

Medical CT at Extreme Scale using Synchrotrons

Professor Anders BJORHOLM DAHL
Technical University of Denmark
August, 2024

Human Organ Atlas Project



Human Organ Atlas Project

Human Organ Atlas

EXPLORE

SEARCH

3D RECONSTRUCTIONS

TUTORIALS

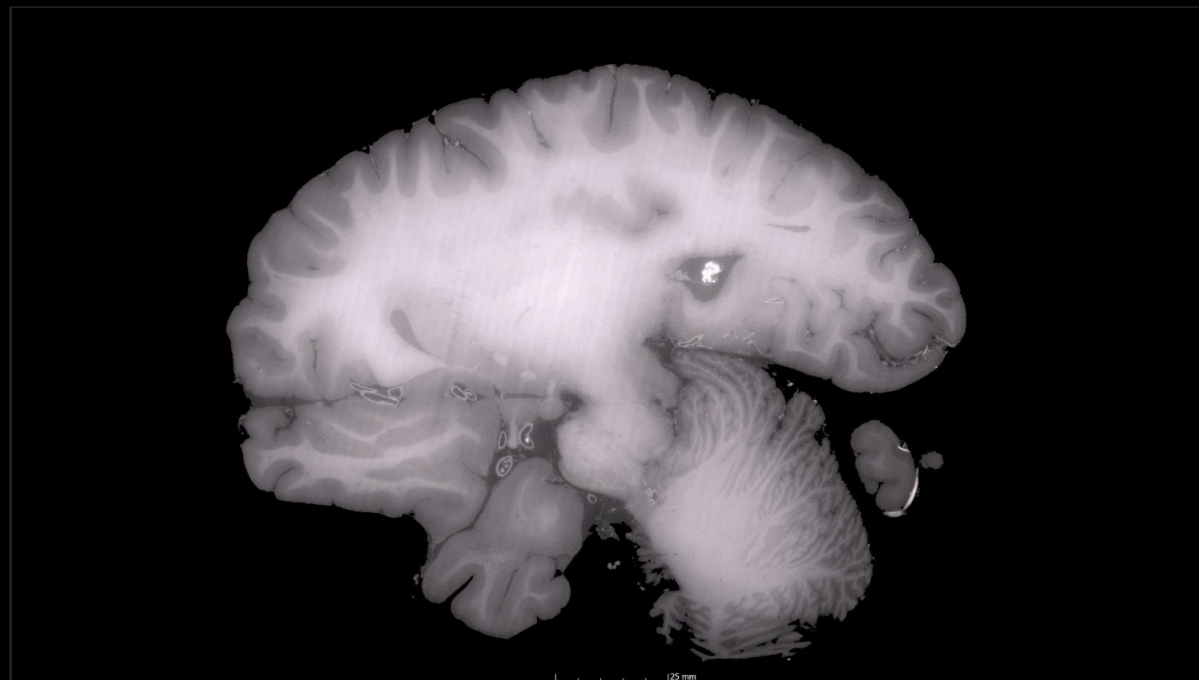
HELP

Welcome to the Human Organ Atlas

The Human Organ Atlas uses **Hierarchical Phase-Contrast Tomography** to span a previously poorly explored scale in our understanding of human anatomy, the micron to whole intact organ scale.

Histology using optical and electron microscopy images cells and other structures with sub-micron accuracy but only on small biopsies of tissue from an organ, while clinical CT and MRI scans can image whole organs, but with a resolution only down to just below a millimetre. **HiP-CT** bridges these scales in 3D, imaging intact organs with ca. 20 micron voxels, and locally down to microns.

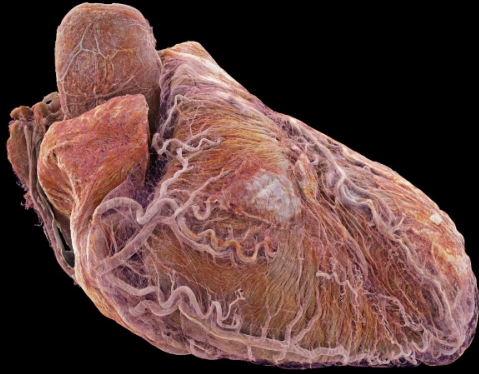
We hope this open access Atlas, enabled by the ESRF-EBS, will act as a reference to provide new insights into our biological makeup in health and disease. To stay up to date, follow [@HiP-CT](#)



HiP-CT imaging and 3D reconstruction of a **complete brain** from the body donor LADAF-2020-31. More videos can be viewed on the [HiP-CT YouTube channel](#).

Organs

Heart



Brain



Left kidney



Right kidney



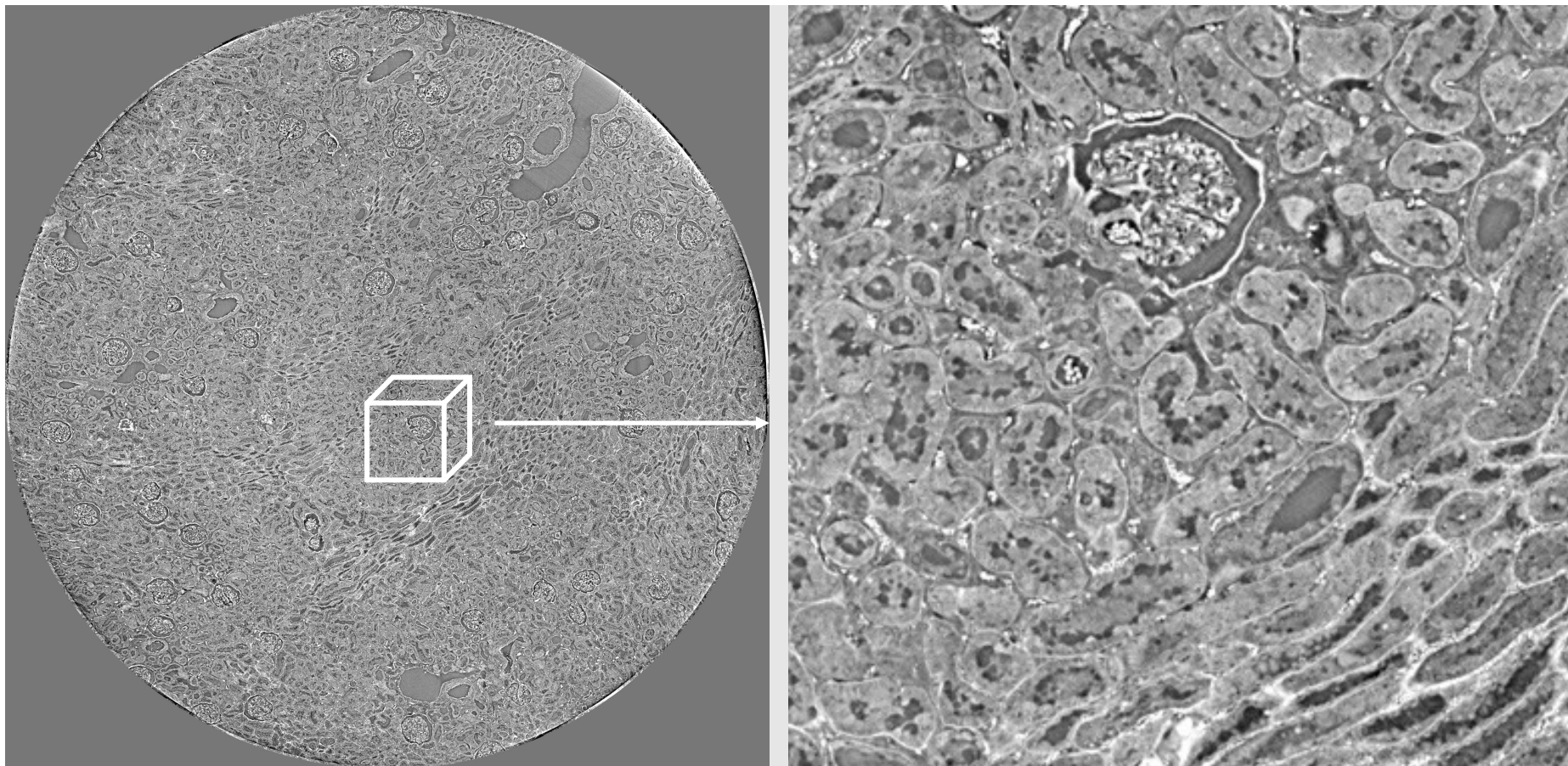
Spleen



Multiple organs
Multiple scales
Large volumes
Available online

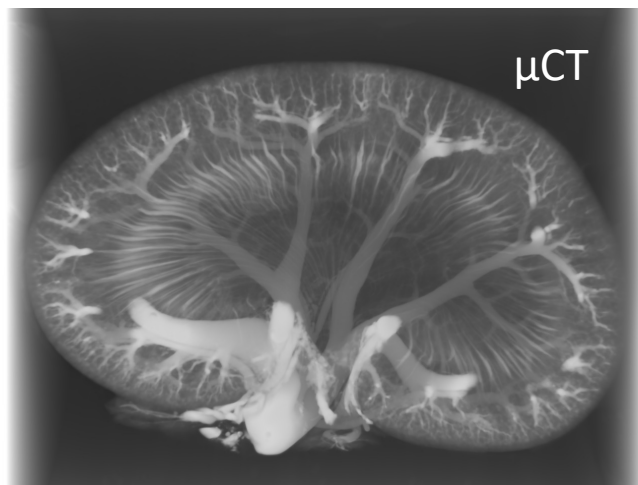
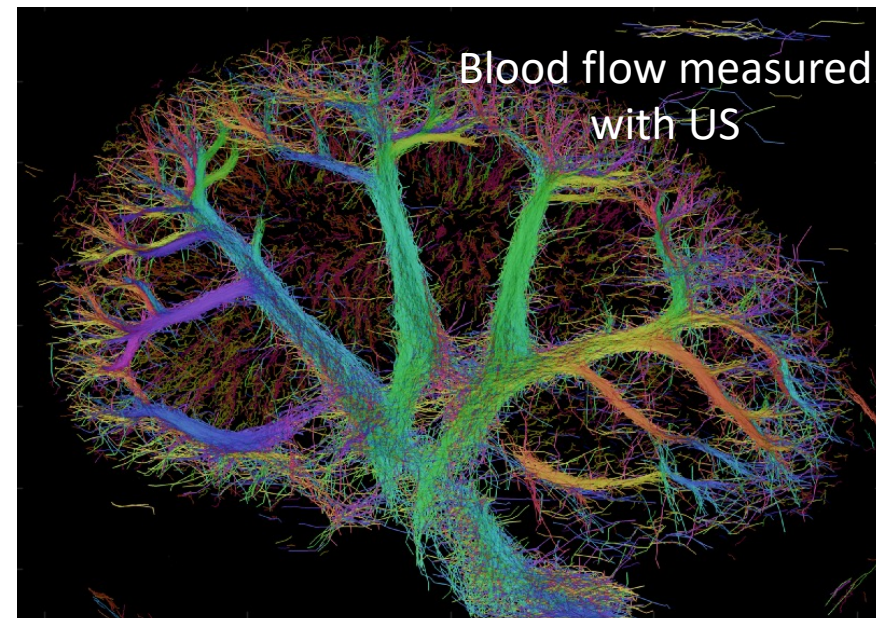
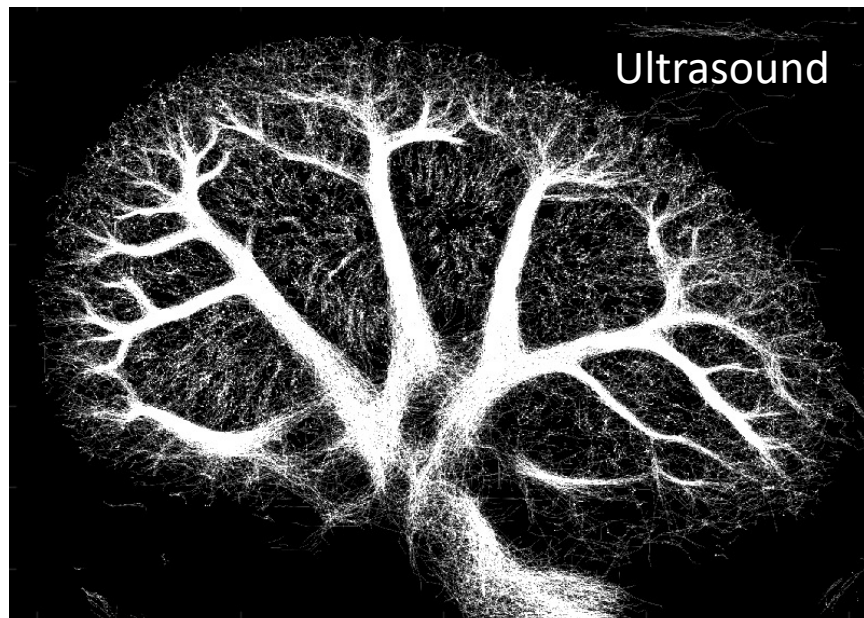
AI for the Human Organ Atlas

Synchrotron CT – from whole organ to nano-meter resolution



Example – optimizing devices

Rat kidney



Imaging pipeline

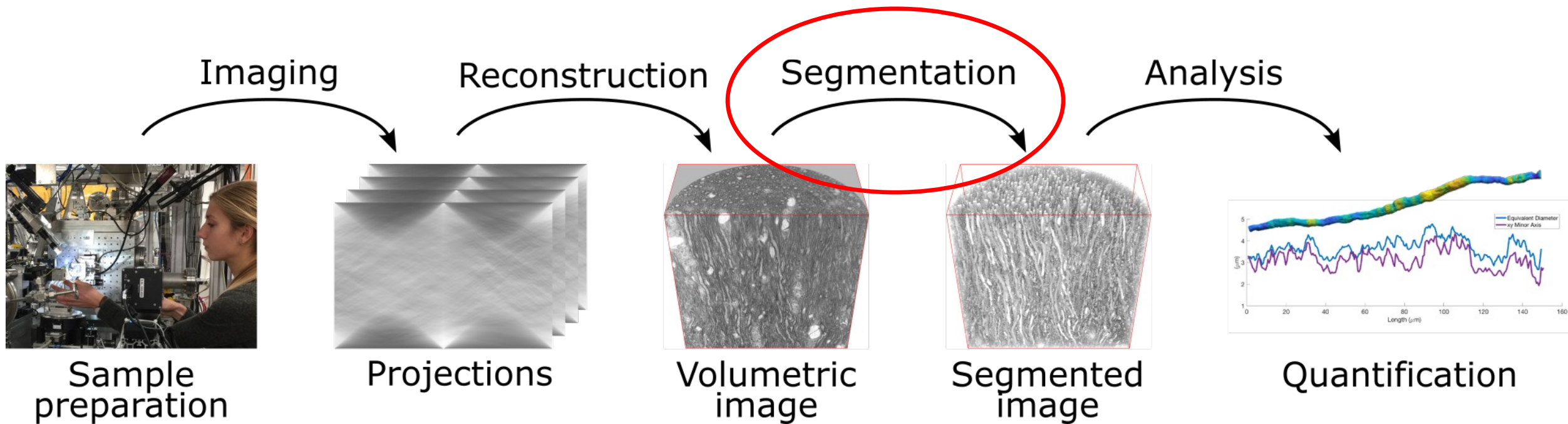
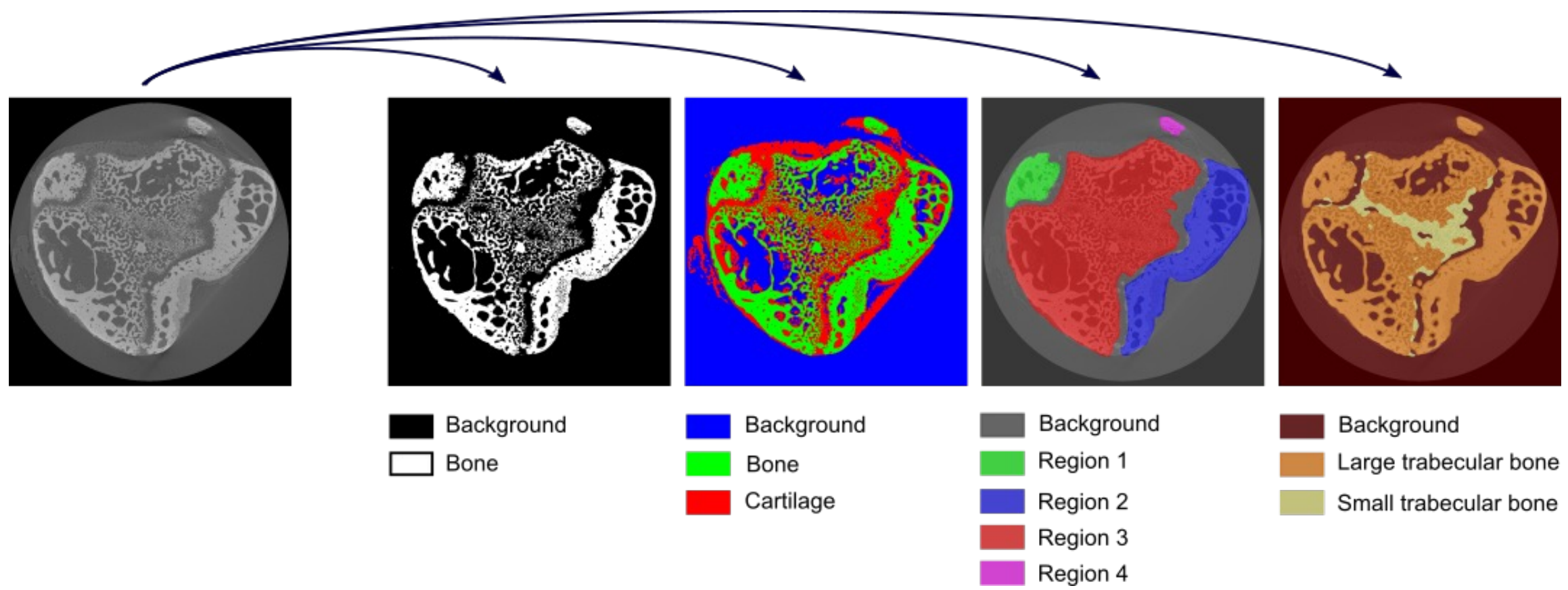


Image segmentation – manual decision



Towards Large Foundational Models

SAM – Segment Anything Model



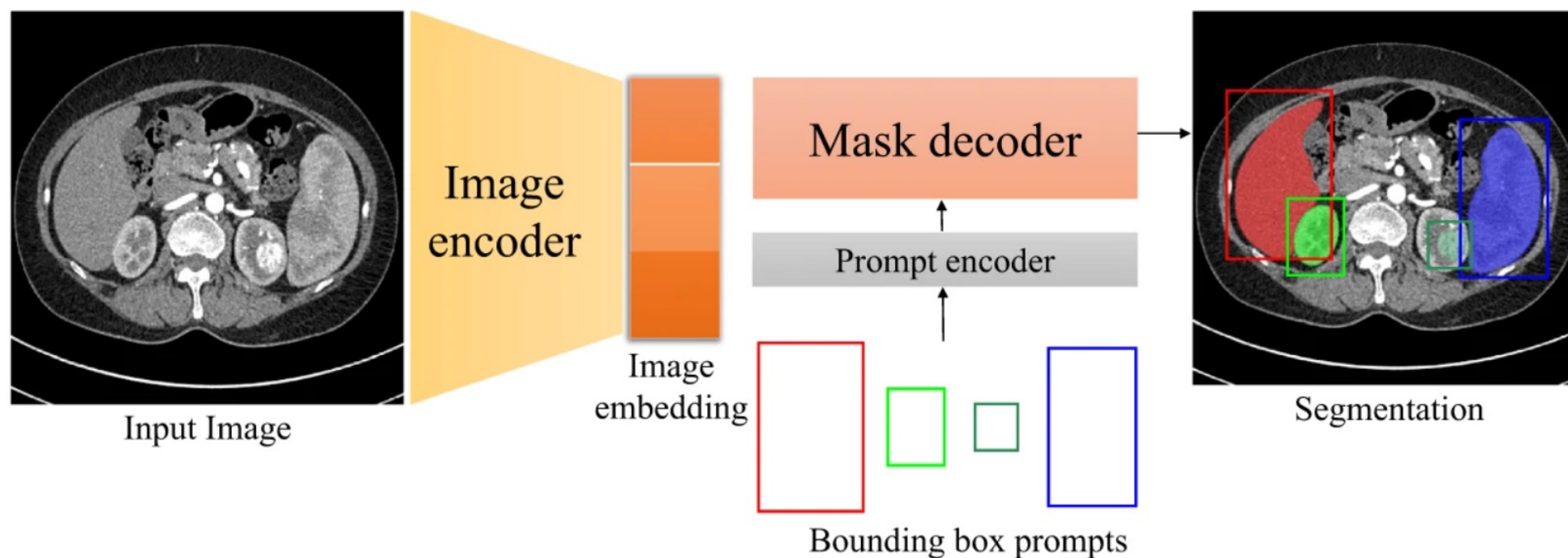
Foundational model

Trained on 11 million images and more than 1 billion labels

Source: <https://segment-anything.com/demo>
Kirillov, Alexander, et al., ICCV, 2023

Foundational Medical Models

MedSAM – Segment Anything in Medical Images



1,570,263 images – 10 imaging modalities
CT, MRI, endoscopy, histology, etc.

Source: Ma, Jun, et al. Nature Communications, 2024

TotalSegmentator

If used for research purposes, please cite our [Radiology AI paper](#).

The results of the models appendicular bones, tissue types, heart chambers highres and face may not be used commercially. All other results are open for any usage.

If this website does not work, please create a issue on [github](#).

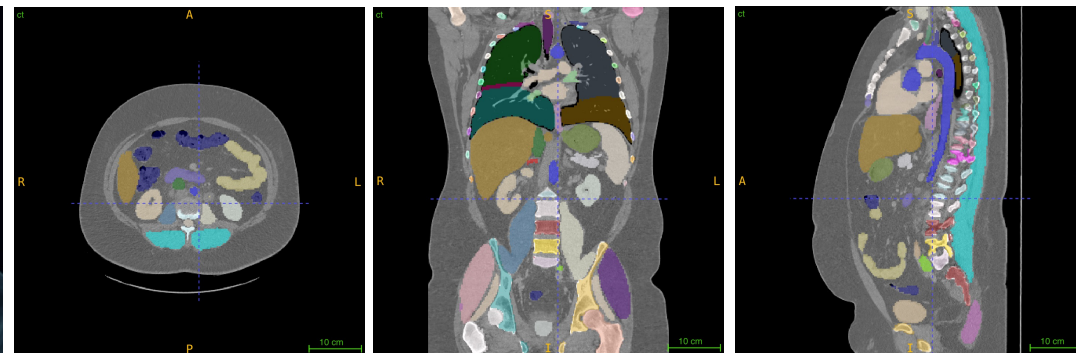
Please help us continue providing TotalSegmentator.com by sharing your thoughts through this quick [form](#). Thank you!

Download results

Upload a new case



Preview rendering of all segmentations



Ground truth



Segmentation

- | # | Segmentation Mask (nifti) |
|---|--|
| 1 | adrenal_gland_left.nii.gz |
| 2 | adrenal_gland_right.nii.gz |
| 3 | aorta.nii.gz |
| 4 | atrial_appendage_left.nii.gz |
| 5 | autochthon_left.nii.gz |

Facts: Trained from 1240 annotated CT scans – 104 anatomical structures

TotalSegmentator v2.0.0

Try out the [TotalSegmentator](#) by uploading any CT data. The upload must meet the following criteria:

- Only a single CT dataset, maximum size is 400 MB
- Upload should be either a zip file of DICOMs or a single NIFTI image

By using this online service you agree that the data can be used to improve the model.

Drop **DICOM.zip** or **NIFTI.nii.gz** here
or click to upload

Selected task
total (default) ▼

Choose a subset to avoid long runtime (if none is selected all are selected)

- Enable fast processing
- Calculate statistics (volume and intensity)

Process data

If used for research purposes, please cite our [Radiology AI paper](#).

The results of the models appendicular bones, tissue types, heartchambers highres and face may not be used commercially.

All other results are open for any usage.

If this website does not work, please create a issue on [github](#).

Segmentation

Radiology: Artificial Intelligence

ORIGINAL RESEARCH

TotalSegmentator: Robust Segmentation of 104 Anatomic Structures in CT Images

Jakob Wasserthal, PhD • Hanns-Christian Breit, MD • Manfred T. Meyer, MD • Maurice Pradella, MD • Daniel Hinck • Alexander W. Sauter, MD • Tobias Heye, MD • Daniel T. Boll, MD • Joshy Cyriac, MSc • Shan Yang, PhD • Michael Bach, PhD • Martin Segeroth, MD

From the Clinic of Radiology and Nuclear Medicine, University Hospital Basel, Basel, Switzerland, Petersgraben 4, 4031 Basel, Switzerland. Received January 25, 2023; revision requested February 27; revision received May 16; accepted June 14. **Address correspondence to** J.W. (email: jakob.wasserthal@usb.ch).

Authors declared no funding for this work.

Conflicts of interest are listed at the end of this article.

See also commentary by Sebro and Mongan in this issue.

Radiology: Artificial Intelligence 2023; 5(5):e230024 • <https://doi.org/10.1148/ryai.230024> • Content codes: **AI CA CT GI MK**

Purpose: To present a deep learning segmentation model that can automatically and robustly segment all major anatomical body CT images.

Materials and Methods: In this retrospective study, 1204 CT examinations (from 2012, 2016, and 2020) were used to segment 104 anatomic structures (27 organs, 59 bones, 10 muscles, and eight vessels) relevant for use cases such as organ volumetry, disease characterization, and surgical or radiation therapy planning. The CT images were randomly sampled from routine clinical studies and thus represent a real-world dataset (different ages, abnormalities, scanners, body parts, sequences, and sites). The authors trained an nnU-Net segmentation algorithm on this dataset and calculated Dice similarity coefficients to evaluate the model's performance. The trained algorithm was applied to a second dataset of 4004 whole-body CT examinations to investigate age-dependent volume and attenuation changes.

Results: The proposed model showed a high Dice score (0.943) on the test set, which included a wide range of clinical data with major abnormalities. The model significantly outperformed another publicly available segmentation model on a separate dataset (Dice score, 0.932 vs 0.871; $P < .001$). The aging study demonstrated significant correlations between age and volume and mean attenuation for a variety of organ groups (eg, age and aortic volume [$r_s = 0.64$; $P < .001$]; age and mean attenuation of the autochthonous dorsal musculature [$r_s = -0.74$; $P < .001$]).

showed a high Dice score (0.943) on the test set, which significantly outperformed another publicly available segmentation model on a separate dataset.

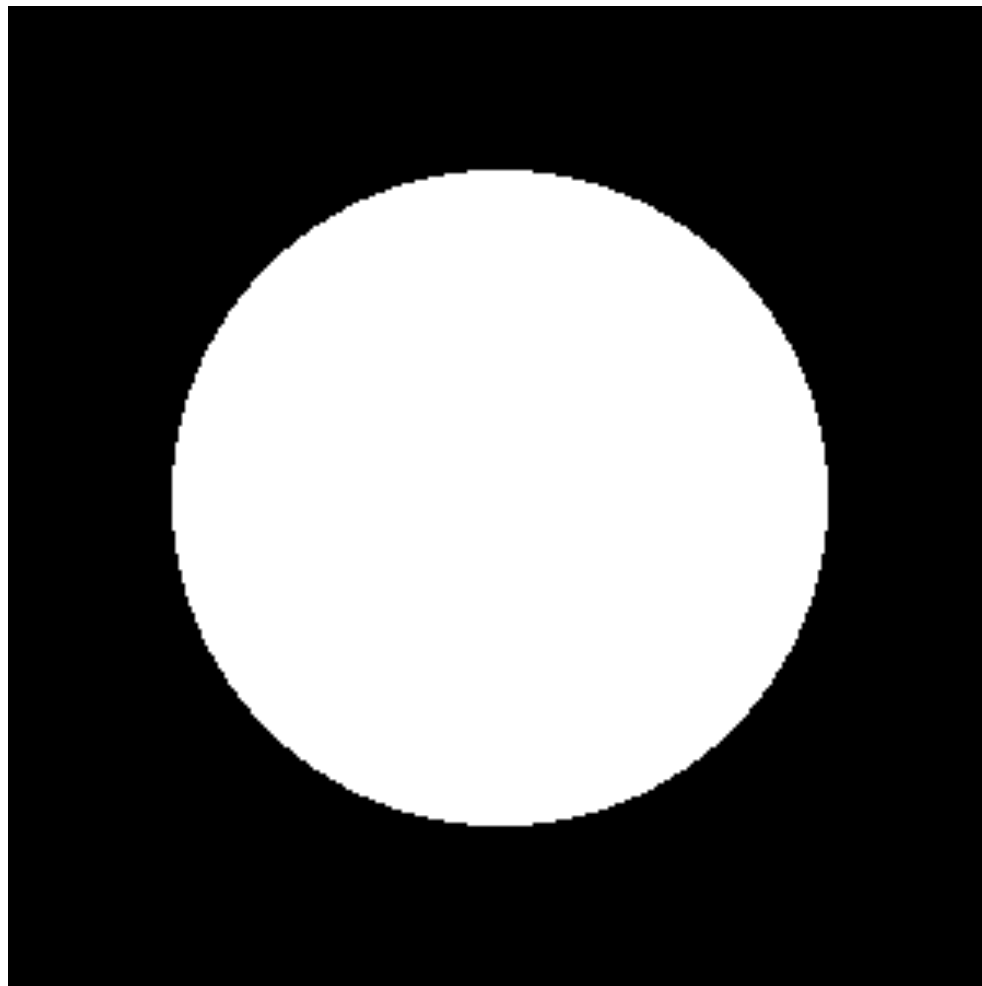
Performance measures

Accuracy:
$$\text{Acc} = \frac{\text{True pixels}}{\text{Total pixels}}$$

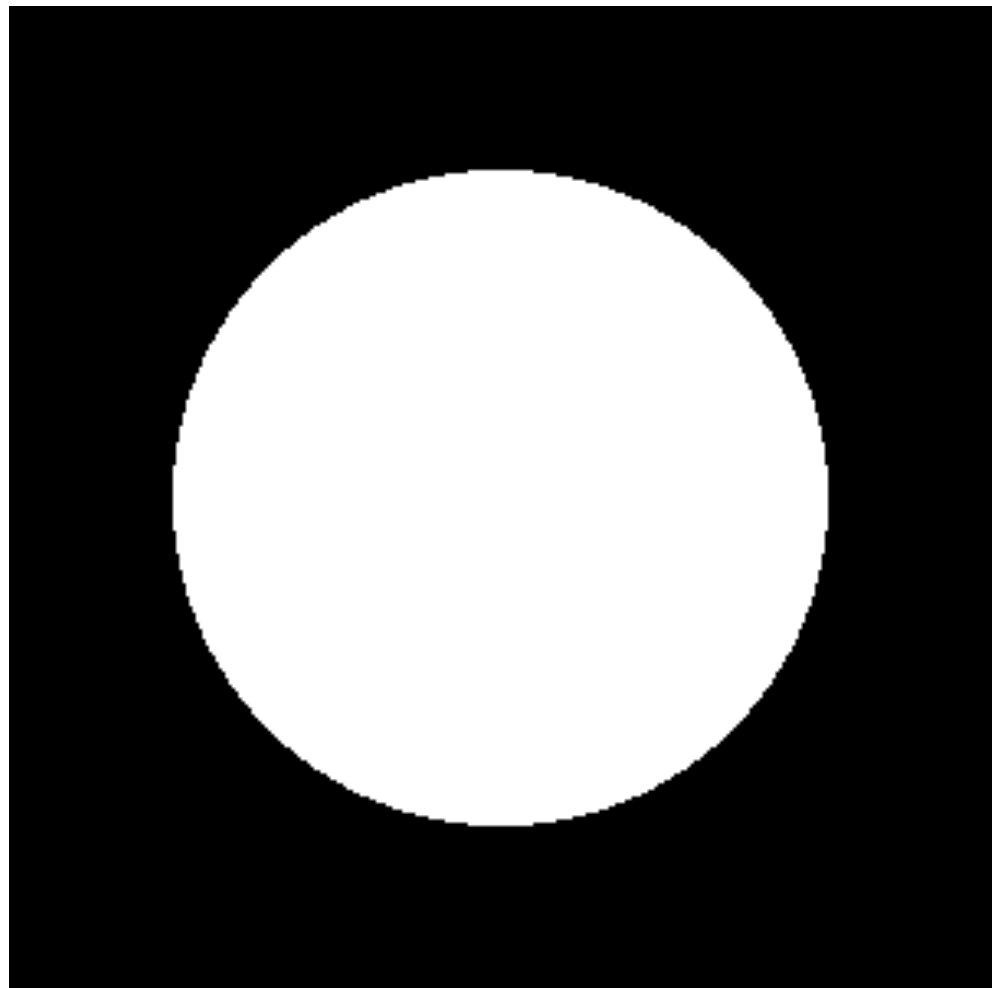
Intersection over Union:
$$\text{IoU} = \frac{|X \cap Y|}{|X \cup Y|}$$

Dice:
$$\text{DSC} = \frac{2|X \cap Y|}{|X| + |Y|}$$

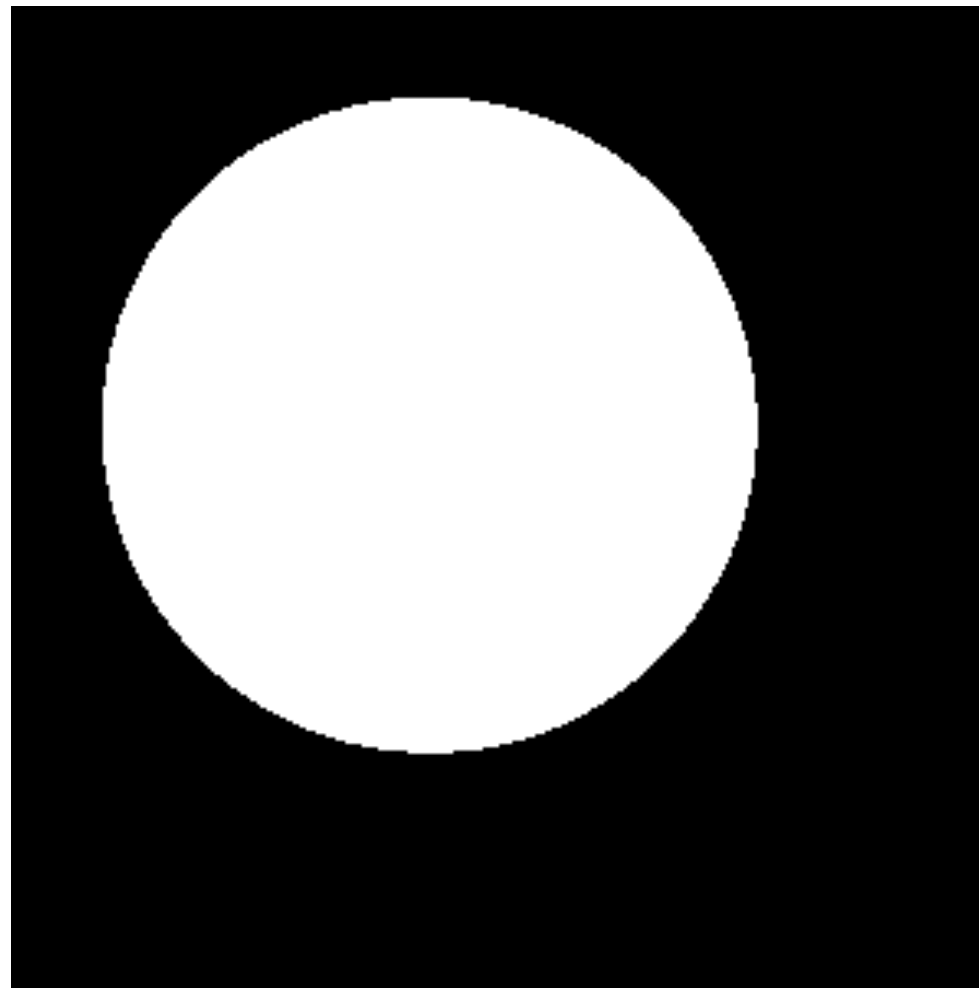
Performance measures



Performance measures

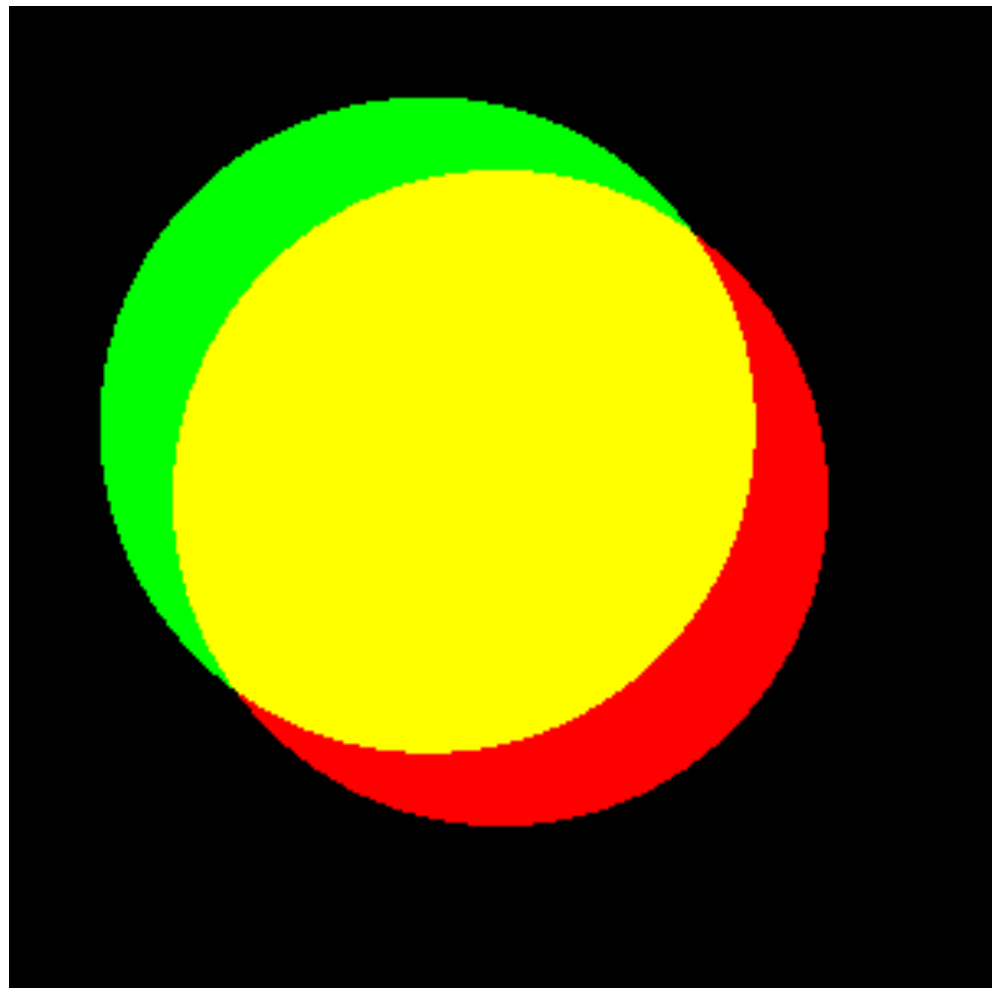


Original



Segmentation

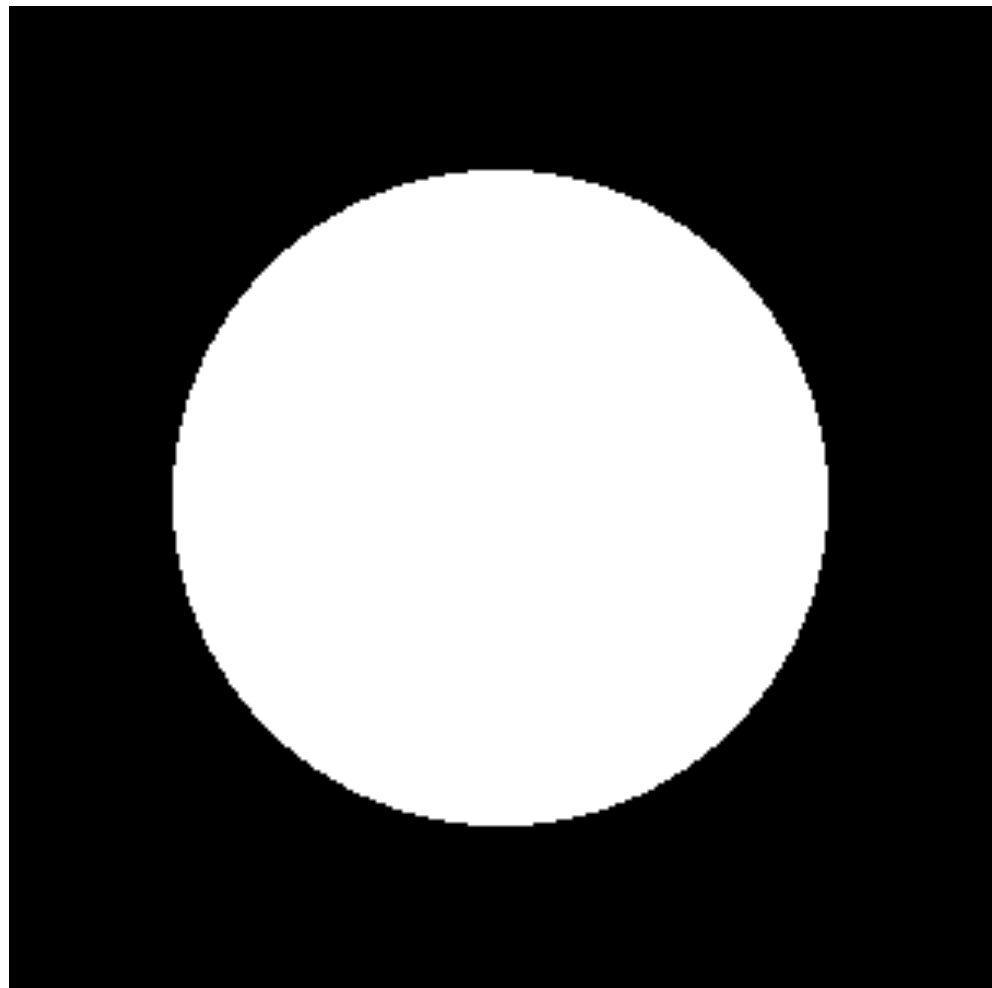
Performance measures



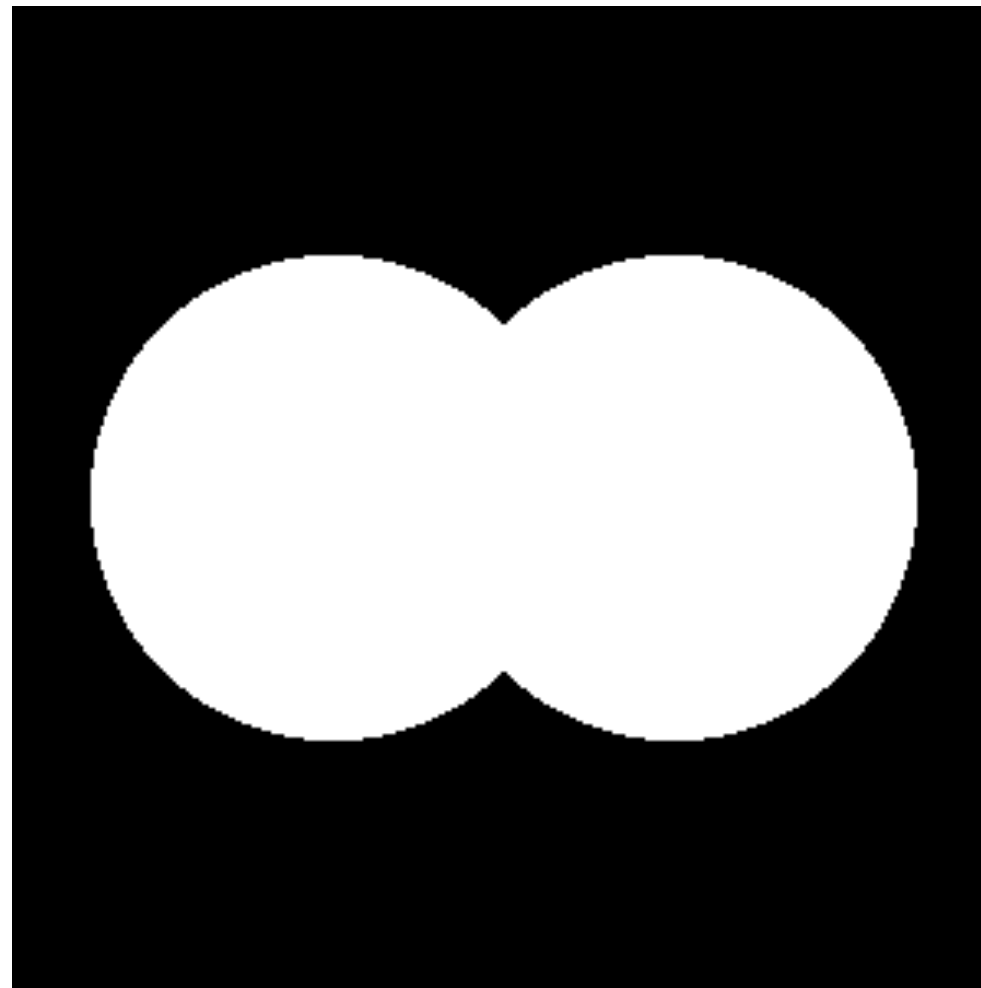
Overlap

Accuracy:	0.861
Intersection over Union:	0.667
Dice:	0.800

Performance measures

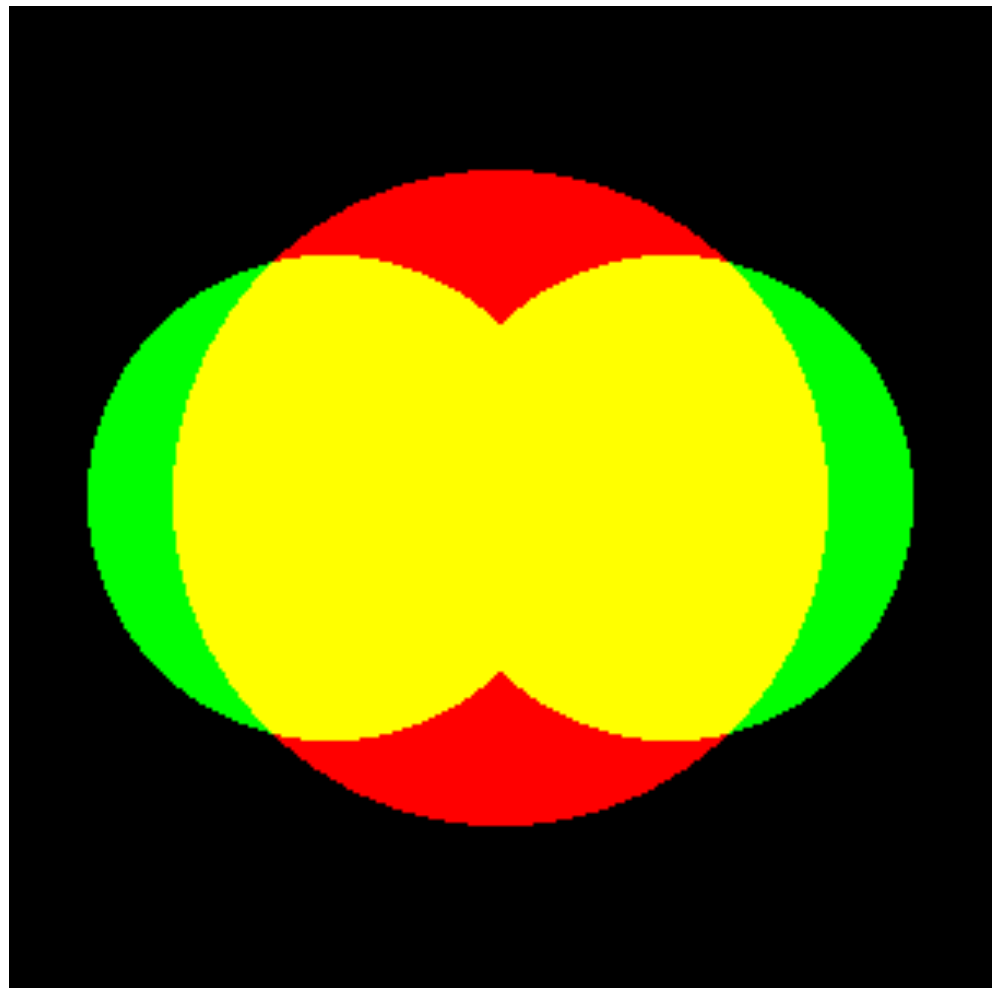


Original



Segmentation

Performance measures



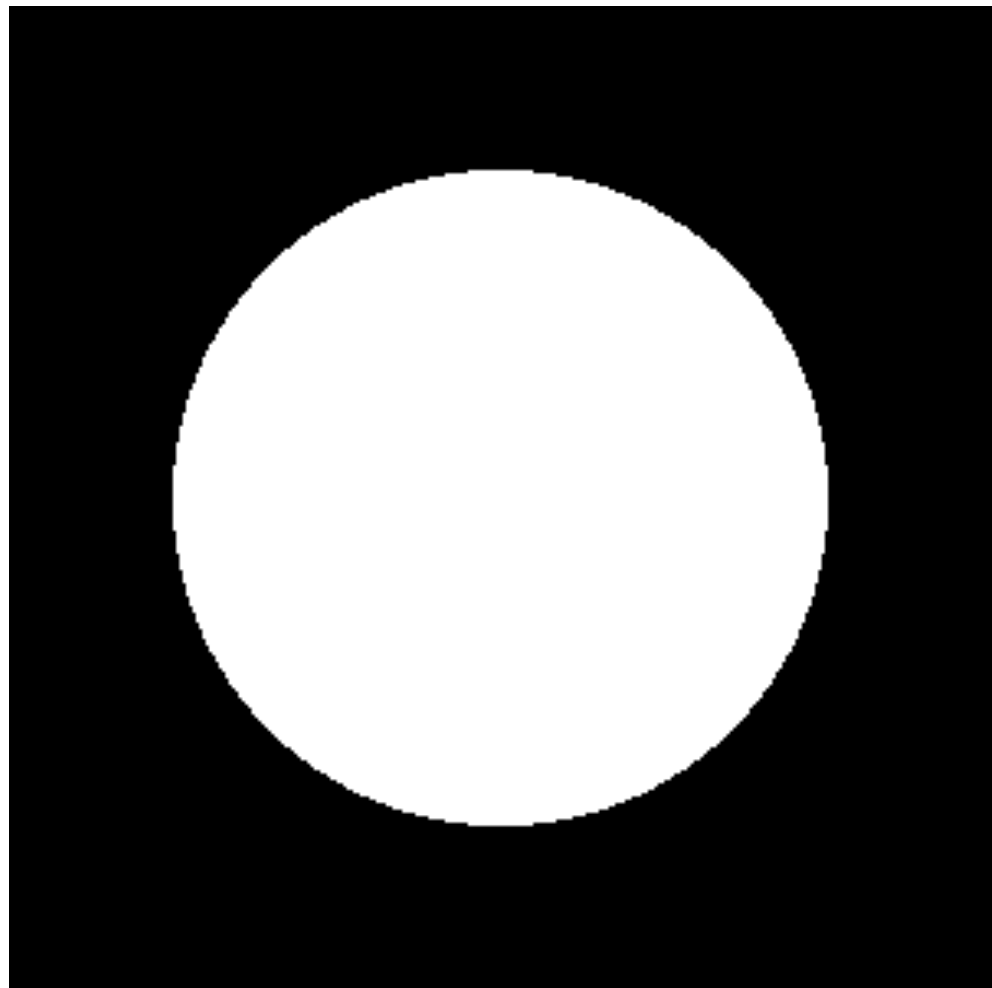
Overlap

Accuracy: 0.864

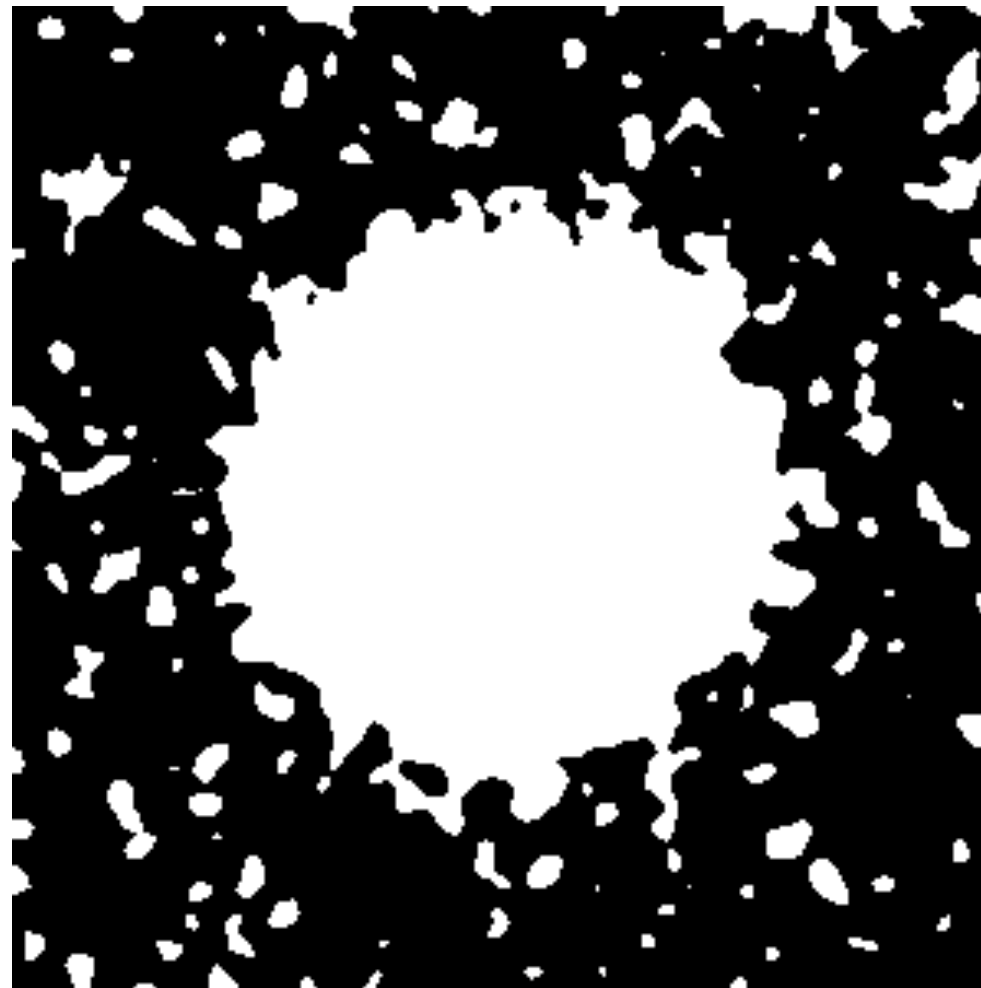
Intersection over Union: 0.673

Dice: 0.804

Performance measures

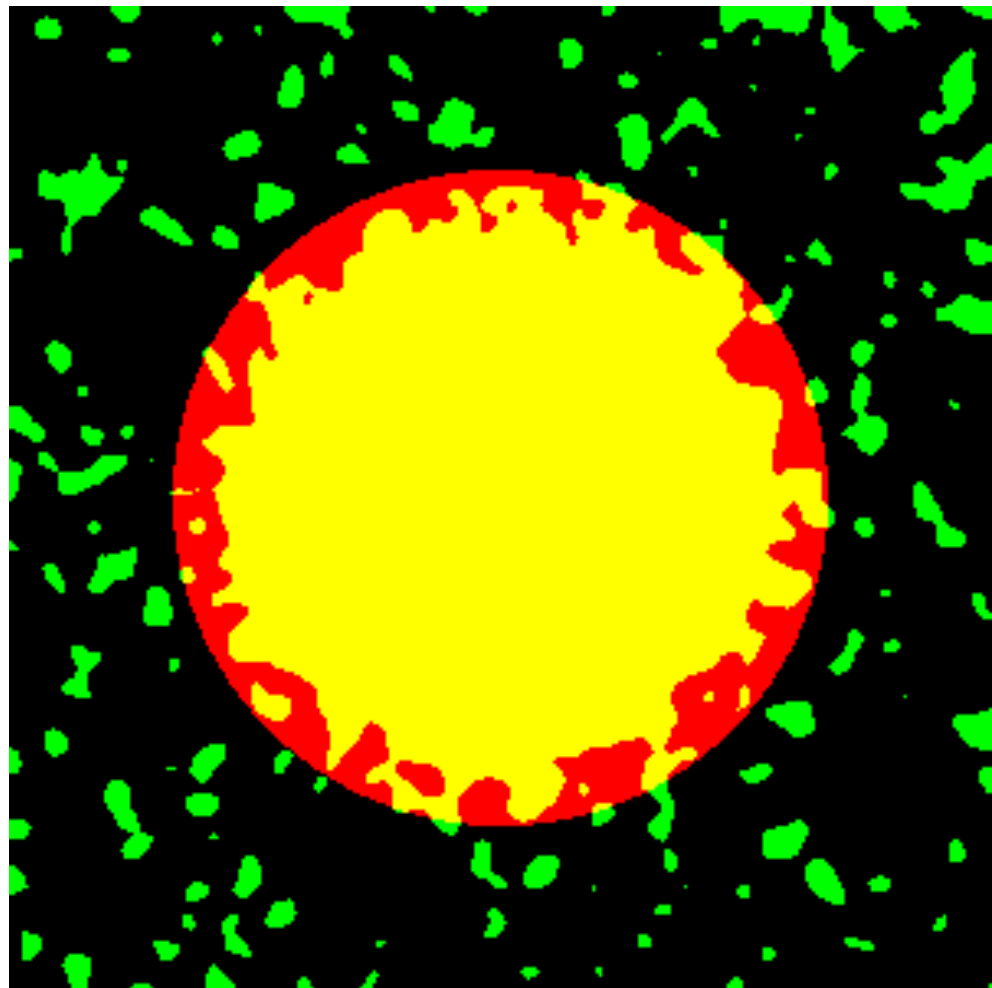


Original



Segmentation

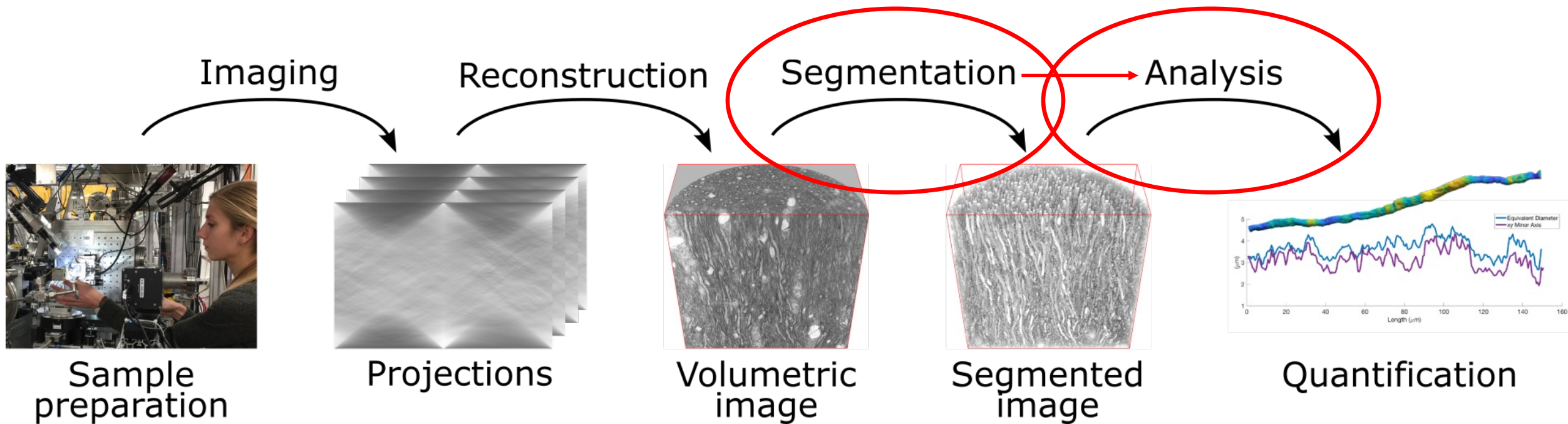
Performance measures



Overlap

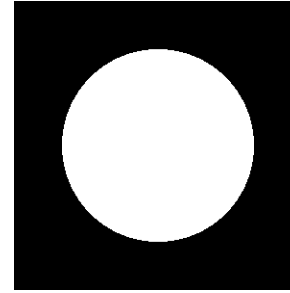
Accuracy:	0.861
Intersection over Union:	0.668
Dice:	0.801

Quantitative measures

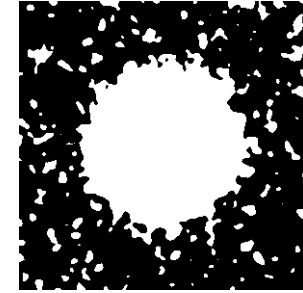


Quantitative measures

Boundary length:



Short



Long

Number of components:

Few (one)

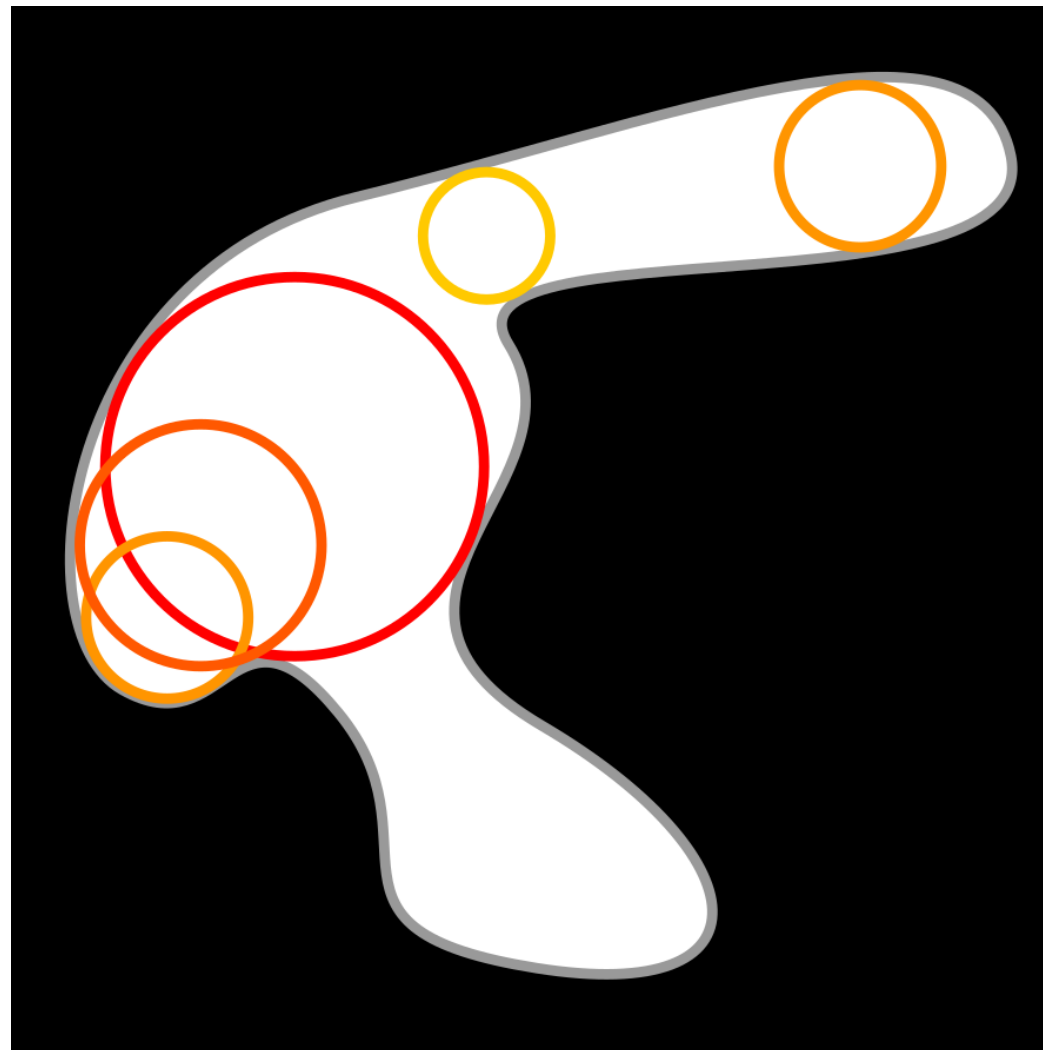
Many

Local thickness/spacing (median):

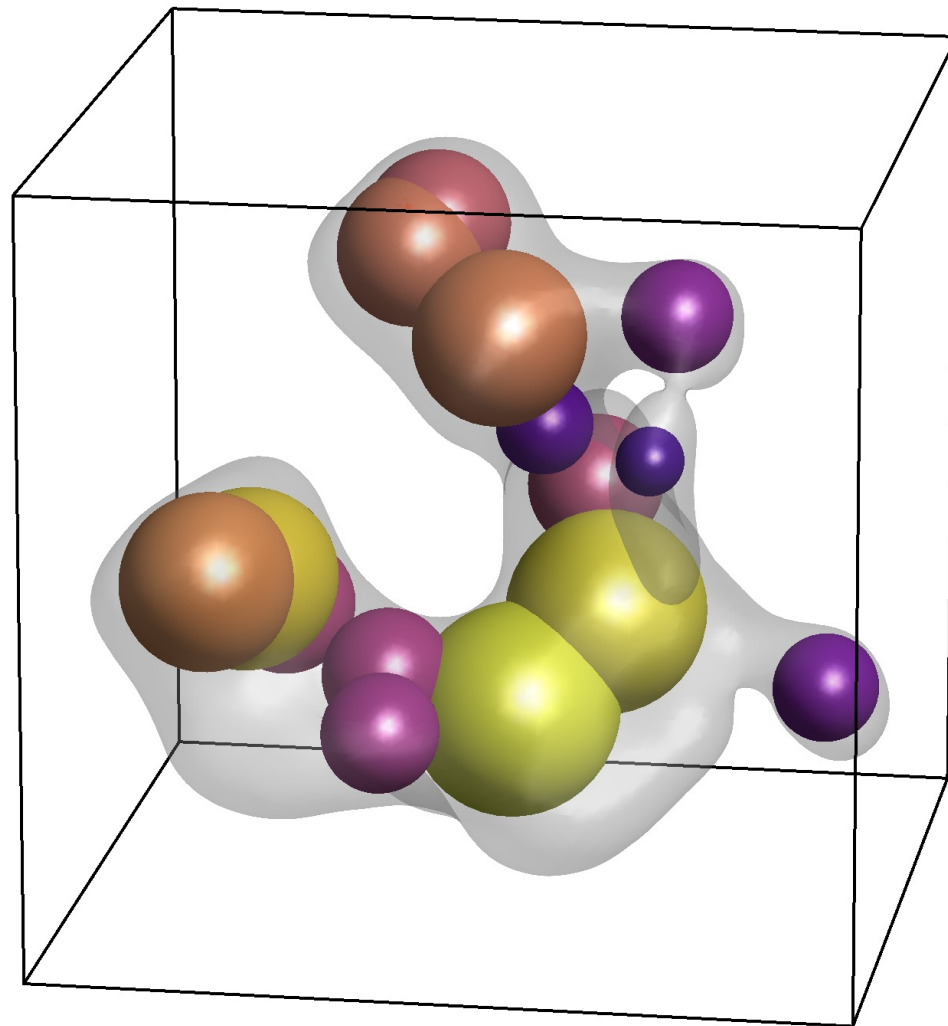
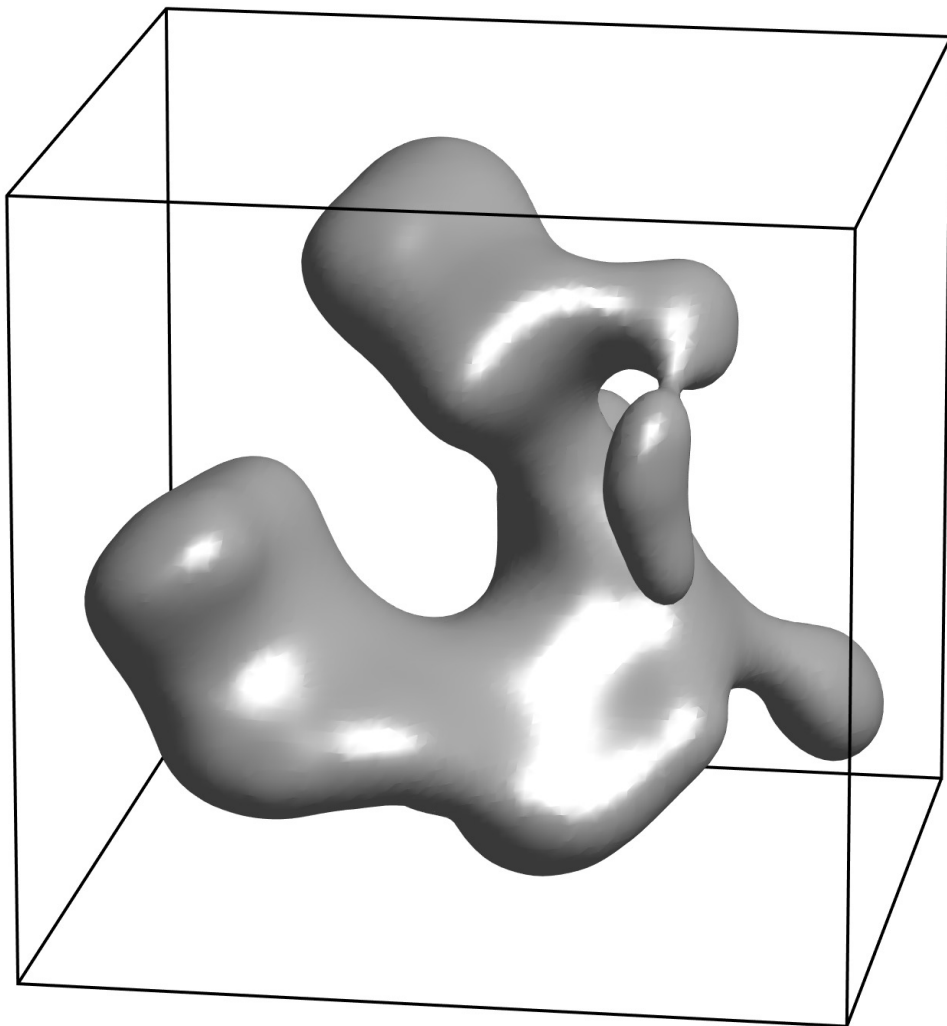
High

Low

Local thickness

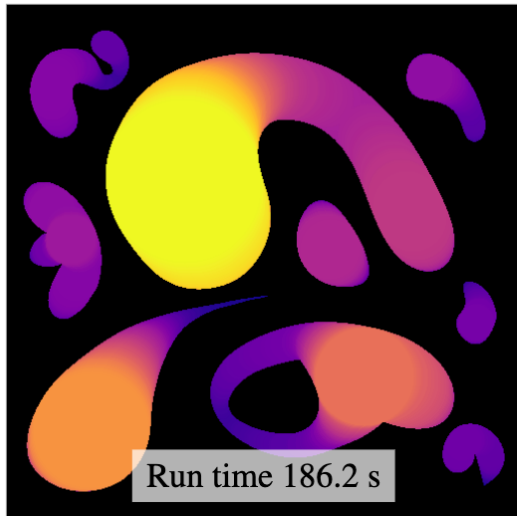


Local Thickness in 3D



Fast Local Thickness

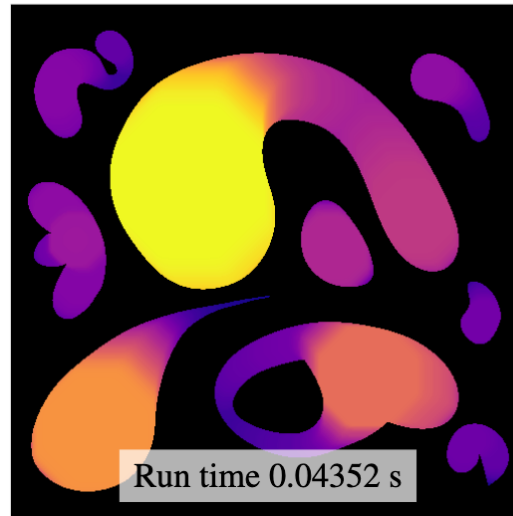
Conventional



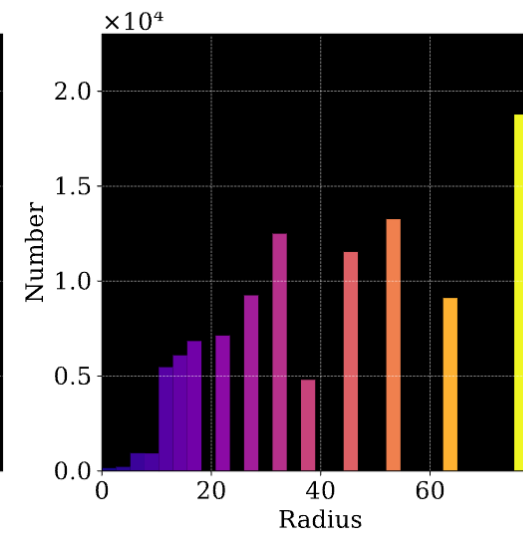
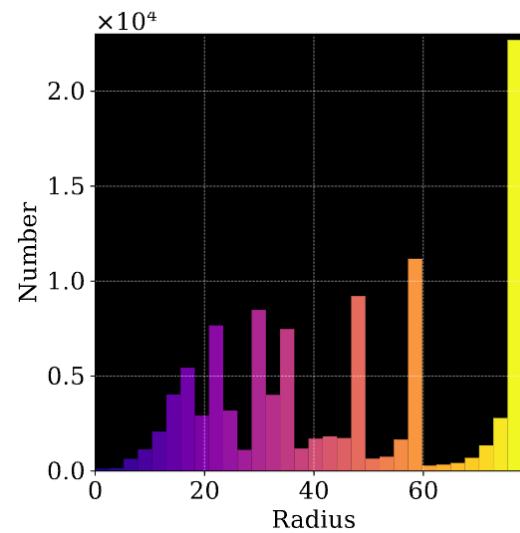
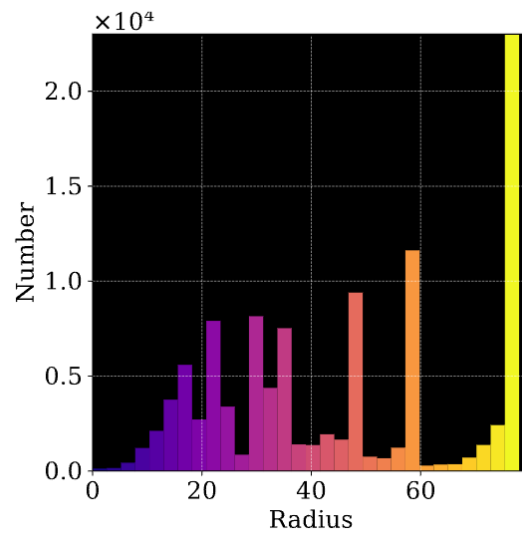
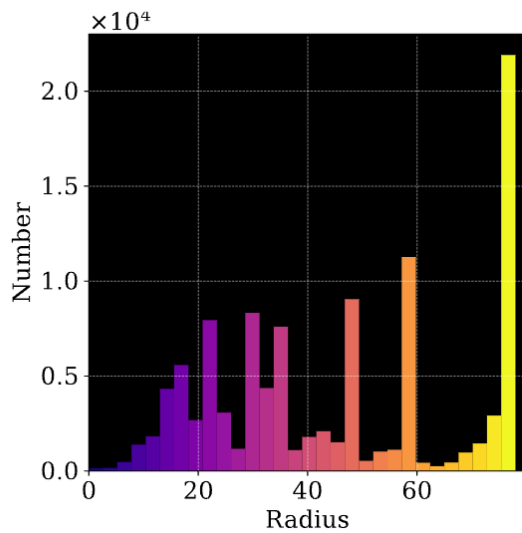
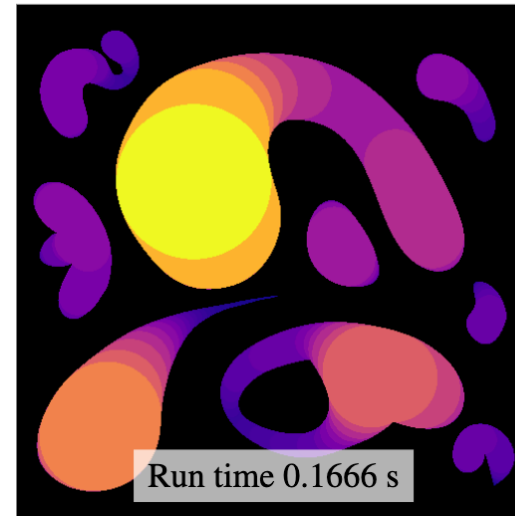
Fast (ours)



Scaled 0.5 (ours)



PoreSpy



Source: V. Dahl & A. Dahl, 2023, CVPR Workshops

Thickness statistics

Distribution of thickness values:

$$\text{mean} = \frac{1}{n} \sum_{i=1}^n h_i$$

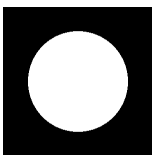
$$\mu_{\log} = \frac{1}{n} \sum_{i=1}^n \log(h_i)$$

$$V_{\log} = \frac{1}{n} \sum_{i=1}^n (\log(h_i) - \mu_{\log})^2$$

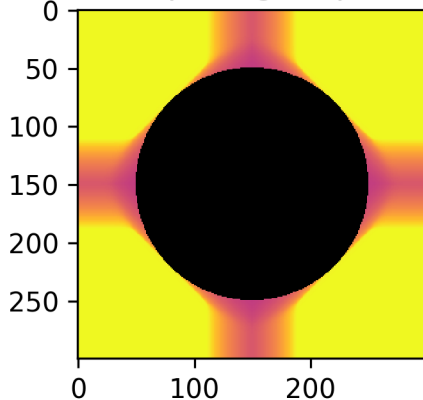
$$\text{median} = \exp(\mu_{\log})$$

$$\text{mode} = \exp(\mu_{\log} - V_{\log})$$

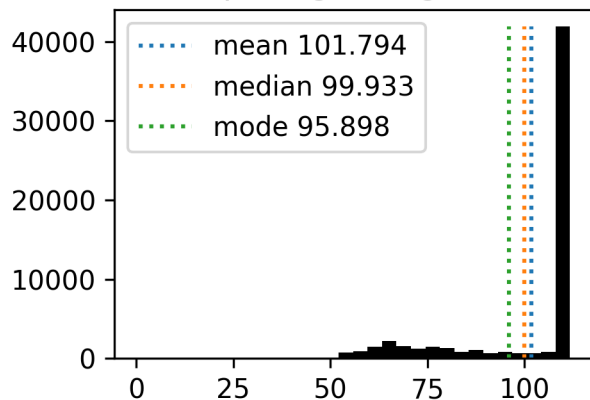
Thickness statistics



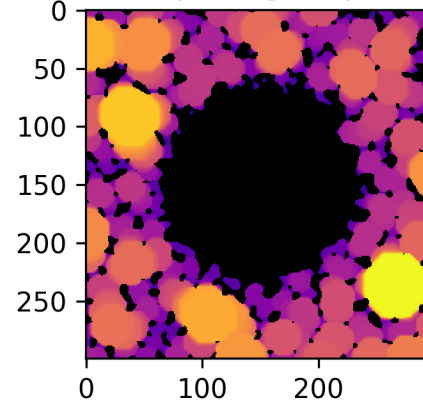
Spacing map



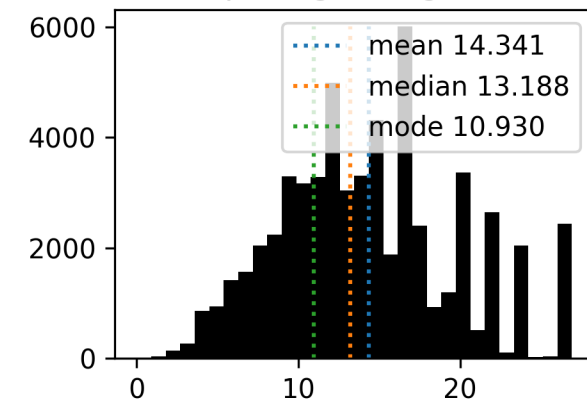
Spacing histogram



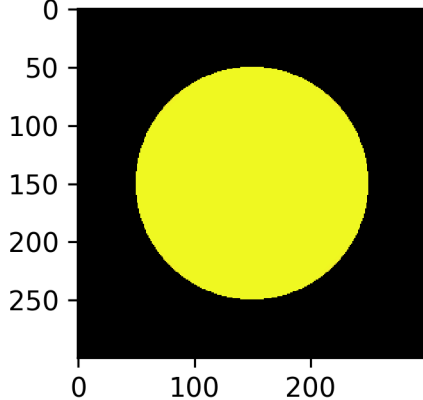
Spacing map



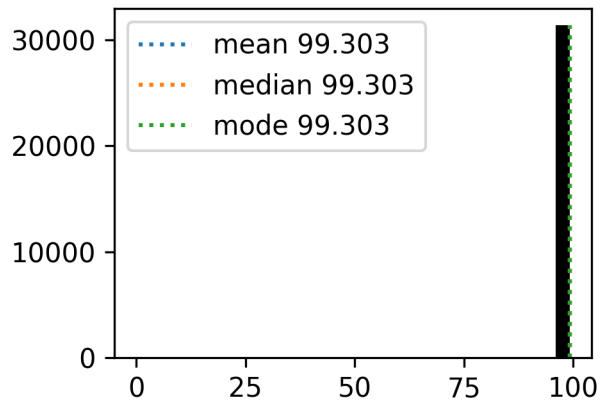
Spacing histogram



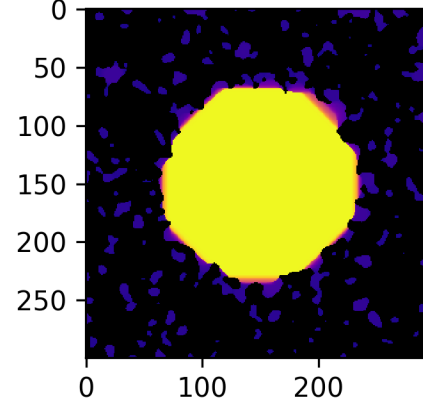
Thickness map



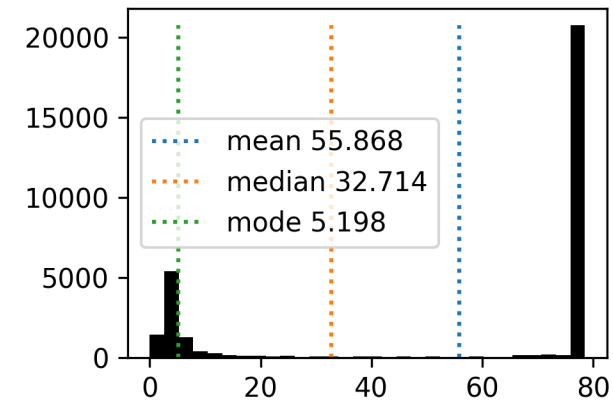
Thickness histogram



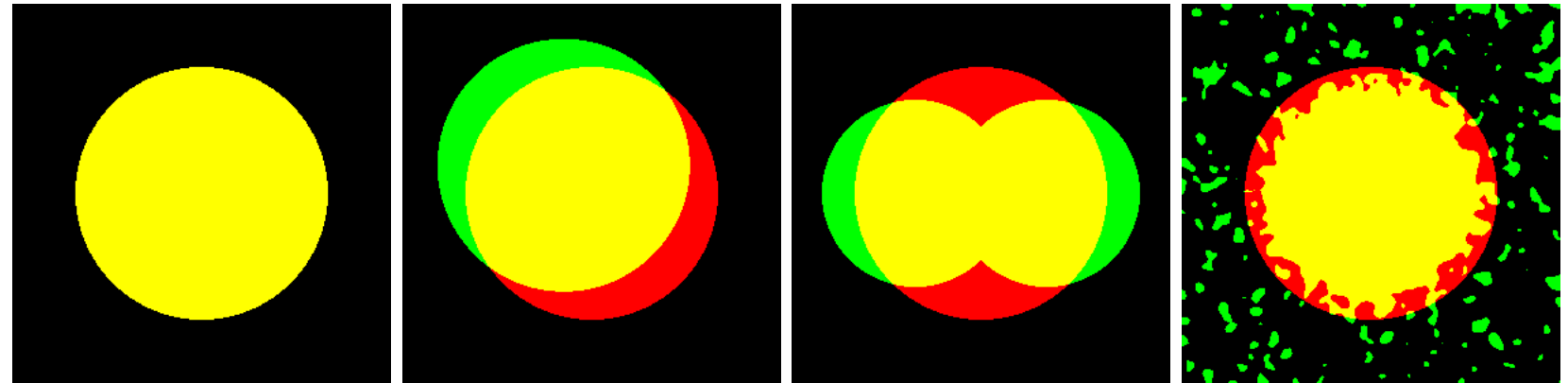
Thickness map



Thickness histogram

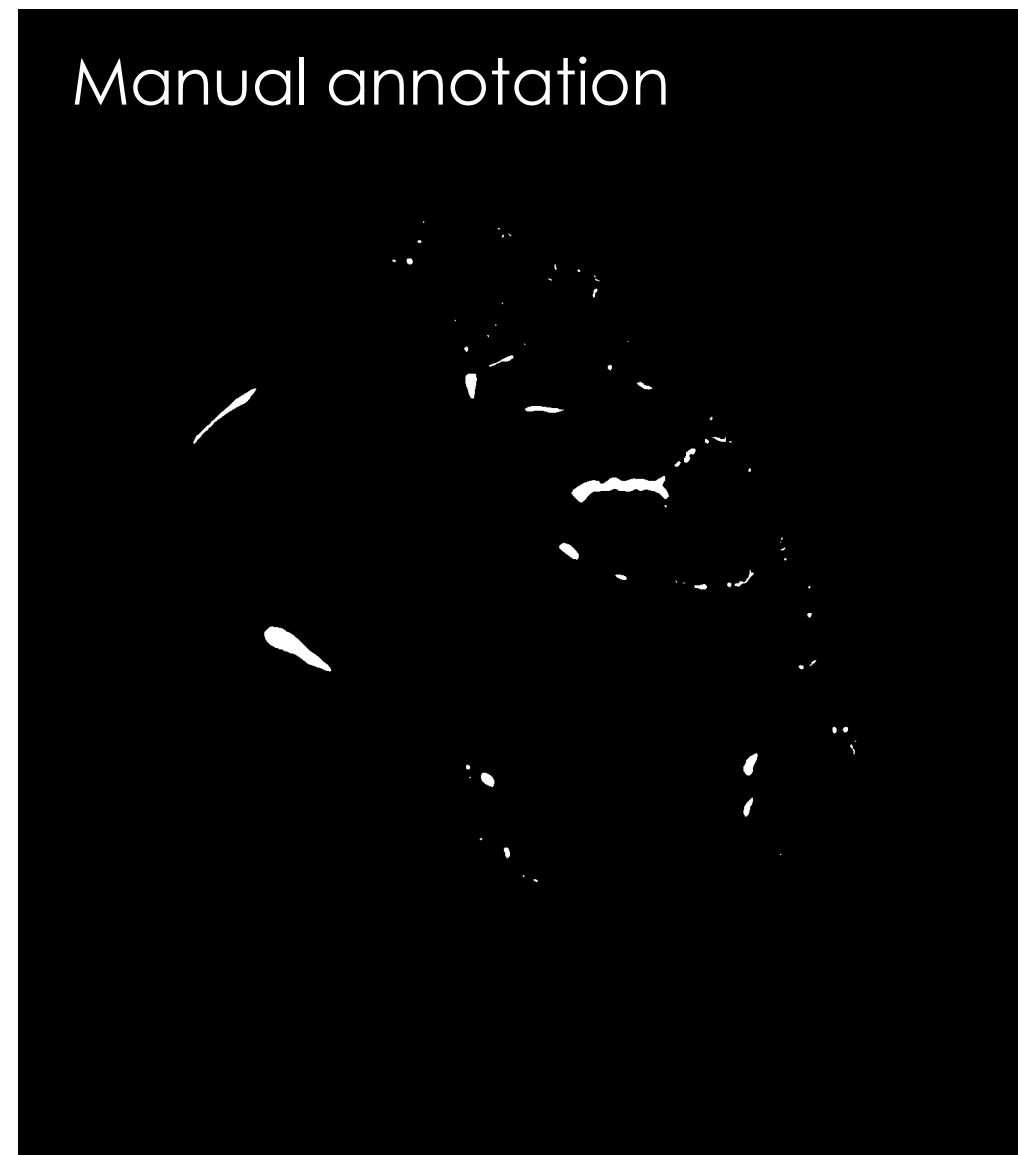
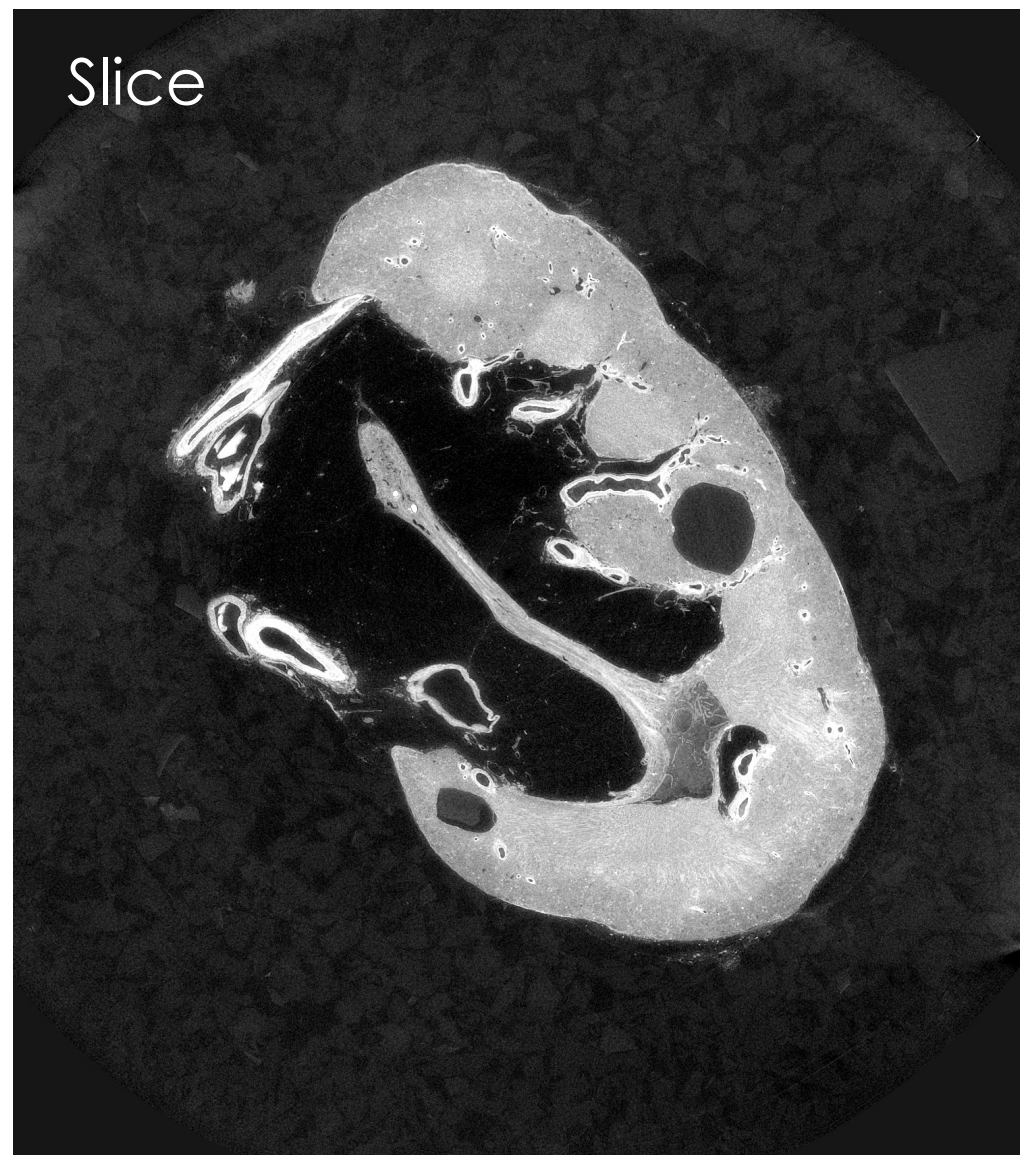


Quantitative measures

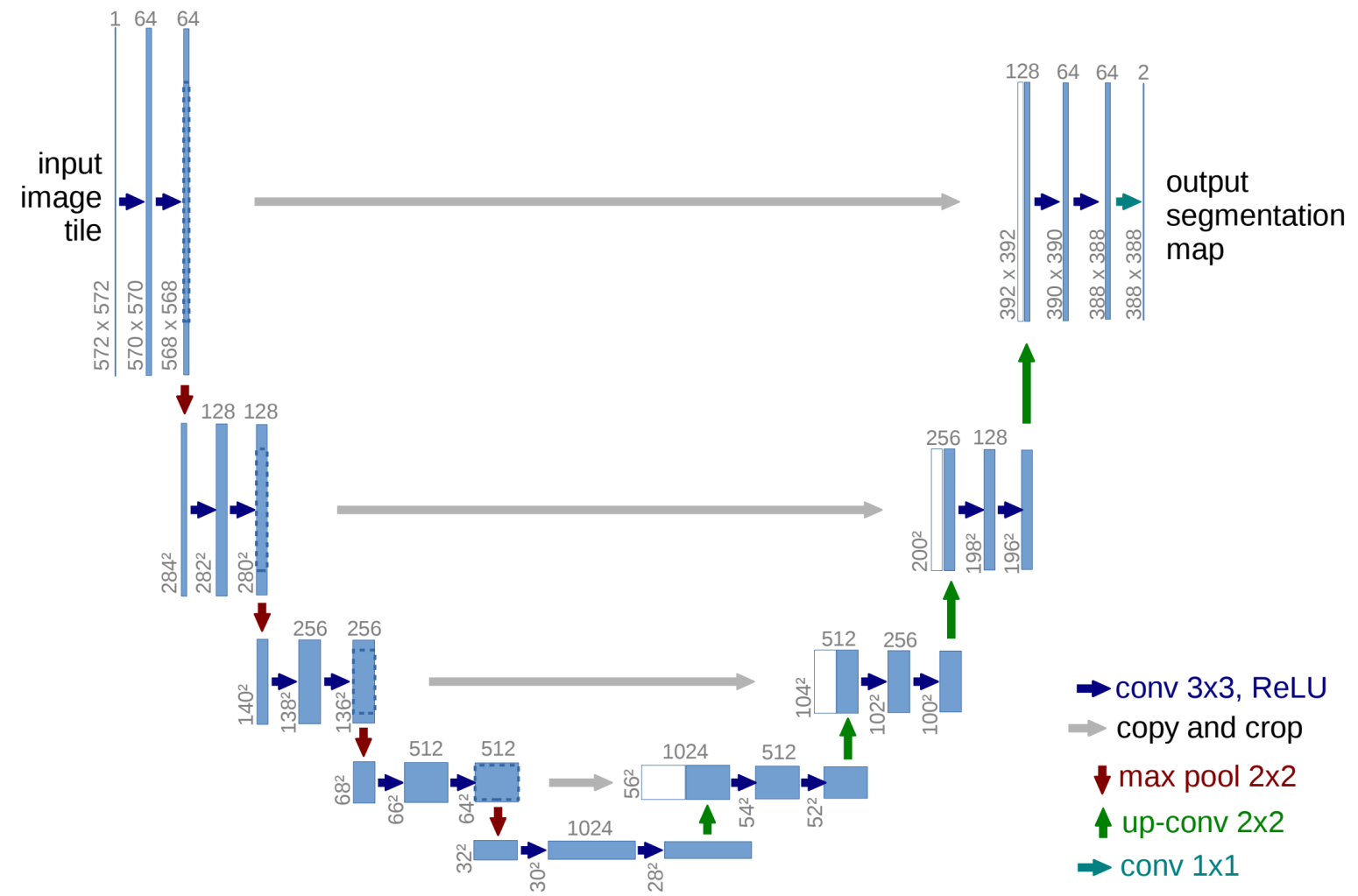


Boundary length ratio	1	1	1.11	6.75
No. of comp. – foreground	1	1	1	135
No. of comp. – background	1	1	1	4
Median thickness	97.8	98.9	72.3	31.4
Median spacing	100.0	105.8	72.1	13.0

Segmentation of kidney data

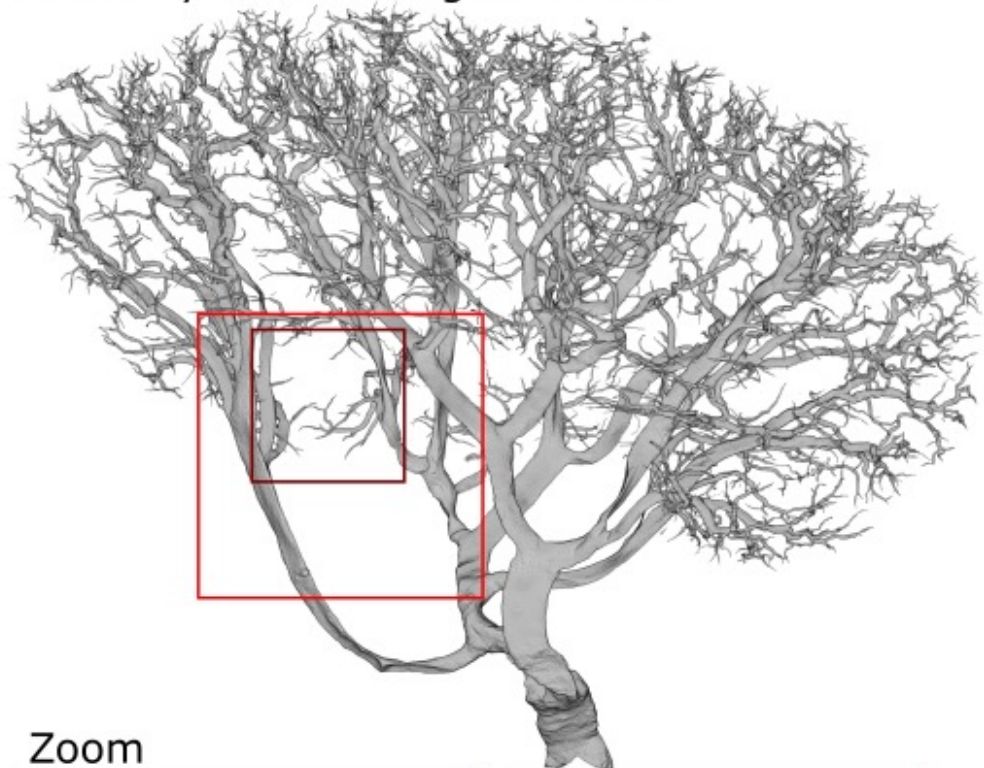


Segmentation of kidney data – U-Net

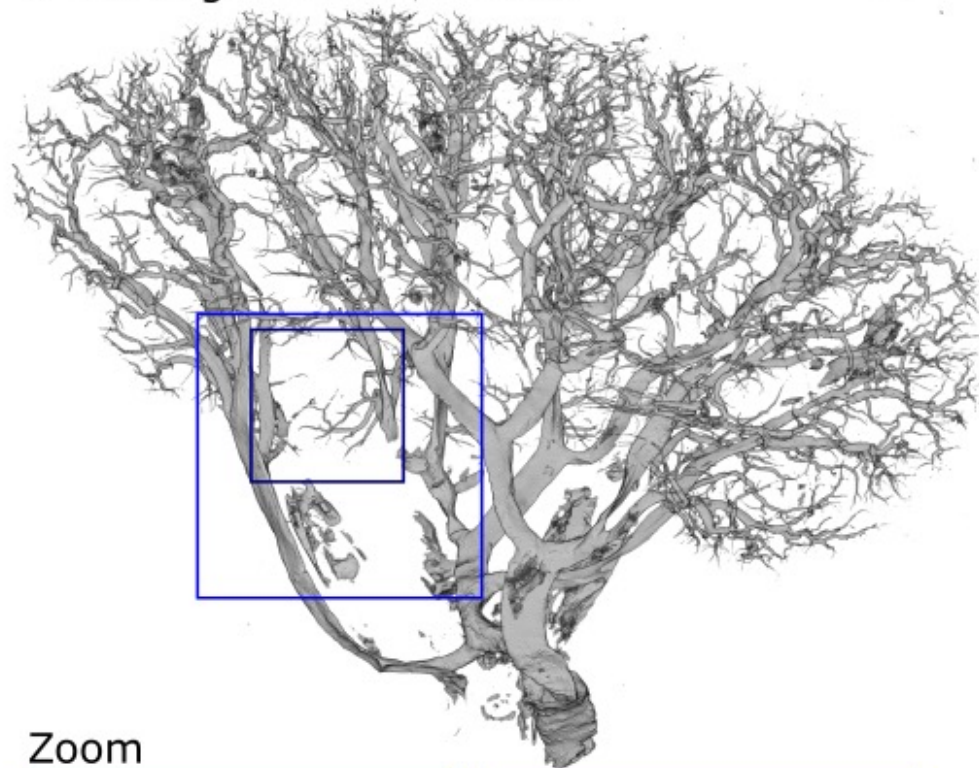


Kidney example

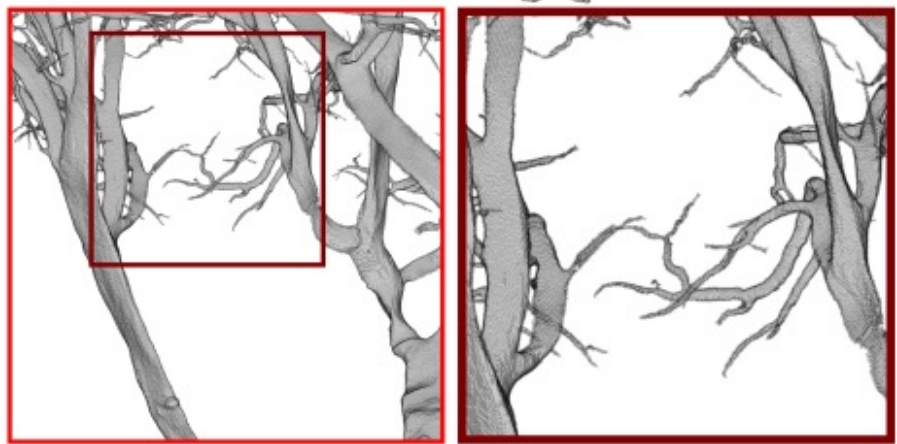
Manually annotated ground truth



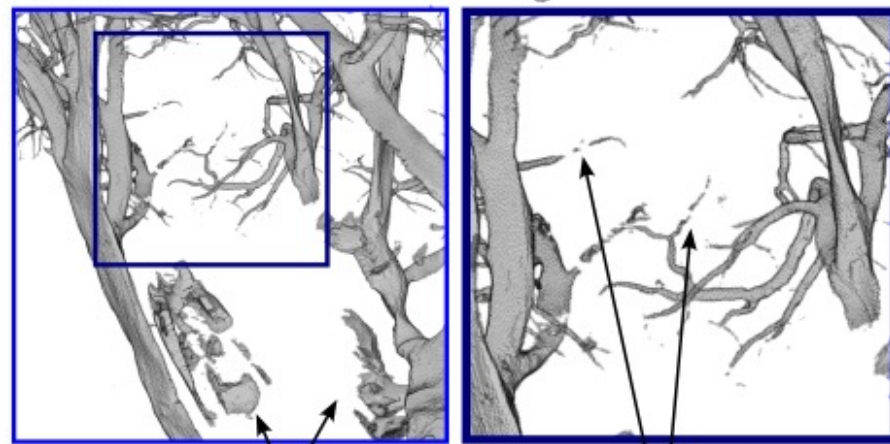
U-Net segmentation result



Zoom



Zoom



Added parts

Broken vessels

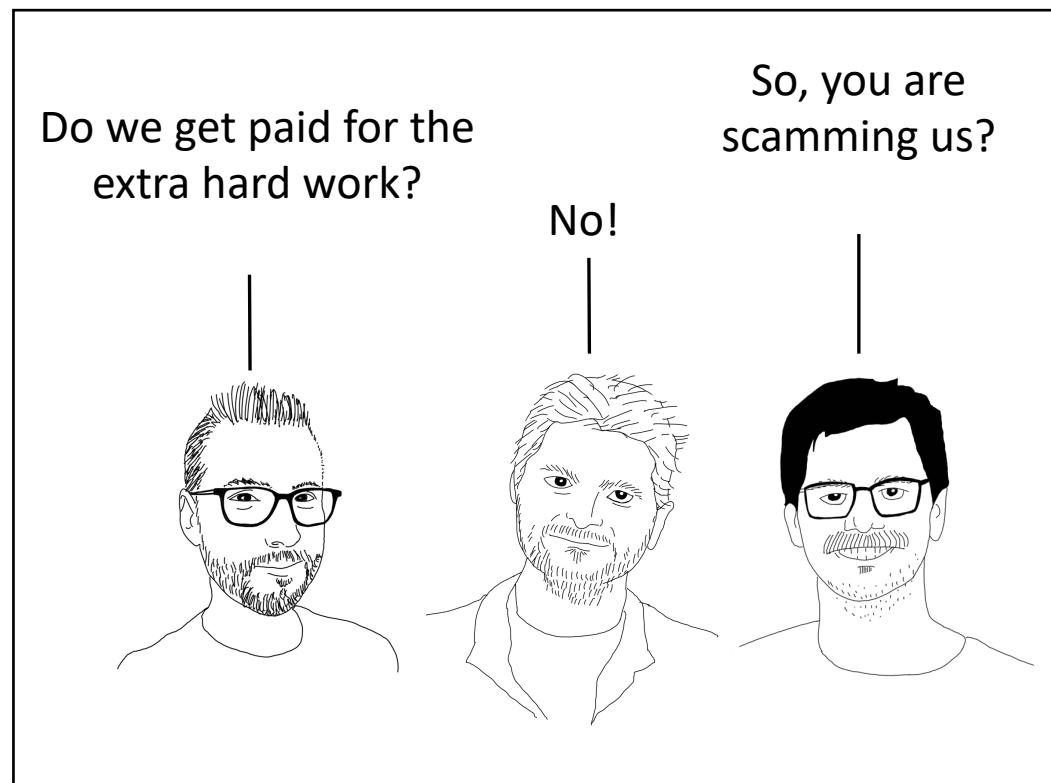
Per slice stats:

Dice:	0.740
# comp. ratio:	1.21
Thick. ratio:	0.919
Space. ratio:	0.970

Conclusion (part one)

- Segmentation measures may not reflect segmentation quality (including accuracy, Dice, and IoU)
- Visualizing and inspecting results is essential
- Need for additional research
 - Quantitative analysis methods
 - Segmentation techniques
 - Etc.

How do we get people to work for free?



Modified from Dilbert

Idea

- Create a dataset – a benchmark for deep learning
 - Inspired by MNIST and CIFAR
 - Volumetric images
 - Easy to use
 - Large scale
- Get other researchers to work on the data
- Collect results and use for other types of problems
- I got the idea, that bugs would be ideal
 - Collaboration with the Natural History Museum
 - Bugs are complex in shape
 - People know about bugs and can relate to them
 - No GDPR

Data collection



Lab



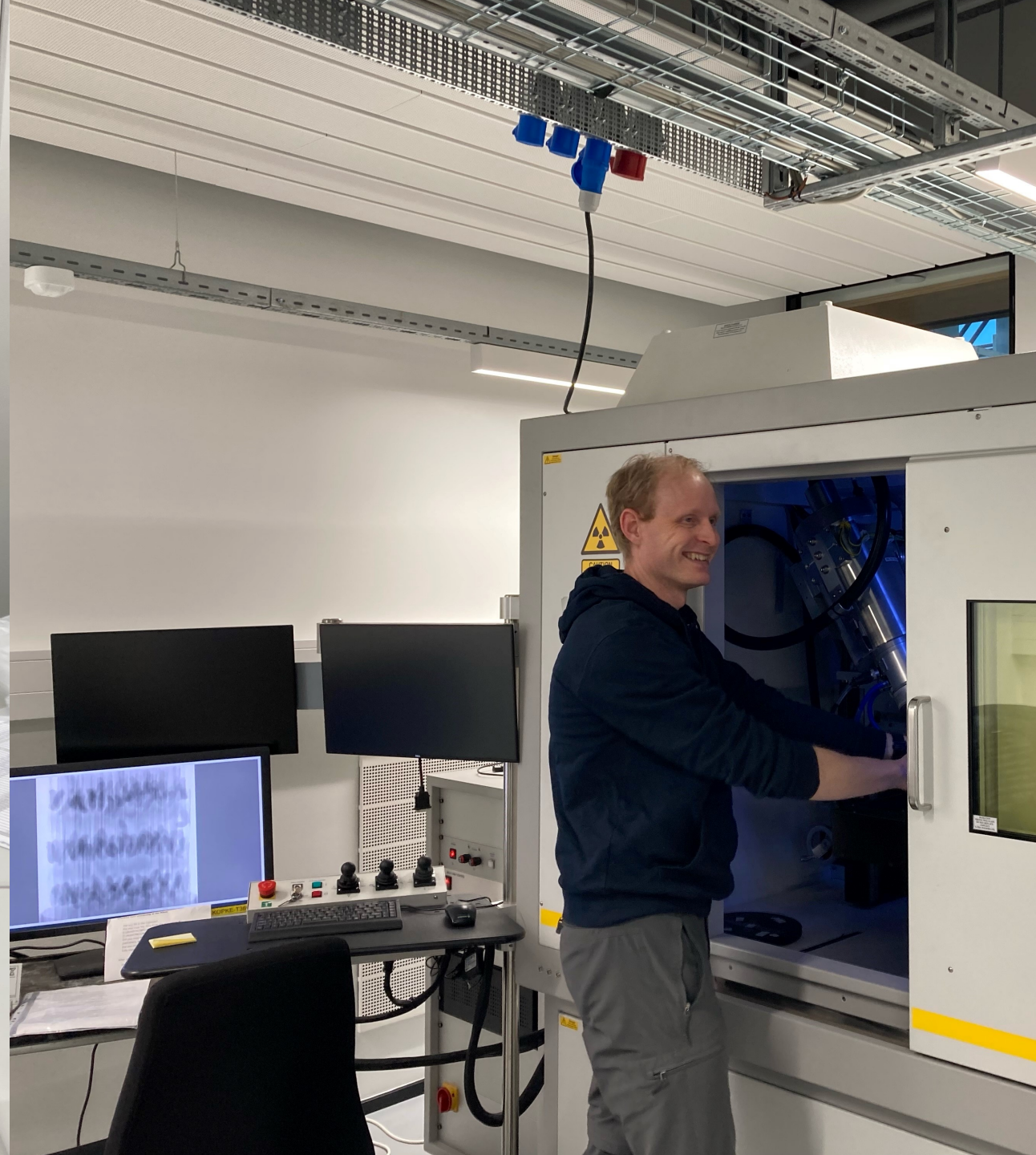
Our freezer at home



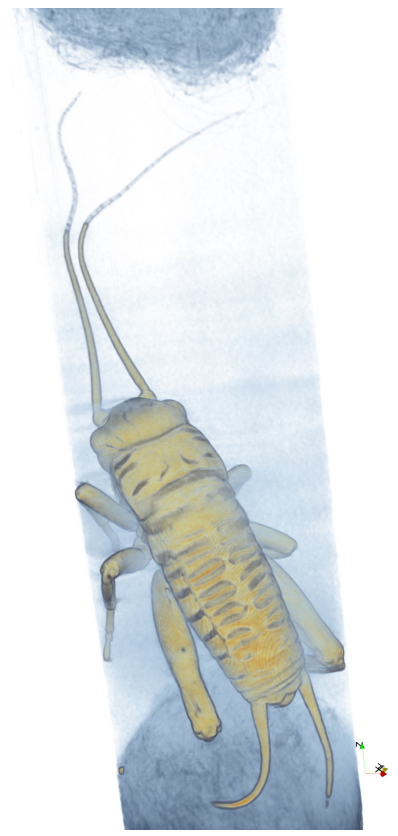
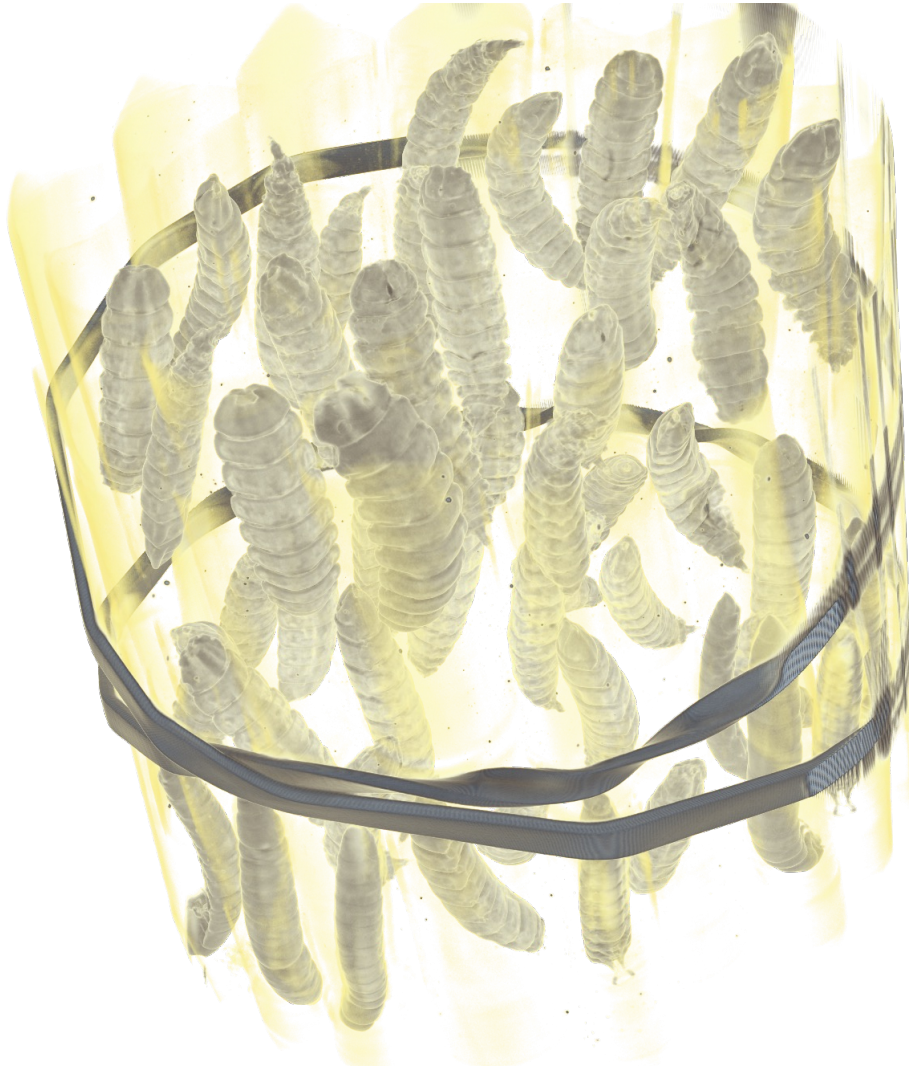
Development of packaging

VIGTIGT (til modtager)
Er pakken sendt med post ved
en temperatur på 5 grader
eller under, skal den i
stuetemperatur, 2 timer
før **UDPAKNING**





Initial data

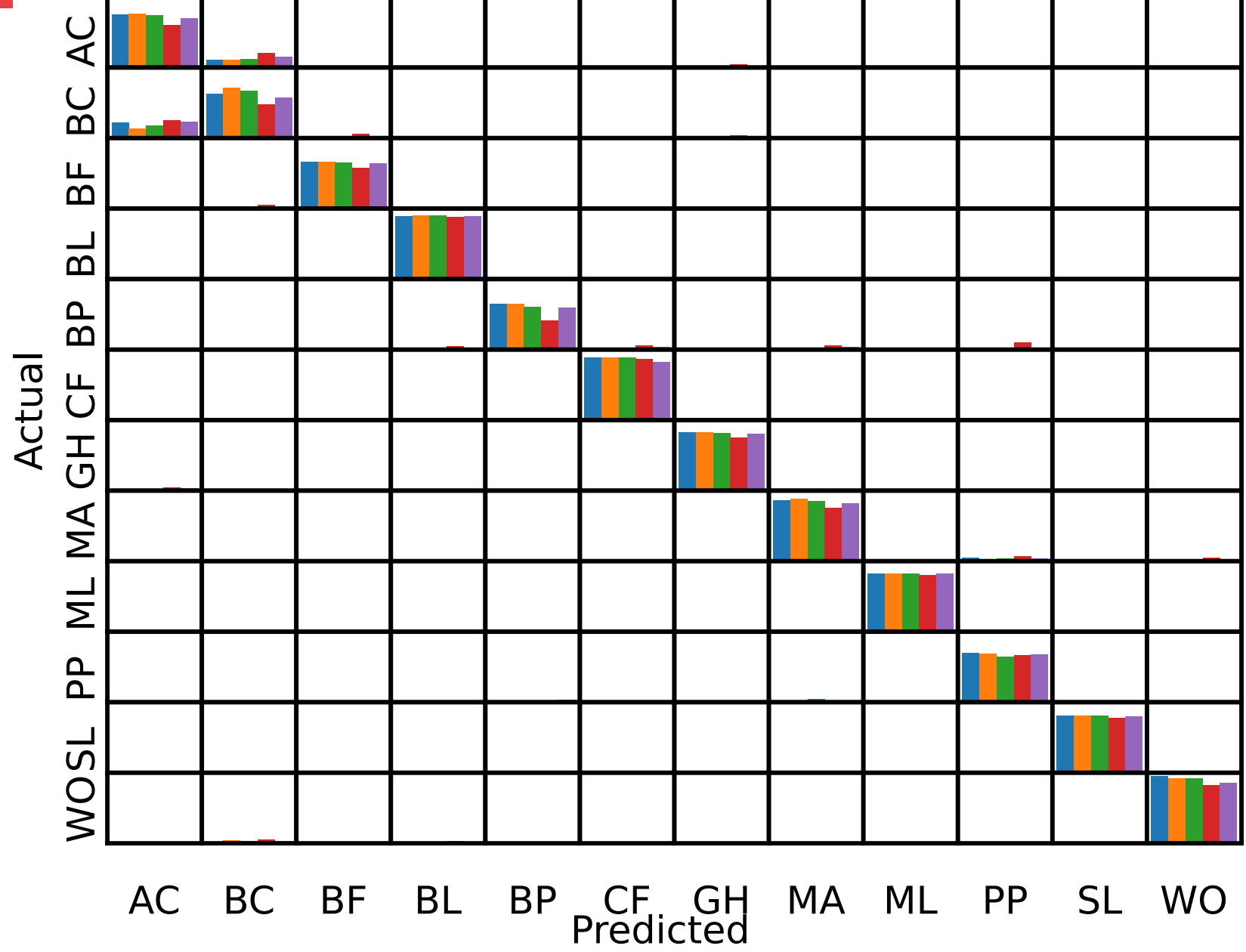


Dataset for classification

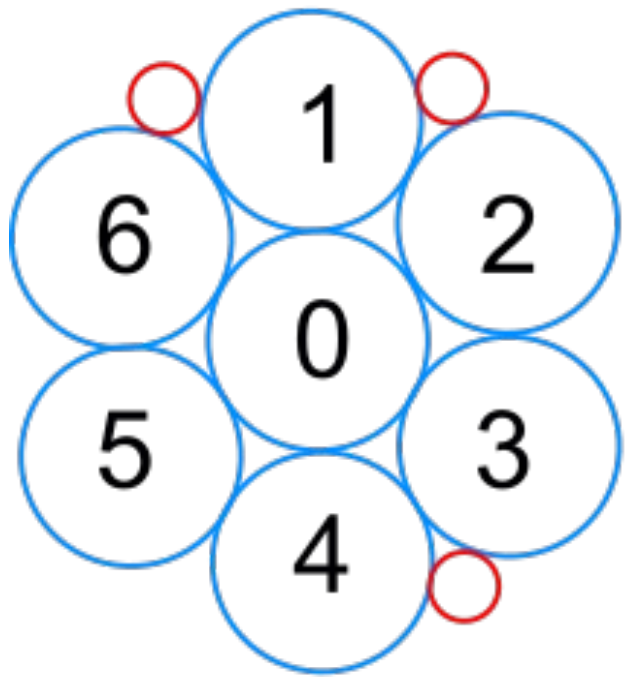
AC	BC	BF	BL	BP	CF	GH	MA	ML	PP	SL	WO
(brown cricket)	(black cricket)	(blow fly)	(buffalo beetle larva)	(blow fly pupa)	(curly-wing fly)	(grasshopper)	(maggot)	(mealworm)	(green bottle fly pupa)	(soldier fly larva)	(woodlice)
724	804	734	780	752	756	760	765	738	769	740	765

Results - classification

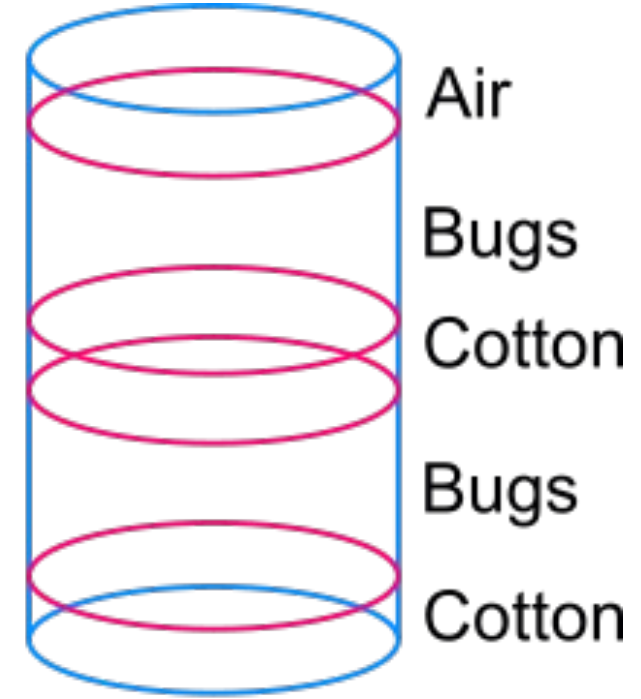
- Almost 100% correct
- Small differences between crickets
- Not much to talk about – solved problem!
- What to do...?



Create a more difficult problem

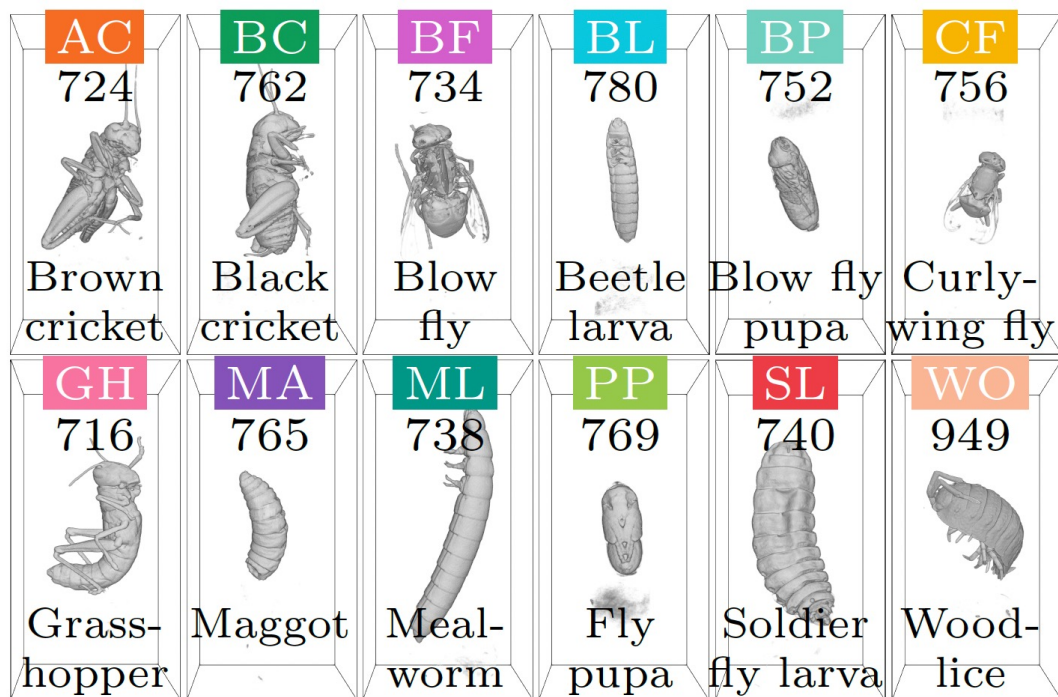


Bundle of test tubes

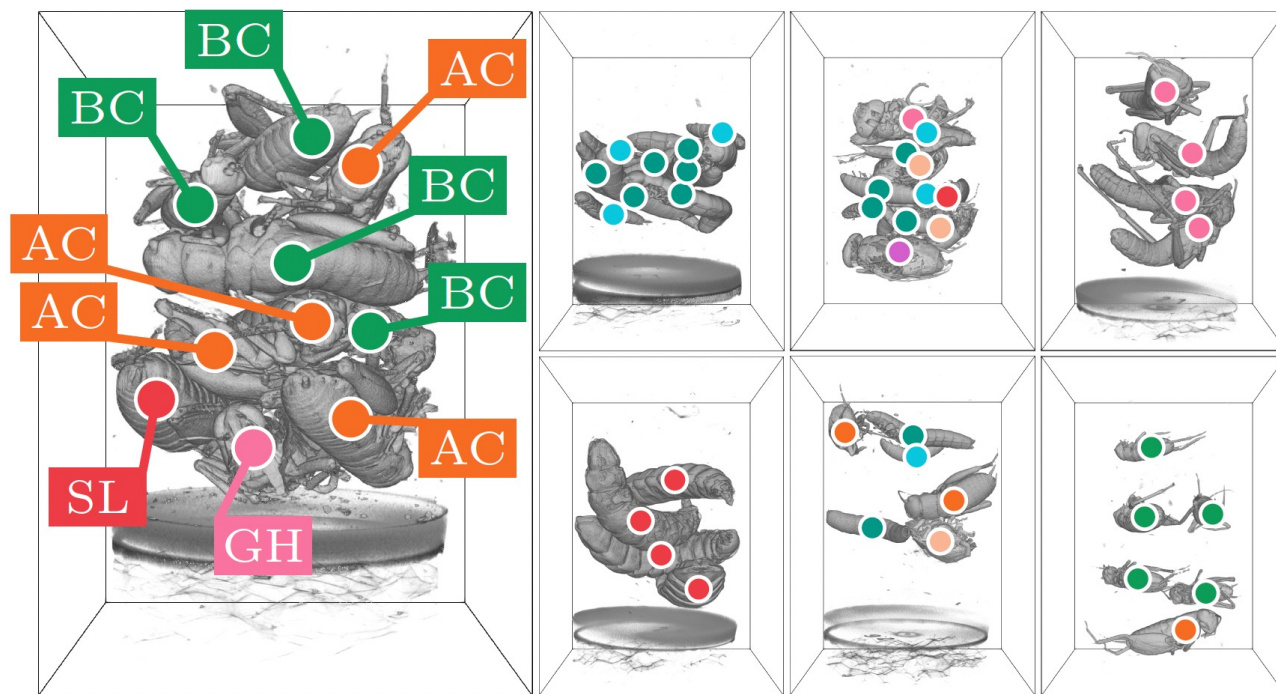


Single test tubes

Small Change – Catastrophic Consequences



Training
Single objects (μ CT volumes)



Test
Mixed objects (μ CT volumes)

Source: Jensen et al., in prep.

Data

Individual – simple to annotate

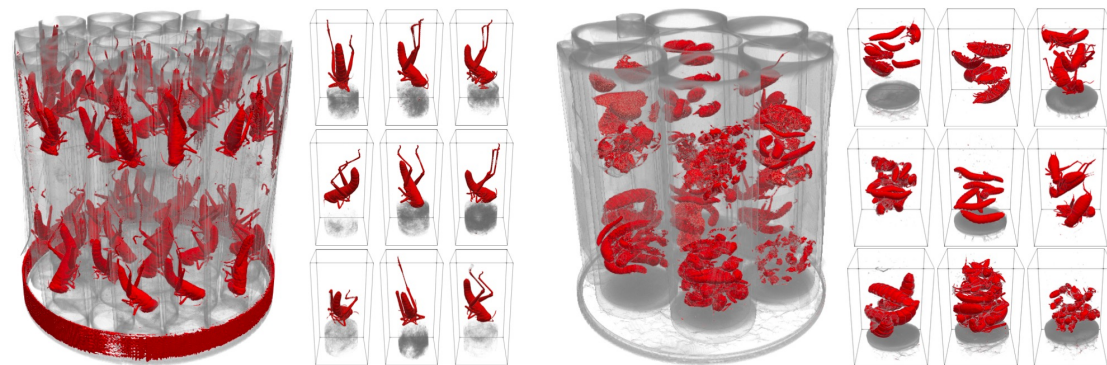


Mixes – complex to annotate

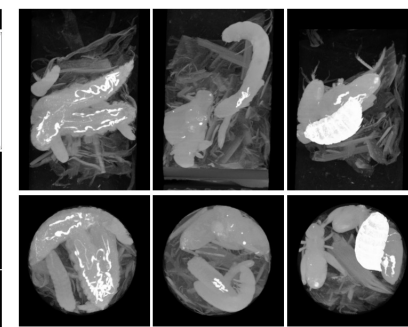


Deep learning benchmark data

- Topic: Object detection and segmentation
- Problem: Annotation is difficult and time-consuming
- Idea: Create a setup where annotation is easy
- Dataset for deep learning:
 - 9154 individual bugs – reflecting shape variation
 - 388 volumes of mixtures
 - Scans with background material (no bug scans)
 - Publish data, baseline solution, and Kaggle Challenge



AC	BC	BF	BL	BP	CF	GH	MA	ML	PP	SL	WO
(brown cricket)	(black cricket)	(blow fly)	(buffalo beetle larva)	(blow fly pupa)	(curly-wing fly)	(grasshopper)	(maggot)	(mealworm)	(green bottle fly pupa)	(soldier fly larva)	(woodlice)
724	804	734	780	752	756	760	765	738	769	740	765



Results on BugNIST challenge

Model	- Trained on	Without class info.			With class info.		
		F1-Score	Precision	Recall	F1-Score	Precision	Recall
U-Net [8]	- Single bugs	0.59 ± 0.18	0.68 ± 0.17	0.60 ± 0.25	0.11 ± 0.16	0.13 ± 0.19	0.11 ± 0.16
	- Synth. mixes	0.60 ± 0.12	0.52 ± 0.17	0.82 ± 0.19	0.11 ± 0.08	0.09 ± 0.08	0.14 ± 0.10
	- Crowded s.m.	0.54 ± 0.13	0.39 ± 0.14	0.97 ± 0.07	0.10 ± 0.08	0.07 ± 0.06	0.18 ± 0.14
Faster R-CNN [54]	- Single bugs	0.56 ± 0.20	1.00 ± 0.04	0.42 ± 0.21	0.11 ± 0.10	0.21 ± 0.19	0.08 ± 0.08
	- Synth. mixes	0.68 ± 0.16	0.63 ± 0.21	0.83 ± 0.22	0.16 ± 0.14	0.15 ± 0.14	0.19 ± 0.18
	- Crowded s.m.	0.27 ± 0.17	0.81 ± 0.24	0.18 ± 0.16	0.06 ± 0.09	0.19 ± 0.30	0.04 ± 0.06
nn- Detection [4]	- Single bugs	0.03 ± 0.02	0.02 ± 0.01	0.91 ± 0.15	0.00 ± 0.01	0.00 ± 0.00	0.09 ± 0.16
	- Synth. mixes	0.50 ± 0.14	0.41 ± 0.17	0.80 ± 0.22	0.10 ± 0.06	0.08 ± 0.06	0.16 ± 0.11
	- Crowded s.m.	0.60 ± 0.19	0.77 ± 0.23	0.58 ± 0.27	0.11 ± 0.12	0.15 ± 0.16	0.11 ± 0.12

FGVC Kaggle challenge @ CVPR



BugNIST2024 Volumetric Out-of-Context Detection

Patrick M. Jensen, Vedrana A. Dahl, Rebecca Engberg, Carsten Gundlach, Hans Martin Kjer, Anders B. Dahl



Background: Labeling densely packed 3D objects for detection is time-consuming.

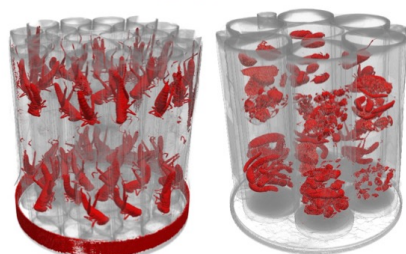
Suggestion: Train detection on isolated, individually scanned objects, where labels are easy to obtain.













Problem: Inferring on densely packaged objects introduces domain shift: out-of-context.

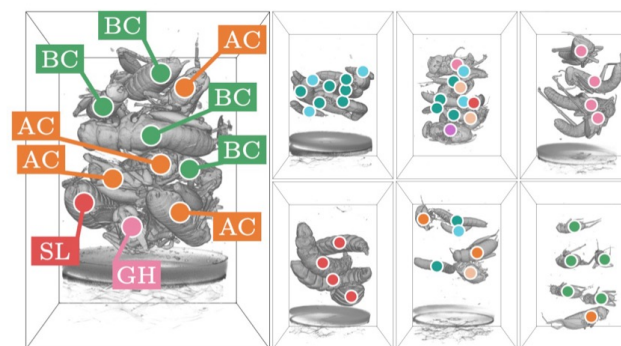
Example objects: Bugs. Due to size suitable for handling and scanning, complex shape, and availability.

Data collection: Bugs placed in tubes, individually or in mixtures (shown below).

Aim: Promote the development of new deep-learning-based methods for 3D volumetric imaging.



AC 724  Brown cricket	BC 761  Black cricket	BF 733  Blow fly	BL 773  Beetle larva	BP 748  Blow fly pupa	CF 756  Curly-wing fly
GH 713  Grasshopper	MA 758  Maggot	ML 737  Mealworm	PP 765  Fly pupa	SL 740  Soldier fly larva	WO 946  Woodlice



BugNIST dataset

- Individual bug volumes: 9185 micro-CT volumes with single bug, 12 bug classes
- Bug mixes: 388 volumes of densely packed bugs, each bug annotated with bug class and center point

Out-of-context detection

- Training: only individual bugs. (These may be used to create synthetic mixes.)
- Testing: bug mixes.

Bugs have the same appearance in the source (individual) and target (mixes) domain, but the surrounding context is different.

kaggle challenge

Participation

- 108 Entrants
- 31 Participants
- 16 Teams
- 91 Submissions

Prizes & Awards

- Kudos
- Joint paper

Team	Public leaderboard	Private leaderboard
Baseline	0.11102	0.12711
Winning team	0.55318	0.54899
Second place	0.45457	0.44450

Reflections: Limited overfitting – similar performance on private and public leaderboards.

- 11 teams beat the baseline
- 4 teams below the baseline

Approach (baseline)

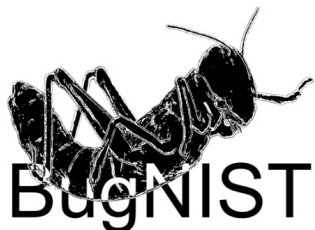
- U-Net with a depth of three trained on individual bugs
- Detection – center points of connected components

Approach (winning team)

- U-Net with a depth of three trained on synthetic mixes
- On-the-fly synthesis and augmentation
- Synthetic mixes inspired by Tetris
- Random augmentations
- Cross-entropy and non-background Dice loss
- Detection – center points of connected components



Data available



Webpage for the BugNIST dataset

[View our competition on Kaggle](#)
Kaggle/bugnist

Download
dataset

Get arXiv
paper

Code on
GitHub

BugNIST - dataset for volumetric analysis

The BugNIST dataset is created to advance methods for classification and detection in 3D. It contains 9542 volumes where 9154 are of individual bugs and 388 are mixtures of bugs and other material. There are 12 types of bugs including larvae, pupae, insects, and woodlice.

In the BugNIST classification challenge, each volume containing a single bug must be classified as one of the 12 types. The original volumes are 900x450x450 voxels, and in addition, we provide the data at different resolutions by downscaling the original scans.

aims to benchmark classification and detection methods, and we have designed the detection challenge such that detection models are trained on scans of individual bugs and tested on bug mixtures. Models capable of solving this task will be independent of the context, i.e., the surrounding material. In cases where the context is unknown or changing, this is a great advantage, which is commonly occurring in 3D μ CT.

What is BugNIST?

BugNIST is a volumetric dataset for object detection and segmentation. BugNIST has several features:

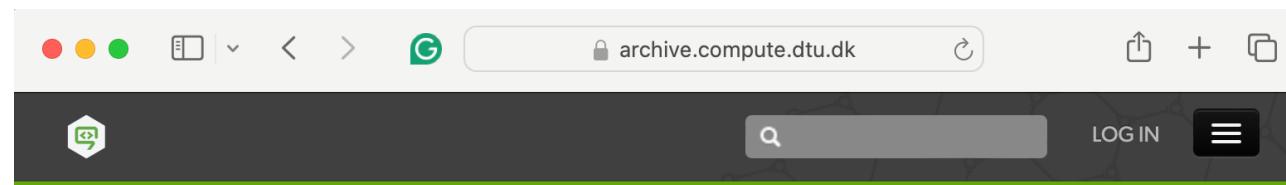
- Object detection in volumetric data
- Segmentation in volumetric data
- 3D μ CT scanning of 12 bug classes
- 9154 volumes of individual bugs
- 388 volumes of bug mixtures with center point annotations
- Volume sizes: 900x450x450 (individual) and 900x650x650 (mixtures)
- Data available in sizes:
 - Original: 900x450x450 (individual) and 900x650x650 (mixtures)
 - Large: 512x256x256 (individual) and 512x370x370 (mixtures)
 - Medium: 256x128x128 (individual) and 256x185x185 (mixtures)
 - Small: 128x64x64 (individual) and 128x92x92 (mixtures)
 - Tiny: 64x32x32 (individual) and 64x46x46 (mixtures)

People:

- Anders Bjorholm Dahl, DTU Compute
- Patrick Møller Jensen, DTU Compute
- Vedrana Andersen Dahl, DTU Compute
- Carsten Gundlach, DTU Physics
- Rebecca Engberg, DTU Compute
- Hans Martin Kjer, DTU Compute

Sponsors: Novo Nordisk Foundation, Villum Foundation

Page is maintained by [abdahl](#) and [QIM](#) team.



zips

// public / projects / BugNIST3D / zips

Browse

Commits



Download .zip

Show Deleted Files

Name	Modified	Size
↑ ..		
📄 bugnist_064.zip	about a month ago	86.68 MB
📄 bugnist_128.zip	about a month ago	540.03 MB
📄 bugnist_256.zip	about a month ago	4.29 GB
📄 bugnist_512.zip	about a month ago	37.29 GB
📄 bugnist_900.zip	about a month ago	237.65 GB
📄 mixed_064.zip	about a month ago	15.62 MB
📄 mixed_128.zip	about a month ago	125.68 MB
📄 mixed_256.zip	about a month ago	1.07 GB
📄 mixed_512.zip	about a month ago	9.12 GB
📄 mixed_900.zip	about a month ago	49.56 GB

Publication

BugNIST – a Large Volumetric Dataset for Object Detection under Domain Shift

Patrick Møller Jensen[✉], Vedrana Andersen Dahl[✉], Rebecca Engberg[✉], Carsten Gundlach[✉], Hans Marin Kjer[✉], and Anders BJORHOLM DAHL[✉]

Technical University of Denmark, Kgs. Lyngby, Denmark
 {patmjen, vand, reen}@dtu.dk, cagu@fysik.dtu.dk, {hmjk, abda}@dtu.dk

Abstract. Domain shift significantly influences the performance of deep learning algorithms, particularly for object detection within volumetric 3D images. Annotated training data is essential for deep learning-based object detection. However, annotating densely packed objects is time-consuming and costly. Instead, we suggest training models on individually scanned objects, causing a domain shift between training and detection data. To address this challenge, we introduce the BugNIST dataset, comprising 9154 micro-CT volumes of 12 bug types and 388 volumes of tightly packed bug mixtures. This dataset is characterized by having objects with the same appearance in the source and target domains, which is uncommon for other benchmark datasets for domain shift. During training, individual bug volumes labeled by class are utilized, while testing employs mixtures with center point annotations and bug type labels. Together with the dataset, we provide a baseline detection analysis, with the aim of advancing the field of 3D object detection methods.

Keywords: Volumetric Dataset, Benchmark, Volumetric Object Detection, Domain Shift.

1 Introduction

Our work on domain shift in volumetric 3D images is motivated by the need for labeled data to train supervised deep learning models for volumetric imaging. The problem that we aim to solve is object detection and classification. We propose to label images of objects scanned as isolated entities as the source domain and use these as a basis to train models for object detection and classification in a complex context of mixed objects and other materials as the target domain. The effort needed for obtaining labels in the two domains is significantly different. If objects are isolated, they can be automatically labeled whereas mixed objects require expensive manual labeling. Automating the labeling based on isolated objects, however, leads to a domain shift between the data in the source domain for training and the data in the target domain for detection and classification. This domain shift is special because the appearance of the objects is the same

arXiv v1:

- **Title:** BugNIST -- A New Large Scale Volumetric 3D Image Dataset for Classification and Detection
- **Authors:** Anders BJORHOLM DAHL, Patrick Møller Jensen, Carsten Gundlach, Rebecca Engberg, Hans Martin Kjer, Vedrana Andersen Dahl
- **Rejected** at ICCV 2023

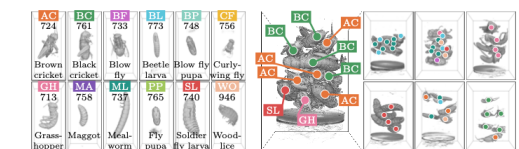
arXiv v2:

- **Title:** BugNIST -- a Large Volumetric Dataset for Object Detection under Domain Shift
- **Authors:** Patrick Møller Jensen, Vedrana Andersen Dahl, Carsten Gundlach, Rebecca Engberg, Hans Martin Kjer, Anders BJORHOLM DAHL
- **Rejected** at CVPR 2024

arXiv v3:

- **Title:** BugNIST -- a Large Volumetric Dataset for Object Detection under Domain Shift
- **Authors:** Patrick Møller Jensen, Vedrana Andersen Dahl, Carsten Gundlach, Rebecca Engberg, Hans Martin Kjer, Anders BJORHOLM DAHL
- **Accepted** at ECCV 2024!

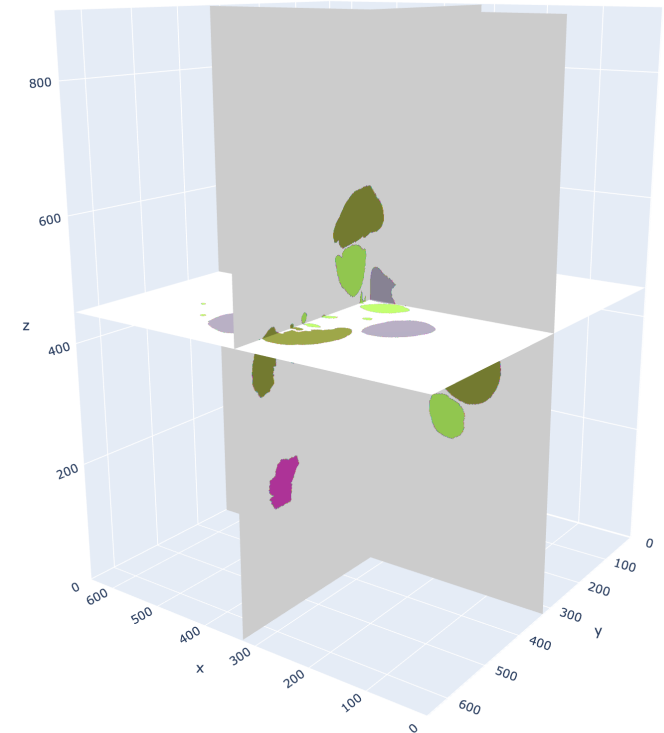
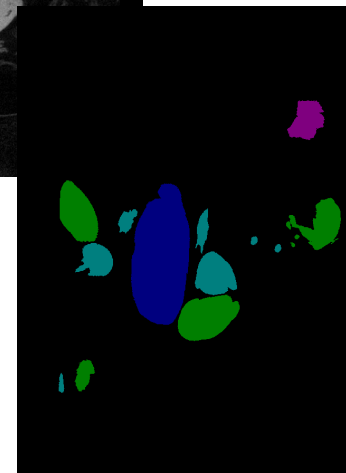
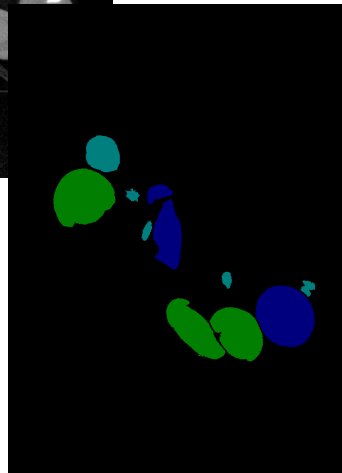
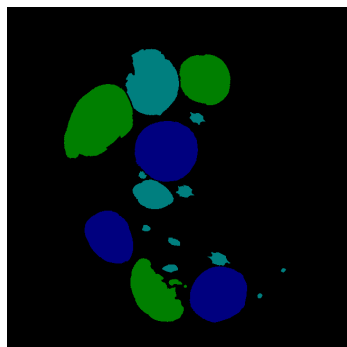
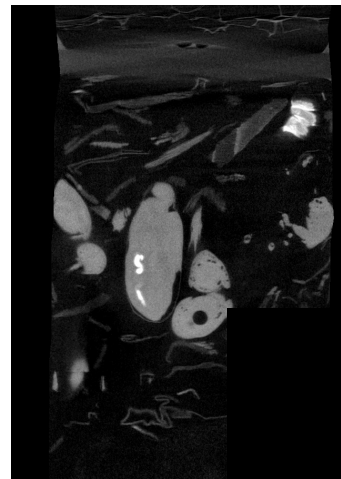
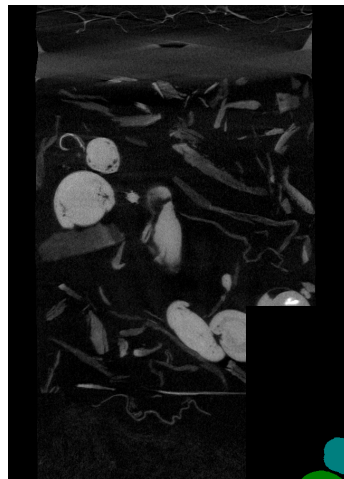
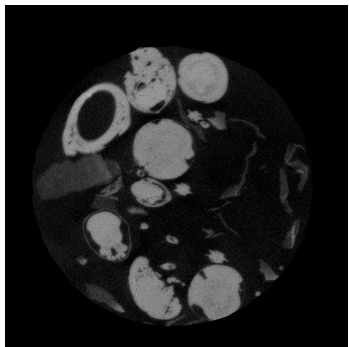
2 P.M. Jensen et al.



(a) 614 volumes of individual bugs (b) 988 volumes of bug mixtures with center point annotations

Future work

- Classification and object detection – not segmentation!
- Problem: Ground truth labels
 - Training data: Individual bugs that are automatically labeled
 - Test data: Mixes where annotation is manual and difficult



Conclusion (part two)

- Domain shift between individuals and mixes was surprisingly large
 - Minimal difference in appearance between individuals and mixes, yet standard deep learning fails!
 - Deep learning-based detection utilizes context
 - Potential research in methods that ignore context (initial investigations)
 - Potential research in generating context (strategy we tested and winners of Kaggle)
- Collecting data
 - Time consuming, exhausting, fun, frustrating...
 - Spend much time testing methods on preliminary data
 - The community expects extremely large datasets
- The data curation is ongoing and will continue
- Datasets with extensive investigations can get published in high-impact venues!

Jon Sparring: Exploring biological shape analysis through topology, geometry and statistics

The lecture will include a hands-on session. On <https://sparring.github.io/> you will find the slides and a zip-file:

- <https://sparring.github.io/bia2024/talk.pdf> including a useful literature list
- https://sparring.github.io/bia2024/spatstat_bia2024.zip which includes `demoRpy2.py` and which has installation instructions for R, R-packages, and python packages:

```
# 1. Install R, which to my experience works best directly from https://cran.r-project.org/
# then start R and install some packages:
# install.packages("spatstat")
# install.packages("lazyeval")
# install.packages("GET")
...
```

Save time during the lecture and install R etc. in advance.

Questions?

Contact:
abda@dtu.dk