

# Configuration Manual

MSc Research Project  
Master of Science in Data Analytics

Saran Das Sivadasan Achary  
Student ID: 23336030

School of Computing  
National College of Ireland

Supervisor: Athanasios Staikopoulos

**National College of Ireland**  
**MSc Project Submission Sheet**  
**School of Computing**



**Student Name:** Saran Das Sivadasan Achary

**Student ID:** 23336030

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**Lecturer:** Athanasios Staikopoulos

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# Configuration Manual

Saran Das Sivadasan Achary  
Student ID: 23336030

## 1 Introduction

This document describes the requirements and steps to be performed for replicating the Risk-Adaptive Triple-Stream Vision Transformer (TS-ViT) model for automated dermatological triage. It specifies the required tools, data processing steps, configuration parameters, and packages required for model development and evaluation.

## 2 Requirements

The main requirements for the model development are:

### Google Colab Pro

Cloud-hosted platform for deep learning model development  
NVIDIA Tesla T4 GPU (16GB VRAM) access  
Preinstalled machine learning libraries  
Eliminates environment setup complexity

### DERM12345 Dataset

Published in Nature Scientific Data (2024) by Yilmaz et al.  
12,345 dermatoscopic images  
Hierarchical organization: 5 superclasses, 15 major classifications, 40 subclassifications  
Available through Harvard Dataverse  
<https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/DAXZ7P>

### Python Environment

Python 3.10.12  
PyTorch 2.2.2 framework  
Dynamic computational graphs  
CUDA acceleration for GPU training

## 3 Specification

The specifications of the system required for developing the model are given below:

### Hardware

- GPU: NVIDIA Tesla T4 (16GB VRAM)
- RAM: 12GB system RAM

- Storage: 10GB for dataset and model checkpoints
- CUDA: Version 11.8 or higher

## Software Specification

- Google Colab Pro with T4 GPU runtime
- Python 3.10.12
- PyTorch 2.2.2
- torchvision 0.17.2
- CUDA 11.8

## Python Libraries Used

- PyTorch
- torchvision
- NumPy
- Pandas
- scikit-learn
- Matplotlib
- Seaborn
- OpenCV
- tqdm

# 4 Installation

## Step 1: Setup Environment

- Access Google Colab website ([colab.research.google.com](https://colab.research.google.com))
- Create a new notebook
- Select Runtime → Change runtime type
- Hardware accelerator: GPU (T4 GPU)

## Step 2: Verify GPU

```
# Device configuration
device = torch.device('cuda' if torch.cuda.is_available() else 'cpu')
print(f"Device: {device}")
print(f"GPU: {torch.cuda.get_device_name(0) if torch.cuda.is_available() else 'None'}")

# Create output directories
os.makedirs('/content/outputs', exist_ok=True)
os.makedirs('/content/checkpoints', exist_ok=True)
os.makedirs('/content/visualizations', exist_ok=True)

... Device: cuda
    GPU: Tesla T4
```

## Step 3: Install PyTorch

```

# Core libraries
import os
import zipfile
import numpy as np
import pandas as pd
from PIL import Image
import matplotlib.pyplot as plt
import seaborn as sns
from tqdm import tqdm
import math

# PyTorch
import torch
import torch.nn as nn
import torch.nn.functional as F
from torch.utils.data import Dataset, DataLoader, WeightedRandomSampler

from torchvision import transforms, models

import timm

```

#### Step 4: Mount Google Drive

```

from google.colab import drive
drive.mount('/content/drive')

Mounted at /content/drive

```

#### Step 5: Create Directory Structure

```

# Create output directories
os.makedirs('/content/outputs', exist_ok=True)
os.makedirs('/content/checkpoints', exist_ok=True)
os.makedirs('/content/visualizations', exist_ok=True)

```

#### Step 6: Set Random Seed

```

def set_seed(seed=42):
    np.random.seed(seed)
    torch.manual_seed(seed)
    torch.cuda.manual_seed_all(seed)
    torch.backends.cudnn.deterministic = True
    torch.backends.cudnn.benchmark = False

set_seed(42)

```

## 5 Data Preparation

### Dataset Acquisition

Download DERM12345 dataset from Harvard Dataverse

<https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/DAXZ7P>

Extract dataset to /content/data/ directory

Verify 12,345 dermatoscopic images present

### Dataset Organization

Total Images: 12,345

Training Set: 7,888 images (80%)

Validation Set: 988 images (10%)

Test Set: 2,485 images (held-out)

### Risk Stratification

Three-tier clinical risk levels:

HIGH RISK: 7,365 images (59.7%)

- Confirmed malignancies: melanoma, basal cell carcinoma, squamous cell carcinoma
- High-risk precursor lesions

MODERATE RISK: 1,315 images (10.7%)

- Dysplastic melanocytic nevi
- Requires periodic surveillance

LOW RISK: 3,665 images (29.7%)

- Benign lesions
- Minimal transformation risk

### Preprocessing Steps

Resize images to 256×256 pixels

Center crop to 224×224 pixels (ViT-B/16 input size)

Convert to PyTorch tensors

Normalize with ImageNet statistics: Mean [0.485, 0.456, 0.406], Std [0.229, 0.224, 0.225]

## 6 Model Building

### Base Architecture (ViT-B/16)

Input size: 224×224 RGB images

Patch size: 16×16 (produces 196 patches)

Embedding dimension: 768

Transformer layers: 12

Attention heads: 12

Total parameters: 86.3 million

Initialization: Random (no ImageNet pretraining)

## TS-ViT Architecture Components

### 1. Shared Transformer Encoder

- Load ViT-B/16 from torchvision with weights=None
- Remove original classification head
- Extract CLS token (768-dim) and 196 patch embeddings

### 2. Global Classification Stream

- Input: CLS token (768 dimensions)
- Two-layer feedforward network:  $768 \rightarrow 384 \rightarrow 3$  dimensions
- Dropout: 0.3
- Purpose: Overall lesion risk assessment

### 3. Spatial Attention Stream

- Input: 196 patch embeddings
- Lightweight attention scoring network
- Softmax normalization for attention weights
- Weighted aggregation of patches
- Output: Attention heatmap + risk logits

### 4. Uncertainty Quantification Stream

- Input: CLS token
- Monte Carlo Dropout: 5 forward passes
- Fully connected network  $\rightarrow$  sigmoid activation
- Output: Confidence estimate and prediction variance

## 7 Comparison

The developed TS-ViT model was evaluated against the following baseline architectures:

### 1. ResNet-50

- Convolutional neural network with residual connections
- Parameters: 25.6 million
- Training: From scratch (no ImageNet pretraining)

### 2. ViT-B/16 (Vanilla)

- Single-stream Vision Transformer
- Parameters: 86.6 million
- Training: From scratch (no ImageNet pretraining)

### 3. MobileNetV3-Large

- Efficient CNN with depth-wise separable convolutions
- Parameters: 5.5 million

- Training: From scratch (no ImageNet pretraining)

| Model                | Accuracy     | Precision    | Recall       | Macro F1     | Brier Score  |
|----------------------|--------------|--------------|--------------|--------------|--------------|
| <b>TS-ViT (Ours)</b> | <b>89.3%</b> | <b>0.799</b> | <b>0.853</b> | <b>0.847</b> | <b>0.074</b> |
| ViT-B/16             | 67.2%        | 0.612        | 0.638        | 0.625        | 0.167        |
| ResNet-50            | 63.8%        | 0.666        | 0.567        | 0.591        | 0.236        |
| MobileNetV3          | 59.4%        | 0.521        | 0.565        | 0.543        | 0.284        |

Table 1. Model comparison

## References

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