



From Data to Segmentation Models: AI for Everybody

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Outline

- Motivation
- Components of segmentation pipeline
 - Hardware (Institutional HPC, Cloud services AWS, Azure, Google cloud)
 - Software (frameworks for training and deployment)
- Applications
 - Clinical (Radiation therapy treatment planning)
 - Research (Consistent data collection for research)
- Demos

Motivation

- Classification
 - predict target class at the patient level from an image or region of interest.
- Detection
 - detection tasks aim to predict the location of potential lesions, often in the form of points, regions, or bounding boxes of interest.
- Segmentation
 - identification of pixels or voxels composing an organ or structure of interest.

Reference: Deep Learning: A Primer for Radiologists, Gabriel Chartrand, Phillip M. Cheng, Eugene Vorontsov, Michal Drozdal, Simon Turcotte, Christopher J. Pal, Samuel Kadoury, and An Tang, RadioGraphics 2017 37:7, 2113-2131

Motivation

➤ Screening and follow-up

- Ardila, D., Kiraly, A.P., Bharadwaj, S. *et al.* End-to-end lung cancer screening with three-dimensional deep learning on low-dose chest computed tomography. *Nat Med* **25**, 954–961 (2019) doi:10.1038/s41591-019-0447-x

➤ Treatment planning – clinical use cases

- Synthetic CT generation from MR (Jiang et al, Wolterink et al, Han et al, etc.)
- Knowledge-based prediction of 3D dose distribution (Shiraishi and Moore, etc.)
- Auto contouring for treatment planning / Adaptive RT

Building blocks of segmentation pipeline

Domain-optimized tools

Training framework

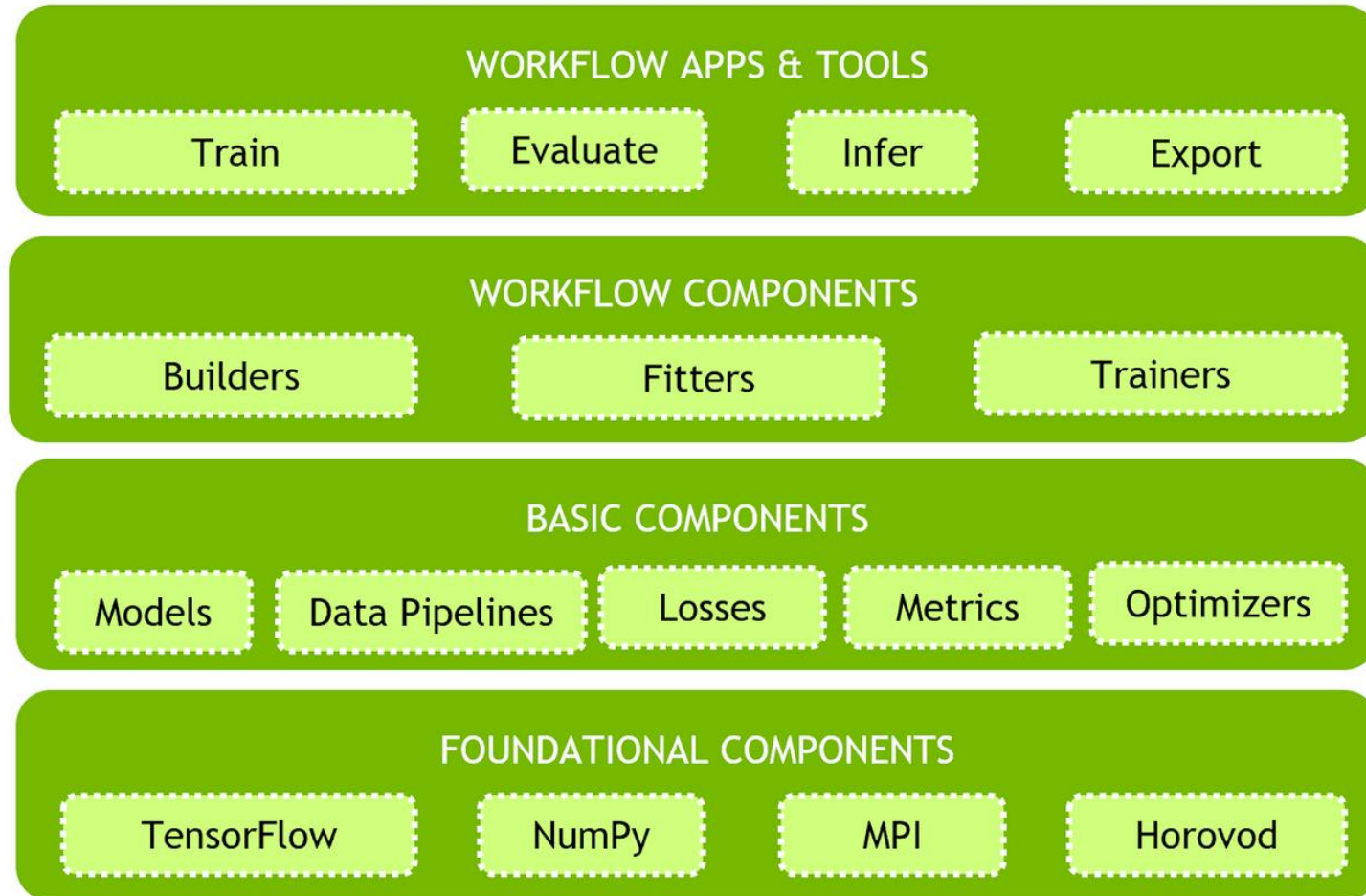
Hardware

Question and Dataset

High Performance Computing (HPC) resources

- Cloud computing with specialized hardware – AWS, Azure, Google cloud, etc.
- Institutional HPC
 - e.g., hpc.mskcc.org
 - 91 nodes, 4640 CPU cores
 - 372 GPUs (4 dedicated to Medical Physics)
 - 3.6PB of fast disk storage, and 6.0PB of ‘warm’ archive storage space
- Clinical HPC
 - 4 nodes, 144 CPU cores
 - 20 GPUs

Software - building blocks

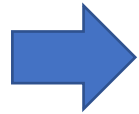


Reference: <https://developer.nvidia.com/blog/annotate-adapt-model-medical-imaging-clara-train-sdk/>

Domain-optimized framework – building blocks

Pre-process

- Parse DICOM
- Select region of interest
- Image filters
- Populate channels



Segment

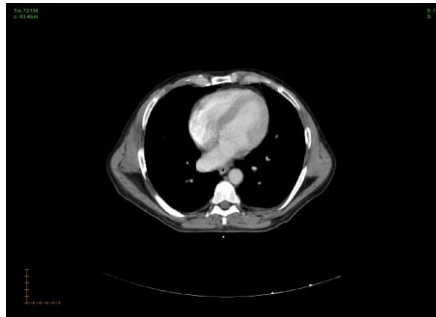
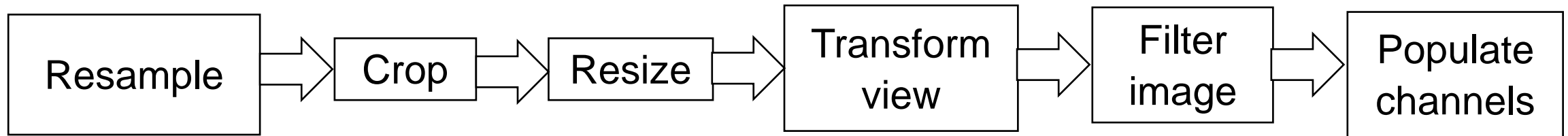
(model and its dependencies)



Post-process

- Label fusion
- Morphological processing

Transformations for medical images



"channels":
[{"imageType":"original", "slice":"current-1"},
{"imageType":"original", "slice":"current"},
{"imageType":"original", "slice":"current+1"}]

Domain-optimized frameworks for medical imaging

- MONAI - PyTorch-based framework for deep learning in healthcare imaging. It provides domain-optimized foundational capabilities for developing healthcare imaging training workflows in a native PyTorch paradigm. (<https://github.com/Project-MONAI/MONAI>)
- NVIDIA Clara – healthcare application framework for AI-powered imaging, genomics, and the development and deployment of smart sensors (<https://docs.nvidia.com/clara>)
- CERR – Models for segmentation of various normal tissues used in radiation therapy treatment planning. (<https://github.com/cerr/CERR>)
- DeepInfer - an open-source toolkit for developing and deploying deep learning models within the 3D Slicer medical image analysis platform (<http://www.deepinfer.org>)

Standardizing the processing pipeline

- NVIDIA-Clara MMAR
- CERR pre/post-processing pipeline
- MONAI “transforms” module

Medical Model Archive (MMAR) in NVIDIA

- The MMAR (Medical Model ARchive) defines a standard structure for organizing all intermediate steps and results produced during the model development life cycle.

```
ROOT
  config
    config_train.json
    config_validation.json
    environment.json
  commands
    set_env.sh
    train.sh
    train_finetune.sh
    train_2gpu.sh
    train_2gpu_finetune.sh
    infer.sh
    validate.sh
    export.sh
  resources
    log.config
    ...
  docs
    license.txt
    Readme.md
    ...
  models (all forms of model: checkpoint, frozen graphs, saved model, TRT)
    model.ckpt.meta, model.ckpt.index, model.ckpt.data
    tensorboard event files
    model.frn.pb, model.trt.pb
```

CERR Pre/post processing settings

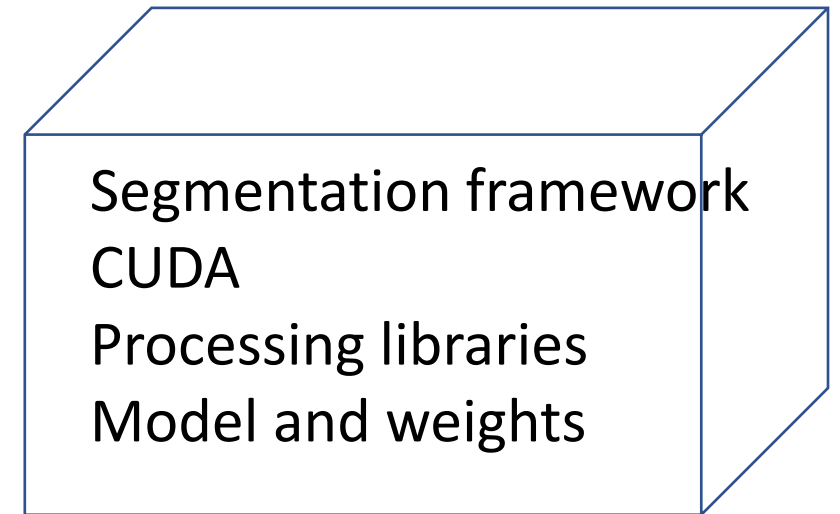
```
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2  "strNameToLabelMap":[
3
4    {"structureName" : "AORTA", "value" : 2},
5    {"structureName" : "LA", "value" : 3},
6    {"structureName" : "LV", "value" : 4},
7    {"structureName" : "RA", "value" : 5},
8    {"structureName" : "RV", "value" : 6},
9    {"structureName" : "IVC", "value" : 7},
10   {"structureName" : "SVC", "value" : 8},
11   {"structureName" : "PA", "value" : 9}
12  ],
13
14  "batchSize" : 1,
15
16  "inputFileType" : "planC",
17
18  "resize" : {"method": "none",
19             "size" : [512,512]},
20
21  "crop" : [{"method": "crop_to_str", "params" : {"structureName": "lung_l"}, "operator" : ""},
22            {"method": "crop_to_str", "params" : {"structureName": "lung_r"}, "operator" : "union"},
23            {"method": "crop_to_str", "params" : {"structureName": "totallung"}, "operator" : "union"}
24  ],
25
26  "passedScanDim" : "2D",
27
28  "reference" : "https://w3.aapm.org/meetings/2019AM/programInfo/programAbs.php?sid=8013&aid=45641"
29
30 }
```

MONAI APIs

- **apps**: high level medical domain specific deep learning applications.
- **config**: for system configuration and diagnostic output.
- **data**: for the datasets, readers/writers, and synthetic data.
- **handlers**: defines handlers for implementing functionality at various stages in the training process.
- **inferers**: defines model inference methods.
- **losses**: classes defining loss functions.
- **optimizers**: classes defining optimizers.
- **transforms**: defines data transforms for preprocessing and postprocessing.
- **utils**: generic utilities intended to be implemented in pure Python or using Numpy, and not with Pytorch, such as namespace aliasing, auto module loading.
- **visualize**: utilities for data visualization.

Model deployment

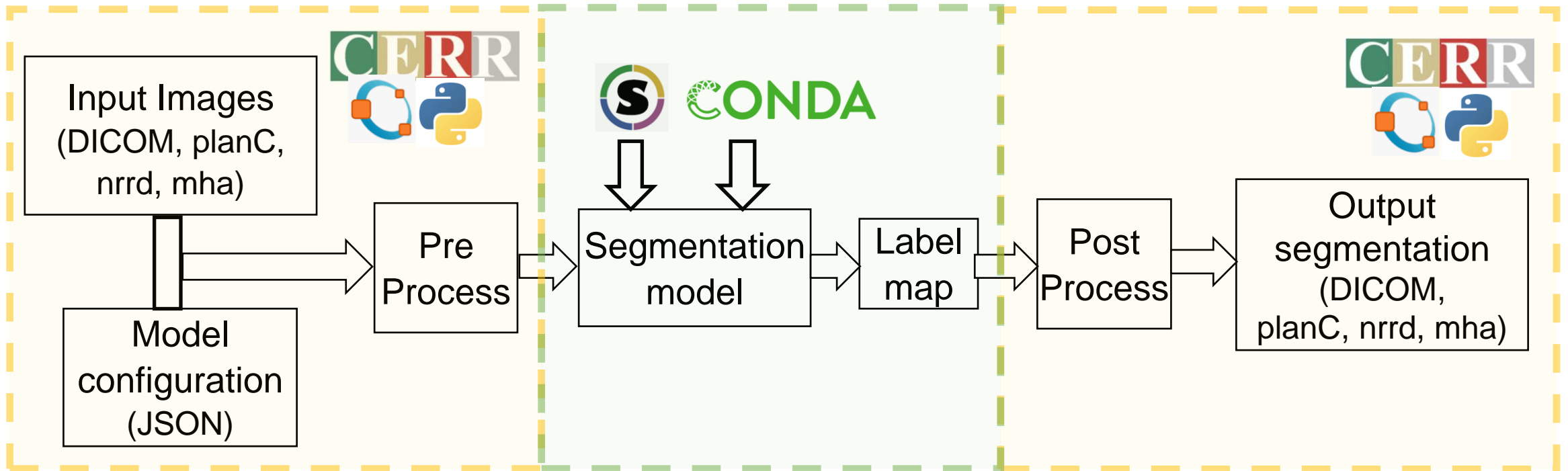
- Singularity containers
 - can be run by users without root privileges.
 - checksums for making the software stacks reproducible
 - compatibility with HPC systems and enterprise architectures
- SingularityHub, DockerHub
- ModelHub (<http://modelhub.ai>) - repository of self-contained deep learning models pretrained for a wide variety of applications.



Model deployment

- Containers
 - Singularity unavailable for Windows.
 - Docker requires admin privilege, so not suitable for bare metal HPC.
 - Containers cannot be run within another container (e.g. Google Colab)
- Anaconda
 - Package manager for Python and R (also supports other
 - Requires dependencies (e.g., CUDA) to be installed on the host machine.

Portable framework for image segmentation



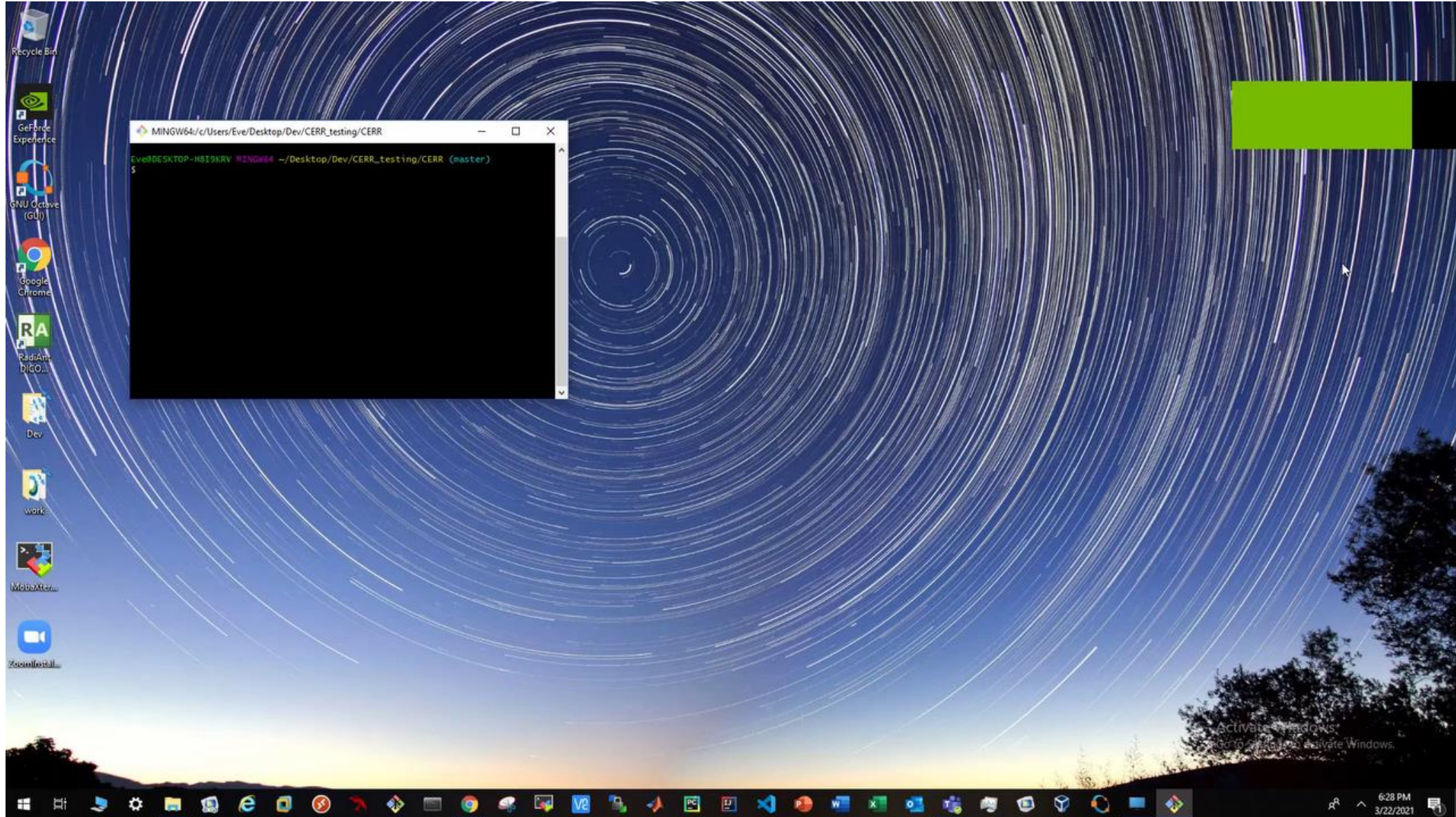
Aditi Iyer, Eve Locastro, Aditya P. Apte, Harini Veeraraghavan, Joseph O. Deasy, Portable framework to deploy deep learning segmentation models for medical images, bioRxiv 2021.03.17.435903; doi:

<https://doi.org/10.1101/2021.03.17.435903>.

Aditya P. Apte, Aditi Iyer, Maria Thor, et al, Library of deep-learning image segmentation and outcomes model- implementations, Physica Medica, Volume 73, 2020, Pages 190-196, ISSN 1120-1797,

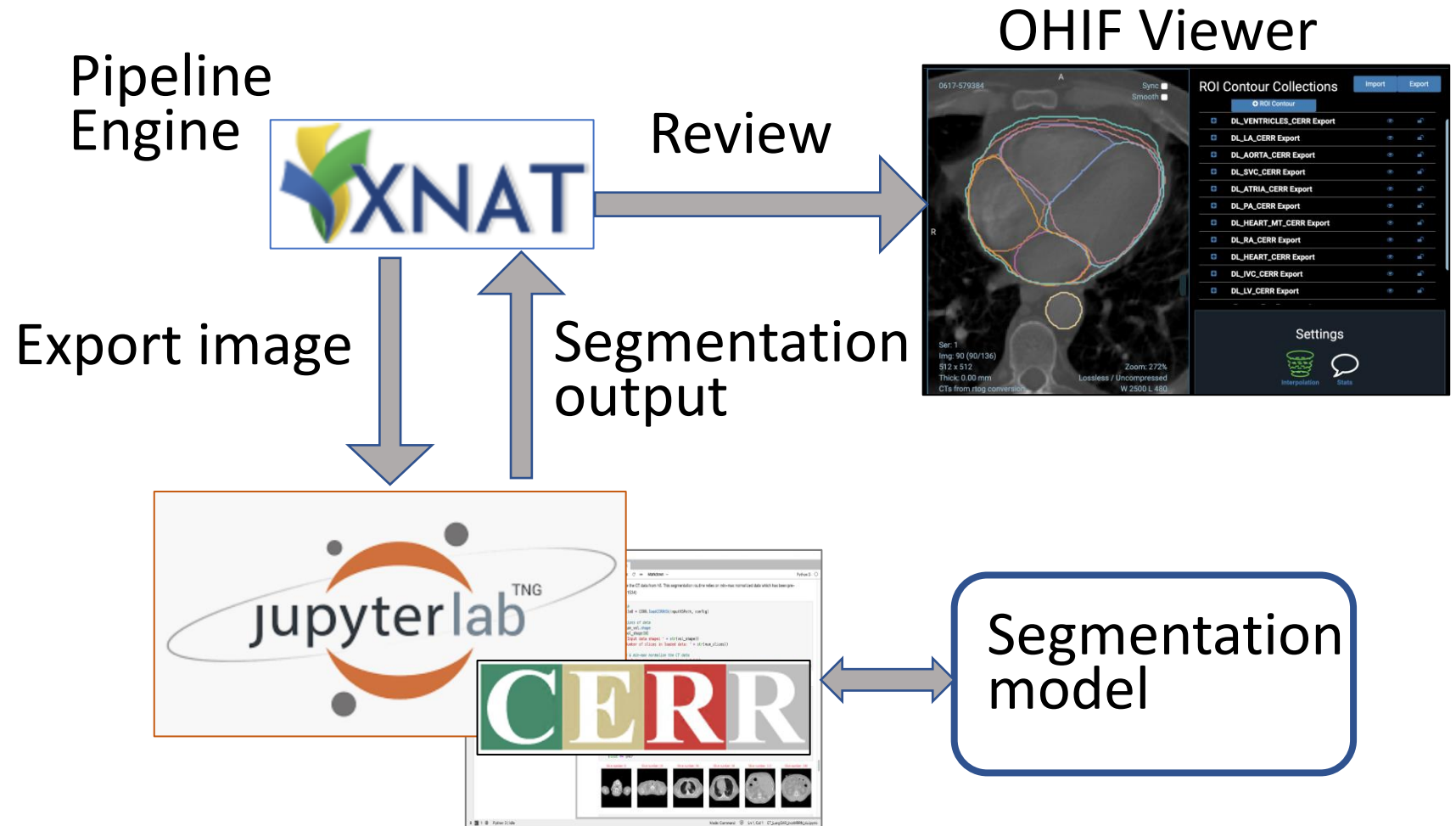
<https://doi.org/10.1016/j.ejmp.2020.04.011>.

AI Segmentation example using CERR

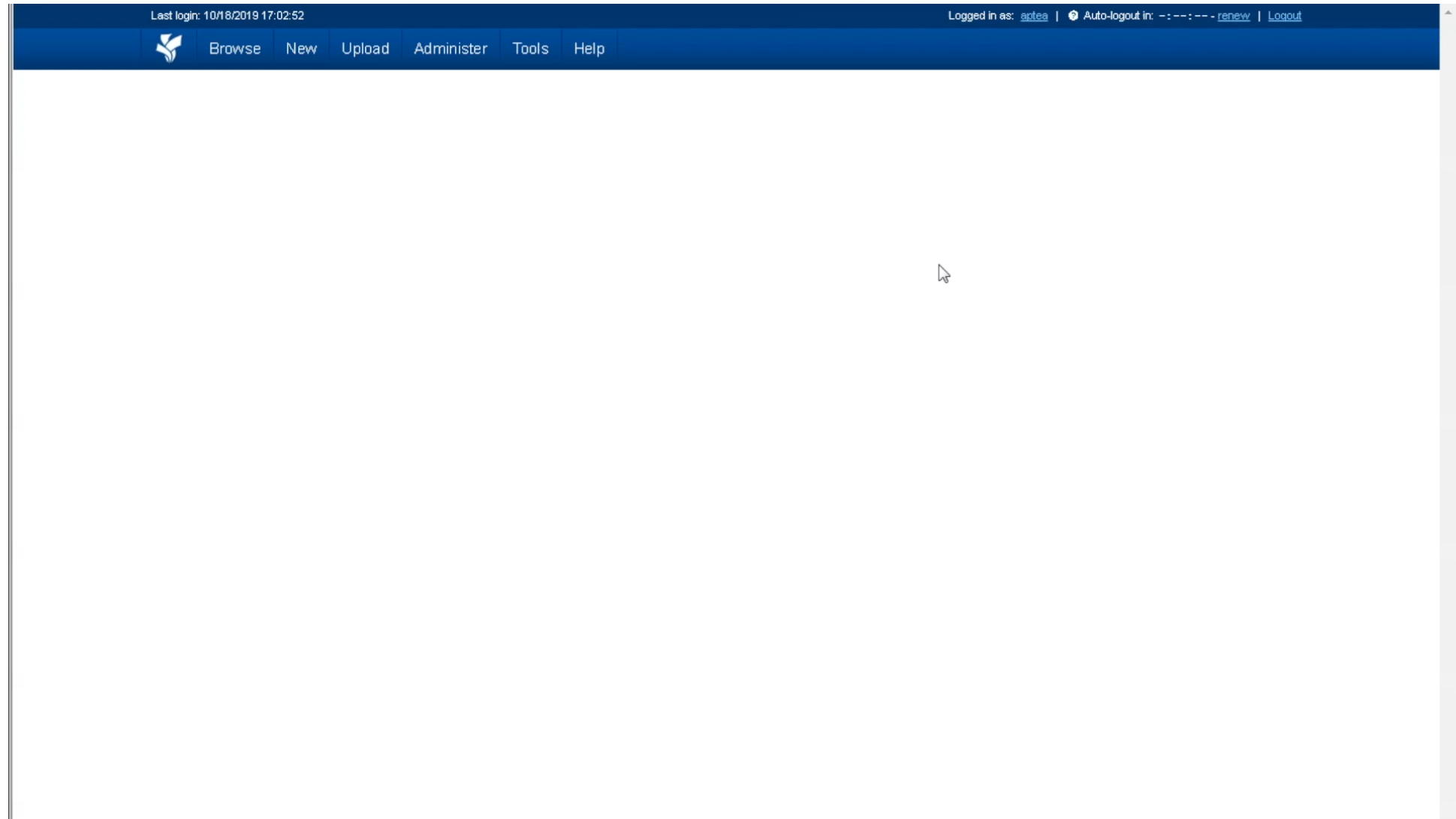


XNAT Pipeline Engine / Event service

- XNAT is an open-source project produced by Neuroinformatics Research Group at the Washington University School of Medicine.
- Centralized data management resource to multiple investigators and research studies.
 - Import, archive, manage and securely distribute imaging datasets.



XNAT segmentation pipeline demo



Fully automatic vs user-assisted contouring

- Semi-automatic:
 - Thresholding, region growing available in clinical software and research tools such as ITKSnap, 3DSlicer, CERR.
- Active-learning
 - FOVIA
 - NVIDIA Clara
 - MONAI-label

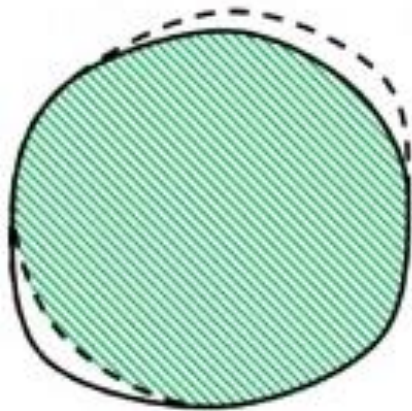
The MONAI-label is a server-client system that facilitates interactive medical image annotation by using AI. It is an open-source and easy-to-install ecosystem that can run locally on a machine with one or two GPUs. Both server and client work on the same/different machine. (Reference: <https://github.com/Project-MONAI/MONAIlabel>)

Example of AI assisted segmentation (DeepGrow3D) in FOVIA

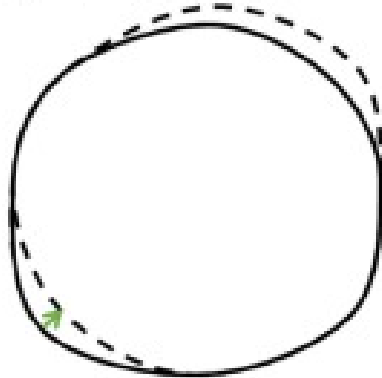


Reference: <https://www.youtube.com/watch?v=bllg2lwSfO4>

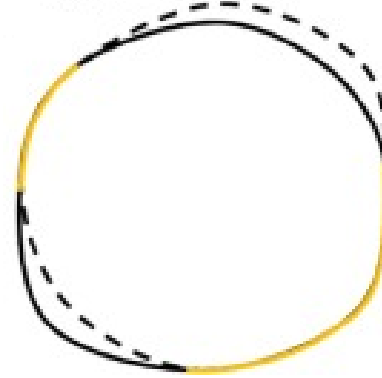
Segmentation performance evaluation



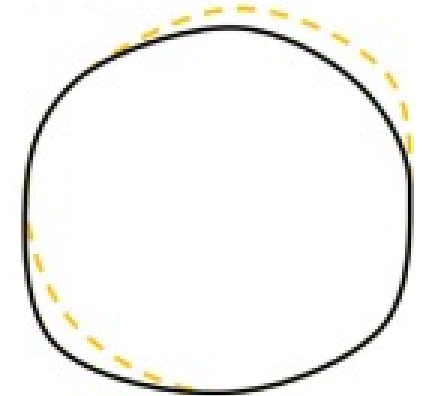
Volumetric DICE



Hausdorff 95 distance



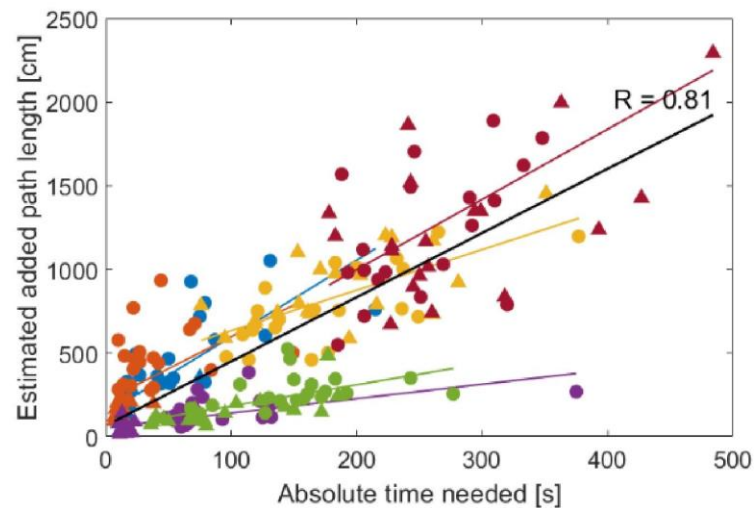
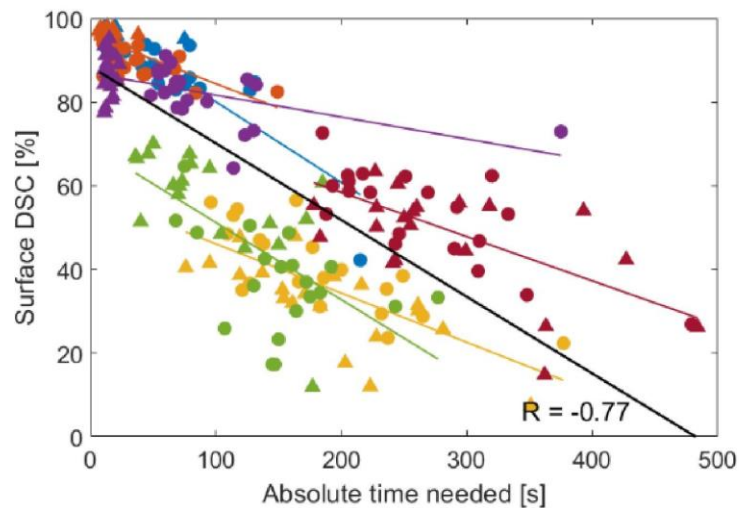
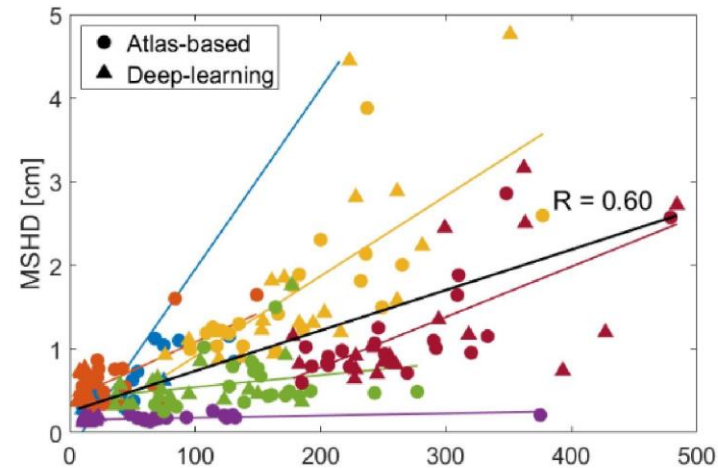
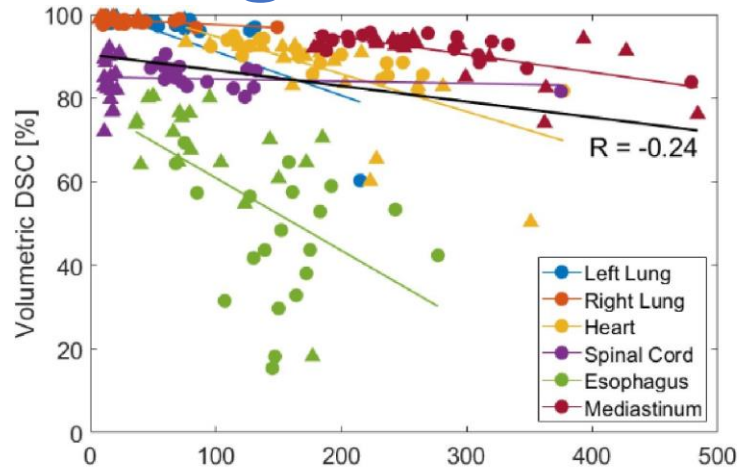
Surface DICE



Added Path Length

Reference: Femke Vaassen, Colien Hazelaar, Ana Vaniqui, et al, Evaluation of measures for assessing time-saving of automatic organ-at-risk segmentation in radiotherapy, Physics and Imaging in Radiation Oncology, Volume 13, 2020, Pages 1-6, ISSN 2405-6316, <https://doi.org/10.1016/j.phro.2019.12.001>

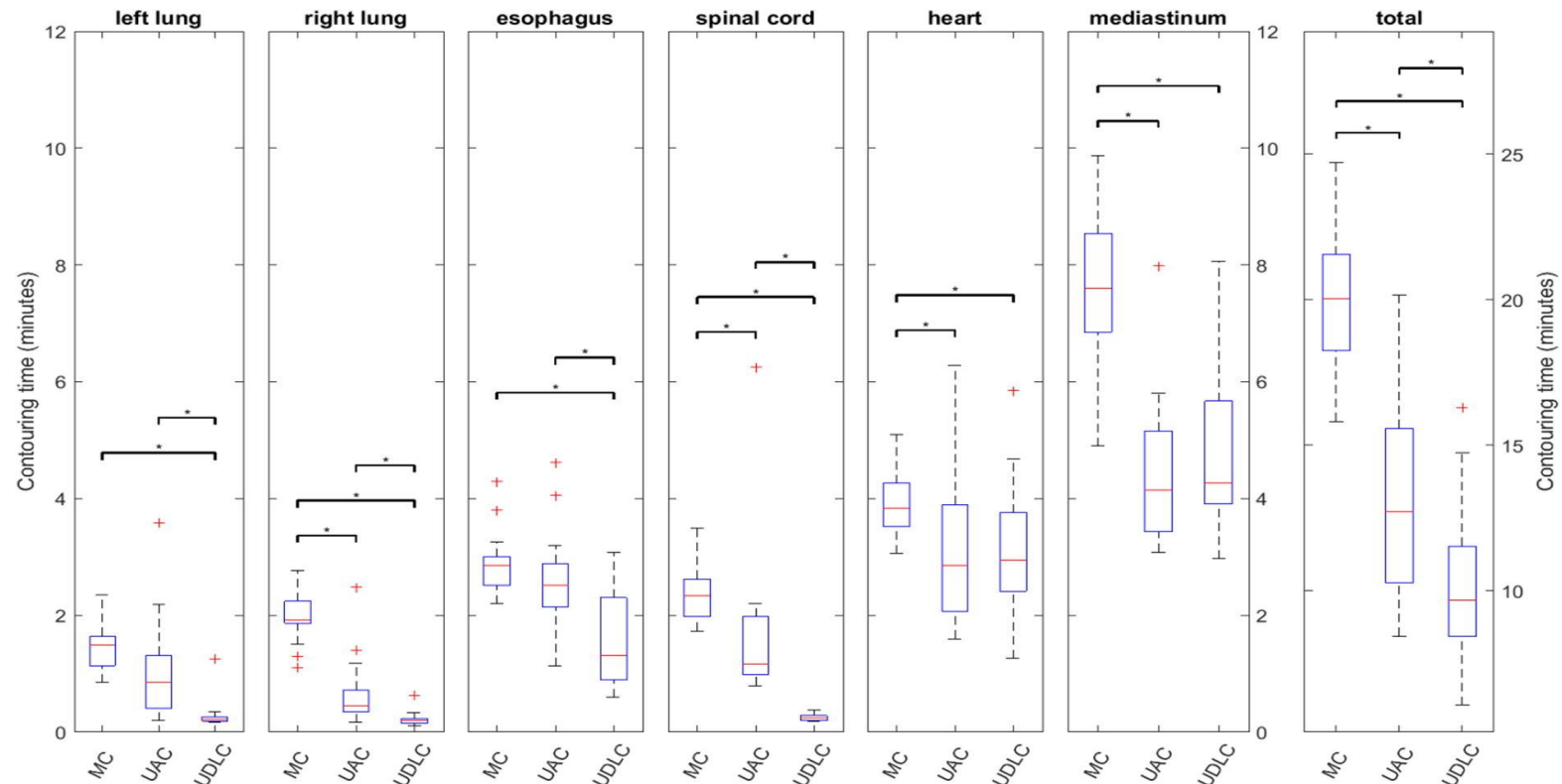
APL correlates with time required for contouring



Reference: Femke Vaassen, Colien Hazelaar, Ana Vaniqui, et al, Evaluation of measures for assessing time-saving of automatic organ-at-risk segmentation in radiotherapy, Physics and Imaging in Radiation Oncology, Volume 13, 2020, Pages 1-6, ISSN 2405-6316, <https://doi.org/10.1016/j.phro.2019.12.001>

Manual vs AI contours – time savings (Thoracic CT)

Comparison between DL and Atlas based contouring for Lung OARs. DL resulted in significant time saving over Atlas based and manual contouring.



Reference: Tim Lustberg, Johan van Soest, Mark Gooding, Clinical evaluation of atlas and deep learning based automatic contouring for lung cancer, Radiotherapy and Oncology, Volume 126, Issue 2, 2018, Pages 312-317, ISSN 0167-8140, <https://doi.org/10.1016/j.radonc.2017.11.012>

Manual vs AI contours – time savings (Prostate CT)

CT acquisition

MAN	DEEP	ATLAS
1) Import CT to TPS	1) Import CT to DEEP software	1) Import CT to TPS
2) Initial contour generation (10.9 ± 4.6 min)	2) Initial contour generation (1.4 ± 0.1 min)	2) Initial contour generation (1.2 ± 0.2 min)
3) Task RO to review contours	3) Export contours to TPS	3) Task RO to review contours
4) RO contour review and editing (4.1 ± 2.5 min)	4) Import CT and contours to TPS	4) RO contour review and editing (10.2 ± 5.7 min)
	5) Task RO to review contours	
	6) RO Contour review and editing (4.7 ± 2.6 min)	
Total: 15.3 min	Total: 6.8 min	Total: 11.7 min

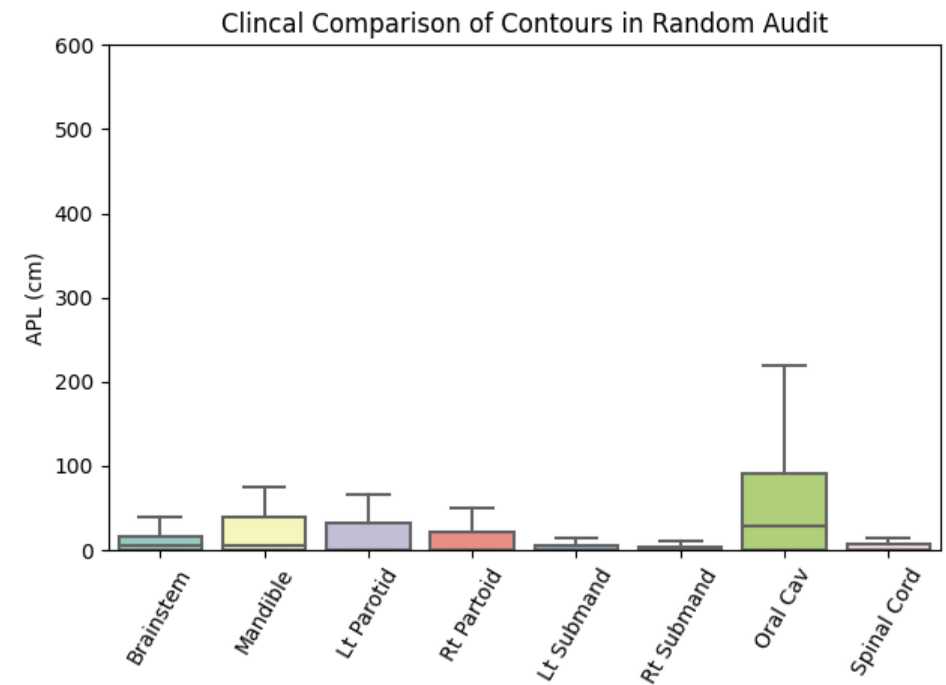
Comparison between DL and Atlas based contouring for Prostate OARs. DL resulted in significant time saving over Atlas based and manual contouring.

Reference: W. Jeffrey Zabel, Jessica L. Conway, Adam Gladwish et al, Clinical Evaluation of Deep Learning and Atlas-Based Auto-Contouring of Bladder and Rectum for Prostate Radiation Therapy, Practical Radiation Oncology, Volume 11, Issue 1, 2021, Pages e80-e89, ISSN 1879-8500,

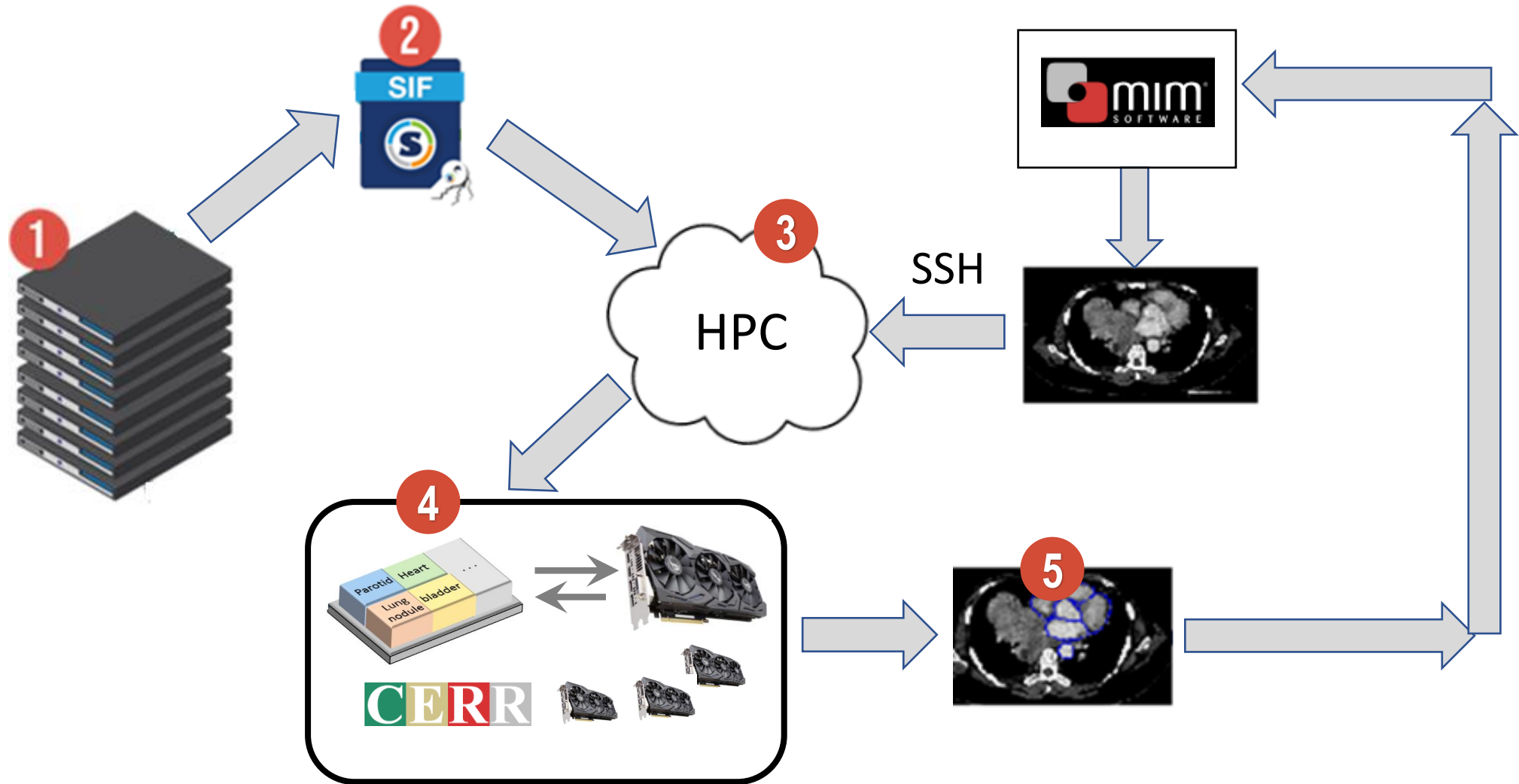
<https://doi.org/10.1016/j.prro.2020.05.013>

Clinical experience at MSKCC (Elguindi *et al*)

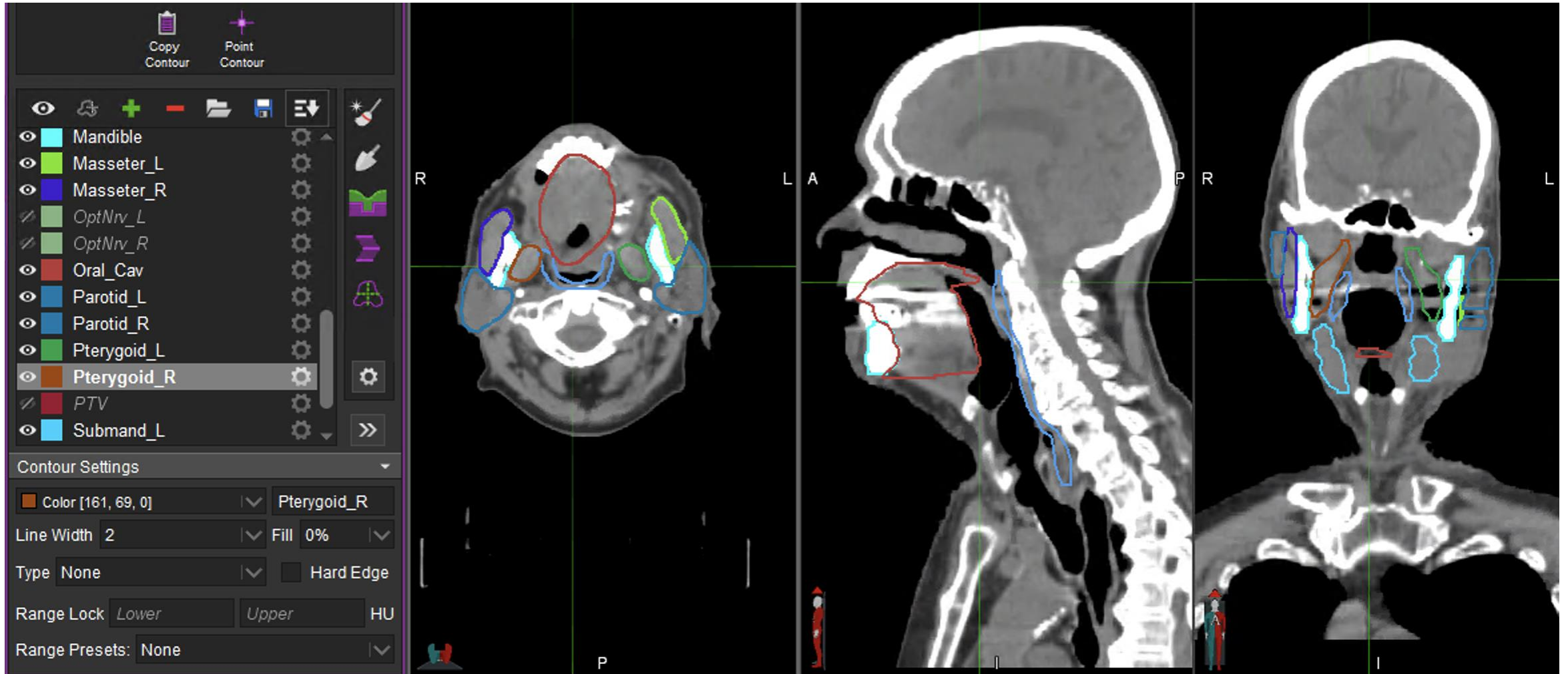
- Rollout for clinical use:
 - Prostate T1 axial MR – 2019 (Elguindi *et al*, Physics and Imaging in Radiation Oncology, Vol.12, pp. 80-86, 2019,)
 - H&N CT (Jiang et al, arXiv:1909.05054 and Iyer et al, bioRxiv 772178)
 - Released May 2020
 - Updated Model: Mid Feb 2021
 - Dataset: 174 patients collected (106 v1, 64 v2), out of approximately 350 patients in total
 - Structures contoured:
 - Left/Right parotids, Left/Right submandibular glands, brainstem, mandible, Cord, Oral Cavity, Left/Right medial pterygoid and Left/Right masseter muscles
 - Average APL: 194.6 cm, average time savings of 8.6 minutes with Left/Right parotids, Left/Right submandibular glands, brainstem.



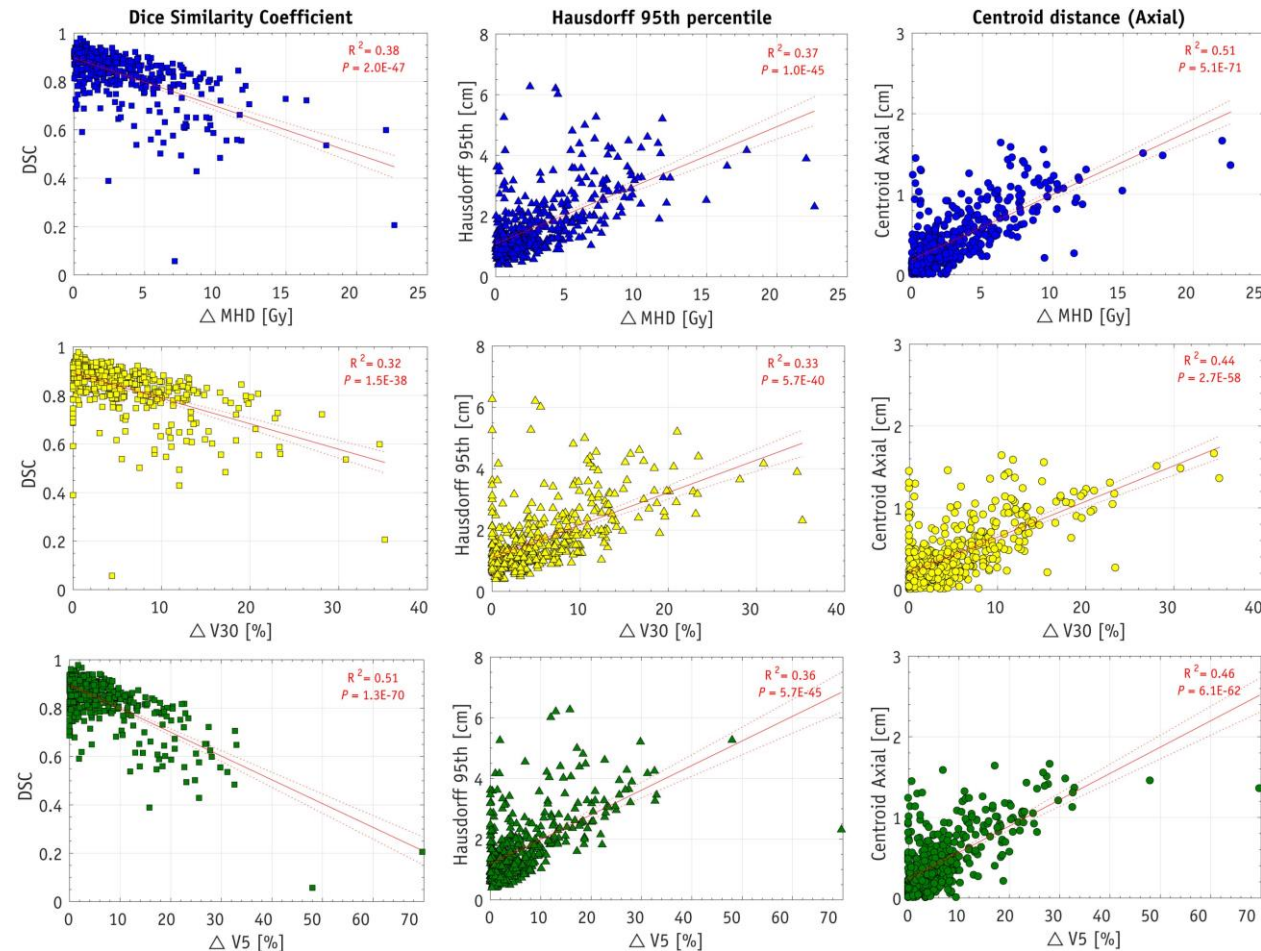
Clinical Workflow: HPC + Containers



Deep learning-based segmentation of OARs in H&N CT scan



Consistent segmentation in clinical trials



Reference: Maria Thor, Aditya Apte, Rabia Haq, et al, Using Auto-Segmentation to Reduce Contouring and Dose Inconsistency in Clinical Trials: The Simulated Impact on RTOG 0617, International Journal of Radiation Oncology*Biophysics, Volume 109, Issue 5, 2021, Pages 1619-1626, ISSN 0360-3016, <https://doi.org/10.1016/j.ijrobp.2020.11.011>

Models available in CERR

SITE	MODALITY	ORGAN/S	MODEL / FRAMEWORK	REFERENCE
Lung	CT	Heart, Heart sub-structures, Pericardium, Atria, Ventricles	DeepLabV3 / Pytorch	Haq et al, Physics and Imaging in Radiation Oncology, Vol 14, pp 61-66, 2020 https://doi.org/10.1016/j.phro.2020.05.009
Lung	CT	Nodules	Incremental MRRN / Keras, Tensorflow	Jiang et al, IEEE Transactions on Medical Imaging, 38(1): 134 – 144 https://doi.org/10.1109/TMI.2018.2857800
Prostate	MRI	Bladder, Prostate and Seminal Vesicles (CTV), Penile Bulb, Rectum, Urethra and Rectal Spacer	DeepLabV3+, Tensorflow-GPU	Elguindi et al, Physics and Imaging in Radiation Oncology, Vol.12, pp. 80-86, 2019, https://doi.org/10.1016/j.phro.2019.11.006
Head & Neck	CT	Masseters (left, right), Medial Pterygoids (left, right), Constrictor muscles (superior, middle, inferior) and Larynx	DeepLabV3+ / Pytorch	Iyer et al, https://www.biorxiv.org/content/10.1101/772178v2.full
Head & Neck	CT	Parotids (left, right), Mandible, Sub-mandibular glands (left, right), Brain stem	Self attention / Pytorch	Jiang et al, https://arxiv.org/abs/1909.05054

Models available in open-source frameworks

- **NVIDIA Clara** (<https://docs.nvidia.com/clara/deploy/BundledPipelines/index.html>)
 - Pipelines for Liver, Spleen, Lung, Lung tumor, Pancreas tumor, Colon tumor, Brain tumor.
- **DeepInfer** (<http://www.deepinfer.org/pages/models/>)
 - Prostate segmentation for T2 MRI, Brain tumor segmentation for Axial T1 MRI and FLAIR
- **ModelHub** (<http://modelhub.ai/>)
 - Liver and liver tumor segmentation for CT, Brain tumor segmentation, prediction of dental artifacts, Right ventricle segmentation from MRI scan,

Deep Learning Criticisms

- Long on data but short on knowledge, medical reasoning, and new insights. (Partho P. Sengupta and Y.S. Chandrashekhar, “Building Trust in AI: Opportunities and Challenges for Cardiac Imaging”, J Am Coll Cardiol Img. 2021 Feb, 14 (2) 520–522)
 - External validation to explore the model generalizability in external patient cohorts obtained from different institutions, geographic boundaries, and different time periods.
 - Approaches to probe and interpret AI techniques have been proposed recently with the emergence of techniques like symbolic AI, knowledge graphs, and their underlying semantic technologies that can provide reasoning mechanisms.

Conclusion

- Numerous open-source frameworks to train and deploy models for clinical and research use.
- Standardizing data processing pipelines enable reproducible application of models
- Encapsulating models in containers makes them readily deployable, hence facilitating their validation on external/unseen datasets.
- AI is already helping to boost productivity in clinic. This is just the beginning!

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- Joseph O. Deasy, Ph.D