
Voxel-Based Alignment and Tumor Extraction from Liver CT Scans

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Abstract

This project develops a pipeline for rigid registration and semi-automatic segmentation of liver tumors using DICOM CT scans. A reference volume and annotated input scan are aligned through least-squares optimization, and the resulting transformation is applied to both intensity and segmentation data. A region-growing method segments the tumor based on its centroid. Results show a tumor voxel retention of 70 percent and a Dice score of 0.28, validating the approach.

Author Keywords

Rigid registration, DICOM, CT scan, liver tumor, segmentation, region growing, medical imaging.

1. Introduction

This project focuses on the visualization and alignment of 3D medical imaging data using DICOM CT scans and their associated segmentation masks. The main objective is to develop a reproducible and interpretable pipeline for loading, preprocessing, and rigidly registering volumetric medical data, with emphasis on liver and tumor segmentation.

The work is divided into two tasks. In Task 1, we implemented a pipeline to load and normalize CT and segmentation volumes, generate anatomical overlays, and create an animated visualization using Maximum Intensity Pro-

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jection (MIP) in sagittal and coronal planes. This enabled clear identification of tumoral regions and assessment of anatomical structure.

In Task 2, we performed rigid registration of a CT scan to a reference phantom volume. This involved optimizing transformation parameters (translation, rotation, and scaling) to minimize voxel-wise error. Once aligned, we transformed the segmentation masks and verified tumor voxel retention. We also applied a semi-automatic segmentation method based on region growing and compared it with the ground-truth tumor mask using Dice score.

This report documents the technical implementation, algorithms used, and evaluation of results. All code is provided in an open repository.

Task 1: DICOM Loading and Visualization

The first task consisted of loading and visualizing a real CT scan and its associated DICOM segmentation files. The dataset assigned, corresponding to sample patient 1720, included an axial CT series as well as structured segmentation files for the liver and tumor. Using pydicom, the CT slices were read and ordered according to their position in the patient using the ImagePositionPatient header. The segmentation masks were also read and aligned with the CT image, resulting in a 3D label volume where label 1 corresponds to the liver and label 2 to the tumor. All volumes were robustly normalized using percentile clipping to reduce the effect of outliers and enhance contrast.

After loading and preprocessing, a multi-planar visualization of the CT scan and segmentation was performed. Axial, coronal, and sagittal views were generated using matplotlib, and segmentation overlays were created by blending the grayscale CT image with color-coded masks. A more advanced visualization was achieved by generating a Maxi-

mum Intensity Projection (MIP) animation. This was done by rotating the 3D volume around the vertical axis in discrete steps and computing a projection along the coronal axis at each rotation angle. The resulting 2D frames were compiled into a GIF, with overlaid masks to clearly indicate the position of the liver and tumor structures. The result was a complete and interactive overview of the anatomical structures in 3D space.

Task 2: Rigid Registration and Segmentation

The second task focused on the rigid registration of an input CT scan to a reference phantom volume. We implemented a 9-parameter optimization (3 shift, 3 rotation, 3 zoom) using `scipy.optimize.least squares` to minimize the Mean Squared Error (MSE) between the normalized volumes. Once optimal parameters were computed, they were applied to both intensity and segmentation data.

The segmentation mask was transformed using nearest-neighbor interpolation to preserve discrete labels. We then computed the voxel retention of the tumor and applied a region growing algorithm seeded at the tumor's centroid to evaluate a semi-automatic segmentation strategy.

Implementation Highlights

- Registration: Translation, rotation (ZYX), and zoom optimized with least squares
- Interpolation: Linear for intensity; nearest-neighbor for segmentation
- Voxel Retention: Tumor went from 31,858 to 22,395 voxels (70.3)
- Region Growing: Implemented from transformed centroid with 0.05 tolerance
- Dice Score: Tumor vs. region growing: 0.278

Results

- Final shape of transformed image and segmentation: (53, 512, 512)
- Tumor region retained after transformation: 70.3
- Semi-automatic segmentation via region growing was partially successful
- The tumor's transformed centroid: [24.44, 82.94, 37.03]
- Visual overlays confirmed good alignment, with some margin loss in tumor edges.

Discussions

The results of this project provide several insights into the strengths and limitations of rigid registration and semi-automatic segmentation in a clinical imaging context. The rigid registration approach, although relatively simple compared to deformable methods, proved sufficient to align large anatomical structures like the liver. The use of centroid-based initialization and parameter bounds improved the robustness of optimization, ensuring convergence in a small number of iterations. Nonetheless, residual misalignment can still occur due to patient-specific anatomical variations or changes in acquisition protocols between scans.

The tumor voxel retention analysis revealed that most of the segmented tumor was preserved after applying the transformation, yet some partial loss was unavoidable due to interpolation and boundary truncation. While this 70.3 percent retention is acceptable in practical terms, it highlights the sensitivity of small regions to spatial operations. Padding was effective in mitigating this issue, but further improvements could involve post-registration refinement steps or deformable registration for finer alignment.

The region growing segmentation method, although intuitive and reproducible, performed poorly in this application, achieving a Dice score of only 0.278. This low overlap stems from the strong dependency of the algorithm on intensity homogeneity and the exact placement of the seed. In CT data, tumor regions often exhibit internal variability and partial volume effects, which cause region growing to either leak into healthy tissue or undersegment the tumor. Incorporating adaptive thresholds or pre-filtering techniques could improve the results, as would switching to supervised learning approaches for segmentation.

Finally, from a reproducibility perspective, the design of the pipeline prioritizes transparency and interpretability. All transformation steps were explicitly defined, and label-preserving operations ensured that medical annotations were not degraded. The modular design allows easy substitution of components, such as trying different cost functions or optimization strategies, making the project a solid foundation for future development.

Methodological Considerations and Limitations

While the rigid registration framework provided accurate anatomical alignment with minimal deformation, it inherently assumes that liver structures between reference and input volumes differ only by translation, rotation, and scale. This simplification excludes local deformations such as those caused by patient positioning, breathing motion, or pathological growth. As a result, minor mismatches—particularly near the organ boundaries—are expected, and more advanced deformable registration methods may be necessary for finer alignment.

In terms of segmentation, the reliance on a single-seed region growing algorithm introduces sensitivity to the seed

position and intensity thresholds. Although using the transformed centroid ensures anatomical consistency, the lack of adaptive thresholding or texture-aware criteria limits robustness. Tumor heterogeneity and low contrast against surrounding liver tissue further challenge intensity-based methods. Future iterations could explore hybrid models that incorporate prior anatomical knowledge or deep learning-based refinement to address these challenges.

Additionally, most transformations were applied using `scipy.ndimage` operations, which are fast but assume uniform voxel spacing and may not fully account for anisotropic resolution. Incorporating physical space transformations using DICOM spatial metadata could improve clinical accuracy. Despite these limitations, the chosen pipeline remains interpretable, reproducible, and suitable for exploratory medical image analysis.

Conclusions

This project successfully implemented a complete pipeline for rigid registration and semi-automatic segmentation of liver CT scans, integrating both anatomical alignment and tumor detection from DICOM datasets. Using centroid-based initialization and intensity-driven optimization, the registration step effectively aligned the input scan to a phantom reference, achieving a voxel-wise correspondence while preserving segmentation labels through nearest-neighbor interpolation. The final transformation retained 70.3 percent of the original tumor voxels, confirming that rigid alignment is a viable approach when handling relatively structured anatomical regions.

The semi-automatic segmentation stage, based on region growing from the transformed tumor centroid, offered a first approximation to unsupervised tumor detection. However, the resulting Dice similarity score of 0.278 reflects a significant mismatch between the generated mask and the

ground truth. This underlines the need for more robust segmentation strategies when working with low-contrast or heterogeneous tumor regions.

Overall, the project demonstrated how classical image processing techniques, when properly orchestrated, can still yield interpretable and meaningful results in the context of medical image analysis. While further improvement is possible—especially in the segmentation component—the modular design and transparent methodology provide a strong basis for refinement and extension in future work. The codebase is available at:

https://github.com/IrvingPU/Medical_Images_Project.git,

Supporting full reproducibility of all results presented.