# PatchCore for Anomaly Detection

This document serves as a detailed guide to help users run the patchcore.py script for anomaly detection. The script is designed to process datasets for training, validation, and testing, and generates anomaly heatmaps stored in a specified output directory.

## **Overview**

The patchcore.py script implements an anomaly detection model using PatchCore with a Resnet backbone (50,101) backbone. It allows users to specify dataset paths and output directories via command-line arguments (CLI).

#### **Features**

- Train an anomaly detection model with a specified training dataset.
- Validate the model with normal and anomalous datasets to find the threshold.
- Test the model and generate anomaly heatmaps.
- Save the heatmaps to a user-specified directory.

# **Prerequisites**

## 1. Environment Setup

Ensure you have Python installed (preferably Python 3.8 or higher). Install the required dependencies by running:

pip install -r requirements.txt

## 2. Directory Structure

Prepare your dataset directory with the following structure:

# **Running the Script**

## **Step 1: Command-Line Arguments**

The script uses command-line arguments to accept dataset paths and output directories. Below is a description of each argument:

Argument	Description
train_dir	Path to the training dataset.
val_normal_dir	Path to the normal validation dataset.
val_anomalous_dir	Path to the anomalous validation dataset.
test_normal_dir	Path to the normal testing dataset.
test_anomalous_dir	Path to the anomalous testing dataset.
output_dir	Path to the output directory where anomaly heatmaps will be saved.
batch_size	(Optional) Batch size for data loaders. Default is 4.

## **Step 2: Example Usage**

To run the script, use the following command:

```
python patchcore.py \
    --train_dir "/path/to/training/normal" \
```

```
--val_normal_dir "/path/to/validation/normal" \
--val_anomalous_dir "/path/to/validation/zflowers" \
--test_normal_dir "/path/to/testing/normal" \
--test_anomalous_dir "/path/to/testing/zflowers" \
--output_dir "./output/anomaly_heatmaps" \
--batch_size 4
```

## Step 3: Output

- The script will train the model using the training dataset.
- It will validate the model and find the best threshold.
- During the testing phase, it will generate anomaly heatmaps for anomalous images and calculate metrics such as accuracy, confusion matrix, and AUROC.

# **Understanding the Outputs**

## **Heatmaps**

- Each heatmap highlights the areas in an image where anomalies are detected.
- Saved in the output directory with filenames like <a href="mailto:anomaly\_visual\_0.png">anomaly\_visual\_0.png</a>, etc.

## Logs

- The script prints the progress of training, validation, and testing phases in the terminal.
- Metrics such as accuracy, confusion matrix, and AUROC are displayed for performance evaluation.

# **Troubleshooting**

#### 1. Missing Dependencies:

If you encounter errors related to missing libraries, ensure you have installed all dependencies from

requirements.txt.

#### 2. Invalid Dataset Paths:

Double-check the paths provided in the CLI arguments. Ensure they point to valid directories containing images.

#### 3. Output Directory Not Found:

If the output directory does not exist, the script will create it automatically.

## **Additional Information**

## **Supported Image Formats**

• The script supports .jpg , .jpeg , and .png image formats.

### **Batch Size**

The batch size can be adjusted based on your system's memory capacity. A
larger batch size may speed up training but requires more memory.