Accelerating medical applications with Xilinx Vitis AI

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Objectives

Medical AI is becoming an essential part of modern healthcare. It increases detection accuracy, lowers cost, achieves earlier disease prediction, and largely uses non-invasive means. In this respect imaging equipment plays a critical role. With the growing applications in this field AI innovations and algorithms associated with medical image processing are evolving rapidly. Hardware implementation of these algorithms offers much better efficiency and lower latency. Xilinx's full-stack deep learning SDK, Vitis AI, along with highly adaptive Xilinx's AI platforms, enable medical equipment manufacturers and developers with rapid prototyping of these highly evolving algorithms, minimizing time-to-market and cost. The re-configurability of Xilinx platforms provides longer life utility of their products as well.

Because of the inherent characteristics of medical images, (higher resolution, large electronic and photonic 3D format, etc.), these images require significant preprocessing before feeding them into an AI inference engine. These preprocessing algorithms require that several complex operations be performed on each pixel in each image, resulting in a large number of operations per second. Implementing these preprocessing algorithms in Xilinx platforms along with the Xilinx's AI inference engine (DPUs) provides near real-time detection, which can be essential in medical care. Xilinx's Vitis AI provides an end-to-end development platform for these whole application acceleration solutions.

In a set of two articles we demonstrate how a medical application developer can take a medical image dataset and develop and evaluate an end-to-end AI accelerated application using Vitis AI, without writing any lower level RTL code. In this first article, we take the open-source Skin Lesions dataset[1], preprocess the images, create a machine learning network and train it on an x86 platform. Then we use the Xilinx's Vitis AI toolset to quantize, compile and evaluate the model in one of the Xilinx's AI inference platforms, the ZCU102 board. In the second article we are going to create an end-to-end solution where the image preprocessing IP, will perform real-time contrast adjustment, brightness adjustment, and inverting and pseudo color operations before feeding them into the Xilinx AI acceleration IPs.

Introduction

The development of an accelerated deep learning application is a two-phase process. Phase 1 is the model creation and training and Phase 2 is the model deployment for inferencing. During the training phase we design a deep neural network for a specific task and train it with a large dataset; in our case the task is to classify the skin lesion images. During inference phase we compile and deploy the trained model with the application logic targeting a specific AI platform, in our case it's the Xilinx's ZCU102 platform. During inference the application logic feeds new data/images to the model for classification. For our skin lesion detection application these phases are described in more detail below.

Phase 1: Model creation and training

1.0 Design Considerations

1.1 Transfer Learning consideration

Training a deep neural network requires a large dataset. Collecting a large number of medical images is always a challenge. Our skin lesion dataset[1] only has 10k images, which is insufficient for training a deep network from scratch. To overcome this challenge, we use a Transfer Learning technique. Transfer Learning can be achieved in two ways, fine-tuning a network pre-trained on general images or fine-tuning a network pre-trained on medical images for a different target organ or task. For ease of availability we chose to use an Inception v3 network pre-trained with ImageNet[2], a dataset of over 14 million general images.

1.2 Dataset size consideration

The size of the dataset is a key parameter in deciding on the level of Transfer Learning. Even with some augmentation our skin dataset is small. The number of parameters in the Inception v3 network is very large, roughly 22 million, so full adaption may result in overfitting. Thus, we chose to proceed with partial adaption.

1.3 Vitis AI considerations

When creating a deep neural network or choosing one for Transfer Learning targeting Xilinx's AI platforms for deployment, we need to make sure all layers, the size of the kernels and the activation functions in the network are supported by the Xilinx Vitis AI stack. Our selected Inception v3 for Transfer Learning is fully supported by the Vitis AI stack. Also, in our network modifications both Dense and Softmax layers are supported (more on this coming later). The kernel size and the input/output dimensions of these newly added layers are within the supported range as well. For more details on the supported layer, kernel size etc. please refer to Xilinx's DPU IP Product Guide PG338.[3]

2.0 Data Preparation: image preprocessing

Supervised training of neural networks for automated diagnosis of pigmented skin lesions requires homogenous, clean and labeled datasets of images. The skin lesion dataset we use is already preprocessed and released as a training set for academic machine learning purposes and is publicly available through the ISIC archive. The images are collected from different populations, by different medical persons at various times with many different dermatoscopes. Given this diversity, various acquisition and cleaning methods are applied during the preprocessing flow. For example, the specimen (a) in Figure 1 below is an original image taken by a dermatoscope. This image has a black border at the bottom left edge. It also has low luminance, yellow hue and the lesion is off center. The image (b) at the right is the processed clean image.

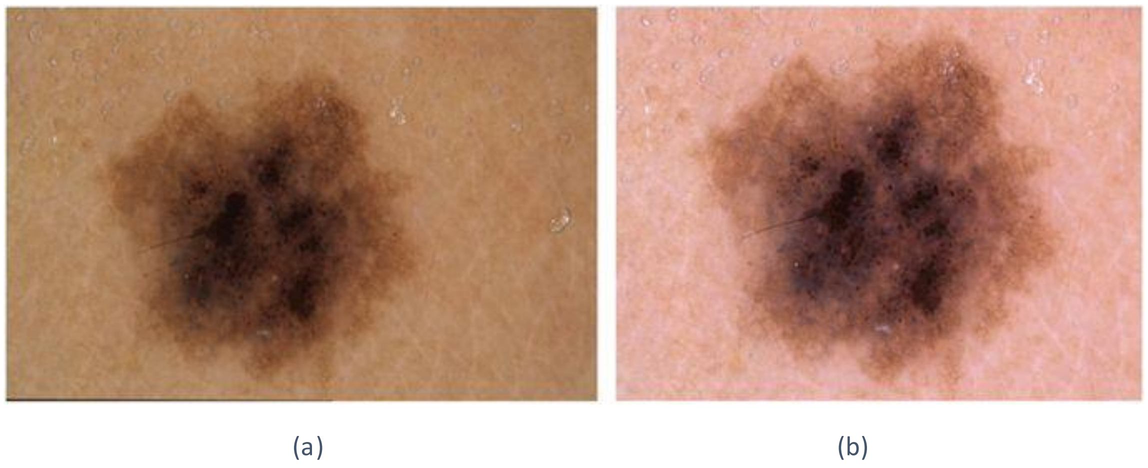


Figure 1: Example preprocessing of a sample skin lesion image a) The original image with black border on the lower left, lesion off center, yellow hue and reduced luminance. b) processed image[4]

Data cleaning is a very important step for convergence during the training flow. Similarly, clean homogeneous specimens are equally important for better detection accuracy during inference. This preprocessing requires significant computations. In the follow-on second article we demonstrate that by implementing these preprocessing algorithms in the hardware in Xilinx's platforms, along with Xilinx's AI inference engine (DPUs), customers can achieve near real-time detection speed.

3.0 Network Design, Training on GPU and Evaluation

The objective of our detection application is to classify skin lesion specimens into seven classes. These seven classes are: nv (Melanocytic nevi), mel (Malignant neoplasm), bkl (Benigh Keratosis), bcc (Basal cell Carcinoma), akiec (Actinic Keratoses), vasc (Vascular Skin) and df (Dermatofibroma).

3.1 Creating a balanced dataset

Analyzing the skin lesion dataset, we see it consists of 10015 images from these seven classes. Class nv has 6705 images, mel has 1113, bkl has 1099, bcc has 514, akiec has 327, vasc has 142 and df has 115. Clearly this dataset is not balanced.

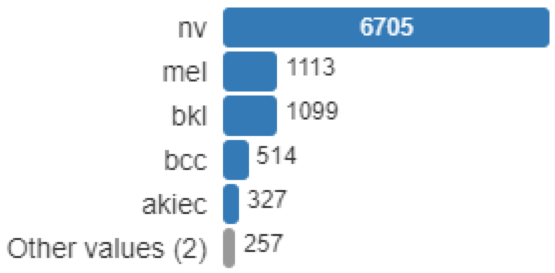


Figure 2: Dataset is not balanced

Training the network with this dataset as-is would create a model which is heavily skewed by a single majority class, nv. To prevent this, we use an offline data augmentation technique to reduce the class imbalance. To create augmented images we use the Keras ImageDataGenerator class as follows,

```
# Data generator
Datagen=ImageDataBenerator(width_shift_range=0.1, height_shift_range=0.1,
rotation_range=180, zoom_range=0.1, horizontal_flip=True, vertical_flip=True,
fill_mode='nearest')
```

We also split the dataset into training and validation sets at a factor of 10:3. For details refer to the Juypter notebook *dataaug.ipnb* located at the GitHub link in the References section at the end of this article[10].

3.2 Network modification

The publicly available Inception v3 network is designed to classify object images into 1001 output classes. To meet our application requirement, we augment the network to support classification between 7 output classes. First the classification layer of the Inception v3 is replaced with a flatten layer. Than two fully connected layers are added right after the flatten layer. Finally, we add a prediction layer (also called Softmax layer) with 7 outputs, one for each category of skin lesion disease. Here is the Keras code snippet where we create the modified network. For details refer to the Juypter notebook, *training.ipnb* located at the GitHub link.

```
# Create an inception_v3 model along with the imagenet pre-trained weights
model=keras.applications.inception_v3.InceptionV3(include_top=False,
weights='imagenet', input_shape=(224, 224, 3))
# Taking the output of the inception_v3 just before last layer
x = iv3_model.layers[-1].output
```

```
# flattening the outputs of the last conv layer
flatten = Flatten()(x)
# adding two fully connected layers. Meeting DPU requirement, keeping output/input
ratio at @ 1/6
dense1 = Dense(2048, activation= 'relu')(flatten)
dense3= Dense(128, activation= 'relu')(dense1)
# adding the prediction layer with 'softmax'
predictions = Dense(7, activation='softmax')(dense3)

# Create the new model with the new outputs
model = Model(inputs=iv3_model.input, outputs=predictions)
```

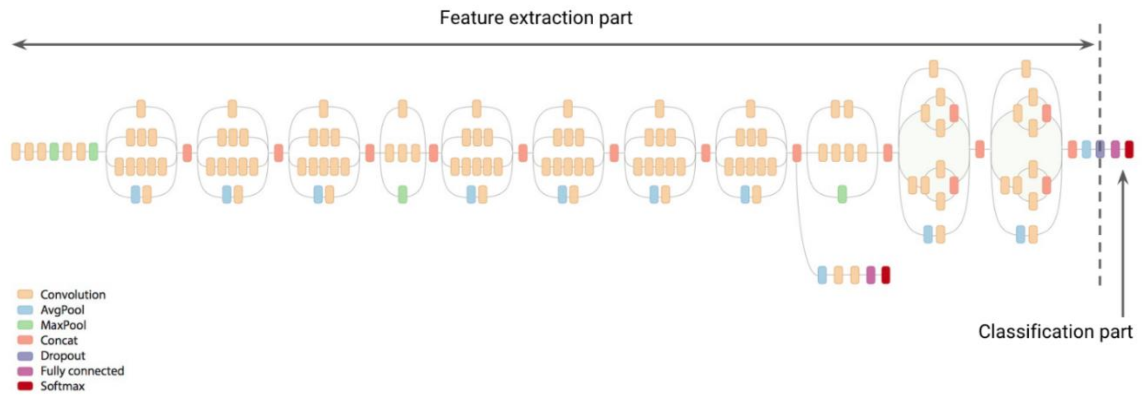


Figure 3: Inception v3 network. It has two parts, Feature extraction and Classification. We replaced the 'Classification part' with a new fully connected classification layer with 7 outputs[9]

3.3 Training flow

For training we freeze the pre-trained weights of all the convolutional layers of the Inception V3. We also randomly initialize the weights of the newly added fully connected layers. Since fine-tuning we choose to use small learning rate during back-propagation runs. The Categorical Cross-entropy algorithm is used for loss calculation while Adam is used to update the weights of the network. Here is the code snippet that we use for training flow. For details refer to the Juypter notebook, *training.ipnb*, also located at the GitHub link.

```
# Freeze the weights of the layers that we aren't training (training the last 23)
for layer in model.layers[:-3]:
   layer.trainable = False
# Compile and prepare the network for training
model.compile(Adam(lr=0.001),                    loss='categorical_crossentropy',
metrics=[categorical_accuracy, top_2_accuracy, top_3_accuracy])
# Declare a checkpoint to save the best trained model
checkpoint = ModelCheckpoint(filepath, monitor='val_categorical_accuracy', verbose=1,
                          save_best_only=True, mode='max')

# Declare how the training flow reduce the learning rate as the learning platos
reduce_lr = ReduceLROnPlateau(monitor='val_categorical_accuracy', factor=0.2,
patience=2,
                          verbose=1, mode='max', min_lr=0.000001)
callbacks_list = [checkpoint, reduce_lr]

# Train the model for 20 epochs
history = model.fit_generator(train_batches,
                          steps_per_epoch=train_steps,
                          class_weight=class_weights,
                          validation_data=valid_batches,
                          validation_steps=val_steps,
                          epochs=20,
                          verbose=1,
                          callbacks=callbacks_list)
```

The training process results in optimal weights and achieves a good classification accuracy of 72.6% and top-3 accuracy of 93.7%.

```
val_cat_acc: 0.7265469035256409
val_top_2_acc: 0.862275450618681
val_top_3_acc: 0.9371257461533099
```

Since we use a Keras framework for the development of the classifier model, the output of the trained weight file is in HDF5 or .h5 format. The Vitis AI quantizer tool accepts .pb format, also known as frozen graph format. We use the following code snippet to convert .h5 file and the network into .pb format. For details refer to *training.ipnb*.

```
from keras import backend as K
frozen_graph = freeze_session(K.get_session(),output_names=[out.op.name for out in
model.outputs])
tf.train.write_graph(frozen_graph, ".", "model/model_incv3_2_6.pb", as_text=False)
```

Phase 2: Port and Evaluate the model on Xilinx's AI platforms

The key advantages of deploying machine learning models on Xilinx's AI platforms are better inference latency and smaller power & memory footprint. We achieve these by quantizing the 32-bit floating point weights of the trained model into lower precision. Also, Xilinx's deep learning processor unit (DPU) is a programmable engine which executes a highly optimized instruction set. Hence, we need to compile the modified

Inception v3 network into instruction sets that can be executed by the DPU. Xilinx's Vitis AI toolchain comes with all necessary tools to quantize and compile our trained model.

1.0 Vitis AI tools bring up

The Vitis AI software is available as a Docker image and is available for download from Docker hub[6]. To install Docker we follow the instructions available at www.docs.Docker.com [7]. We clone the Vitis AI 1.0 GitHub repository and pull Xilinx/vitis-aitools-1.0.0-cpu Docker image from Docker hub. Step by step instructions are available in the Vitis AI guide UG1414 [5]. Here are the command snippets:

```
# pull the vitis-ai tools image from Docker hub
$ Docker pull xilinx/vitis-ai:tools-1.0.0-cpu
#Clone the Vitis AI repository
$ git clone https://github.com/xilinx/vitis-ai
# Launch the Docker container
$ cd Vitis-AI
$ ./Docker_run.sh  xilinx/vitis-ai:tools-1.0.0-cpu
# Once inside the container at /workspace, activate the vitis-ai-tensorflow conda
environment
$ conda activate vitis-ai-tensorflow
```

2.0 Quantization of the weights

Currently Xilinx's AI platforms support 8 bit precision. To quantize the trained weights we took advantage of the via_q_tensorflow application that comes pre-installed in the Vitis AI tools Docker. We call the via_q_tensorflow with the parameters shown in the table below. For additional options and parameters refer to UG1414.

```
# Quantize the trained weights of skinl model
$ vai_q_tensorflow quantize \
                --input_frozen_graph ${TF_NETWORK_PATH}/${FROZEN_MODEL}  \
                --input_fn  ${INPUT_FN} \
                --input_nodes ${INPUT_NODES} \
                --output_nodes ${OUTPUT_NODES}\
                --input_shapes ?,224,224,3 \
                --calib_iter 10 \
                --method 1 \
                --gpu 0 \
                --output_dir ${TF_NETWORK_PATH}/qoutput
```

Name	Type	Description
--input_frozen_graph	String	Frozen inference GraphDef file; the *model/model_incv3_2_6.pb* we created during Phase 1

--input_nodes	String	A list of input node names of the frozen graph
--output_nodes	String	A list of output nodes of the frozen graph
--input_shapes	String	A list of 4d shapes of all input_nodes.
--input_fn	String	This function feeds the input calibration images to the graph. The function format is module_name.input_fn_name.
--method	Int32	The method for quantization. We use 0: Non-overflow method
--calib_iter	Int32	The iterations of calibration. Total number of images for calibration = calib_iter * batch_size.
--output_dir	string	The directory in which to save the quantization results.

We gather the input_node name, the output_node name and input_shape by executing the vitis_ai_tensorflow application with 'inspect' option as shown below,

```
$ vai_q_tensorflow inspect
            --input_frozen_graph=model_incv3_2_6.pb

Op types used: 912 Const, 350 Identity, 87 Relu, 86 Conv2D, 86 Fill, 86 FusedBatchNorm,
12 ConcatV2, 9 AvgPool, 4 MaxPool, 3 BiasAdd, 3 MatMul, 1 Pack, 1 Placeholder, 1 Prod,
1 Reshape, 1 Shape, 1 Softmax, 1 StridedSlice
Found 1 possible inputs: (name=input_1, type=float(1), shape=[?,224,224,3])
Found 1 possible outputs: (name=dense_3/Softmax, op=Softmax)
```

The calibration image set is a subset of the training/validation dataset or actual application images. We copied 300 calibration images during the 'data augmentation' step in Phase-1. For details refer to the Juypter notebook *dataaug.ipnb.*

For input_fn we modified the input_fn.py that comes with the Vitis AI examples in the repository. We modify the *calib_input(..)* function in the *input_fn.py*. It reads the calibration images batch by batch and returns a numpy dictionary of *{input_node_name, numpy.Array_images}*

For convenience we create a bash script *dnnq_skinl.sh* with the quantization function call. Once we have all necessary parameters we update the script and execute it within the Docker container under conda environment *vitis-ai-tensorflow*

```
$ ./dnnq_skinl.sh
```

Once the quantization is done, the summary displays as shown below:

```
INFO: Calibration Done.
INFO: Generating Deploy Model...
INFO: Deploy Model Generated.
```

```
******************** Quantization Summary ********************
INFO: Output:
  quantize_eval_model: qoutput/quantize_eval_model.pb
  deploy_model: qoutput/deploy_model.pb
```

During quantization two files are generated in the output directory named *qoutput/*. The *deploy_model.pb* file contains the quantized trained weights. We use this file in the next section during network compilation. The *quantize_eval_model.pd* file can be used for model evaluation which we will cover in a future article.

3.0 Compilation of the network graph

The Vitis AI tools Docker comes with Vitis AI VAI_C, a domain-specific compiler. It efficiently maps the network model into a highly optimized instruction sequence for the Xilinx's Deep learning Processor Unit (DPU). We call the via_c_tensorflow with the parameters shown in the table below. For additional options and parameters refer to UG1414.

```
# Compile the skinl network
$ vai_c_tensorflow --frozen_pb qoutput/deploy_model.pb \
            --arch {ARCH} \
            --output_dir coutput/output_ZCU102/ \
           --net_name skinl
```

Parameters	Description
--arch	DPU architecture configuration file for VAI_C compiler in JSON format. It contains the dedicated options for the DPU. We used the configuration file for the ZCU102 board, located at /opt/vitis_ai/compiler/arch/dpuv2/ZCU102/ZCU102.json
--frozen_pb	Path of TensorFlow frozen protobuf file. It is the deploy_model.pg file we generated during the quntization flow.
--output_dir	Path of output directory after compilation process. We choose '*coutput/output_ZCU102/*'
--net_name	Name of DPU kernel for network model after compiled, its skinl

For convenience we create a bash script *dnnc_skinl.sh* with the compilation function call. We update the script with all necessary parameters and execute it within the Docker container under conda environment *vitis-ai-tensorflow*

```
$ ./dnnc_skinl.sh
```

Depending on the node operators in the input network the compilation flow generates two categories of kernels. In our case, the skinl_0 is the accelerator kernel which is to be executed by the DPU in the HW. This kernel is composed within the generated object file *dpu_skinl_0.elf* in the *coutput/output_ZCU102* folder. And skinl_1 is the softmax kernel created to be executed by the cpu. However, in this application we gather the input and output dimensions from the skinl_1 kernel parameters and use them to create a Python function CPUCalculateSoftmax(..) which does the softmax calculation in the host cpu. More details on this are covered in the evaluation section below. Compilation also generates a meta.json file in the same folder. This file contains runtime library paths. We copy the /coutput/ folder using scp to the ZCU102 board. A portion of the output of the compilation flow is shown below:

```
Kernel topology "skinl_kernel_graph.jpg" for network "skinl"
kernel list info for network "skinl"
                    Kernel ID : Name
                         0 : skinl_0
                         1 : skinl_1
```

4.0 Model evaluation on ZCU102

Xilinx's ZCU102 is an excellent platform for evaluating accelerated machine learning applications targeted for edge deployment. This board features a Zynq UltraScale+ device, DDR4 memory, a rich set of peripherals and interfaces and expansion capability.[8]

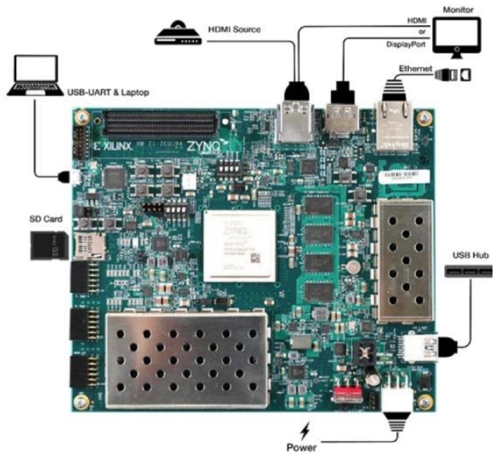


Figure 5: ZCU102 platform with JTAG, SD card and Ethernet ports.

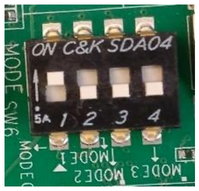


Figure 4: Switch SW6 on ZCU102 board, configured for SD boot

We configure the ZCU102 board so that it boots from an SD card, and connect it to the network via its ethernet port. For simplicity and ease of application evaluation we create a board image with a pre-installed Juypter notebook. The Juypter notebook launches automatically at the end of platform boot. We access the Juypter notebook on a browser at http://board_ip_address:8888. We gather the board_ip_address by accessing it via jtag-over-usb from a laptop. For more details on the configuration options, settings and accessing it via jtag and SSH refer to the user guide UG1414.

Creating the application:

Once the board is up and running we create the lesion detection application in the Juypter notebook environment. Vitis AI applications can be created using C++ or Python APIs. All required API libraries are already installed in the board image. This image is available for download from the GitHub link. We create the application using Python APIs.

The first step of creating a Vitis AI application in Python is to transform the DPU object file, *dpu_skinl_0.elf,* we generated in the network compilation step above into a shared library. We achieve this by using the Arm GCC toolchain. Refer to the Juypter notebook *skinl_app.ipnb.* The naming format of the shared library must be "libdpumodelModelName.so", in our case its *libdpumodelskinl.so.* We place the shared library in the /dpuv2_rundir/ subdirectory which is in the same path level of the *skinl_app.ipnb* script. The command used is as follows:

```
# Transform the dpu_skinl_0.elf into shard library libdpumodelskinl.so
 !/usr/bin/aarch64-xilinx-linux-gcc   -fPIC   -shared   ../coutput/output_ZCU102/dpu_skinl_0.elf  -o
libdpumodelskinl.so
```

Vitis AI comes with a 'Runner Class' which provides the abstraction for FPGA initialization and methods for scheduling compute tasks to the DPU. We instantiate the Vitis Runner object with the syntax shown below; the /vitis_rundir/ is the path to the folder containing *libdpumodelskinl.so* and *meta.json* files.

```
# Instantiate the runner for the DPU
 dpu = runner.Runner(path+'/dpuv2_rundir/' )
```

Now we place the input image data in the memory in a format such that DPU can read and process. To do that we gather the input and output tensors of the DPU using the following API calls. The outputs are in Python list format.

```
# get the input and output tensors
inputTensors = dpu.get_input_tensors()
outputTensors = dpu.get_output_tensors()
```

We estimate the input and output dimensions from the input and output Tensors lists as follows:

```
shapeIn = (batchSize,) + tuple([inputTensors[0].dims[i] for i in range(inputTensors[0].ndims)][1:])
outputHeight = outputTensors[0].dims[2]
outputWidth = outputTensors[0].dims[3]
outputChannel = outputTensors[0].dims[1]
```

We use these dimensions to create input and output data buffers in the memory:

```
outputData.append(np.empty((batchSize,outputSize), dtype = np.float32, order = 'C'))
inputData.append(np.empty((shapeIn), dtype = np.float32, order = 'C'))
```

We than populate the input buffer with the lesion images we want to do detection as follows:

```
#place input images in to the input buffer
k = steps * batchSize
for j in range(batchSize):
    imageRun = inputData[0]
    imageRun[j,...]
    =img[j+k].reshape(inputTensors[0].dims[1],inputTensors[0].dims[2],inputTensors[0].dims[3])
```

Finally, we schedule the compute task to the DPU with the location of the input buffer and the output buffer, where it dumps the computed outputs. Once DPU execution completes the results are available in the outputData buffer.

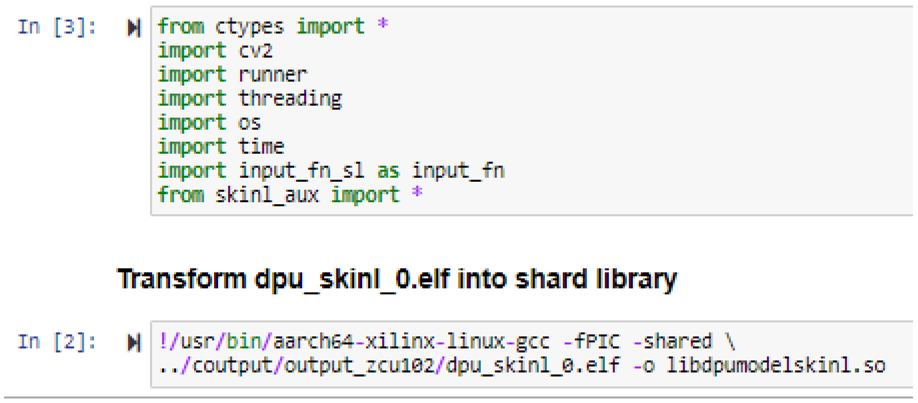
```
dpu.execute_async(inputData,outputData)
```

Finally, we execute the Softmax computation in the CPU by calling *CPUCalcSoftmax(..)* with the outputData. The *CPUCalcSoftmax(..)* is a Python function defined in the *skil_aux.py* file.

```
CPUCalcSoftmax(outputData[0][j], outputSize)
```

The output of the Softmax function is a list of detected classes of the batch of lesion images we fed via inputData buffer. In the Jupyter notebook *skinl_app.ipnb* we used 600 images and demonstrated the estimation of the model accuracy and the average frame/sec (FPS) of the application.

Screen captures from Jupyter notebook running on zcu102 platform:

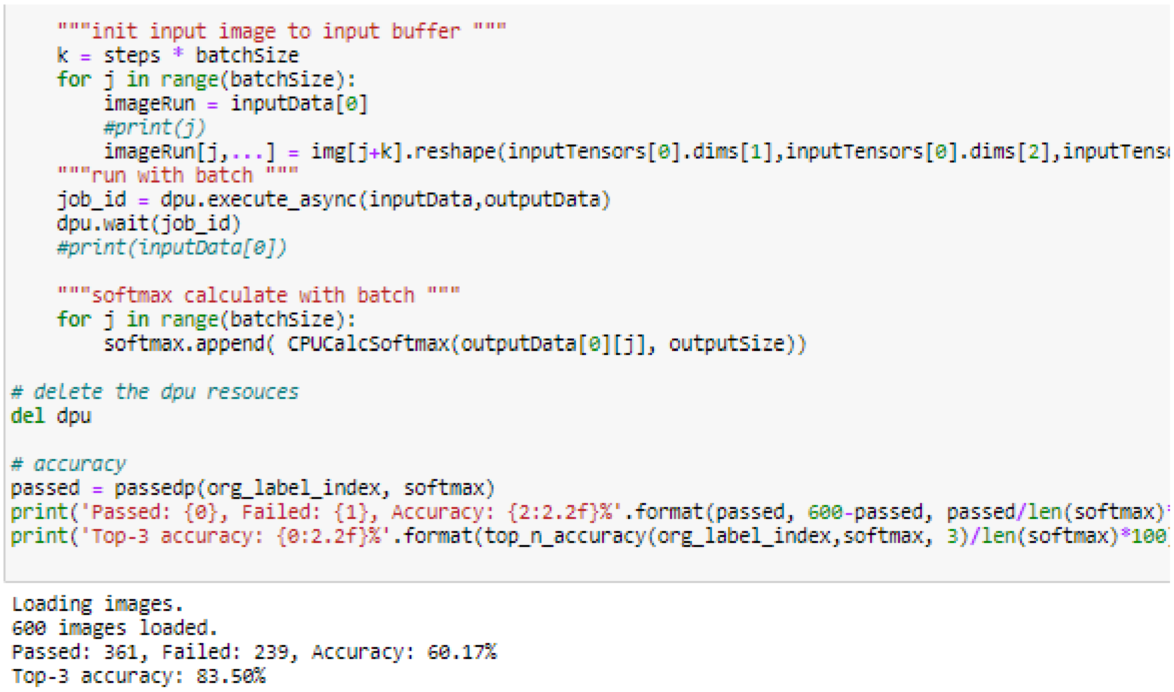


```
In [3]:  from ctypes import *
         import cv2
         import runner
         import threading
         import os
         import time
         import input_fn_sl as input_fn
         from skinl_aux import *
```

Transform dpu_skinl_0.elf into shard library

```
In [2]:  !/usr/bin/aarch64-xilinx-linux-gcc -fPIC -shared \
         ../coutput/output_zcu102/dpu_skinl_0.elf -o libdpumodelskinl.so
```

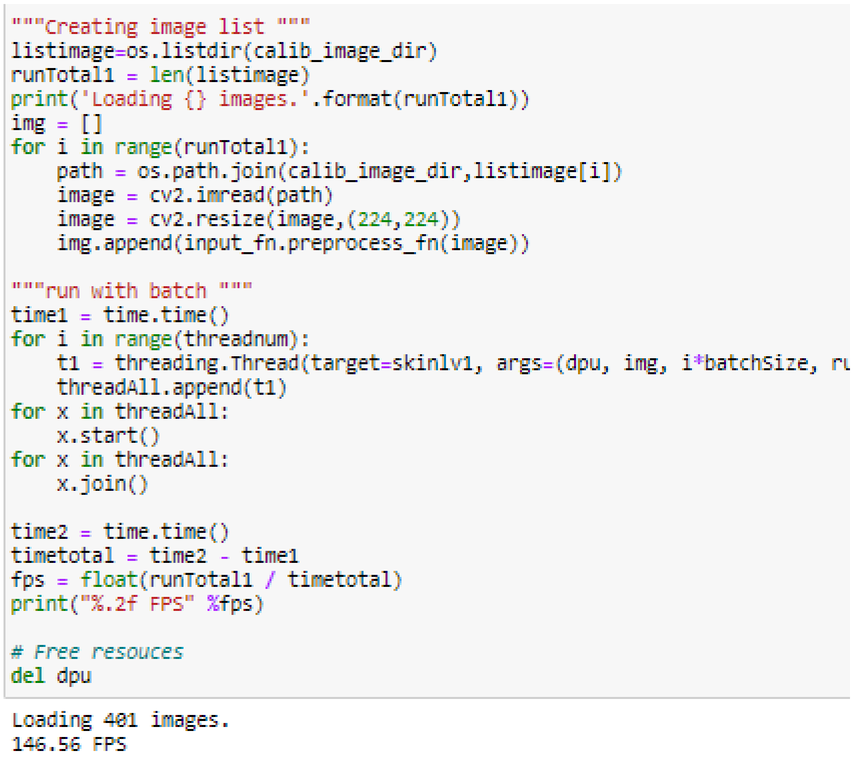
Figure 6: python loadable shared library creation on zcu102 board platform



```
    """init input image to input buffer """
    k = steps * batchSize
    for j in range(batchSize):
        imageRun = inputData[0]
        #print(j)
        imageRun[j,...] = img[j+k].reshape(inputTensors[0].dims[1],inputTensors[0].dims[2],inputTens
    """run with batch """
    job_id = dpu.execute_async(inputData,outputData)
    dpu.wait(job_id)
    #print(inputData[0])

    """softmax calculate with batch """
    for j in range(batchSize):
        softmax.append( CPUCalcSoftmax(outputData[0][j], outputSize))

# delete the dpu resouces
del dpu

# accuracy
passed = passedp(org_label_index, softmax)
print('Passed: {0}, Failed: {1}, Accuracy: {2:2.2f}%'.format(passed, 600-passed, passed/len(softmax)
print('Top-3 accuracy: {0:2.2f}%'.format(top_n_accuracy(org_label_index,softmax, 3)/len(softmax)*100
```

```
Loading images.
600 images loaded.
Passed: 361, Failed: 239, Accuracy: 60.17%
Top-3 accuracy: 83.50%
```

Figure 8: DPU classification and Top-3 estimation on zcu102 platform



```
"""Creating image list """
listimage=os.listdir(calib_image_dir)
runTotal1 = len(listimage)
print('Loading {} images.'.format(runTotal1))
img = []
for i in range(runTotal1):
    path = os.path.join(calib_image_dir,listimage[i])
    image = cv2.imread(path)
    image = cv2.resize(image,(224,224))
    img.append(input_fn.preprocess_fn(image))

"""run with batch """
time1 = time.time()
for i in range(threadnum):
    t1 = threading.Thread(target=skinlv1, args=(dpu, img, i*batchSize, ru
    threadAll.append(t1)
for x in threadAll:
    x.start()
for x in threadAll:
    x.join()

time2 = time.time()
timetotal = time2 - time1
fps = float(runTotal1 / timetotal)
print("%.2f FPS" %fps)

# Free resouces
del dpu
```

```
Loading 401 images.
146.56 FPS
```

Figure 7: FPS estimation on zcu102.

The GitHub link in the references section contains the following items. These are available for download,

1) The Vitis AI tools docker image with the Juypter notebook *dataaug.ipnb, training.ipnb,* and related files and libraries
2) The SD image with *skinl_app.ipnb* and related files and necessary libraries.

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