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**Optimization and Inferencing using Intel distributed OpenVino Toolkit (Local Workstation)**

**How to optimize a TensorFlow model through Intel distributed OenVino toolkit:**

# Step 1: Copy all developed TensorFlow models:

m\_maize\_tensorflowmodel.pb, m\_potato\_tensorflowmodel.pb and m\_tomato\_tensorflowmodel.pb

from

/home/**fakrul**/Documents/PlantPathology/Model/32/tf

\*\*\*\*fakrul will be replaced by your home directory name.

to

model optimizer of openvino

/opt/intel/openvino/deployment\_tools/model\_optimizer

1. Go to the location, /opt/intel/openvino/deployment\_tools/model\_optimizer

**$cd /opt/intel/openvino/deployment\_tools/model\_optimizer**

1. Copy all tensorflow models by giving the following commands:

**$ cp /home/fakrul/Documents/PlantPathology/Model/32/tf/m\_maize\_tensorflowmodel.pb .**

**$ cp /home/fakrul/Documents/PlantPathology/Model/32/tf/m\_potato\_tensorflowmodel.pb .**

**$ cp /home/fakrul/Documents/PlantPathology/Model/32/tf/m\_tomato\_tensorflowmodel.pb .**

# Step 2: Optimization of all TensorFlow Models

Give the following commands in the shell to generate IR, BIN and mapping files.

**Optimization of Potato model:**

***root@tsiailab:/opt/intel/openvino/deployment\_tools/model\_optimizer$ python3 mo\_tf.py --input\_model m\_potato\_tensorflowmodel.pb --output\_dir /opt/intel/openvino/deployment\_tools/model\_optimizer --input\_shape [1,32,32,3]***

You will get the following messages:

[ SUCCESS ] Generated IR model.

[ SUCCESS ] XML file: /opt/intel/openvino/deployment\_tools/model\_optimizer/m\_potato\_tensorflowmodel.xml

[ SUCCESS ] BIN file: /opt/intel/openvino/deployment\_tools/model\_optimizer/m\_potato\_tensorflowmodel.bin

[ SUCCESS ] Total execution time: 5.21 seconds.

\*You will find that corresponding BIN, MAPPING and XML files are generated.

**Optimization of Tomato model:**

**root@tsiailab:/opt/intel/openvino/deployment\_tools/model\_optimizer$ python3 mo\_tf.py --input\_model m\_tomato\_tensorflowmodel.pb --output\_dir /opt/intel/openvino/deployment\_tools/model\_optimizer --input\_shape [1,32,32,3]**

You will get the following message and ignore all warnings.

[ SUCCESS ] Generated IR model.

[ SUCCESS ] XML file: /opt/intel/openvino/deployment\_tools/model\_optimizer/m\_tomato\_tensorflowmodel.xml

[ SUCCESS ] BIN file: /opt/intel/openvino/deployment\_tools/model\_optimizer/m\_tomato\_tensorflowmodel.bin

[ SUCCESS ] Total execution time: 4.99 seconds.

\*You will find that corresponding BIN, MAPPING and XML files are generated.

**Optimization of Maize model:**

**root@tsiailab:/opt/intel/openvino/deployment\_tools/model\_optimizer$ python3 mo\_tf.py --input\_model m\_maize\_tensorflowmodel.pb --output\_dir /opt/intel/openvino/deployment\_tools/model\_optimizer --input\_shape [1,32,32,3]**

[ SUCCESS ] Generated IR model.

[ SUCCESS ] XML file: /opt/intel/openvino/deployment\_tools/model\_optimizer/m\_maize\_tensorflowmodel.xml

[ SUCCESS ] BIN file: /opt/intel/openvino/deployment\_tools/model\_optimizer/m\_maize\_tensorflowmodel.bin

[ SUCCESS ] Total execution time: 5.01 seconds.

\*You will find that corresponding BIN, MAPPING and XML files are generated.

**How to inference an optimized model through Intel distributed OpenVino toolkit:**

\*\*\*\*General instructions:

1. Load the openvino environment

Run below in your shell

**$ source /opt/intel/openvino/bin/setupvars.sh**

1. There is a python script developed to create/to load the inference engine and network files, “**tsiai\_inference\_model.py**” to run on the optimized model of tomato, potato and maize.
2. There are 3 (three) levels of files created for each plant for inferencing to classify the diseases with probability. Items with the highest probability will be shown at the top.
3. Input for inferencing:

PHL.JPG means/contains a potato healthy leaf image

TLB.JPG means/contains a tomato late blight image

MHL.JPG means/contains a maize maize healthy leaf image

**tomato.labels** contains**-** All tomato diseases classification

**root@tsiailab:/opt/intel/openvino/deployment\_tools/model\_optimizer$ cat tomato.labels**

0="EarlyBlight"

1="LateBlight"

2="LeafCurl"

3="LeafMold"

4="Healthy"

**potato.labels** contains- All potato diseases classification

**root@tsiailab:/opt/intel/openvino/deployment\_tools/model\_optimizer# cat potato.labels**

0="EarlyBlight"

1="LateBlight"

2="Healthy"

**maize.labels** contains- All maize diseases classification

**root@tsiailab:/opt/intel/openvino/deployment\_tools/model\_optimizer# cat maize.labels**

0="CommonRust"

1="GrayLeafSpot"

2="NorthernLeafBlight"

3="Healthy"

1. You can control the prediction items through the parameter “**-nt**”; for example:

* **nt “3”** means show top 3 probability(Potato model can classify 3 categories, 2 diseases and healthy leaf that’s why we will use -nt “3” when we will inference potato model )
* **nt “5”** means show top 5 probability(Tomato model can classify 5 categories, 4 diseases and healthy leaf )
* **nt “4”** means show top 4 probability(Maize model can classify 4 categories, 3 diseases and healthy leaf)

**Inference of Potato Model:**

Run below command in your shell:

**root@tsiailab:/opt/intel/openvino/deployment\_tools/model\_optimizer$ python3**

**tsiai\_inference\_model.py -m "m\_potato\_tensorflowmodel.xml" -i "PHL.JPG" -d "CPU" --labels "potato.labels" -nt "3"**

You will get the following messages:

[ INFO ] Creating Inference Engine

[ INFO ] Loading network files:

m\_potato\_tensorflowmodel.xml

m\_potato\_tensorflowmodel.bin

[ INFO ] Preparing input blobs

[ WARNING ] Image PHL.JPG is resized from (256, 256) to (32, 32)

[ INFO ] Batch size is 1

[ INFO ] Loading model to the plugin

[ INFO ] Starting inference in synchronous mode

[ INFO ] Processing output blob

[ INFO ] Top 3 results:

Image PHL.JPG

classid probability

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2="Healthy"0.9689336

1="LateBlight"0.0310663

0="EarlyBlight"0.0000000

**Inference of Tomato Model:**

Run below command in your shell:

**root@tsiailab:/opt/intel/openvino/deployment\_tools/model\_optimizer$ python3 tsiai\_inference\_model.py -m "m\_tomato\_tensorflowmodel.xml" -i "TLB.JPG" -d "CPU" --labels "tomato.labels" -nt "5"**

You will get the message,

[ INFO ] Creating Inference Engine

[ INFO ] Loading network files:

m\_tomato\_tensorflowmodel.xml

m\_tomato\_tensorflowmodel.bin

[ INFO ] Preparing input blobs

[ WARNING ] Image TLB.jpg is resized from (256, 256) to (32, 32)

[ INFO ] Batch size is 1

[ INFO ] Loading model to the plugin

[ INFO ] Starting inference in synchronous mode

[ INFO ] Processing output blob

[ INFO ] Top 5 results:

Image TLB.JPG

classid probability

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1="LateBlight" 0.9993267

0="EarlyBlight"0.0006714

2="LeafCurl"0.0000017

3="LeafMold"0.0000002

4="Healthy"0.0000000

**Inference of Maize Model:**

Run below command in your shell:

**root@tsiailab:/opt/intel/openvino/deployment\_tools/model\_optimizer# python3 tsiai\_inference\_model.py -m "m\_maize\_tensorflowmodel.xml" -i "MHL.JPG" -d "CPU" --labels "maize.labels" -nt "4"**

You will get the following messages:

[ INFO ] Creating Inference Engine

[ INFO ] Loading network files:

m\_maize\_tensorflowmodel.xml

m\_maize\_tensorflowmodel.bin

[ INFO ] Preparing input blobs

[ WARNING ] Image MHL.jpg is resized from (256, 256) to (32, 32)

[ INFO ] Batch size is 1

[ INFO ] Loading model to the plugin

[ INFO ] Starting inference in synchronous mode

[ INFO ] Processing output blob

[ INFO ] Top 4 results:

Image MHL.JPG

classid probability

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3="Healthy" 1.0000000

0="CommonRust" 0.0000000

1="GrayLeafSpot" 0.0000000

2="NorthernLeafBlight" 0.0000000