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

**How to optimize TensorFlow model through intel distributed openvino 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 model 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 Model

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 message:

[ 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 optimized model through intel distributed openvino toolkit.**

\*\*\*\*General instruction:

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 a total of 3 levels 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

1. **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 message,

[ 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 in your shell:

1. **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 mazie model:**

Run below in your shell:

1. **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 message,

[ 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