## Paper

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## Project description

will update later...

## How to use

### Installation

You can use python setup.py develop to install the environment directly, or manually install the following packages. requirement pkgs=[ 'numpy', 'torch=2.3.0', 'torchvision', 'six', 'h5py', 'Pillow', 'scipy', 'scikit-learn', 'metric-learn', 'faiss\_gpu']

cd ClusterContrast

pip install -e .

### Data Preparation

You need to train the whole dataset before using the query search engine, after it has been trained, the user can use the list of the locations as the query engine input. Here is the method for preparing the dataset: python make\_blindDS\_maui.py -- INPUT\_DIR <Path to the input dir containing biomarker images> -- OUTPUT\_DIR <Path to the output dir> --BBXS\_FILE <Path to the bbxs\_detection.txt file generated from cell nuclei detection module> --channel\_names <List of filnames for channels in the order: [dapi, histone, neun, s100, olig2, iba1, reca1]>

Alternatively, there are several default variables that you can change by your need, please check the code in the file. The input biomarker images are the whole brain images and the output are the cropped [175,172,10] patches. Below is a sample of how to run the code. python make\_blindDS\_maui.py \ -- INPUT\_DIR=/project/roysam/rwmills/data/brain/MDA\_GBM/1168457/intra\_cor rected/ \ --OUTPUT\_DIR=/project/roysam/rwmills/repos/cluster-contrast reid/examples/data/MDA\_GBM\_1168457\_whole.2/ \ --

BBXS\_FILE=/project/roysam/rwmills/data/brain/MDA\_GBM/1168457/detection \_results/bbxs\_detection.txt \ --DAPI=R1C1.tif \ --HISTONES=R1C2.tif \ --NEUN=R1C3.tif \ --S100=R1C4.tif \ --OLIG2=R1C5.tif \ --IBA1=R1C6.tif \ --RECA1=R2C2.tif \ --other1=R2C3.tif \ --other2=R2C4.tif \ -- other3=R2C5.tif \

You can see the example of the data in the bbs\_detection.txt. We recommend you set the file arc as below:

cluster-contrast-reid

├── clustercontrast

├── exaples

│ └──data

│ └──logs

│ └──pretrained

├── results

├── runs c

├── setup.py

### Train

To train the network, we need several args, here is the explanation: CUDA\_VISIBLE\_DEVICES=0,1,2,3 In default, we train the network in 4 GPUs, corresponding to the variable -j, if you are using another number of GPUs, you need to change the variable -j to the number of the GPUs -b batch size -a backbone network --iters number

of the epoch --momentum the momentum of the encoder update rate -- eps max neighbor distance for DBSCAN -- k1 hyperparameter for KNN -- k2 hyperparameter for outline

One example for training: CUDA\_VISIBLE\_DEVICES=0,1,2,3 python examples/cluster\_contrast\_train\_usl\_infomap.py -b 256 -a resnet50 -d market1501 --iters 200 --momentum 0.1 --eps 0.5 --k1 15 --k2 4 --num instances 16 --logs-dir /project/roysam/rwmills/repos/cluster contrast-reid/examples/logs/infomap/ --height 50 --width 50

### Query

Run the code in BooleanUser\_lhuang.ipynb to see how to interact with your query and the output display with the machine learning model. Before that, you need to prepare the following files:

* pre-trained matrix
* atlas borders
* Target whole brain image

...More Details...

## Acknowledgments

Will update later

## License

If you use this codebase in your work, please consider citing:

@article{update later,

author = {update later},

title = {update later},

journal = {update later},

year = {update later},

doi = {update later},

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