

Predicting Invasive Ductal Carcinoma (IDC) in tissue slices.

Motivation

Invasive Ductal Carcinoma (IDC) is the most common type of breast cancer. It's malignant and able to form metastases which makes it especially dangerous. Often a biopsy is done to remove small tissue samples. Then a pathologist has to decide whether a patient has IDC, another type of breast cancer or is healthy. In addition, sick cells need to be located to find out how advanced the disease is and which grade should be assigned. This has to be done manually and is a time-consuming process. Furthermore, the decision depends on the expertise of the pathologist and his or her equipment. Therefore, deep learning could be of great help to automatically detect and locate tumor tissue cells and to speed up the process. In order to exploit the full potential, one could build a pipeline using massive amounts of tissue image data of various hospitals that were evaluated by different experts. This way, one would be able to overcome the dependence on the pathologist, which would be especially useful in regions where no experts are available.

Our goal

The goal is to create a deep learning model that can be used to ease the work of the pathologist so that they can check the tissue samples in greater batches and in a more efficient manner.

This requires the model to be highly accurate, i.e. above 85% accuracy, and have good recall in both negative and positive classes.

What is meant by invasive ductal carcinoma?

This illustration created by [Mikael Häggström](#) shows the anatomy of a healthy breast. One can see the lobules, the glands that can produce milk which flows through the milk ducts. Ductal carcinoma starts to develop in the ducts, whereas lobular carcinoma has its origin in the lobules. Invasive carcinoma is able to leave its initial tissue compartment and can form metastases.

#importing necessary libraries

```
from numpy.random import seed
seed(101)

import pandas as pd
import numpy as np

import tensorflow

from tensorflow.keras.models import Sequential
```

```
from tensorflow.keras.layers import Dense, Dropout, Conv2D,
MaxPooling2D, Flatten
from tensorflow.keras.optimizers import Adam
from tensorflow.keras.metrics import categorical_crossentropy
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.models import Model
from tensorflow.keras.callbacks import EarlyStopping,
ReduceLROnPlateau, ModelCheckpoint
```

```
import os
from os import listdir
import cv2
```

```
import imageio
import skimage
import skimage.io
import skimage.transform
```

```
from sklearn.utils import shuffle
from sklearn.metrics import confusion_matrix
from sklearn.model_selection import train_test_split
from skimage.io import imread
import itertools
import shutil
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
```

Removing duplicate folders to save space before running the notebook

```
shutil.rmtree('/kaggle/working/all_images_dir', ignore_errors=True)
shutil.rmtree('/kaggle/working/base_dir', ignore_errors=True)
```

Exploring the Data Structure

```
files = listdir("../input/breast-histopathology-images/")
print(len(files))
```

280

#looking at first 10 folders

```
files[0:10]
```

```
['13689',
 '12872',
 '8957',
 '14321',
 '12933',
 '8950',
 '9320',
 '8974',
```

```
'14213',  
'14189']
```

In each folder there are several images and each folder name is the id of the patient

```
base_path =  
"../input/breast-histopathology-images/IDC_regular_ps50_idx5/"  
folder = listdir(base_path)  
print("No. of Patients:", len(folder))
```

No. of Patients: 279

We have to find the number of total images in the dataset

```
total_images = 0  
for n in range(len(folder)):  
    patient_id = folder[n]  
    for c in [0, 1]:  
        patient_path = base_path + patient_id  
        class_path = patient_path + '/' + str(c) + '/'  
        subfiles = listdir(class_path)  
        total_images += len(subfiles)
```

```
print("Total Images in dataset: ", total_images )
```

Total Images in dataset: 277524

Organizing the data into pandas data frame

```
data = pd.DataFrame(index=np.arange(0, total_images),  
columns=["patient_id", "path", "target"])
```

```
k = 0  
for n in range(len(folder)):  
    patient_id = folder[n]  
    patient_path = base_path + patient_id  
    for c in [0, 1]:  
        class_path = patient_path + "/" + str(c) + "/"  
        subfiles = listdir(class_path)  
        for m in range(len(subfiles)):  
            image_path = subfiles[m]  
            data.iloc[k]["path"] = class_path + image_path  
            data.iloc[k]["target"] = c  
            data.iloc[k]["patient_id"] = patient_id  
            k += 1
```

```
data.head()
```

	patient_id	path	target
0	13689	../input/breast-histopathology-images/IDC_regu...	0
1	13689	../input/breast-histopathology-images/IDC_regu...	0
2	13689	../input/breast-histopathology-images/IDC_regu...	0
3	13689	../input/breast-histopathology-images/IDC_regu...	0
4	13689	../input/breast-histopathology-images/IDC_regu...	0

Shape of data frame

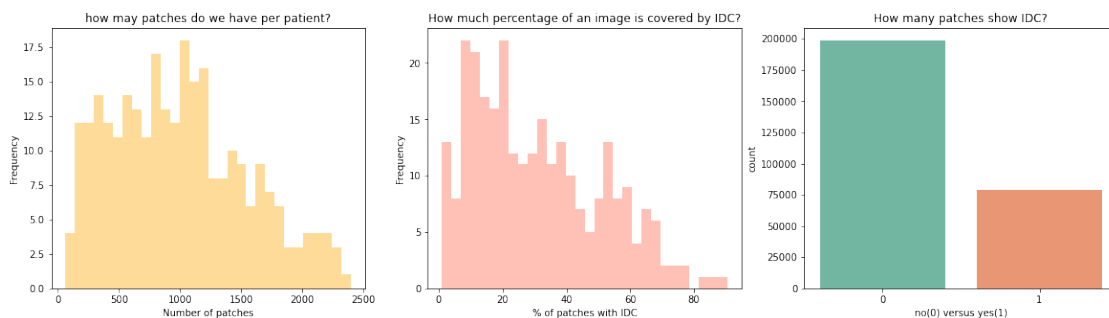
```
data.shape
```

```
(277524, 3)
```

Exploring the data

```
cancer_perc = data.groupby("patient_id").target.value_counts() /  
data.groupby("patient_id").target.size()  
cancer_perc = cancer_perc.unstack()
```

```
fig, ax = plt.subplots(1, 3, figsize = (20,5))  
sns.distplot(data.groupby('patient_id').size(), ax=ax[0],  
color='Orange', kde=False, bins=30)  
ax[0].set_xlabel('Number of patches')  
ax[0].set_ylabel('Frequency')  
ax[0].set_title('how may patches do we have per patient?')  
sns.distplot(cancer_perc.loc[:, 1]*100, ax=ax[1], color="Tomato",  
kde=False, bins=30)  
ax[1].set_title("How much percentage of an image is covered by IDC?")  
ax[1].set_ylabel("Frequency")  
ax[1].set_xlabel("% of patches with IDC");  
sns.countplot(data.target, palette="Set2", ax=ax[2]);  
ax[2].set_xlabel("no(0) versus yes(1)")  
ax[2].set_title("How many patches show IDC?");
```



Insights

- The number of image patches per patient varies a lot.
- Some patients have more than 80 % patches that show IDC! Consequently the tissue is full of cancer or only a part of the breast was covered by the tissue slice that is focused on the IDC cancer.
- The classes of IDC versus no IDC are imbalanced.

converting target to int

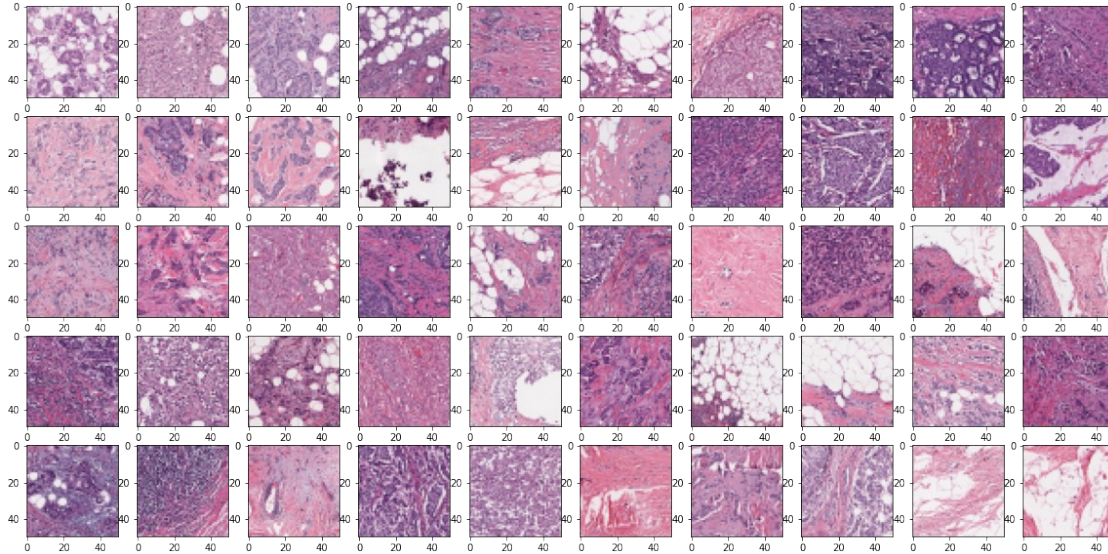
```
data.target = data.target.astype(np.int)
```

Displaying Cancer Tissue Samples

```
cancer_selection = np.random.choice(data[data.target ==  
1].index.values, size=50, replace=False)
```

```
fig, ax = plt.subplots(5, 10, figsize=(20, 10))
```

```
for n in range(5):
    for m in range(10):
        idx = cancer_selection[m + 10*n]
        image = imread(data.loc[idx, "path"])
        ax[n,m].imshow(image)
        ax[n,m].grid(False)
```

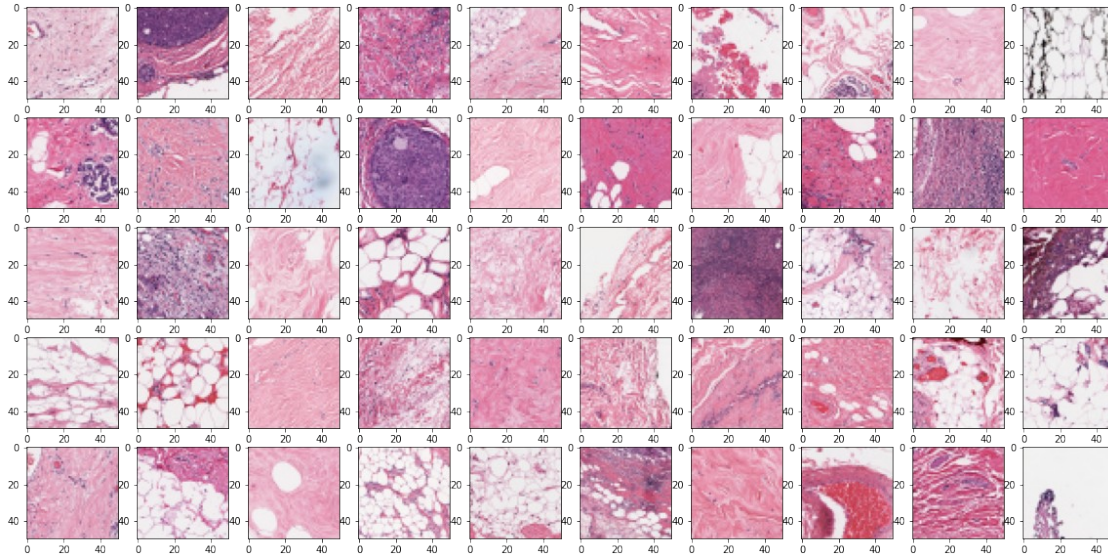


Displaying Non-Cancer Tissue Samples

```
non_cancer_selection = np.random.choice(data[data.target == 0].index.values, size=50, replace=False)
```

```
fig, ax = plt.subplots(5, 10, figsize=(20, 10))
```

```
for n in range(5):
    for m in range(10):
        idx = non_cancer_selection[m + 10*n]
        image = imread(data.loc[idx, "path"])
        ax[n,m].imshow(image)
        ax[n,m].grid(False)
```



Insights

- Cancer Tissue appears to be more violet.
- But some non-cancer tissue is also violet.

Preparing the dataset

Creating directory to store all images

```
all_images_dir = 'all_images_dir'
```

```
if os.path.isdir(all_images_dir):
```

```
    pass
```

```
else:
```

```
    os.mkdir(all_images_dir)
```

This code copies all images from their separate folders into the same

folder called all_images_dir.

```
...
```

The directory structure is like:

```
    patient_id:
```

```
        0
```

```
        1
```

```
...
```

```
patient_list = folder
```

```
for patient in patient_list:
```

```
    path_0 =
```

```
    "../input/breast-histopathology-images/IDC_regular_ps50_idx5/" +
```

```
str(patient) + '/0'
    path_1 =
"../input/breast-histopathology-images/IDC_regular_ps50_idx5/" +
str(patient) + '/1'
```

```
# create list of all files in folder 0
```

```
file_list_0 = listdir(path_0)
```

```
#create a list of all files in folder 1
```

```
file_list_1 = listdir(path_1)
```

```
# moving the 0 class images to all_images_dir
```

```
for fname in file_list_0:
```

```
    src = os.path.join(path_0, fname)
```

```
    dst = os.path.join(all_images_dir, fname)
```

```
    shutil.copyfile(src, dst)
```

```
# moving the 1 class images to all_images_dir
```

```
for fname in file_list_1:
```

```
    src = os.path.join(path_1, fname)
```

```
    dst = os.path.join(all_images_dir, fname)
```

```
    shutil.copyfile(src, dst)
```

```
# Total number of images
```

```
len(listdir(all_images_dir))
```

```
277524
```

```
Creating dataframe of all images
```

```
image_list = os.listdir('all_images_dir')
```

```
df_data = pd.DataFrame(image_list, columns=['image_id'])
```

```
df_data.head()
```

```
                                image_id
0  13403_idx5_x2101_y901_class1.png
1   9324_idx5_x1001_y201_class1.png
2   9325_idx5_x1751_y451_class0.png
3  12954_idx5_x2701_y401_class0.png
4  12905_idx5_x1151_y2001_class0.png
```

```
# Defining helper functions
```

```
def extract_patient_id(x):
```

```
    a = x.split('_')
```



```

    patient_id = a[0]

    return patient_id

def extract_target(x):

    a = x.split('_')
    b = a[4]
    target = b[5]

    return target

# creating new column named patient_id
df_data['patient_id'] = df_data['image_id'].apply(extract_patient_id)

#creating new column named target
df_data['target'] = df_data['image_id'].apply(extract_target)

df_data.head(10)

```

	image_id	patient_id	target
0	13403_idx5_x2101_y901_class1.png	13403	1
1	9324_idx5_x1001_y201_class1.png	9324	1
2	9325_idx5_x1751_y451_class0.png	9325	0
3	12954_idx5_x2701_y401_class0.png	12954	0
4	12905_idx5_x1151_y2001_class0.png	12905	0
5	12910_idx5_x951_y701_class1.png	12910	1
6	10272_idx5_x1951_y2101_class0.png	10272	0
7	13689_idx5_x1501_y1951_class0.png	13689	0
8	14211_idx5_x1201_y451_class1.png	14211	1
9	15840_idx5_x2351_y551_class0.png	15840	0

```

# class distribution of the images

```

```

df_data['target'].value_counts()

```

```

0    198738
1     78786
Name: target, dtype: int64

```

Balance the class distribution

- We can see that the class 1 images are higher in number than that of class 0
- So to prevent this we balance the dataset
- We do this so that the Neural Network does not lean on favouring only one class


```
SAMPLE_SIZE = 78786
```

```
# take a sample of the majority class 0 (total = 198738)
```

```
df_0 = df_data[df_data['target'] == '0'].sample(SAMPLE_SIZE,  
random_state=101)
```

```
# take a sample of class 1 (total = 78786)
```

```
df_1 = df_data[df_data['target'] == '1'].sample(SAMPLE_SIZE,  
random_state=101)
```

```
# concat the two dataframes
```

```
df_data = pd.concat([df_0, df_1], axis=0).reset_index(drop=True)
```

```
# Check the new class distribution
```

```
df_data['target'].value_counts()
```

```
0      78786
```

```
1      78786
```

```
Name: target, dtype: int64
```

Creating train and test sets

```
y = df_data['target']
```

```
df_train, df_val = train_test_split(df_data, test_size=0.10,  
random_state=101, stratify=y)
```

```
print(df_train.shape)
```

```
print(df_val.shape)
```

```
(141814, 3)
```

```
(15758, 3)
```

Creating Directory Structure

```
# Creating new base directory
```

```
base_dir = 'base_dir'
```

```
os.mkdir(base_dir)
```

```
# Creating train directory inside base directory
```

```
train_dir = os.path.join(base_dir, 'train_dir')
```

```
os.mkdir(train_dir)
```

```
# Creating validation directory inside base directory
```

```
val_dir = os.path.join(base_dir, 'val_dir')
```

```
os.mkdir(val_dir)
```

```
# create new folders inside train_dir
```

```
a_no_idc = os.path.join(train_dir, 'a_no_idc')
```

```
os.mkdir(a_no_idc)
```

```
b_has_idc = os.path.join(train_dir, 'b_has_idc')
```

```
os.mkdir(b_has_idc)
```

```

# create new folders inside val_dir
a_no_idc = os.path.join(val_dir, 'a_no_idc')
os.mkdir(a_no_idc)
b_has_idc = os.path.join(val_dir, 'b_has_idc')
os.mkdir(b_has_idc)

# check that the folders have been created
os.listdir('base_dir/train_dir')

['b_has_idc', 'a_no_idc']

# Set the id as the index in df_data
df_data.set_index('image_id', inplace=True)

train_list = list(df_train['image_id'])
val_list = list(df_val['image_id'])

# Transferring the train images
for image in train_list:

    try:
        fname = image
        target = df_data.loc[image, 'target']

        if target == '0':
            label = 'a_no_idc'
        if target == '1':
            label = 'b_has_idc'

        # source path to image
        src = os.path.join(all_images_dir, fname)
        # destination path to image
        dst = os.path.join(train_dir, label, fname)
        # move the image from the source to the destination
        shutil.move(src, dst)
    except:
        continue

for image in val_list:

    try:
        fname = image
        target = df_data.loc[image, 'target']

        if target == '0':
            label = 'a_no_idc'
        if target == '1':

```

```

label = 'b_has_idc'

# source path to image
src = os.path.join(all_images_dir, fname)
# destination path to image
dst = os.path.join(val_dir, label, fname)
# move the image from the source to the destination
shutil.move(src, dst)

except:
    continue

# check how many val images we have in each folder
print(len(os.listdir('base_dir/train_dir/a_no_idc')))
print(len(os.listdir('base_dir/train_dir/b_has_idc')))

70907
70907

Setting up image generators
train_path = 'base_dir/train_dir'
valid_path = 'base_dir/val_dir'

num_train_samples = len(df_train)
num_val_samples = len(df_val)
train_batch_size = 10
val_batch_size = 10

train_steps = np.ceil(num_train_samples / train_batch_size)
val_steps = np.ceil(num_val_samples / val_batch_size)

IMAGE_SIZE = 50

datagen = ImageDataGenerator(rescale = 1.0 / 255,
                             rotation_range = 90,
                             zoom_range = 0.2,
                             horizontal_flip=True,
                             vertical_flip=True)

train_gen = datagen.flow_from_directory(train_path,
target_size=(IMAGE_SIZE, IMAGE_SIZE),
                                     batch_size=train_batch_size,
                                     class_mode='categorical')

val_gen = datagen.flow_from_directory(valid_path,

```

```
target_size=(IMAGE_SIZE,IMAGE_SIZE),  
                                     batch_size=val_batch_size,  
                                     class_mode='categorical')
```

```
# Note: shuffle=False causes the test dataset to not be shuffled  
test_gen = datagen.flow_from_directory(valid_path,
```

```
target_size=(IMAGE_SIZE,IMAGE_SIZE),  
                                     batch_size=1,  
                                     class_mode='categorical',  
                                     shuffle=False)
```

```
Found 141814 images belonging to 2 classes.  
Found 15758 images belonging to 2 classes.  
Found 15758 images belonging to 2 classes.
```

```
# Building the model
```

```
kernel_size = (3,3)  
pool_size= (2,2)  
first_filters = 32  
second_filters = 64  
third_filters = 128
```

```
dropout_conv = 0.3  
dropout_dense = 0.3
```

```
model = Sequential()  
model.add(Conv2D(first_filters, kernel_size, activation = 'relu',  
                 input_shape = (IMAGE_SIZE, IMAGE_SIZE, 3)))  
model.add(Conv2D(first_filters, kernel_size, activation = 'relu'))  
model.add(Conv2D(first_filters, kernel_size, activation = 'relu'))  
model.add(MaxPooling2D(pool_size = pool_size))  
model.add(Dropout(dropout_conv))
```

```
model.add(Conv2D(second_filters, kernel_size, activation = 'relu'))  
model.add(Conv2D(second_filters, kernel_size, activation = 'relu'))  
model.add(Conv2D(second_filters, kernel_size, activation = 'relu'))  
model.add(MaxPooling2D(pool_size = pool_size))  
model.add(Dropout(dropout_conv))
```

```
model.add(Conv2D(third_filters, kernel_size, activation = 'relu'))  
model.add(Conv2D(third_filters, kernel_size, activation = 'relu'))  
model.add(Conv2D(third_filters, kernel_size, activation = 'relu'))  
model.add(MaxPooling2D(pool_size = pool_size))  
model.add(Dropout(dropout_conv))
```

```
model.add(Flatten())  
model.add(Dense(256, activation = "relu"))
```

```
model.add(Dropout(dropout_dense))
model.add(Dense(2, activation = "softmax"))
```

```
model.summary()
```

Model: "sequential"

Layer (type)	Output Shape	Param #
conv2d (Conv2D)	(None, 48, 48, 32)	896
conv2d_1 (Conv2D)	(None, 46, 46, 32)	9248
conv2d_2 (Conv2D)	(None, 44, 44, 32)	9248
max_pooling2d (MaxPooling2D)	(None, 22, 22, 32)	0
dropout (Dropout)	(None, 22, 22, 32)	0
conv2d_3 (Conv2D)	(None, 20, 20, 64)	18496
conv2d_4 (Conv2D)	(None, 18, 18, 64)	36928
conv2d_5 (Conv2D)	(None, 16, 16, 64)	36928
max_pooling2d_1 (MaxPooling2D)	(None, 8, 8, 64)	0
dropout_1 (Dropout)	(None, 8, 8, 64)	0
conv2d_6 (Conv2D)	(None, 6, 6, 128)	73856
conv2d_7 (Conv2D)	(None, 4, 4, 128)	147584
conv2d_8 (Conv2D)	(None, 2, 2, 128)	147584
max_pooling2d_2 (MaxPooling2D)	(None, 1, 1, 128)	0
dropout_2 (Dropout)	(None, 1, 1, 128)	0
flatten (Flatten)	(None, 128)	0
dense (Dense)	(None, 256)	33024
dropout_3 (Dropout)	(None, 256)	0
dense_1 (Dense)	(None, 2)	514
Total params: 514,306		
Trainable params: 514,306		

Non-trainable params: 0

Training the model

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

filepath = "model.h5"
checkpoint = ModelCheckpoint(filepath, monitor='val_acc', verbose=1,
                             save_best_only=True, mode='max')

reduce_lr = ReduceLRonPlateau(monitor='val_acc', factor=0.5,
                              patience=3,
                              verbose=1, mode='max',
                              min_lr=0.00001)

callbacks_list = [checkpoint, reduce_lr]

history = model.fit_generator(train_gen, steps_per_epoch=train_steps,
                             validation_data=val_gen,
                             validation_steps=val_steps,
                             epochs=50, verbose=1,
                             callbacks=callbacks_list)

try:
    model.save('/kaggle/working/model.h5')
except:
    pass

try:
    model.save('model.h5')
except:
    pass

Epoch 1/50
14182/14182 [=====] - 340s 24ms/step - loss:
0.4692 - accuracy: 0.7887 - val_loss: 0.4049 - val_accuracy: 0.8269
Epoch 2/50
14182/14182 [=====] - 332s 23ms/step - loss:
0.4087 - accuracy: 0.8226 - val_loss: 0.4081 - val_accuracy: 0.8180
Epoch 3/50
14182/14182 [=====] - 326s 23ms/step - loss:
0.3867 - accuracy: 0.8353 - val_loss: 0.3728 - val_accuracy: 0.8473
Epoch 4/50
14182/14182 [=====] - 327s 23ms/step - loss:
0.3739 - accuracy: 0.8415 - val_loss: 0.3684 - val_accuracy: 0.8455
Epoch 5/50
14182/14182 [=====] - 324s 23ms/step - loss:
0.3647 - accuracy: 0.8464 - val_loss: 0.3470 - val_accuracy: 0.8511
```

Epoch 6/50
14182/14182 [=====] - 323s 23ms/step - loss:
0.3591 - accuracy: 0.8493 - val_loss: 0.3482 - val_accuracy: 0.8533
Epoch 7/50
14182/14182 [=====] - 325s 23ms/step - loss:
0.3543 - accuracy: 0.8524 - val_loss: 0.3556 - val_accuracy: 0.8478
Epoch 8/50
14182/14182 [=====] - 328s 23ms/step - loss:
0.3500 - accuracy: 0.8535 - val_loss: 0.3478 - val_accuracy: 0.8542
Epoch 9/50
14182/14182 [=====] - 328s 23ms/step - loss:
0.3457 - accuracy: 0.8561 - val_loss: 0.3478 - val_accuracy: 0.8519
Epoch 10/50
14182/14182 [=====] - 326s 23ms/step - loss:
0.3407 - accuracy: 0.8577 - val_loss: 0.3333 - val_accuracy: 0.8640
Epoch 11/50
14182/14182 [=====] - 327s 23ms/step - loss:
0.3397 - accuracy: 0.8583 - val_loss: 0.4116 - val_accuracy: 0.8118
Epoch 12/50
14182/14182 [=====] - 325s 23ms/step - loss:
0.3367 - accuracy: 0.8597 - val_loss: 0.3186 - val_accuracy: 0.8676
Epoch 13/50
14182/14182 [=====] - 326s 23ms/step - loss:
0.3342 - accuracy: 0.8604 - val_loss: 0.3264 - val_accuracy: 0.8650
Epoch 14/50
14182/14182 [=====] - 324s 23ms/step - loss:
0.3315 - accuracy: 0.8621 - val_loss: 0.3201 - val_accuracy: 0.8684
Epoch 15/50
14182/14182 [=====] - 325s 23ms/step - loss:
0.3299 - accuracy: 0.8635 - val_loss: 0.3211 - val_accuracy: 0.8657
Epoch 16/50
14182/14182 [=====] - 328s 23ms/step - loss:
0.3269 - accuracy: 0.8648 - val_loss: 0.3124 - val_accuracy: 0.8701
Epoch 17/50
14182/14182 [=====] - 325s 23ms/step - loss:
0.3256 - accuracy: 0.8647 - val_loss: 0.3464 - val_accuracy: 0.8636
Epoch 18/50
14182/14182 [=====] - 327s 23ms/step - loss:
0.3239 - accuracy: 0.8648 - val_loss: 0.3109 - val_accuracy: 0.8700
Epoch 19/50
14182/14182 [=====] - 327s 23ms/step - loss:
0.3221 - accuracy: 0.8663 - val_loss: 0.3212 - val_accuracy: 0.8646
Epoch 20/50
14182/14182 [=====] - 327s 23ms/step - loss:
0.3226 - accuracy: 0.8660 - val_loss: 0.3245 - val_accuracy: 0.8596
Epoch 21/50
14182/14182 [=====] - 323s 23ms/step - loss:
0.3181 - accuracy: 0.8685 - val_loss: 0.3063 - val_accuracy: 0.8749
Epoch 22/50
14182/14182 [=====] - 324s 23ms/step - loss:

0.3189 - accuracy: 0.8682 - val_loss: 0.3315 - val_accuracy: 0.8601
Epoch 23/50
14182/14182 [=====] - 322s 23ms/step - loss:
0.3160 - accuracy: 0.8688 - val_loss: 0.3215 - val_accuracy: 0.8681
Epoch 24/50
14182/14182 [=====] - 326s 23ms/step - loss:
0.3151 - accuracy: 0.8696 - val_loss: 0.3072 - val_accuracy: 0.8736
Epoch 25/50
14182/14182 [=====] - 328s 23ms/step - loss:
0.3159 - accuracy: 0.8696 - val_loss: 0.3171 - val_accuracy: 0.8690
Epoch 26/50
14182/14182 [=====] - 325s 23ms/step - loss:
0.3127 - accuracy: 0.8716 - val_loss: 0.3016 - val_accuracy: 0.8731
Epoch 27/50
14182/14182 [=====] - 325s 23ms/step - loss:
0.3133 - accuracy: 0.8714 - val_loss: 0.3138 - val_accuracy: 0.8766
Epoch 28/50
14182/14182 [=====] - 324s 23ms/step - loss:
0.3126 - accuracy: 0.8707 - val_loss: 0.3118 - val_accuracy: 0.8766
Epoch 29/50
14182/14182 [=====] - 325s 23ms/step - loss:
0.3100 - accuracy: 0.8717 - val_loss: 0.3131 - val_accuracy: 0.8723
Epoch 30/50
14182/14182 [=====] - 327s 23ms/step - loss:
0.3098 - accuracy: 0.8717 - val_loss: 0.3077 - val_accuracy: 0.8665
Epoch 31/50
14182/14182 [=====] - 322s 23ms/step - loss:
0.3079 - accuracy: 0.8727 - val_loss: 0.3309 - val_accuracy: 0.8544
Epoch 32/50
14182/14182 [=====] - 317s 22ms/step - loss:
0.3077 - accuracy: 0.8730 - val_loss: 0.3245 - val_accuracy: 0.8638
Epoch 33/50
14182/14182 [=====] - 314s 22ms/step - loss:
0.3084 - accuracy: 0.8728 - val_loss: 0.2947 - val_accuracy: 0.8793
Epoch 34/50
14182/14182 [=====] - 315s 22ms/step - loss:
0.3070 - accuracy: 0.8735 - val_loss: 0.3013 - val_accuracy: 0.8755
Epoch 35/50
14182/14182 [=====] - 307s 22ms/step - loss:
0.3074 - accuracy: 0.8727 - val_loss: 0.3074 - val_accuracy: 0.8760
Epoch 36/50
14182/14182 [=====] - 304s 21ms/step - loss:
0.3073 - accuracy: 0.8737 - val_loss: 0.3310 - val_accuracy: 0.8539
Epoch 37/50
14182/14182 [=====] - 303s 21ms/step - loss:
0.3058 - accuracy: 0.8736 - val_loss: 0.2985 - val_accuracy: 0.8799
Epoch 38/50
14182/14182 [=====] - 313s 22ms/step - loss:
0.3042 - accuracy: 0.8756 - val_loss: 0.2916 - val_accuracy: 0.8785
Epoch 39/50

```

14182/14182 [=====] - 327s 23ms/step - loss:
0.3110 - accuracy: 0.8733 - val_loss: 0.3210 - val_accuracy: 0.8575
Epoch 40/50
14182/14182 [=====] - 329s 23ms/step - loss:
0.3064 - accuracy: 0.8738 - val_loss: 0.3022 - val_accuracy: 0.8745
Epoch 41/50
14182/14182 [=====] - 331s 23ms/step - loss:
0.3047 - accuracy: 0.8739 - val_loss: 0.3000 - val_accuracy: 0.8760
Epoch 42/50
14182/14182 [=====] - 330s 23ms/step - loss:
0.3044 - accuracy: 0.8749 - val_loss: 0.2983 - val_accuracy: 0.8766
Epoch 43/50
14182/14182 [=====] - 328s 23ms/step - loss:
0.3030 - accuracy: 0.8760 - val_loss: 0.2971 - val_accuracy: 0.8736
Epoch 44/50
14182/14182 [=====] - 325s 23ms/step - loss:
0.3060 - accuracy: 0.8746 - val_loss: 0.3233 - val_accuracy: 0.8752
Epoch 45/50
14182/14182 [=====] - 321s 23ms/step - loss:
0.3155 - accuracy: 0.8704 - val_loss: 0.3342 - val_accuracy: 0.8737
Epoch 46/50
14182/14182 [=====] - 321s 23ms/step - loss:
0.3072 - accuracy: 0.8730 - val_loss: 0.3349 - val_accuracy: 0.8420
Epoch 47/50
14182/14182 [=====] - 325s 23ms/step - loss:
0.3041 - accuracy: 0.8748 - val_loss: 0.3076 - val_accuracy: 0.8777
Epoch 48/50
14182/14182 [=====] - 323s 23ms/step - loss:
0.3037 - accuracy: 0.8756 - val_loss: 0.3210 - val_accuracy: 0.8582
Epoch 49/50
14182/14182 [=====] - 324s 23ms/step - loss:
0.3025 - accuracy: 0.8767 - val_loss: 0.3383 - val_accuracy: 0.8562
Epoch 50/50
14182/14182 [=====] - 329s 23ms/step - loss:
0.3097 - accuracy: 0.8746 - val_loss: 0.3269 - val_accuracy: 0.8749

```

```
model.save('model.h5')
```

Evaluating the model

```
# get the metric names so we can use evaluate_generator
```

```
model.metrics_names
```

```
['loss', 'accuracy']
```

```
# Here the best epoch will be used.
```

```
model.load_weights('model.h5')
```

```
val_loss, val_acc = \
model.evaluate_generator(test_gen,
                        steps=len(df_val))
```

```
print('val_loss:', val_loss)
print('val_acc:', val_acc)
```

```
val_loss: 0.32337668538093567
val_acc: 0.8747302889823914
```

Plotting the training curves

display the loss and accuracy curves

```
import matplotlib.pyplot as plt
```

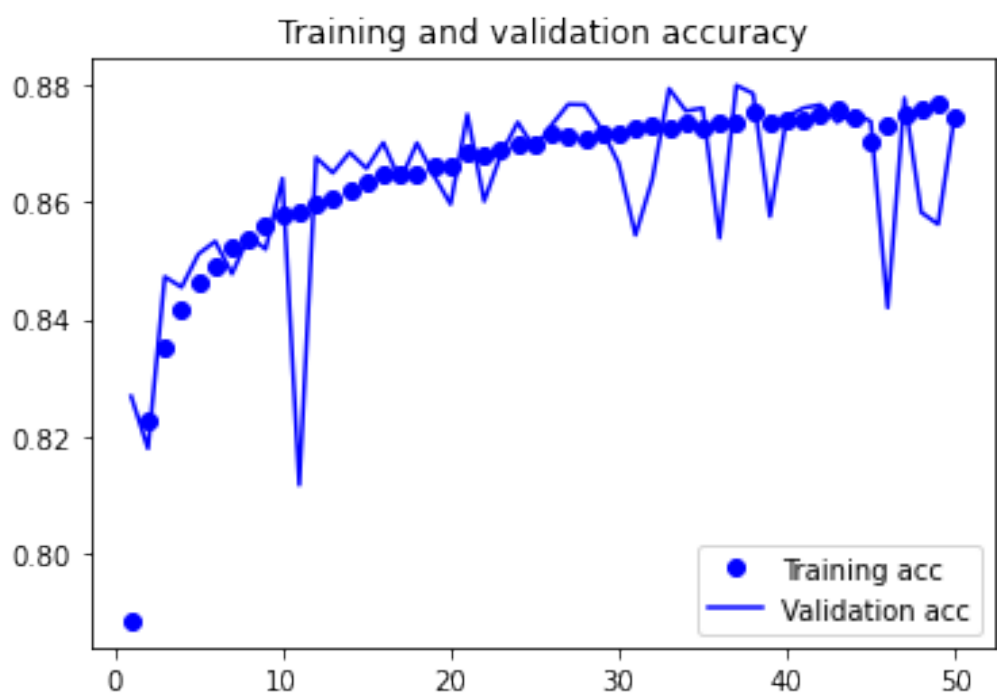
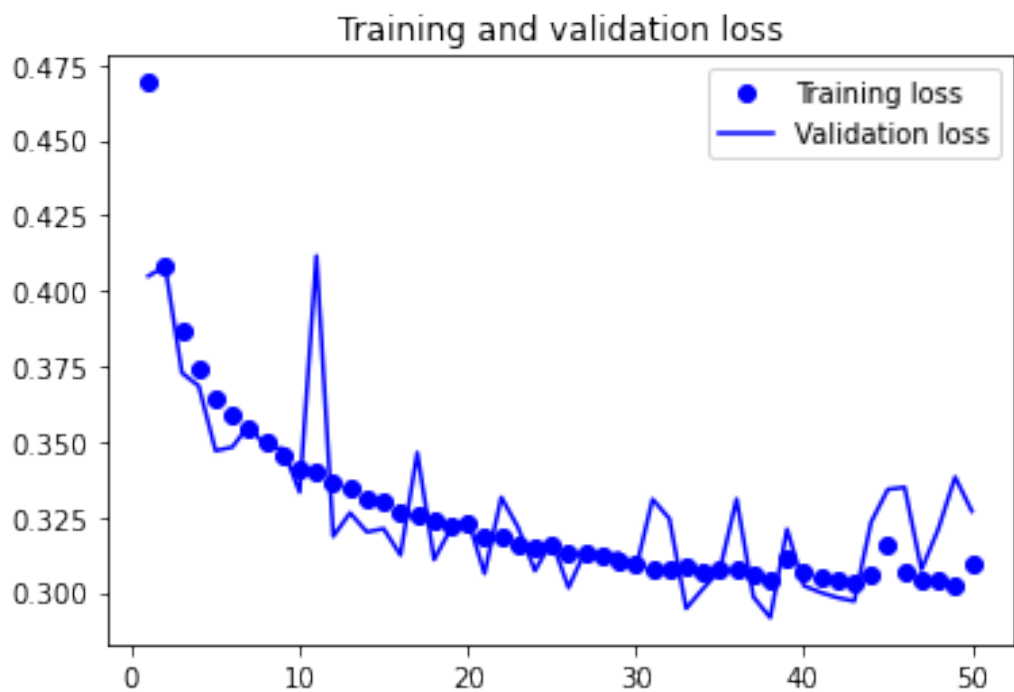
```
acc = history.history['accuracy']
val_acc = history.history['val_accuracy']
loss = history.history['loss']
val_loss = history.history['val_loss']
```

```
epochs = range(1, len(acc) + 1)
```

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

```
plt.plot(epochs, acc, 'bo', label='Training acc')
plt.plot(epochs, val_acc, 'b', label='Validation acc')
plt.title('Training and validation accuracy')
plt.legend()
plt.figure()
```

<Figure size 432x288 with 0 Axes>



<Figure size 432x288 with 0 Axes>

[Make a prediction on the val set](#)

We need these predictions to calculate the AUC score, print the Confusion Matrix and calculate the F1 score.

```

# make a prediction
predictions = model.predict_generator(test_gen, steps=len(df_val),
verbose=1)

15758/15758 [=====] - 54s 3ms/step

predictions.shape

(15758, 2)

# This is how to check what index keras has internally assigned to
each class.
test_gen.class_indices

{'a_no_idc': 0, 'b_has_idc': 1}

# Put the predictions into a dataframe.
# The columns need to be ordered to match the output of the previous
cell

df_preds = pd.DataFrame(predictions, columns=['no_idc', 'has_idc'])

df_preds.head()

   no_idc  has_idc
0  0.690448  0.309552
1  0.685284  0.314716
2  0.293493  0.706507
3  0.332423  0.667577
4  0.829533  0.170467

# Get the true labels
y_true = test_gen.classes

# Get the predicted labels as probabilities
y_pred = df_preds['has_idc']

```

Calculating the AUC Score

```

from sklearn.metrics import roc_auc_score

roc_auc_score(y_true, y_pred)

0.9459758550448937

```

Creating the confusion matrix

```

def plot_confusion_matrix(cm, classes,
                           normalize=False,
                           title='Confusion Matrix',
                           cmap=plt.cm.Blues):
    if normalize:
        cm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]
        print("Normalized confusion matrix")

```

```

else:
    print('Confusion matrix, without normalization')

print(cm)

plt.imshow(cm, interpolation='nearest', cmap=cmap)
plt.title(title)
plt.colorbar()
tick_marks = np.arange(len(classes))
plt.xticks(tick_marks, classes, rotation=45)
plt.yticks(tick_marks, classes)

fmt = '.2f' if normalize else 'd'
thresh = cm.max() / 2.
for i, j in itertools.product(range(cm.shape[0]),
range(cm.shape[1])):
    plt.text(j, i, format(cm[i, j], fmt),
             horizontalalignment="center",
             color="white" if cm[i, j] > thresh else "black")

plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.tight_layout()

# Get the labels of the test images.

test_labels = test_gen.classes

test_labels.shape

(15758,)

# argmax returns the index of the max value in a row
cm = confusion_matrix(test_labels, predictions.argmax(axis=1))

# Print the label associated with each class
test_gen.class_indices

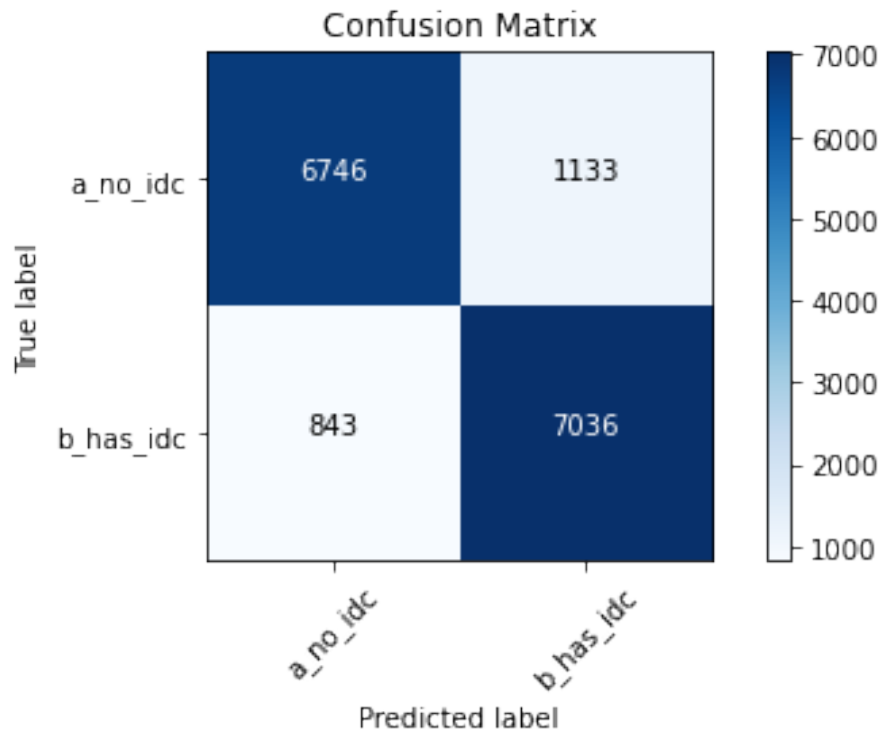
{'a_no_idc': 0, 'b_has_idc': 1}

# Define the labels of the class indices. These need to match the
# order shown above.
cm_plot_labels = ['a_no_idc', 'b_has_idc']

plot_confusion_matrix(cm, cm_plot_labels, title='Confusion Matrix')

Confusion matrix, without normalization
[[6746 1133]
 [ 843 7036]]

```



Creating a classification Report

```
from sklearn.metrics import classification_report
```

```
# Generate a classification report
```

```
# For this to work we need y_pred as binary labels not as probabilities
```

```
y_pred_binary = predictions.argmax(axis=1)
```

```
report = classification_report(y_true, y_pred_binary,
                               target_names=cm_plot_labels)
```

```
print(report)
```

	precision	recall	f1-score	support
a_no_idc	0.89	0.86	0.87	7879
b_has_idc	0.86	0.89	0.88	7879
accuracy			0.87	15758
macro avg	0.88	0.87	0.87	15758
weighted avg	0.88	0.87	0.87	15758

Recall = Given a class, will the classifier be able to detect it? **Precision** = Given a class prediction from a classifier, how likely is it to be correct? **F1 Score** = The harmonic mean of the recall and precision. Essentially, it punishes extreme values.

Conclusion

- From the above report we can see that the model gives us admirable results.
- The model can be improved.
- The recall for each class should be ideally be above 0.90
- The present recall which the model produces is good enough.
- For use in the real world the recall can be further improved.
- This model can help pathologists detect cancer on tissue faster
- The manual examining of tissue slides would not be required