Business Case

Metastasis is the spread of cancer cells to new areas of the body, often by way of the lymph system or bloodstream. A metastatic cancer, or metastatic tumor, is one that has spread from the primary site of origin, or where it started, into different areas of the body.

Tumors formed from cells that have spread are called secondary tumors. The cancer may have spread to areas near the primary site, called regional metastasis, or to parts of the body that are farther away, called distant metastasis.

Cancer that has spread from the primary, or original, site to other places in the body is generally classified as advanced cancer. When the cancer has spread only to nearby tissues or lymph nodes, it is called locally advanced cancer. When the cancer has spread to other parts of the body, it is called metastatic cancer. The liver, lungs, lymph nodes and bones are common areas of metastasis.

Even when metastatic cancer spreads to a new location, it is still named after the area of the body where it started. For example, a person with breast cancer that has spread to the bones is said to have breast cancer with bone metastases. If a cancer has spread widely throughout the body before it is discovered and it is unknown exactly where it started, it is called cancer of unknown primary origin.

One of the most important tests when someone is diagnosed with metastatic breast cancer is a tumor biopsy. A biopsy is the removal of a small amount of tissue for examination under a microscope. A biopsy can be done for many parts of the body, including lymph nodes, lungs, liver, bone, skin, or body fluids.

The process is time consuming and always a chance for a human error. As a part of the biopsy test, a small part of the tissue is put on a glass slide under a microscope for the pathologist to examine. Then the pathologist scans through the region to find malignant areas.

ML Problem Statement

With the current day technology. The glass slides under a microscope can be made digital. The dataset consisted of 220,025 image patches with Metastatic negative and positive. The main goal of the model is accuratly identifying in order to help clinical tast and save time and reduce error.

Metastatic Model

Dataset

We will use Kaggle's version of the PCam (PatchCamelyon) dataset. It's part of the Histopathologic Cancer Detection competition where the challenge is to identify metastatic tissue in histopathologic scans of lymph node sections.

The dataset consists of 220,025 image patches of size 96x96 (130,908 Metastatic negative and 89,117 Metastatic positive).

The images are in tiff format. Many web browsers, including Chrome, don't support the tiff format. Thus the web app wil not be able to accept tiff images. Before training, we will convert these images to png format. This will ensure that the model will be trained on images of similar quality to what we expect a user to submit. Source - https://www.kaggle.com/vbookshelf/part-2-breast-cancer-analyzer-web-app (https://www.kaggle.com/vbookshelf/part-2-breast-cancer-analyzer-web-app)

Required Libraries and Files

In [4]:
```
import tensorflow
from numpy.random import seed
seed(106)
tensorflow.random.set_seed(106)
import pandas as pd
import numpy as np
import tensorflow as tf
from tensorflow import keras
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.layers import Conv2D, MaxPooling2D
from tensorflow.keras.layers import Dense, Dropout, Flatten, Activa
tion
from tensorflow.keras.models import Sequential
from tensorflow.keras.callbacks import EarlyStopping, ReduceLROnPla
teau, ModelCheckpoint
from tensorflow.keras.optimizers import Adam

import os
import cv2

from sklearn.utils import shuffle
from sklearn.metrics import confusion_matrix
from sklearn.model_selection import train_test_split
import itertools
import shutil
import matplotlib.pyplot as plt
%matplotlib inline
```

In [5]:
```
IMAGE_SIZE = 96
IMAGE_CHANNELS = 3
#From the dataset feed we know there is a class imbalance.
#To counter that we will take our sample size as 85000
SAMPLE_SIZE = 85000
```

Files that are available

In [6]:
```
os.listdir('histopathologic-cancer-detection')
```

Out[6]:
```
['train_labels.csv', '.DS_Store', 'test', 'train', 'sample_submiss
ion.csv']
```

In [7]:
```
#Number of Images in train and test
print(len(os.listdir('histopathologic-cancer-detection/train')))
print(len(os.listdir('histopathologic-cancer-detection/test')))
```

```
220025
57458
```

In [9]:
```
#Creating a data frame containing all images
df_data = pd.read_csv('histopathologic-cancer-detection/train_label
s.csv')

#As per https://www.kaggle.com/vbookshelf/part-2-breast-cancer-anal
yzer-web-app
# removing this image because it caused a training error previously
df_data = df_data[df_data['id'] != 'dd6dfed324f9fcb6f93f46f32fc800f
2ec196be2']

# removing this image because it's black
df_data = df_data[df_data['id'] != '9369c7278ec8bcc6c880d99194de09f
c2bd4efbe']


print(df_data.shape)
```

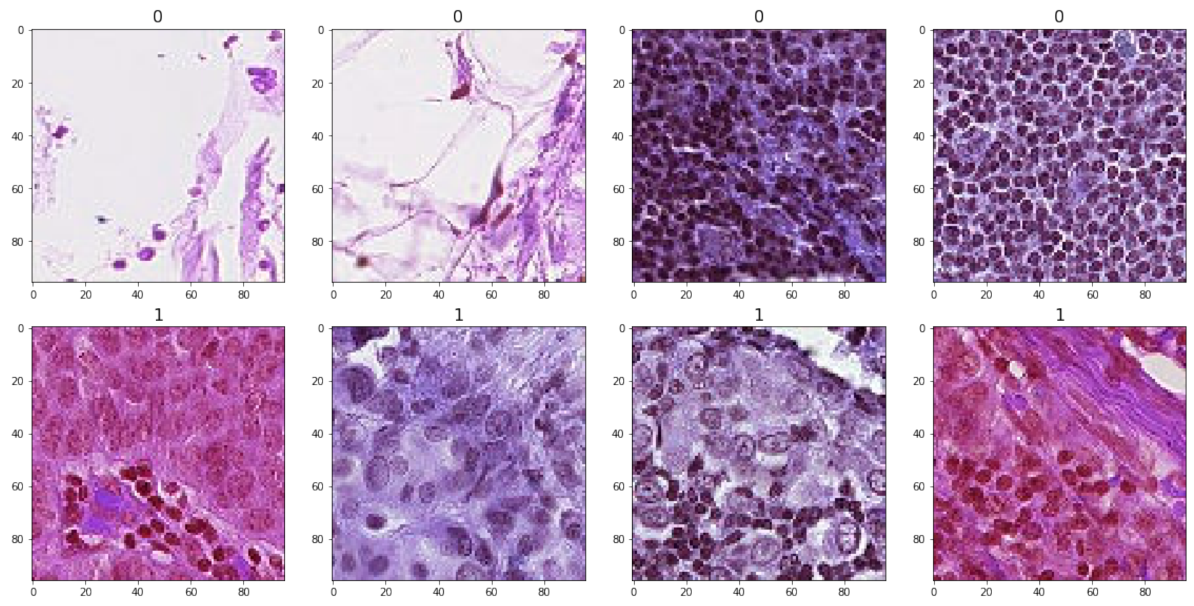
```
(220023, 2)
```

Class Imbalance

As mentioned earlier checking for class distribution

In [10]:
```
# source: https://www.kaggle.com/gpreda/honey-bee-subspecies-classi
fication

def draw_category_images(col_name,figure_cols, df, IMAGE_PATH):

    """
    Give a column in a dataframe,
    this function takes a sample of each class and displays that
    sample on one row. The sample size is the same as figure_cols w
hich
    is the number of columns in the figure.
    Because this function takes a random sample, each time the func
tion is run it
    displays different images.
    """


    categories = (df.groupby([col_name])[col_name].nunique()).index
    f, ax = plt.subplots(nrows=len(categories),ncols=figure_cols,
                         figsize=(4*figure_cols,4*len(categories)))
# adjust size here
    # draw a number of images for each location
    for i, cat in enumerate(categories):
        sample = df[df[col_name]==cat].sample(figure_cols) # figure
_cols is also the sample size
        for j in range(0,figure_cols):
            file=IMAGE_PATH + sample.iloc[j]['id'] + '.tif'
            im=cv2.imread(file)
            ax[i, j].imshow(im, resample=True, cmap='gray')
            ax[i, j].set_title(cat, fontsize=16)
    plt.tight_layout()
    plt.show()
```

In [11]:
```
IMAGE_PATH = 'histopathologic-cancer-detection/train/'

draw_category_images('label',4, df_data, IMAGE_PATH)
```



Creating Train and Validation datasets

Frim train we will be creating validation datasets

In [12]:
```
df_data.head()
```

Out[12]:

	id	label
0	f38a6374c348f90b587e046aac6079959adf3835	0
1	c18f2d887b7ae4f6742ee445113fa1aef383ed77	1
2	755db6279dae599ebb4d39a9123cce439965282d	0
3	bc3f0c64fb968ff4a8bd33af6971ecae77c75e08	0
4	068aba587a4950175d04c680d38943fd488d6a9d	0

In [14]:
```
# What is the class distribution?

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

Out[14]:
```
0    130907
1     89116
Name: label, dtype: int64
```

Since class 1's are 89116 and class o's are 130907 we will reduce class 1's to aviod classimablance. In order to achive this I have defined my sample size as 85000

In [15]:
```
# take a random sample of class 0 with size equal to num samples in
class 1
df_0 = df_data[df_data['label'] == 0].sample(SAMPLE_SIZE, random_st
ate = 101)
# filter out class 1
df_1 = df_data[df_data['label'] == 1].sample(SAMPLE_SIZE, random_st
ate = 101)

# concat the dataframes
df_data = pd.concat([df_0, df_1], axis=0).reset_index(drop=True)
# shuffle
df_data = shuffle(df_data)

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

Out[15]:
```
1    85000
0    85000
Name: label, dtype: int64
```

Now Dataframe df_data consists of equal number of class 1's and 0's

In [16]:
```
# train_test_split

# stratify=y creates a balanced validation set.
y = df_data['label']

df_train, df_val = train_test_split(df_data, test_size=0.20, random
_state=101, stratify=y)

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

```
(136000, 2)
(34000, 2)
```

In [17]:
```
df_train['label'].value_counts()
```

Out[17]:
```
1    68000
0    68000
Name: label, dtype: int64
```

In [18]:
```
df_val['label'].value_counts()
```

Out[18]:
```
1    17000
0    17000
Name: label, dtype: int64
```

Directory Structure

As this is a classification problem, and in order to train the model better. I will be creating direcotries

In [19]:
```
# Create a new directory
base_dir = 'base_dir'
os.mkdir(base_dir)


#[CREATE FOLDERS INSIDE THE BASE DIRECTORY]

# now we create 2 folders inside 'base_dir':

# train_dir
    # a_no_met_tissue
    # b_has_met_tissue

# val_dir
    # a_no_met_tissue
    # b_has_met_tissue



# create a path to 'base_dir' to which we will join the names of th
e new folders
# train_dir
train_dir = os.path.join(base_dir, 'train_dir')
os.mkdir(train_dir)

# val_dir
val_dir = os.path.join(base_dir, 'val_dir')
os.mkdir(val_dir)



# [CREATE FOLDERS INSIDE THE TRAIN AND VALIDATION FOLDERS]
# Inside each folder we create seperate folders for each class

# create new folders inside train_dir
no_met_tissue = os.path.join(train_dir, 'a_no_met_tissue')
os.mkdir(no_met_tissue)
has_met_tissue = os.path.join(train_dir, 'b_has_met_tissue')
os.mkdir(has_met_tissue)


# create new folders inside val_dir
no_met_tissue = os.path.join(val_dir, 'a_no_met_tissue')
os.mkdir(no_met_tissue)
has_met_tissue = os.path.join(val_dir, 'b_has_met_tissue')
os.mkdir(has_met_tissue)
```

In [20]:
```
# check that the folders have been created
os.listdir('base_dir/train_dir')
```

Out[20]:
```
['a_no_met_tissue', 'b_has_met_tissue']
```

Image Transfer

Transfering images into respective folders

In [21]:
```
# Set the id as the index in df_data
df_data.set_index('id', inplace=True)
```

In [25]:
```
# Get a list of train and val images
train_list = list(df_train['id'])
val_list = list(df_val['id'])



# Transfer the train images

for image in train_list:

    # the id in the csv file does not have the .tif extension there
fore we add it here
    fname_tif = image + '.tif'
    # get the label for a certain image
    target = df_data.loc[image,'label']

    # these must match the folder names
    if target == 0:
        label = 'a_no_met_tissue'
    if target == 1:
        label = 'b_has_met_tissue'

    # source path to image
    src = os.path.join('histopathologic-cancer-detection/train', fn
ame_tif)
    # change the new file name to png
    fname_png = image + '.png'
    # destination path to image
    dst = os.path.join(train_dir, label, fname_png)


    # read the file as an array
    cv2_image = cv2.imread(src)
    # save the image at the destination as a png file
    cv2.imwrite(dst, cv2_image)



# Transfer the val images

for image in val_list:

    # the id in the csv file does not have the .tif extension there
```

```
fore we add it here
    fname_tif = image + '.tif'
    # get the label for a certain image
    target = df_data.loc[image,'label']

    # these must match the folder names
    if target == 0:
        label = 'a_no_met_tissue'
    if target == 1:
        label = 'b_has_met_tissue'


    # source path to image
    src = os.path.join('histopathologic-cancer-detection/train', fn
ame_tif)
    # change the new file name to png
    fname_png = image + '.png'
    # destination path to image
    dst = os.path.join(val_dir, label, fname_png)


    # read the file as an array
    cv2_image = cv2.imread(src)
    # save the image at the destination as a png file
    cv2.imwrite(dst, cv2_image)
```

In [26]:

```
# check how many train images we have in each folder

print(len(os.listdir('base_dir/train_dir/a_no_met_tissue')))
print(len(os.listdir('base_dir/train_dir/b_has_met_tissue')))
```

```
68001
68001
```

In [27]:

```
# check how many val images we have in each folder

print(len(os.listdir('base_dir/val_dir/a_no_met_tissue')))
print(len(os.listdir('base_dir/val_dir/b_has_met_tissue')))
```

```
17000
17000
```

Mode Buidling

Image Augumentation

In [28]:
```
train_path = 'base_dir/train_dir'
valid_path = 'base_dir/val_dir'
test_path = '../input/test'

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)
```

In [29]:
```
datagen = ImageDataGenerator(rescale=1.0/255,rotation_range=15,zoom
_range=[0.9, 1.25],brightness_range=[0.5, 1.5],height_shift_range=0
.1)


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

val_gen = datagen.flow_from_directory(valid_path,
                                        target_size=(IMAGE_SIZE,IMA
GE_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,IMA
GE_SIZE),
                                        batch_size=1,
                                        class_mode='categorical',
                                        shuffle=False)
```

```
Found 136000 images belonging to 2 classes.
Found 34000 images belonging to 2 classes.
Found 34000 images belonging to 2 classes.
```

In [30]:
```
kernel_size = (3,3)
pool_size= (2,2)
first_filters = 32
second_filters = 64
third_filters = 128
#fourth_filters = 256



dropout_conv = 0.3
dropout_dense = 0.3


model = Sequential()
model.add(Conv2D(first_filters, kernel_size, strides = 1, padding = 
"same", activation = 'relu',
                 input_shape = (IMAGE_SIZE, IMAGE_SIZE, 3)))
model.add(Conv2D(first_filters, kernel_size, strides = 1, padding = 
"same", activation = 'relu'))
model.add(Conv2D(first_filters, kernel_size, strides = 1, padding = 
"same", activation = 'relu'))
model.add(MaxPooling2D(pool_size = pool_size))
model.add(Dropout(dropout_conv))

model.add(Conv2D(second_filters, kernel_size, strides = 1, padding 
= "same", activation ='relu'))
model.add(Conv2D(second_filters, kernel_size, strides = 1, padding 
= "same", activation ='relu'))
model.add(Conv2D(second_filters, kernel_size, strides = 1, padding 
= "same", activation ='relu'))
model.add(MaxPooling2D(pool_size = pool_size))
model.add(Dropout(dropout_conv))

model.add(Conv2D(third_filters, kernel_size, strides = 2, padding = 
"same", activation ='relu'))
model.add(Conv2D(third_filters, kernel_size, strides = 2, padding = 
"same", activation ='relu'))
model.add(Conv2D(third_filters, kernel_size, strides = 2, padding = 
"same", 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, 96, 96, 32)        896       
_________________________________________________________________
conv2d_1 (Conv2D)            (None, 96, 96, 32)        9248      
_________________________________________________________________
conv2d_2 (Conv2D)            (None, 96, 96, 32)        9248      
_________________________________________________________________
max_pooling2d (MaxPooling2D) (None, 48, 48, 32)        0         
_________________________________________________________________
dropout (Dropout)            (None, 48, 48, 32)        0         
_________________________________________________________________
conv2d_3 (Conv2D)            (None, 48, 48, 64)        18496     
_________________________________________________________________
conv2d_4 (Conv2D)            (None, 48, 48, 64)        36928     
_________________________________________________________________
conv2d_5 (Conv2D)            (None, 48, 48, 64)        36928     
_________________________________________________________________
max_pooling2d_1 (MaxPooling2 (None, 24, 24, 64)        0         
_________________________________________________________________
dropout_1 (Dropout)          (None, 24, 24, 64)        0         
_________________________________________________________________
conv2d_6 (Conv2D)            (None, 12, 12, 128)       73856     
_________________________________________________________________
conv2d_7 (Conv2D)            (None, 6, 6, 128)         147584    
_________________________________________________________________
conv2d_8 (Conv2D)            (None, 3, 3, 128)         147584    
_________________________________________________________________
max_pooling2d_2 (MaxPooling2 (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
_________________________________________________________________
```

```
In [31]: model.compile(Adam(lr=0.0001), loss='binary_crossentropy',
                       metrics=['accuracy'])
```

In [32]:
```
# Get the labels that are associated with each index
print(val_gen.class_indices)
```

```
{'a_no_met_tissue': 0, 'b_has_met_tissue': 1}
```

In [35]:
```
filepath = "Metastatic_Model.h5"
checkpoint = ModelCheckpoint(filepath, monitor='val_accuracy', verb
ose=1,
                             save_best_only=True, mode='max')

reduce_lr = ReduceLROnPlateau(monitor='val_accuracy', factor=0.5, p
atience=2,
                                   verbose=1, mode='max', min_lr=0.
00001)


callbacks_list = [checkpoint, reduce_lr]

history = model.fit_generator(train_gen, steps_per_epoch=train_step
s,
                    validation_data=val_gen,
                    validation_steps=val_steps,
                    epochs=10, verbose=1,
                   callbacks=callbacks_list)
```

```
Epoch 1/10
13599/13600 [============================>.] - ETA: 0s - loss: 0.3
610 - accuracy: 0.8431
Epoch 00001: val_accuracy improved from -inf to 0.85635, saving mo
del to Metastatic_Model.h5
13600/13600 [==============================] - 4873s 358ms/step -
loss: 0.3610 - accuracy: 0.8431 - val_loss: 0.3306 - val_accuracy:
0.8564
Epoch 2/10
13599/13600 [============================>.] - ETA: 0s - loss: 0.3
250 - accuracy: 0.8610
Epoch 00002: val_accuracy improved from 0.85635 to 0.87044, saving
model to Metastatic_Model.h5
13600/13600 [==============================] - 4878s 359ms/step -
loss: 0.3250 - accuracy: 0.8610 - val_loss: 0.2963 - val_accuracy:
0.8704
Epoch 3/10
13599/13600 [============================>.] - ETA: 0s - loss: 0.3
018 - accuracy: 0.8722
Epoch 00003: val_accuracy improved from 0.87044 to 0.88738, saving
model to Metastatic_Model.h5
13600/13600 [==============================] - 4873s 358ms/step -
loss: 0.3018 - accuracy: 0.8723 - val_loss: 0.2679 - val_accuracy:
0.8874
Epoch 4/10
13599/13600 [============================>.] - ETA: 0s - loss: 0.2
841 - accuracy: 0.8818
Epoch 00004: val_accuracy did not improve from 0.88738
```

```
13600/13600 [==============================] - 4886s 359ms/step -
loss: 0.2841 - accuracy: 0.8818 - val_loss: 0.2791 - val_accuracy:
0.8840
Epoch 5/10
13599/13600 [============================>.] - ETA: 0s - loss: 0.2
701 - accuracy: 0.8889
Epoch 00005: val_accuracy improved from 0.88738 to 0.89974, saving
model to Metastatic_Model.h5
13600/13600 [==============================] - 4882s 359ms/step -
loss: 0.2701 - accuracy: 0.8889 - val_loss: 0.2421 - val_accuracy:
0.8997
Epoch 6/10
13599/13600 [============================>.] - ETA: 0s - loss: 0.2
588 - accuracy: 0.8934
Epoch 00006: val_accuracy did not improve from 0.89974
13600/13600 [==============================] - 4873s 358ms/step -
loss: 0.2588 - accuracy: 0.8933 - val_loss: 0.3098 - val_accuracy:
0.8712
Epoch 7/10
13599/13600 [============================>.] - ETA: 0s - loss: 0.2
488 - accuracy: 0.8983
Epoch 00007: val_accuracy improved from 0.89974 to 0.90785, saving
model to Metastatic_Model.h5
13600/13600 [==============================] - 4880s 359ms/step -
loss: 0.2488 - accuracy: 0.8983 - val_loss: 0.2265 - val_accuracy:
0.9079
Epoch 8/10
13599/13600 [============================>.] - ETA: 0s - loss: 0.2
413 - accuracy: 0.9033
Epoch 00008: val_accuracy improved from 0.90785 to 0.91382, saving
model to Metastatic_Model.h5
13600/13600 [==============================] - 4872s 358ms/step -
loss: 0.2413 - accuracy: 0.9033 - val_loss: 0.2159 - val_accuracy:
0.9138
Epoch 9/10
13599/13600 [============================>.] - ETA: 0s - loss: 0.2
330 - accuracy: 0.9062
Epoch 00009: val_accuracy did not improve from 0.91382
13600/13600 [==============================] - 4884s 359ms/step -
loss: 0.2330 - accuracy: 0.9062 - val_loss: 0.2141 - val_accuracy:
0.9128
Epoch 10/10
13599/13600 [============================>.] - ETA: 0s - loss: 0.2
269 - accuracy: 0.9096
Epoch 00010: val_accuracy did not improve from 0.91382

Epoch 00010: ReduceLROnPlateau reducing learning rate to 4.9999998
73689376e-05.
13600/13600 [==============================] - 4888s 359ms/step -
loss: 0.2269 - accuracy: 0.9096 - val_loss: 0.2403 - val_accuracy:
0.8979
```

In [36]:
```
# get the metric names so we can use evaulate_generator
model.metrics_names
```

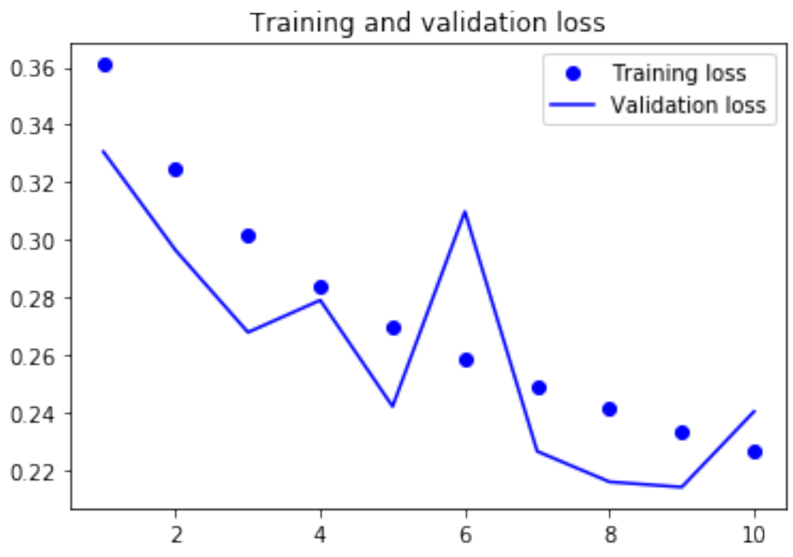
Out[36]:
```
['loss', 'accuracy']
```

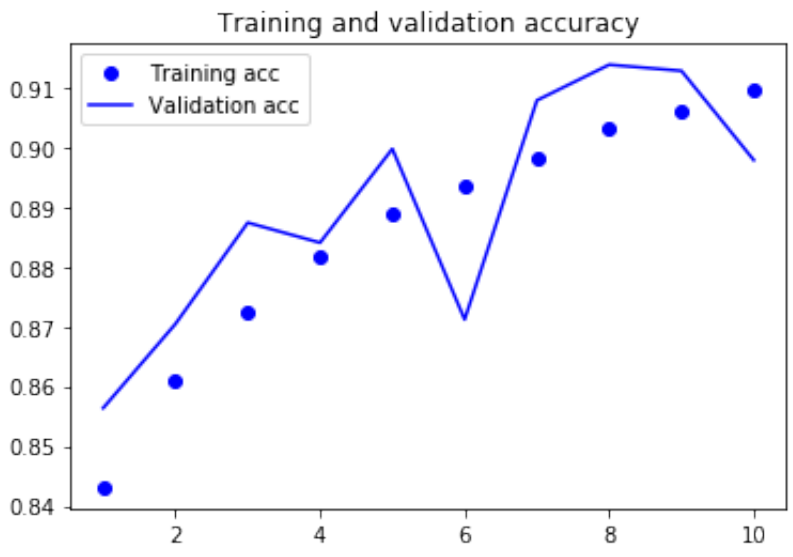
In [37]:
```
# Here the best epoch will be used.

model.load_weights('Metastatic_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: 0.213540935480198
val_acc: 0.9144118
```

In [39]:
```
# 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()
```

```
Out[39]: <Figure size 432x288 with 0 Axes>
```





```
<Figure size 432x288 with 0 Axes>
```

Prediction on Val set

```
In [40]: # make a prediction
         predictions = model.predict_generator(test_gen, steps=len(df_val),
         verbose=1)

         34000/34000 [==============================] - 593s 17ms/step
```

```
In [41]: # This is how to check what index keras has internally assigned to
         each class.
         test_gen.class_indices

Out[41]: {'a_no_met_tissue': 0, 'b_has_met_tissue': 1}
```

In [42]:
```
# Put the predictions into a dataframe.
# The columns need to be oredered to match the output of the previo
us cell

df_preds = pd.DataFrame(predictions, columns=['no_met_tissue', 'has
_met_tissue'])

df_preds.head()
```

Out[42]:

	no_met_tissue	has_met_tissue
0	0.982293	0.017707
1	0.988207	0.011793
2	0.980404	0.019596
3	0.986494	0.013506
4	0.789523	0.210477

In [43]:
```
# Get the true labels
y_true = test_gen.classes

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

What is the AUC Score?

In [44]:
```
from sklearn.metrics import roc_auc_score

roc_auc_score(y_true, y_pred)
```

Out[44]:
```
0.9707840224913493
```

Confusion Matrix

In [45]:
```
# Source: Scikit Learn website
# http://scikit-learn.org/stable/auto_examples/
# model_selection/plot_confusion_matrix.html#sphx-glr-auto-examples
-model-
# selection-plot-confusion-matrix-py


def plot_confusion_matrix(cm, classes,
                          normalize=False,
                          title='Confusion matrix',
                          cmap=plt.cm.Blues):
    """
    This function prints and plots the confusion matrix.
    Normalization can be applied by setting `normalize=True`.
    """
    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.shap
e[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()
```

In [46]:
```
# Get the labels of the test images.

test_labels = test_gen.classes
```

In [47]:
```
test_labels.shape
```

Out[47]:
```
(34000,)
```

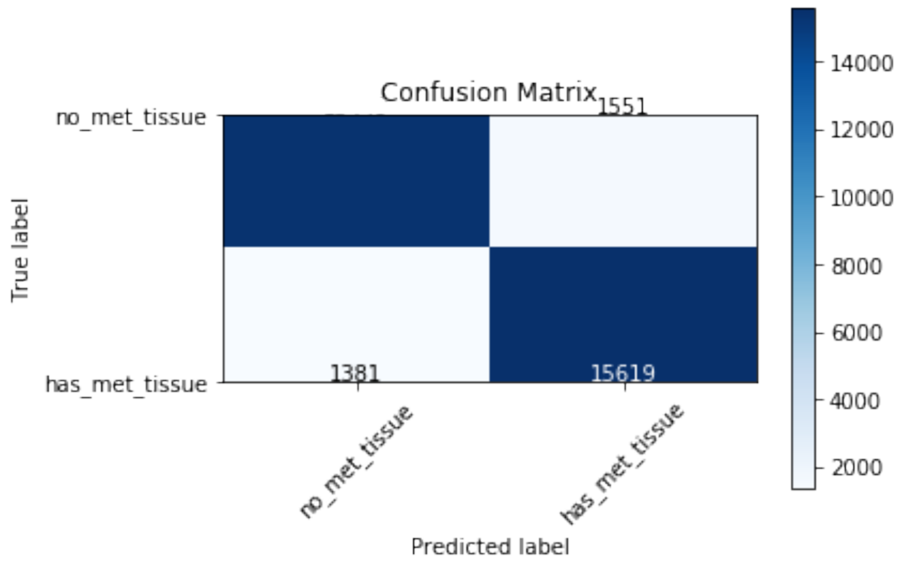
In [48]:
```
# argmax returns the index of the max value in a row
cm = confusion_matrix(test_labels, predictions.argmax(axis=1))
```

In [49]:
```
# Print the label associated with each class
test_gen.class_indices
```

Out[49]:
```
{'a_no_met_tissue': 0, 'b_has_met_tissue': 1}
```

In [50]:
```
# Define the labels of the class indices. These need to match the
# order shown above.
cm_plot_labels = ['no_met_tissue', 'has_met_tissue']

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

```
Confusion matrix, without normalization
[[15449  1551]
 [ 1381 15619]]
```



In [51]:
```
from sklearn.metrics import classification_report

# Generate a classification report

# For this to work we need y_pred as binary labels not as probabili
ties
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

 no_met_tissue       0.92      0.91      0.91     17000
has_met_tissue       0.91      0.92      0.91     17000

      accuracy                           0.91     34000
     macro avg       0.91      0.91      0.91     34000
  weighted avg       0.91      0.91      0.91     34000
```

In [ ]:

Citation

https://www.cancercenter.com/metastasis (https://www.cancercenter.com/metastasis)
https://www.cancer.net/cancer-types/breast-cancer-metastatic/diagnosis
(https://www.cancer.net/cancer-types/breast-cancer-metastatic/diagnosis)

In [ ]: