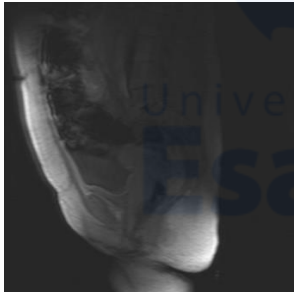
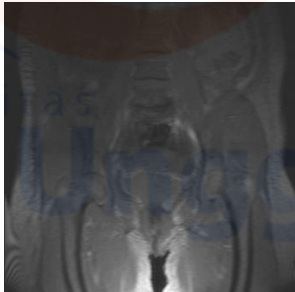
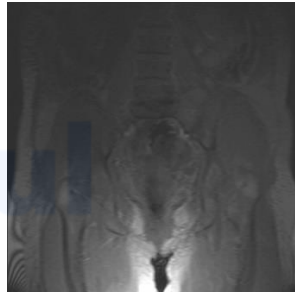
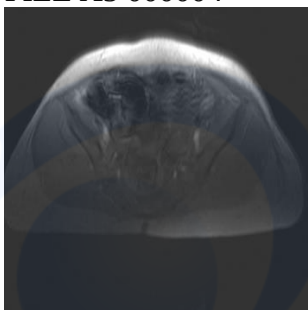
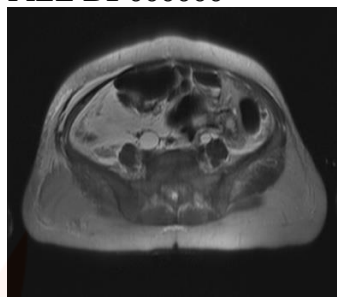
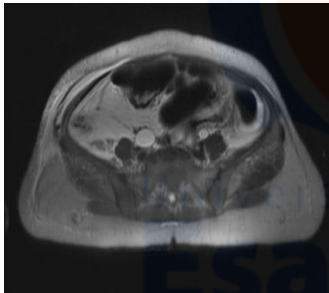
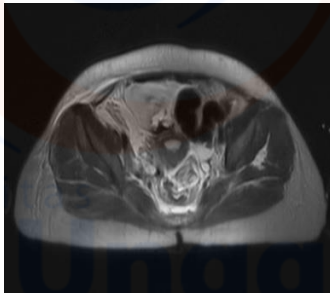
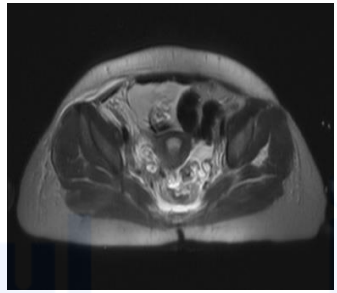
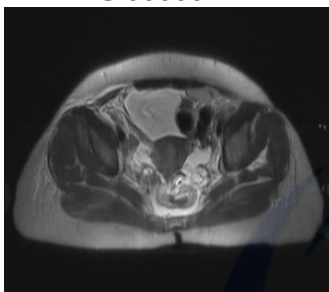
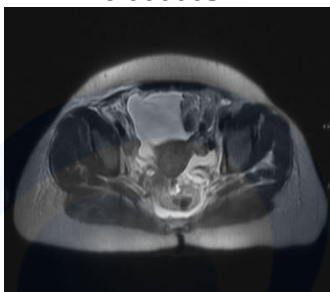
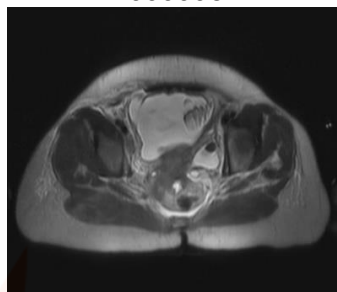
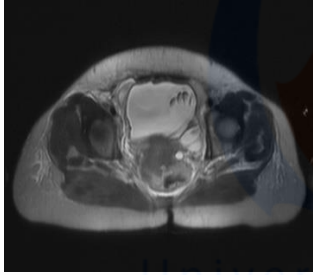
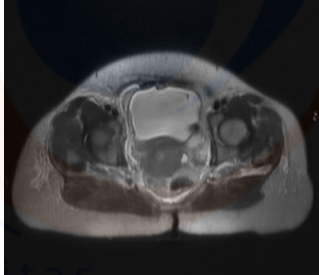
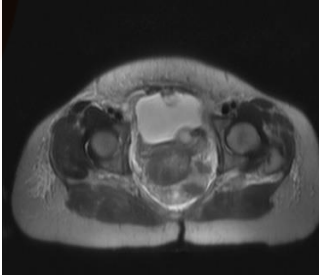
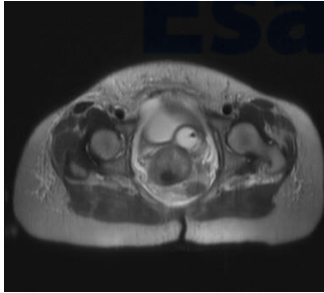
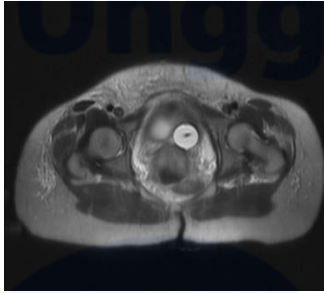
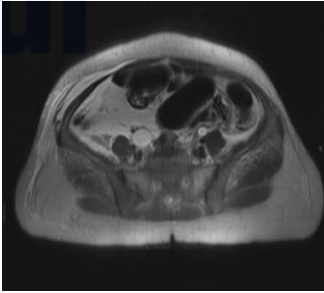
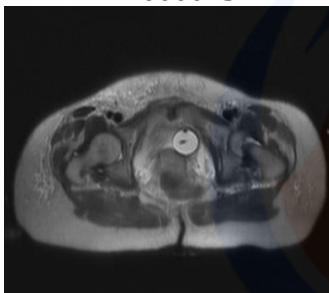
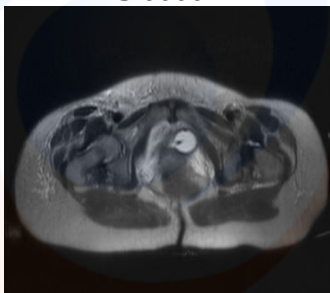
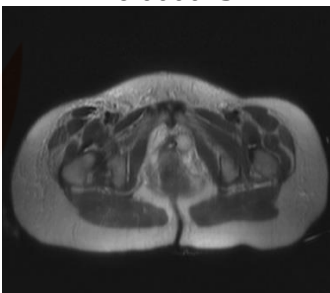
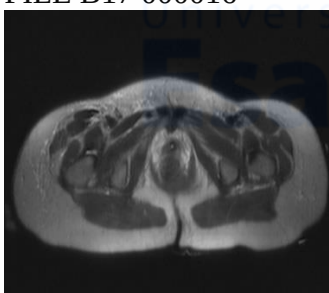
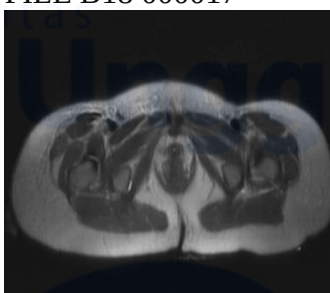
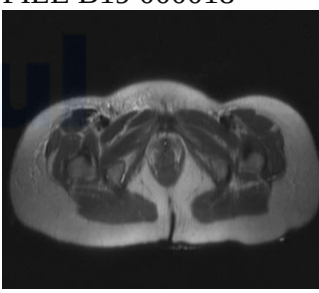
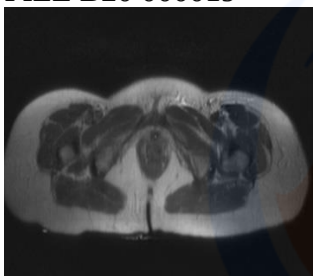
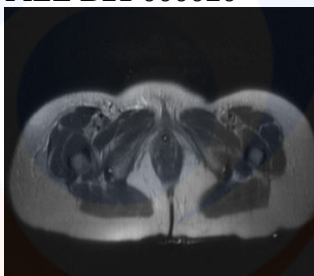
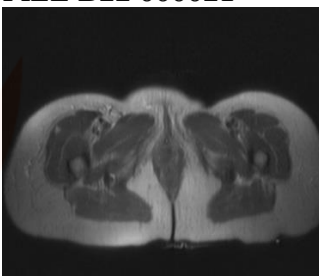
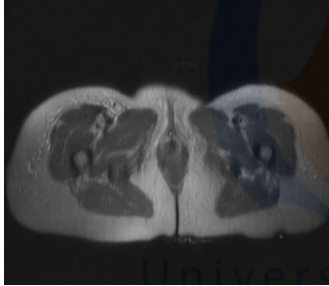
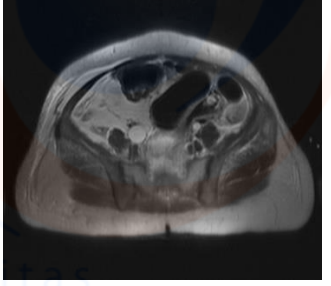
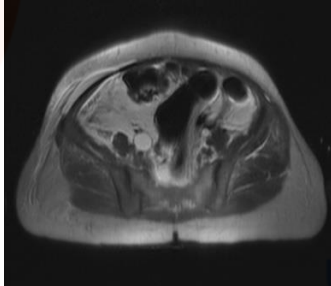
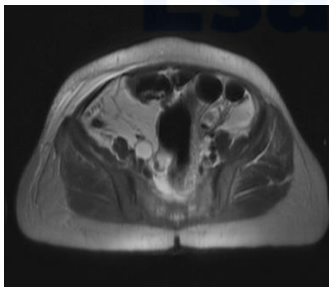
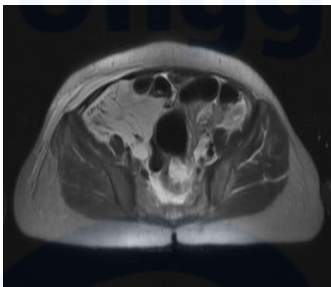
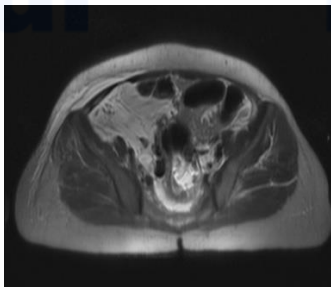
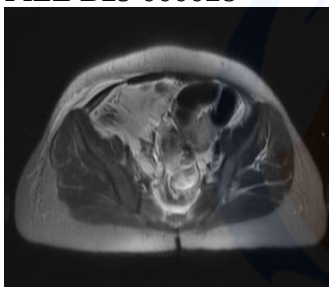
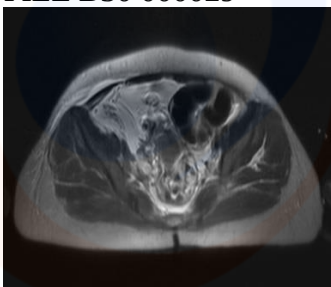
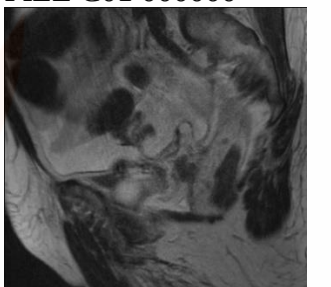
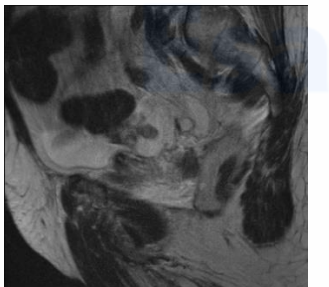
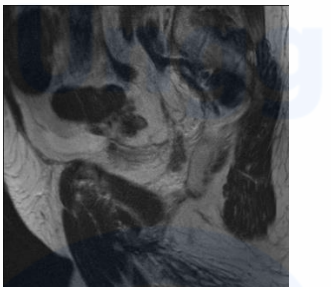
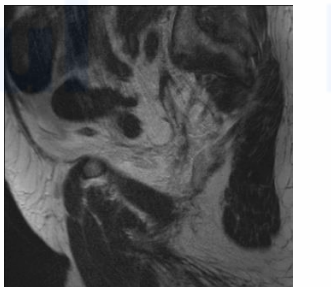


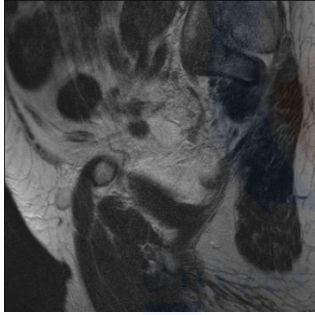
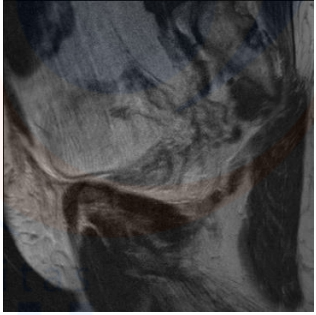
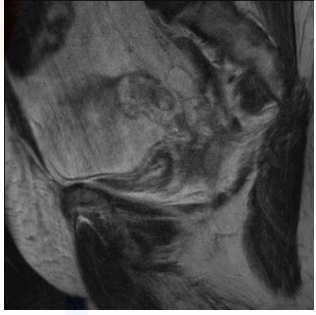
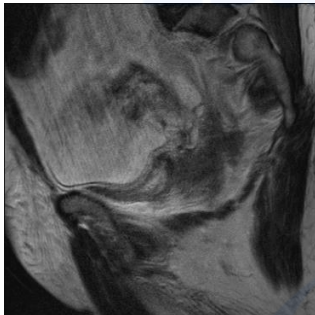
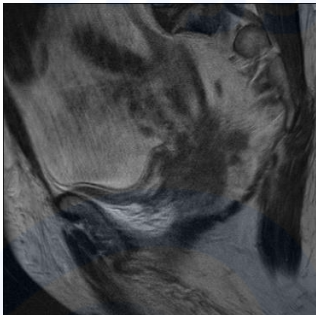
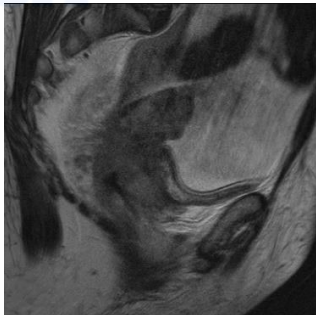
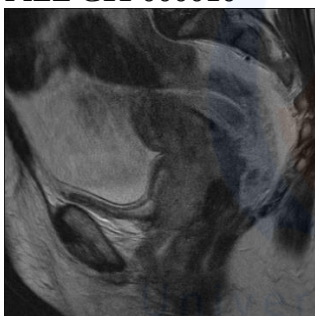
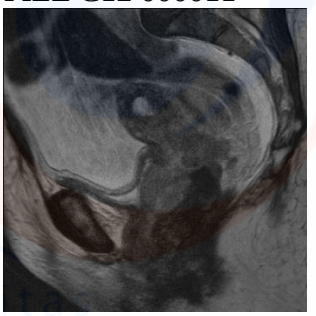
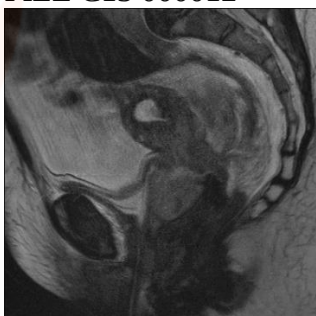
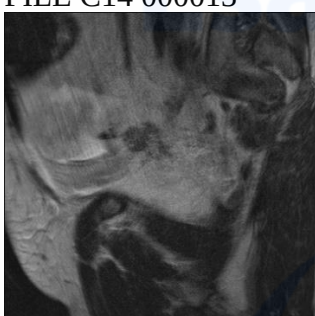
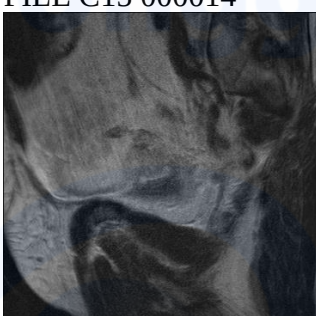
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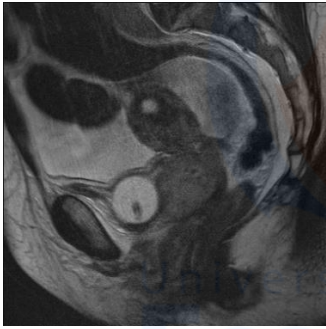
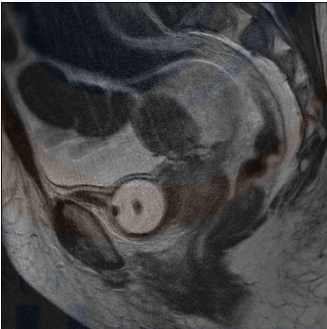
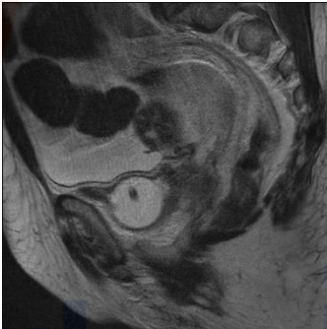
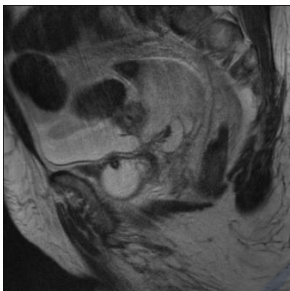
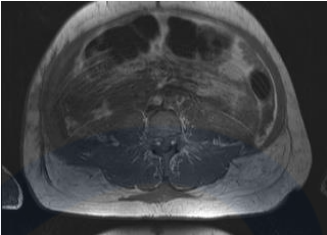
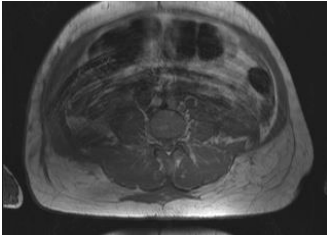
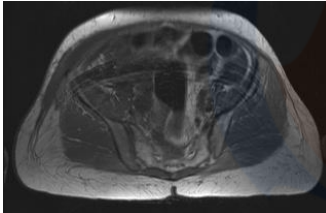
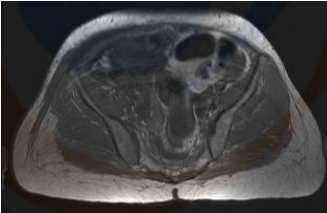
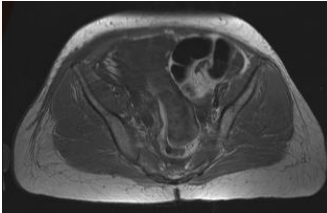
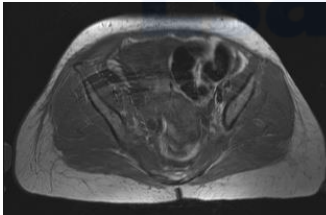
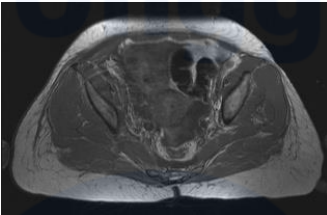
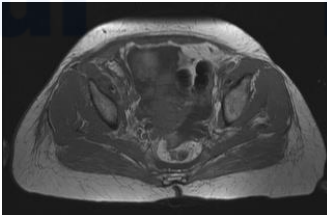
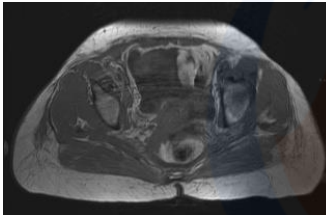
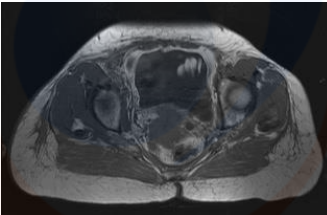
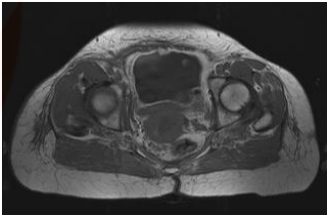
1. Dataset (cancerimagingarchive.net)

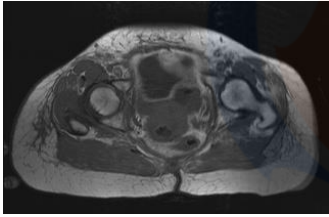
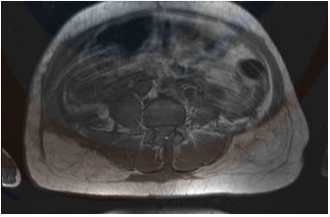
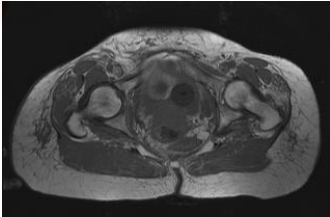
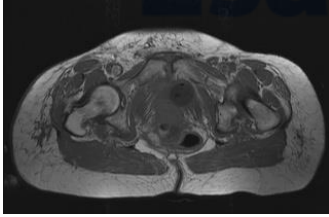
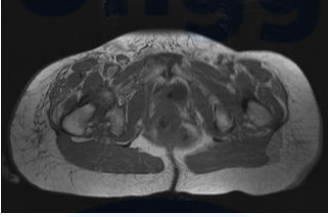
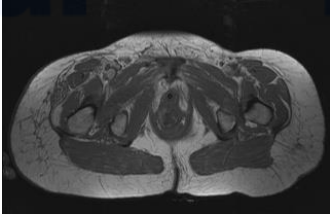
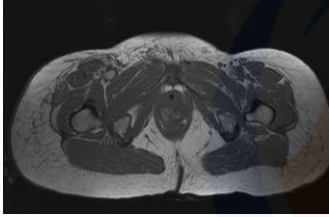
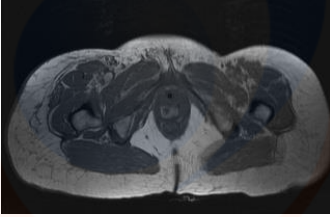
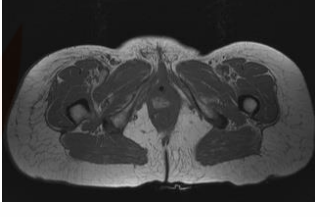
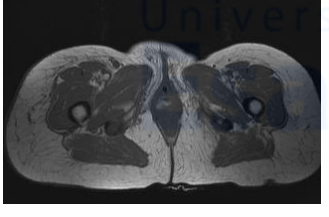
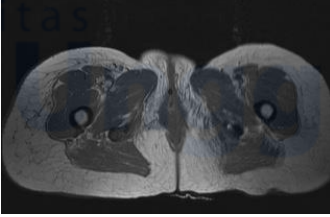
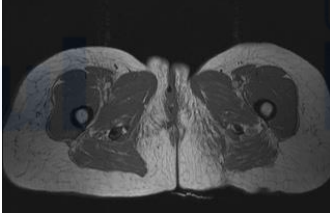
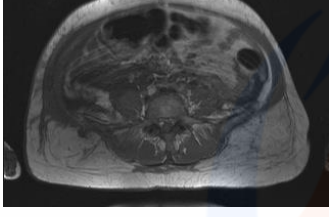
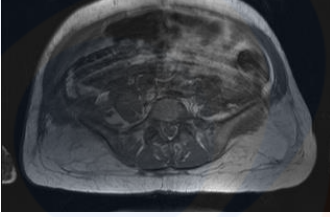
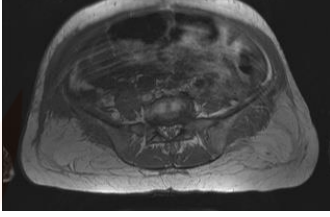
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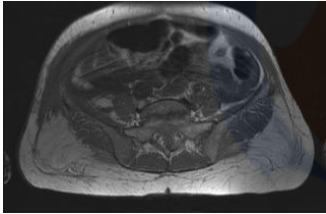
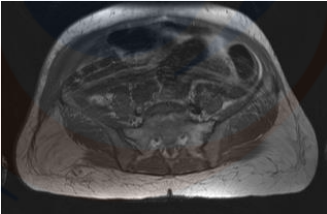
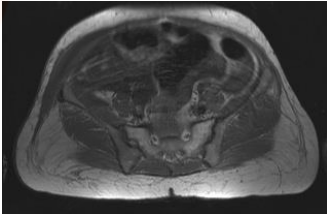
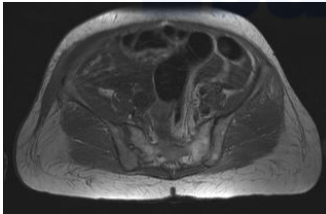
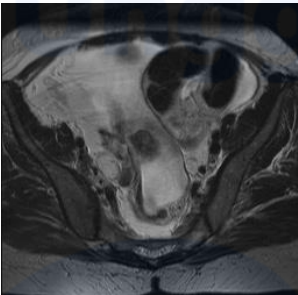
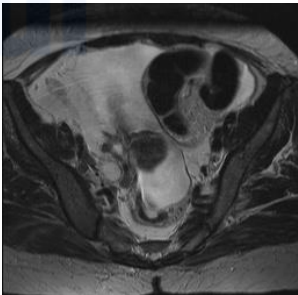
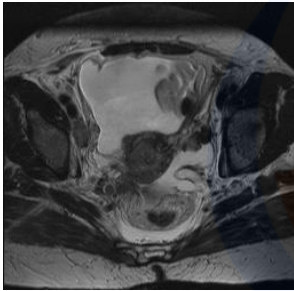
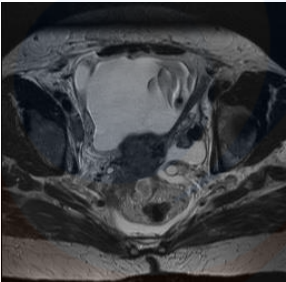
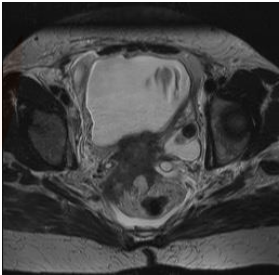
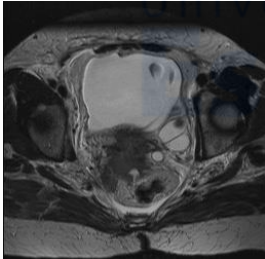
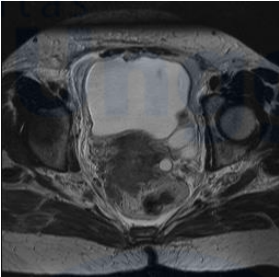
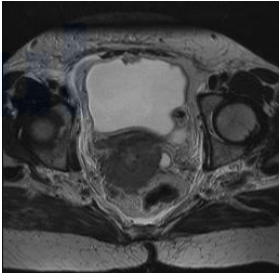
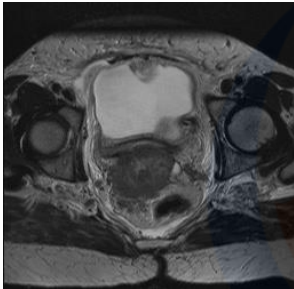
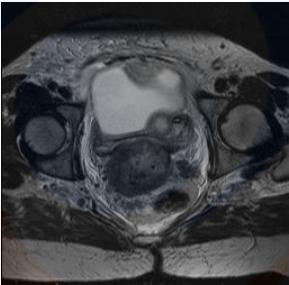
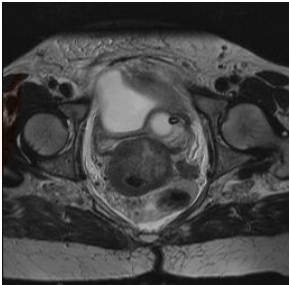
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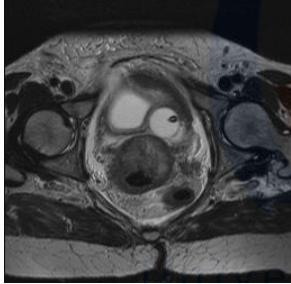
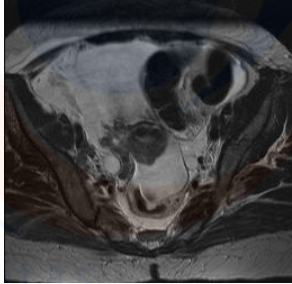
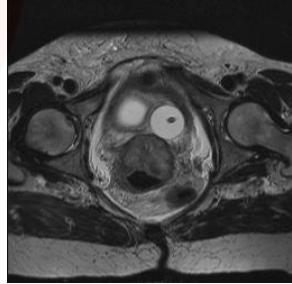
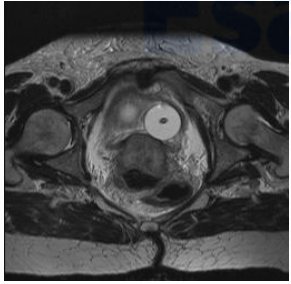
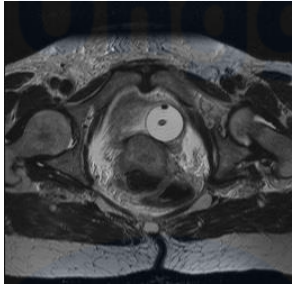
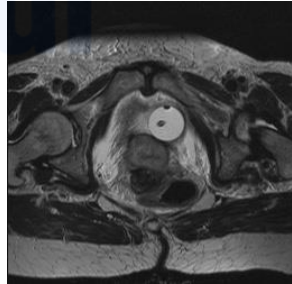
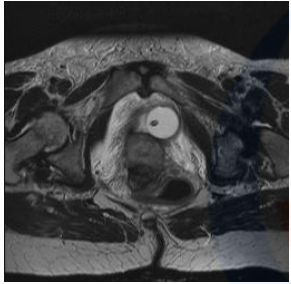
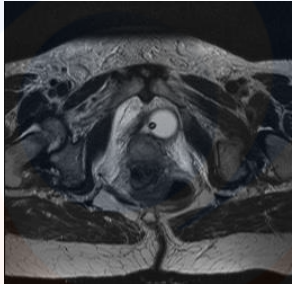
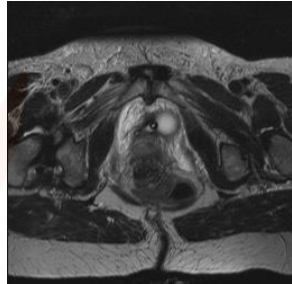
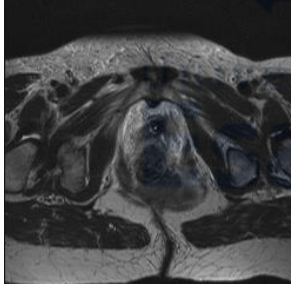
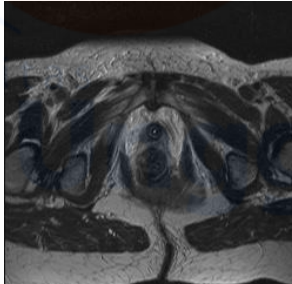
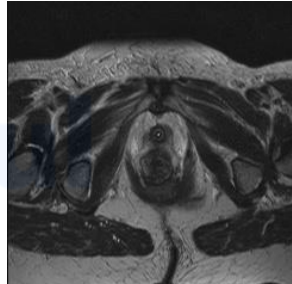
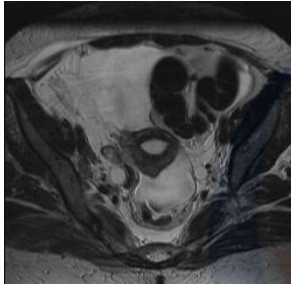
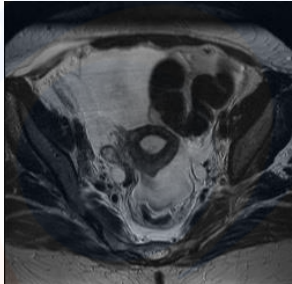
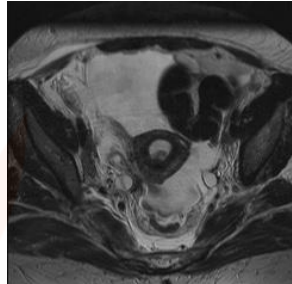
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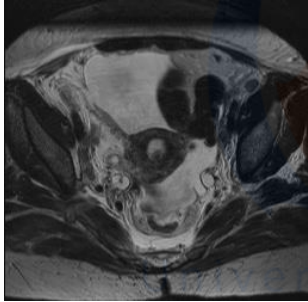
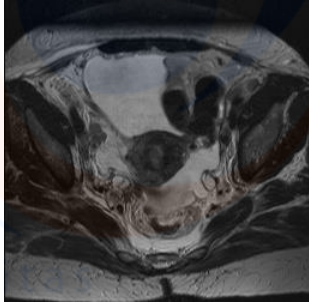
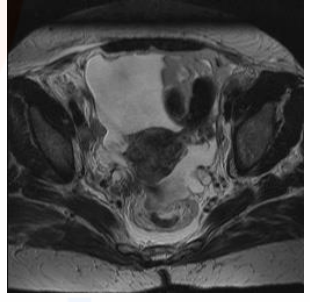
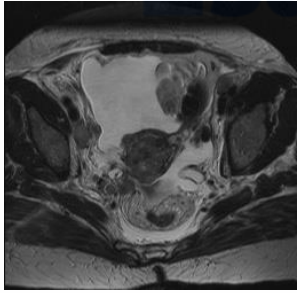
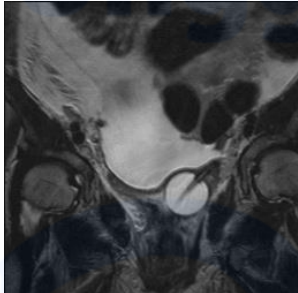
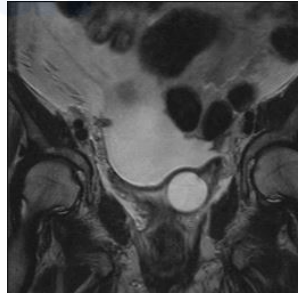
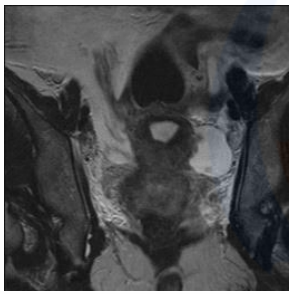
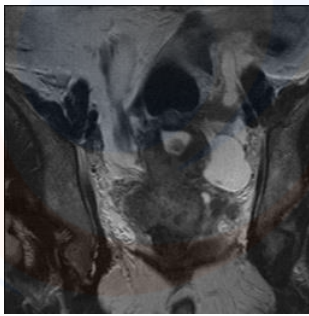
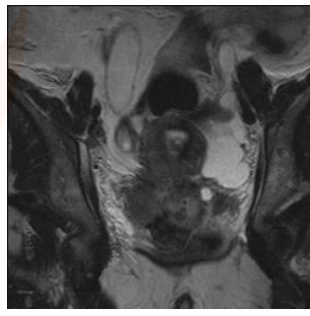
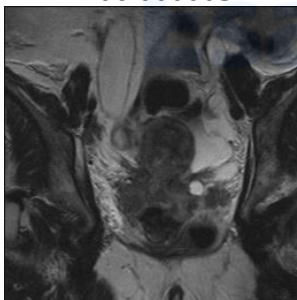
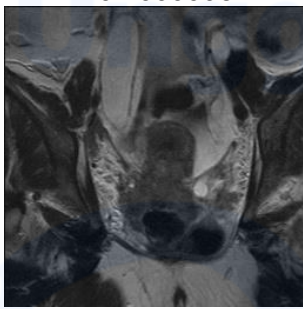
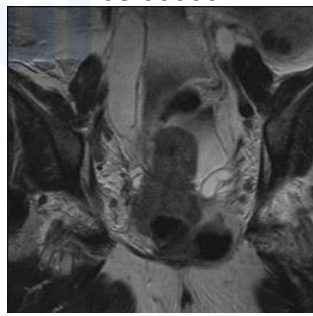
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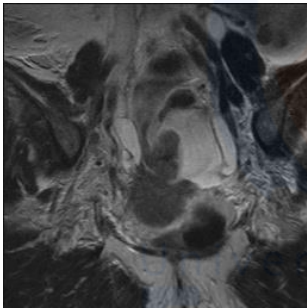
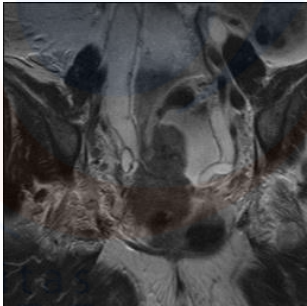
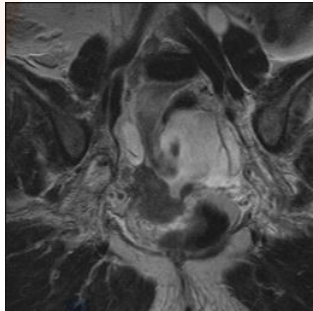
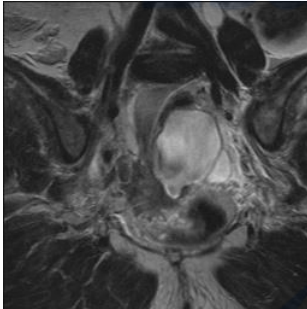
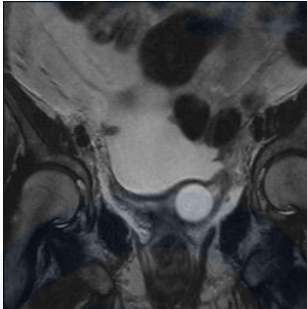
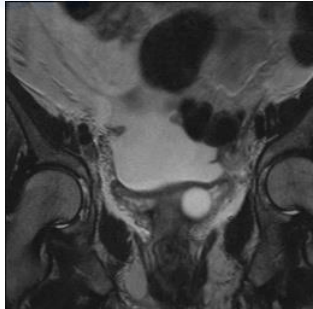
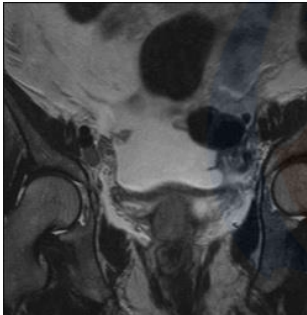
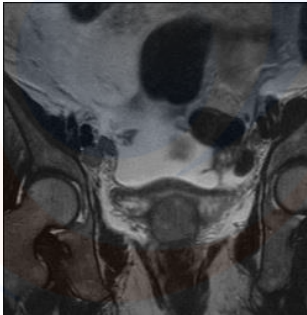
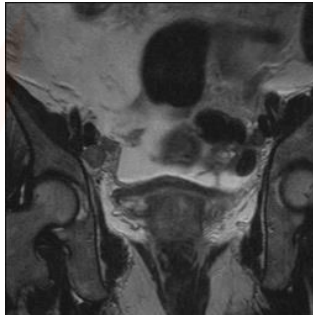
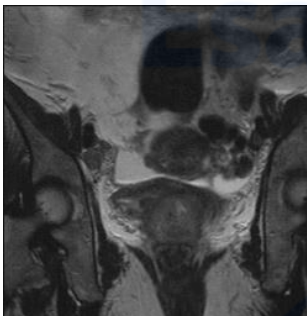
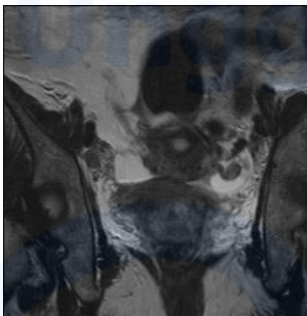
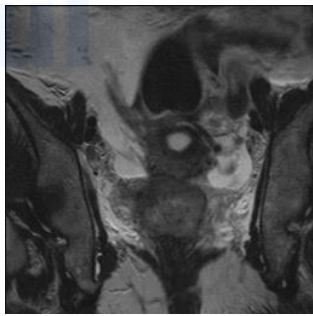
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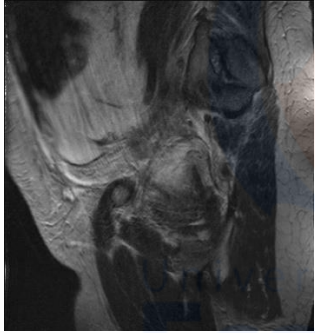
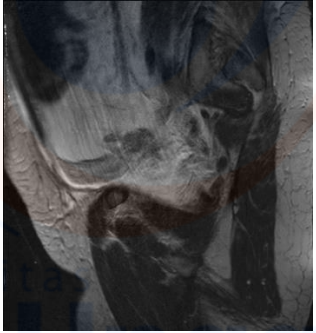
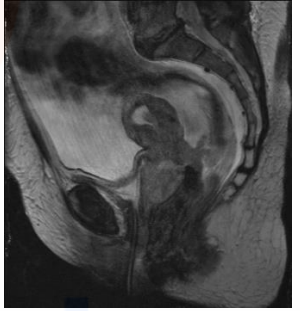
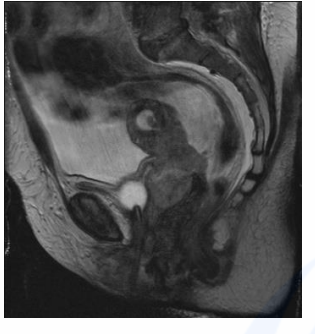
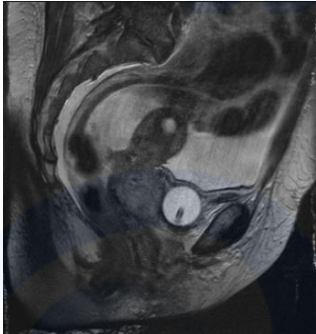
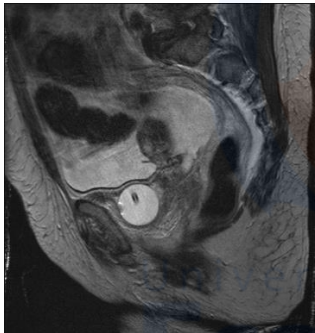
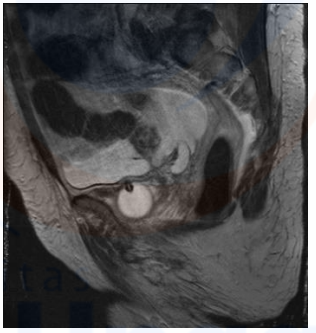
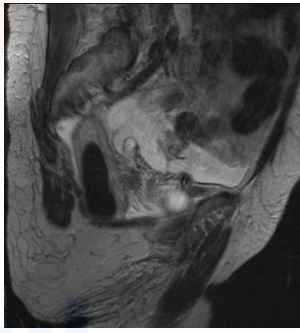
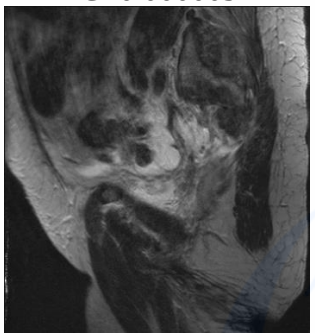
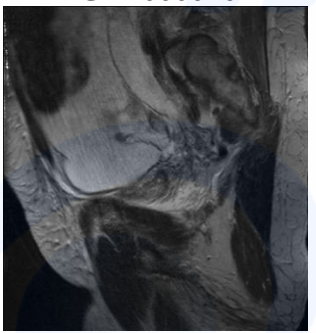
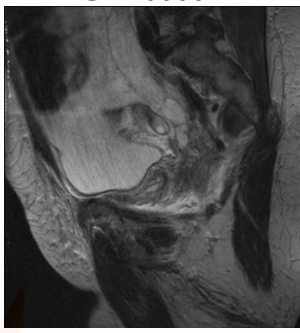
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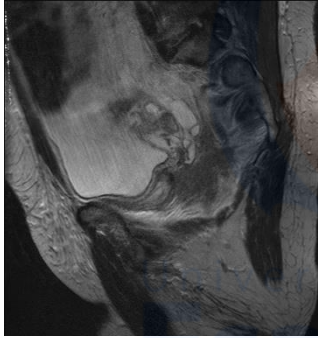
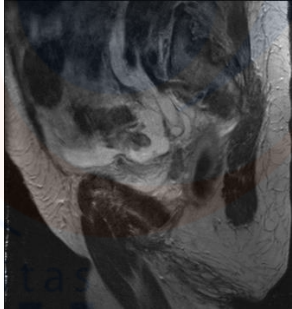
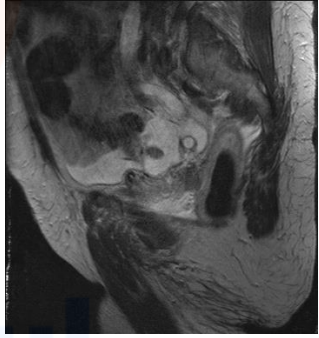
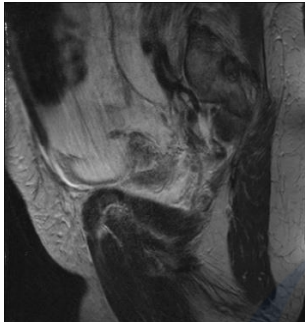
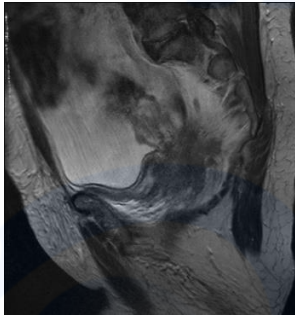
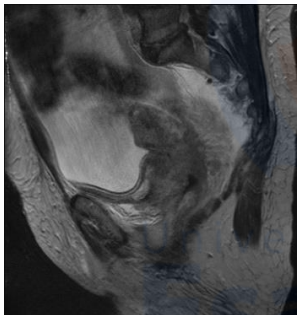
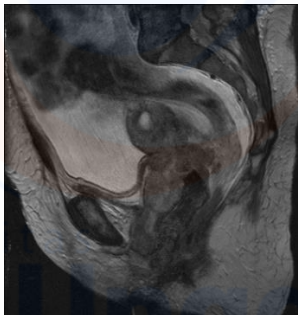
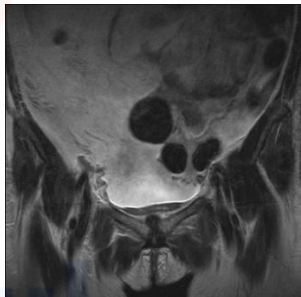
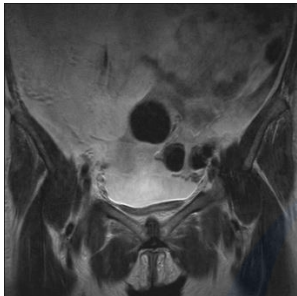
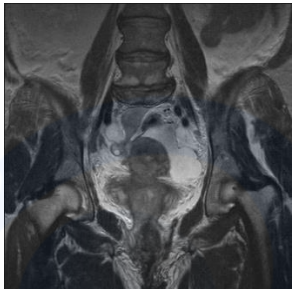
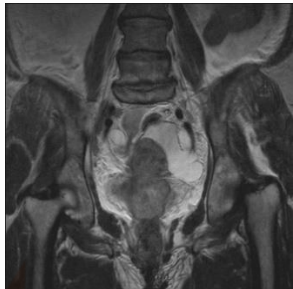
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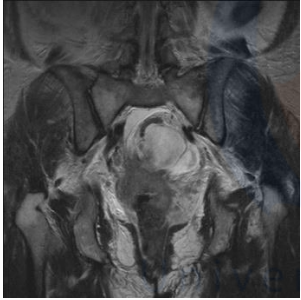
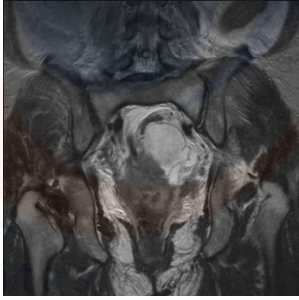
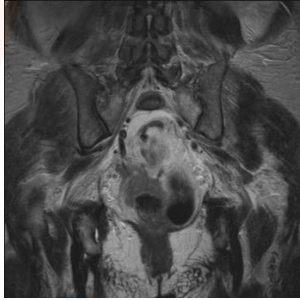
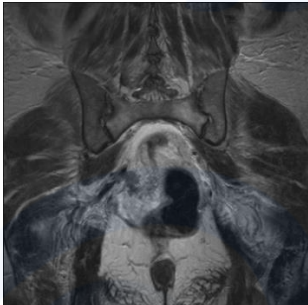
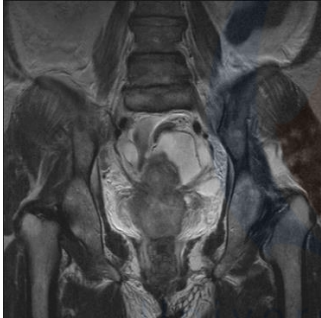
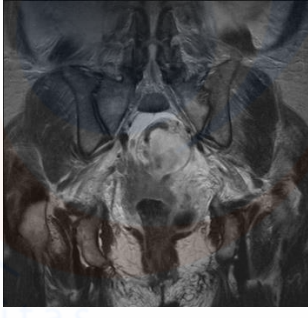
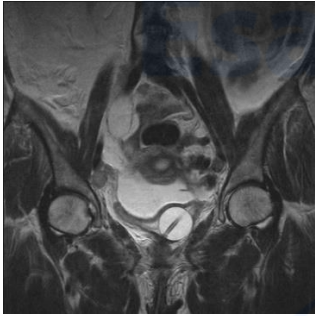
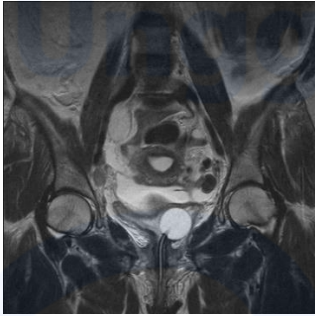
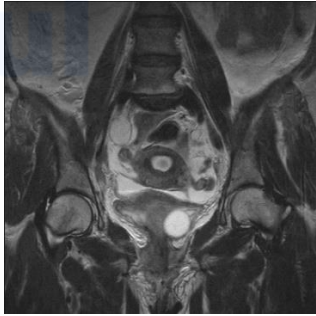
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FILE H14 000013 	FILE H15 000014 	FILE H16 000015 

2. Source Code

a. Build Data Set

```
from main import config
from imutils import paths
import random
import shutil
import os

imagePaths =
list(paths.list_images(config.ORIG_INPUT_DATASET))
random.seed(42)
random.shuffle(imagePaths)

i = int(len(imagePaths) * config.TRAIN_SPLIT)
trainPaths = imagePaths[:i]
testPaths = imagePaths[i:]

i = int(len(trainPaths) * config.VAL_SPLIT)
valPaths = trainPaths[:i]
trainPaths = trainPaths[i:]

datasets = [
    ("training", trainPaths, config.TRAIN_PATH),
    ("validation", valPaths, config.VAL_PATH),
    ("testing", testPaths, config.TEST_PATH)
]

for (dType, imagePaths, baseOutput) in datasets:

    print("[INFO] building '{}' split".format(dType))

    if not os.path.exists(baseOutput):
        print("[INFO] 'creating {}' directory".format(baseOutput))
        os.makedirs(baseOutput)

    for inputPath in imagePaths:

        filename = inputPath.split(os.path.sep)[-1]
        label = filename[-5:-4]
```



```

labelPath = os.path.sep.join([baseOutput, label])

if not os.path.exists(labelPath):
    print("[INFO] 'creating {}'
directory".format(labelPath))
    os.makedirs(labelPath)

p = os.path.sep.join([labelPath, filename])
shutil.copy2(inputPath, p)

```

b. Config
import os

```

ORIG_INPUT_DATASET = "datasets/orig"

```

```

BASE_PATH = "datasets/idc"

```

```

TRAIN_PATH = os.path.sep.join([BASE_PATH, "training"])
VAL_PATH = os.path.sep.join([BASE_PATH, "validation"])
TEST_PATH = os.path.sep.join([BASE_PATH, "testing"])

```

```

TRAIN_SPLIT = 0.8

```

```

VAL_SPLIT = 0.1

```

c. Model

```

from keras.models import Sequential
from keras.layers.normalization import BatchNormalization
from keras.layers.convolutional import SeparableConv2D
from keras.layers.convolutional import MaxPooling2D
from keras.layers.core import Activation
from keras.layers.core import Flatten
from keras.layers.core import Dropout
from keras.layers.core import Dense
from keras import backend as K

```

```

class CancerNet:
    @staticmethod
    def build(width, height, depth, classes):

```

```

model = Sequential()
inputShape = (height, width, depth)
chanDim = -1

if K.image_data_format() == "channels_first":
    inputShape = (depth, height, width)
    chanDim = 1

    model.add(SeparableConv2D(32, (3, 3), padding="same",
        input_shape=inputShape))
    model.add(Activation("relu"))
    model.add(BatchNormalization(axis=chanDim))
    model.add(MaxPooling2D(pool_size=(2, 2)))
    model.add(Dropout(0.2))

    model.add(SeparableConv2D(64, (3, 3),
padding="same"))
    model.add(Activation("relu"))
    model.add(BatchNormalization(axis=chanDim))
    model.add(SeparableConv2D(64, (3, 3),
padding="same"))
    model.add(Activation("relu"))
    model.add(BatchNormalization(axis=chanDim))
    model.add(MaxPooling2D(pool_size=(2, 2)))
    model.add(Dropout(0.2))

    model.add(SeparableConv2D(128, (3, 3),
padding="same"))
    model.add(Activation("relu"))
    model.add(BatchNormalization(axis=chanDim))
    model.add(SeparableConv2D(128, (3, 3),
padding="same"))
    model.add(Activation("relu"))
    model.add(BatchNormalization(axis=chanDim))
    model.add(SeparableConv2D(128, (3, 3),
padding="same"))
    model.add(Activation("relu"))
    model.add(BatchNormalization(axis=chanDim))
    model.add(MaxPooling2D(pool_size=(2, 2)))
    model.add(Dropout(0.2))

    model.add(Flatten())
    model.add(Dense(256))
    model.add(Activation("relu"))
    model.add(BatchNormalization())

```

```
model.add(Dropout(0.2))
```

```
model.add(Dense(256))  
model.add(Activation("relu"))  
model.add(BatchNormalization())  
model.add(Dropout(0.2))
```

```
model.add(Dense(256))  
model.add(Activation("relu"))  
model.add(BatchNormalization())  
model.add(Dropout(0.2))
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```

```
model.add(Dense(classes))  
model.add(Activation("softmax"))  
model.summary()  
model.compile(loss='mse', optimizer='rmsprop')  
return model
```

d. Train

```
# USAGE
```

```
# python train_model.py
```

```
# set the matplotlib backend so figures can be saved in the  
background
```

```
import matplotlib  
matplotlib.use("Agg")
```

```
from keras.preprocessing.image import ImageDataGenerator  
from keras.callbacks import LearningRateScheduler
```



```
from keras.optimizers import Adagrad
from keras.utils.vis_utils import plot_model
from keras.utils import np_utils
from sklearn.metrics import classification_report
from sklearn.metrics import confusion_matrix
from main.cancernet import CancerNet
from main import config
from imutils import paths
import matplotlib.pyplot as plt
import numpy as np
import argparse
import os
```

```
ap = argparse.ArgumentParser()
ap.add_argument("-p", "--plot", type=str, default="plot.png",
                help="path to output loss/accuracy plot")
args = vars(ap.parse_args())
```

```
NUM_EPOCHS = 30
INIT_LR = 1e-2
BS = 32
```

```
trainPaths = list(paths.list_images(config.TRAIN_PATH))
totalTrain = len(trainPaths)
totalVal = len(list(paths.list_images(config.VAL_PATH)))
totalTest = len(list(paths.list_images(config.TEST_PATH)))
```

```
trainLabels = [int(p.split(os.path.sep)[-2]) for p in trainPaths]
trainLabels = np_utils.to_categorical(trainLabels)
classTotals = trainLabels.sum(axis=0)
classWeight = classTotals.max() / classTotals
```

```
trainAug = ImageDataGenerator(
    rescale=1 / 255.0,
    rotation_range=20,
    zoom_range=0.05,
    width_shift_range=0.1,
    height_shift_range=0.1,
    shear_range=0.05,
    horizontal_flip=True,
    vertical_flip=True,
    fill_mode="nearest")
```

```
valAug = ImageDataGenerator(rescale=1 / 255.0)
```

```
trainGen = trainAug.flow_from_directory(  
    config.TRAIN_PATH,  
    class_mode="categorical",  
    target_size=(48, 48),  
    color_mode="rgb",  
    shuffle=True,  
    batch_size=BS)
```

```
valGen = valAug.flow_from_directory(  
    config.VAL_PATH,  
    class_mode="categorical",  
    target_size=(48, 48),  
    color_mode="rgb",  
    shuffle=False,  
    batch_size=BS)
```

```
testGen = valAug.flow_from_directory(  
    config.TEST_PATH,  
    class_mode="categorical",  
    target_size=(48, 48),  
    color_mode="rgb",  
    shuffle=False,  
    batch_size=BS)
```

```
model = CancerNet3.build(width=48, height=48, depth=3,  
    classes=2)  
opt = Adagrad(lr=INIT_LR, decay=INIT_LR / NUM_EPOCHS)  
model.compile(loss="binary_crossentropy", optimizer=opt,  
    metrics=["accuracy"])
```

```
H = model.fit_generator(  
    trainGen,  
    steps_per_epoch=totalTrain // BS,  
    validation_data=valGen,  
    validation_steps=totalVal // BS,  
    class_weight=classWeight,
```

```

epochs=NUM_EPOCHS)

print("[INFO] evaluating network...")
testGen.reset()
predIdxs = model.predict_generator(testGen,
    steps=(totalTest // BS) + 1)

predIdxs = np.argmax(predIdxs, axis=1)

print(classification_report(testGen.classes, predIdxs,
    target_names=testGen.class_indices.keys()))

cm = confusion_matrix(testGen.classes, predIdxs)
total = sum(sum(cm))
acc = (cm[0, 0] + cm[1, 1]) / total
sensitivity = cm[0, 0] / (cm[0, 0] + cm[0, 1])
specificity = cm[1, 1] / (cm[1, 0] + cm[1, 1])

print(cm)
print("acc: {:.4f}".format(acc))
print("sensitivity: {:.4f}".format(sensitivity))
print("specificity: {:.4f}".format(specificity))

N = NUM_EPOCHS
plt.style.use("ggplot")
plt.figure()
plt.plot(np.arange(0, N), H.history["loss"], label="train_loss")
plt.plot(np.arange(0, N), H.history["val_loss"], label="val_loss")
plt.plot(np.arange(0, N), H.history["acc"], label="train_acc")
plt.plot(np.arange(0, N), H.history["val_acc"], label="val_acc")
plt.title("Training Loss and Accuracy on Dataset")
plt.xlabel("Epoch #")
plt.ylabel("Loss/Accuracy")
plt.legend(loc="lower left")
plt.savefig(args["plot"])

plot_model(model, to_file='vgg.png')

```