USING THREE-DIMENSIONAL MODELING TO ANALYZE VASCULAR CHANGES AROUND PRIMARY LUNG TUMORS

Siri Ravuri[1], Shruti Siva Kumar[2], Walter O'Dell[1]

[1]Departments of Radiation Oncology[1], and Biomedical Engineering[2], University of Florida, Gainesville, FL

BME RadOnc

MIACA Lab

University of Florida

I. INTRODUCTION

- Lung cancer is typically diagnosed once primary lung tumors are visible through CT and/or PET scans, and generally become more difficult to treat as the tumor growth progresses.
- This investigation is aimed at using three-dimensional modeling techniques to characterize changes in the vascular tree structures around primary lung tumors, including ratio of parent-child branch radii, vessel tortuosity, and bifurcation angles.
- Normalized ranges of a healthy patient will be used as a point of comparison for vascular disorders such as chronic pulmonary arterial hypertension (PAH) and changes in vascular structure around a growing tumor.
- This research has the potential to detect lung cancer earlier, to distinguish between active and benign disease, and further understand the vascular changes and vascular damage that occurs with the growth of primary lung tumors.

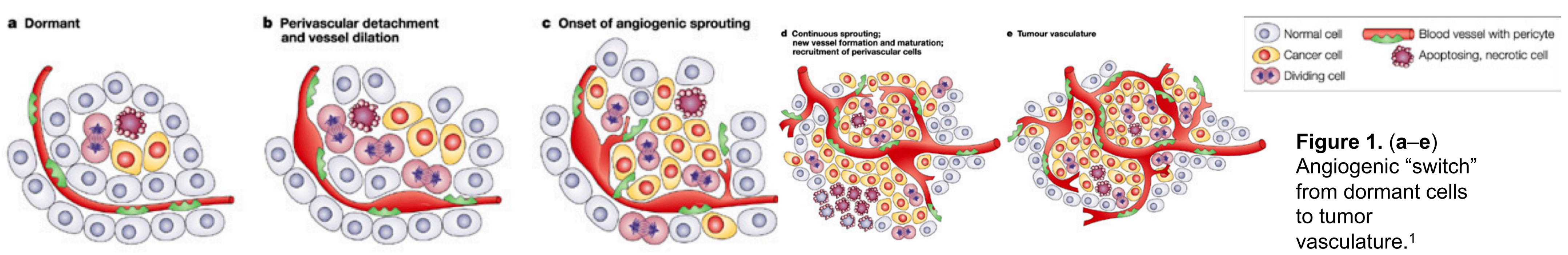


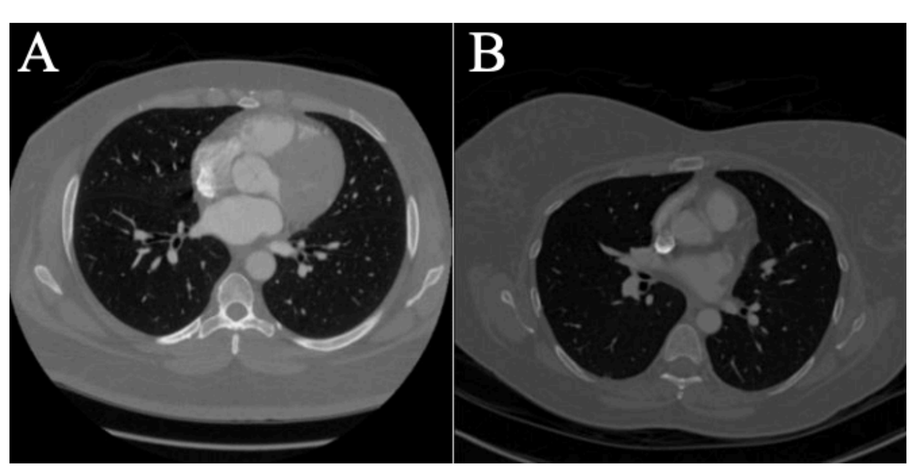
Figure 1. (a–e) Angiogenic "switch" from dormant cells to tumor vasculature.[1]

OBJECTIVE :
To use three-dimensional modelling to quantify and create an interactive environment through which researchers can study lung structure and identify early markers of vascular change, particularly around developing lung tumours.

II.METHODOLOGY: IMAGING AND SEGMENTATION

IMAGE ACQUISITION

- Multiple patient CT scans are being used to analyze various vascular properties.
- The control, healthy adult dataset was supplied by Dr. Ender Finol from the University of Texas in San Antonio.
- The datasets of primary lung tumors are supplied by patients enrolled in an on-going IRB approved study.
- Chest CTs of breast cancer patients with metastases to the lung are being gathered under a 2nd IRB approved study.



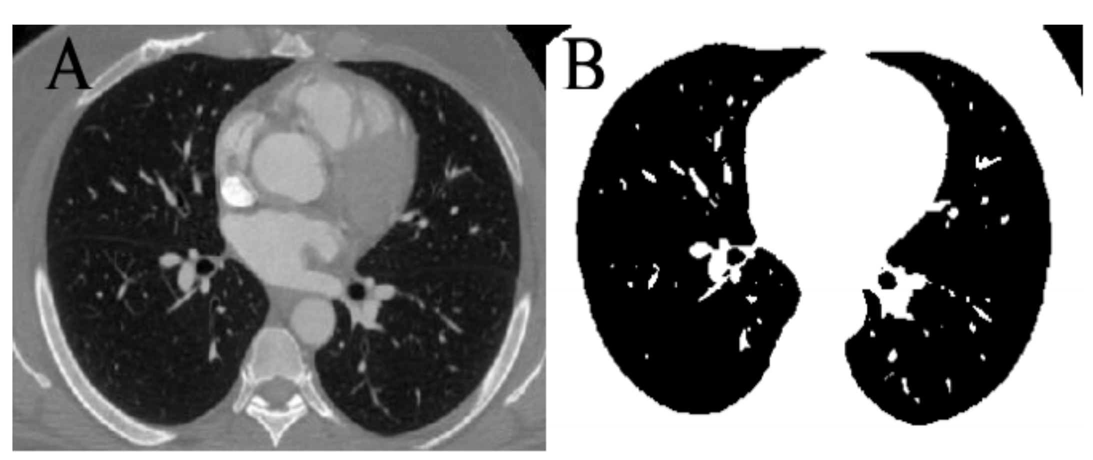


Figure 1 CT scans from [A] healthy controls and [B] a patient with primary lung cancer. **Figure 2** [A] Original image cropped to chest. [B] Lungs segmented using thresholding

LUNG VESSEL SEGMENTATION

- In-house software built upon the NIH ImageJ platform was used first to segment the lung volumes from the CT datasets. This is completed by cropping the images to the chest region and using thresholding to isolate the necessary parts of the image.
- Thresholding removes unnecessary elements or sorts for specific parts of an image by setting parameters that the pixel or voxel (3-D pixel) must meet to be kept and/or identified.[2]
- A semi-automatic, snake-based approach is used to isolate the hilar region from the CT scans.
- The vascular structures are segmented using a region-growing method starting from a manually-selected seed point.
- The tree structure is traversed and labeled, extracting for each branch its length, radius, tortuosity, bifurcation angles, etc.[3]
- The tree structure can then be mathematically modeled in 3D for more accurate estimates of each branch parameter.[4]
- The branch parameter values around each tumor or benign nodule were compared to that from the contralateral hemi-lung of the same patient, or from the healthy volunteer.

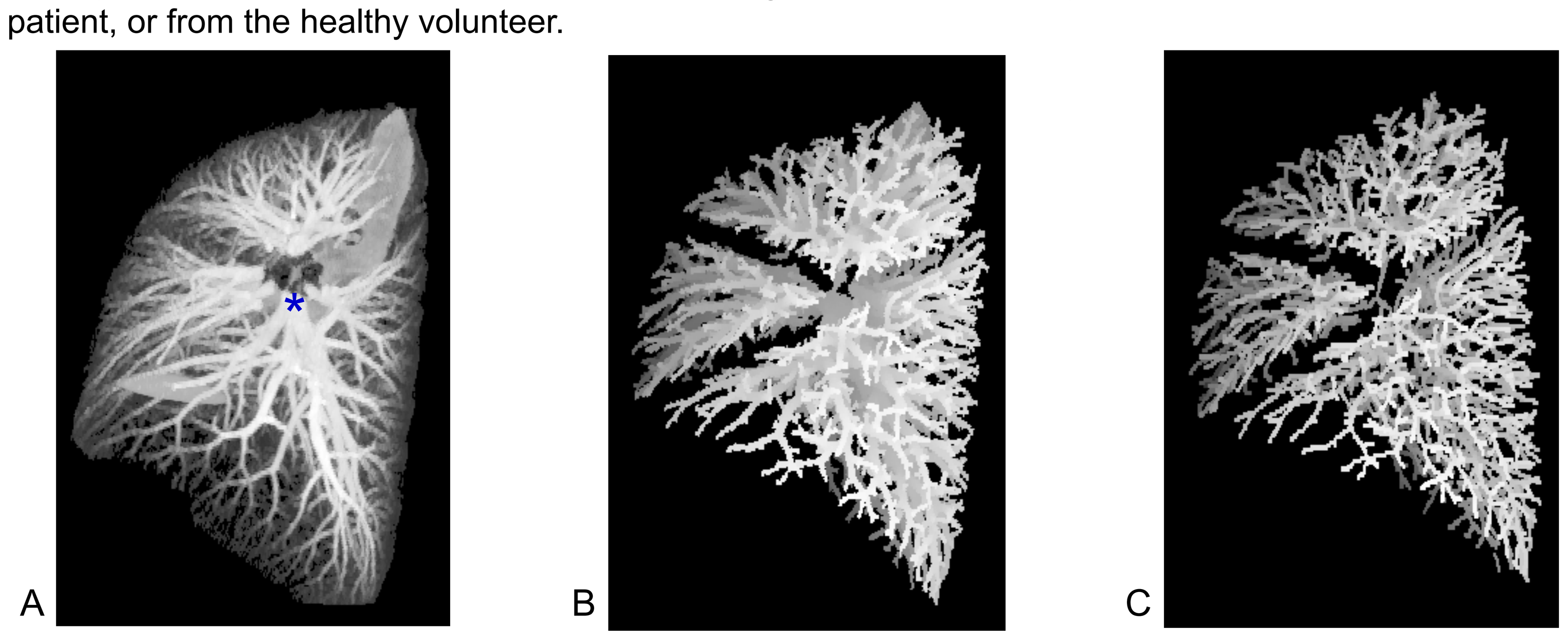


Figure 3: [A] The lung volume mask applied to the 3D CT dataset shows primarily the lung vessels. [B] Seeded region growing from the blue star in [A] extracts just the connected vascular components. [C] Skeletonization of the vascular tree then permits the evaluation of the tree structure.

III. RESULTS

ANALYSIS OF VASCULAR CHARACTERISTICS

- The final set of methods used in this investigation were created for analytical purposes.
- There are many different vascular properties in the lungs that have not been studied in-depth since the 1970s.[5]
- The main features that were analyzed include the average tortuosity, angle bifurcation, and ratio of parent to child branch radius.

RESULTS

- A comparison of the tumor-encompassed vessel tree versus the control vessel tree using the radius to tortuosity correlation was made.
- A Mann-Whitney U Test/Wilcoxon rank sum test for significant was conducted.
- A significant difference (p-value < 0.001) between the average tortuosity in each bin for the vessels with a radius between 0 and 3 mm.

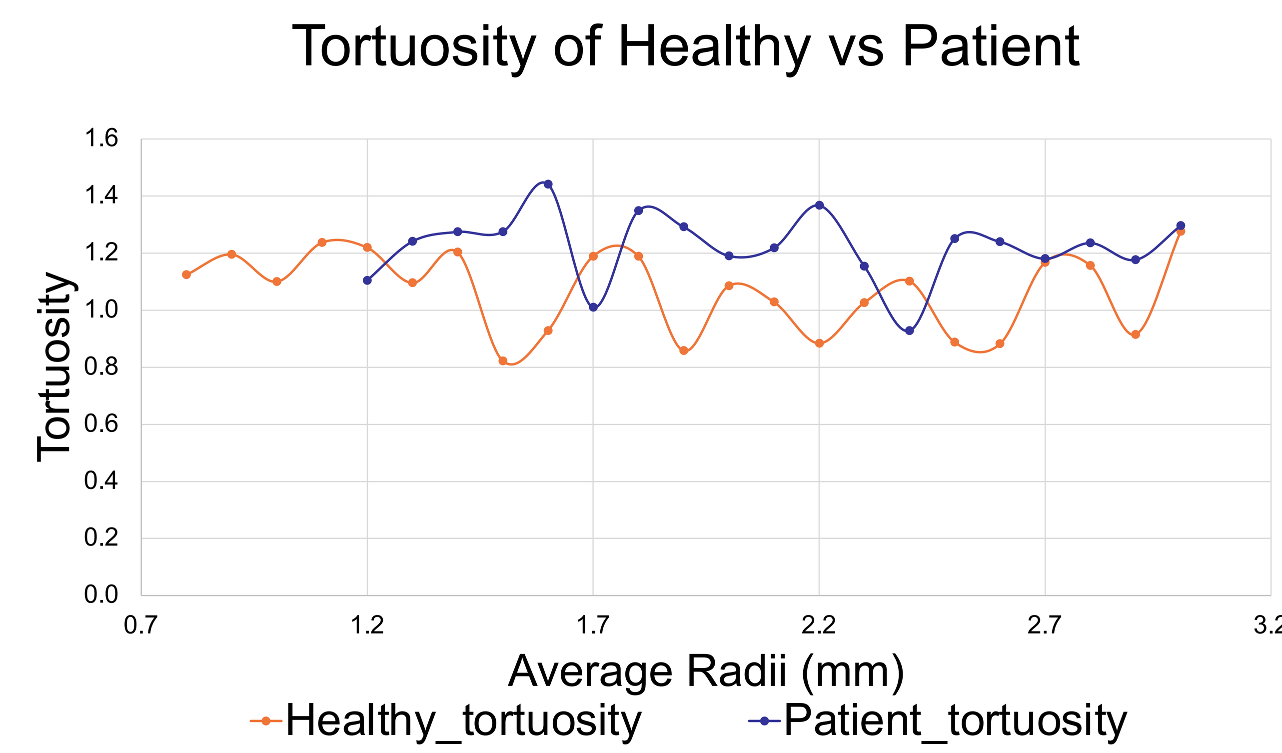


Figure 4: Distribution of the tortuosity in relation to the average radii in mm of the healthy lung and patient lung. Tortuosity is measured as the distance along the vessel centerline divided by the distance between the vessel endpoints.

IV. DISCUSSION and CONCLUSION

- I have demonstrated the ability to quantify vascular tree architecture in human subjects with potential to measure abnormal architecture in lungs with developing tumors.
- The immediate next step is to apply these methods to local regions around a suspected tumor to test whether changes in vascular architecture are present and observable.
- Future work will apply this analysis using sub-trees of varying size to find the most discriminating size scale.
- An analysis of the effects of imaging parameters (CT slice thickness, in-plane pixel dimensions) will also be conducted to calibrated the vascular metrics across scans (See Poster #1647).
- A study of patients with lung tumors will also be made by comparing a healthy hemi-lung vs a hemi-lung with a tumor.
- We will then compare vascular changes in a larger cohort that includes benign nodules, and lesions from different primary and metastatic tumor types.

IV. REFERENCES

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