Chest Cancer Classification using MLflow-DVC-AWS

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ABSTRACT

This MLDevOps project uses the VGG16 CNN model for object detection and classification algorithm which is able to classify upto 1000 images of 1000 different categories with 92.7% accuracy. TensorFlow with Keras was chosen to be used in the model to provide an approachable, highly-productive interface for detecting Adenocarcinoma (Adenocarcinoma is a type of cancerous tumor that can occur in several parts of the body. It is defined as neoplasia of epithelial tissue that has glandular origin, glandular characteristics, or both.) cancer in the chest through chest CT scan datasets with a focus on modern deep learning.

We first train the model with the required basic parameters and log the experiments into MLflow. Then we modify the parameters and rerun the experiment each time and push the logs into MLflow where we compare the results of all the experiments and choose the best parameters based on Accuracy & Loss metrics that have been defined in the source code.

Once we have automated our pipelines, we integrate our source code into Dagshub which acts as a remote server/repository for our project. We then implement DVC (Data Version Control) through a .yaml file to orchestrate our entire pipeline.

We then create an IAM role, an EC2 server and a Elastic Container Registry to host our devops project on AWS Cloud. We create a local self-hosted runner in our github/gitlab Project which stores the AWS Secrets to connect to the AWS Resources.

After setup is complete, when we make a source code update and push the changes to github/gitlab, the pipelines get built and output can be seen on the public IPV4 address of our Amazon EC2 Instance configured on port 8080. In this web page, when we upload a CT scanned image of a chest, the website will tell whether Adenocarcinoma cancer is present or not.

Objective of the Project

The objective of this project is to build an end to end implementation of a chest cancer(Adenocarcinoma) detection system with CICD Deployment through Dagshub remote server for experiment tracking(through the MLflow UI), DVC for Orchestration of the CI/CD pipelines and AWS Cloud for final deployment.

Tools and Requirements

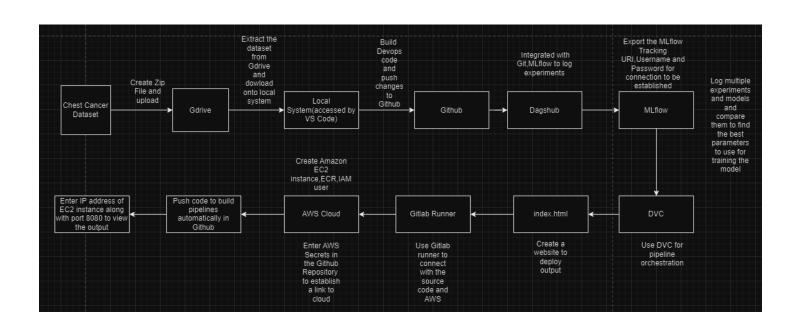
Requirements-

- tensorflow==2.12.0
- Pandas
- gdown
- Dvc
- mlflow==2.2.2
- notebook
- Numpy
- matplotlib
- seaborn
- python-box==6.0.2
- pyYAML
- tqdm
- ensure==1.0.2
- joblib
- types-PyYAML scipy
- Flask
- Flask-Cors
- -e.

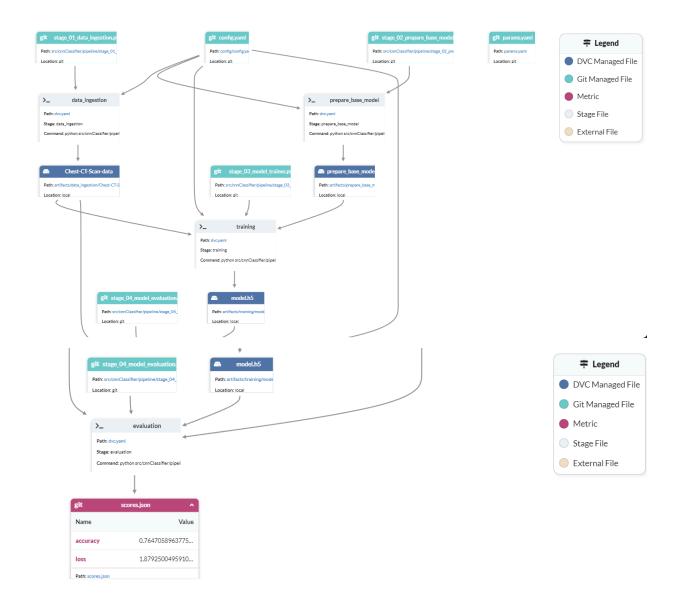
Tools-

- VSCode
- Github
- MLFlow
- DVC
- Gitlab
- Dagshub
- Docker
- AWS
- HTML,CSS,Bootstrap

System Architecture Diagram



Data Flow Diagram



System Configuration for MLflow

We use DagsHub which can integrate with MLflow to provide an easy way to track experiment parameters and metrics, and provides a built-in integration with Git and dataset management meaning that all our experiments become fully reproducible.

Environment Variables -

- os.environ["MLFLOW_TRACKING_URI"]="https://dagshub.com/SuhasMeda/End-to-End-Che st-Cancer-Classification-using-MLflow-DVC.mlflow"
- os.environ["MLFLOW TRACKING USERNAME"]="****"
- os.environ["MLFLOW_TRACKING_PASSWORD"]="****"

System Configuration Source Code -

```
import tensorflow as tf
model = tf.keras.models.load model("artifacts/training/model.h5")
from dataclasses import dataclass
from pathlib import Path
@dataclass(frozen=True)
class EvaluationConfig:
  path of model: Path
  training data: Path
  all params: dict
  mlflow uri: str
  params image size: list
  params_batch_size: int
from cnnClassifier.constants import *
from cnnClassifier.utils.common import read yaml, create directories, save json
class ConfigurationManager:
  def init (
    self,
    config filepath = CONFIG_FILE_PATH,
    params filepath = PARAMS FILE PATH):
    self.config = read yaml(config filepath)
    self.params = read yaml(params filepath)
    create directories([self.config.artifacts root])
  def get evaluation config(self) -> EvaluationConfig:
```

```
eval config = EvaluationConfig(
       path of model="artifacts/training/model.h5",
       training data="artifacts/data ingestion/Chest-CT-Scan-data",
mlflow uri="https://dagshub.com/SuhasMeda/End-to-End-Chest-Cancer-Classification-using-MLflow-DVC.mlfl
ow",
       all params=self.params,
       params image size=self.params.IMAGE SIZE,
       params batch size=self.params.BATCH SIZE
    )
    return eval config
import tensorflow as tf
from pathlib import Path
import mlflow
import mlflow.keras
from urllib.parse import urlparse
class Evaluation:
  def init (self, config: EvaluationConfig):
    self.config = config
  def valid generator(self):
    datagenerator kwargs = dict(
       rescale = 1./255,
       validation split=0.30
    )
    dataflow kwargs = dict(
       target size=self.config.params image size[:-1],
       batch_size=self.config.params_batch_size,
       interpolation="bilinear"
    )
     valid datagenerator = tf.keras.preprocessing.image.ImageDataGenerator(
       **datagenerator kwargs
    )
```

```
self.valid generator = valid datagenerator.flow from directory(
    directory=self.config.training data,
    subset="validation",
    shuffle=False,
    **dataflow kwargs
  )
@staticmethod
def load model(path: Path) -> tf.keras.Model:
  return tf.keras.models.load model(path)
def evaluation(self):
  self.model = self.load model(self.config.path of model)
  self. valid generator()
  self.score = model.evaluate(self.valid generator)
  self.save score()
def save score(self):
  scores = {"loss": self.score[0], "accuracy": self.score[1]}
  save json(path=Path("scores.json"), data=scores)
def log into mlflow(self):
  mlflow.set registry uri(self.config.mlflow uri)
  tracking url type store = urlparse(mlflow.get tracking uri()).scheme
  with mlflow.start run():
    mlflow.log params(self.config.all params)
    mlflow.log metrics(
       {"loss": self.score[0], "accuracy": self.score[1]}
    # Model registry does not work with file store
    if tracking url type store != "file":
       mlflow.keras.log model(self.model, "model", registered model name="VGG16Model")
    else:
       mlflow.keras.log model(self.model, "model")
```

```
try:
    config = ConfigurationManager()
    eval_config = config.get_evaluation_config()
    evaluation = Evaluation(eval_config)
    evaluation.evaluation()
    evaluation.log_into_mlflow()
except Exception as e:
    raise e
```

System Configuration for DVC

We use DVC for orchestrating our pipelines with the help of our "dvc.yaml" file.

DVC commands used in our project -

dvc init - a new . dvc/ directory is created for configuration, default cache location, and other internal files and directories, that are hidden from the user.

dvc repro - It provides an interface to rerun the commands in the pipeline defined by the stage files in the current workspace.

dvc dag - It is used to display the dependency graph of the stages in our pipeline, as defined in the dvc.yaml file found in the project.

dvc.yaml file -

```
stages:
```

```
data_ingestion:
    cmd: python src/cnnClassifier/pipeline/stage_01_data_ingestion.py
    deps:
    - src/cnnClassifier/pipeline/stage_01_data_ingestion.py
    - config/config.yaml
```

outs:

- artifacts/data ingestion/Chest-CT-Scan-data

prepare base model:

cmd: python src/cnnClassifier/pipeline/stage_02_prepare_base_model.py deps:

- src/cnnClassifier/pipeline/stage_02_prepare_base_model.py
- config/config.yaml

params:

- IMAGE SIZE
- INCLUDE TOP
- CLASSES
- WEIGHTS
- LEARNING_RATE

outs:

- artifacts/prepare_base_model

training:

cmd: python src/cnnClassifier/pipeline/stage_03_model_trainer.py deps:

- src/cnnClassifier/pipeline/stage 03 model trainer.py
- config/config.yaml
- artifacts/data ingestion/Chest-CT-Scan-data
- artifacts/prepare base model

params:

- IMAGE SIZE
- EPOCHS
- BATCH SIZE
- AUGMENTATION

outs:

- artifacts/training/model.h5

evaluation:

cmd: python src/cnnClassifier/pipeline/stage_04_model_evaluation.py deps:

- src/cnnClassifier/pipeline/stage_04_model_evaluation.py
- config/config.yaml

- artifacts/data_ingestion/Chest-CT-Scan-data
- artifacts/training/model.h5

params:

- IMAGE SIZE
- BATCH SIZE

metrics:

- scores.json:

Pre-requirements for Auto Training for AI/ML

We use code for converting image to Base64 format and vice versa for getting the final output.

Workflow -

- 1. Update config.yaml
- 2. Update params.yaml
- 3. Update the entity
- 4. Update the configuration manager in src config
- 5. Update the components
- 6. Update the pipeline
- 7. Update the main.py
- 8. Update the dvc.yaml

from dataclasses import dataclass from pathlib import Path

@dataclass(frozen=True)
class TrainingConfig:
 root_dir: Path
 trained_model_path: Path
 updated_base_model_path: Path

```
training data: Path
  params epochs: int
  params batch size: int
  params is augmentation: bool
  params image size: list
from cnnClassifier.constants import *
from cnnClassifier.utils.common import read yaml, create directories
import tensorflow as tf
class ConfigurationManager:
  def init (
    self,
    config filepath = CONFIG FILE PATH,
    params filepath = PARAMS FILE PATH):
    self.config = read yaml(config filepath)
    self.params = read yaml(params filepath)
    create directories([self.config.artifacts root])
  def get training config(self) -> TrainingConfig:
    training = self.config.training
    prepare base model = self.config.prepare base model
    params = self.params
    training data = os.path.join(self.config.data ingestion.unzip dir, "Chest-CT-Scan-data")
    create directories([
       Path(training.root dir)
    ])
    training config = TrainingConfig(
       root dir=Path(training.root dir),
       trained model path=Path(training.trained model path),
       updated base model path=Path(prepare base model.updated base model path),
       training data=Path(training data),
       params epochs=params.EPOCHS,
       params batch size=params.BATCH SIZE,
```

```
params is augmentation=params.AUGMENTATION,
       params image size=params.IMAGE SIZE
    )
    return training config
import os
import urllib.request as request
from zipfile import ZipFile
import tensorflow as tf
import time
class Training:
  def init (self, config: TrainingConfig):
    self.config = config
  def get base model(self):
    self.model = tf.keras.models.load model(
       self.config.updated base model path
    )
  def train valid generator(self):
    datagenerator kwargs = dict(
       rescale = 1./255,
       validation split=0.20
    )
    dataflow kwargs = dict(
       target size=self.config.params image size[:-1],
       batch_size=self.config.params_batch_size,
       interpolation="bilinear"
    )
    valid datagenerator = tf.keras.preprocessing.image.ImageDataGenerator(
       **datagenerator kwargs
    )
    self.valid generator = valid datagenerator.flow from directory(
```

```
directory=self.config.training data,
    subset="validation",
    shuffle=False,
    **dataflow kwargs
  )
  if self.config.params is augmentation:
    train datagenerator = tf.keras.preprocessing.image.ImageDataGenerator(
       rotation range=40,
       horizontal flip=True,
       width shift range=0.2,
       height shift range=0.2,
       shear range=0.2,
       zoom range=0.2,
       **datagenerator kwargs
    )
  else:
    train datagenerator = valid datagenerator
  self.train generator = train datagenerator.flow from directory(
    directory=self.config.training data,
    subset="training",
    shuffle=True,
    **dataflow kwargs
  )
@staticmethod
def save model(path: Path, model: tf.keras.Model):
  model.save(path)
def train(self):
  self.steps per epoch = self.train generator.samples // self.train generator.batch size
  self.validation steps = self.valid generator.samples // self.valid generator.batch size
  self.model.fit(
    self.train generator,
```

```
epochs=self.config.params_epochs,
       steps_per_epoch=self.steps_per_epoch,
       validation steps=self.validation steps,
       validation data=self.valid generator
     )
     self.save_model(
       path=self.config.trained_model_path,
       model=self.model
     )
try:
  config = ConfigurationManager()
  training_config = config.get_training_config()
  training = Training(config=training config)
  training.get base model()
  training.train_valid_generator()
  training.train()
except Exception as e:
  raise e
```

Output



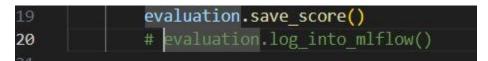
Screenshots

```
End-to-End-Chest-Cancer-Classification-using-MLflow-DVC > logs > E running_logs.log

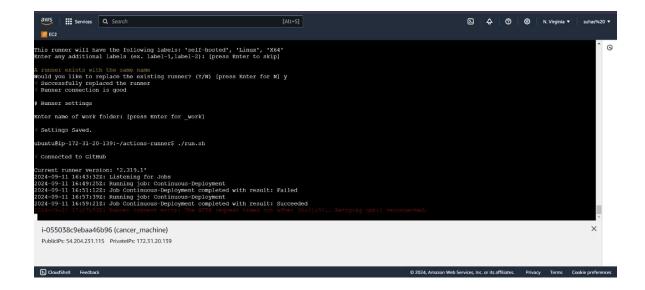
[2024-09-05 15:24:59, 311: INFO: main: kelcome to cnnClassifier]
[2024-09-05 18:02:51,194: INFO: common: yaml file: config\config.yaml loaded successfully]
[2024-09-05 18:02:51,199: INFO: common: yaml file: params.yaml loaded successfully]
[2024-09-05 18:02:51,199: INFO: common: created directory at: artifacts]
[2024-09-05 18:02:51,209: INFO: common: created directory at: artifacts/data_ingestion]
[2024-09-05 18:04:58,115: INFO: common: yaml file: params.yaml loaded successfully]
[2024-09-05 18:04:58,117: INFO: common: yaml file: params.yaml loaded successfully]
[2024-09-05 18:04:58,118: INFO: common: yaml file: params.yaml loaded successfully]
[2024-09-05 18:04:58,118: INFO: common: created directory at: artifacts/data_ingestion]
[2024-09-05 18:04:58,121: INFO: common: created directory at: artifacts/data_ingestion]
[2024-09-05 18:04:58,121: INFO: common: created directory at: artifacts/data_ingestion]
[2024-09-05 18:04:58,121: INFO: common: created directory at: artifacts/data_ingestion]
[2024-09-05 18:09:57,775: INFO: main: >>>>> stage Data ingestion stage started <<<<<<|>[2024-09-05 19:09:57,7718: INFO: main: >>>>> stage Data ingestion stage started <<<<<|>[2024-09-05 19:09:57,7718: INFO: common: yaml file: config\config.yaml loaded successfully]
[2024-09-05 19:09:57,7718: INFO: common: yaml file: config\config.yaml loaded successfully]
[2024-09-05 19:09:57,7718: INFO: common: created directory at: artifacts/data_ingestion]
[2024-09-05 19:09:57,7728: INFO: common: created directory at: artifacts/data_ingestion]
[2024-09-05 19:09:57,7728: INFO: common: created directory at: artifacts/data_ingestion]
[2024-09-05 19:09:57,720: INFO: common: created directory at: artifacts/data_ingestion]
[2024-09-05 19:09:57,720: INFO: data_ingestion: Downloading data from https://drive.google.com/file/d/ImsuE90pYbpYd8HYbZ_2j-vun7a3DJNI1/vi
[2024-09-05 19:09:57,720: INFO: data_ingestion: Downloaded data from https://drive.google.com/file/d/Ims
```

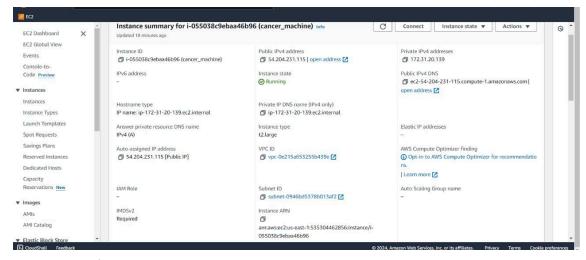
```
# - name: Stop and remove container if running
# run: |
# docker ps -q --filter "name=cnncls" | grep -q . && docker stop cnncls && docker rm -fv cnncls
```

uncomment 2nd time onwards in the main.yaml file when executing cancer project

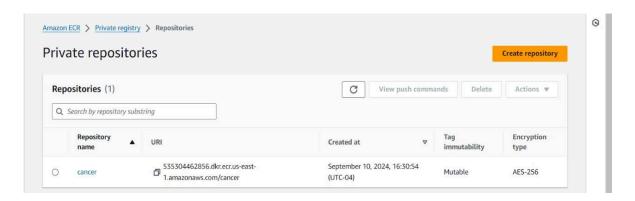


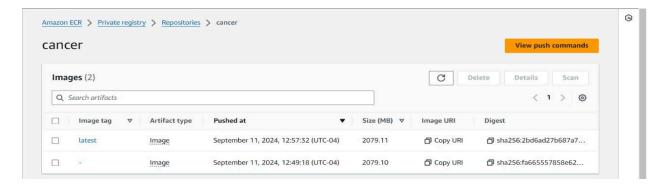
uncomment in stage 04 model evaluation.py file to get logs in mlflow



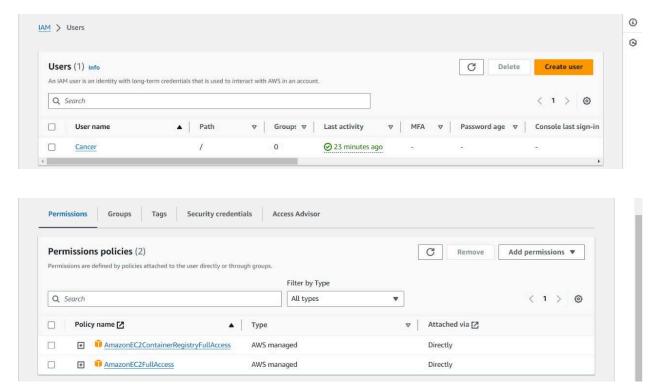


Ec2 Instance in AWS





ECR Registry in AWS to store the docker images



IAM User who has the policies required to access the EC2 instance in AWS.

Future Scope of Enhancement

- Use the Data version control (DVC) to enable rollbacking of models in MLFlow
- Replace Dagshub with a MLFlow Server inside nova dev server(on-premise remote server)
- Enable dataset traceability through model weight files
- Pipeline Deployment capability to a server or edge machine (done)
- Parameterize the entire code through a .yaml file or a .env file

References

- https://dvc.org/doc
- https://mlflow.org/docs/latest/index.html
- https://dagshub.com/docs/
- https://www.tensorflow.org/guide/keras
- https://medium.com/@mygreatlearning/everything-you-need-to-know-about-vgg16-7315defb59
 18
- https://www.youtube.com/@dswithbappy
- https://docs.github.com/en/actions/hosting-your-own-runners/managing-self-hosted-runners/adding-self-hosted-runners
- https://base64.guru/converter/decode/image