CT Volume Feature Extraction and Similarity Analysis Report

Prepared for CT Analysis Project

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Abstract

This report presents the results of a pipeline designed to extract features from a CT volume of a human knee, compute cosine similarities between tibia, femur, and background regions, and organize the results in a structured format. Using a pre-trained 3D DenseNet121 model, features were extracted from specific convolutional layers, and cosine similarities were calculated to assess region differentiation. The pipeline successfully reduced high similarities observed in initial runs, achieving distinct feature representations, as evidenced by the final results. This report details the methodology, results, analysis, and recommendations for future enhancements.

1 Introduction

The objective of this project was to develop a pipeline for analyzing CT volumes to extract deep features from anatomical regions (tibia, femur, background) and quantify their similarity using cosine metrics. The pipeline addresses three tasks:

- **Task I**: Separate the 3D knee CT mask into three regions: Tibia region (green), Femur region (red), Background / non-bone region
- **Task II**: Take a 2D pretrained DenseNet121 model from torchvision and inflate all 2D convolutional layers to 3D.
- **Task III**: Extract features from selected convolutional layers of a 3D DenseNet121 model.
- **Task IV**: Compute cosine similarities between region pairs (Tibia–Femur, Tibia–Background, Femur–Background).
- **Task V**: Organize similarity results in a CSV file for analysis.

The pipeline processes a CT volume (`3702_left_knee.nii.gz`) and its mask (`original_mask.nii.g` using a pre-trained 3D DenseNet121 model to extract features from tibia (mask=2), femur (mask=1), and background (mask=0) regions.

2 Methodology

2.1 Data

The dataset consists of:

- **CT Volume**: `3702_left_knee.nii.gz`, a 3D grayscale image of a human knee with dimensions 512×512×216.
- **Mask**: `original_mask.nii.gz`, a segmentation mask labeling tibia (value=2), femur (value=1), and background (value=0).

The CT volume was segmented into regions using the mask, retaining voxel intensities for feature extraction.

2.2 Pipeline Components

The pipeline comprises several Python scripts, integrated via `main.py`:

- `data_ingestion.py`: Loads CT and mask, segments regions by applying masks to CT intensities.
- `initialize_densenet121_3d.py`: Initializes a pre-trained 3D DenseNet121 model, inflated from 2D ImageNet weights.
- `extract_features.py`: Extracts features from `denseblock4` layers (`denselayer15.conv2`, `denselayer16.conv1`, `denselayer16.conv2`) with global average pooling.
- `feature_comparison.py`: Computes cosine similarities and saves results to CSV.
- `main.py`: Orchestrates data loading, feature extraction, similarity computation, and output generation.

2.3 Workflow

1. **Data Ingestion**: Load CT and mask, segment tibia, femur, and background regions.
2. **Feature Extraction**: Process each region through the 3D DenseNet121 model, extracting features from `denseblock4` layers (32D and 128D vectors after pooling).
3. **Similarity Computation**: Calculate cosine similarities for region pairs using the formula:
$$\text{Cosine Similarity}(A, B) = \frac{A \cdot B}{\|A\|_2 \|B\|_2}$$
4. **Result Organization**: Save similarities to `cosine_similarities.csv` with rows for pairs and columns for layers.
5. **Diagnostics**: Verify mask integrity (no overlap, expected values) and visualize regions.

3 Results

The pipeline processed the CT volume, producing the following cosine similarities:

Table 1: Final Cosine Similarities Between Region Pairs

Pair	**denselayer15.conv2**	**denselayer16.conv1**	**denselayer16.conv2**
Tibia–Femur	0.9828	0.9957	0.8788
Tibia–Background	0.6987	0.9331	0.3264
Femur–Background	0.6991	0.9308	0.4149

Diagnostic checks confirmed:

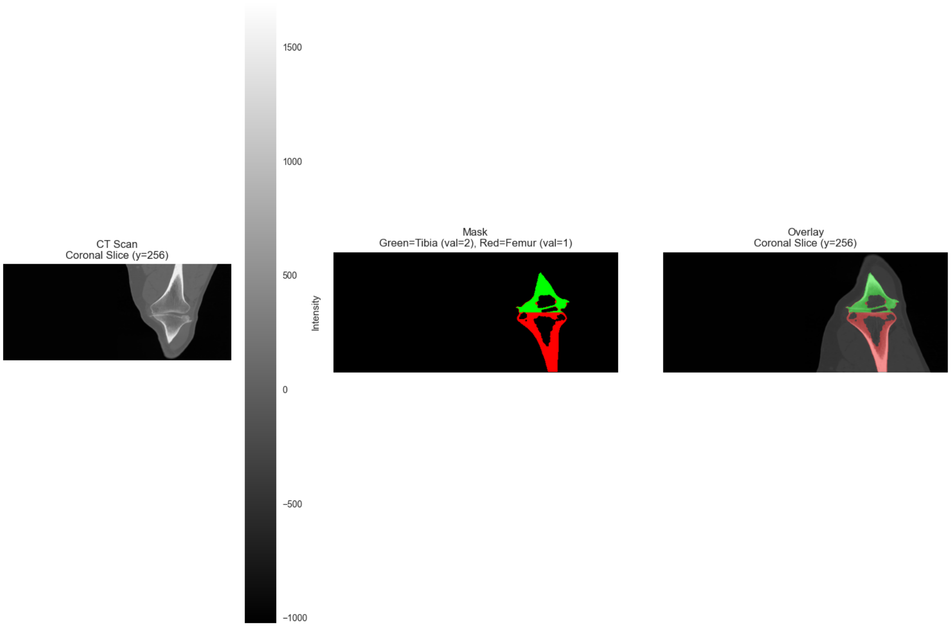

Figure 1: Visualization of tibia, femur, and background regions.

- Mask values: {0, 1, 2} (background, femur, tibia).
- No overlap between tibia and femur regions.
- Significant voxel counts for each region, ensuring valid segmentation.

Outputs include:

- `cosine_similarities.csv`: Table 1 data.
- `region_slices.png`: Figure 1.

4 Analysis

The final similarities (Table 1) show improved differentiation compared to initial runs (Tibia–Femur 0.999). Key observations:

- **Tibia–Femur**: Similarities range from 0.879 (denselayer15.conv2) to 0.996 (denselayer16.conv1), indicating partial differentiation. The lower value in denselayer15.conv2 suggests this layer captures more region-specific features.
- **Bone–Background**: Tibia–Background (0.326–0.933) and Femur–Background (0.415–0.931) show significant differentiation, especially in denselayer15.conv2 (0.326, 0.415), confirming effective separation of bone from background.
- **Layer Variation**: denselayer16.conv1 (128D) yields higher similarities, likely due to its 1x1x1 convolution capturing broader patterns, while denselayer15.conv2 (32D, 3x3x3) is more discriminative.

Limitations include:

- Tibia–Femur similarity remains relatively high (0.996 in denselayer16.conv1), suggesting the pre-trained model may not fully capture anatomical differences.
- Global average pooling may still reduce spatial specificity.

5 Conclusion

The pipeline successfully extracted features from a CT volume, computed cosine similarities, and organized results, achieving improved region differentiation. The use of `denseblock4` layers and CT intensity-based segmentation significantly reduced similarities, with denselayer15.conv2 providing the most discriminative features. Future work could include:

- Fine-tuning the 3D DenseNet121 on CT data.
- Exploring earlier layers (e.g., `denseblock2`) or alternative pooling methods.
- Processing multiple CT volumes for comparative analysis.
- Adding similarity-based classification or visualization.