

Anatomy Completor: A Multi-class Completion Framework for 3D Anatomy Reconstruction

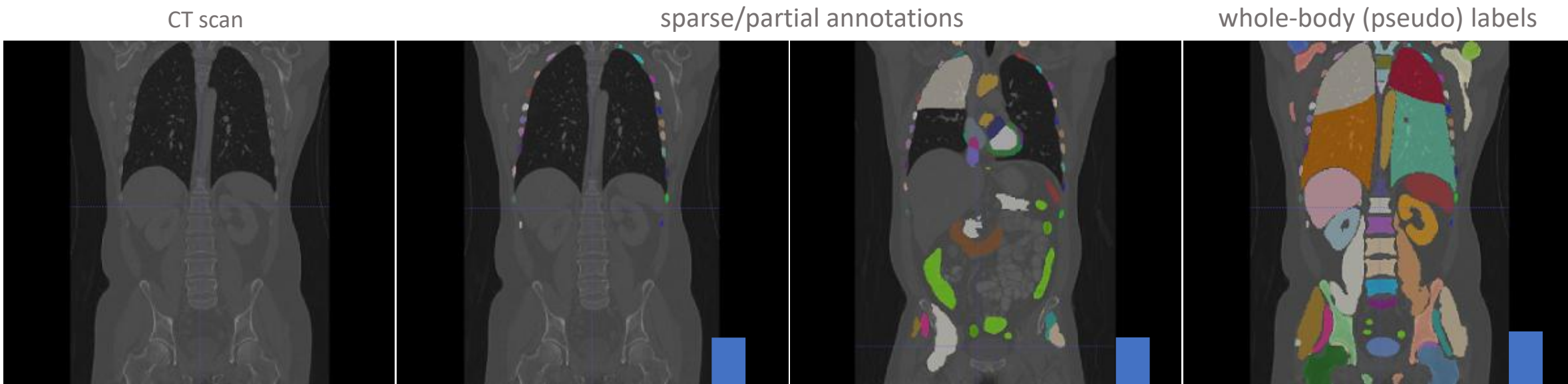
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Problem Statement

For an unannotated CT dataset, given partial manual annotations, how to automatically generate whole-body (pseudo) annotations?

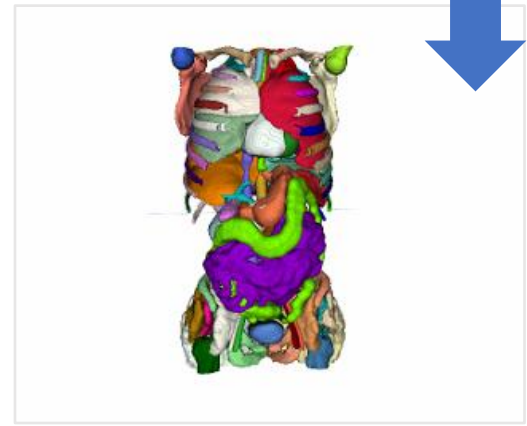
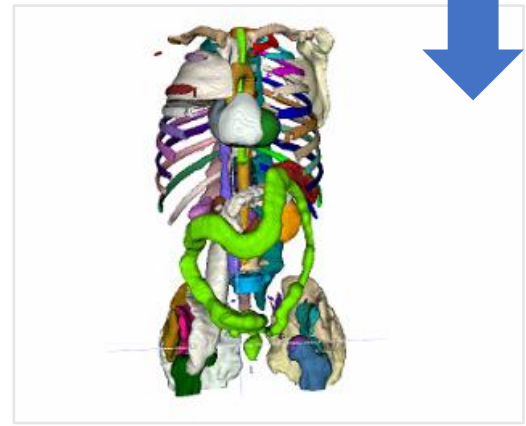
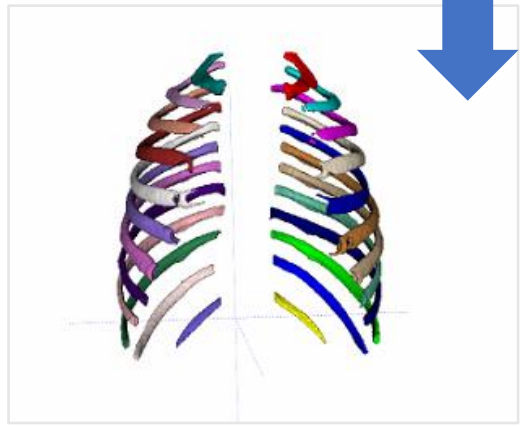


CT scan

sparse/partial annotations

whole-body (pseudo) labels

3D shape completion (image from [1])



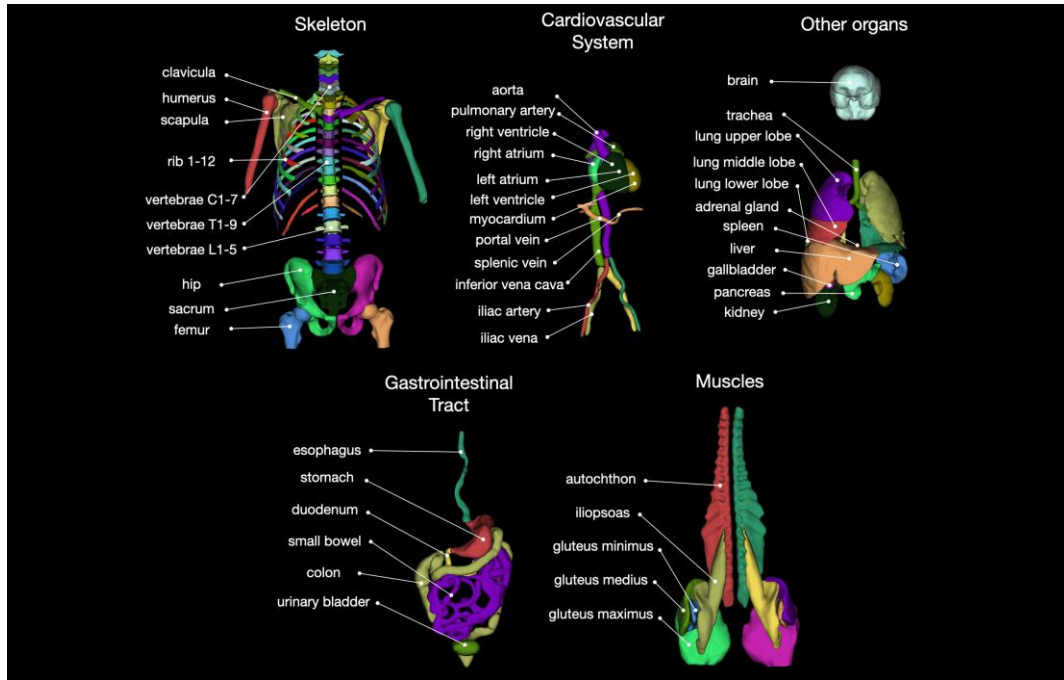
input: partial labels

target: whole-body labels

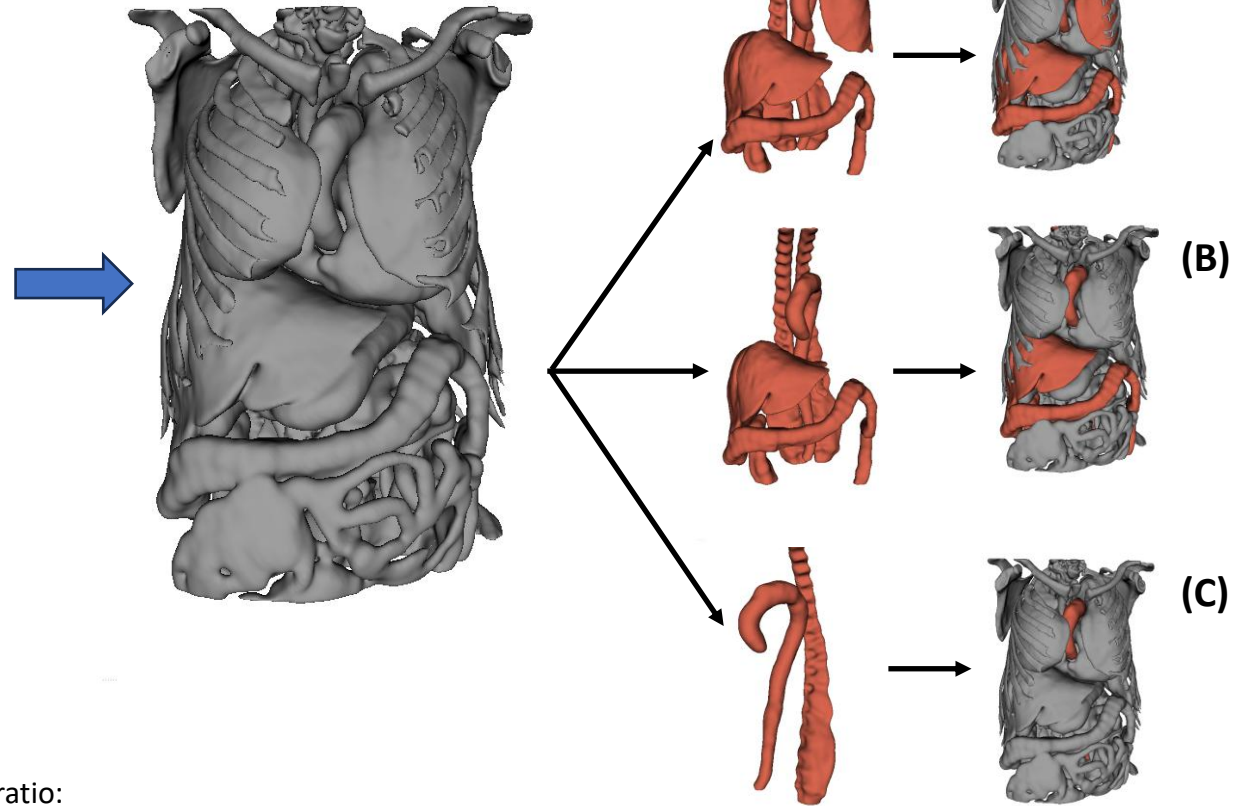
[1] Chu, L., et al. *Unsupervised shape completion via deep prior in the neural tangent kernel perspective*. ACM Transactions on Graphics (TOG), 2021

Dataset Creation: Single Class Dataset

TotalSegmentator whole-body segmentations [1]



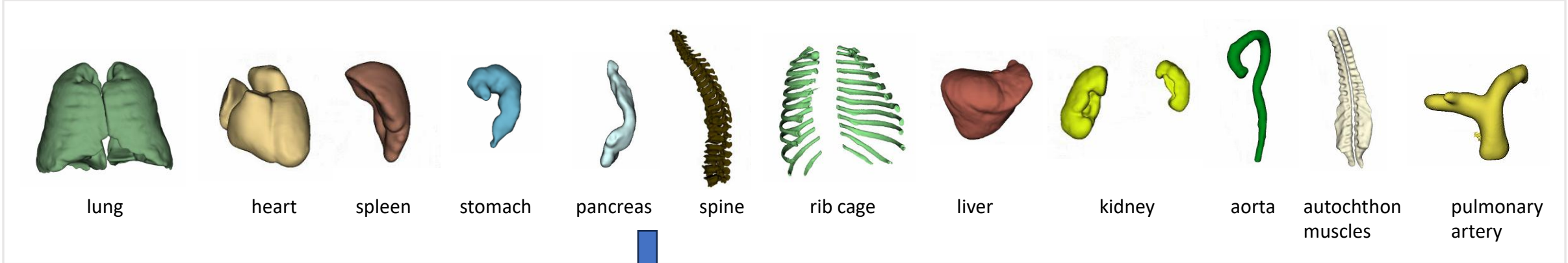
a set of whole-body (104) anatomies



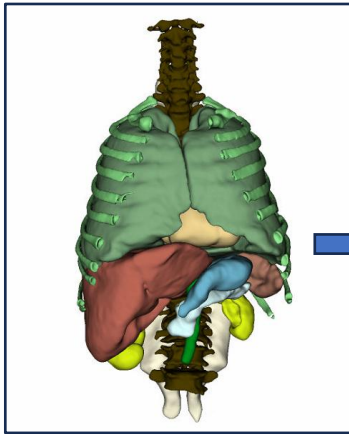
- 737 sets of whole-body anatomies (451 training, 286 evaluation)
- Each set contains 104 anatomies
- To create partial labels, remove some of the anatomies based on their volume ratio:
 - anatomies with a volume ration of **10%** and above are removed **(A)**
 - anatomies with a volume ration of **20%** and above are removed **(B)**
 - anatomies with a volume ration of **40%** and above are removed **(C)**

Single-class dataset: anatomies are not distinguished (different anatomies have the same label "1". The background is "0")

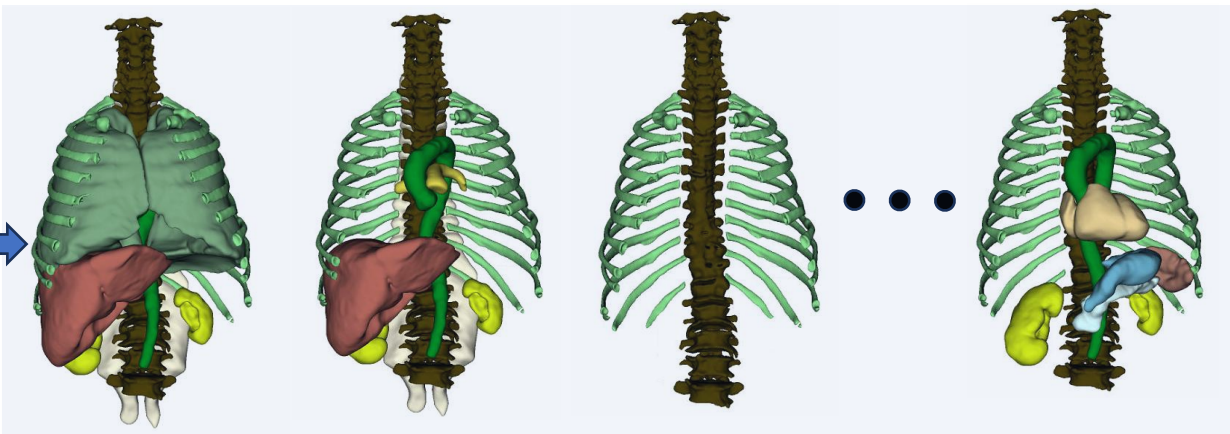
Dataset Creation: Multi-class Dataset



- 12 anatomies (lung, heart, spleen, etc) -> 12 classes
- 18 sets of 12-class anatomies
- create 10 partial labels from each set by randomly removing some of the labels: $18 \times 10 = 180$ training samples



target for reconstruction



10 partial labels (input)

Method: 3D Denoising Auto-encoder (DAE)

- Learning a **many-to-one** mapping

$$\mathcal{F} : \{x_n^m\}_{m=1}^M \rightarrow y_n, n = 1, 2, \dots, N$$

- Learning a **one-to-one (residual)** mapping

$$\mathcal{F}_{res} : \{x_n^m\}_{m=1}^M \rightarrow \{y_n - x_n^m\}_{m=1}^M, n = 1, 2, \dots, N$$

- Loss function: two variants of **Dice** loss

many-to-one mapping

$$\mathcal{L}_{\mathcal{F}} = \sum_{m=1}^M \sum_{n=1}^N \mathcal{L}_{dice}(y_n, \tilde{y}_n^m)$$

residual mapping

$$\mathcal{L}_{\mathcal{F}_{res}} = \sum_{m=1}^M \sum_{n=1}^N \mathcal{L}_{dice}(y_n, \tilde{x}_n^m + x_n^m)$$

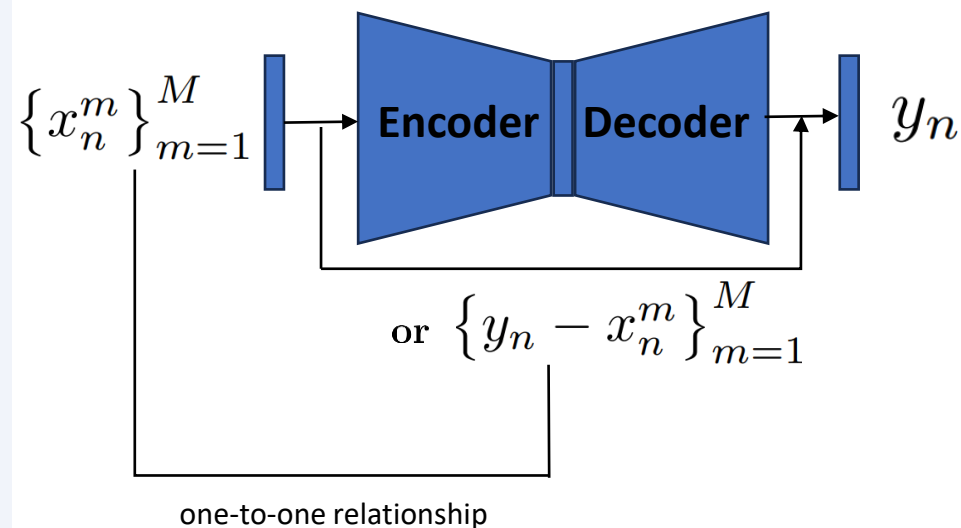
x_n^m the m th partial label from set n

y_n full label from set n

$\{y_n - x_n^m\}_{m=1}^M$ the missing labels of set n

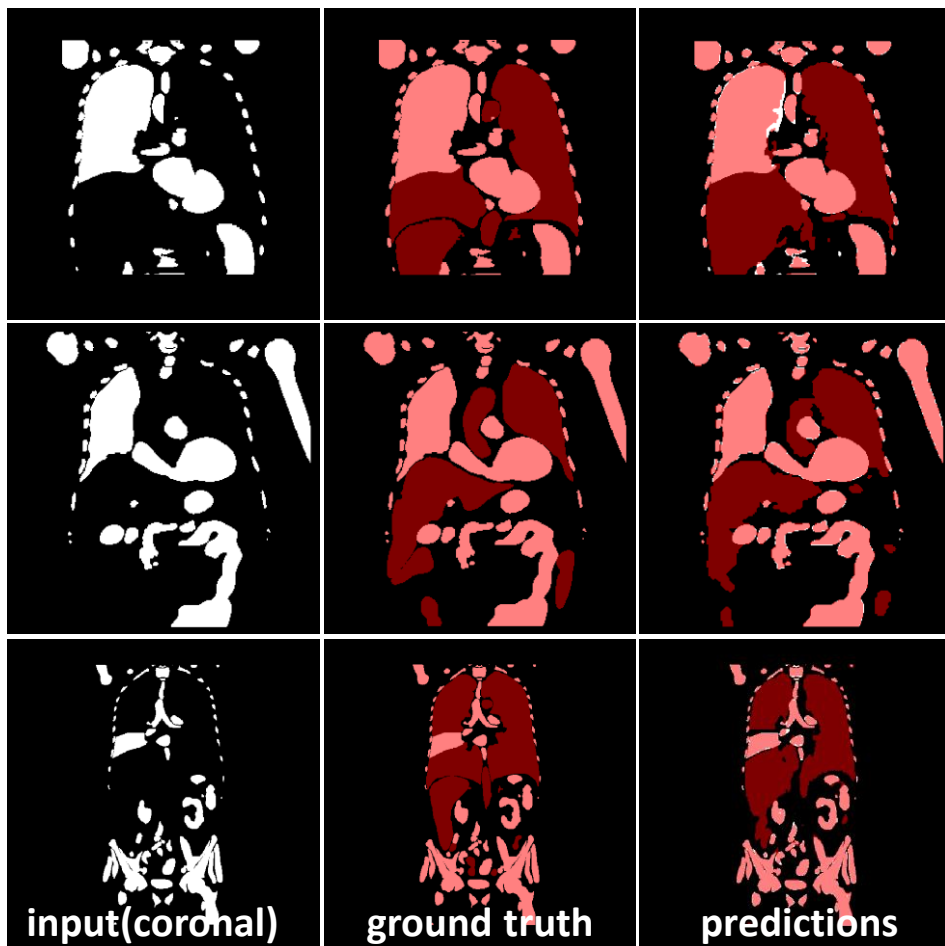
\mathcal{L}_{dice} Dice loss

- a one-to-one mapping is easier to learn than a many-to-one mapping
- DAE can detect what are missing in the input (which are random), and reconstruct them. DAE is expected to learn every possible combinations.
- increasing M (the number of partial labels) increases the DAE's ability to do so

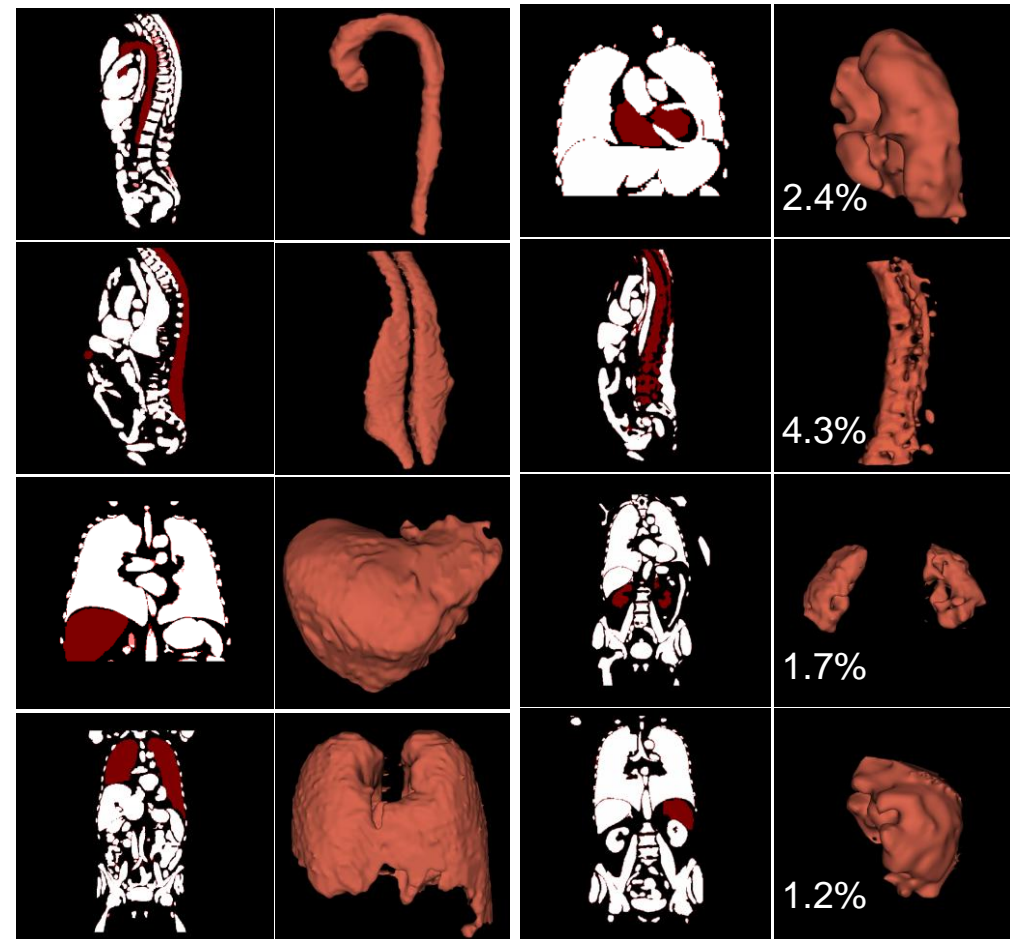


Results: Single-class Reconstruction (104 anatomies, 1 class)

multiple anatomies are missing

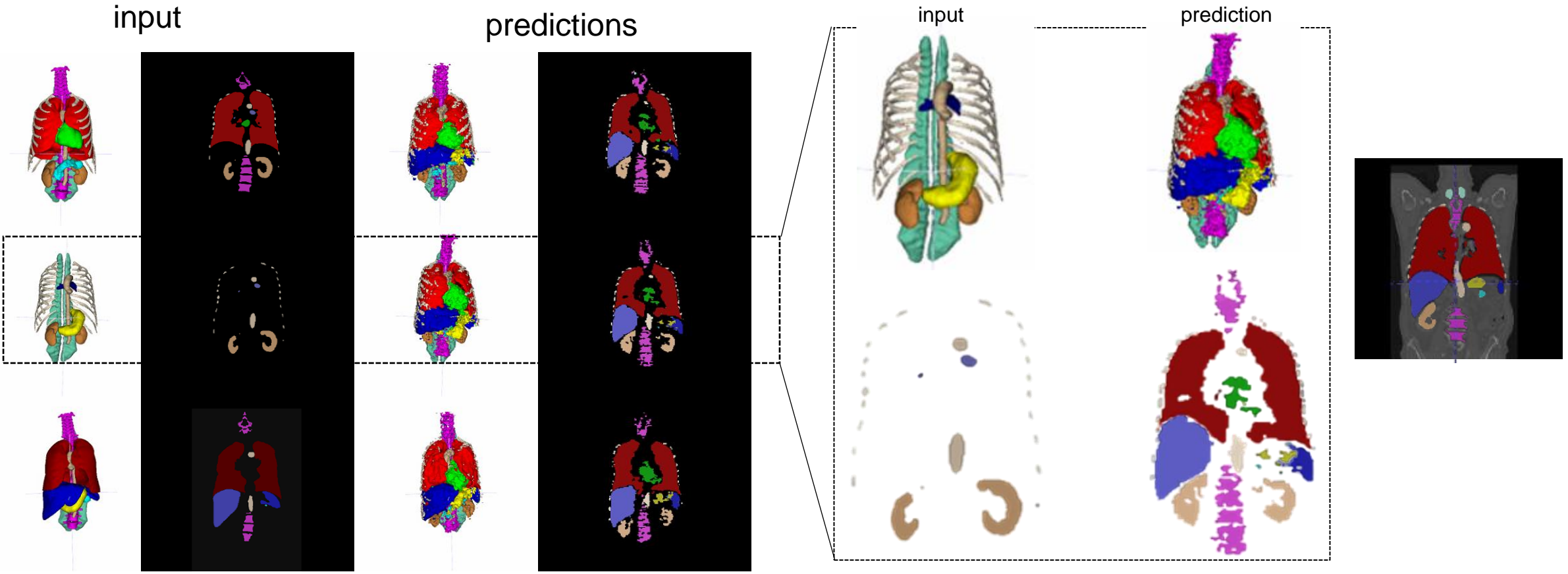


a single anatomy is missing



- on three test sets D_{test1} (10%), D_{test2} (20%), D_{test3} (40%), the DSC (standard deviation) are **0.865 (0.074)**, **0.904 (0.039)**, **0.931 (0.030)**
- better performance in reconstructing larger missing anatomies (D_{test3} 40%)

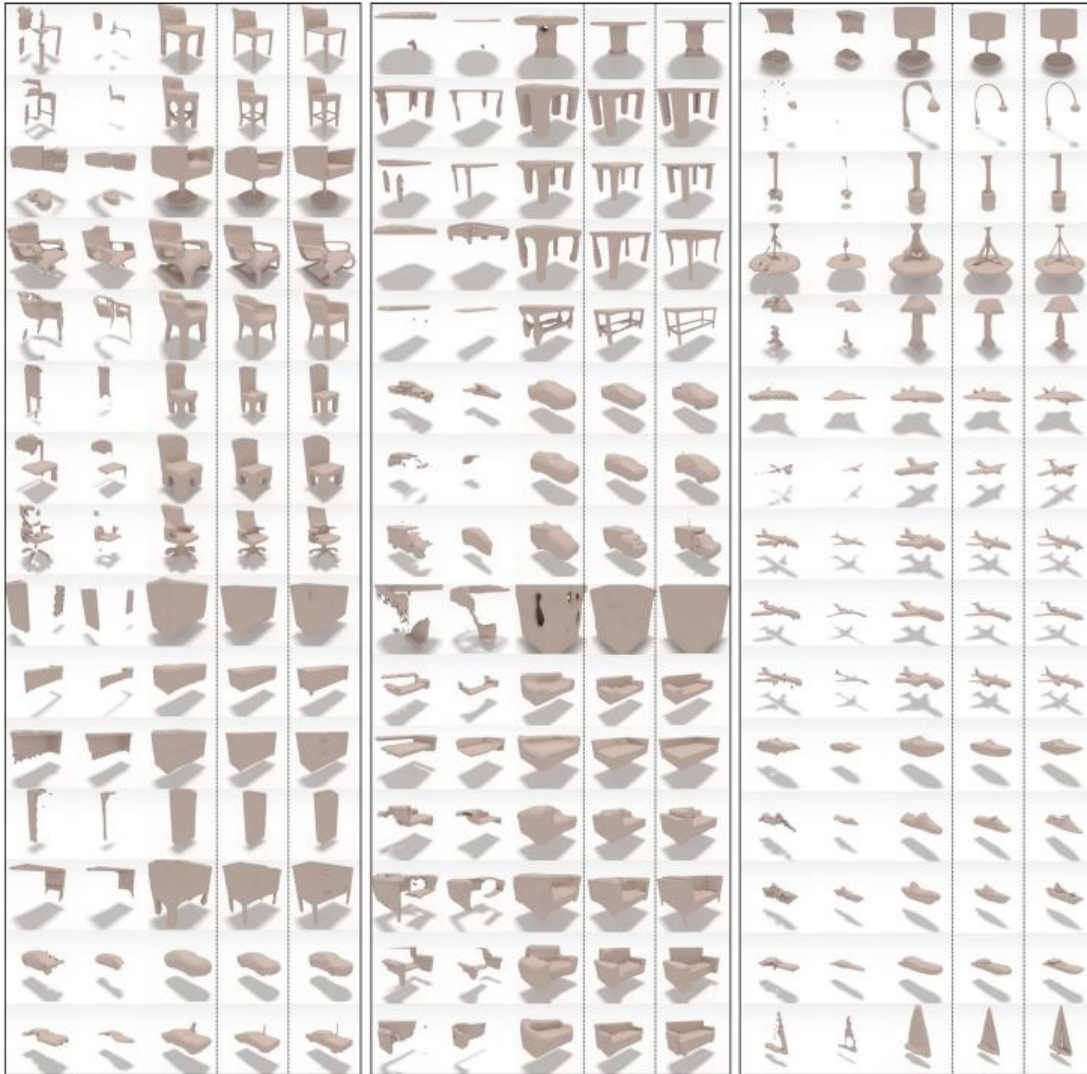
Results: Multi-class Reconstruction (12 anatomies, 12 classes)



- Generate whole-body pseudo labels for an unannotated dataset (to train a whole-body segmentation network)
- Annotate the rib cage (and a few anchoring organs), and generate pseudo labels for the remaining anatomies
- How to choose the proper anchors, so that the positions of the reconstructed anatomies match the corresponding CT scan the best?

MedShapeNet

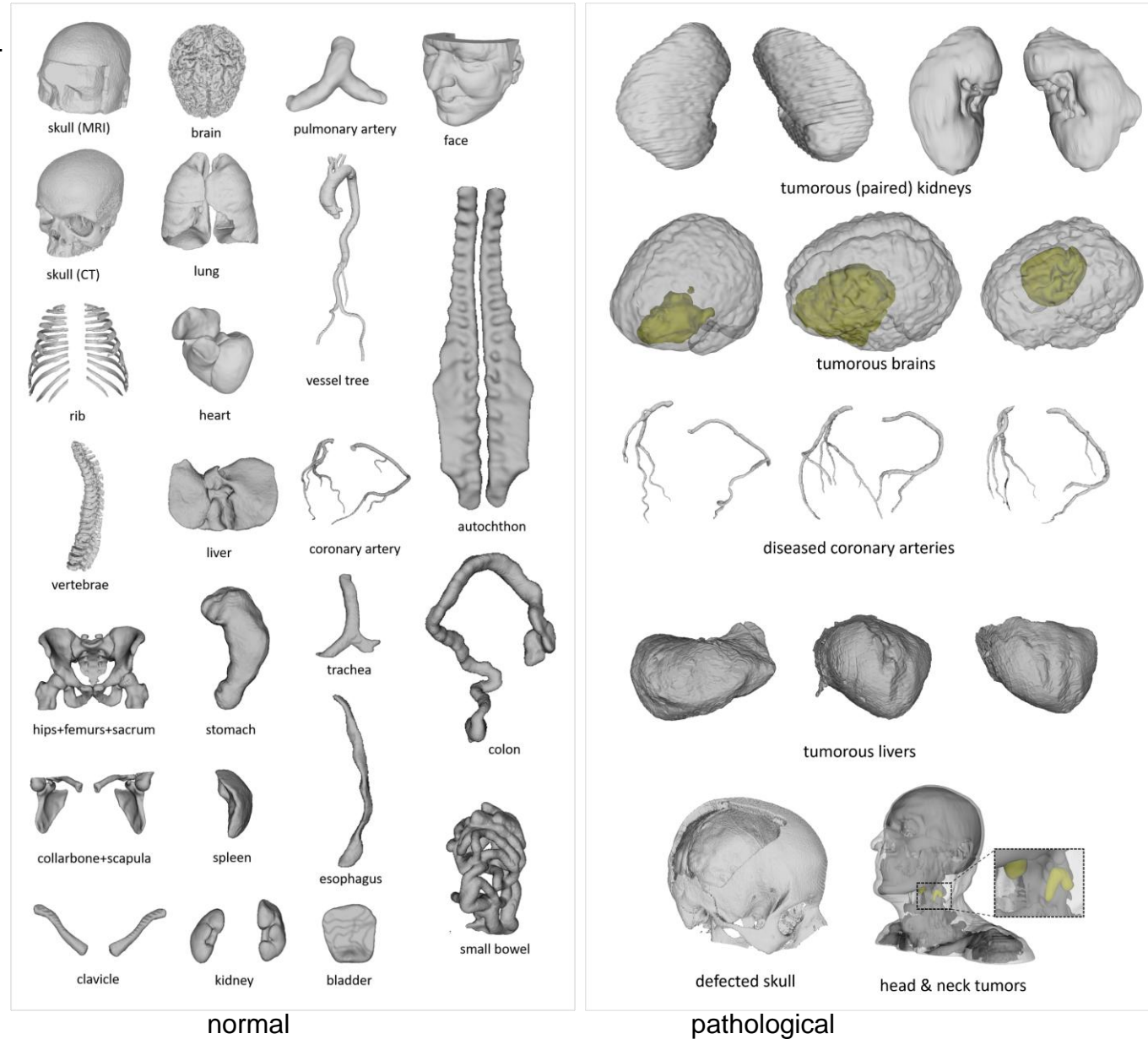
ShapeNet: 3D CAD models of real-world objects: chair, desk, car, airplane...



benchmark dataset: 3D shape completion, retrieval/classification, reconstruction...

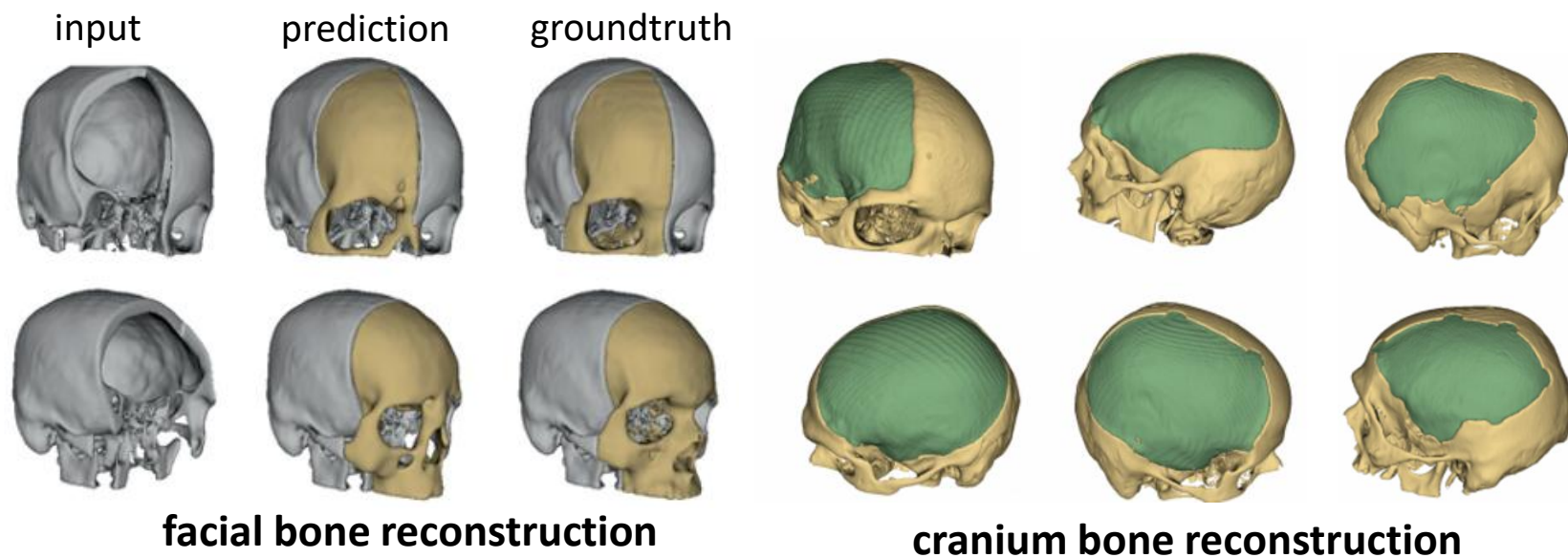
<https://shapenet.org/>

MedShapeNet: (1) 3D models of normal and pathological human anatomies extracted from the imaging data of real patients. (2) a medical version of **ShapeNet**.



<https://medshapenet.ikim.nrw/>

MedShapeNet: other shape reconstruction applications



benchmark datasets and codes:

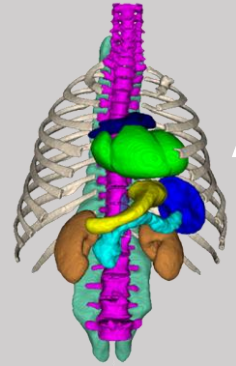
<https://github.com/Jianningli/medshapenet-feedback/>

Conclusion

- Derived a benchmark dataset from whole-body segmentations for anatomical shape reconstruction (a subset of MedShapeNet)
- Proposed and evaluated a simple shape completion framework to generate whole-body pseudo-labels from partial/sparse manual annotations
- Achieved reasonable quantitative and qualitative results

Future Work

- Include more (ideally whole-body) anatomies for multi-class anatomy completion
- Perform quantitative evaluation for each anatomy included
- Evaluate the multi-class completion framework in a whole-body segmentation task



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