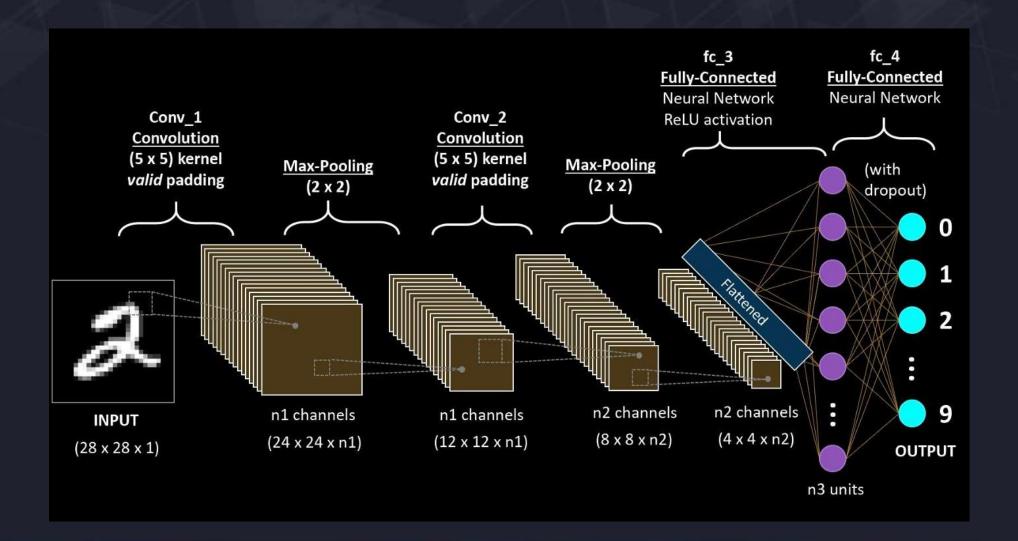


Histopatholgic Cancer Detection







```
CO
```

```
LR = 0.001
def build compile model2():
 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 Structure
  model = Sequential()
  model.add(Conv2D(first_filters, kernel_size, activation='relu', input_shape=(*IMG_SIZE, IMG_CHANNELS)))
  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(1, activation="sigmoid"))
  model.compile(Adam(learning_rate=LR), loss='binary_crossentropy',
             metrics=['accuracy'])
  return model
```

Workflow



Charger le data set

Préparer le data set



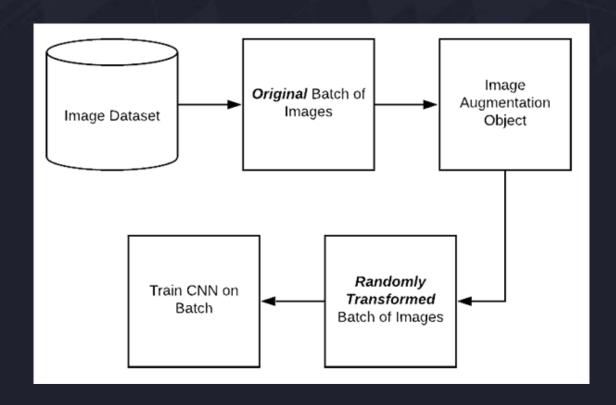
Entrainer les modèles (Forward & Back Propagation)

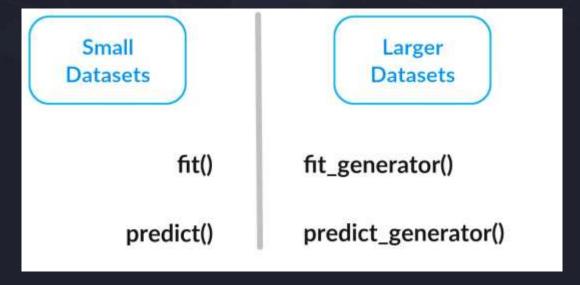
Tester les modèles (Forward Propagation)

Analyser statistiquement les résultats prédictifs



ImageDataGenerator

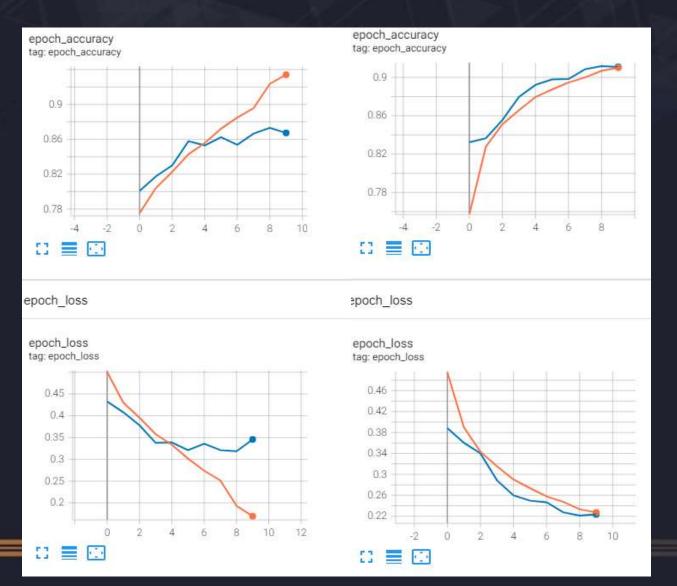




Note: fit_generator et predict_generator are deprecated. fit and predict support generators.









Binary Classifcation Metrics

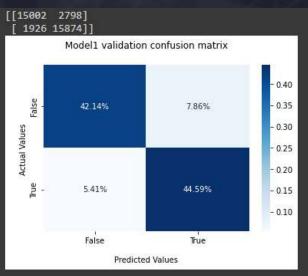
Metric	Formula
True positive rate, recall	$\frac{\mathrm{TP}}{\mathrm{TP}+\mathrm{FN}}$
False positive rate	$\frac{\text{FP}}{\text{FP+TN}}$
Precision	$\frac{\mathrm{TP}}{\mathrm{TP} + \mathrm{FP}}$
Accuracy	$\frac{\mathrm{TP} + \mathrm{TN}}{\mathrm{TP} + \mathrm{TN} + \mathrm{FP} + \mathrm{FN}}$
F-measure	$\frac{2 \cdot \text{precision} \cdot \text{recall}}{\text{precision} + \text{recall}}$

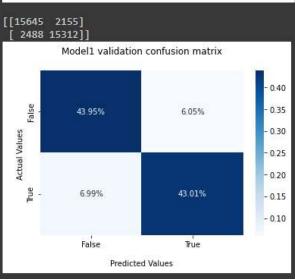


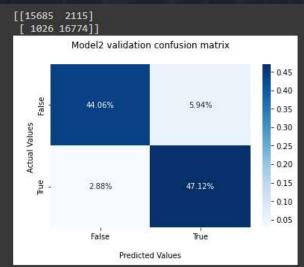


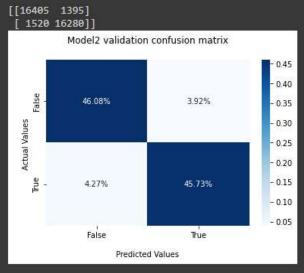
threshold = 0.5





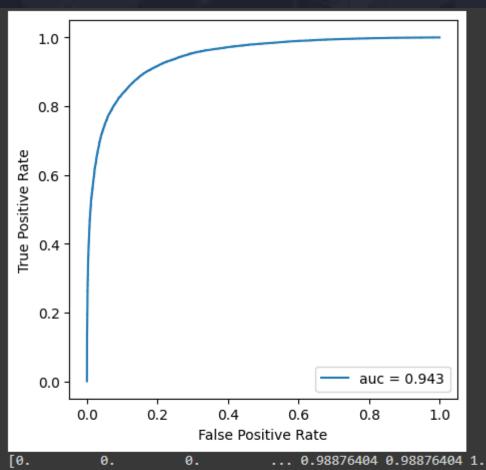




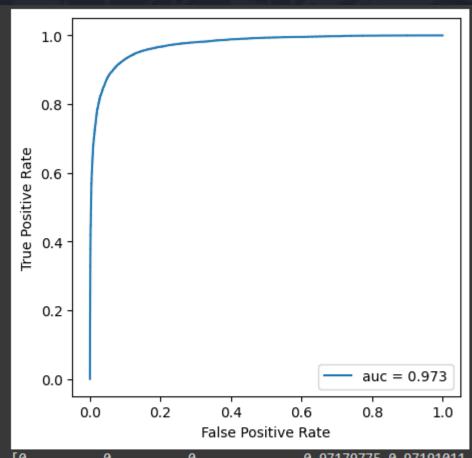








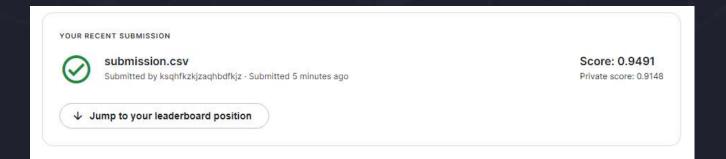
[0. 0. 0. 0.98876404 0.98876404 1.]
[0.00000000e+00 5.61797753e-05 2.80898876e-04 ... 9.99943820e-01
1.00000000e+00 1.00000000e+00]
[1.9999968e+00 9.9999678e-01 9.9999499e-01 ... 1.1485952e-05 1.1462010e-05
3.4040716e-14]
BEST THRESHOLD: 0.65364665



```
[0. 0. 0. 0. 0.97179775 0.97191011 1. ]
[0.00000000e+00 5.61797753e-05 2.24719101e-04 ... 1.00000000e+00
1.00000000e+00 1.00000000e+00]
[1.9999986e+00 9.9999857e-01 9.9999774e-01 ... 2.2486486e-03 2.2478900e-03
6.2224061e-09]
BEST THRESHOLD: 0.64063287
```







	Class 1	Class 0
Breast	9/10	8/10
Lung	9/10	10/10
Colon	6/10	3/10

Results summary
Results in ./untitled_project
Showing 10 best trials
<keras_tuner.engine.objective.
Trial summary
Hyperparameters:
LR: 0.001
dropout_conv: 0.2
dropout_dense: 0.3
n_layers: 3

Score: 0.19306489825248718

Trial summary Hyperparameters: LR: 0.001

dropout_conv: 0.3
dropout_dense: 0.2

n_layers: 3

Score: 0.20378223061561584

Trial summary
Hyperparameters:
LR: 0.0005
dropout_conv: 0.3
dropout_dense: 0.2

n_layers: 4

Score: 0.32328590750694275

Trial summary
Hyperparameters:
LR: 0.0005
dropout_conv: 0.3
dropout dense: 0.3

n_layers: 4

Score: 0.6931468844413757

Trial summary
Hyperparameters:
LR: 0.001
dropout_conv: 0.2
dropout_dense: 0.3

n_layers: 4

Score: 0.6931471228599548