
A Collaborative Approach To AI Research: *Designing AI for Hepatocellular Carcinoma*



A presentation by Dr. Sunil Jeph and OpenVessel LLC



Dr. Sunil Jeph

Director of Computer Vision
Research, CRRG

Assistant Professor of Radiology
Penn State College of Medicine

OpenVessel Presenters



Leslie Wubbel
CEO & Founder



Nathaniel Leies
Business Dev &
Marketing



Alex Schweizer
Product Developer

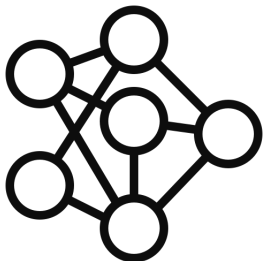


OpenVessel LLC is an
AI research consultant.

We provide *data science
consultation and solutions
to academic physicians*
to power their AI research.



OpenVessel | What We Do



Collaboratively
*engineer AI / ML
solutions* with
investigators.



Collaboratively *design
experiments*, and
oversee the entire
experiment process.



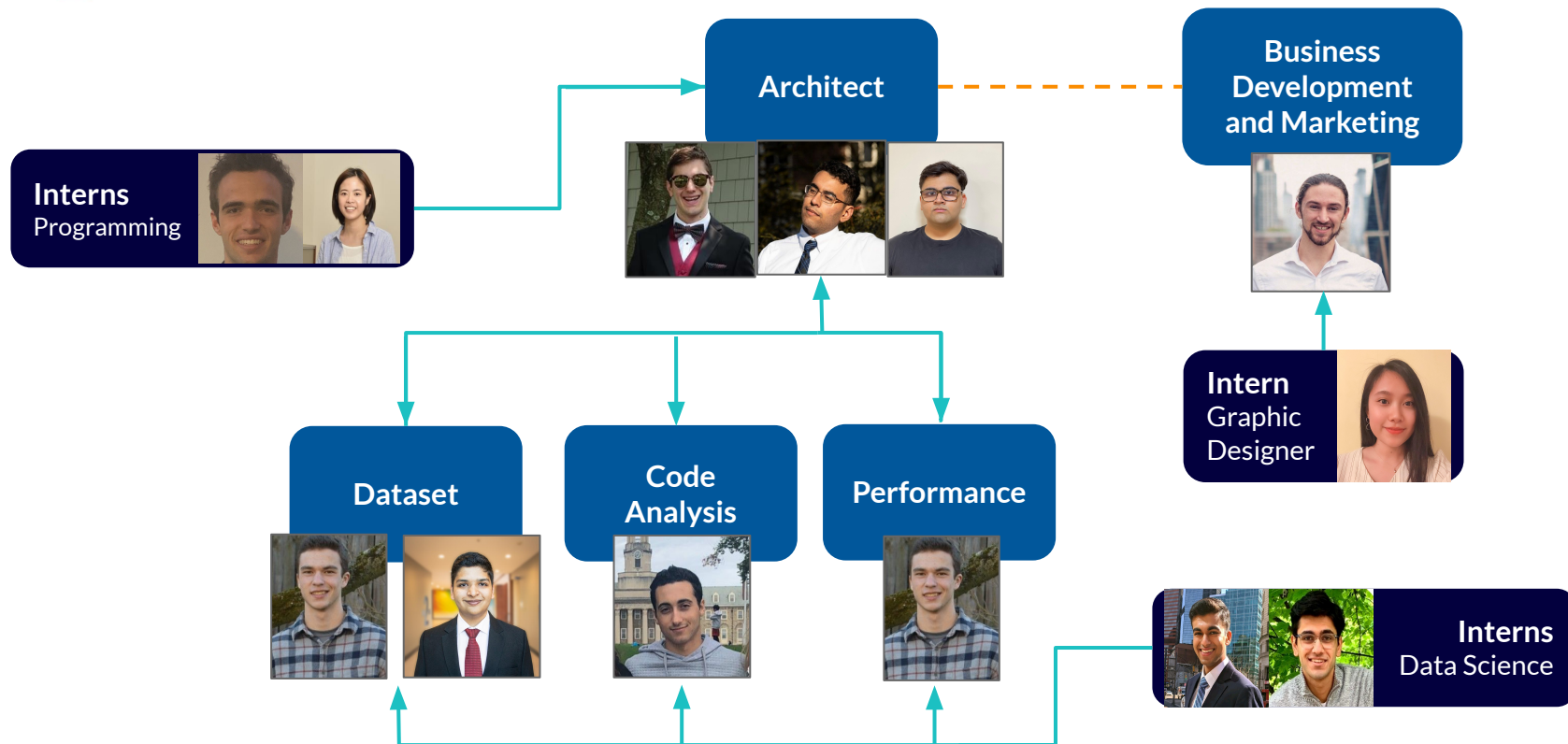
*Co-author impactful
research* and successful
funding applications.



Establish a foundation
of data-science
research upon which
*our clients can build
their success.*



OpenVessel | Our Team



Working with Penn State College of Medicine

*December
2020*



Contacted CRRG | Offered pro-bono Medical AI project

Promise: Recruit and train PSU undergraduate interns

*January
2021*



Connected with Dr. Jeph | Identified clinical problem

*January –
February*



Developed **OpenVessel Deep Learning AI Model**

Collaborated with Dr. Jeph: Biweekly meetings | Phone calls | Slack

*March
2021*



Demonstrate Deep Learning AI Model | Develop abstracts



Our Project Goal with Dr. Jeph

Engineer a model that can ***detect and classify*** hepatocellular carcinoma (HCC).

SCOPE OF WORK

- Train model with open-access liver CTs
- Record results
- Create abstracts
- Utilize model in publications, promoting PSU College of Medicine



OpenVessel

Timelines & Deliverables

March 2nd 2021

March - June

June 30th 2021

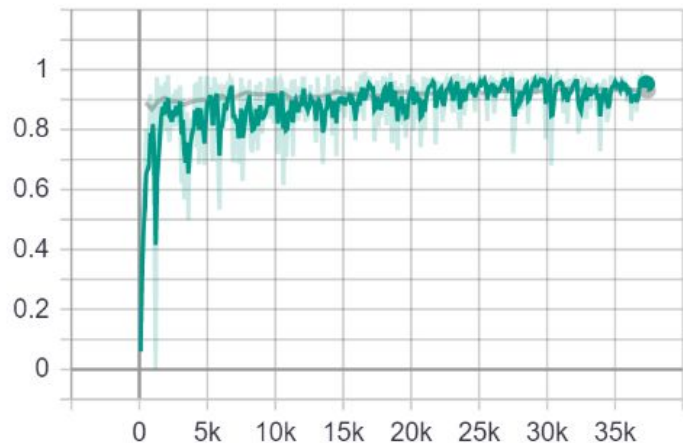


Dr. Jeph's Previous AI Research

Automatic Segmentation of Autosomal Dominant Polycystic Kidney Disease Using Deep Learning with Multi-institutional Validation

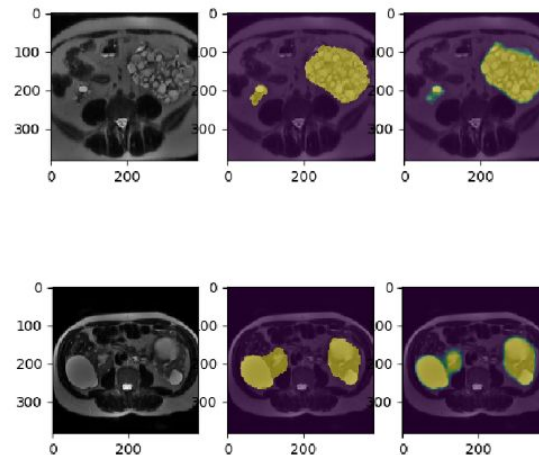
Akshay Goel MD, Sunil Jeph MD, Sadjad Riyahi MD, Martin Prince MD

dice_metric



Gray = Validation, Green = Training

Sample Predictions on Validation (input, ground truth, prediction)



Clinical Problem

Dr. Jeph requested that we address **liver research**.

"Primary liver cancer is the second most common cause of cancer death" [1].

Opportunity to introduce **multiphase CT** data from Penn State to the OpenVessel model.



Above: Dr. Jeph introduced OpenVessel team to LIRADS classification and the multiphase CT modality in a collaborative meeting.

OpenVessel AI / ML Consultation



Client Ask

Create a data model that will continue Dr. Jeph's research on segmentation/data modeling. Interested in AI for the liver.

What OpenVessel Offered

Building a deep learning model to segment and classify liver cancer. Access to openly available liver CTs and AI codebases provided a starting point.



Liver Tumor Segmentation (LiTS) Dataset

We used the LiTS Dataset, available through the [LiTS Challenge](https://lits-challenge.com), an AI competition launched in 2017.

SPECIFICATIONS

- 130 CT Scans
- 57.6 GB
- Contains pixel volumes and labels
- Variance in contrast levels

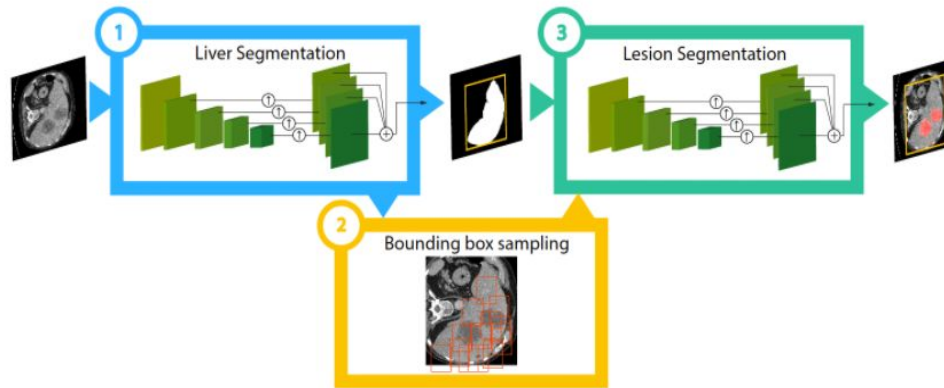
ABNORMALITIES

- Primary & secondary cancers
- Variance in lesion shapes and sizes
- Variance in number of lesions per study

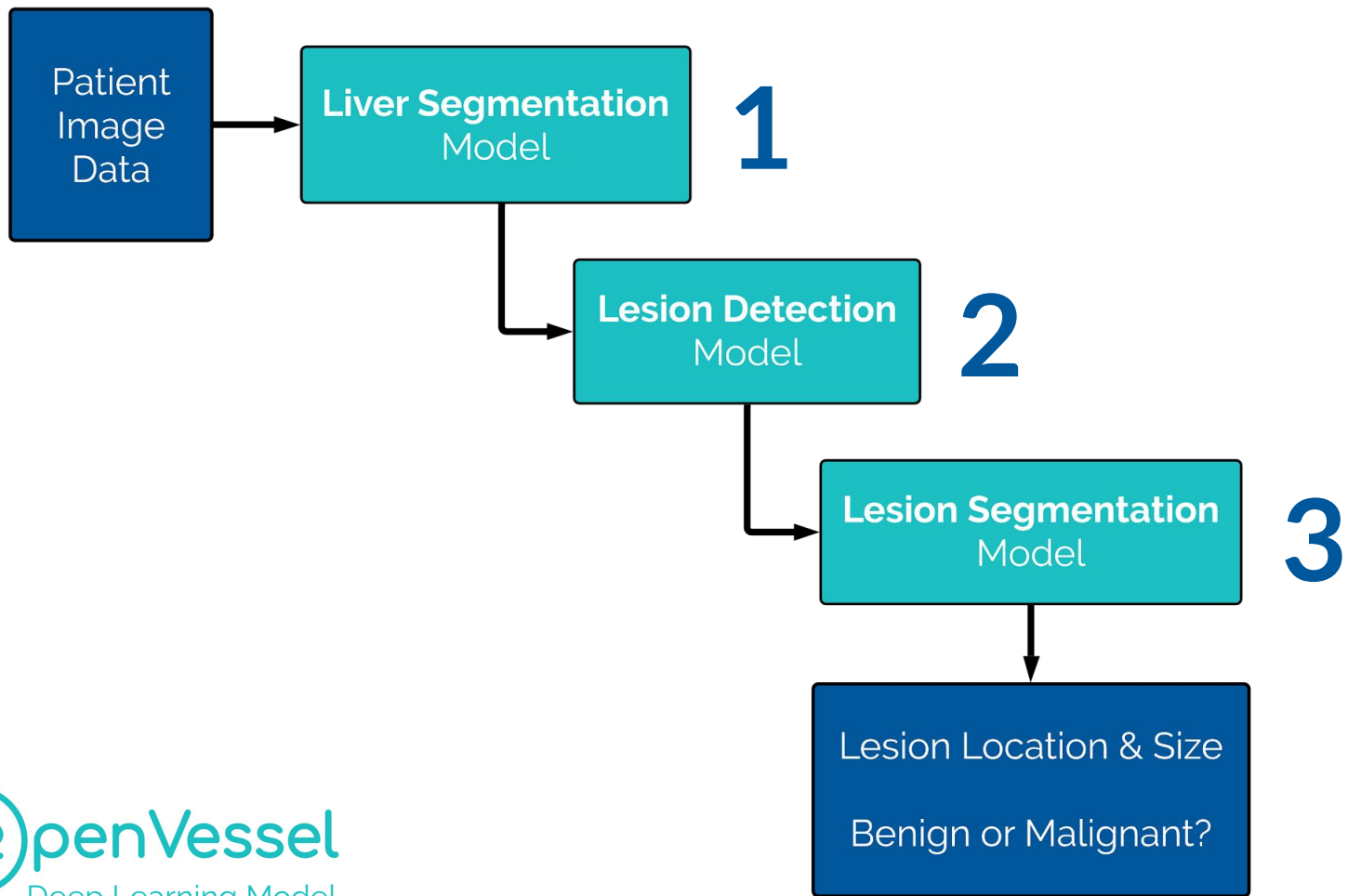


OpenVessel Deep Learning Model

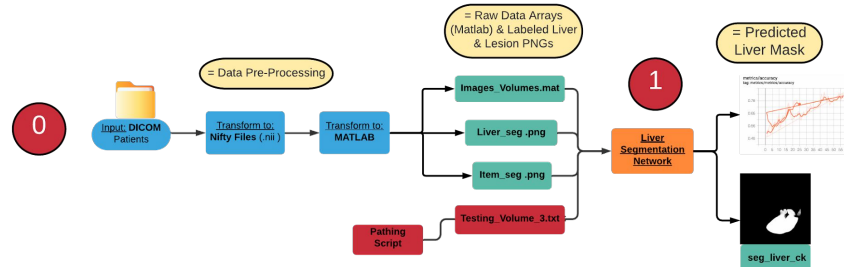
- Started with Barcelona Tech Deep Learning Model (2017), an open source code base
- We validated the model by rebuilding it
- Automated manual processes
- Debugged extensive problems
- Arrived at OpenVessel Deep Learning Model (2021)



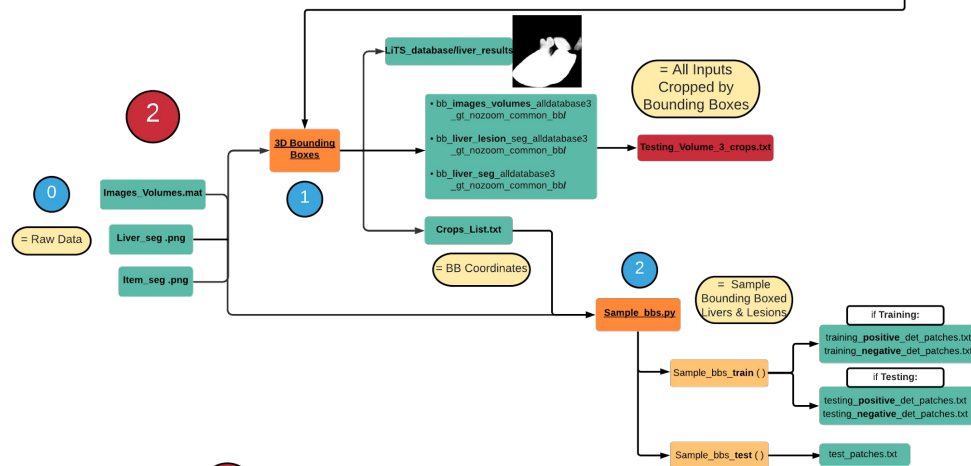
Above: Barcelona Tech Model



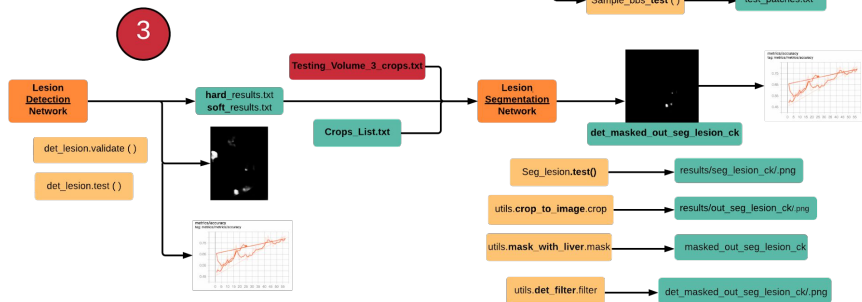
1 Preprocessing and Liver Segmentation



2 Lesion Detection



3 Lesion Segmentation



Work Timeline | 2 Month Progress



GitHub

[OpenVessel Github Repository](#)

Estimated Total Hours
1,680

Number of FTEs
6

**Average employee
contribution per week**
35 hours





OpenVessel

Bringing AI closer to healthcare.

<https://www.dev.openvessel.org/> openvessel@openvessel.org

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Python 0 2 1 0 Updated 3 hours ago



liverseg-2017-nipsws

Forked from [imatge-upc/liverseg-2017-nipsws](#)
Detection-aided Liver Lesion Segmentation

Python MIT 47 1 4 0 Updated 3 hours ago



Top languages

Python JavaScript HTML

People

14 >




```
(MyVenv) PS D:\L_pipe\greg_branch\liverseg-2017-nipsws> python .\main.py  
Running step: seg_liver_test
```

```
Started loading files...
```

```
Done initializing Dataset
```

```
[]
```

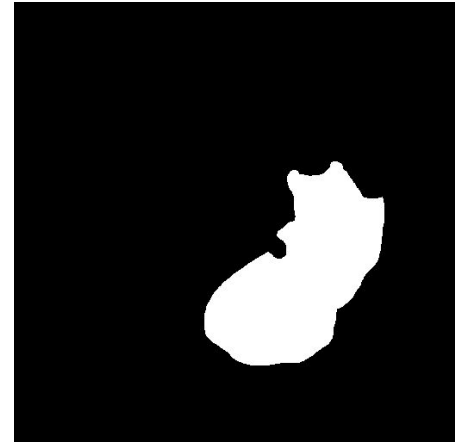
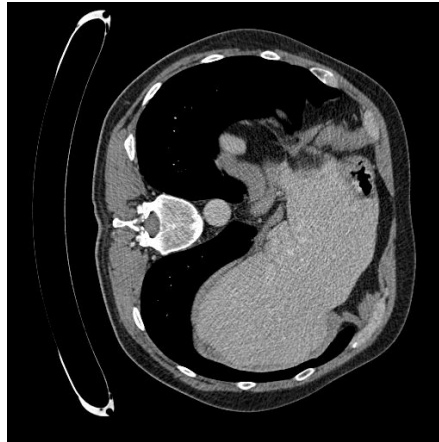
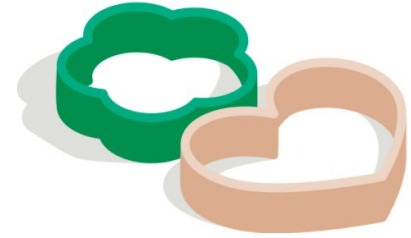
RESULTS



Terms to Know: Segmentation & Mask

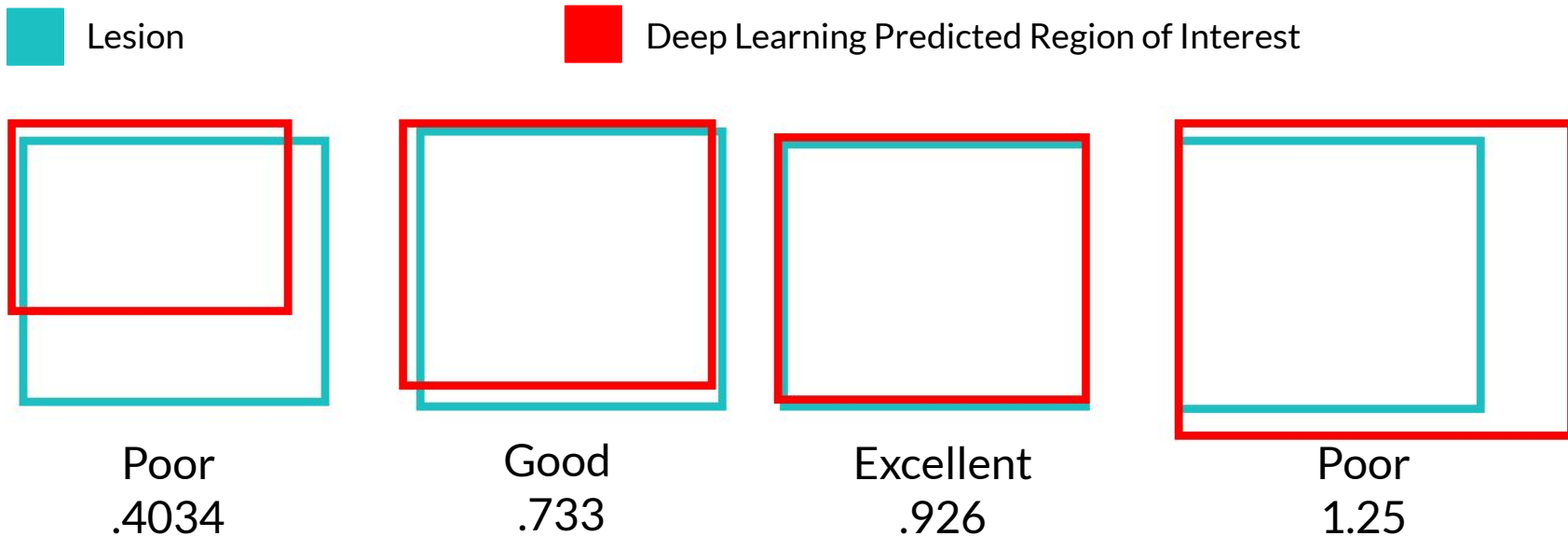
Segmentation of a Mask-

- Divides images into *parts or sections*
- Generates a **mask** that *outlines an object*
- By analyzing the HU values

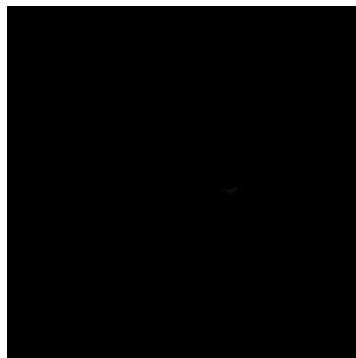


Understanding Evaluation Metrics | DICE Score

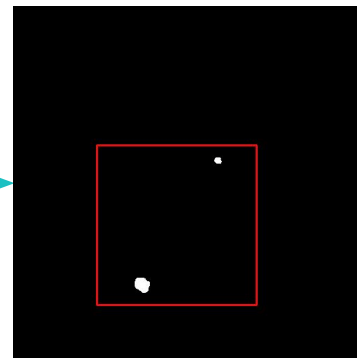
DICE is a metric describing how well a model identifies a lesion. Computed through overlap.



VISUAL OUTPUTS



Predicted Liver Mask



Detected Lesions

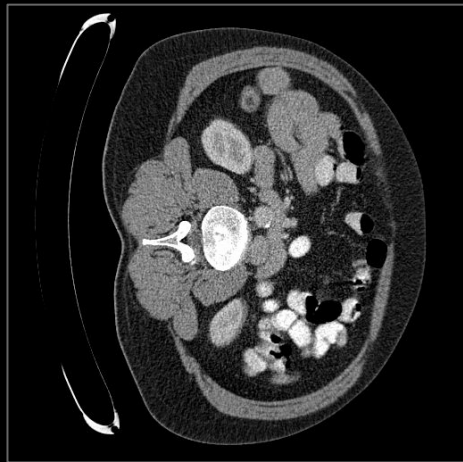


Predicted Lesion Mask

	Technical Description	DICE SCORE	Time
Liver Segmentation	Liver mask predicted by the model & segmented out of the region of interest (ROI) in the patient.	0.8233	4.11 m
Lesion Detection	Network classifies areas of interest in liver mask as positive (containing lesions) or negative.	0.68	1.90 m
Lesion Segmentation	The positive lesions are segmented out as results.	0.71	4.36 m

1 *Visual Results*

Liver Segmentation Network



Normal Patient CT Scan

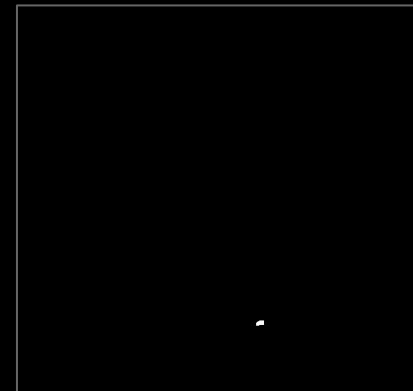
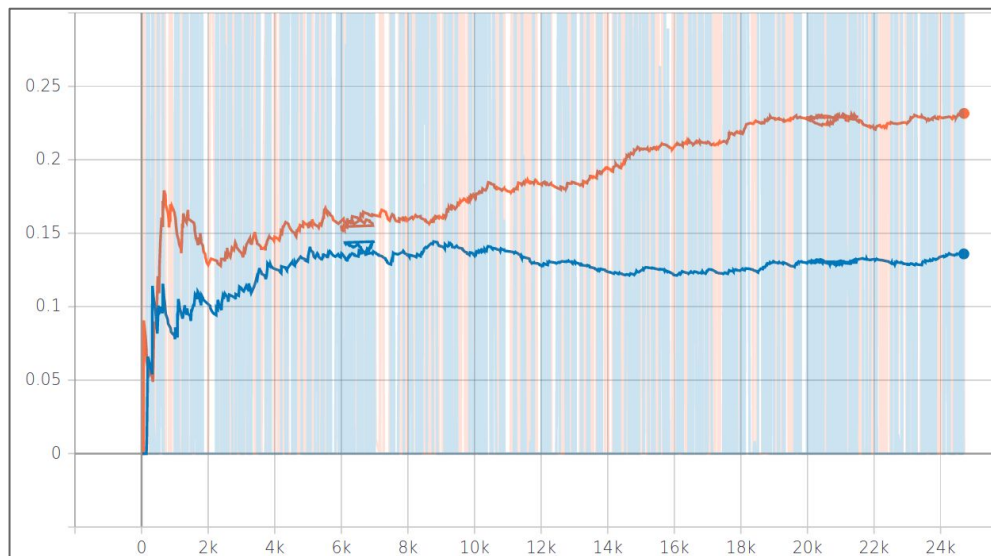


Deep Learning Predicted Result

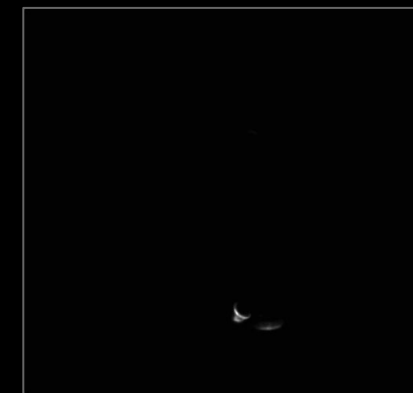
1 *Liver Segmentation Network*

Metrics

DICE SCORE - 0.8233 | TEST TIME - 4.11 Minutes



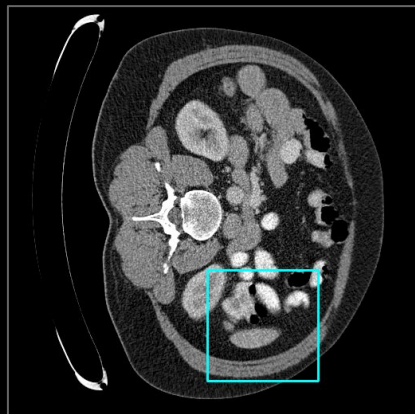
Liver identify by Radiologist



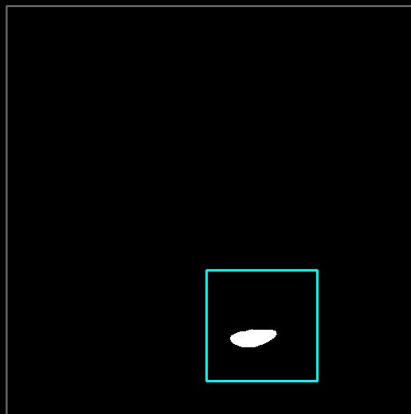
Deep Learning Predicted Result



2 Lesion Detection Network



Normal Patient CT Scan



Deep Learning Predicted Result

png')

Done step: compute_bbs_from_gt_liver

Time taken: 71 seconds or 1.0 minutes 11s to

Running step: sample_bbs_test

Done step: sample_bbs_test

Time taken: 6 seconds or 0.0 minutes 6s to ru

Running step: det_lesion_test

Started loading training files...

Started loading validation files...

Started loading testing files...

Done initializing Dataset

INFO:tensorflow:Restoring parameters from D:\

Testing D:\L_pipe\liver_open\liverseg-2017-ni

Testing D:\L_pipe\liver_open\liverseg-2017-ni

Testing D:\L_pipe\liver_open\liverseg-2017-ni

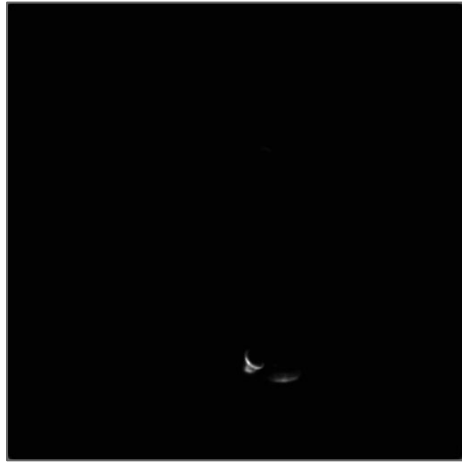
Testing D:\L_pipe\liver_open\liverseg-2017-ni

Testing D:\L_pipe\liver_open\liverseg-2017-ni

Testing D:\L_pipe\liver_open\liverseg-2017-ni

2 Lesion Detection Network

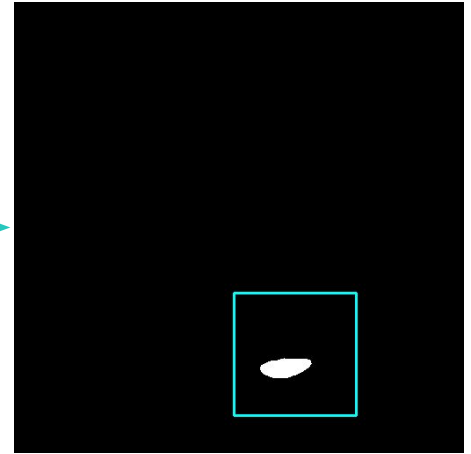
512 x 512 Liver Mask



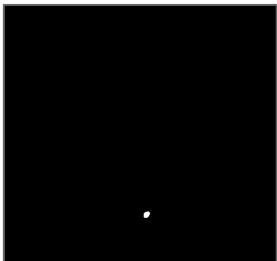
Zoomed Liver Mask



Sampled Liver Mask

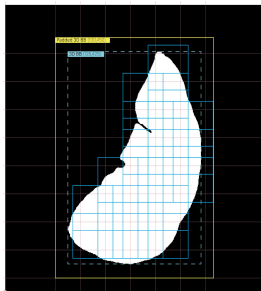


Sample = Inputs to Lesion Detection Network



Why samples?

- ***Simpler*** inputs for ***faster*** computation & better ***accuracy***
- Can create ***extra data*** among scarcity



What is a "sample"?

- 50 x 50 sample boxes w/ 15 pixel ***margins of error***
- A ***positive*** sample > 50 lesion pixels
- A ***negative*** sample < 50 lesion pixels



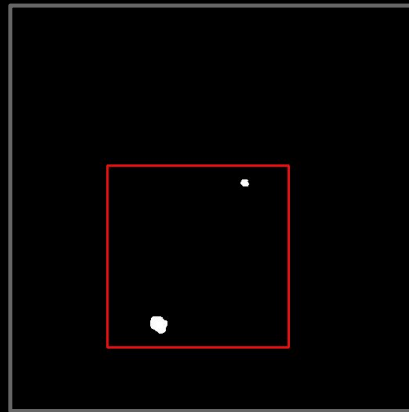
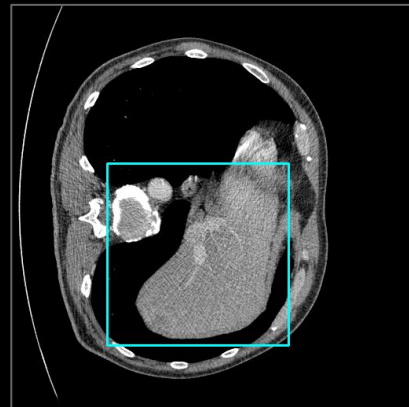
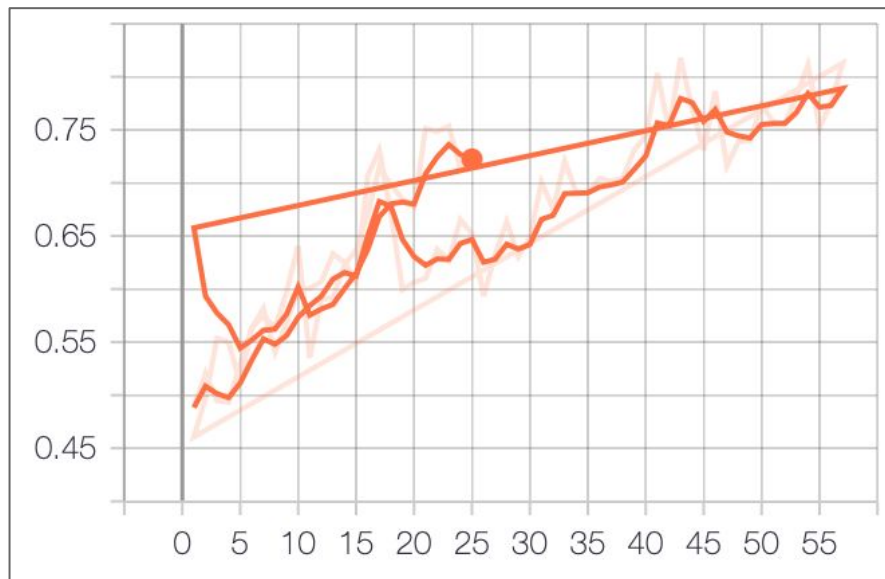
How do we determine which predicted lesions are segmented?

- If probability of lesion > 50% = a ***hard result***
- If probability of lesion < 50% = a ***soft result***

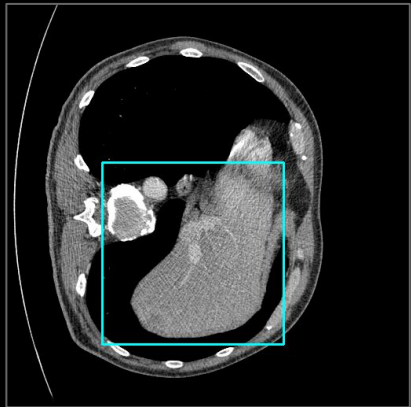


2 Lesion Detection Network Metrics

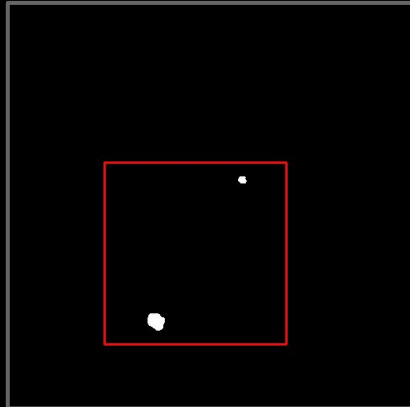
DICE SCORE - 0.68 | TEST TIME - 1.90 Minutes



2 Lesion Detection Network



Normal Patient CT Scan



Deep Learning Predicted Result

png')

Done step: compute_bbs_from_gt_liver

Time taken: 71 seconds or 1.0 minutes 11s to

Running step: sample_bbs_test

Done step: sample_bbs_test

Time taken: 6 seconds or 0.0 minutes 6s to ru

Running step: det_lesion_test

Started loading training files...

Started loading validation files...

Started loading testing files...

Done initializing Dataset

INFO:tensorflow:Restoring parameters from D:\

Testing D:\L_pipe\liver_open\liverseg-2017-ni

Testing D:\L_pipe\liver_open\liverseg-2017-ni

Testing D:\L_pipe\liver_open\liverseg-2017-ni

Testing D:\L_pipe\liver_open\liverseg-2017-ni

Testing D:\L_pipe\liver_open\liverseg-2017-ni

Testing D:\L_pipe\liver_open\liverseg-2017-ni

3

Lesion Segmentation Network

Lesion identified by radiologist

Deep Learning Predicted Result

[TERMINAL](#)
[DEBUG CONSOLE](#)
[PROBLEMS](#)
8
[OUTPUT](#)

[illegible]

Done step: det_lesion_test

Time taken: 152 seconds or 2.0 minutes 32s to r

Running step: seg_lesion_test

Started loading files...

Done initializing Dataset

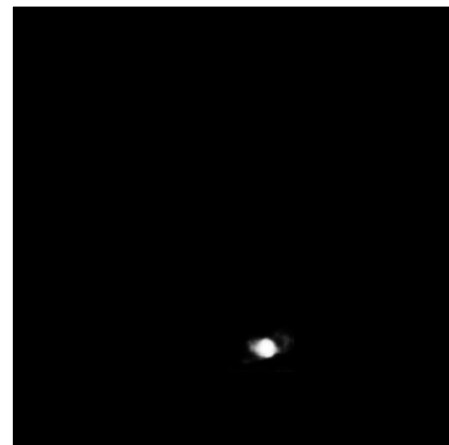
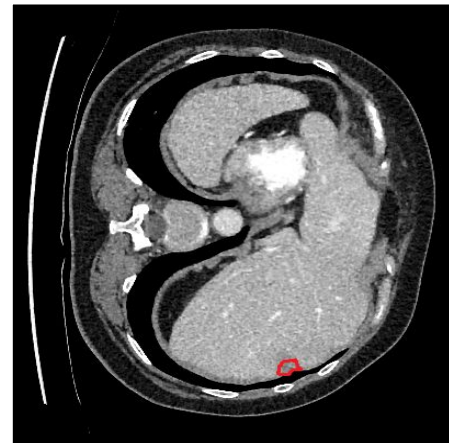
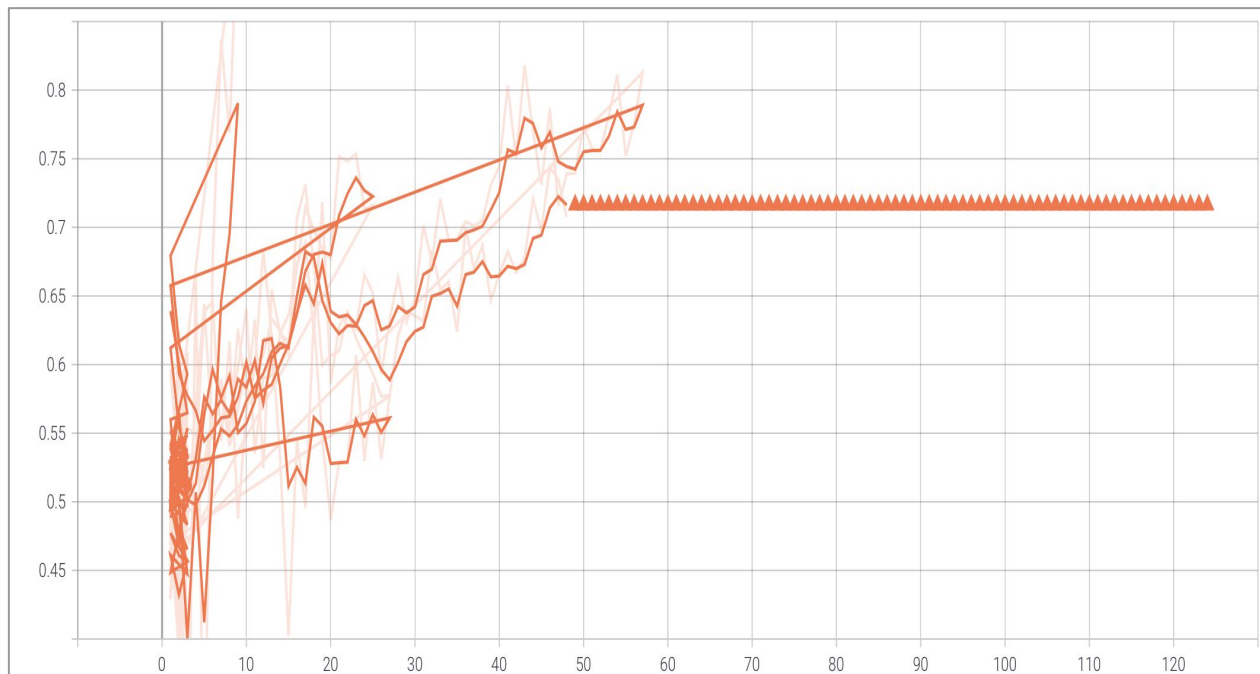
segmenting lesions

```
INFO:tensorflow:Restoring parameters from D:\L
```

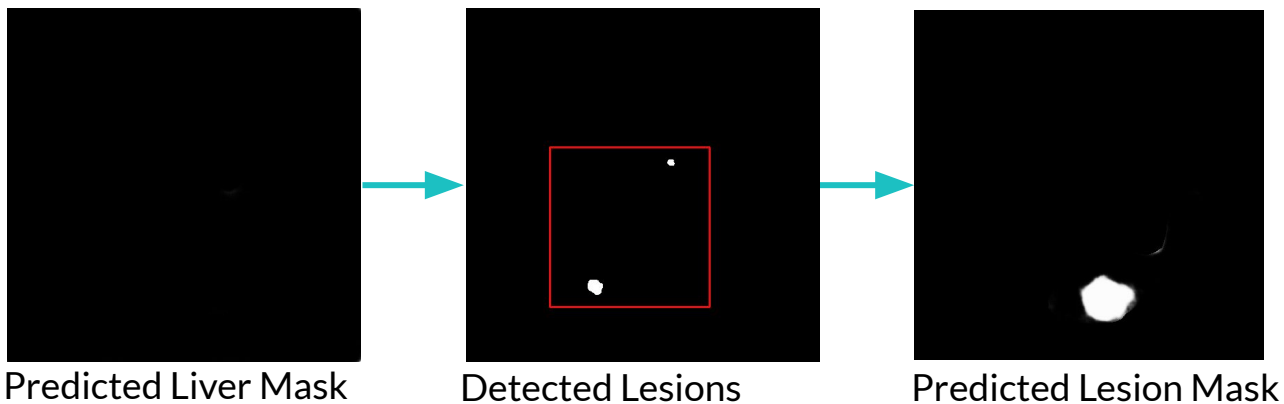
Saving D:\L_pipe\greg_branch\liverseg-2017-nips

3 Lesion Detection Network Metrics

DICE SCORE - 0.71 | TEST TIME - 4.36 Minutes



VISUAL OUTPUTS



	Technical Description	DICE SCORE	Time
Liver Segmentation	Liver mask predicted by the model & segmented out of the region of interest (ROI) in the patient.	0.8233	4.11 m
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NEXT STEPS

March - June 2021



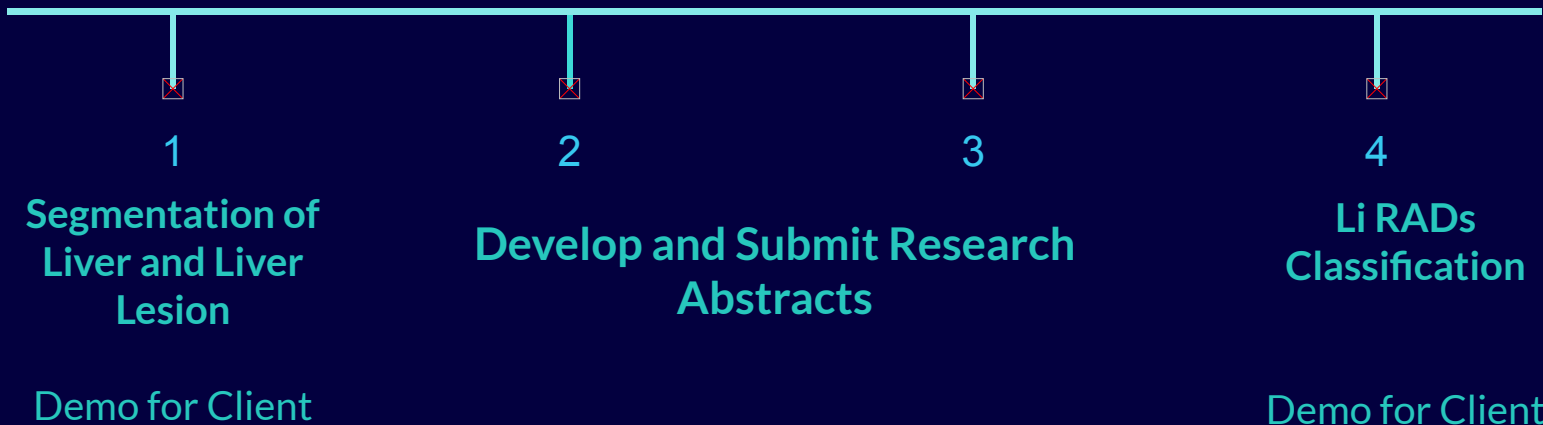
OpenVessel

Timelines & Deliverables

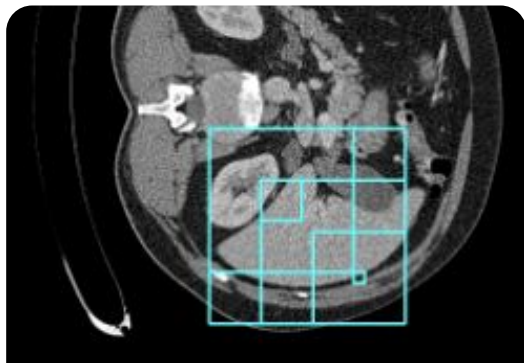
March 2nd 2021

March - June

June 30th 2021



Specific Objectives



Improving DICE Lesion Detection

Adaptive Thresholding

Google Collab/ Jupyter notebooks



**ROAR
Supercomputer**

User Interface



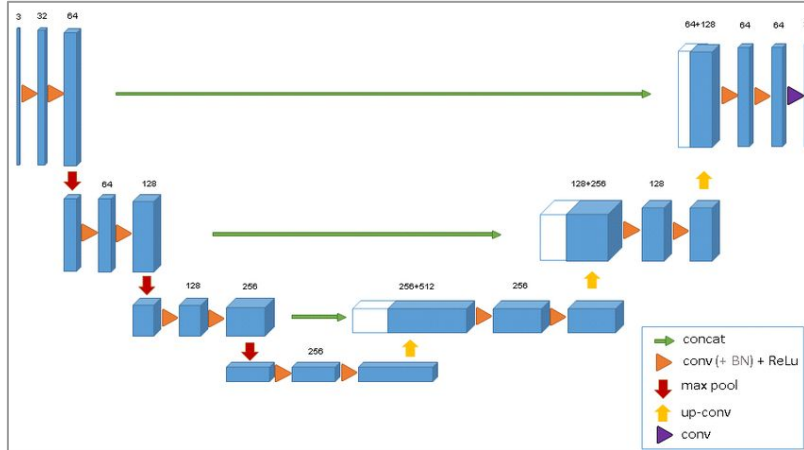
Dr. Jeph's Li-RADs Classification Data

Release Healthy Livers Dataset



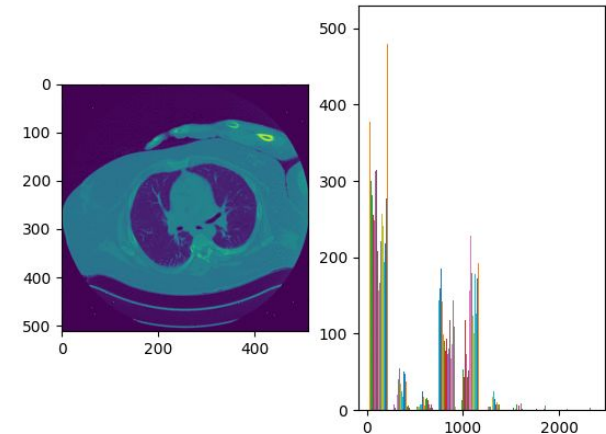
How to improve DICE?

- Engineering preprocessing
- Better bounding boxes
- Implement 3D U-net



Adaptive Thresholding

Dataset analysis & Adaptive Thresholding
Research (dataset description [report](#))



 K-means-to-binaryclass.ipynb ☆
File Edit View Insert Runtime Tools Help Last edited on Aug 30, 2020

Table of contents

First Layer of Masking

Second Layer of Masking

Exporting code to new image dataset training and test

Section

+ Code + Text

First Layer of Masking

Statistical input per 2D image or per slice

```
[ ] from google.colab import drive
drive.mount('/content/drive/')

!pip install pydicom
import numpy as np
import pydicom
import pandas as pd
import os
from pydicom import dcmread
dicom_stack = "/content/drive/My Drive/Vessel Outline storage/Input data/FUMPE_DATA/Patient_data/PAT001"

def load_scan(path):
    ## slices = [] is an array
    slices = [dcmread(path + '/' + s) for s in os.listdir(path)]
    slices.sort(key = lambda x: int(x.InstanceNumber))
    try:
        slice_thickness = np.abs(slices[0].ImagePositionPatient[2] - slices[1].ImagePositionPatient[2])
    except:
        slice_thickness = np.abs(slices[0].SliceLocation - slices[1].SliceLocation)

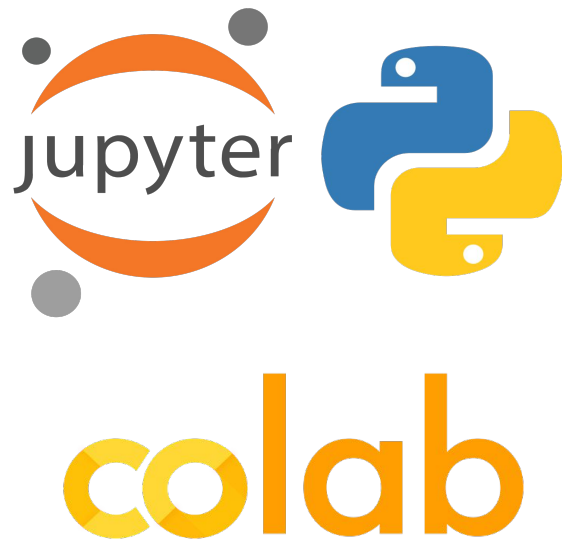
    for s in slices:
        s.SliceThickness = slice_thickness

    return slices

return slices

slice_thickness = slice_thickness

for s in slices:
```



PSU Supercomputer



Industrial level Research

- Run 5+ models all at once
- Unlimited storage
- CPU
- GPUs



Dr. Justin Matthew Petucci



Test User Interface for Researchers

×

ML python.exe path

./MyVenv/Scripts/python.exe

ML entry point

./backend/main.py



Liver-Lesion detection model interface

Output folder (absolute path)

C:/Users/grego/OneDrive/Projects/OpenVessel/StreamlitApp/results

Results of ML model will appear here

Name of function to run in ML entry point file

test

Run model on a collection of patients

Dataset folder (absolute path)

C:/Users/grego/OneDrive/Projects/OpenVessel/StreamlitApp/data

Folder should follow the structure **dataset_folder/105/1.dcm**

Run Collection

Running ML on collection

Running ML on patient 105

Running ML on patient 106

Or run model on a single patient

Upload set of DICOM files from a single scan



Drag and drop files here

Limit 200MB per file • DCM

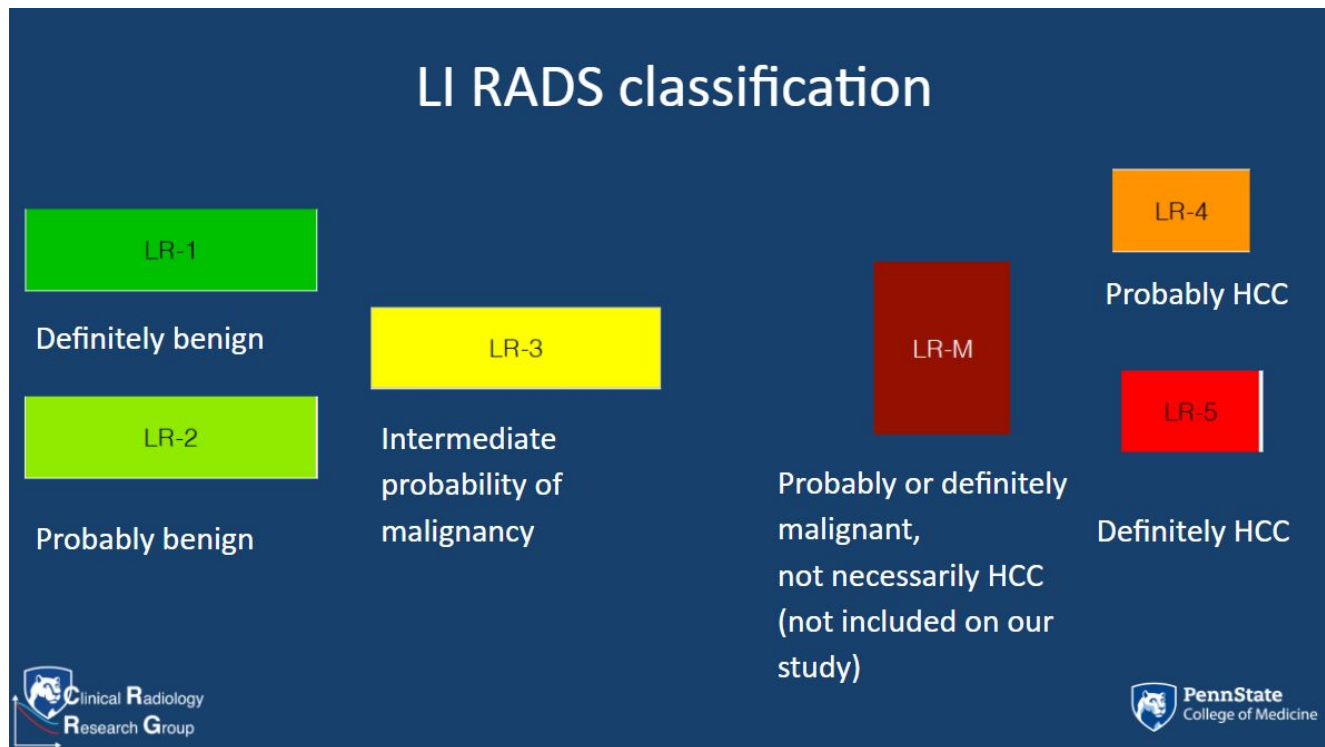
Browse files

Run Single Patient



LiRADs Classification

LiRADs classification research (dataset description [report](#))



Work Cited

- [1] Patrick Bilic, et al. (2019). "The Liver Tumor Segmentation Benchmark (LiTS)." arXiv: 1901.04056v1.
- [2] Kevis-Kokitsi Maninis and Jordi Pont-Tuset and Pablo Andrés Arbeláez and Luc Van Gool (2016). Deep Retinal Image Understanding *CoRR*, *abs/1609.01103*.
- [3] Özgün Çiçek, Ahmed Abdulkadir, Soeren S. Lienkamp, Thomas Brox, & Olaf Ronneberger. (2016). 3D U-Net: Learning Dense Volumetric Segmentation from Sparse Annotation.

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