





Towards 3D Atlas of Human Body

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- **1. Annotation** (5 min) We annotated 25 anatomical structures in 9,262 CT volumes
 - NeurIPS-2023 Semi-automated annotation
 - Three versions: AbdomenAtlas 1.0, 1.1, Pro
- 2. Dataset (10min) We developed data synthesis strategies to enrich tumor examples
 - CVPR-2023 Liver tumor synthesis
 - CVPR-2024 Liver, pancreatic, & kidney tumor synthesis
 - Next version: AbdomenAtlas X
- **3.** Algorithm (10min) We released a set of supervised pre-trained vision-language models
 - ICCV-2023 & MICCAI-2023 Vision-language models
 - ICLR-2024 Supervised pre-training
- **4.** Ending (2 min) A large, open algorithmic benchmark

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Data \rightarrow Information \rightarrow Knowledge \rightarrow Application



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We created AbdomenAtlas of 22,682 CT volumes and 3.2M annotated masks



AbdomenAtlas 1.0

publicly available! 5,195 CT volumes and 46K annotated masks *https://www.zongweiz.com/dataset*





AbdomenAtlas 1.1

coming in MICCAI-2024 challenge 9,262 CT volumes and 231K annotated masks *https://www.zongweiz.com/dataset*





Highlight 1. Multicenter CT scans (3M)



Highlight 2. Fully annotated 25 structures





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Fine-tuning Convolutional Neural Networks for Biomedical Image Analysis: Actively and Incrementally*

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Abstract

Intense interest in applying convolutional neural networks (CNNs) in biomedical image analysis is wide spread, but its success is impeded by the lack of large annotated datasets in biomedical imaging. Annotating biomedical images is not only tedious and time consuming, but also demanding of costly, specialty-oriented knowledge and skills, which are not easily accessible. To dramatically reduce annotation cost, this paper presents a novel method called AIFT (active, incremental fine-tuning) to naturally integrate active learning and transfer learning into a single framework. AIFT starts directly with a pre-trained CNN to seek "worthy" samples from the unannotated for annotation, and the (fine-tuned) CNN is further fine-tuned continuously by incorporating newly annotated samples in each iteration to enhance the CNN's performance incrementally. We have evaluated our method in three different biomedical imaging applications, demonstrating that the cost of annotation can be cut by at least half. This performance is attributed to the several advantages derived from the advanced active and incremental capability of our AIFT method.

Total citations Cited by 473

but its success is impeded by the lack of such large annotated datasets in biomedical imaging. Annotating biomedical images is not only tedious and time consuming, but also demanding of costly, specialty-oriented knowledge and skills, which are not easily accessible. Therefore, we seek to answer this critical question: How to dramatically reduce the cost of annotation when applying CNNs in biomedical imaging. In doing so, we present a novel method called AIFT (active, incremental fine-tuning) to naturally integrate active learning and transfer learning into a single framework. Our AIFT method starts directly with a pre-trained CNN to seek "salient" samples from the unannotated for annotation, and the (fine-tuned) CNN is continuously finetuned by incrementally enlarging the training dataset with newly annotated samples. We have evaluated our method in three different applications including colonoscopy frame classification, polyp detection, and pulmonary embolism (PE) detection, demonstrating that the cost of annotation can be cut by at least half.

This outstanding performance is attributed to a simple yet powerful observation: To boost the performance of C-NNs in biomedical imaging, multiple patches are usual-



annotation







We summarized a **taxonomy** of common errors made by AIs and humans [Qiao et al., RSNA 2023]



Aorta Inconsistent labeling protocols





Stomach uncertainty in empty areas



Postcava ambiguous & blurry boundaries

- 1. Annotation Summary
- We created AbdomenAtlas 1.1 for 25 anatomical structures
- But, scaling annotations for tumors remains challenging
 - Pathology reports
 - Manual annotations
 - Collaborations (academia, industry, & hospital)

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Observation: early-stage tumors (< 2cm) tend to have *similar imaging characteristics* in computed tomography (CT), whether they originate in the liver, pancreas, or kidneys.



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Generative AI models (e.g., diffusion models) trained on **liver tumor** examples Observation: early-stage tumors (< 2cm) tend to have *similar imaging characteristics* in computed tomography (CT), whether they originate in the liver, pancreas, or kidneys.





Generative AI models (e.g., diffusion models) trained on **liver tumor** examples

- 1. We used Diffusion Model to overfit tumor appearance
- 2. We address out-of-distribution by using diverse CT volumes





Generative AI models (e.g., diffusion models) trained on liver tumor examples

Medical professionals cannot tell which are real and which are synthetic tumors



Training AI on synthetic tumors performs as well as training it on real tumors

CT



Al prediction trained on real tumors with per-voxel annotation DSC = 58% [52% - 63%] Al prediction trained on synthetic tumors *with no annotation* DSC = 60% [55% - 65%]



Diffusion Model can generate enormous small tumors for training AI models

- AI trained on synthetic tumors AI trained on real tumors
- ground truth



Observation: Compared with real tumors, AI trained on synthetic tumors improves Sensitivity from 52% to 62% for detecting small tumors (0-5mm). *We evaluated on real tumors!*

Diffusion Model can generate enormous small tumors for training AI models

AI trained on synthetic tumorsAI trained on real tumorsground truth



Observation: Compared with real tumors, Al trained on synthetic tumors improves Sensitivity from 52% to 62% for detecting small tumors (0-5mm). *We evaluated on real tumors!*

- Needed for early detection
 - o Early signs of cancer can be subtle
 - o 1/2 of liver cancer are missed by radiologists

Diffusion Model can generate enormous small tumors for training AI models

Al trained on synthetic tumors Al trained on real tumors ground truth



Observation: Compared with real tumors, Al trained on synthetic tumors improves Sensitivity from 52% to 62% for detecting small tumors (0-5mm). *We evaluated on real tumors!*

- Needed for early detection
 - o Early signs of cancer can be subtle
 - o 1/2 of liver cancer are missed by radiologists
- Needed for AI development
 - o CT scans with early cancer are limited
 - o Annotations for early cancer are hard

AbdomenAtlas X – coming soon! (Chen et al., CVPR 2024) 9,262 CT volumes and 66K tumor masks https://www.zongweiz.com/dataset

- 2. Dataset Summary
- We generated synthetic tumor data in the liver, pancreas, & kidneys
- But, generalizable tumor synthesis to other organs is challenging
 - The assumption—early tumors are similar—is problematic
 - Medical knowledge is needed CV plus Radiology

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Two potential tumors are framed in bounding boxes.



Medical Segmentation Decathlon

#	₩	User (Team)	₩	Created	1\$₽	Mean Position	
1st		🚳 zongwei.zhou 🏖 (universal_model)		13 Feb. 2023		5.6	
2nd		Swin_UNETR 2		12 Nov. 2021		10.1	
3rd		🚑 ahatamiz2 🚔		12 Nov. 2021		10.1	
4th		🛞 Isensee 🚔		6 Dec. 2019		12.3	
5th		AndyL		24 Nov. 2022		12.5	
6th		🛞 heyufan1995		30 Oct. 2020		12.8	
7th		😛 qsyeung 🚔		5 Jan. 2023		12.9	
8th		🌐 vishwesh.nath 峇		11 Nov. 2021		13.5	

Acknowledgement: Universal Model adopted the checkpoint released by Tang et al., CVPR 2022 (NVIDIA). This checkpoint was *self-supervised* pre-trained from 5,000 CT volumes. But wait, we have AbdomenAtlas 1.1 now!



De-noising [Vincent et al., 2010] Positioning [Doersch et al., 2015] In-painting [Pathak et al., 2016] Jigsaw [Noroozi and Favaro, 2016] DeepCluster [Caron et al., 2018] Restoration [Chen et al., 2019]



[Zhou et al., MICCAI 2019] MICCAI Young Scientist Award MedIA Best Paper Award

Rubiks Cube [Zhuang et al., MICCAI 2019] Swin UNETR [Tang et al., CVPR 2022]

UniMiSS [Xie et al., ECCV 2022]



Option 1. Self-supervised pre-training



Option 1. Self-supervised pre-training



Option 2. Supervised pre-training

AbdomenAtlas 1.1

Supervised > Self-supervised data & computation efficiency





data for pre-training

transferring to tumor segmentation



annotated data for fine-tuning



The FELIX Project: Deep Networks To Detect Pancreatic Neoplasms

Yingda Xia^{1,†}, Qihang Yu^{1,†}, Linda Chu^{2,†}, Satomi Kawamoto^{2,†}, Seyoun Park², Fengze Liu¹, Jieneng Chen¹, Zhuotun Zhu¹, Bowen Li¹, Zongwei Zhou¹, Yongyi Lu¹, Yan Wang¹, Wei Shen¹, Lingxi Xie¹, Yuyin Zhou¹, Christopher Wolfgang³, Ammar Javed³, Daniel Fadaei Fouladi², Shahab Shayesteh², Jefferson Graves², Alejandra Blanco², Eva S. Zinreich², Benedict Kinny-Köster³, Kenneth Kinzler^{4,6,7,8}, Ralph H. Hruban⁵, Bert Vogelstein^{4,6,7,8,9}, Alan L. Yuille^{1,*}, Elliot K. Fishman^{2,*}

¹Department of Computer Science, Johns Hopkins University; ²Department of Radiology and Radiological Science, Johns Hopkins Medicine; ³Department of Surgery, New York University; ⁴Department of Oncology, Johns Hopkins Medicine; ⁵Department of Pathology, Johns Hopkins Medicine; ⁶Ludwig Center, Johns Hopkins University School of Medicine; ⁷Sidney Kimmel Comprehensive Cancer Center, Johns Hopkins University School of Medicine; ⁸Sol Goldman Pancreatic Cancer Research Center, Johns Hopkins University School of Medicine; ⁹Howard Hughes Medical Institute, Johns Hopkins Medical Institutions

Abstract Tens of millions of abdominal images are performed with computed tomography (CT) in the U.S. each year but pancreatic cancers are sometimes not initially detected in these images. We here describe a suite of algorithms (named FELIX) that can recognize pancreatic lesions from CT images without human input. Using FELIX, >90% of patients with pancreatic ductal adenocarcinomas were detected at a specificity of >90% in patients without pancreatic disease. FELIX may be able to assist radiologists in identifying pancreatic cancers earlier, when surgery and other treatments offer more hope for long-term survival.



Extending Supervised Pretraining on Large Organ Dataset to Universal Lesion Segmentation

Yannick Kirchhoff, Maximilian R. Rokuss, Saikat Roy, Klaus H. Maier-Hein German Cancer Research Center (DKFZ), Heidelberg, Germany

Method Description:

Our method uses a lightweight nnUNet [1] pretrained on a large organ segmentation dataset. We used supervised pretraining on the Abdomen Atlas 1.0 [2,3] dataset with 8 annotated organs over 5000 CT samples. Our work demonstrates that we can efficiently train the smallest possible models to learn robust representations of CT images from a large organ database which does not have any label overlaps with the ULS23 labelset. Our priority is not solely about reaching the very best Dice score. Instead, we aim for a very lightweight design while maintaining comparable accuracy.

References:

[1] Isensee, Fabian, et al. "nnU-Net: a self-configuring method for deep learning-based biomedical image segmentation." Nature methods 18.2 (2021): 203-211.

[2] Qu, Chongyu, et al. "Abdomenatlas-8k: Annotating 8,000 CT volumes for multi-organ segmentation in three weeks." Advances in Neural Information Processing Systems 36 (2024).

[3] Li, Wenxuan, Alan Yuille, and Zongwei Zhou. "How well do supervised models transfer to 3d image segmentation?." The Twelfth International Conference on Learning Representations. 2023.

- 3. Algorithm Summary
- Language is the key to unify multiple vision tasks
 - High-performance & generalizable
 - Accommodating new classes/tasks
- Let's start the debate between self-supervised vs. supervised pre-training

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AbdomenAtlas 1.0

@ISBI 2024 Challenge



IEEE INTERNATIONAL SYMPOSIUM ON BIOMEDICAL IMAGING ISBBI 2024 27-30 MAY, 2024 - ATHENS, GREECE WIGADON ANNOV 2024 - ATHENS, GREECE

Backbone	Author	Institute	Publication	Backbone	Author	Institute	Publication
U-Net	O. Ronneberger	Uni Freiburg	MICCAI	nnU-Net	Fabian Isensee	DKFZ	Nat. Methods
nnFormer	Hong-Yu Zhou	НКО	TIP	SAT	Ziheng Zhao	SJTU 14 0	arXiv
CoTr	Yutong Xie	NPU	MICCAI	Swin UNETR	Ali Hatamizadeh	NVIDIA	MICCAIW
UniverSeg	Victor Ion Butoi	MIT	ICCV	UniSeg	Yiwen Ye	NPU	MICCAI
UNet++	Zongwei Zhou	ASU	тмі	MagicNet	Duowen Chen	ECNU 8 co	CVPR
TransUNet	Jieneng Chen	JHU	ICMLW	MedSegDiff	Junde Wu	NUS	AAAI
Swin-Unet	Ни Сао	Huawei	ECCVW	3D UNeXt	Jeya Maria Jose	JHU 9 st	MICCAI
DINTS	Yufan He	JHU	CVPR				

So far, 53 groups have confirmed the contribution—we will invite more authors of famous backbones for medical segmentation.

Zongwei Zhou zzhou82@jh.edu Code, Dataset, & Model:

https://github.com/MrGiovanni/AbdomenAtlas



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Satomi · Kawamoto · Seyoun Park · Christopher Wolfgang · Ammar Javed
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Li · Yu-Cheng Chou · Angtian Wang · Yixiong Chen · Yuxiang Lai · Jincheng
Wang · Huimin Xue · Yining Cao · Haoqi Han · Xiaorui Lin · Yutong Tang · Meihua Li · Yujiu Ma · Jinghui Xu · Jiawei Liu · Zheyuan Zhang



Reference

Scaling Annotations

- C. Qu, T. Zhang, H. Qiao, J. Liu, Y. Tang, A. Yuille, and Z. Zhou*. "Annotating 8,000 Abdominal CT Volumes for Multi-Organ Segmentation in Three Weeks." NeurIPS 2023. <u>https://github.com/MrGiovanni/AbdomenAtlas</u>
- W. Li, A. Yuille, Z. Zhou*. "How Well Do Supervised 3D Models Transfer to Medical Imaging Tasks?" ICLR 2024. https://github.com/MrGiovanni/SuPreM

Scaling Datasets

- Q. Hu, Y. Chen, J. Xiao, S. Sun, J. Chen, A. Yuille, Z. Zhou*. "Label-Free Liver Tumor Segmentation." CVPR 2023. <u>https://github.com/MrGiovanni/SyntheticTumors</u>
- Q. Chen, X. Chen, H. Song, Z. Xiong, A. Yuille, C. Wei, Z. Zhou*. "Towards Generalizable Tumor Synthesis." CVPR 2024. https://github.com/MrGiovanni/DiffTumor
- Y. Lai, X. Chen, A. Wang, A. Yuille, Z. Zhou*. "From Pixel to Cancer: Cellular Automata in Computed Tomography." MICCAI 2024. <u>https://github.com/MrGiovanni/Pixel2Cancer</u>

Scaling Algorithms

 J. Liu, Y. Zhang, J. Chen, Y. Lu, Y. Yuan, A. Yuille, Y. Tang*, Z. Zhou*. "CLIP-Driven Universal Model for Organ Segmentation and Tumor Detection." ICCV 2023. <u>https://github.com/ljwztc/CLIP-Driven-Universal-Model</u>
 Y. Zhang, X. Li, H. Chen, A. Yuille, Y. Liu*, Z. Zhou*. "Learning without Forgetting for Continual Abdominal Multi-Organ and Tumor Segmentation." MICCAI 2023. <u>https://github.com/MrGiovanni/ContinualLearning</u>