QIN Segmentation Challenge Dry Run Status

Update 10/9/2012

Jayashree Kalpathy-Cramer

Purpose

Task: CT-based lung nodule segmentation

Evaluate algorithms

Accuracy, stability, user interaction

Dry-run Goals

Run through entire pipeline (identify data, make available for distribution, download data, segment, submit segmentation results, compare, statistics)

Support for different annotation formats

Datasets

FDA phantom (single study, 2 nodules of interest)

Known size, shape and location (no mask)

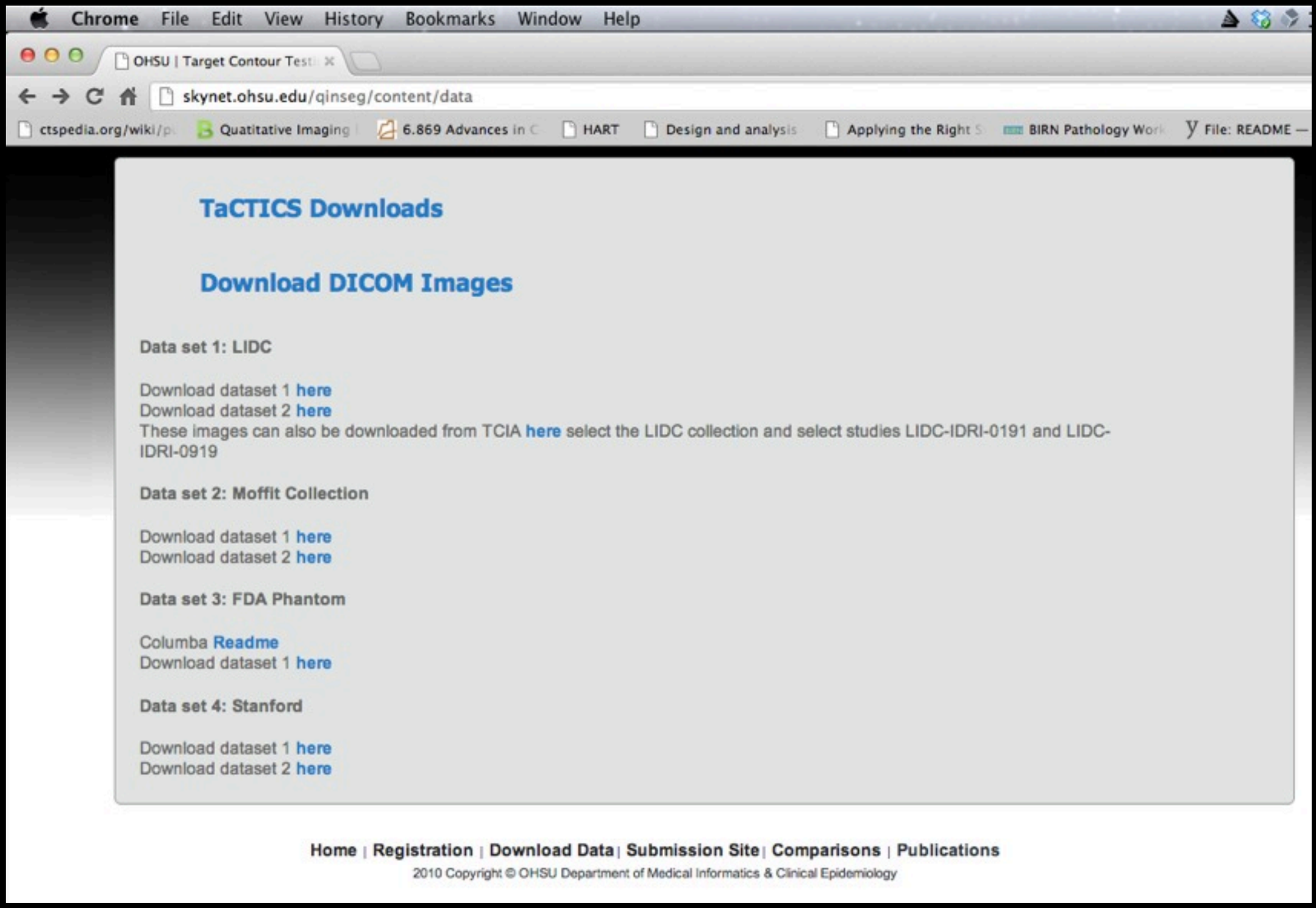
LIDC (2 studies with 1 nodule each (>3mm))

4 manual annotations (contour points)

Moffitt (2 studies with 1 nodule of interest each)

Stanford (2 studies with 1 nodule of interest each)

Raw Data Also Available At...

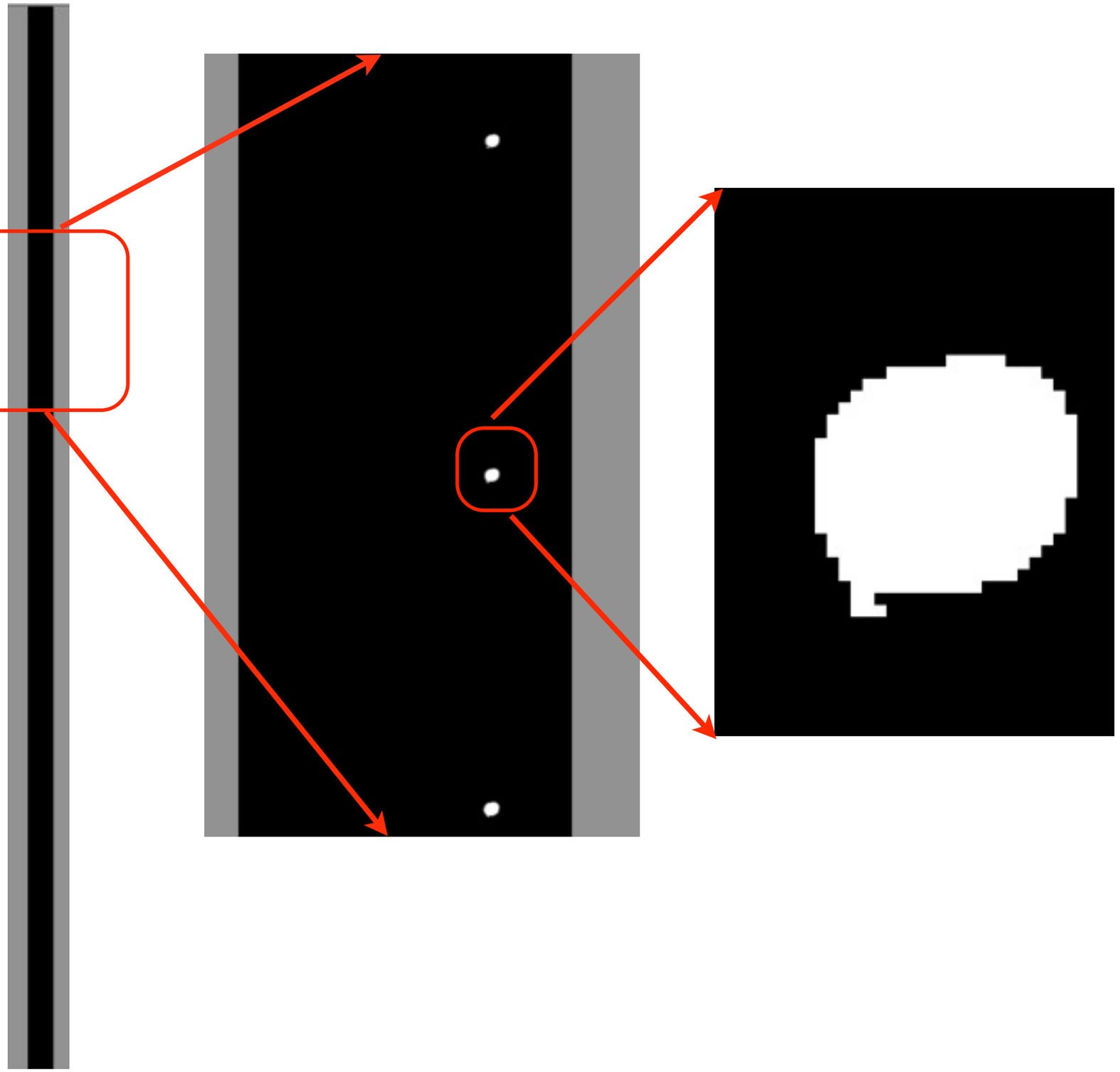


http://skynet.ohsu.edu/qinseg/content/data

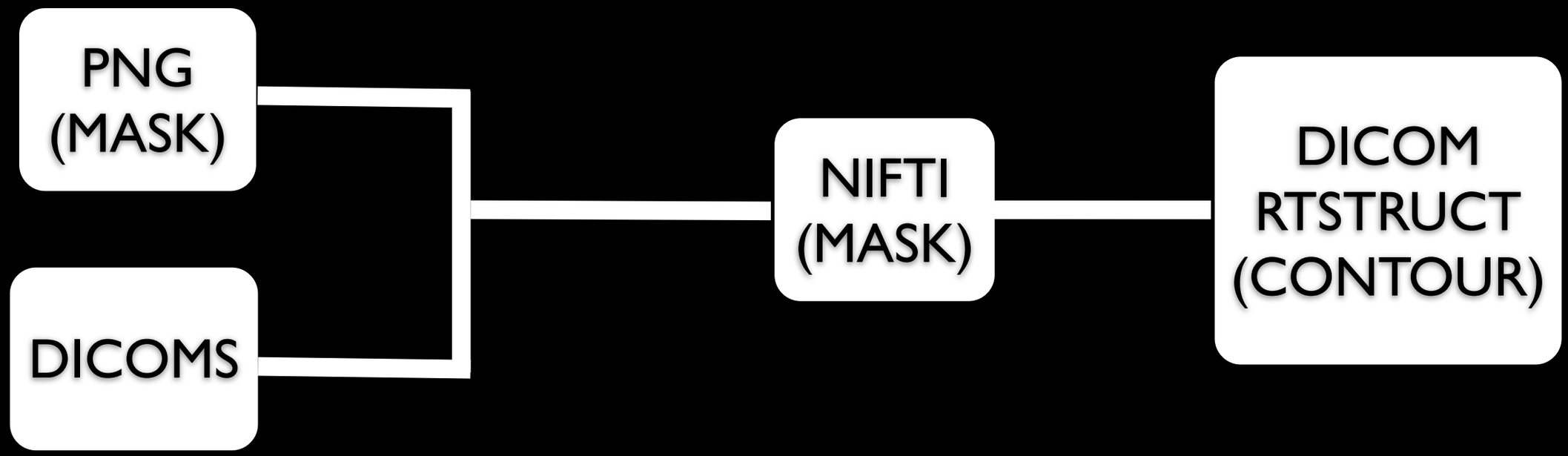
Segmentation Formats

Moffitt and Columbia

Single PNG file (stacked)



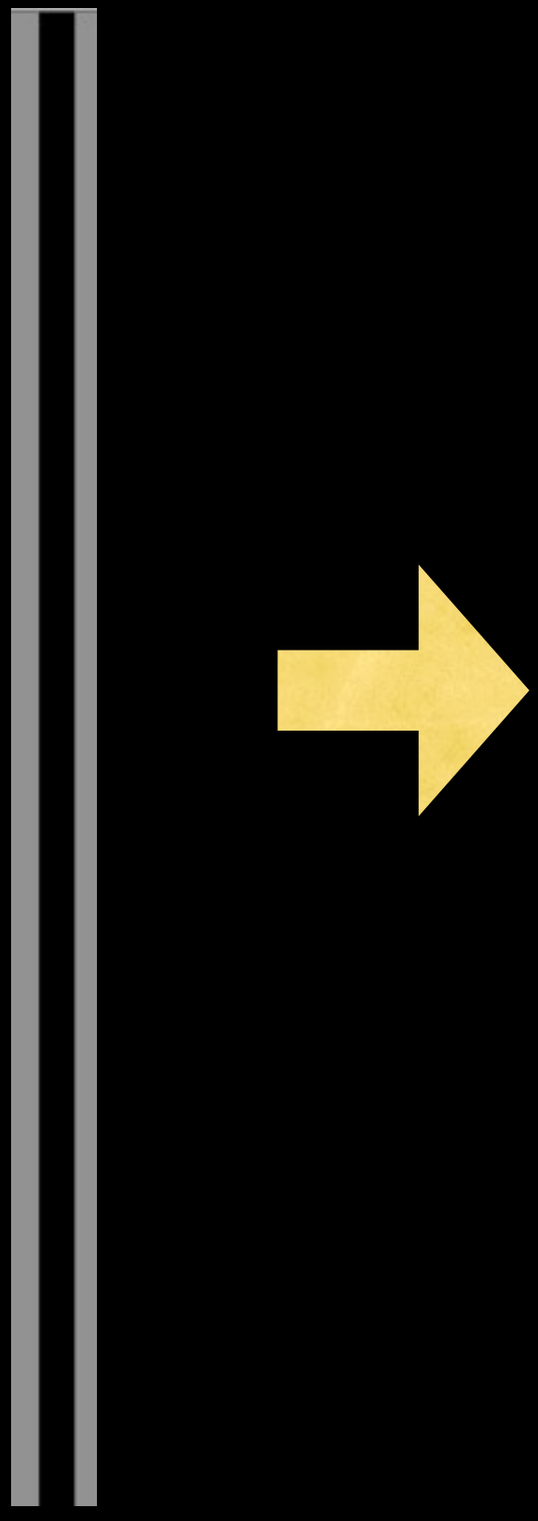
Conversion Script

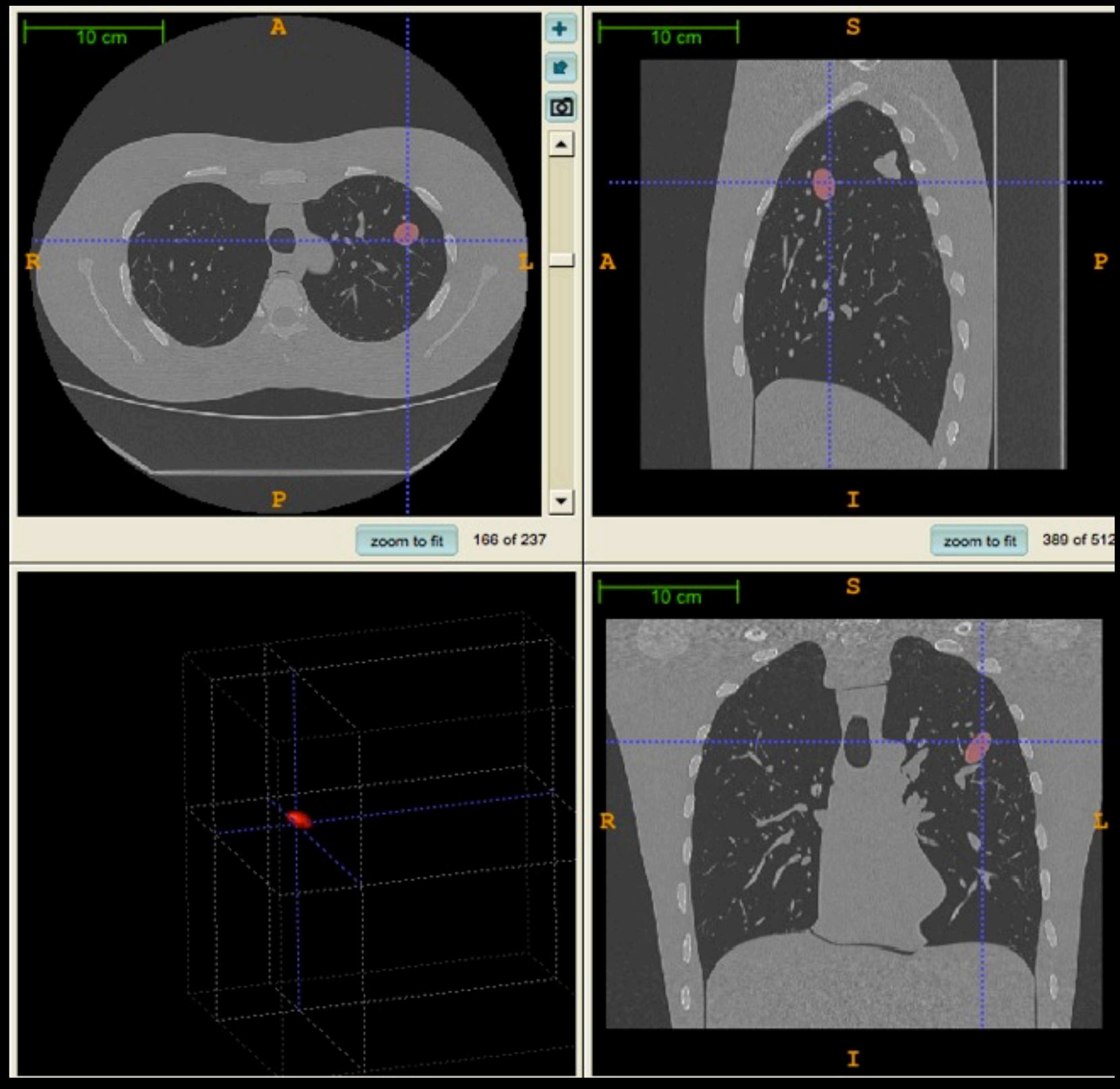


MATLAB C++

Ruby

Output Mask




10 cm
A
R
L
P
zoom to fit
166 of 237
10 cm
S
A
P
I
zoom to fit
389 of 512
10 cm
S
R
L
I

LIDC XML format

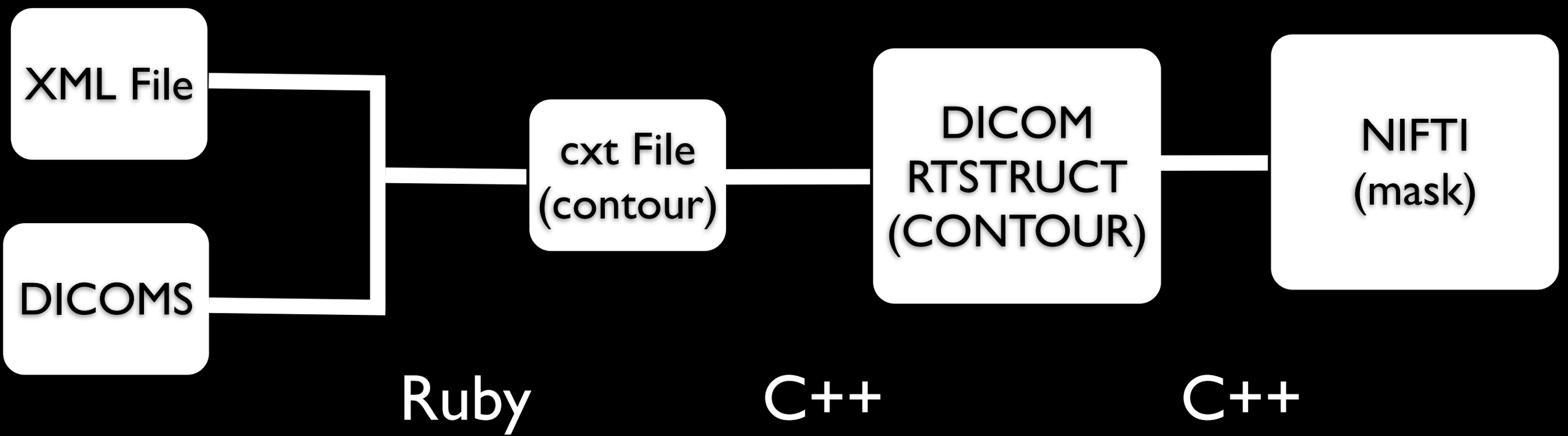
```
<?xml version="1.0" encoding="UTF-8"?>
<LidcReadMessage uid="1.3.6.1.4.1.14519.5.2.1.6279.6001.1307390644735.0" xmlns="http://www.nih.gov" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
xsi:schemaLocation="http://www.nih.gov  http://troll.rad.med.umich.edu/lidc/LidcReadMessage.xsd">
<ResponseHeader>
    <Version>1.8</Version>
    <MessageId>NIH179</MessageId>
        <DateRequest>2006-02-16</DateRequest>
        <TimeRequest>00:00:00</TimeRequest>
    <RequestingSite>removed</RequestingSite>
    <ServicingSite>removed</ServicingSite>
    <TaskDescription>Second unblinded read</TaskDescription>
    <CtImageFile>removed</CtImageFile>
    <SeriesInstanceUid>1.3.6.1.4.1.14519.5.2.1.6279.6001.2353649787
    <DateService>2008-08-29</DateService>
    <TimeService>13:13:05</TimeService>
<ResponseDescription>1 - Reading complete</ResponseDescription>
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```

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    <readingSession>
        <annotationVersion>3.12</annotationVersion>
        <servicingRadiologistID>anon</servicingRadiolo
        <unblindedReadNodule>...
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        <unblindedReadNodule>...
        <unblindedReadNodule>...
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    <nonNodule>...
</readingSession>
```

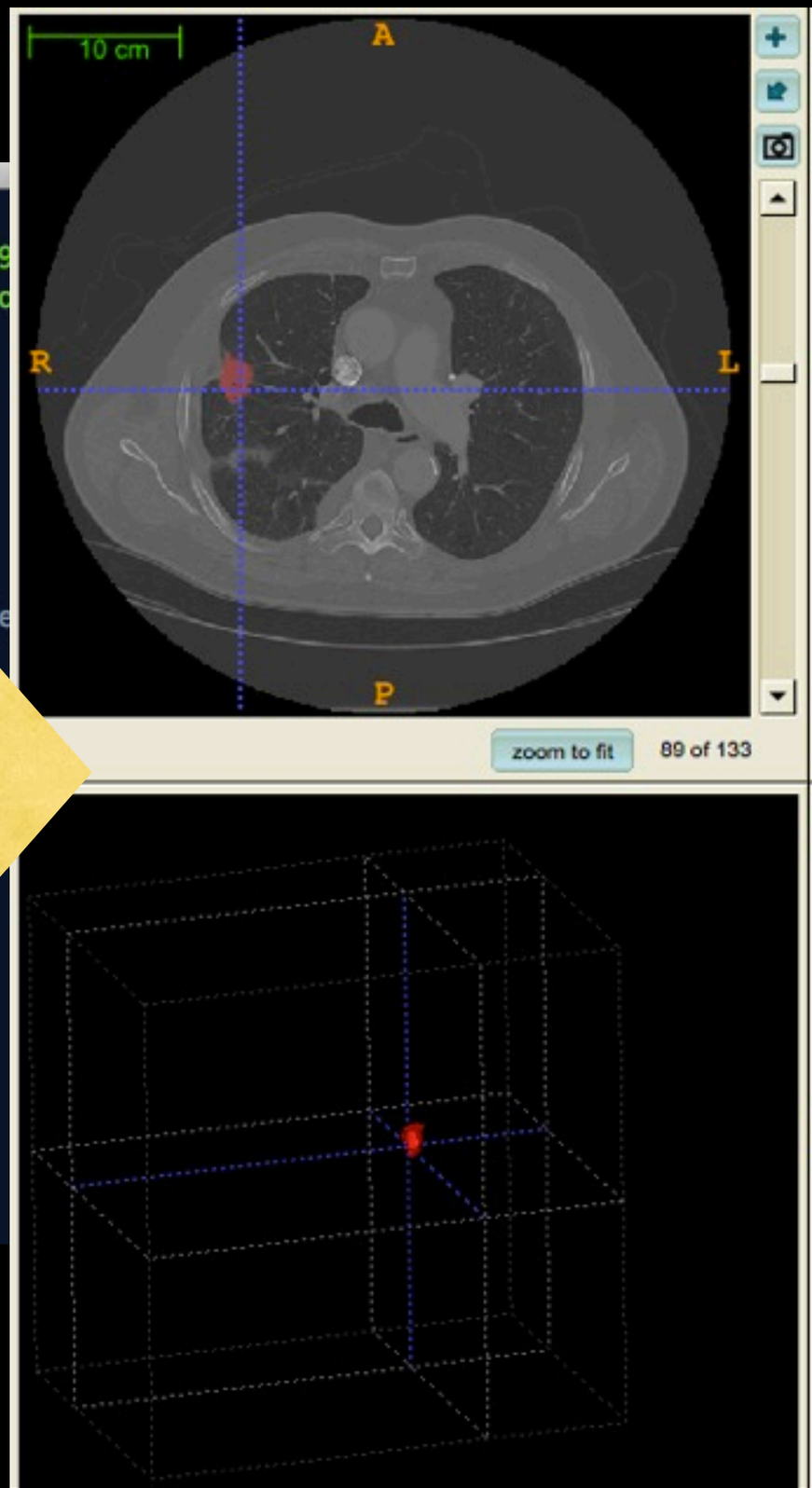
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    <unblindedReadNodule>
<noduleID>IL057_156959</noduleID>
<characteristics>
    <subtlety>4</subtlety>
    <internalStructure>1</internalStructure>
    <calcification>6</calcification>
    <sphericity>2</sphericity>
    <margin>4</margin>
    <lobulation>4</lobulation>
    <spiculation>4</spiculation>
    <texture>5</texture>
    <malignancy>5</malignancy>
</characteristics>
<roi>
    <imageZposition>-226.054993</imageZposition>
    <imageSOP_UID>1.3.6.1.4.1.14519.5.2.1.6279.6001.479209658786776331963534777579</im
    <inclusion>TRUE</inclusion>
    <edgeMap>
        <xCoord>376</xCoord>
        <yCoord>331</yCoord>
    </edgeMap>
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        <yCoord>330</yCoord>
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    <edgeMap>
        <xCoord>378</xCoord>
        <yCoord>329</yCoord>
    </edgeMap>
    <edgeMap>
        <xCoord>379</xCoord>
        <yCoord>328</yCoord>
```

Single File with contour points for up to 4 raters and many nodules

Conversion Script



```
<?xml version="1.0" encoding="UTF-8"?>
<LidcReadMessage uid="1.3.6.1.4.1.14519.5.2.1.6279
xsi:schemaLocation="http://www.nih.gov  http://tro
<ResponseHeader>
    <Version>1.8</Version>
    <MessageId>NIH179</MessageId>
        <DateRequest>2006-02-16</DateRequest>
        <TimeRequest>00:00:00</TimeRequest>
    <RequestingSite>removed</RequestingSite>
    <ServicingSite>removed</ServicingSite>
    <TaskDescription>Second unblinded read</TaskDe
    <CtImageFile>removed</CtImageFile>
    <SeriesInstanceUid>1.3.6.1.4.1.14519.5.2.1.62
    <DateService>2008-08-29</DateService>
    <TimeService>13:13:05</TimeService>
<ResponseDescription>1 - Reading complete</Respon
<StudyInstanceUID>1.3.6.1.4.1.14519.5.2.1.6279.60
    <readingSession>…
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    <readingSession>…
    <readingSession>…
</LidcReadMessage>
```

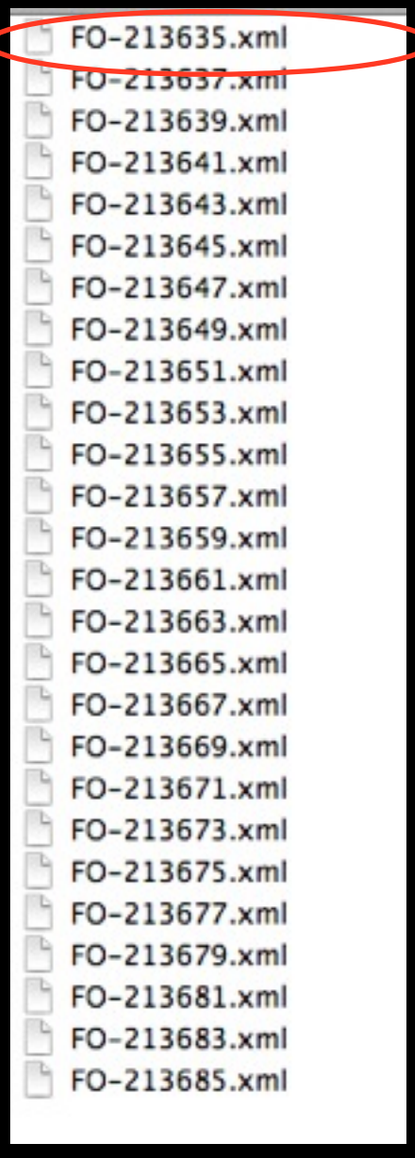


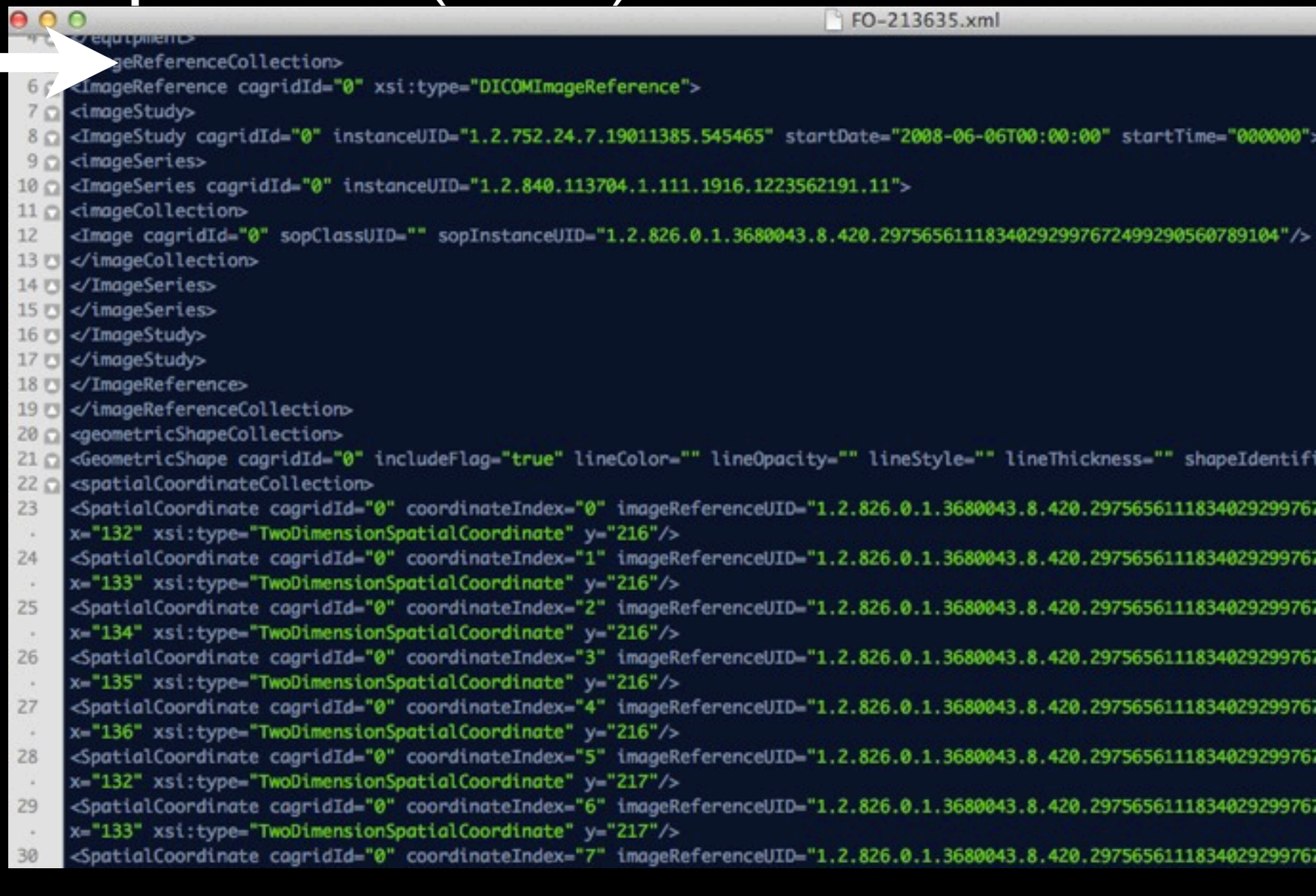


Stanford- AIM

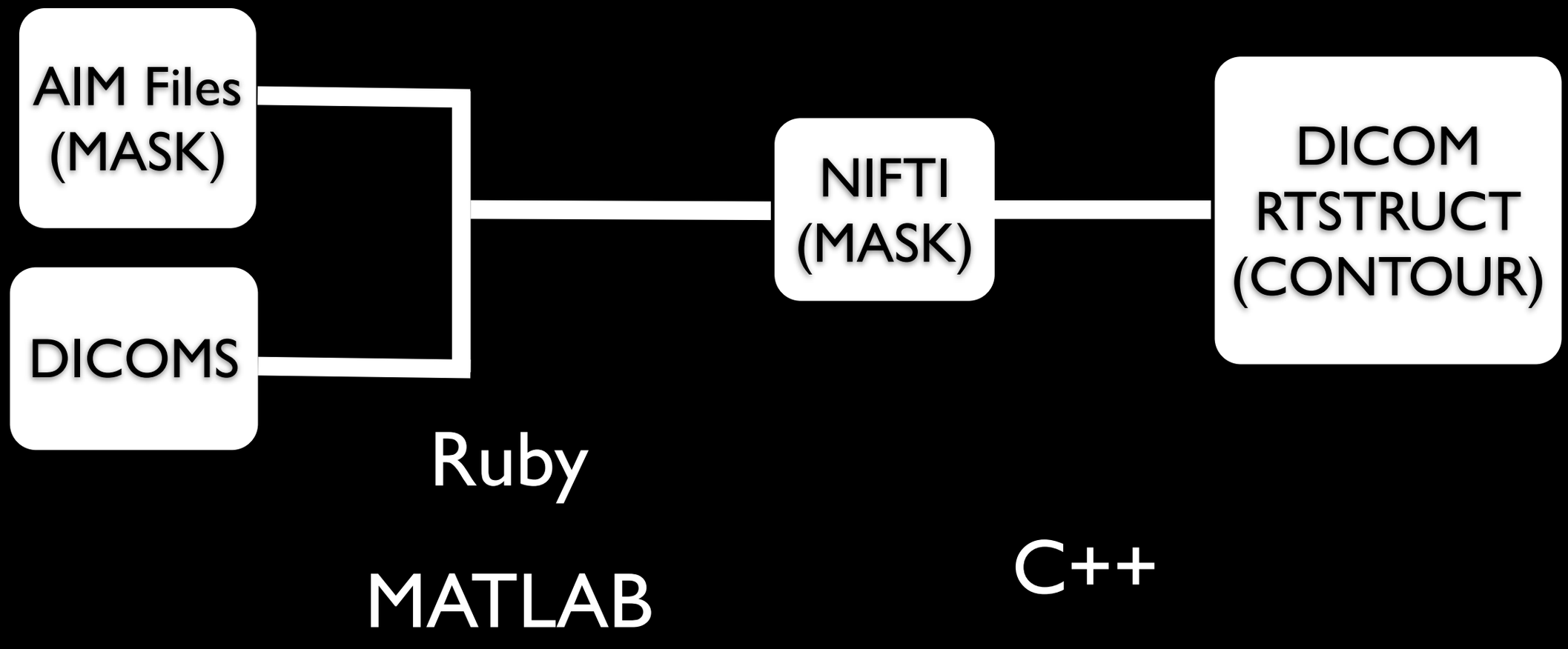
Multiple AIM files per nodule

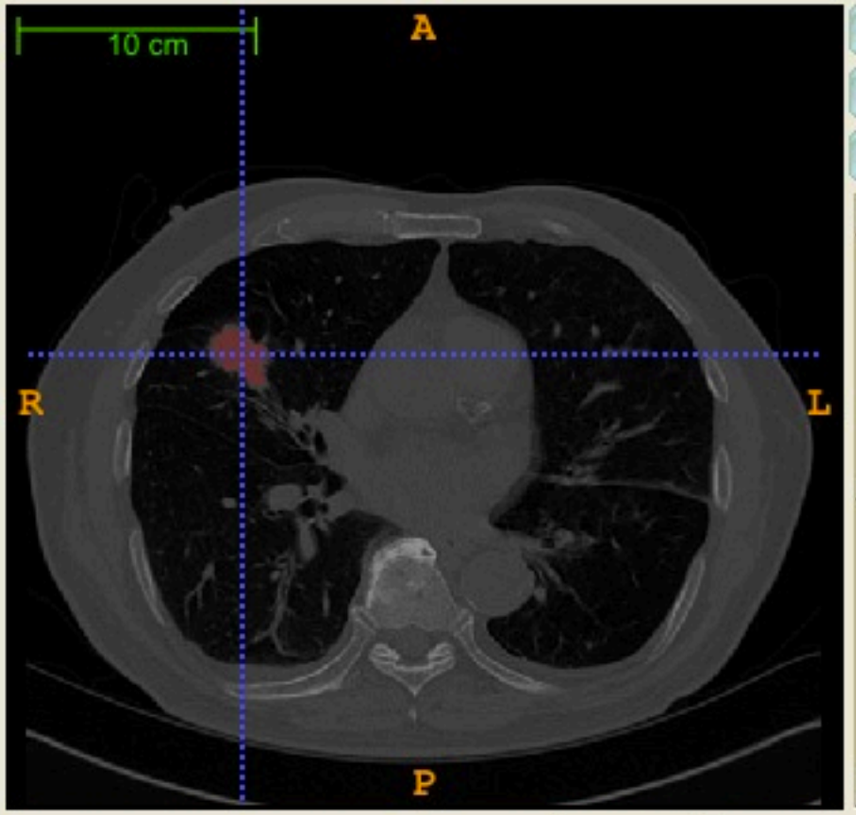
Single AIM file per slice (mask)



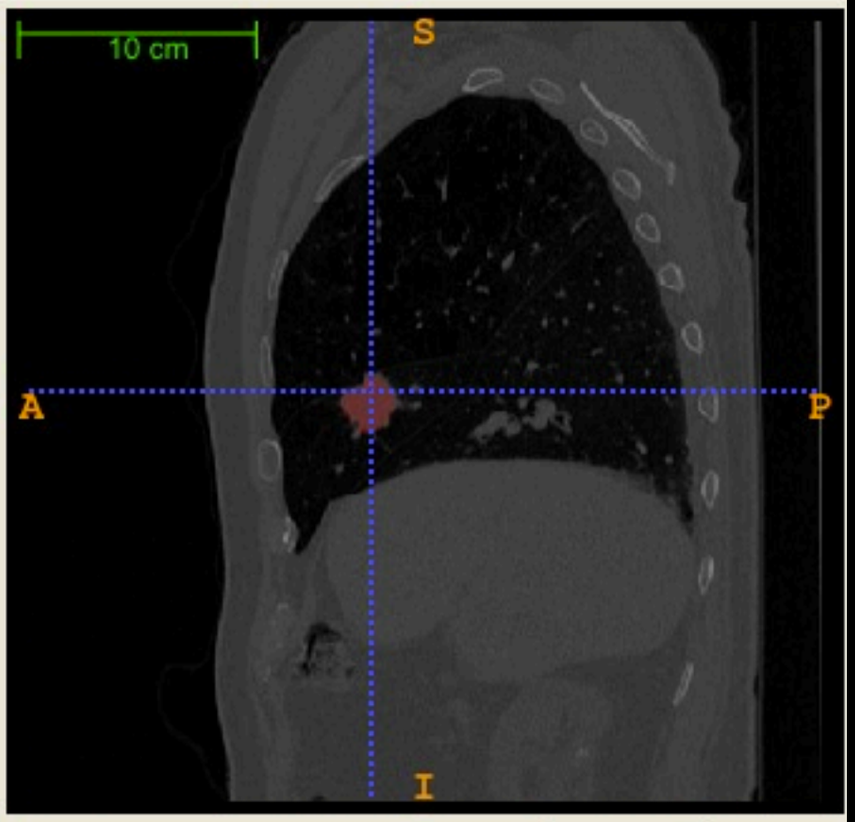


Conversion Script

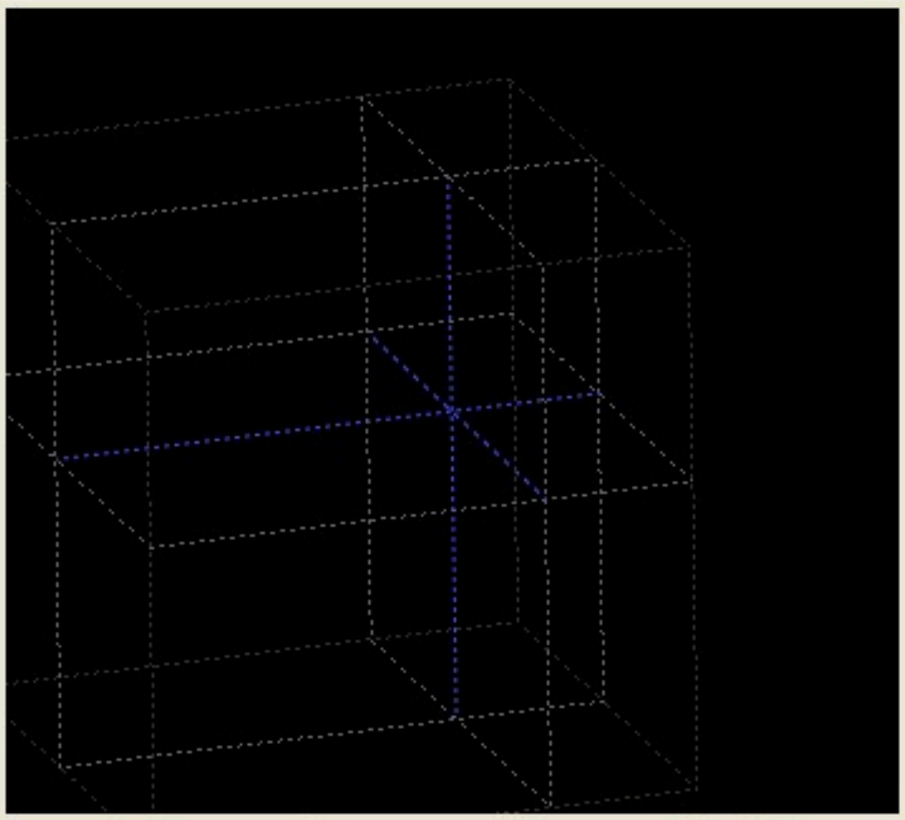


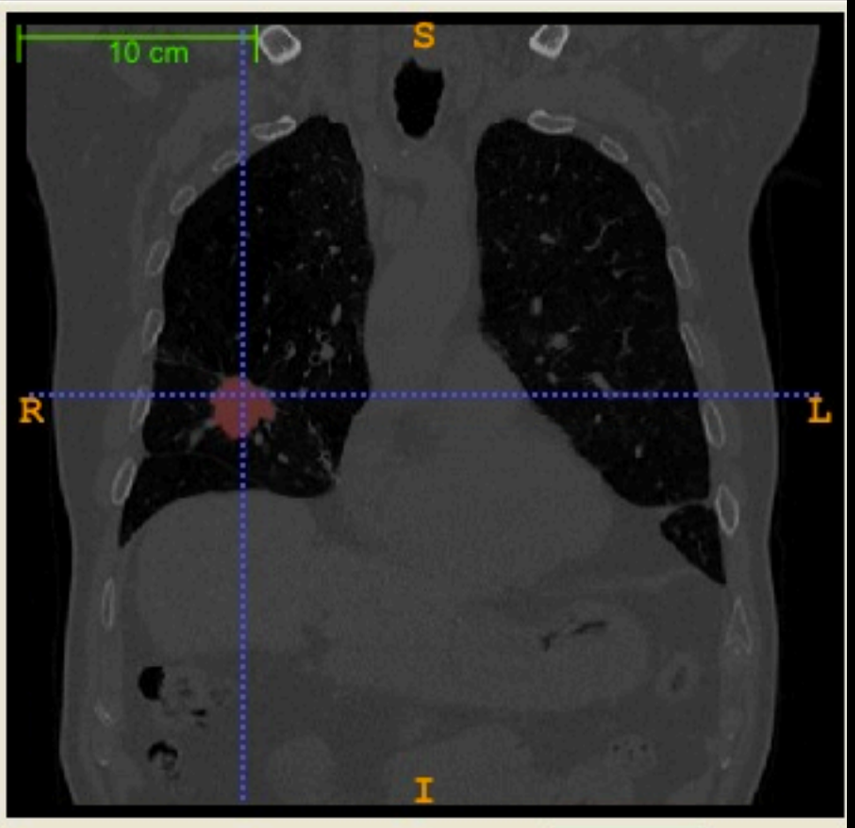


zoom to fit 173 of 329



zoom to fit 139 of 512



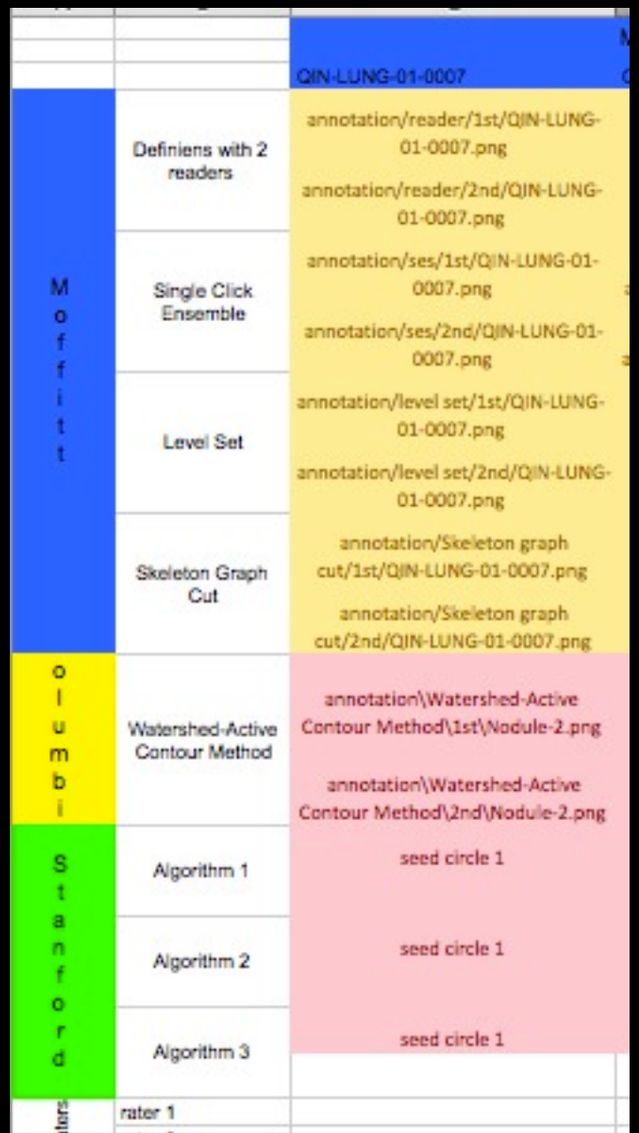


Current Status of Submission (dry run)

		Moffitt		LIDC		CUMC (FDA) Phantom		Stanford	
		QIN-LUNG-01-0007	QIN-LUNG-01-0013	LIDC-IDRI_0191	LIDC-IDRI_0919	GEVCT-1.25L-100mAs-L3		EP-1mm-CT	UR-1.25mm-CT
Moffitt	Definiens with 2 readers	annotation/reader/1st/QIN-LUNG-01-0007.png annotation/reader/2nd/QIN-LUNG-01-0007.png	annotation/reader/1st/QIN-LUNG-01-0013.png annotation/reader/2nd/QIN-LUNG-01-0013.png						
	Single Click Ensemble	annotation/ses/1st/QIN-LUNG-01-0007.png annotation/ses/2nd/QIN-LUNG-01-0007.png	annotation/ses/1st/QIN-LUNG-01-0013.png annotation/ses/2nd/QIN-LUNG-01-0013.png						
	Level Set	annotation/level set/1st/QIN-LUNG-01-0007.png annotation/level set/2nd/QIN-LUNG-01-0007.png	annotation/level set/1st/QIN-LUNG-01-0013.png annotation/level set/2nd/QIN-LUNG-01-0013.png						
	Skeleton Graph Cut	annotation/Skeleton graph cut/1st/QIN-LUNG-01-0007.png annotation/Skeleton graph cut/2nd/QIN-LUNG-01-0007.png	annotation/Skeleton graph cut/1st/QIN-LUNG-01-0013.png annotation/Skeleton graph cut/2nd/QIN-LUNG-01-0013.png						
olumbi	Watershed-Active Contour Method	annotation\Watershed-Active Contour Method\1st\Nodule-2.png annotation\Watershed-Active Contour Method\2nd\Nodule-2.png	annotation\Watershed-Active Contour Method\1st\Nodule-11.png annotation\Watershed-Active Contour Method\2nd\Nodule-11.png	ershed-Active Contour Method\1st\No ershed-Active Contour Method\2nd\No	ershed-Active Contour Method\1st\No ershed-Active Contour Method\2nd\N	ershed-Active Contour Method\1st\No ershed-Active Contour Method\2nd\No	annotation\Watershed-Active Contour Method\1st\Nodule-11.png annotation\Watershed-Active Contour Method\2nd\Nodule-11.png	Watershed-Active Contour Watershed-Active Contour	ed-Active Contour Method\1st\Nodule-11.png ed-Active Contour Method\2nd\Nodule-11.png
Stanford	Algorithm 1	seed circle 1	seed circle 1	seed circle 1	seed circle 1	seed circle 1	seed circle 1	seed circle 1	seed circle 1
	Algorithm 2	seed circle 1	seed circle 1	seed circle 1	seed circle 1	seed circle 1	seed circle 1	seed circle 1	seed circle 1
	Algorithm 3	seed circle 1	seed circle 1	seed circle 1	seed circle 1	seed circle 1	seed circle 1	seed circle 1	seed circle 1

Dry Run Results (not typical of expected results)

MOFFIT_0007



		QIN-LUNG-01-0007
Moffitt	Definiens with 2 readers	annotation/reader/1st/QIN-LUNG-01-0007.png annotation/reader/2nd/QIN-LUNG-01-0007.png
	Single Click Ensemble	annotation/ses/1st/QIN-LUNG-01-0007.png annotation/ses/2nd/QIN-LUNG-01-0007.png
	Level Set	annotation/level set/1st/QIN-LUNG-01-0007.png annotation/level set/2nd/QIN-LUNG-01-0007.png
	Skeleton Graph Cut	annotation/Skeleton graph cut/1st/QIN-LUNG-01-0007.png annotation/Skeleton graph cut/2nd/QIN-LUNG-01-0007.png
Columbi	Watershed-Active Contour Method	annotation\Watershed-Active Contour Method\1st\Nodule-2.png annotation\Watershed-Active Contour Method\2nd\Nodule-2.png
Stanford	Algorithm 1	seed circle 1
	Algorithm 2	seed circle 1
	Algorithm 3	seed circle 1
	rater 1	

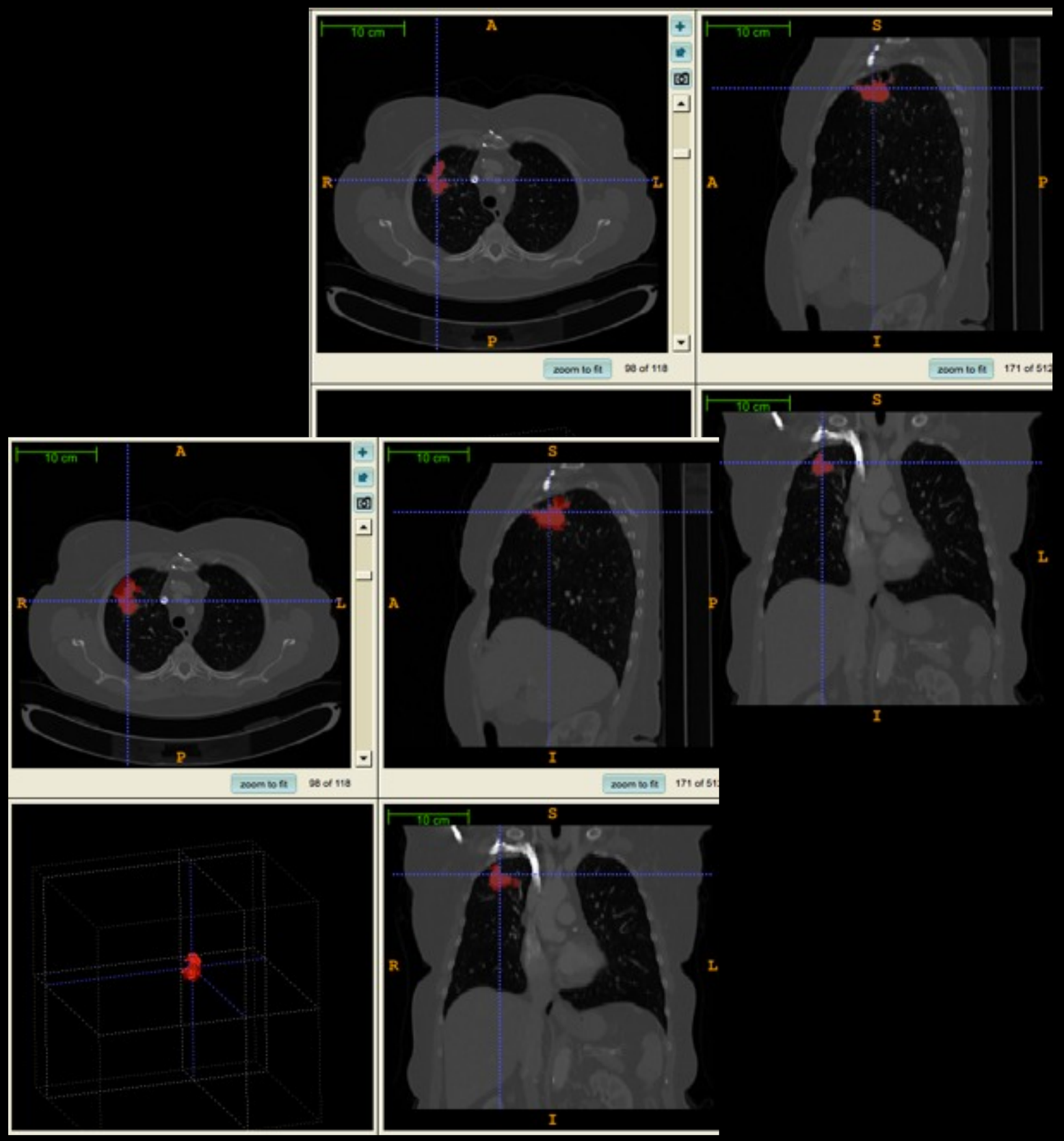
Non-optimized

Different levels of interaction

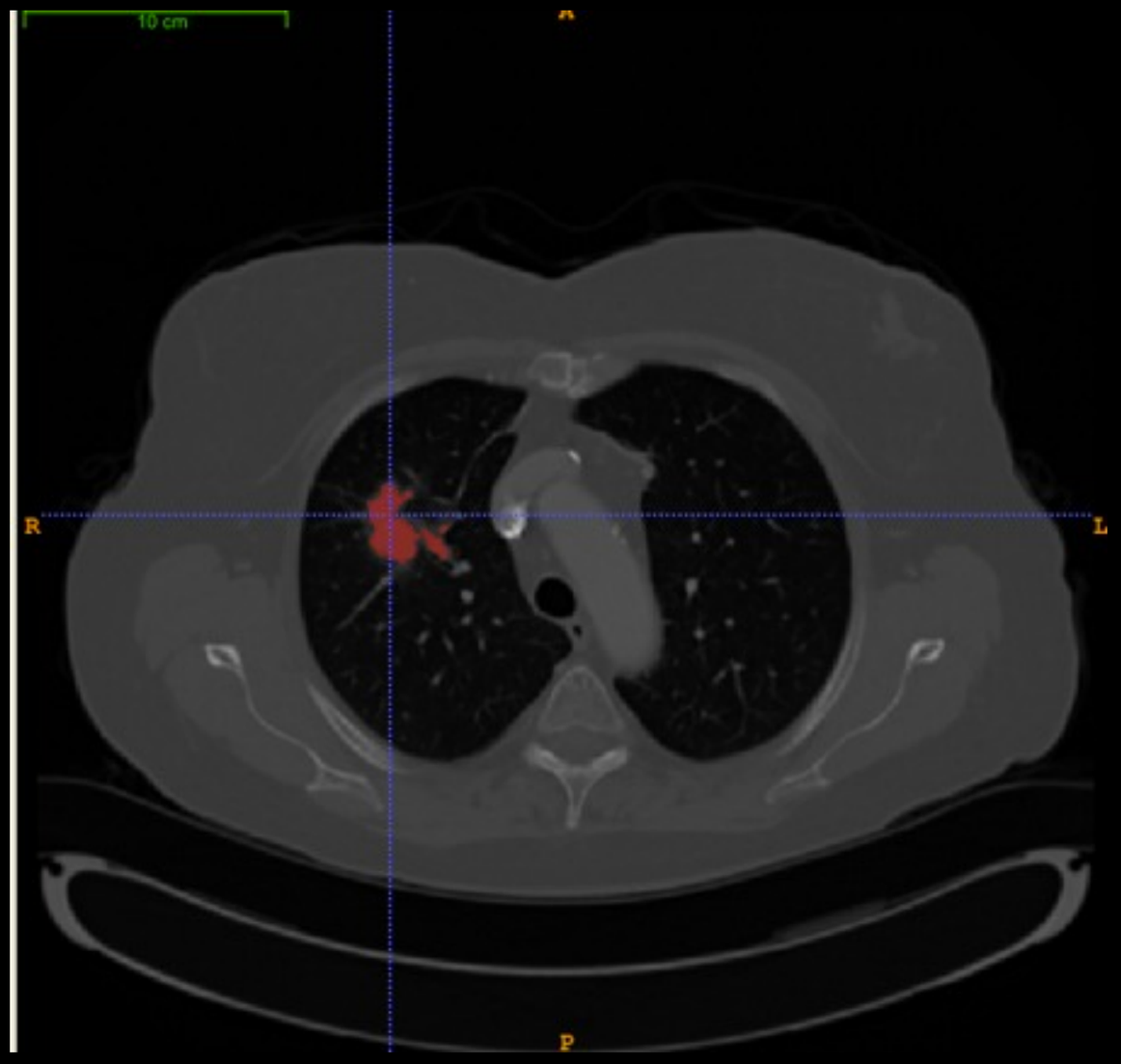
automatic vs.manual

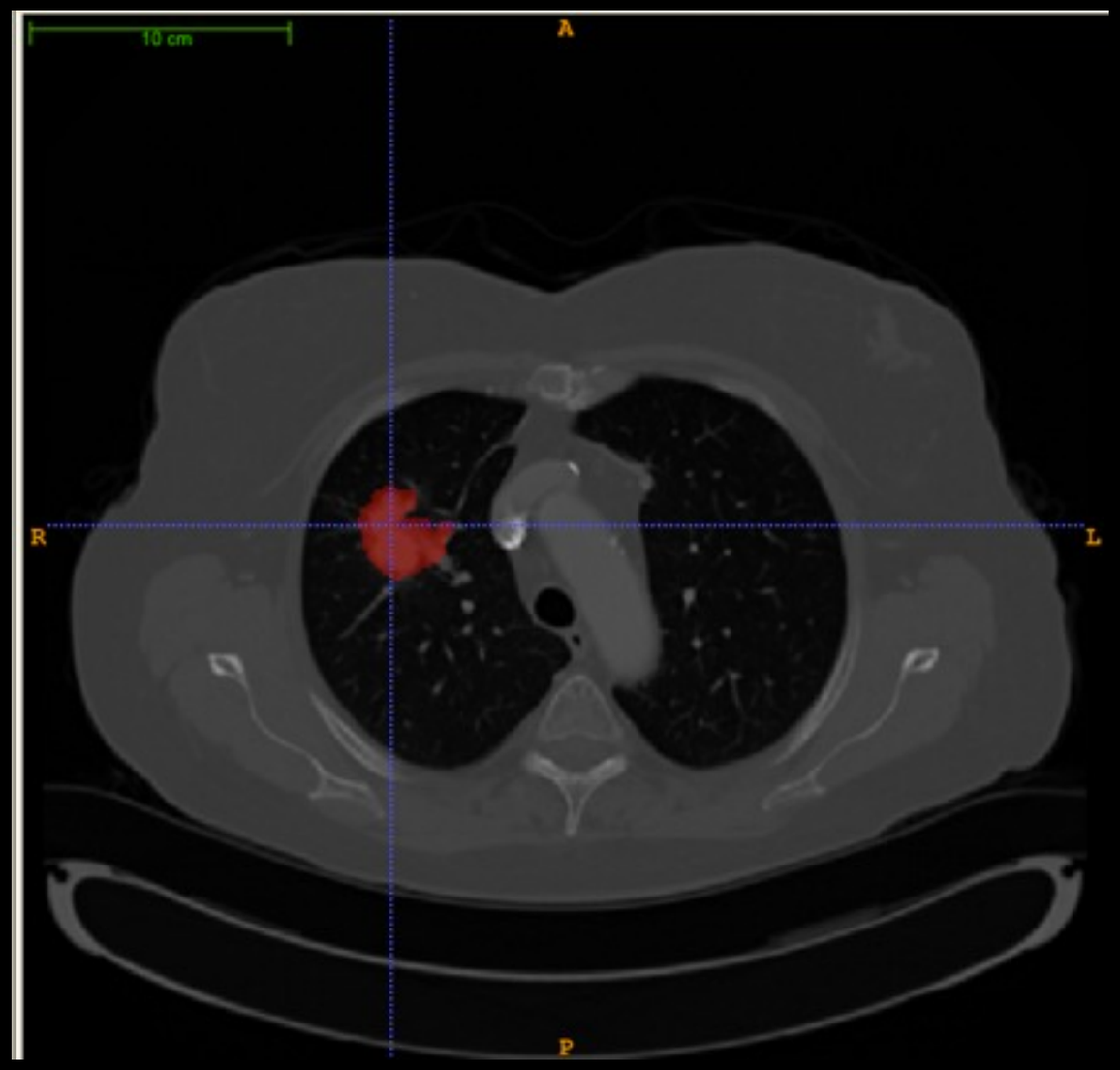
Volumes

Run	Volume
CUMC_0007_01.nii	12495
CUMC_0007_02.nii	12681
GC_0007_01.nii	13960
GC_0007_02.nii	11687
LS_0007_01.nii	13443
LS_0007_02.nii	13318
RR_0007_01.nii	13908
RR_0007_02.nii	13629
SC_0007_01.nii	12354
SC_0007_02.nii	11781
stan_MOFF_0007_01.nii	22021
stan_MOFF_0007_02.nii	17045
stan_MOFF_0007_03.nii	16915



MOFF_0007





Dice Overlap (pairwise)

Average of Dice	Column Lab											
Row Labels	CUMC_0007_	GC_0007_01.	GC_0007_02.	LS_0007_01.r	LS_0007_02.r	RR_0007_01.r	RR_0007_02.r	SC_0007_01.r	SC_0007_02.r	stan_MOFF_0	stan_MOFF_0	stan_MOFF_0
CUMC_0007_01.nii	0.95	0.89	0.90	0.90	0.91	0.92	0.92	0.92	0.92	0.63	0.70	0.69
CUMC_0007_02.nii		0.87	0.88	0.90	0.91	0.91	0.90	0.93	0.90	0.62	0.68	0.68
GC_0007_01.nii			0.91	0.87	0.87	0.91	0.91	0.90	0.89	0.66	0.69	0.69
GC_0007_02.nii				0.87	0.87	0.88	0.88	0.91	0.90	0.62	0.67	0.67
LS_0007_01.nii					0.99	0.89	0.88	0.91	0.87	0.62	0.68	0.68
LS_0007_02.nii						0.90	0.88	0.91	0.88	0.62	0.68	0.68
RR_0007_01.nii							0.97	0.92	0.92	0.65	0.72	0.71
RR_0007_02.nii								0.91	0.93	0.66	0.72	0.72
SC_0007_01.nii									0.93	0.62	0.69	0.69
SC_0007_02.nii										0.63	0.70	0.70
stan_MOFF_0007_01.nii											0.83	0.83
stan_MOFF_0007_02.nii												0.98

Hausdorff Distance (pairwise)

Current Status of Converters

All converters written and appear to be correct

- More exhaustive validation in progress
- Adding more error checking to code
- Converting to C++ (?)

Can handle contours or masks

PNG, LIDC-xml or AIM-xml

Format for Segmentation Challenge

- DICOM (seg or RT)
  - Standard (preferable)
  - Can use TCIA to store them
  - None of the current sites use this
  - DICOM-RT does not handle donuts (need to ‘keyhole’)
  - Tools to create these not readily available?
    - Slicer?
  - Storing meta data?

Considerations for next round

Goal of challenge and identification of appropriate metrics

Scale (how many studies, algorithms, repetitions)

Meta-data to be collected (minimal was collected this time)

Segmentation format

Format for Segmentation Challenge

AIM

Can store a lot of metadata
inference, calculated features etc

Not currently set up for 3D segmentations
May need to create multiple AIM files per nodule (one per slice)
not ideal?
Tools to create/visualize these?
Store non-image related meta data?

Format for Segmentation Challenge

LIDC-XML

can potentially store metadata

single file for multiple raters, nodules

Request for next round

File Naming convention

if all files are names the same (even if in different folders) causes problems when uploaded to website

batch processing easier if files named similarly

e.g. STAN_MOFF_0007_01_01

Location_collection_study_nodule_run