

Retraining Inception V3 Model

Commands for Linux Terminal

To run these commands, python must be installed as well as TensorFlow and Bazel. Also the github repository for tensorflow models must be forked or cloned into the machine. The link for this repository is in the References section on the report.

1. Preparing the datasets

```
cd tensorflow-models/inception
bazel build //inception:build_image_data

bazel-bin/inception/build_image_data \
  --train_directory="/home/cc/newSets/TRAIN" \
  --validation_directory="/home/cc/newSets/VALIDATION" \
  --output_directory="/home/cc/newSets/my-custom-data0" \
  --labels_file="/home/cc/newSets/labels.txt" \
  --train_shards=128 \
  --validation_shards=24 \
  --num_threads=8
```

2. Fine-tune the pretrained model with the lung cancer data sets.

```
cd tensorflow-models/inception
bazel build //inception:flowers_train

bazel-bin/inception/flowers_train \
  --train_dir="/home/cc/newSets/OutputModel" \
  --data_dir="/home/cc/newSets/my-custom-data" \
  --pretrained_model_checkpoint_path="/home/cc/inception-v3-model/inception-v3/model.ckpt-157585" \
  --fine_tune=True \
  --initial_learning_rate=0.001 \
  --input_queue_memory_factor=1
```

3. Evaluate fine-tuned model

```
cd tensorflow-models/inception
bazel build //inception:flowers_eval

bazel-bin/inception/flowers_eval \
  --eval_dir="/home/cc/newSets/eval" \
  --data_dir="/home/cc/newSets/my-custom-data" \
  --subset=validation \
  --num_examples=500 \
  --checkpoint_dir="/home/cc/newSets/OutputModel" \
  --input_queue_memory_factor=1 \
  --run_once
```