As the input to the network is 256 by 256 (instead of the original 1024 by 1024) and the network downsamples a number of times without import csv import random import pydicom

any meaningful upsampling (the final upsampling is just to match in 256 by 256 mask) the final prediction is very crude. If the network

• Firstly a convolutional neural network is used to segment the image, using the bounding boxes directly as a mask.

Secondly connected components is used to separate multiple areas of predicted pneumonia.

Finally a bounding box is simply drawn around every connected component.

Load pneumonia locations

downsamples 4 times the final bounding boxes can only change with at least 16 pixels. import numpy as np import pandas as pd from skimage import io from skimage import measure from skimage.transform import resize import tensorflow as tf from tensorflow import keras from matplotlib import pyplot as plt import matplotlib.patches as patches

Network

Approach

At the end of the network a single upsampling layer converts the output to the same shape as the input.

 The network consists of a number of residual blocks with convolutions and downsampling blocks with max pooling. In []: import os

In []: | # empty dictionary # load table # open reader

pneumonia locations = {} # skip header

Table contains [filename: pneumonia location] pairs per row.

else:

Load filenames

random.shuffle(filenames)

print('n valid samples', len(valid filenames)) n_train_samples = len(filenames) - n_valid_samples

print('Images with pneumonia:', len(pneumonia locations))

ns = [len(value) for value in pneumonia_locations.values()]

In []: | print('Total train images:',len(filenames))

plt.xlabel('Pneumonia per image') plt.xticks(range(1, np.max(ns)+1))

heatmap = np.zeros((1024, 1024))

x, y, w, h = value

for value in values:

ws.append(w) hs.append(h)

for values in pneumonia locations.values():

heatmap[y:y+h, x:x+w] += 1

plt.title('Pneumonia location heatmap')

plt.title('Pneumonia height lengths') plt.hist(hs, bins=np.linspace(0,1000,50))

plt.title('Pneumonia width lengths')

plt.hist(ws, bins=np.linspace(0,1000,50))

self.augment = augment self.predict = predict self.on_epoch_end()

def load (self, filename):

create empty mask

msk = np.zeros(img.shape)

load dicom file as numpy array

get filename without extension filename = filename.split('.')[0] # if image contains pneumonia

loop through pneumonia

resize both image and mask

img = np.fliplr(img) msk = np.fliplr(msk)# add trailing channel dimension $img = np.expand_dims(img, -1)$ msk = np.expand dims(msk, -1)

def __loadpredict__(self, filename): # load dicom file as numpy array

> imgs = np.array(imgs) msks = np.array(msks) return imgs, msks

return everything

random.shuffle(self.filenames)

return full batches only

def on epoch end(self): if self.shuffle:

if self.predict:

In []: def create_downsample(channels, inputs):

x = keras.layers.LeakyReLU(0)(x)

x = keras.layers.MaxPool2D(2)(x)

def create resblock(channels, inputs):

x = keras.layers.LeakyReLU(0)(x)

x = keras.layers.LeakyReLU(0)(x)

channels = channels * 2

for b in range(n blocks):

x = keras.layers.LeakyReLU(0)(x)

define iou or jaccard loss function

y_true = tf.reshape(y_true, [-1]) y_pred = tf.reshape(y_pred, [-1])

smooth = tf.ones(tf.shape(intersect))

loss=iou bce loss,

return lr*(np.cos(np.pi*x/epochs)+1.)/2

create train and validation generators folder = '../input/stage_1_train_images'

metrics=['accuracy', mean iou])

def iou_loss(y_true, y_pred):

combine bce loss and iou loss def iou bce loss(y true, y pred):

def mean_iou(y_true, y_pred): y_pred = tf.round(y_pred)

create network and compiler

model.compile(optimizer='adam',

cosine learning rate annealing

def cosine annealing(x):

lr = 0.001epochs = 25

return 1 - score

mean iou as a metric

x = create downsample(channels, x)

x = create_resblock(channels, x)

outputs = keras.layers.UpSampling2D(2**depth)(x) model = keras.Model(inputs=inputs, outputs=outputs)

intersection = tf.reduce_sum(y_true * y_pred)

intersect = tf.reduce_sum(y_true * y_pred, axis=[1, 2, 3])

model = create_network(input_size=256, channels=32, n_blocks=2, depth=4)

learning rate = tf.keras.callbacks.LearningRateScheduler(cosine annealing)

plt.plot(history.epoch, history.history["acc"], label="Train accuracy") plt.plot(history.epoch, history.history["val_acc"], label="Valid accuracy")

plt.plot(history.epoch, history.history["mean_iou"], label="Train_iou") plt.plot(history.epoch, history.history["val mean iou"], label="Valid iou")

x = keras.layers.BatchNormalization (momentum=0.9) (x)

x = keras.layers.Conv2D(1, 1, activation='sigmoid')(x)

return keras.layers.add([x, inputs])

def len (self):

Network

return x

input

residual blocks

return model

Train network

In []:

for d in range(depth):

return img, msk

resize image

if filename in self.pneumonia locations:

x, y, w, h = location msk[y:y+h, x:x+w] = 1

if augment then horizontal flip half the time

if self.augment and random.random() > 0.5:

img = pydicom.dcmread(os.path.join(self.folder, filename)).pixel array

img = resize(img, (self.image_size, self.image_size), mode='reflect')

img = pydicom.dcmread(os.path.join(self.folder, filename)).pixel array

img = resize(img, (self.image_size, self.image_size), mode='reflect')

return int(np.ceil(len(self.filenames) / self.batch size))

x = keras.layers.Conv2D(channels, 1, padding='same', use bias=False)(x)

x = keras.layers.Conv2D(channels, 3, padding='same', use bias=False)(x)

x = keras.layers.Conv2D(channels, 3, padding='same', use_bias=False)(x)

x = keras.layers.Conv2D(channels, 3, padding='same', use bias=False)(inputs)

score = (intersection + 1.) / (tf.reduce sum(y true) + tf.reduce sum(y pred) - intersection + 1.)

return 0.5 * keras.losses.binary_crossentropy(y_true, y_pred) + 0.5 * iou_loss(y_true, y_pred)

train gen = generator(folder, train filenames, pneumonia locations, batch size=32, image size=256, shuf

axarr[axidx].add patch(patches.Rectangle((x,y),width,height,linewidth=2,edgecolor='b',facec

union = tf.reduce_sum(y_true, axis=[1, 2, 3]) + tf.reduce_sum(y_pred, axis=[1, 2, 3])

return tf.reduce mean((intersect + smooth) / (union - intersect + smooth))

return int(len(self.filenames) / self.batch size)

x = keras.layers.BatchNormalization(momentum=0.9)(inputs)

x = keras.layers.BatchNormalization(momentum=0.9)(inputs)

x = keras.layers.BatchNormalization (momentum=0.9) (x)

def create_network(input_size, channels, n_blocks=2, depth=4):

inputs = keras.Input(shape=(input size, input size, 1))

msk = resize(msk, (self.image size, self.image size), mode='reflect') > 0.5

for location in self.pneumonia_locations[filename]: # add 1's at the location of the pneumonia

print('Minimum pneumonia height:', np.min(hs)) print('Minimum pneumonia width: ', np.min(ws))

n valid samples = 2560

Exploration

plt.figure() plt.hist(ns)

plt.show()

plt.figure()

plt.figure()

plt.show() plt.figure()

plt.show()

plt.imshow(heatmap)

ws = []hs = []

 If a filename contains multiple pneumonia, the table contains multiple rows with the same filename but different pneumonia locations. • If a filename contains no pneumonia it contains a single row with an empty pneumonia location. The code below loads the table and transforms it into a dictionary. The dictionary uses the filename as key and a list of pneumonia locations in that filename as value. • If a filename is not present in the dictionary it means that it contains no pneumonia. with open(os.path.join('../input/stage 1 train labels.csv'), mode='r') as infile: reader = csv.reader(infile) next (reader, None) # loop through rows for rows in reader:

retrieve information

filename = rows[0]location = rows[1:5]

pneumonia = rows[5]

if pneumonia == '1': # convert string to float to int

if row contains pneumonia add label to dictionary # which contains a list of pneumonia locations per filename location = [int(float(i)) for i in location] # save pneumonia location in dictionary if filename in pneumonia locations: pneumonia locations[filename].append(location) pneumonia locations[filename] = [location] In []: # load and shuffle filenames folder = '../input/stage 1 train images' filenames = os.listdir(folder) # split into train and validation filenames

train filenames = filenames[n valid samples:] valid filenames = filenames[:n valid samples] print('n train samples', len(train_filenames))

Data generator The dataset is too large to fit into memory, so we need to create a generator that loads data on the fly. The generator takes in some filenames, batch_size and other parameters. The generator outputs a random batch of numpy images and numpy masks. In []: class generator(keras.utils.Sequence): def init (self, folder, filenames, pneumonia locations=None, batch size=32, image size=256, shuf fle=True, augment=False, predict=False): self.folder = folder self.filenames = filenames self.pneumonia locations = pneumonia locations self.batch size = batch size self.image size = image size self.shuffle = shuffle

add trailing channel dimension img = np.expand dims(img, -1)return img def getitem (self, index): # select batch filenames = self.filenames[index*self.batch size:(index+1)*self.batch size] # predict mode: return images and filenames if self.predict: imgs = [self.__loadpredict__(filename) for filename in filenames] # create numpy batch imgs = np.array(imgs) return imgs, filenames # train mode: return images and masks else: # load files items = [self. load (filename) for filename in filenames] # unzip images and masks imgs, msks = zip(*items)# create numpy batch

fle=True, augment=True, predict=False) valid_gen = generator(folder, valid_filenames, pneumonia_locations, batch_size=32, image_size=256, shuf fle=False, predict=False) history = model.fit_generator(train_gen, validation_data=valid_gen, callbacks=[learning_rate], epochs=2 5, workers=4, use_multiprocessing=True) In []: plt.figure(figsize=(12,4)) plt.subplot(131) plt.plot(history.epoch, history.history["loss"], label="Train loss") plt.plot(history.epoch, history.history["val loss"], label="Valid loss") plt.legend() plt.subplot(132)

plt.legend() plt.subplot(133)

plt.legend() plt.show()

In []: for imgs, msks in valid gen:

axidx = 0

create figure

predict batch of images preds = model.predict(imgs)

axarr = axarr.ravel()

loop through batch

plot image

threshold true mask comp = msk[:, :, 0] > 0.5# apply connected components comp = measure.label(comp) # apply bounding boxes predictionString = ''

> height = y2 - ywidth = x2 - x

threshold predicted mask comp = pred[:, :, 0] > 0.5# apply connected components comp = measure.label(comp) # apply bounding boxes predictionString = ''

f, axarr = plt.subplots(4, 8, figsize=(20,15))

for img, msk, pred in zip(imgs, msks, preds):

for region in measure.regionprops(comp): # retrieve x, y, height and width

for region in measure.regionprops(comp):

y, x, y2, x2 = region.bbox

axarr[axidx].imshow(img[:, :, 0])

retrieve x, y, height and width y, x, y2, x2 = region.bboxheight = y2 - ywidth = x2 - xaxarr[axidx].add patch(patches.Rectangle((x,y),width,height,linewidth=2,edgecolor='r',facec olor='none')) axidx += 1plt.show() # only plot one batch break **Predict test images**

olor='none'))

In []: # load and shuffle filenames folder = '../input/stage 1 test images' test filenames = os.listdir(folder) print('n test samples:', len(test_filenames)) # create test generator with predict flag set to True test gen = generator(folder, test filenames, None, batch size=25, image size=256, shuffle=False, predic # create submission dictionary submission dict = {} # loop through testset

for imgs, filenames in test gen: # predict batch of images preds = model.predict(imgs)

resize predicted mask

threshold predicted mask comp = pred[:, :, 0] > 0.5# apply connected components comp = measure.label(comp) # apply bounding boxes predictionString = ''

for pred, filename in zip(preds, filenames):

for region in measure.regionprops(comp):

pred = resize(pred, (1024, 1024), mode='reflect')

loop through batch

retrieve x, y, height and width y, x, y2, x2 = region.bboxheight = y2 - ywidth = x2 - x# proxy for confidence score conf = np.mean(pred[y:y+height, x:x+width]) # add to predictionString predictionString += str(conf) + ' ' + str(x) + ' ' + str(y) + ' ' + str(width) + ' ' + str(# add filename and predictionString to dictionary filename = filename.split('.')[0] submission dict[filename] = predictionString # stop if we've got them all if len(submission_dict) >= len(test_filenames): break

save dictionary as csv file sub = pd.DataFrame.from dict(submission dict,orient='index') sub.index.names = ['patientId'] sub.columns = ['PredictionString'] sub.to csv('submission.csv')

In []: