exploration

April 24, 2025

1 0 Setup

[1]:
```
import os
import data_utils as utils
import data_pipeline as pipeline
import pandas as pd
import numpy as np
import tensorflow as tf
import matplotlib.pyplot as plt
import seaborn as sns
from PIL import Image
from tensorflow.keras.preprocessing.image import ImageDataGenerator
```

[2]:
```
# define globals
RAW_DIR = "../data/raw"
PROCESSED_DIR = "../data/processed"
IMG_HEIGHT = IMG_WIDTH = 299
TARGET_HEIGHT = TARGET_WIDTH = 224
BATCH_SIZE = 128
```

2 1 - Loading data

[3]:
```
# define data directories
data_dir = "../data/raw"

train_dir = os.path.join(data_dir, "train")
val_dir = os.path.join(data_dir, "val")
test_dir = os.path.join(data_dir, "test")

train_covid_dir = os.path.join(train_dir, "COVID")
train_normal_dir = os.path.join(train_dir, "NORMAL")

val_covid_dir = os.path.join(val_dir, "COVID")
val_normal_dir = os.path.join(val_dir, "NORMAL")

test_covid_dir = os.path.join(test_dir, "COVID")
test_normal_dir = os.path.join(test_dir, "NORMAL")
```

[4]:
```
# initialize image generators with rescaling
train_img_gen = ImageDataGenerator()
val_img_gen = ImageDataGenerator()
test_img_gen = ImageDataGenerator()

# load train data
train_generator = train_img_gen.flow_from_directory(
    train_dir,
    target_size=(IMG_HEIGHT, IMG_WIDTH),
    batch_size=BATCH_SIZE,
    class_mode="binary",
)

# load val data
val_generator = val_img_gen.flow_from_directory(
    val_dir,
    target_size=(IMG_HEIGHT, IMG_WIDTH),
    batch_size=BATCH_SIZE,
    class_mode="binary",
)

# load test data
test_generator = test_img_gen.flow_from_directory(
    test_dir,
    target_size=(IMG_HEIGHT, IMG_WIDTH),
    batch_size=BATCH_SIZE,
    class_mode="binary",
)
```

```
Found 1600 images belonging to 2 classes.
Found 400 images belonging to 2 classes.
Found 200 images belonging to 2 classes.
```

3 2 - Data exploration

[5]:
```
# get number of images in each directory
num_covid_train = len(os.listdir(train_covid_dir))
num_normal_train = len(os.listdir(train_normal_dir))

num_covid_val = len(os.listdir(val_covid_dir))
num_normal_val = len(os.listdir(val_normal_dir))

num_covid_test = len(os.listdir(test_covid_dir))
num_normal_test = len(os.listdir(test_normal_dir))

print("training data")
print(f"covid: {num_covid_train}")
print(f"normal: {num_normal_train}")

print("\nvalidation data")
print(f"covid: {num_covid_val}")
print(f"normal: {num_normal_val}")

print("\ntest data")
print(f"covid: {num_covid_test}")
print(f"normal: {num_normal_test}")
```

```
training data
covid: 800
normal: 800

validation data
covid: 200
normal: 200

test data
covid: 100
normal: 100
```

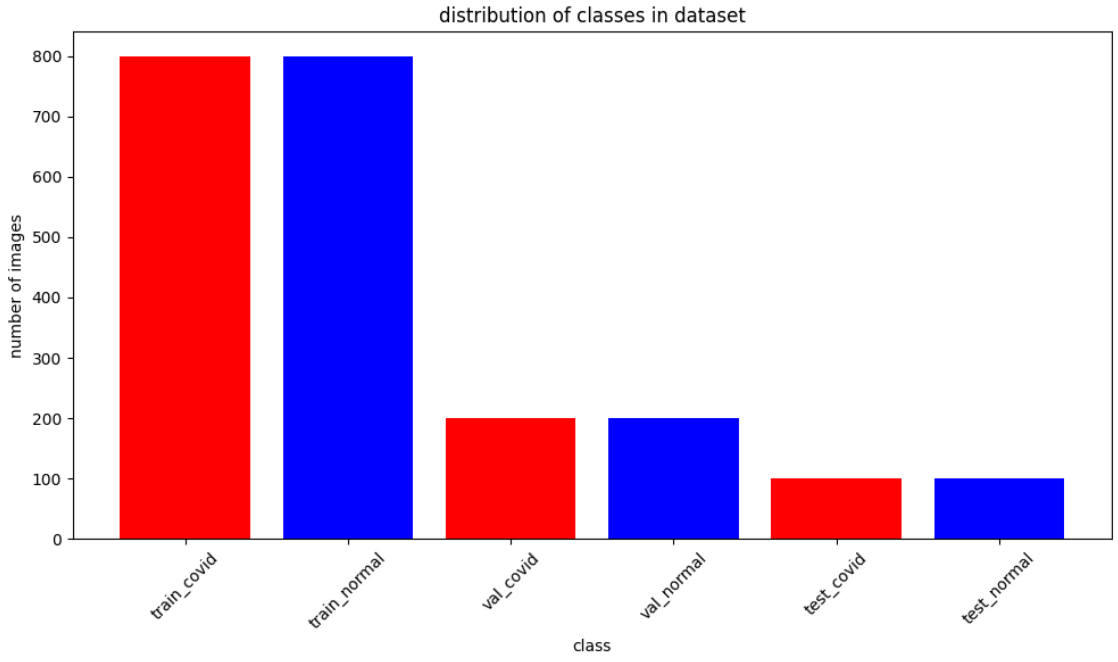
[6]:
```
# combine paths
all_paths = pipeline.get_image_paths(RAW_DIR)
```

[7]:
```
# check image size
utils.check_image_size(all_paths)
```

```
reference image size: (299, 299)
all images have the same size
(checked all 2200 images)
```

[8]:
```
# show distribution of classes
# add previously generated counts to dict
```

```
class_counts = {
    "train_covid": num_covid_train,
    "train_normal": num_normal_train,
    "val_covid": num_covid_val,
    "val_normal": num_normal_val,
    "test_covid": num_covid_test,
    "test_normal": num_normal_test,
}

# create bar plot
plt.figure(figsize=(10, 6))
plt.bar(
    class_counts.keys(),
    class_counts.values(),
    color=["red", "blue", "red", "blue", "red", "blue"],
)
plt.xlabel("class")
plt.ylabel("number of images")
plt.title("distribution of classes in dataset")
plt.xticks(rotation=45)
plt.tight_layout()
plt.show()
```



[9]:
```
# plot a few samples from each class
```

```
train_covid_paths = [path for path in all_paths if path.
 ↪startswith(train_covid_dir)]
train_normal_paths = [path for path in all_paths if path.
 ↪startswith(train_normal_dir)]

# sample 5 images from each class
covid_samples = np.random.choice(train_covid_paths, 5, replace=False)
normal_samples = np.random.choice(train_normal_paths, 5, replace=False)

# load images as grayscale
covid_images = [np.array(Image.open(path).convert("L")) for path in␣
 ↪covid_samples]
normal_images = [np.array(Image.open(path).convert("L")) for path in␣
 ↪normal_samples]

# plot covid images
print("covid samples:")
utils.plotImages(covid_images)

# plot normal images
print("normal samples:")
utils.plotImages(normal_images)
```

```
covid samples:
```

```
normal samples:
```

[10]:
```
# get other paths
val_covid_paths = [path for path in all_paths if path.startswith(val_covid_dir)]
val_normal_paths = [path for path in all_paths if path.
 ↪startswith(val_normal_dir)]
test_covid_paths = [path for path in all_paths if path.
 ↪startswith(test_covid_dir)]
test_normal_paths = [path for path in all_paths if path.
 ↪startswith(test_normal_dir)]

# calculate stats for each dataset
train_stats = utils.calculate_pixel_stats(train_covid_paths +␣
 ↪train_normal_paths)
val_stats = utils.calculate_pixel_stats(val_covid_paths + val_normal_paths)
test_stats = utils.calculate_pixel_stats(test_covid_paths + test_normal_paths)

# display stats in a table
stats_df = pd.DataFrame({"train": train_stats, "val": val_stats, "test":␣
 ↪test_stats}).T

print("pixel intensity statistics:")
display(stats_df)
```

```
pixel intensity statistics:
```

	global_mean	global_std	global_min	global_max	per_image_mean_avg	\
train	135.030773	62.210686	0.0	255.0	135.030773	
val	137.376634	64.901636	0.0	255.0	137.376634	
test	139.270291	66.004260	0.0	255.0	139.270291	

	per_image_mean_std	per_image_std_avg	per_image_std_std
train	23.773935	55.622600	14.529134
val	24.497091	58.744112	12.698197
test	25.340164	59.667862	12.417112

[11]:
```
# compare summary stats across outcome classes
covid_stats = utils.calculate_pixel_stats(
    train_covid_paths + val_covid_paths + test_covid_paths
)
normal_stats = utils.calculate_pixel_stats(
    train_normal_paths + val_normal_paths + test_normal_paths
)

# display stats in a table
class_stats_df = pd.DataFrame({"covid": covid_stats, "normal": normal_stats}).T

print("pixel intensity statistics:")
display(class_stats_df)
```

```
pixel intensity statistics:
```

```
        global_mean  global_std  global_min  global_max  per_image_mean_avg  \
covid     143.893189   59.213480         0.0       255.0          143.893189
normal    127.792218   65.736219         0.0       255.0          127.792218

        per_image_mean_std  per_image_std_avg  per_image_std_std
covid            24.169832          51.466770          16.529580
normal           21.147788          61.649027           8.568486
```

4 3 - Preprocessing

[12]:
```
# downsample images
print(f"downsampling {len(all_paths)} images")
processed_paths = []
for path in all_paths:
    input_path = path
    output_path = path.replace(RAW_DIR, PROCESSED_DIR)
    pipeline.downsample_image(input_path, output_path, TARGET_HEIGHT,␣
 ↪TARGET_WIDTH)
    processed_paths.append(output_path)
```

```
downsampling 2200 images
```

[13]:
```
# calculate mean and standard deviation of downsampled train images
processed_train_paths = [path for path in processed_paths if "train" in path]
print(
    f"calculating mean and standard deviation of {len(processed_train_paths)}␣
 ↪train images"
)
mean, std = pipeline.calc_mean_std(processed_train_paths)
print(f"mean: {mean}, std: {std}")
```

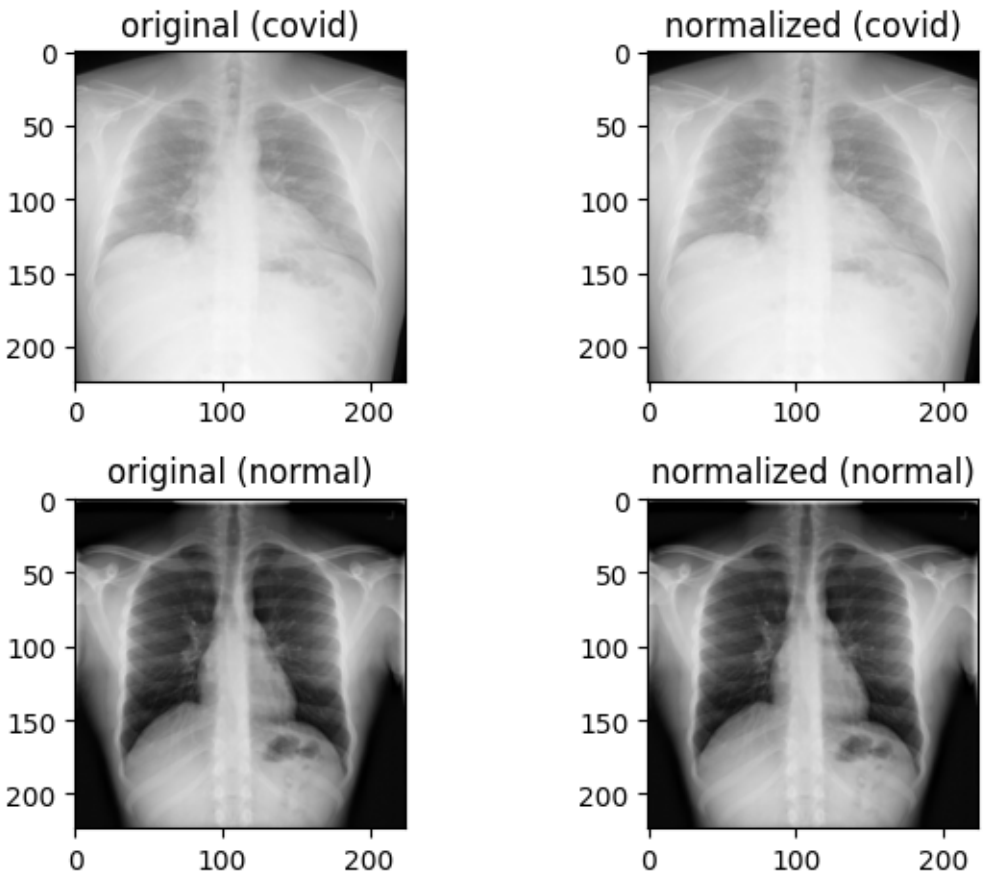
```
calculating mean and standard deviation of 1600 train images
mean: 135.03696812220983, std: 62.192818138566
```

NB: There was of course no need to recalculate the mean and standard deviation here, but the above cells uses the data_pipeline.py file implementation to normalize the images

In the actual pipeline, the images are normalized as part of the data generator, but here we do so manually for illustration purposes

[14]:
```
# get paths for each class
processed_val_paths = [path for path in processed_paths if "val" in path]
processed_val_covid_paths = [path for path in processed_val_paths if "COVID" in␣
 ↪path]
processed_val_normal_paths = [path for path in processed_val_paths if "NORMAL"␣
 ↪in path]
```

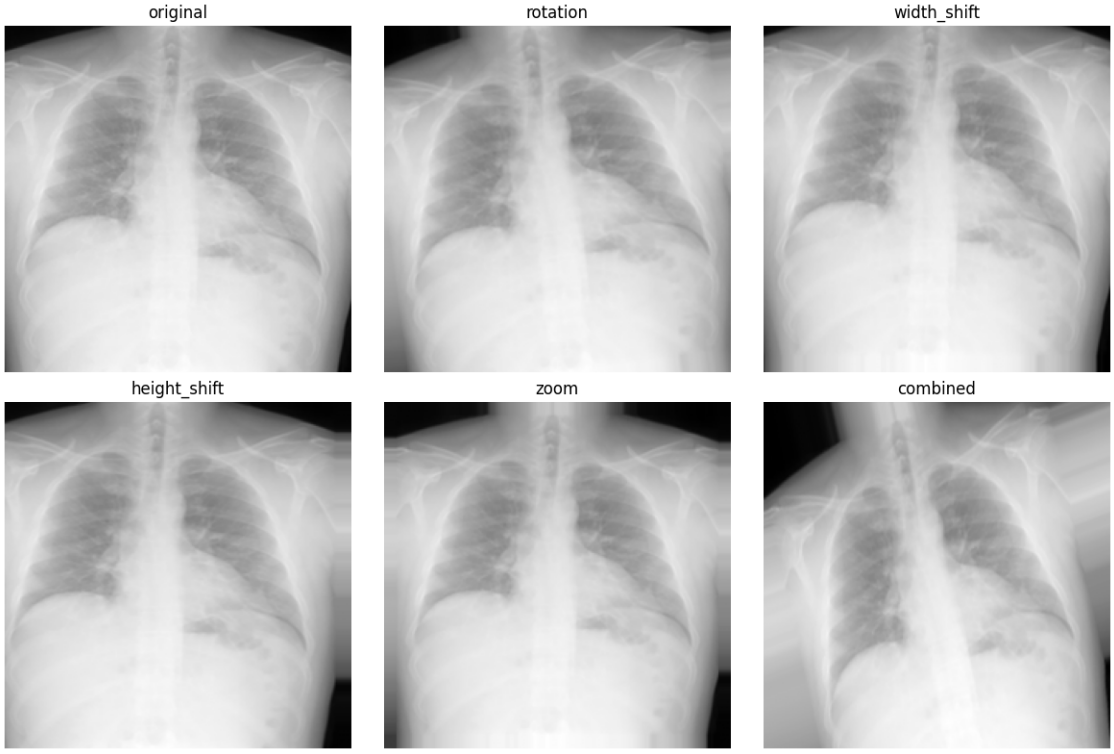
```
# sample random image from each class
covid_sample = np.random.choice(processed_val_covid_paths, 1, replace=False)
normal_sample = np.random.choice(processed_val_normal_paths, 1, replace=False)

# load images
covid_img = np.array(Image.open(covid_sample[0]).convert("L"))
normal_img = np.array(Image.open(normal_sample[0]).convert("L"))

# normalize images
covid_img_normalized = (covid_img - mean) / (std + 1e-7)
normal_img_normalized = (normal_img - mean) / (std + 1e-7)

# plot
fig, axes = plt.subplots(2, 2)

# show original images
axes[0, 0].imshow(covid_img, cmap="gray")
axes[0, 0].set_title("original (covid)")
axes[1, 0].imshow(normal_img, cmap="gray")
axes[1, 0].set_title("original (normal)")

# show normalized images
axes[0, 1].imshow(np.array(covid_img_normalized), cmap="gray")
axes[0, 1].set_title("normalized (covid)")
axes[1, 1].imshow(np.array(normal_img_normalized), cmap="gray")
axes[1, 1].set_title("normalized (normal)")

plt.tight_layout()
plt.show()
```

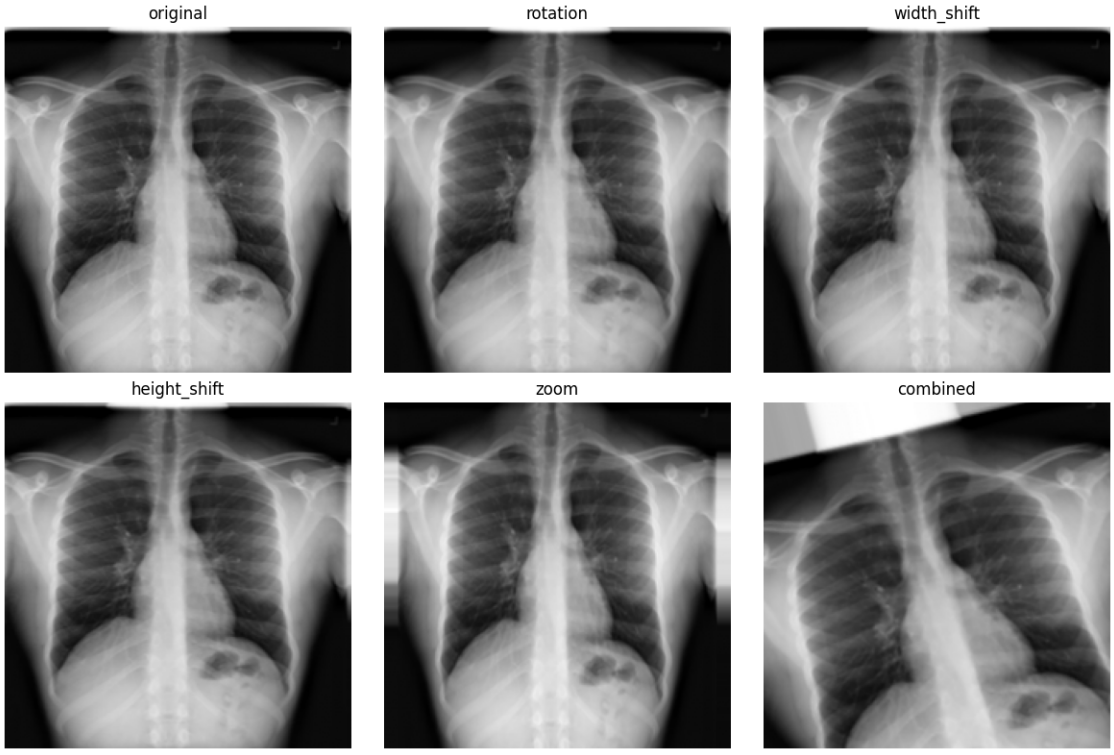


5 4 - Augmentation

NB: In the actual data pipeline, we will augment the images using flow_from_directory, but for now, we can just augment the images and plot them manually

[15]:
```
# using same samples as before
utils.visualize_augmentations(covid_img_normalized)
utils.visualize_augmentations(normal_img_normalized)
```


original
rotation
width_shift
height_shift
zoom
combined


original
rotation
width_shift
height_shift
zoom
combined