

Diagnoses of Pulmonary Embolism from Non-Contrast 4DCT Using Image Processing-Derived Quantitative Perfusion Scores

Hsu-Ting Kuo,¹ Yi-Kuan Liu,¹ Girish Nair,² Danielle Turner-Lawrence,³ Lili Zhao,⁴ Craig Stevens,⁵ Jorge Cisneros¹, and Edward Castillo^{*,1,5}

¹ Department of Biomedical Engineering, The University of Texas at Austin, TX, USA, ² Department of Internal Medicine, William Beaumont University Hospital, Royal Oak, MI, USA,

³ Department of Emergency Medicine, William Beaumont University Hospital, Royal Oak, MI, USA, ⁴ Department of Biostatistics and Health Informatics, William Beaumont University Hospital, Royal Oak, MI, USA,

⁵ Department of Radiation Oncology, William Beaumont University Hospital, Royal Oak, MI, USA

Introduction

Chest computed tomography angiography (CTA) is the current gold standard for pulmonary embolism (PE) diagnosis (Fig. 1). However, patients with an allergy to iodinated contrast or renal insufficiency are often ineligible for CTA in the Emergency Department setting. For these cases, an alternative method for PE diagnosis based on non-contrast imaging is needed. CT-derived perfusion (CTP) is a novel image processing modality that employs mathematical modeling and scientific computing to quantify pulmonary perfusion from an inhale/exhale CT image pair acquired without contrast (4DCT). The resulting CT-P information can potentially be used to identify hypo-perfused regions associated with PE. In this study, we introduce a thresholding approach for identifying patients with PE on non-contrast 4DCT using lobar CTP measurements.

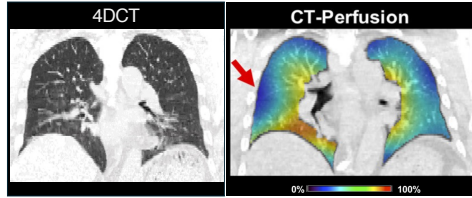


Figure 1. 4DCT scan and 4DCT-derived perfusion. For visualization, the intensity values within each image were converted to percentile values (color scale). The red arrows indicate a “wedge” perfusion defect in a region.

4DCT data

We conducted an Institutional Review Board-approved imaging trial with 129 patients at our institutional Emergency Center with suspected PE. Each patient received a CTA for PE diagnosis and a non-contrast 4DCT scan within 48 hours of the CTA acquisition.

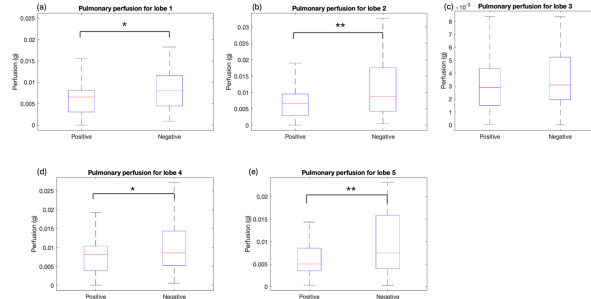


Figure 2. Boxplots of perfusion data for lobe 1 to 5. The medians of pulmonary perfusion in the 64 positive cases are lower than those in the 59 negative cases for each lobe. Statistical differences between the positive and negative groups were calculated using a two-sample t-test after the outliers were removed (11 cases for positive and negative respectively). P-values for Lobe 1 to 5 in graphs (a)-(e) are 0.027, 0.003, 0.352, 0.023, 0.007. *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$.

Methods

We removed 6 cases out of the 129 cases due to severe failure of the segmentation pipeline. 64 positive and 59 cases were used to train the model.

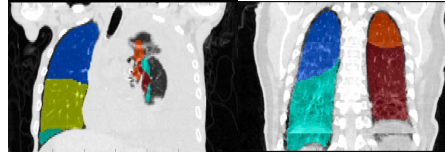


Figure 3. PE cases with segmentation failures. Our segmentation model failed on cases with lobectomy and significant artifacts.

Particle swarm optimization optimizes the threshold parameters for the lobes to minimize the loss function below:

$$Loss(T) = -\min\left(\frac{N_p^{predicted}}{N_p^{labeled}}, \frac{N_n^{predicted}}{N_n^{labeled}}\right) - 0.15 \times \frac{S_p}{N_p} + 0.15 \times \frac{S_n}{N_n}$$

The objective function will be used to evaluate the fitness of the solutions in this population, and if the value of the objective function for the validation set or the training set, whichever is greater, is smaller than -0.7, the optimization will stop, and the solutions in this population will be used as the optimal solutions.

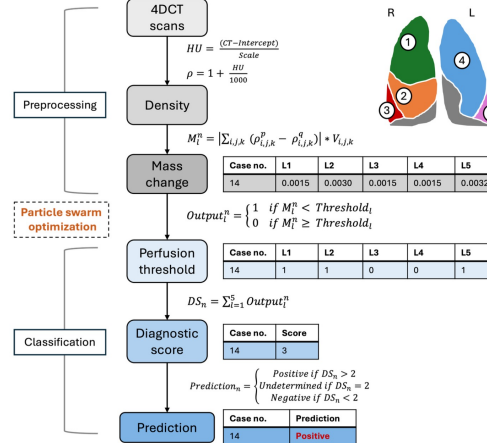


Figure 4. Overview of the model, including the preprocessing and classification parts.

L1-L5 denotes lobe 1 to lobe 5 as labeled in the top-right lung figure and case 14 was used as an example. We extracted the pulmonary per- fusion data from the 4DCT images by converting the CT numbers into density and further calculating the mass change in each lobe using the density. To classify the cases into positive and negative, we found the threshold for pulmonary perfusion in each lobe and used the thresholds to convert mass change data into a 1×5 binary matrix for each case. By summing up the binary matrix, we get the diagnostic score. Finally, we classified cases with a score > 2 as positive, < 2 as negative, and $= 2$ as inconclusive.

Results

Using LOOCV, our model achieved accuracy = 0.72, sensitivity = 0.75, and specificity = 0.69 with 17% inconclusive cases. Without allowing any inconclusive cases, the accuracy = 0.66 with sensitivity = 0.60 and specificity = 0.73 (Table 1). It was clearly shown that allowing cases to be inconclusive can in- crease the accuracy of our model prediction.

Table 1. Model performance. Sensitivity, specificity, and accuracy were evaluated on the test dataset. The inconclusive (Inc) rate was calculated on the training data during the optimization process.

	Sen	Spe	Acc	Inc (%)
W/o Inc	0.60	0.73	0.66	0
With Inc	0.75	0.69	0.72	17

Table 2. Average (Avg) and standard deviation (Stdev) of threshold values for each lobe over cross-validation runs. The standard deviation for each lobe is lower than 0.005, validating the robustness of the thresholds found using our optimization approach.

	L1	L2	L3	L4	L5
Avg	2.75E-3	1.23E-2	1.78E-3	9.93E-3	6.50E-3
Stdev	0.0041	0.0009	0.0005	0.0046	0.0008

Discussions and Conclusions

Strengths

- A diagnostic model with minimal complexity that enables accurate results with a small dataset.
- First PE diagnostic model based on non-contrast CT scans.

Limitations

- Lack of severe cases in the dataset.
- Complex 4DCT reconstruction, which created image artifacts.
- Highly effort dependent.

Future directions

- Breath-hold CT
- Focus more on improving the sensitivity of the model based on clinical needs.
- Animal models

In this study, we developed a 4DCT-based computational model that allows for accurate and rapid diagnosis of pulmonary embolism with a sensitivity of 0.75 and a specificity of 0.69 using only pulmonary perfusion. Our model optimizes the threshold for pulmonary perfusion in each lobe using Particle Swarm Optimization, converts pulmonary perfusion data into binary matrices, sums up the binary matrix for each case to generate a diagnostic score, and classifies each case while allowing some cases to be inconclusive.

Acknowledgments

4DCT data acquisition was funded through University of Michigan Fast Forward Medical Innovation's MTRAC for Life Sciences Innovation Hub, a partnership with University of Michigan Tech Transfer and the State of Michigan. This work was partially funded by 4DMedical, which develops respiratory imaging technologies for clinical and research use.