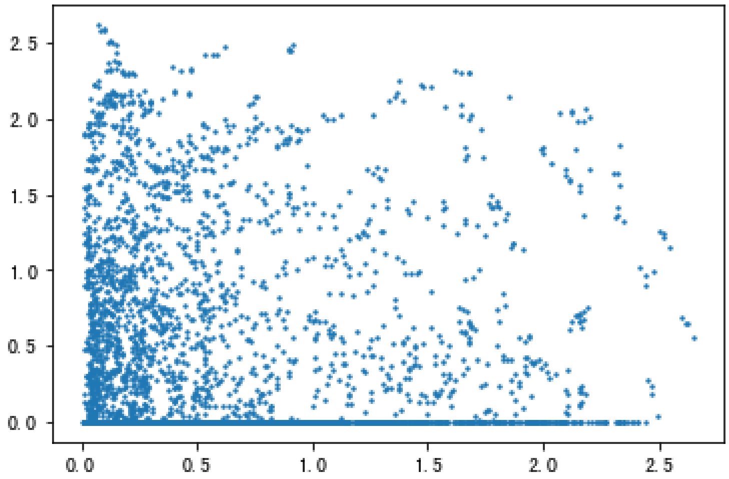
level1 tf to genes plot

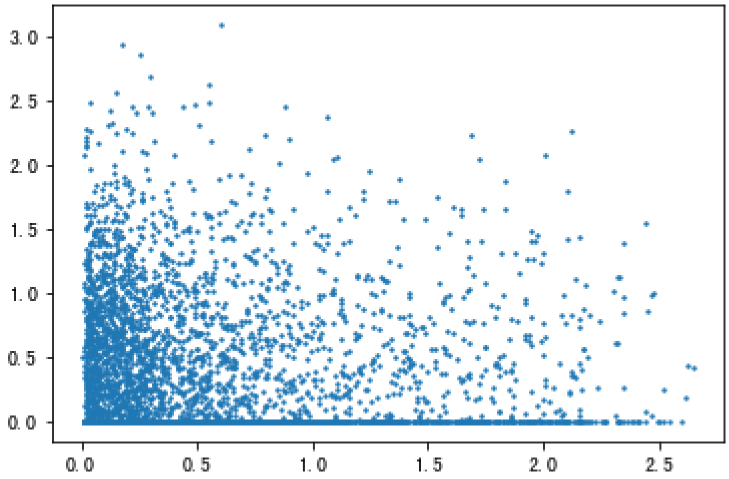


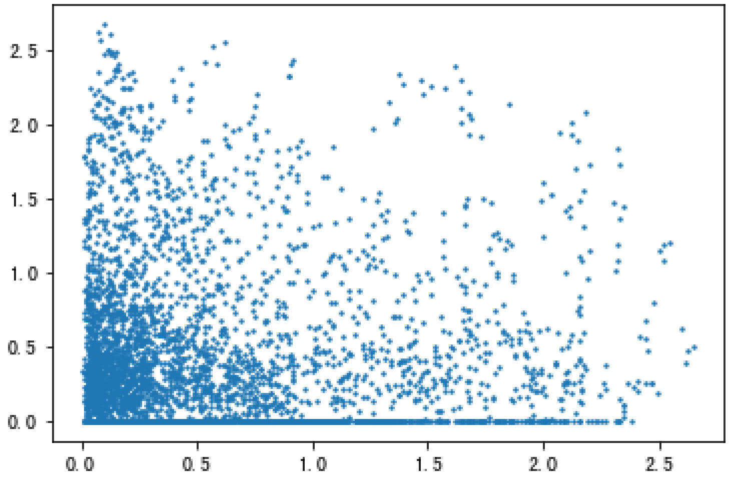
level3 tf to genes plot



tf reconstruction plots (L1 L2 L3)





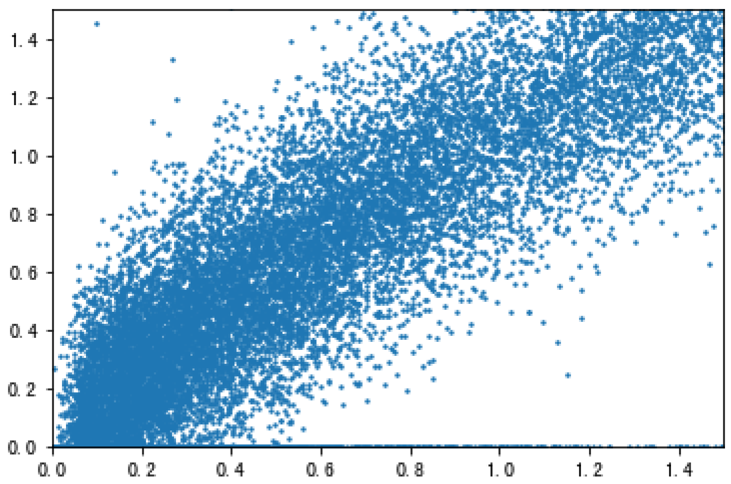


In-silico perturbation Visualization

First I get the mean tfs value of each cell type

```
test_z =  np.array([np.mean(adata[adata.obs['cell_type'].str.startswith('PERK_IRE1_pMJ154') ,tfs
np.mean(adata[adata.obs['cell_type'].str.startswith('ATF6_PERK_pMJ150') ,tfs_pmbc].X,axis=0),
np.mean(adata[adata.obs['cell_type'].str.startswith('ATF6_IRE1_pMJ152') ,tfs_pmbc].X,axis=0)
])
```

Utilizing L1 tf to predict the genes will be better.


1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4