

2018 IEEE VIP-CUP

2018 IEEE Video and Image Processing Cup “Lung Cancer Radiomics”

Supported by:

**IEEE Signal Processing Society (SPS)
Concordia Institute for Information System Engineering (CIISE), Concordia University
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Intelligent Signal & Information Processing (I-SIP) Lab**

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2018 IEEE Video and Image Processing (VIP) Cup: Lung Cancer Radiomics

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INTRODUCTION

The volume, variety, and velocity of medical imaging data generated for medical diagnosis are exploding. Interpretation of such large amount of diagnostic images, however, highly depends on the experience of the radiologist can be extremely time-consuming. Referred to as Radiomics, the ability to process such large amounts of data promises to decipher the un-decoded information within medical images; Develop predictive and prognosis models to design personalized diagnosis; Allow comprehensive study of tumor phenotype, and; Assess tissue heterogeneity for diagnosis of different type of cancers. More specifically, Radiomics refers to the process of extracting and analyzing several features (e.g., attenuation, shape, size, and location) from medical images with the ultimate goal of obtaining predictive or prognostic models. Segmentation and prediction are considered as critical steps among different processing tasks within the Radiomics pipeline, and are the focus of this competition. The 2018 VIP-CUP challenge is on segmentation and prediction of Lung Cancer Tumor region via screening Computed Tomography (CT) scans. Images from several patients along with the annotations will be provided for training and validation purposes. The evaluation will be performed based on test sets provided closer to the submission deadline.

PARTICIPATION GUIDELINES

Teams satisfying the eligibility criteria outlined below, are invited to participate in the VIP-CUP. Detailed competition instructions together with the data sources will be provided at <https://users.encs.concordia.ca/i-sip/2018VIP-Cup>.

Eligibility Criteria: Each team must be composed of: (i) One faculty member (the Supervisor); (ii) At most one graduate student (the Tutor), and; (iii) At least three but no more than ten undergraduates. At least three of the undergraduate team members must be either IEEE Signal Processing Society (SPS) members or SPS student members. Postdocs and research associates are not considered as faculty members. A graduate student is a student having earned at least a 4-year University degree at the time of submission. An undergraduate student is a student without a 4-year degree. Questions about the 2018 VIP-CUP should be directed to Dr. Arash Mohammadi.

- **Eligibility of 3rd and 4th-year Undergraduate Students:** All undergraduate students are eligible to participate in the VIP-Cup. They do not have to be in the first two years of their program.
- **Eligibility of 1st and 2nd-year Masters Students whose Bachelor's degree was 3 years:** First and second-year Master's students are eligible to act a graduate student member of a team, but not as an undergraduate member (regardless of the duration of their bachelor's degree). A team may have at most one graduate student member. Furthermore, graduate students are expected to act as tutors for the team, not as primary participants.

Since the VIP-Cup is an undergraduate oriented competition, Master's students are not eligible to participate as regular team members, only as graduate student mentors/tutors.

- **Eligibility of Students in a 5-year program that will culminate in a Master's degree:** Students who do not hold a bachelors and are in their 4th year of a 5-year program that will culminate in a master's degree are eligible to participate in the VIP-Cup as regular undergraduate team members.

ENROLLING IN THE PIAZZA INTERACTIVE PAGE

Please join the VIPCUP2018 page created on the Piazza to interact with organizing committee members; ask questions, and; access supporting documents. Below are the steps to join the Piazza page:

- Go to <https://piazza.com>
- Click the “Sing Up” tab on the top left corner of the page, and select “Students Get Stared”
- In the “Search Schools:” type in “IEEE SPS” and select the pop-up option.
- Select **Summer 2018** term.
- In Class 1 tab:
 - Write “VIPCUP2018: IEEE Video and Image Processing (VIP) Cup 2018”
 - Password is “sps007”.
 - Select “Join as: Student”.
 - Click on Join the Class.
- Proceed with signing up to get access to the VIP-CUP Piazza page

TENTATIVE SCHEDULE

Competition Webpage & Preliminary Info:	May 1st, 2018	Results Submission:	August 28th, 2018
Data are Available Online:	May 25th, 2018	Finalist Teams Announced:	September 8th, 2018
Team registration on IEEE VIP-Cup:	July 15, 2018	VIP Cup at ICIP in Athens:	October 7th, 2018
Test Data Will be Released:	August 14, 2018		

1 Radiomics Segmentation Challenge

The volume, variety, and velocity of medical imaging data is exploding, making it impractical for clinicians to properly utilize the available information resources in an efficient fashion. At the same time, interpretation of such large amount of medical imaging data by humans is significantly error prone reducing the possibility of extracting informative data. The ability to process such large amounts of data promises to decipher the un-decoded information within medical images; Develop predictive and prognosis models to design personalized diagnosis; Allow comprehensive study of tumor phenotype, and; Assess tissue heterogeneity for diagnosis of different type of cancers. Recently, there has been a great surge of interest on Radiomics, which refers to the process of extracting and analyzing several semi-quantitative (e.g., attenuation, shape, size, and location) and quantitative features (e.g., wavelet decomposition, histogram, and gray-level intensity) from medical images with the ultimate goal of obtaining predictive or prognostic models. Radiomics workflow, typically, consists of the following four main processing tasks:

- (i) Image acquisition/modality;
- (ii) Image segmentation;
- (iii) Feature extraction and qualification, and;
- (iv) Statistical analysis and model building.

The Radiomics features can be extracted from different imaging modalities including Magnetic Resonance Imaging (MRI); Positron Emission Tomography (PET), and; Computed Tomography (CT). Among these imaging modalities, the CT is the most used because of its imaging sensitivity, high resolution and isotropic acquisition in locating the lung lesions.

The 2018 IEEE VIP-CUP consists of the following Task:

Segmentation of Tumor region in Lung CT Images, is the initial task of the 2018 VIP-Cup challenge. *Segmentation* (i.e., providing contour or bounding box) and *Localization* (i.e., a class label is supposed to be assigned to each pixel) are considered as the critical step within the Radiomics workflow, as typically Radiomics features are extracted from segmented sections. Although, manual delineation of the gross tumour is the conventional (standard) clinical approach, it is time consuming and extensively sensitive to inter-observer variability. Automatic and semi-automatic segmentation methods together with their ability to minimize manual error and increase consistency of delineating regions are of paramount importance. In recent years, different tumor segmentation methods have been proposed, which can be categorized generally as follows:

- Thresholding Methods;
- Histogram-based Methodologies;
- Active contours;
- Morphological Methods;
- Deformable Models;
- Clustering approaches;
- Graph-cut Mechanisms;
- Markov Random fields, and;
- Neural Networks and Deep Networks.

2 Dataset

The challenge dataset contains images from non-small cell lung cancer (NSCLC) subjects selected from NSCLC-Radiomics dataset [1, 2] provided by The Cancer Imaging Archive (TCIA) [3]. The first training data consist of pre-treatment CT scans from 100 subjects, together with manual delineation by a radiation oncologist of the 3D volume of the gross tumor volume. Fig 1 illustrates an example of CT images of lung cancer patients with tumor contours. Test data will be realised, on a later date, including unseen CT images without inclusion of the annotations. Please also consider the following further comments:

- Consider 2D segmentation problem, however, the information from neighbouring slices can be used too.
- The final training set consists of 260 subjects with all slices.
- There are 2 set of initial training datasets:

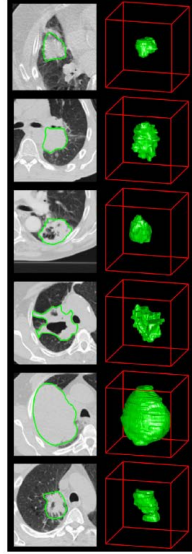


Figure 1: Example computed tomography (CT) images of lung cancer patients. CT images with tumour contours [2].

- (i) 100 subjects with all slices, and;
 - (ii) A selected set of subjects with tumor only slices.
- Use folder names including "PatientID" as an identifier for each subject, e.g., "LUNG1-001".
 - Annotations are provided through an extra DICOM file for each patient (Each patient folder has two subfolders. One including the original images and one including the annotations). By reading the annotation DICOM file you have access to an attribute called "contour data" that consists of contour points for tumors.
 - To view the RTSTRUCT segmentation on top of the images (visualize RTSTRUCT files over the CT scan) you can use the following two options:
 - *Dicompyler*: An open-source platform that can visualize DICOM images and their segmentations; <http://www.dicompyler.com/>.
 - *Slicer*: Another open-source platform that can visualize DICOM images and their segmentations. This software can also provide reconstruction of other angles (for further understandings); <https://www.slicer.org/>.

3 Evaluation Criteria

The segmented contours provided by the competitors will be compared against the manual contours for all test images using evaluation metrics similar to the following ones.

C1- Dice Coefficient: This is a measure of relative overlap, where 1 represents perfect agreement and 0 represents no overlap.

$$\text{Evaluation Criteria 1: } D = \frac{2|X \cap Y|}{|X| + |Y|}, \quad (1)$$

where \cap denotes the intersection operator, X and Y are the ground truth and test regions. Please note that dice coefficient (D) has a restricted range of $[0, 1]$. As recommended in literature of image validation, a good overlap occurs when $D > 0.700$. Please consider the following two conventions in computation of Dice coefficient: (i) For True-Negative (i.e., there is no tumor and the processing algorithm correctly detected the absence of the tumor), the dice coefficient would be 1, and; (ii) For False-Positive (i.e., there is no tumor but the processing algorithm mistakenly segmented the tumor), the dice coefficient would be 0.

C2- Mean surface distance: The directed average Hausdorff measure is the average distance of a point in X to its closest point in Y , i.e.,

$$\vec{d}_{H,\text{avg}}(X, Y) = \frac{1}{|X|} \sum_{x \in X} \min_{y \in Y} d(x, y). \quad (2)$$

The (undirected) average Hausdorff measure is the average of the two directed average Hausdorff measures given by

$$\text{Evaluation Criteria 2: } d_{H,\text{avg}}(X, Y) = \frac{\vec{d}_{H,\text{avg}}(X, Y) + \vec{d}_{H,\text{avg}}(Y, X)}{2} \quad (3)$$

C3- Hausdorff distance (95% Hausdorff distance): The directed percent Hausdorff measure, for a percentile r , is the r th percentile distance over all distances from points in X to their closest point in Y . For example, the directed 95% Hausdorff distance is the point in X with distance to its closest point in Y is greater or equal to exactly 95% of the other points in X . In mathematical terms, denoting the r th percentile as K_r , this is given by

$$\vec{d}_{H,r}(X, Y) = K_r \left(\min_{y \in Y} d(x, y) \right) \forall x \in X \quad (4)$$

The (undirected) percent Hausdorff measure is defined again with the mean:

$$\text{Evaluation Criteria 3: } d_{H,r}(X, Y) = \frac{\vec{d}_{H,r}(X, Y) + \vec{d}_{H,r}(Y, X)}{2} \quad (5)$$

4 Final Submission Guidelines

The final datasets that are provided for training, validation and test purposes are included in the Database folder of the VIP-CUP, and are as follows:

- **Training Dataset:** The 260 subjects that are included in the folder entitled “VIP_CUP18_TrainingData” are intended to be used for training purposes. The labels (RTStruct files) for these patients are provided.
- **Validation Dataset:** The 40 subjects that are included in the folder entitled “VIP_CUP18_ValidationData,” are intended to be used for validation purposes, i.e., each team provides a CSV file presenting their results for these 40 subjects.
 - The labels (RTStruct files) for these patients are provided, therefore, each team can evaluate their algorithms and report the results.
 - The validation data should not be used for the training purposes.
- **Test Dataset:** The 40 subjects that are included in the folder entitled “VIP_CUP18_TestData,” are intended to be used for test purposes.
 - The labels (RTStruct files) for these patients are NOT provided.
 - For the 40 test subjects, as the true labels are not available, each team needs to provide the segmentation results in Binary Image format.
 - The Test data should not be used for the training purposes.

IMPORTANT: The final datasets provided for training, validation, and test purposes have several different annotations other than the tumor ones targeted in the VIP-CUP. To access the tumor annotation, the address to tumor contour is as follows:

ROIContourSequence -- > Item_2 -- > ContourSequence -- > Item_ (slice number) -- > ContourData

SUBMISSION PACKAGE: Each team must submit a “.zip” package including 4 main items as specified in Fig. 2.

- The submitted package needs to be in “.zip” format and named as follows:

“VIP_CUP” + “underscore” + “TeamName”.zip (for example, VIP_CUP_ TeamA.zip)
- The name Must be one word (NO spaces) or separated with underscores (.).
- The name of each of the four components should start with the “TeamName” as shown in Fig. 2. For example, the submitted package for “TeamA”, will include the following 4 items: TeamA.exe; TeamA.zip; TeamA.csv, and; TeamA.pdf.

The specification of each of the 4 required components is outlined below:

1. Code Executable: The executable file (e.g., “TeamA.exe”) must be prepared based on the following instructions:

- The executable file must take as an input the path to the “test-directory-folder” which contains all patient folders that are to be analyzed.
- The “test-directory-folder” could be “VIP_CUP18_ValidationData” or “VIP_CUP18_TestData” or any other folder which has similar contents (with different folder names).
- The “test-directory-folder” will only contain patient folders.

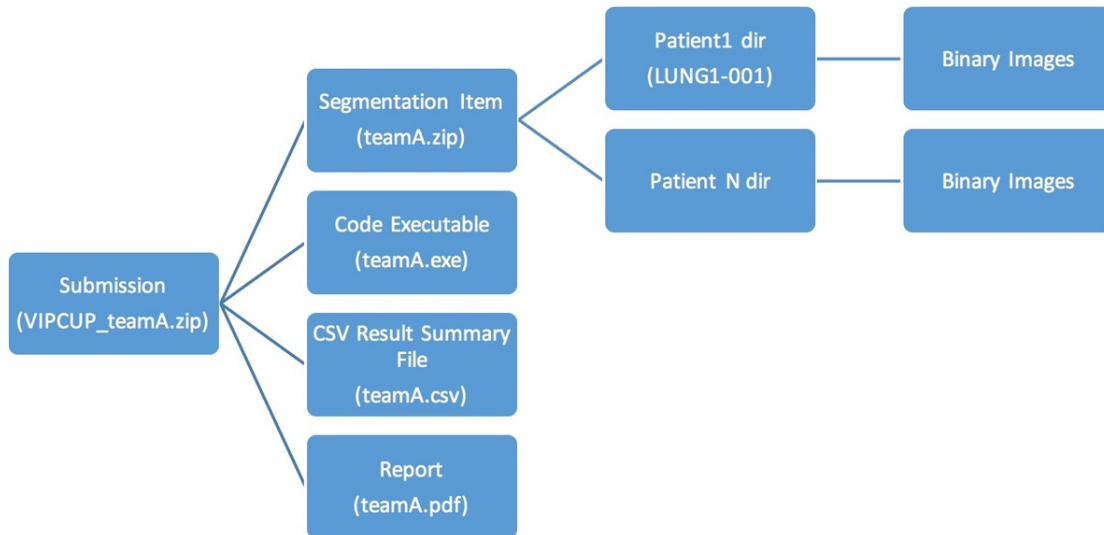


Figure 2: Different items that must be included in the final submission package as a “.zip” file.

PATIENT ID	CRITERIA 1 results	CRITERIA 2 results	CRITERIA 3 results
LUNG1-001			
....			
LUNG1 N			

Figure 3: An example of the submitted CVS result file.

- If the patient folders within “test-directory-folder” do have the associated labels (RTStruct files), then the output of the executable should create the CSV file containing all results (as specified below). For instance, if as the input to the executable file, we provide the path to the “VIP_CUP18.ValidationData” folder, the output should be a CSV file exactly similar to the submitted one.
 - If the provided patient folders do not have any labels (RTStruct files), then the executable should return a folder containing all patient folders where in each folder segmentation results are presented as Binary images. For instance, if as the input to the executable file, we provide the path to the “VIP_CUP18.TestData” folder which does not include labels, the output should be segmentation results exactly similar to the ones included for instance in the “TeamA.zip”.
- 2. CSV File:** The “CSV” file provides the final evaluation results based on the three identified criteria (i.e., Eqs. 1, 3, and 5) over **The Validation Data Set** (i.e., the 40 subjects included in the “VIP_CUP18.ValidationData” folder for which the labels (RTStruct files) are provided). The CSV file included in the submission package must be prepared based on the following specifications:
- The CSV file needs to provide the results for all the 40 subjects provided in the “VIP-CUP18-ValidationData” based on the three identified criteria (i.e., Eqs. 1, 3, and 5).
 - For each subject report the average value of each criteria for all of tat patient’s slices.
 - The CSV file contents need to be similar to the example provided in Fig. 3. Please note the first row describing the content of the columns should not be in your submitted CSV file. It is intended only for clarification purposes.
- 3. Segmentation File:** This item (e.g., “TeamA.zip”) provides the segmentation results for **The Test Data Set** (i.e., the 40 subjects included in the “VIP-CUP18-TestData” folder for which the labels (RTStruct files) are not provided). This segmentation file must be prepared based on the following specifications, for ease of reference we use for example “TeamA.zip” file:
- The “TeamA.zip” file must contain the Binary images in “.png” format and of the same resolution (size) as that of the input images.

- The “TeamA.zip” needs to have 40 folders named exactly the same as the folders in the “VIP-CUP18-TestData” folder.
- Each folder within the “TeamA.zip” needs to have binary images for all the slices provided for that specific patient.

4. Report: The report should be similar to an IEEE conference paper providing: (i) Required background; (ii) Any signal processing and pre-processing algorithms used; (iii) Information regarding the algorithms used to perform the segmentation tasks; (iv) Explicitly provide details on other data sources, trained models, and/or similar items (if any) that is/are used for training purposes; (v) Potential novelties of the processing algorithms, and; (vi) Presents and discuss the evaluation results.

- The report file needs to be in PDF format
- The report file needs to be prepared based on IEEE templates in “double-column”, “single-spaced” format. IEEE - Manuscript Templates for Conference Proceedings can be downloaded from the following link:
<https://www.ieee.org/conferences/publishing/templates.html>
- The report file is limited to 6 pages.

References

- [1] Aerts, Hugo J. W. L., Rios Velazquez, Emmanuel, Leijenaar, Ralph T. H., Parmar, Chintan, Grossmann, Patrick, Carvalho, Sara, Lambin, Philippe, “Data From NSCLC-Radiomics,” *The Cancer Imaging Archive*, 2015.
- [2] Aerts, H. J. W. L., Velazquez, E. R., Leijenaar, R. T. H., Parmar, C., Grossmann, P., Cavalho, S., Lambin, P., “Decoding Tumour Phenotype by Noninvasive Imaging using a Quantitative Radiomics Approach,” *Nature Communications*, Nature Publishing Group, 2014.
- [3] “The Cancer Imaging Archive (TCIA),” <http://www.cancerimagingarchive.net/>.