



# Functional Imaging Quantitation for Radiation Therapy Planning in Head and Neck Cancer

*John Buatti, MD*

*Department of Radiation Oncology*

*University of Iowa*

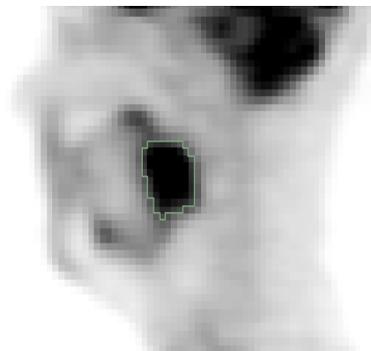
# Specific Aims

- Specific Aim 2:
- Develop novel semi-automated tools for reproducible tumor definitions applicable to quantitative image-based response assessment that will be compared with manual methods.

# Image Analysis Output

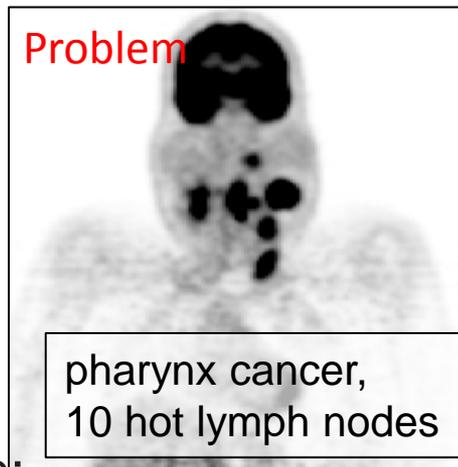
1. Volume of interest (VOI) masks for structures with uptake:
  - Reference regions (similar to PERCIST<sup>+</sup>)
  - Primary cancer
  - Lymph nodes
  - Etc.
2. Quantitative indices derived from segmented VOIs:
  - SUVmax, SUVpeak, SUVaverage, Volume, Metabolic Tumor Volume (MTV), ...
  - Indices may also be based on CT data

*<sup>+</sup> R.Wahl et al. From RECIST to PERCIST: Evolving Considerations for PET response criteria in solid tumors. J Nucl Med. 2009.*



# Advantages of Approach

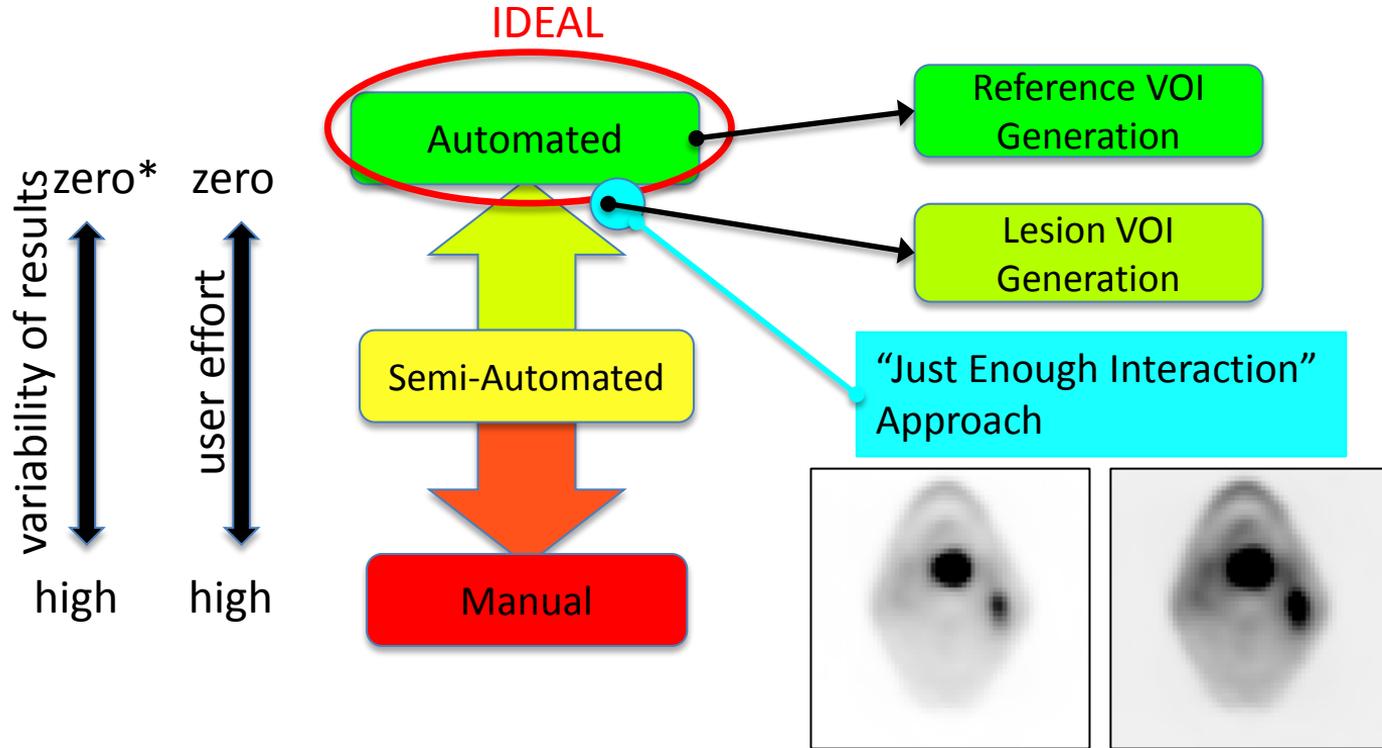
- Flexibility:
  - switch from
    - MTV  $\rightarrow$  SUV<sub>peak</sub>
    - reference region: liver  $\rightarrow$  cerebellum
    - ...
- New quantitative indices can be calculated retrospectively
- If outcome data or surrogate end points are available:
  - Select indices utilizing machine learning techniques
- Transparent process
- Digital volumetric models for RT targeting
- ...



Q: Why not frequently utilized?

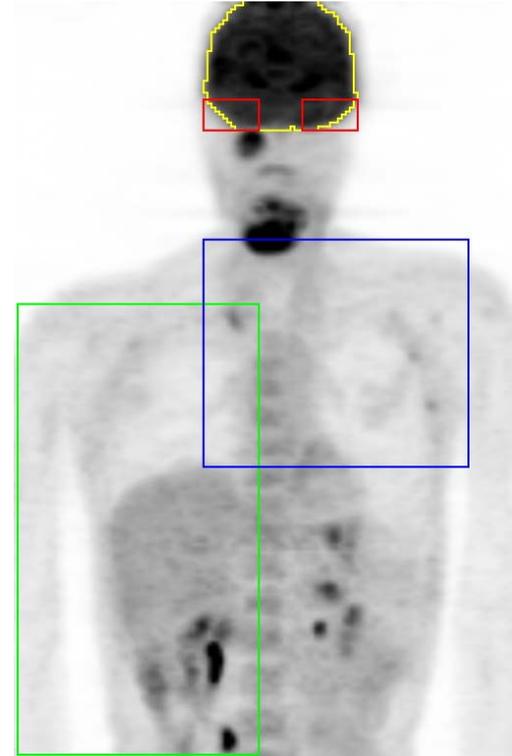
# Segmentation Approach

→ key for success (usability)



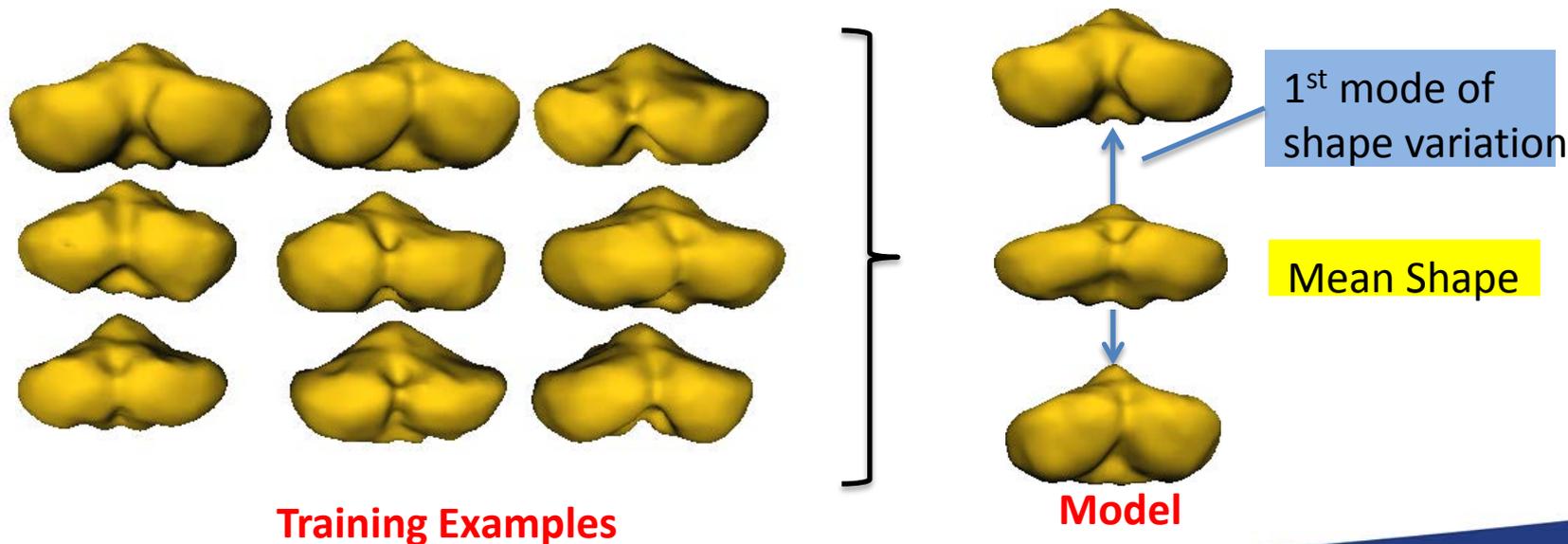
# Automated Reference VOI Generation

- Methods for
  - Cerebellum (full)
  - Liver (tri-axial ellipsoid)
  - Aortic arch (tube, CT image)
- “Search regions” based on a brain segmentation
  - Gray-value threshold, morphology, size analysis

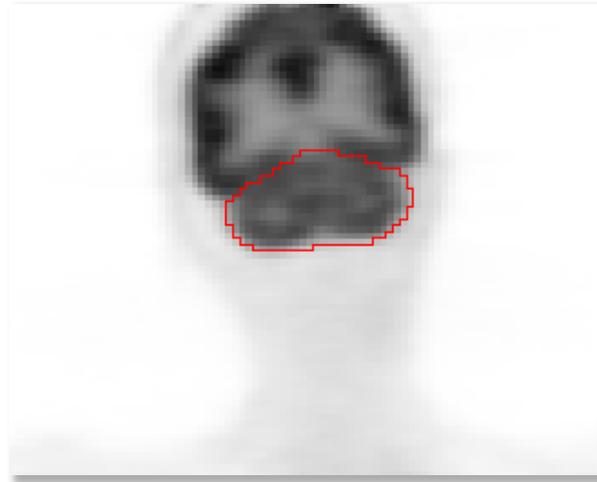
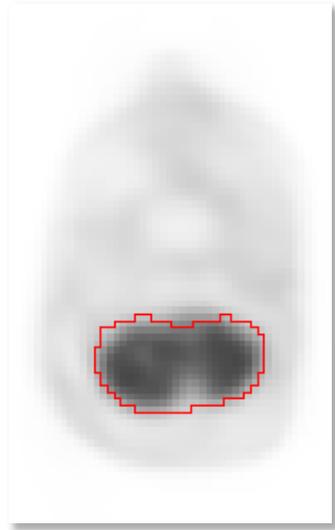


# Cerebellum VOI Algorithm

- Based on a **Robust Active Shape Model**
- Learn shapes of cerebella → model
- Match model to new image data → VOI



# Example of a Resulting Cerebellum VOI



# Validation – Image Data

- 134 PET/CT scans from 49 subjects with H&N cancer
- F-18 FDG (370 MBq $\pm$ 10%)
- Uptake time 90 min  $\pm$  10%
- Subjects fasted >4h
- Blood glucose <200 mg/dl
- Arms down
- 128x128 pixel matrix (3.5 x 3.5 x 3.4 mm) or  
168 x 168 pixel matrix (3.4mm x 3.4mm x 2.0mm)

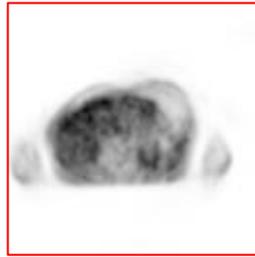
# Validation - Uptake in Cerebellum

- Independent reference standard:
  - Experts manually traced the cerebellum in 4 cross-sections (1 axial, 1 coronal, 2 sagittal [left & right hemisphere])
  - 2 experts: 134, 1 expert: 44, and 1 expert: 20
  - Average SUV from all 4 cross-sections
  - Consensus-true SUV model based on expert results + statistical analysis approach

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# Liver VOI Generation



PET volume



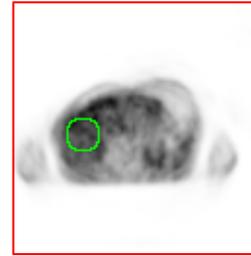
> 1 SUV



Hole closing



Distance  
transform

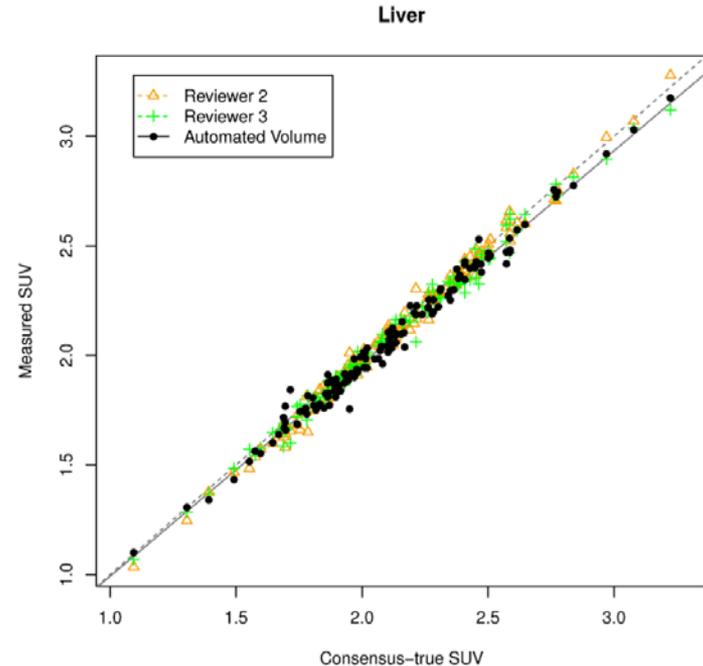


VOI

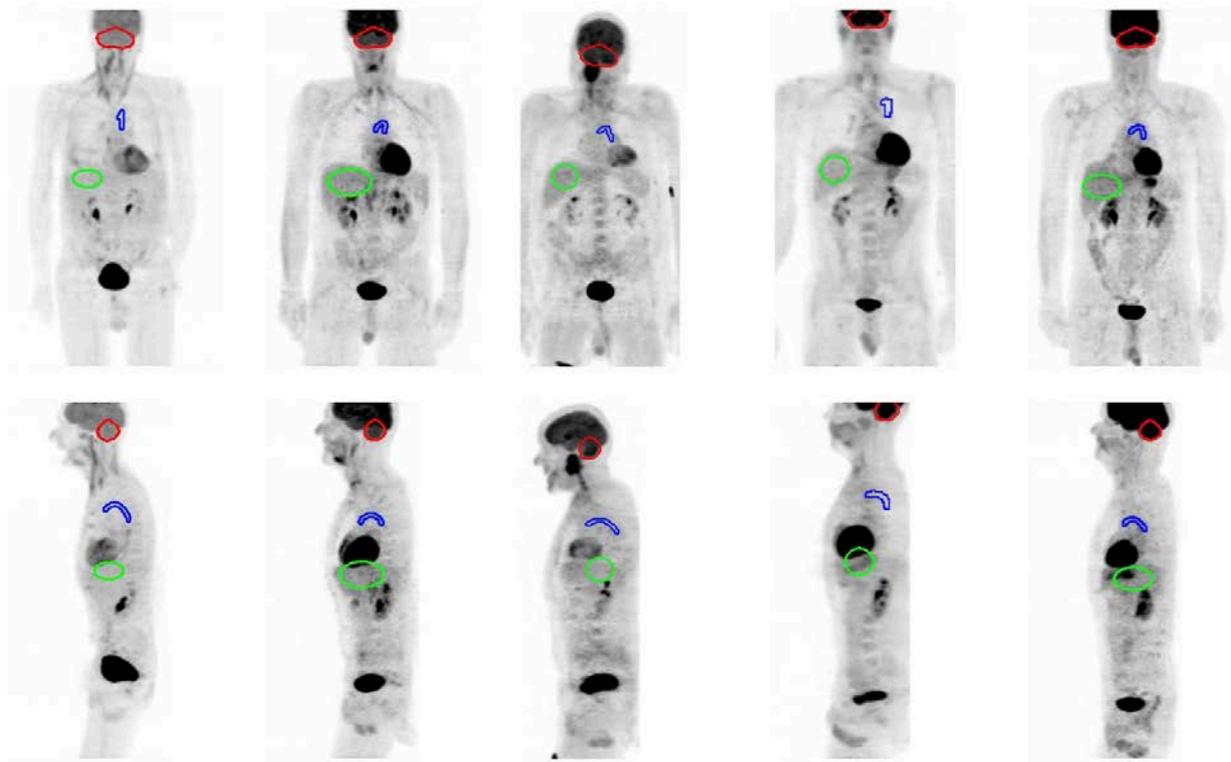
# Validation - Uptake in Liver

- Reference: 2 experts
- Tracing in one axial, sagittal and coronal slice
- Same 134 scans
- Same analysis steps

Site	Auto	Intercept $\beta_0$ (SUV)	Slope $\beta_1$ (-)
Liver	Volume	0.02 (-0.23, 0.15)	0.97 (0.94, 1.00)



# Examples of Automatically Defined Reference VOI (1)



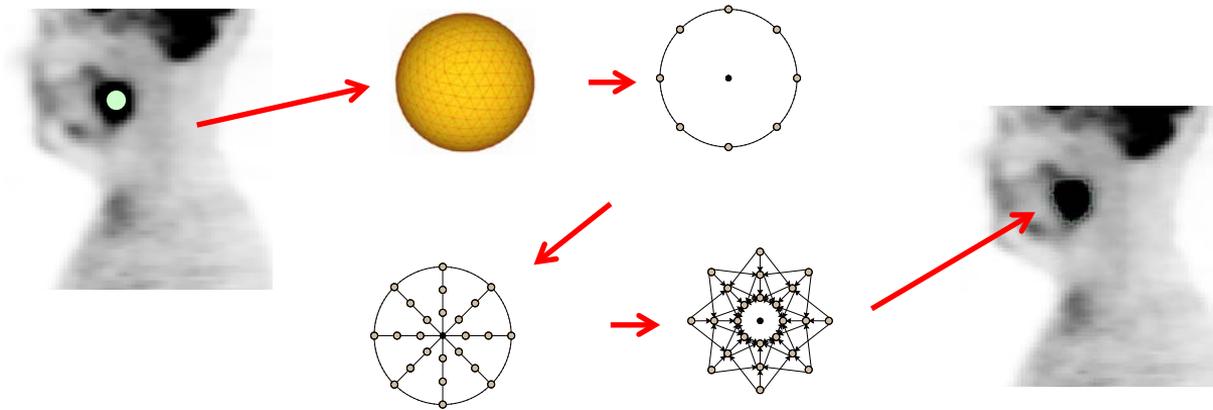
# Comparison Automated vs. Manual

Decrease in total variability if the automated method was used instead of the manual method:

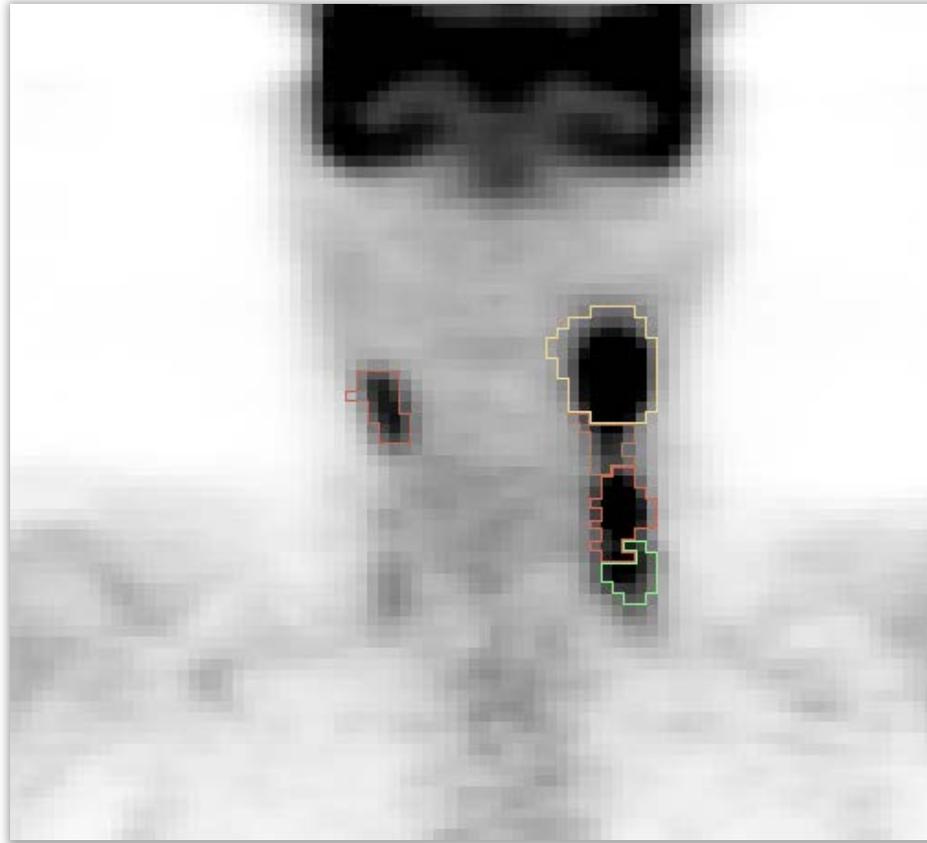
<b>Cerebellum</b>	<b>4-Slice</b>	<b>99.2% *</b>
	<b>Volume</b>	<b>89.8% *</b>
<b>Aortic arch</b>	<b>Volume</b>	<b>76.7% *</b>
<b>Liver</b>	<b>Volume</b>	<b>54.7%</b>

# VOI Generation for Lesions

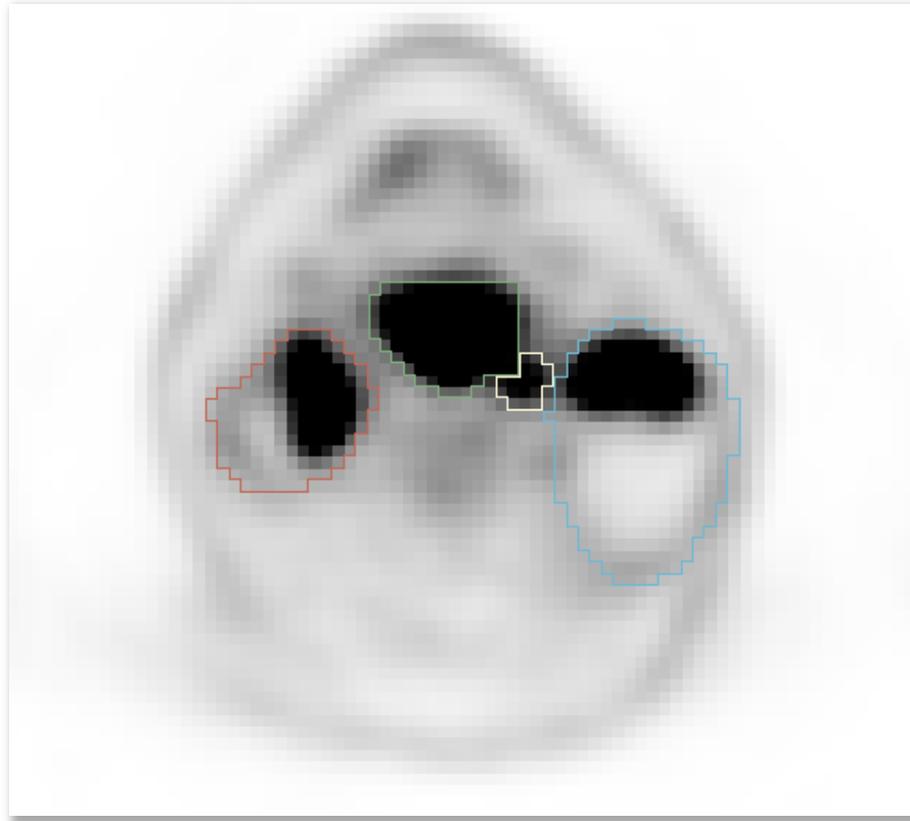
- Segmentation problem  $\rightarrow$  graph-based optimization approach (Optimal Surface Segmentation)
- Graph + cost function (design is critical!)
- Integrated into 3D Slicer ([www.slicer.org](http://www.slicer.org))



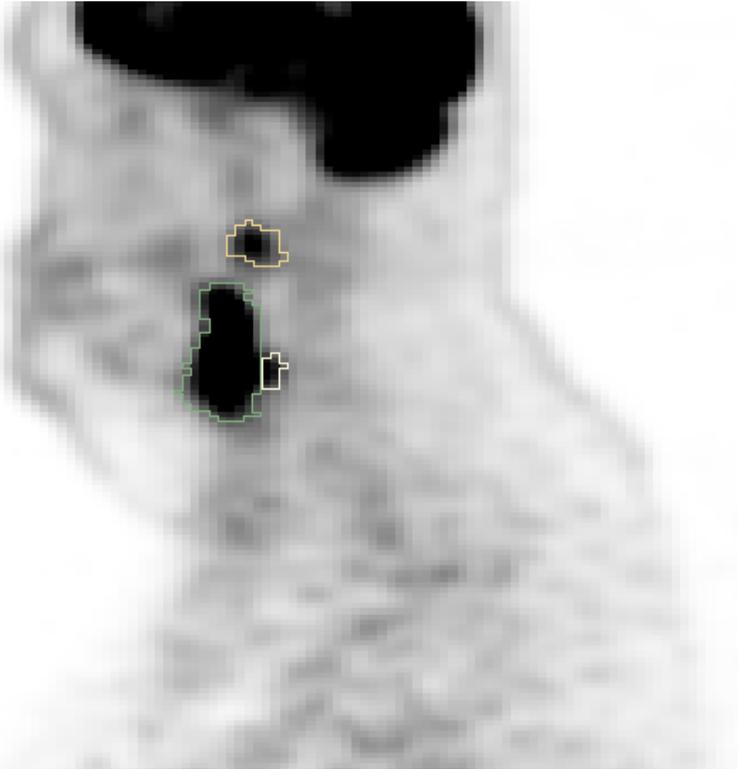
# Complexity issues



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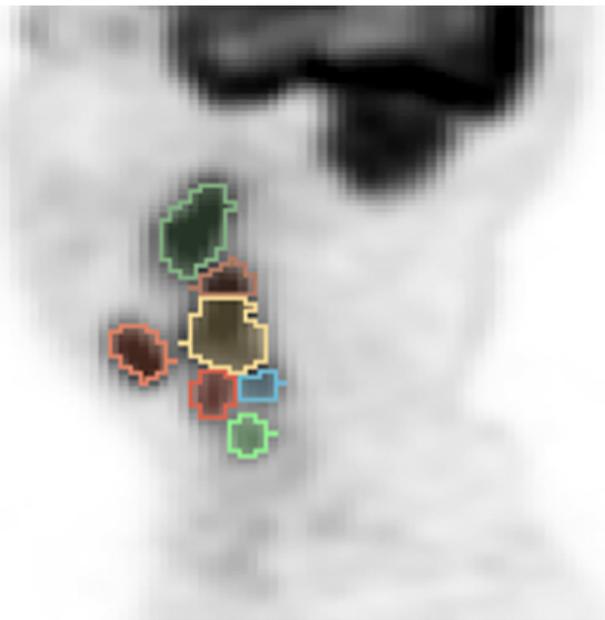
# Generating Data



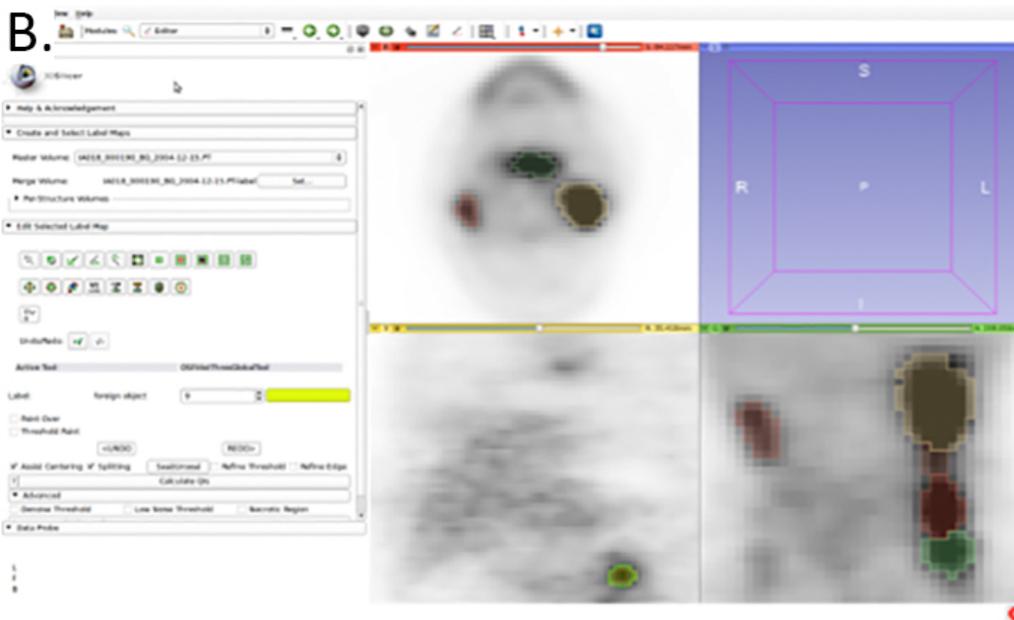
- SUV Max, Mean
- Metabolic Tumor Volume
- Range Pixel Values
- Volume over/x SUV
- Normalization against
  - Liver/Blood Flow
- Lowest Quartile
- Highest Quartile
- Etc.....

# PET Module Tool

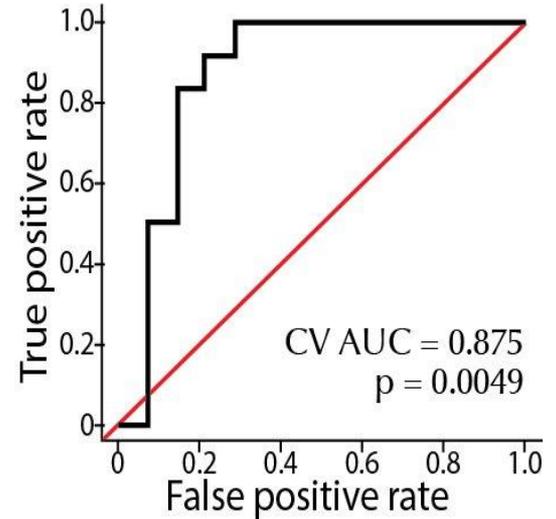
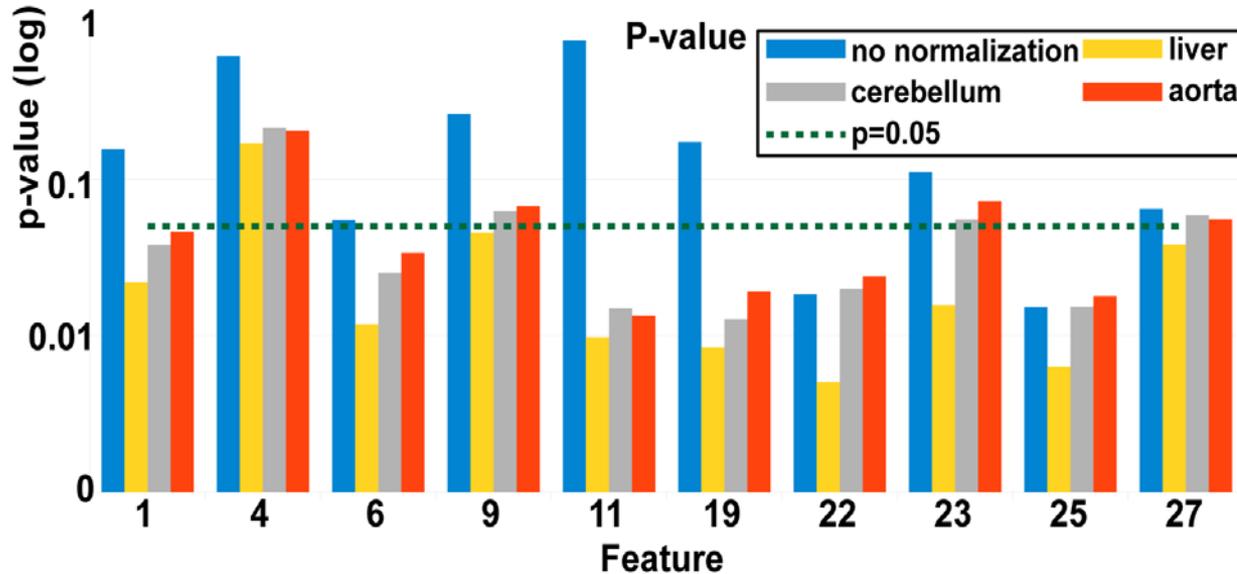
A.



B.



# Types of Analyses





# Validation Study

- Using a set of 60 cases with 230 lesions
  - 3 investigators randomly contoured each case using manual (twice) or PET module tool (twice)
  - 2760 contoured lesions
  - Compared for internal consistency and against best estimate of ground truth

# Automated tool agreement

**Table 1**

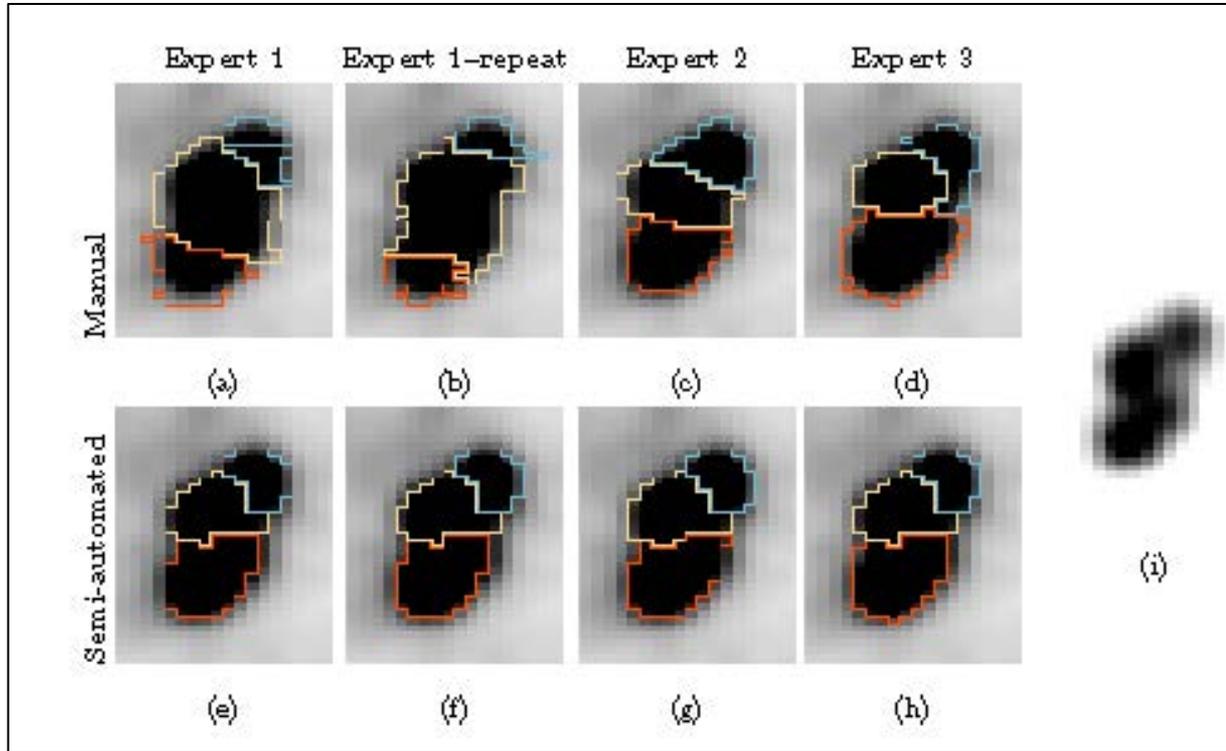
Agreement	N	Manual		Semi-automated	
		Mean	95% CI	Mean	95% CI
Within Operator	690	77.0	(74.7–79.4)	92.6	(90.2–94.9)
Between Operator	690	79.8	(78.4–81.2)	94.1	(92.7–95.6)

*Table 1. Estimated mean dice coefficients for intra and inter-operator segmentation agreement.*

**Table 2**

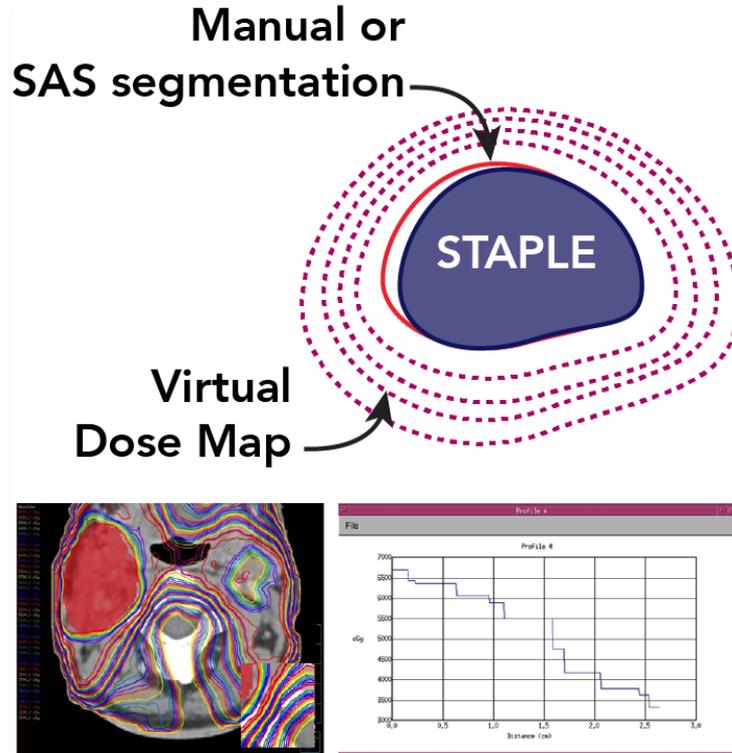
Method	Time (minutes)	95% CI (minutes)
Manual	8.88 ± 7.1	(6.47, 11.28)
Semiauto	3.74 ± 3.3	(2.40, 5.08)

*Table 2. Estimated mean times with standard deviation and 95% confidence intervals (CI) for manual and semi-automated segmentations.*



Example of intra- and inter-operator segmentation agreement for manual and semi-automated segmentation methods. (a-d) Manual slice-by-slice segmentation results. (e-h) Semi-automated full 3D segmentation results. (i) Same PET image as in images (a-h), but with a different gray-value transfer function, showing uptake peaks corresponding to individual lymph nodes in close proximity.

# Tumor Control Probability



*(Top) A virtual dose map was generated from each manual contour (Manual-C) or semi-automated segmentation (SAS). (Bottom) Its dose gradient was - 2.7 % per mm, adapted from a clinical head-and-neck intensity-modulated radiation therapy (IMRT) plan.*

# Tumor Control Probability

	Differences (SAS – Manual-C)		
	$\Delta$ EUD	$\Delta$ Logistic TCP	$\Delta$ Poisson TCP
Mean	-0.3	-1.2%	-1.1%
Median	-0.3	-1.0%	-1.0%
Intra-Observer Variability Standard Deviations	0	-0.9%	-0.8%
Inter-Observer Variability Standard Deviations	-1.2	-4.7%	-4.7%

*The differences between SAS and Manual-C in terms of EUD, Logistic TCP and Poisson TCP when using STAPLE as a ground truth tumor contour. For all cases, SAS resulted in significantly lower (i.e. “-“) both intra- and inter-observer variability standard deviations regardless of TCP modeling ( $p < 0.0043$ ).*

# Conclusions

- Quantitative imaging represents an opportunity to improve both our ability to consistently identify targets for radiation therapy as well as improve response assessment and prognostication of cancer
- Algorithmic tools are critical components to leverage the big data source and will be combined (multiparametric) with both other imaging and radiogenomics.

# Conclusions

- As the complexity increases, the ability of strictly simple principles that have commonly guided therapy decision making is likely to go away
- Final thought on algorithms and target identification in light of TCP and NTCP