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## LAMPIRAN

### 1. Lampiran Code program

Berikut merupakan *Source Code* yang digunakan pada pengimplementasian arsitektur CNN dalam mengklasifikasikan kanker kulit.

In [1]: *import library*

```
import Numpy as np
import matplotlib.pyplot as plt
import cv2
import os
from os import listdir

import keras
from keras.preprocessing import image
from keras import backend as K
from keras.layers import Input
from keras.optimizers import Adam

from keras.preprocessing.image import ImageDataGenerator
from keras.preprocessing import image
from keras.preprocessing.image import img_to_array
from Sklearn.preprocessing import MultiLabelBinarizer
from Sklearn.preprocessing import LabelBinarizer
from Sklearn.model_selection import train_test_split

import tensorflow as tf
from tensorflow.keras import optimizers
from tensorflow.keras.models import Sequential, Model
from keras.layers import Conv2D, MaxPooling2D, Dense, Input,
Activation, Dropout, GlobalAveragePooling2D, \
    BatchNormalization, concatenate, AveragePooling2D, Flatten
```

Ln [2]: *directory dataset*

```
%cd "/content/drive/MyDrive/SkinCancer_10/cancer/actinic keratosis"
# read an image
img = cv2.imread('ISIC_0053826.jpg')
# show image format
print(img)
```

In [3]: *inisialisasi hyperparameter*

```
EPOCHS = 100
INIT_LR = 1e-4
default_image_size = tuple((224, 224))
directory_root = "/content/drive/MyDrive/SKIN_CANCER"
width = 224
height = 224
depth = 3
```

#### In [4]: Konversi Citra Menjadi Array

```
def convert_image_to_array(image_dir):
    try:
        image = cv2.imread(image_dir)
        if image is not None :
            image = cv2.resize(image, default_image_size)
            return img_to_array(image)
        else :
            return np.array([])
    except Exception as e:
        print("Error :", e)
        return None
```

```
image_list, label_list = [], []
try:
    print("[INFO] Loading images ...")
    root_dir = listdir(directory_root)
    for directory in root_dir :
        # remove .DS_Store from list
        if directory == ".DS_Store" :
            root_dir.remove(directory)

    for Skin_folder in root_dir :

        Skin_cancer_folder_list =
listdir(f"{directory_root}/{Skin_folder}")

        for cancer_folder in Skin_cancer_folder_list :
            # remove .DS_Store from list
            if cancer_folder == ".DS_Store" :
                Skin_cancer_folder_list.remove(cancer_folder)

        for Skin_cancer_folder in Skin_cancer_folder_list:
            print(f"[INFO] Processing {Skin_cancer_folder} ...")
            Skin_cancer_folder_list =
listdir(f"{directory_root}/{Skin_folder}/{Skin_cancer_folder}/")

            for single_plant_disease_image in
Skin_cancer_folder_list :
                if single_plant_disease_image == ".DS_Store" :

Skin_cancer_folder_list.remove(single_plant_disease_image)

                for image in Skin_cancer_folder_list[:300]:
                    image_directory =
f"{directory_root}/{Skin_folder}/{Skin_cancer_folder}/{image}"
                    if image_directory.endswith(".jpg") == True or
image_directory.endswith(".JPG") == True:

image_list.append(convert_image_to_array(image_directory))
                    label_list.append(Skin_cancer_folder)
            print("[INFO] Image loading completed")
except Exception as e:
    print(f"Error : {e}")
```

In [6]: pelabelan citra

```
label_binarizer = LabelBinarizer()
image_labels = label_binarizer.fit_transform(label_list)
n_classes = len(label_binarizer.classes_)
labels = os.listdir(directory_root)
print("Consist of " + str(n_classes) + " Classes")
```

In [7]: normalisasi data citra

```
print("Normalizing data ..")
np_image_list = np.array(image_list, dtype=np.float16) / 225.0
```

In [8]: *Splitting* data

```
x_train, x_test, y_train, y_test =
train_test_split(np_image_list, image_labels, test_size=0.2)
len(x_test), len(x_train)
```

In [9]: augmetasi citra

```
aug = ImageDataGenerator(
    rotation_range=25,
    width_shift_range=0.1,
    height_shift_range=0.1,
    shear_range=0.2,
    zoom_range=0.2,
    vertical_flip=True,
    horizontal_flip=True,
    fill_mode="nearest")
```

In [10]: arsitektur model

```
#Arsitektur VGG16
import tensorflow as tf
from tensorflow.keras.applications.VGG16 import VGG16
model = tf.keras.Sequential([
    VGG16(
        include_top=False,
        weights='imagenet',
        input_shape=(224, 224, 3)),
    tf.keras.layers.Flatten(),
    tf.keras.layers.Dense(1024, activation='relu'),
    tf.keras.layers.Dropout(0.5),
    tf.keras.layers.Dense(10, activation='softmax')
])
```

```
#Arsitektur DenseNet121
import tensorflow as tf
from tensorflow.keras.applications.densenet import DenseNet121
model = tf.keras.Sequential([
    DenseNet121(
        include_top=False,
        weights='imagenet',
        input_shape=(224, 224, 3)),
    tf.keras.layers.Flatten(),
    tf.keras.layers.Dense(1024, activation='relu'),
    tf.keras.layers.Dropout(0.5),
```

```
tf.keras.layers.Dense(10, activation='softmax')
])
```

```
#Arsitektur NASNetMobile
import tensorflow as tf
from tensorflow.keras.applications.nasnet import NASNetMobile
model = tf.keras.Sequential([
    NASNetMobile(
        include_top=False,
        weights='imagenet',
        input_shape=(224, 224, 3)),
    tf.keras.layers.Flatten(),
    tf.keras.layers.Dense(1024, activation='relu'),
    tf.keras.layers.Dropout(0.5),
    tf.keras.layers.Dense(10, activation='softmax')
])
```

```
optimizer = Adam(lr=0.0001)
model.compile(loss='categorical_crossentropy', optimizer=optimizer,
metrics=['accuracy'])
model.summary()
```

In [12]: training model

```
%%time
history = model.fit(
    aug.flow(x_train, y_train, batch_size=64),
    validation_data=(x_test, y_test),
    steps_per_epoch=len(x_train) // 64,
    epochs=100,
    verbose=1)
```

```
scores = model.evaluate(x_test, y_test)
print(f"Test Accuracy: {scores[1]*100}")
```

In [14]: menampilkan plot accuracy

```
acc = history.history['accuracy']
val_acc = history.history['val_accuracy']
loss = history.history['loss']
val_loss = history.history['val_loss']
epochs = range(1, len(acc) + 1)
#Train and validation accuracy
plt.plot(epochs, acc, 'b', label='Training accuracy')
plt.plot(epochs, val_acc, 'r', label='Validation accuracy')
plt.title('Training and Validation accuracy')
plt.legend()

plt.figure()
#Train and validation loss
plt.plot(epochs, loss, 'b', label='Training loss')
plt.plot(epochs, val_loss, 'r', label='Validation loss')
plt.title('Training and Validation loss')
plt.legend()
plt.show()
```

In [15]: menampilkan *Confusion Matrix*

```
import seaborn as sns

ax = plt.subplot()
sns.heatmap(model_densenet, annot=True, ax = ax)

ax.set_xlabel('Predict labels')
ax.set_title('Confusion Matrix')
ax.xaxis.set_ticklabels(label_binarizer.classes_, rotation=90)
ax.yaxis.set_ticklabels(label_binarizer.classes_, rotation=0)
```

In [16]: menampilkan kurva ROC

```
plt.figure(1, figsize=(10, 10))
plt.plot([0, 1], [0, 1], 'k--')
for i in range(len(label_binarizer.classes_)):
    fpr, tpr, thresholds = roc_curve(y_test[:, i], model_pred[:, i])
    individual_auc = auc(fpr, tpr)
    plt.plot(fpr, tpr, label= (label_binarizer.classes_[i] + ' (area =
    {})'.format(individual_auc)))

plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC curve')
plt.legend(loc='best')
plt.show()
```

In [17]: menampilkan *precision, Recall, F1-score*

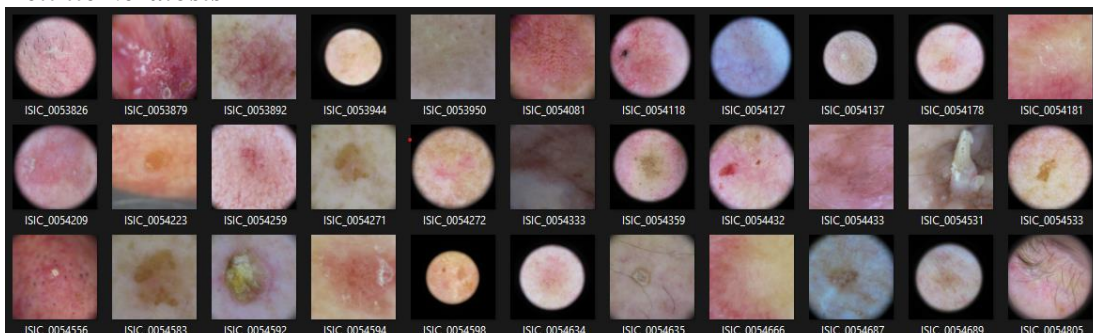
```
from Sklearn.metrics import classification_report
print (classification_report(y_test,y_pred))
```

*source code Android*

<https://github.com/Ajrana/AppSkinCancer>

## 2. Lampiran Gambar

### *Actinic keratosis*





*basal cell carcinoma*



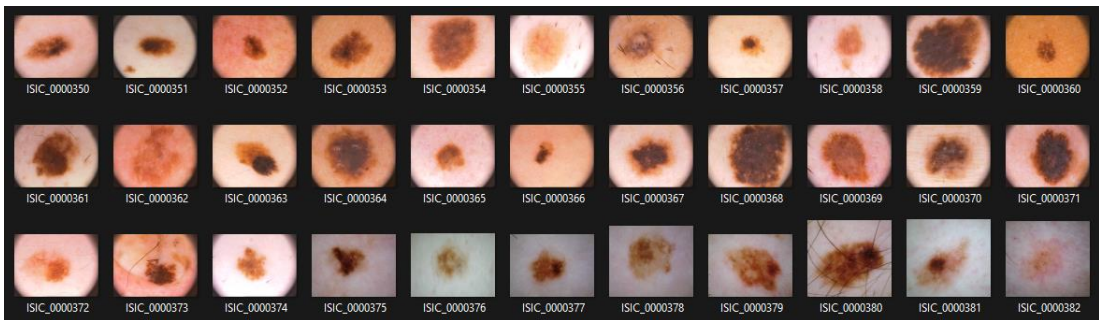
*Dermatofibroma*



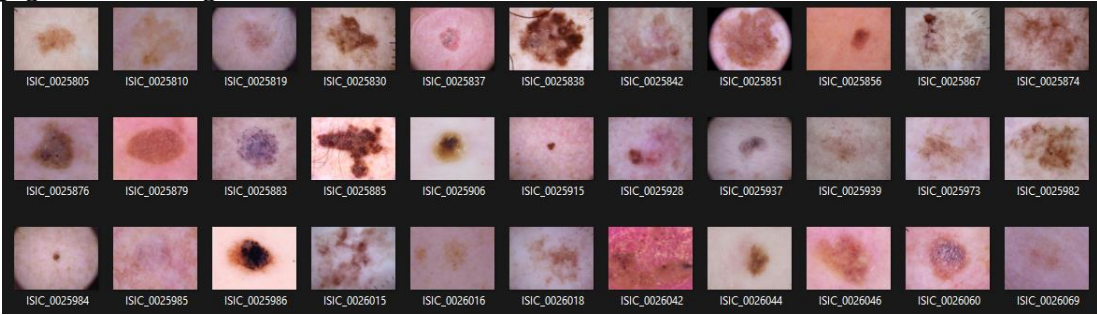
*melanoma*



*Nevus*



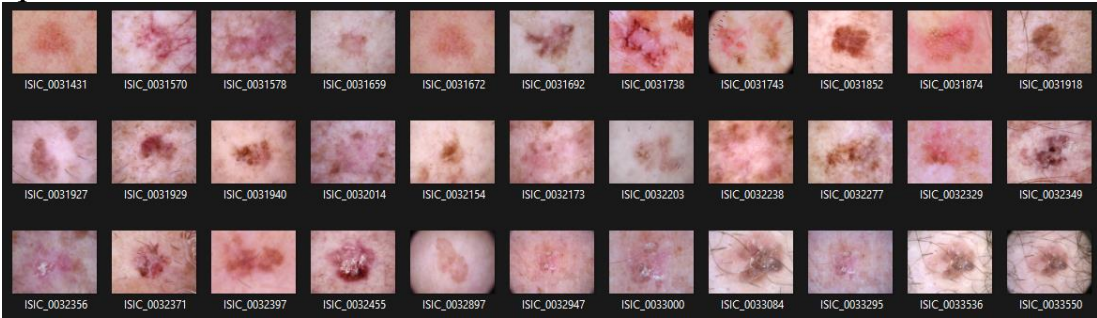
*pigmented benign keratosis*



*seborrheic keratosis*



*squamous cell carcinoma*



*vascular lesion*

