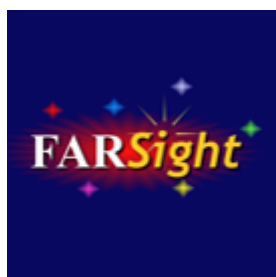


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A Visual Query-Driven Search Engine for Brain Tissue Image Analysis

Paper



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_mauai.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 filenames 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_mauai.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 | bash.sh | 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:

- pretrained matrix
- atlas_borders
- Target whole brain image

...More Details...

Acknowledgements

- 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},  
}
```