SFU SIMON FRASER UNIVERSITY

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Medical Image Analysis Lab

ISBI 2025
2025 IEEE International Symposium on Biomedical Imaging
April 14-17, 2025 | Houston, TX, USA

Disentangled PET Lesion Segmentation

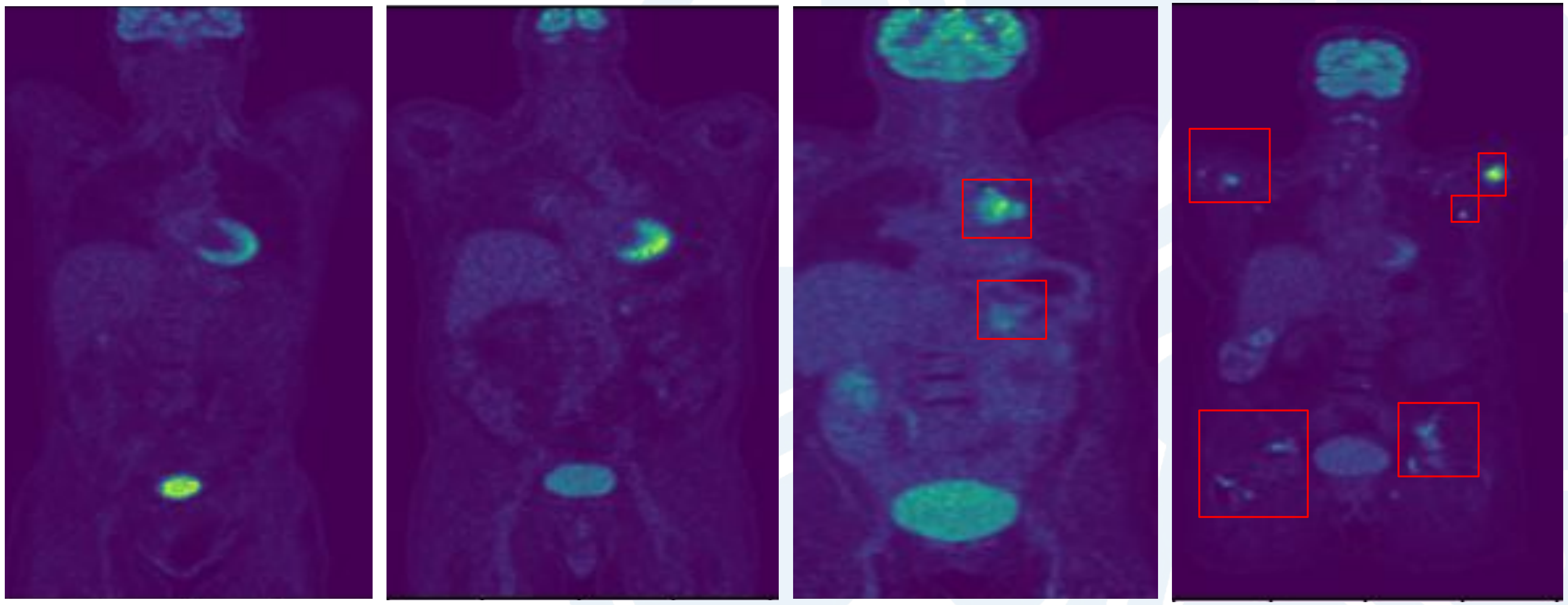
Tanya Gatsak, Kumar Abhishek, Hanene Ben Yedder, Saeid Asgari Taghanaki, Ghassan Hamarneh

Medical Image Analysis Lab, Simon Fraser University, Canada

Introduction

Positron emission tomography (PET) is an invaluable tool in medicine.

- Used in oncology for cancer staging, diagnosis, and monitoring.



Clinicians analyse PET to identify healthy vs abnormal uptake patterns.

Manual annotation of disease is laborious and can suffer from inter- and intraobserver variability necessitating automated methods.

Introduction

Automatic lesion segmentation methods aim to learn disease features.

Disentanglement of images is proving beneficial in many settings.

- Separate underlying sources of variation into semantic latent vectors.
- Better understand the structure of data, enhance model interpretability.

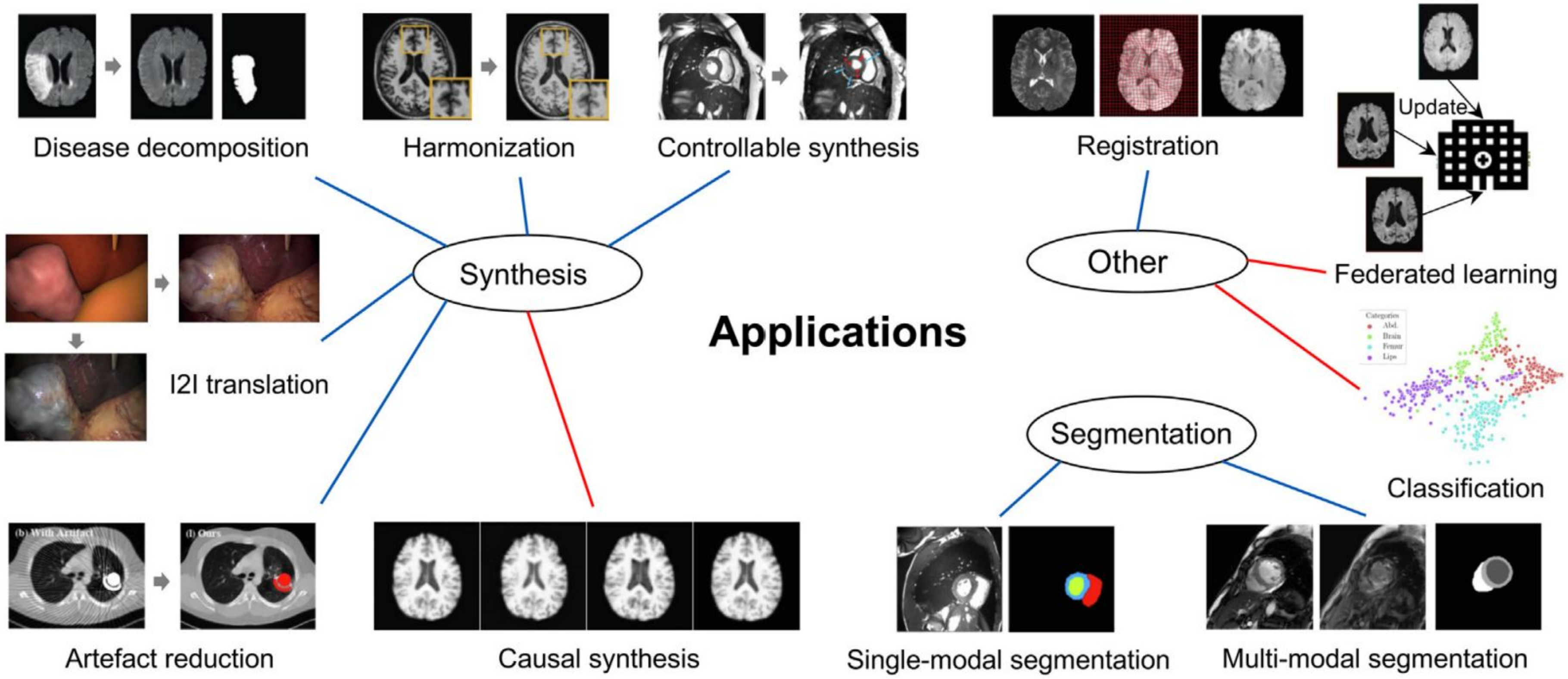
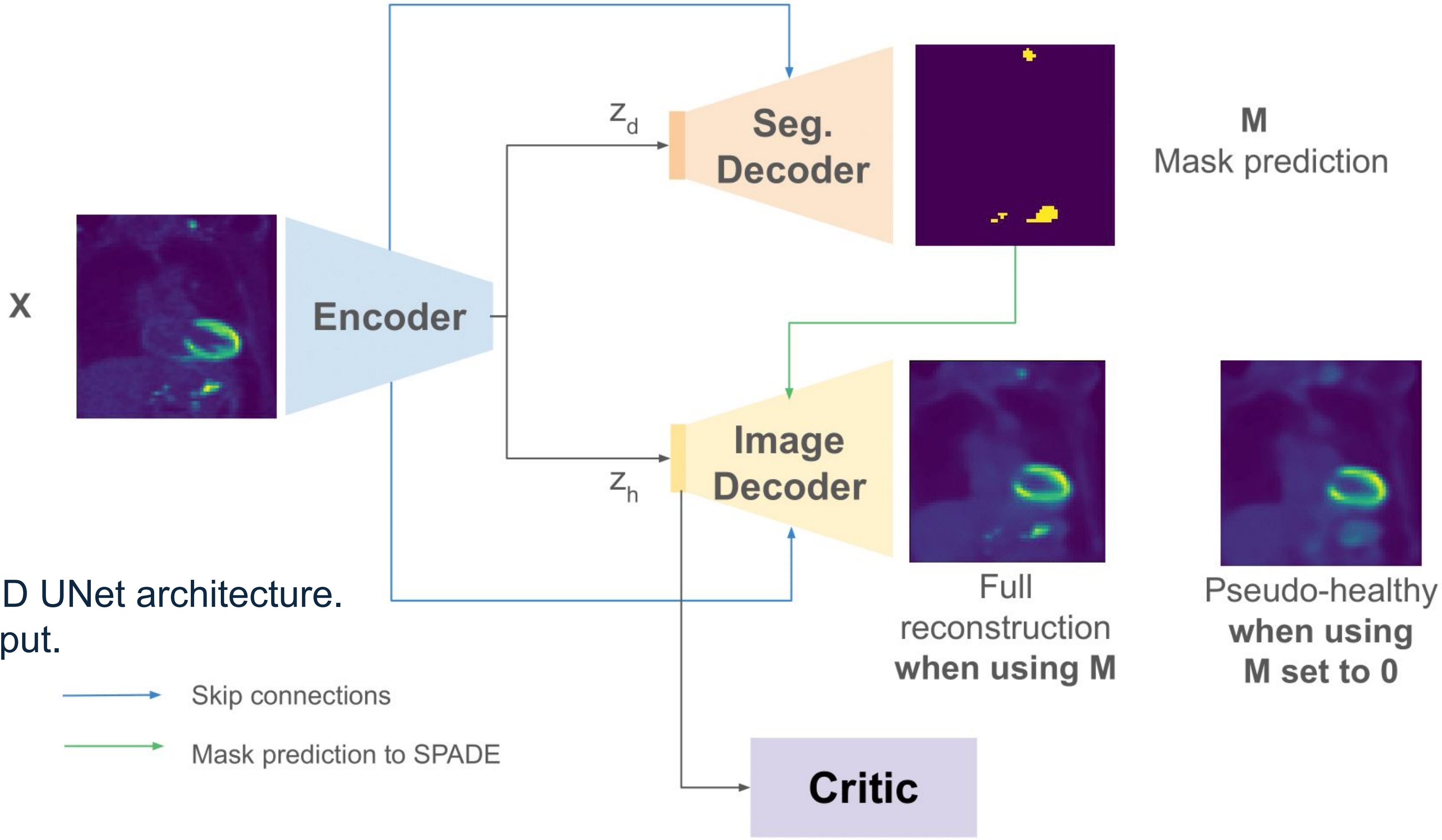


Image courtesy[1]

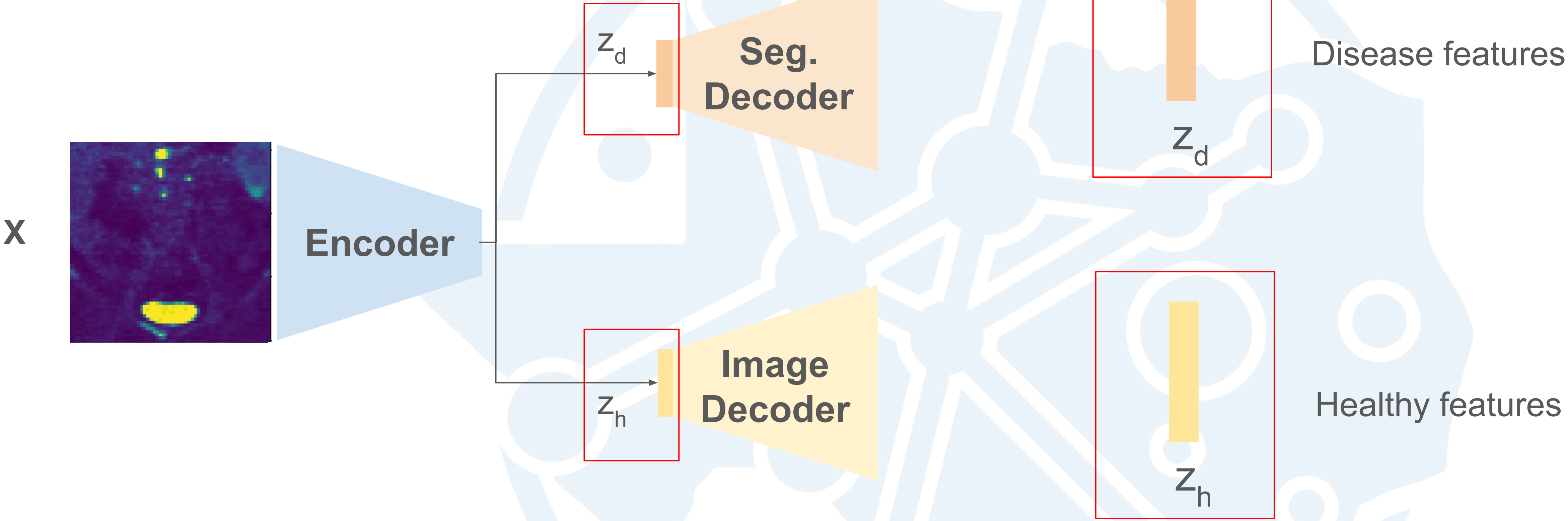
PET-Disentangler

PET lesion segmentation leveraging a 3D disentanglement framework to disentangle healthy and disease features.



- Modified 3D UNet architecture.
- 3D PET input.

Method overview: PET-Disentangler



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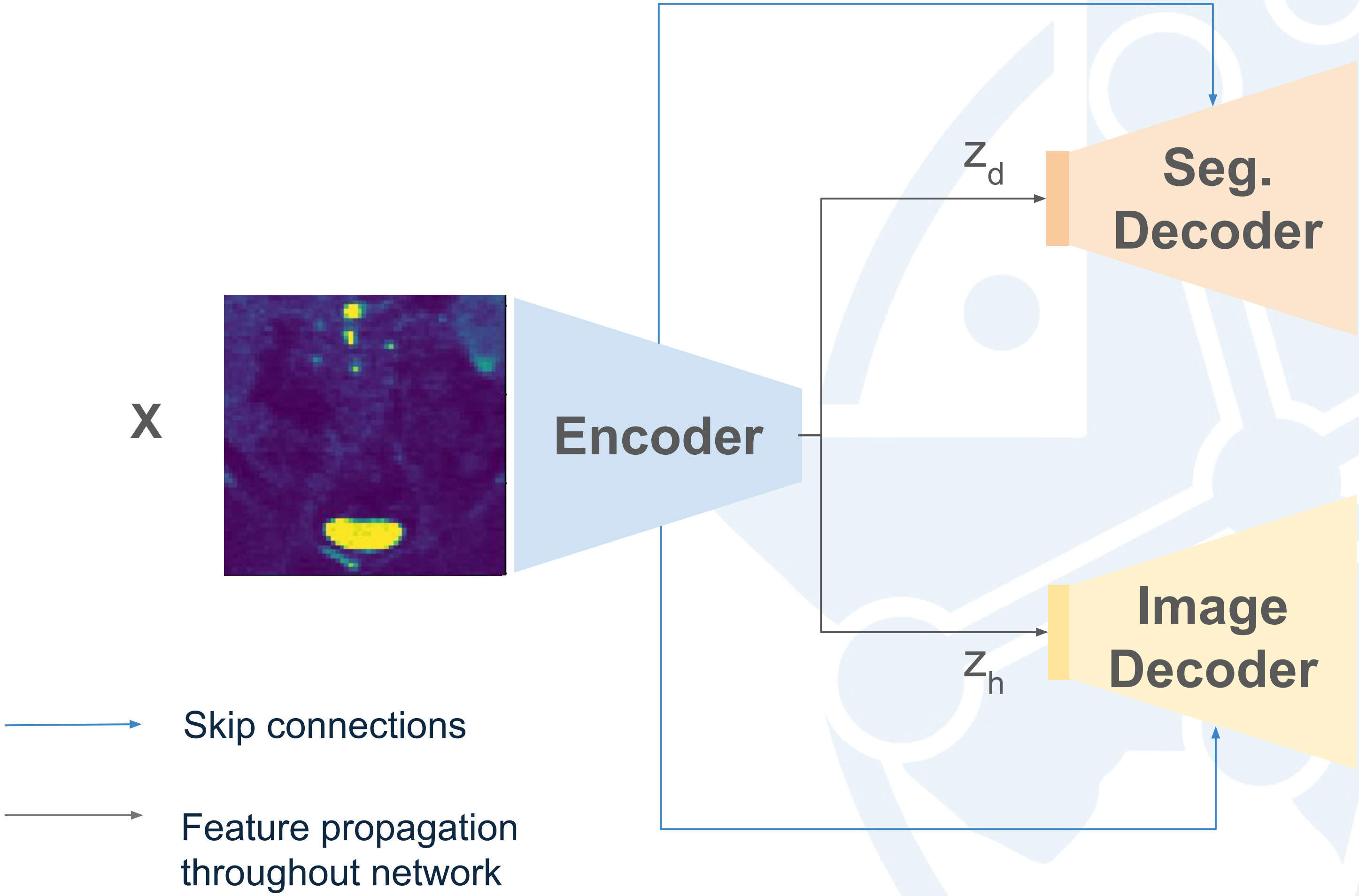
Method overview: PET-Disentangler



X

Encoder

z_d

Seg. Decoder

z_h

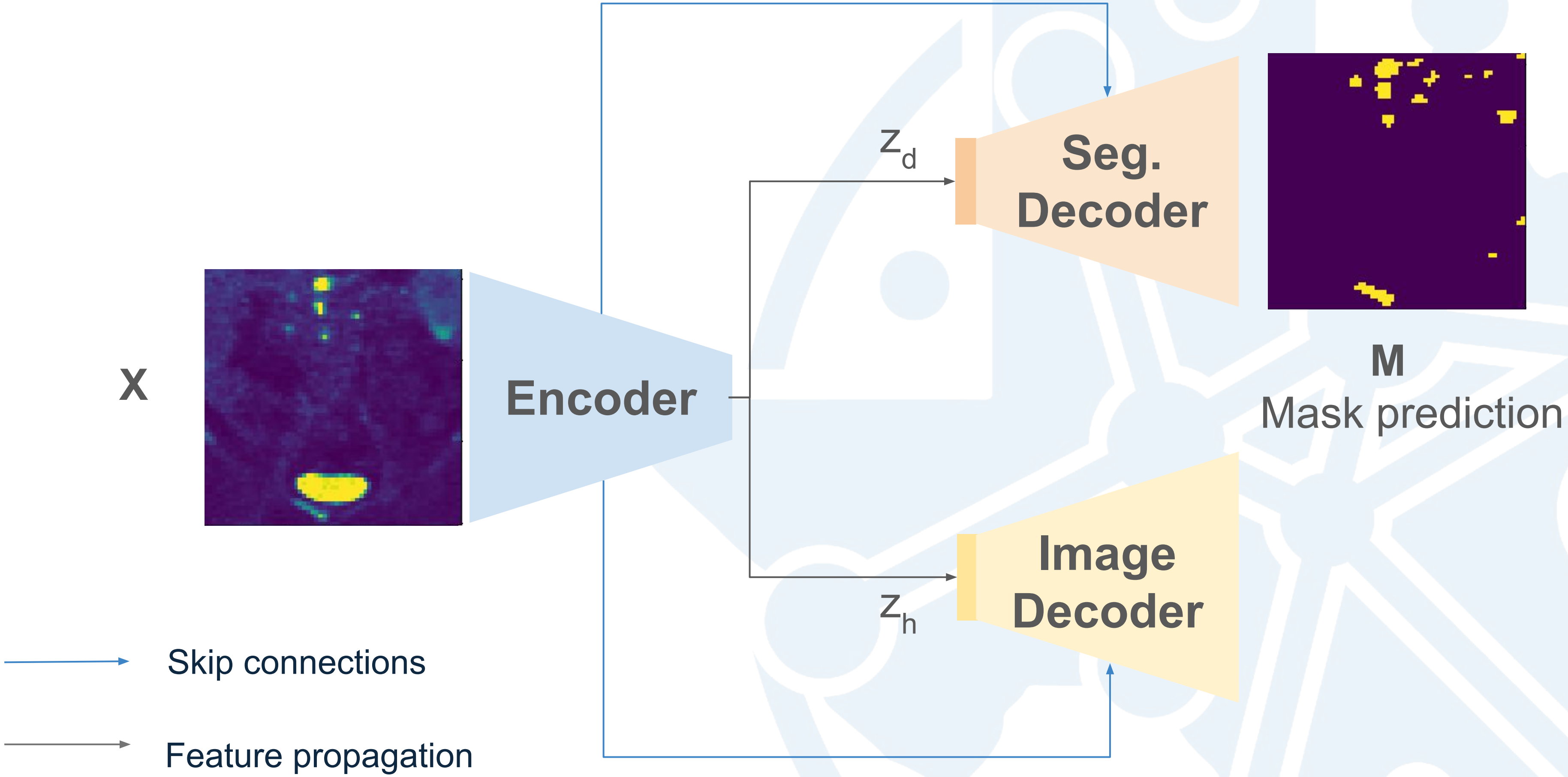
Image Decoder

Skip connections

Feature propagation throughout network

- Modified 3D UNet architecture.
- 3D PET input.

Method overview: PET-Disentangler

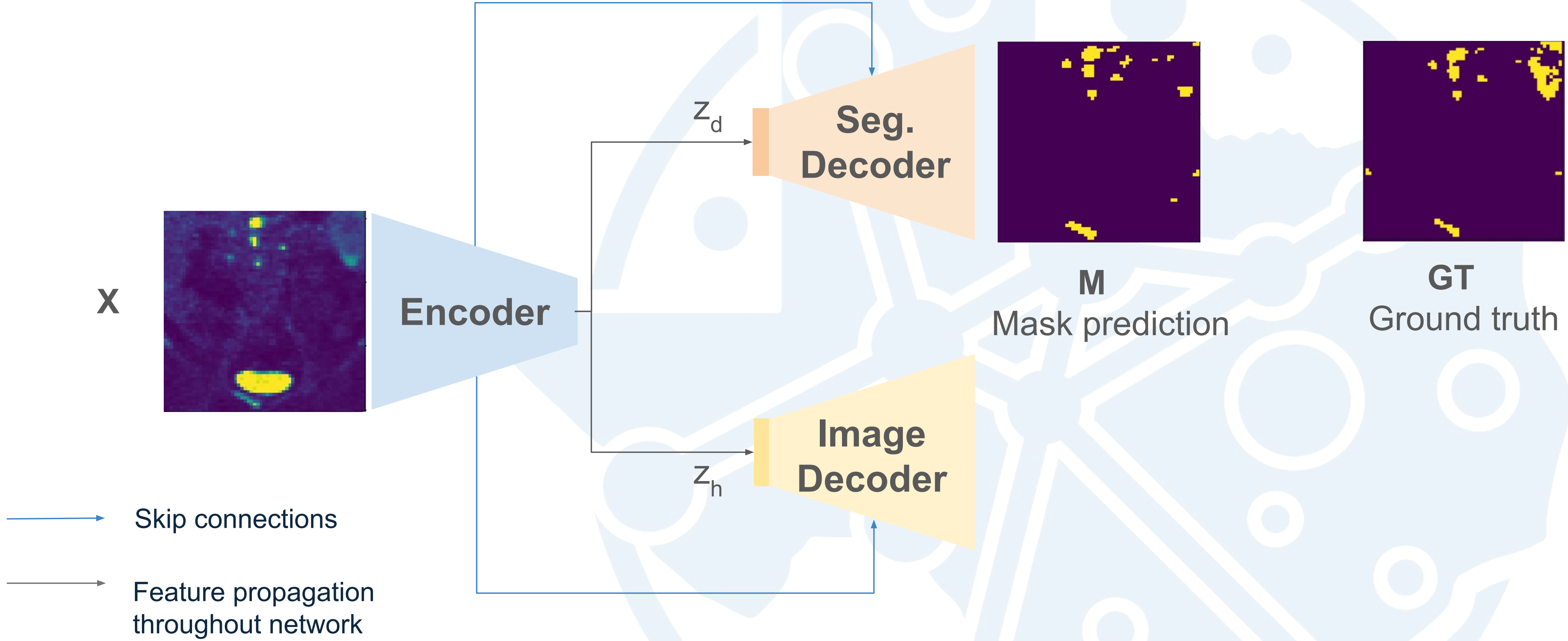


Skip connections

Feature propagation throughout network

- Modified 3D UNet architecture.
- 3D PET input.

Method overview: PET-Disentangler


X

Encoder

z_d

Seg. Decoder

z_h

Image Decoder

M
Mask prediction

GT
Ground truth

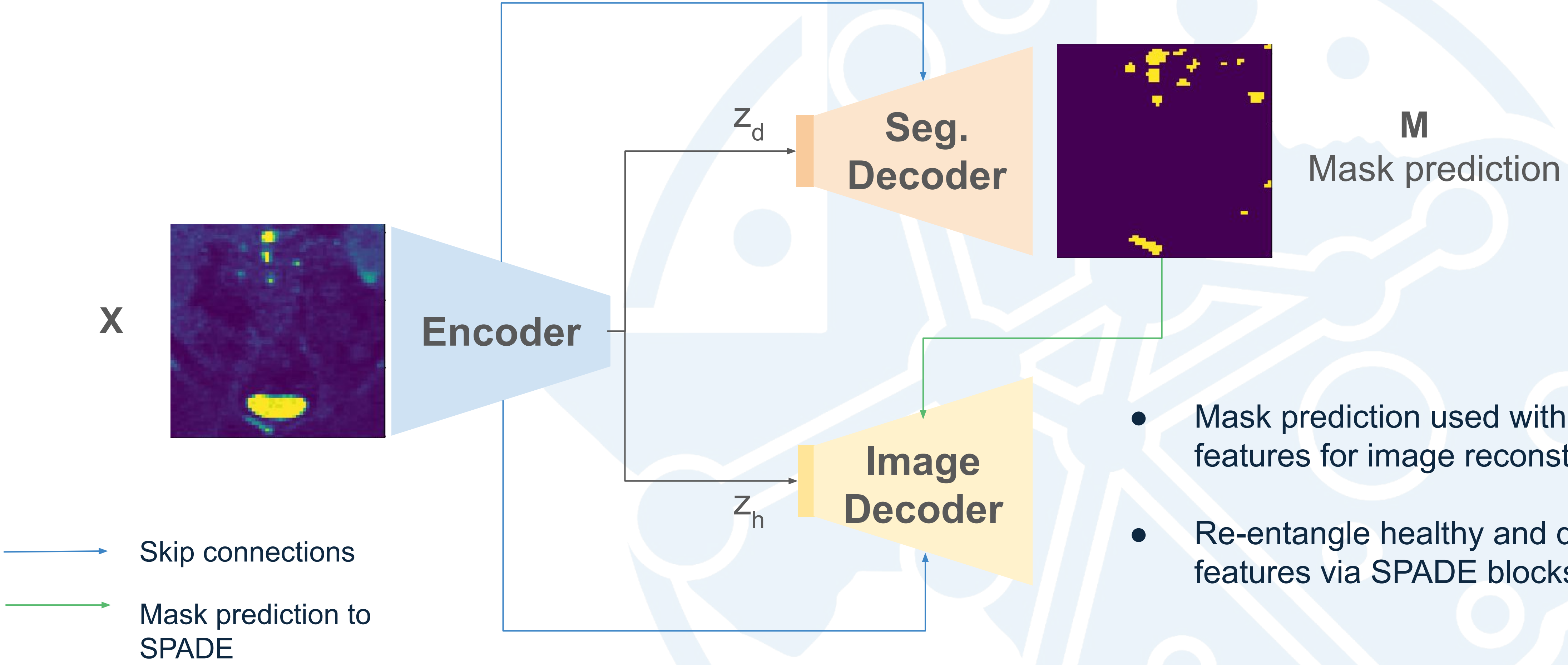
Skip connections

Feature propagation throughout network

$$L_{seg} = L_{ComboLoss}(M, M_{GT}) = L_{Dice} + L_{CE}$$

- Modified 3D UNet architecture.
- 3D PET input.

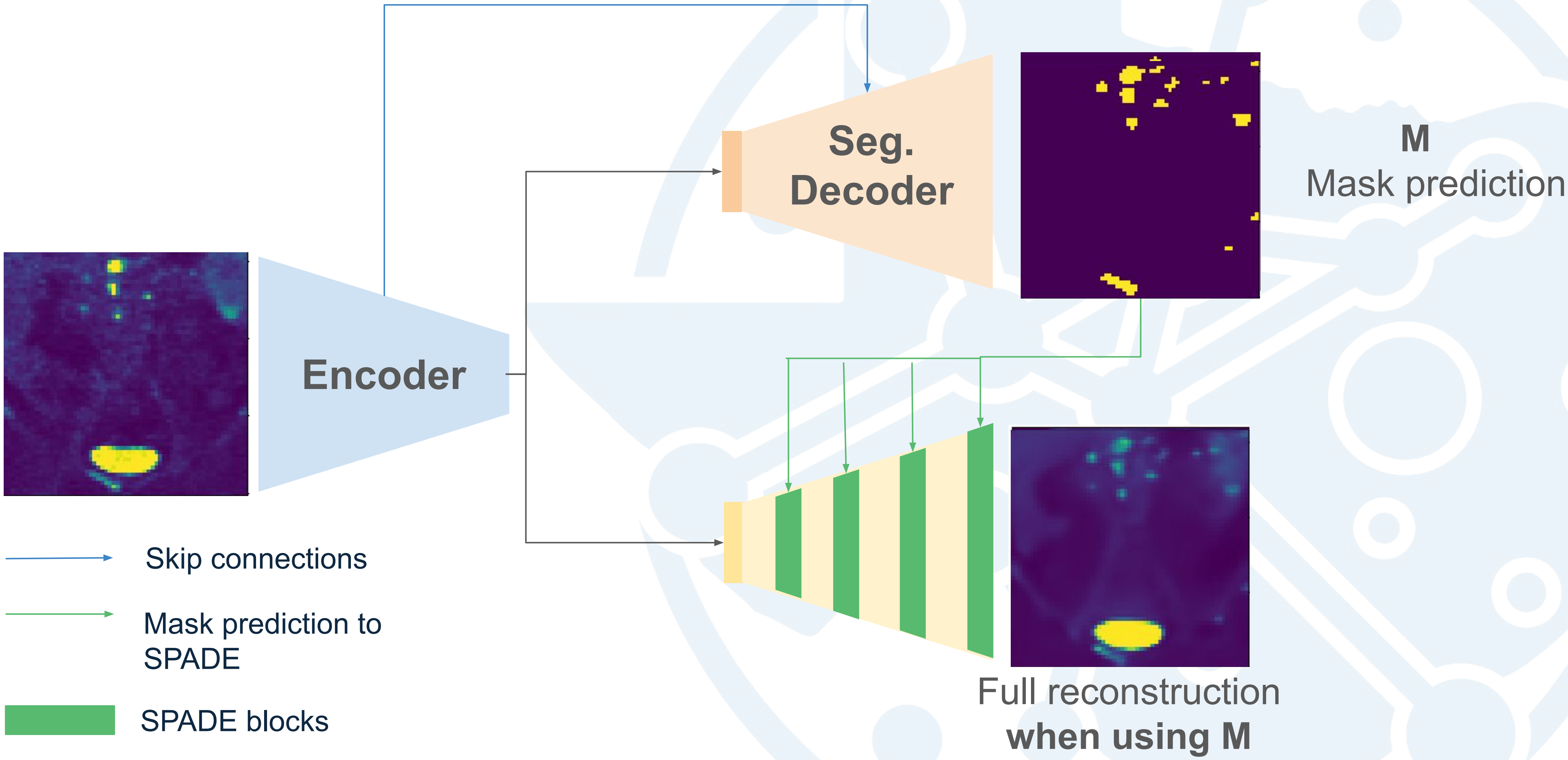
Method overview: PET-Disentangler



- Mask prediction used with healthy features for image reconstruction.
- Re-entangle healthy and disease features via SPADE blocks.

- Modified 3D UNet architecture.
- 3D PET input.

Image decoder and reconstruction



Seg. Decoder

M

Mask prediction

Encoder

Full reconstruction

when using M

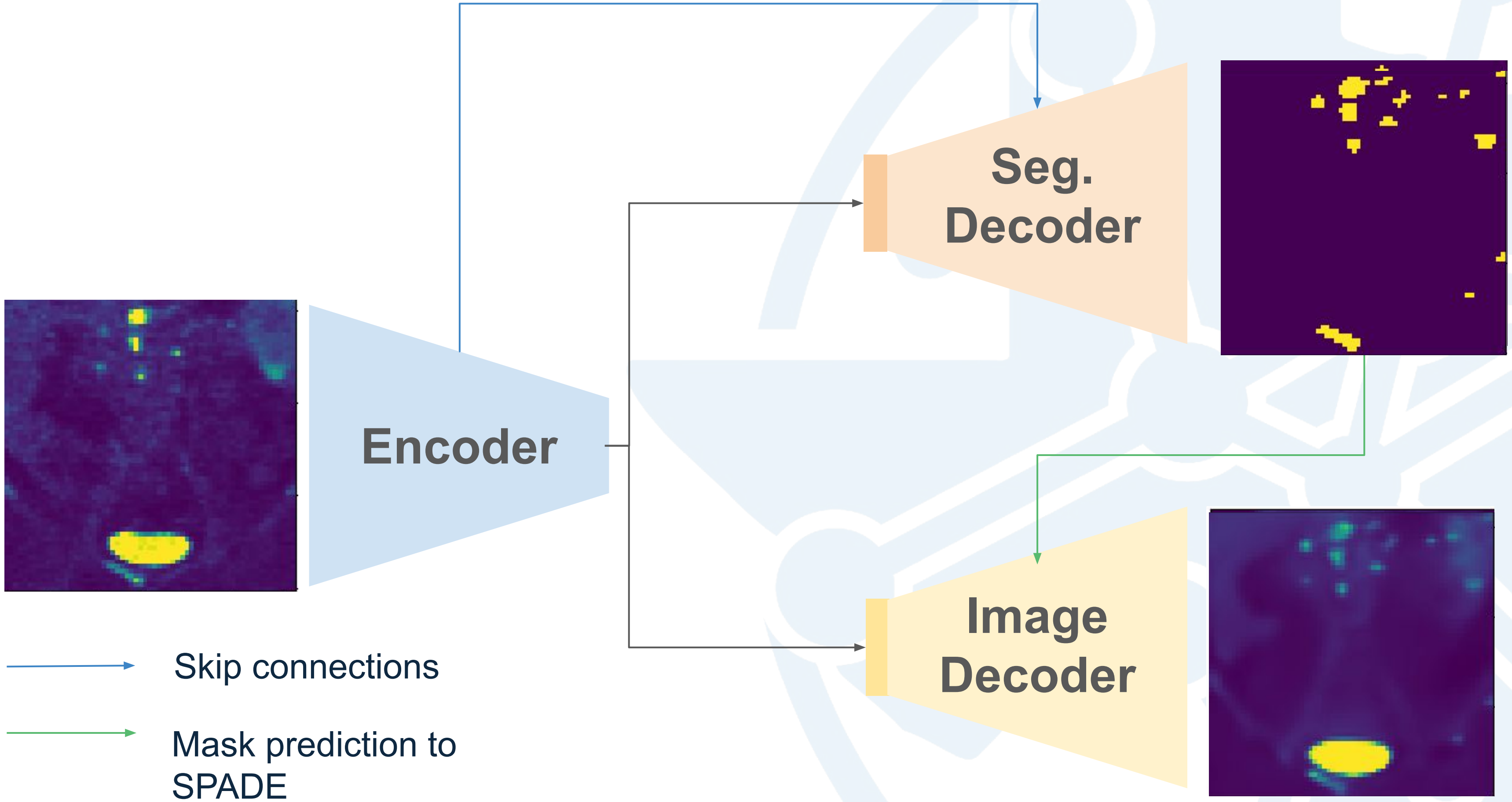
→ Skip connections

→ Mask prediction to SPADE

🟩 SPADE blocks

Downsample masks to each resolution within image decoder.

Image decoder and reconstruction



Encoder

Seg. Decoder

M
Mask prediction

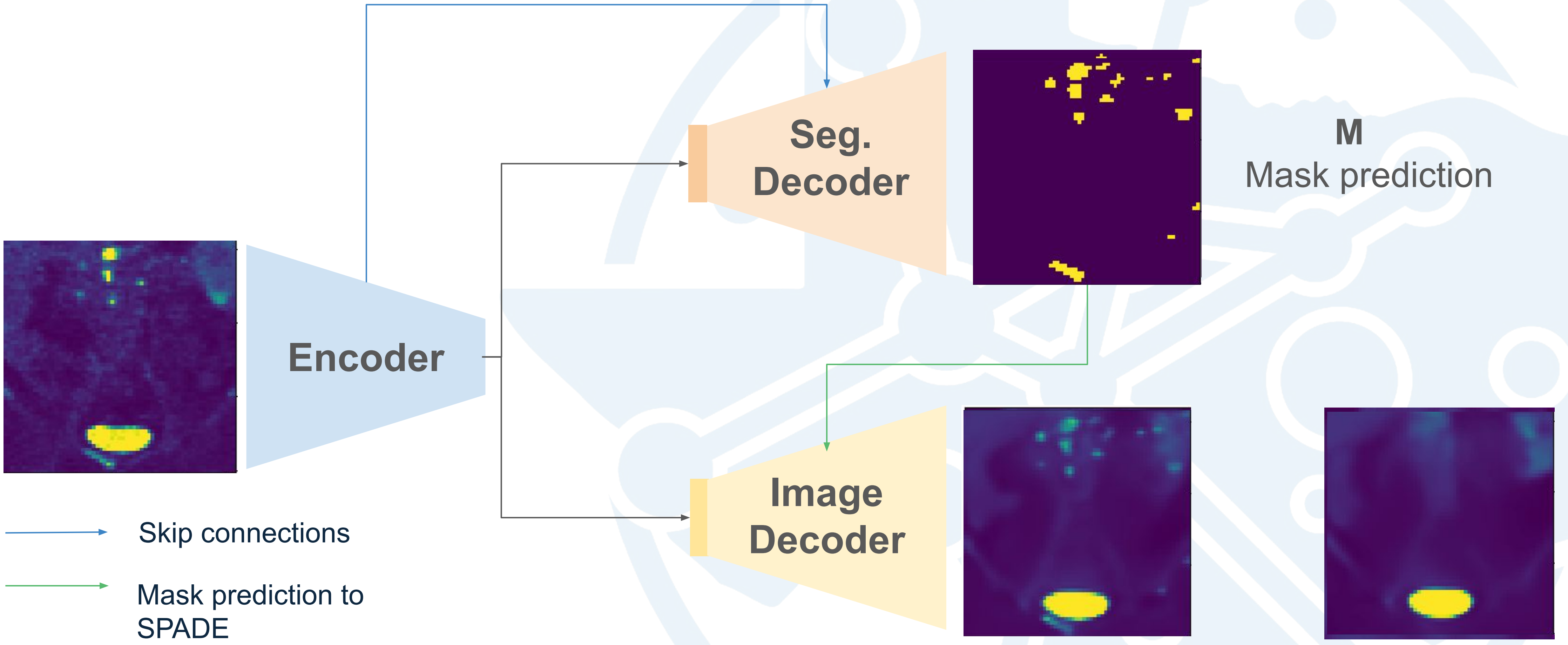
Image Decoder

Full reconstruction
when using M

Skip connections

Mask prediction to SPADE

Image decoder and reconstruction



Encoder

Seg. Decoder

Image Decoder

M
Mask prediction

Skip connections

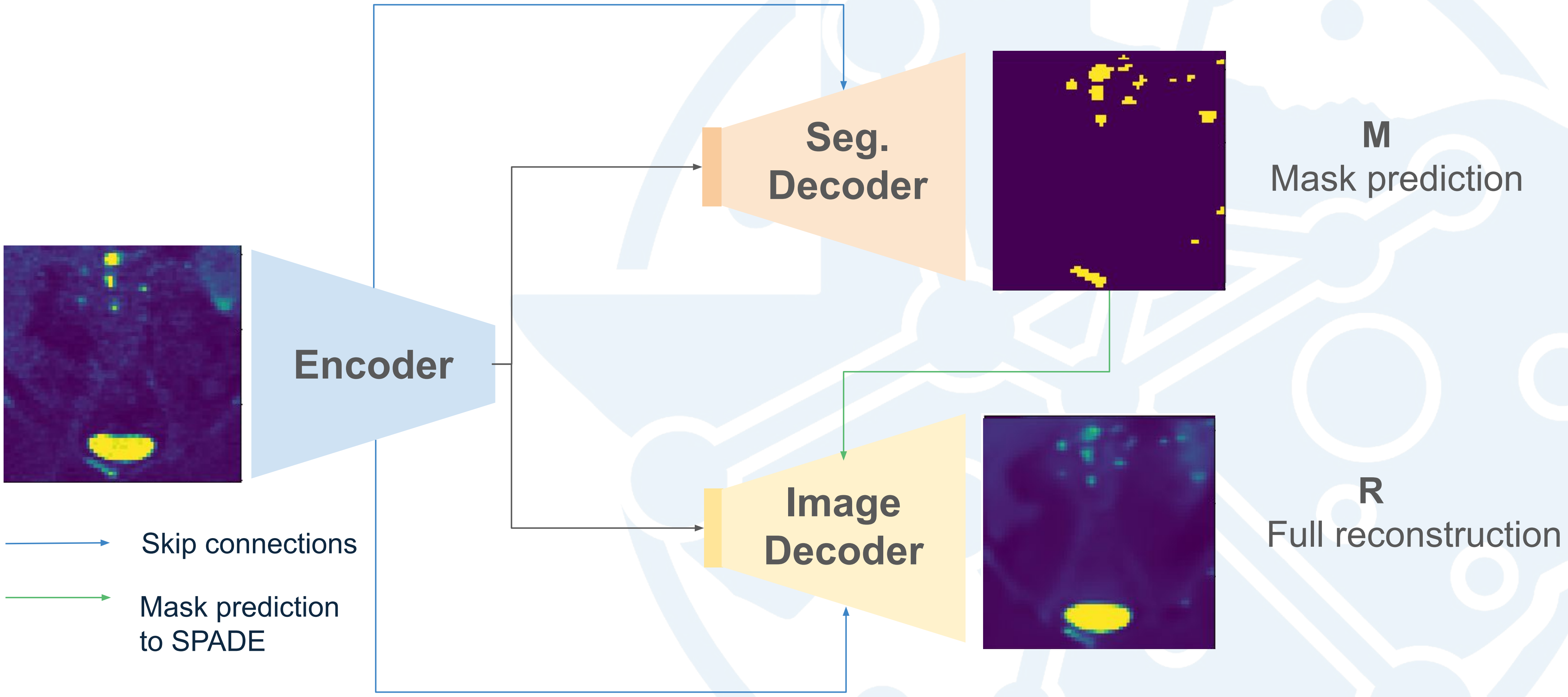
Mask prediction to SPADE

Full reconstruction **when using M**

Pseudo-healthy **when using M set to 0**

Note: **Full reconstruction** and **Pseudo-healthy** should look the same when X is **healthy**

Image decoder and reconstruction



Encoder

Seg. Decoder

M
Mask prediction

Image Decoder

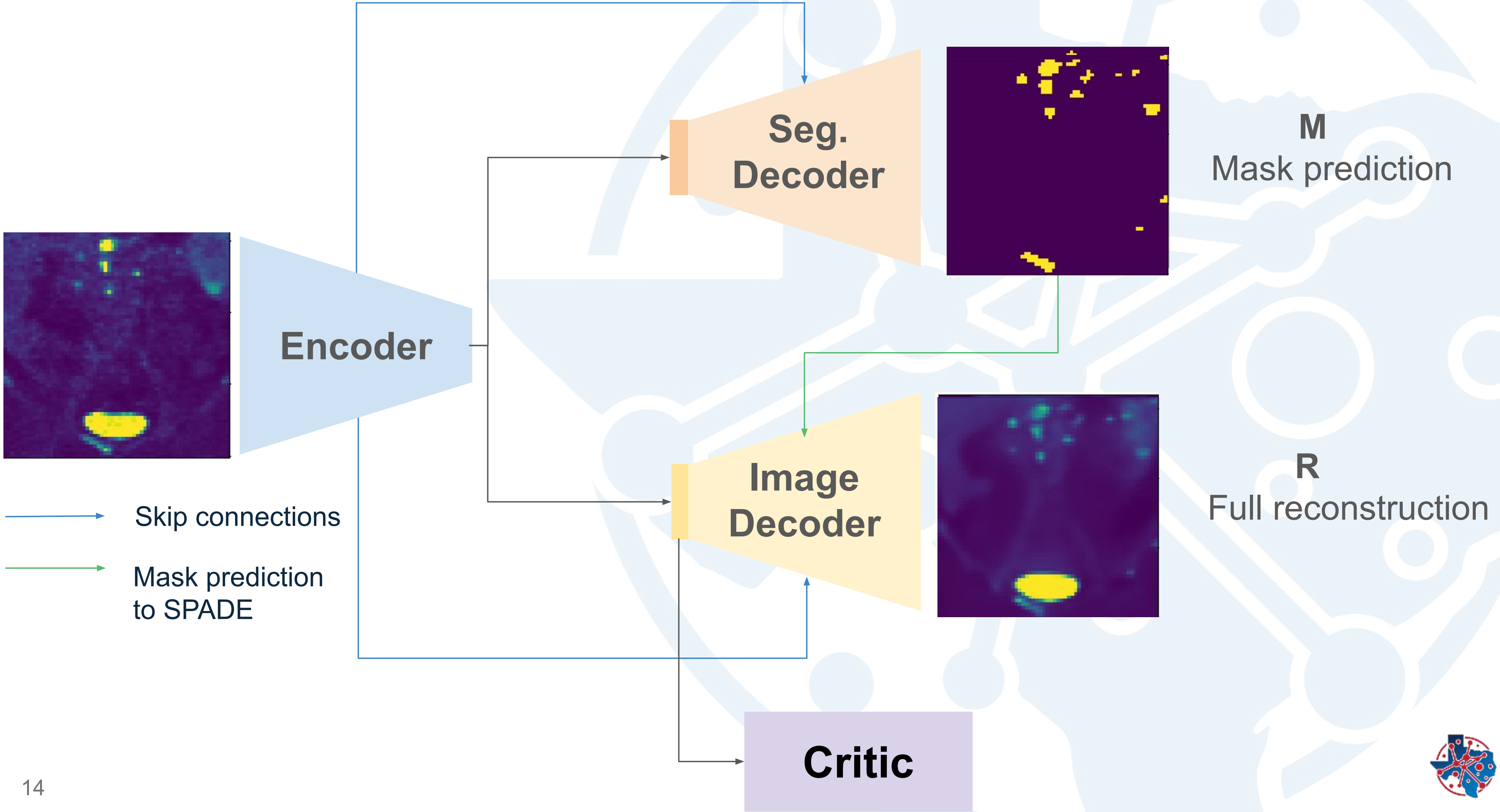
R
Full reconstruction

Skip connections

Mask prediction
to SPADE

$$L_{recon} = ||X - R||_1 + ||X - R||_2$$

Critic network for healthy distribution matching



Encoder

Seg. Decoder

M
Mask prediction

Image Decoder

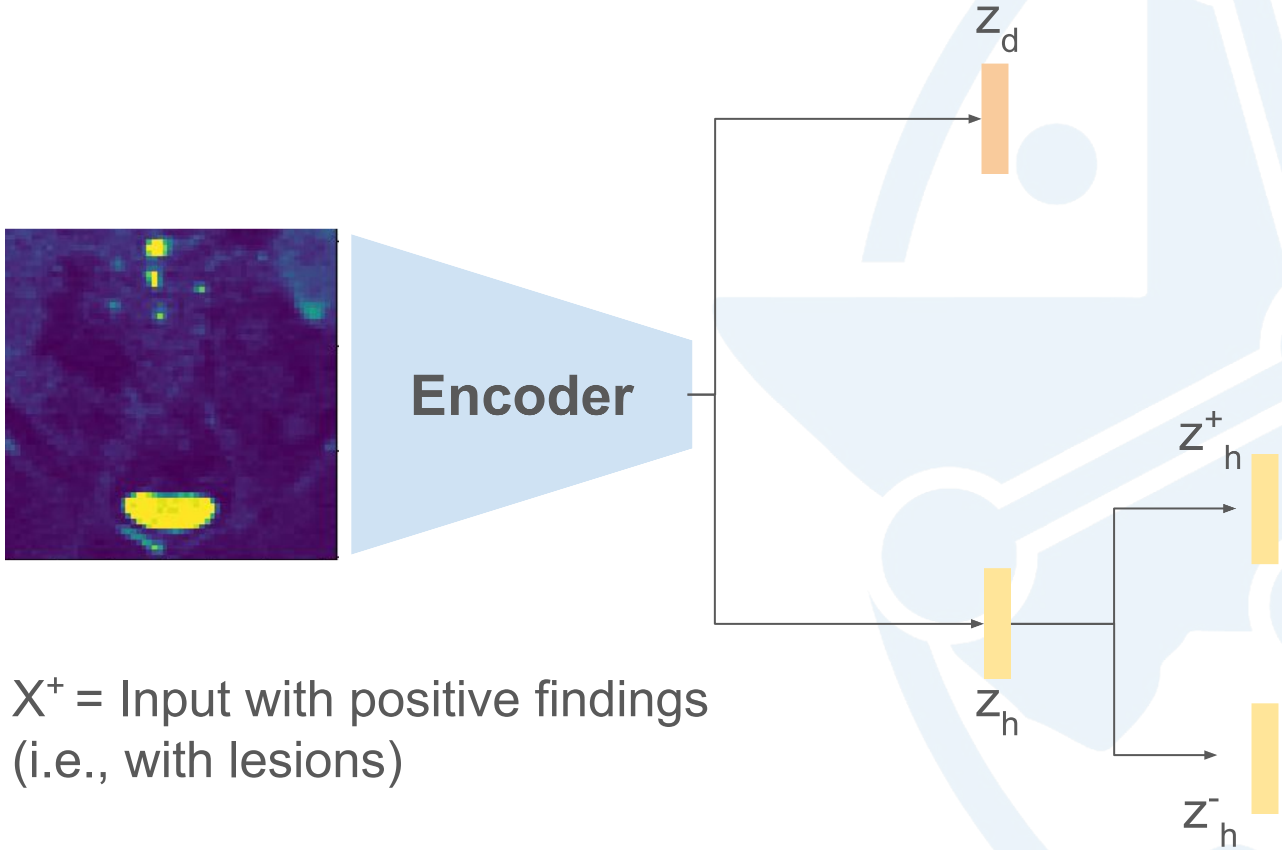
R
Full reconstruction

Critic

Skip connections

Mask prediction to SPADE

Critic network for healthy distribution matching



X^+ = Input with positive findings (i.e., with lesions)

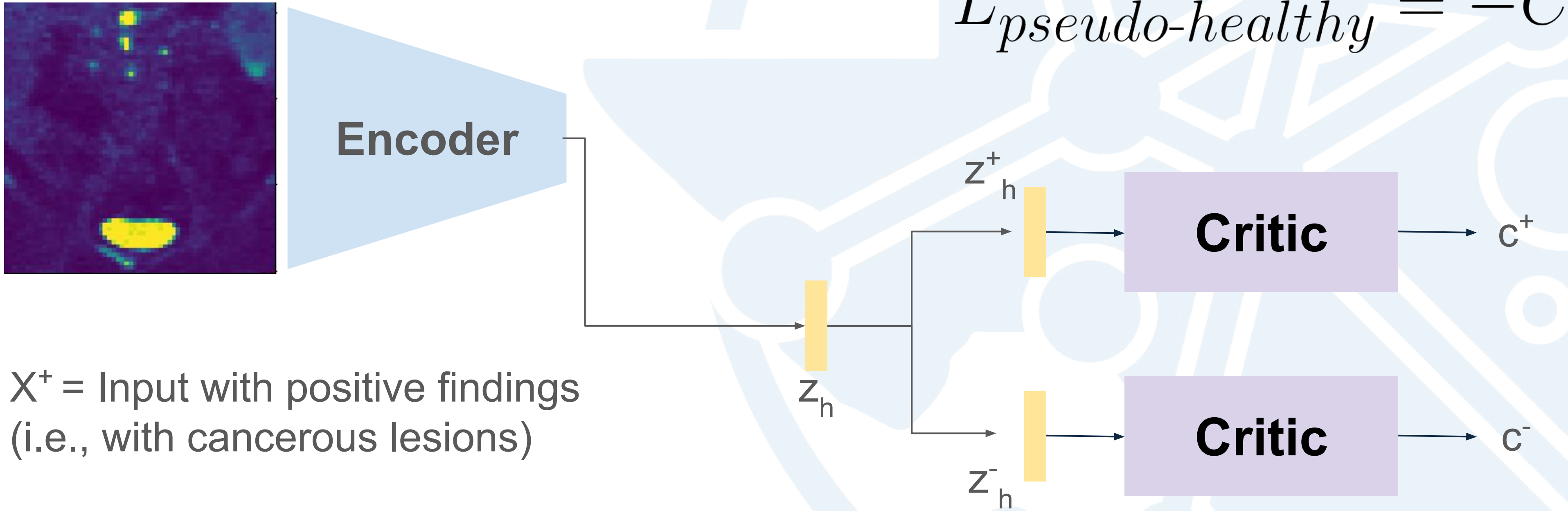
X^- = Input with negative findings (i.e., without lesions)

Critic network for healthy distribution matching

$$L_{critic} = \left(-\left(C(z_h^-) - C(z_h^+)\right) + \lambda_{GP}\left(||\nabla_{z_m} C(z_m)||_2 - 1\right)^2\right) \cdot w_c$$

$$z_m = \alpha z_h^- + (1 - \alpha) z_h^+$$

$$L_{pseudo\text{-}healthy} = -C(z_h^+)$$


Encoder

z_h

z^+_h

z^-_h

Critic

Critic

c^+

c^-

X^+ = Input with positive findings (i.e., with cancerous lesions)

X^- = Input with negative findings (i.e., without cancerous lesions)

Overall objective function

The critic is optimized separately from the rest of the network components.

The critic loss is used to optimize the critic.

The overall objective function to optimize the encoder, segmentation decoder, and image decoder is:

$$L_{overall} = w_s L_{seg} + w_r L_{recon} + w_{ph} L_{pseudo\text{-}healthy}$$

Experiments

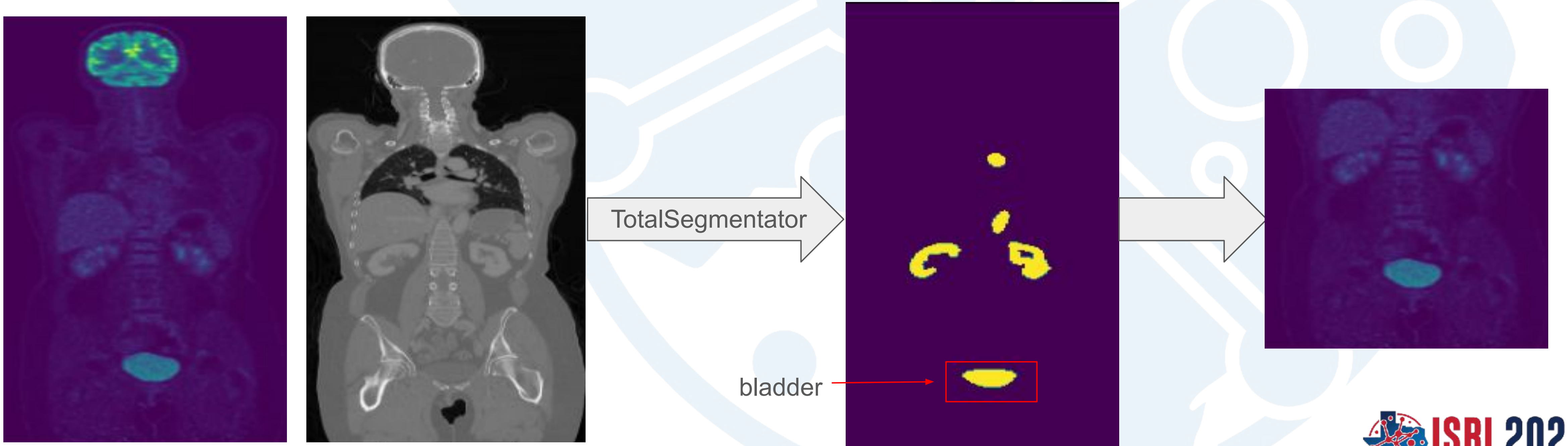
	Objective	Segmentation	Reconstruction	Disentanglement
SegOnly	Learn disease features	✓	✗	✗
SegRecon	Learn disease and image features	✓	✓	✗
SegReconHealthy	Learn disease and healthy features	✓	Healthy examples	✗
PET-Disentangler	Learn disease and healthy features	✓	✓	✓

Experiments

TCIA Wholebody FDG-PET/CT dataset[2]

- 513 scans without lesions, 501 scans with lesions.

Leverage TotalSegmentator[3] to obtain aligned subvolumes for the dataset centered around bladder.



PET

Corresponding CT

Results

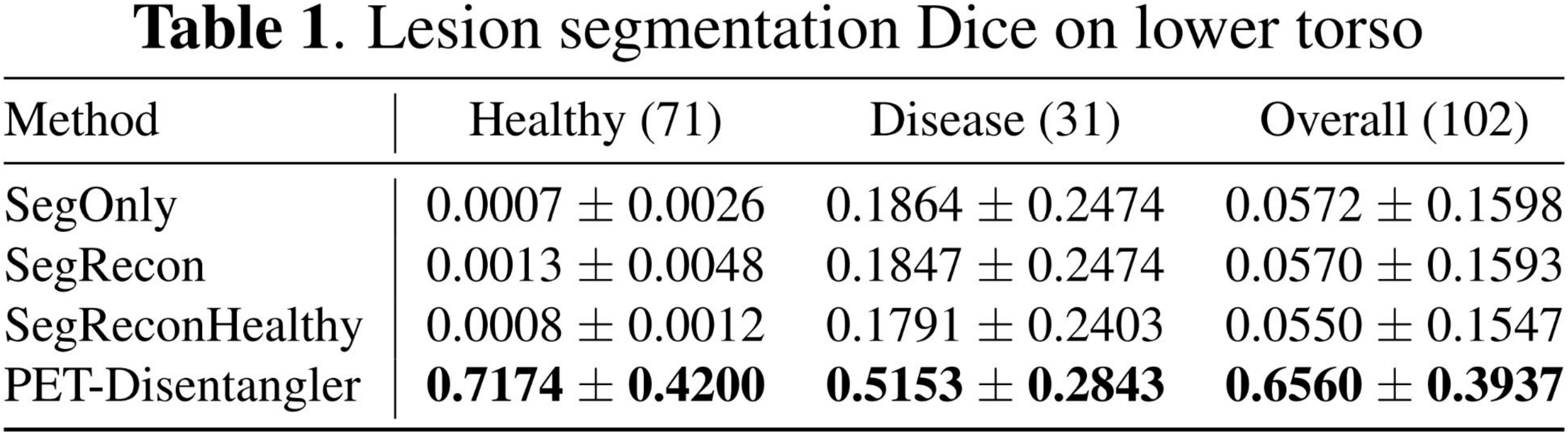
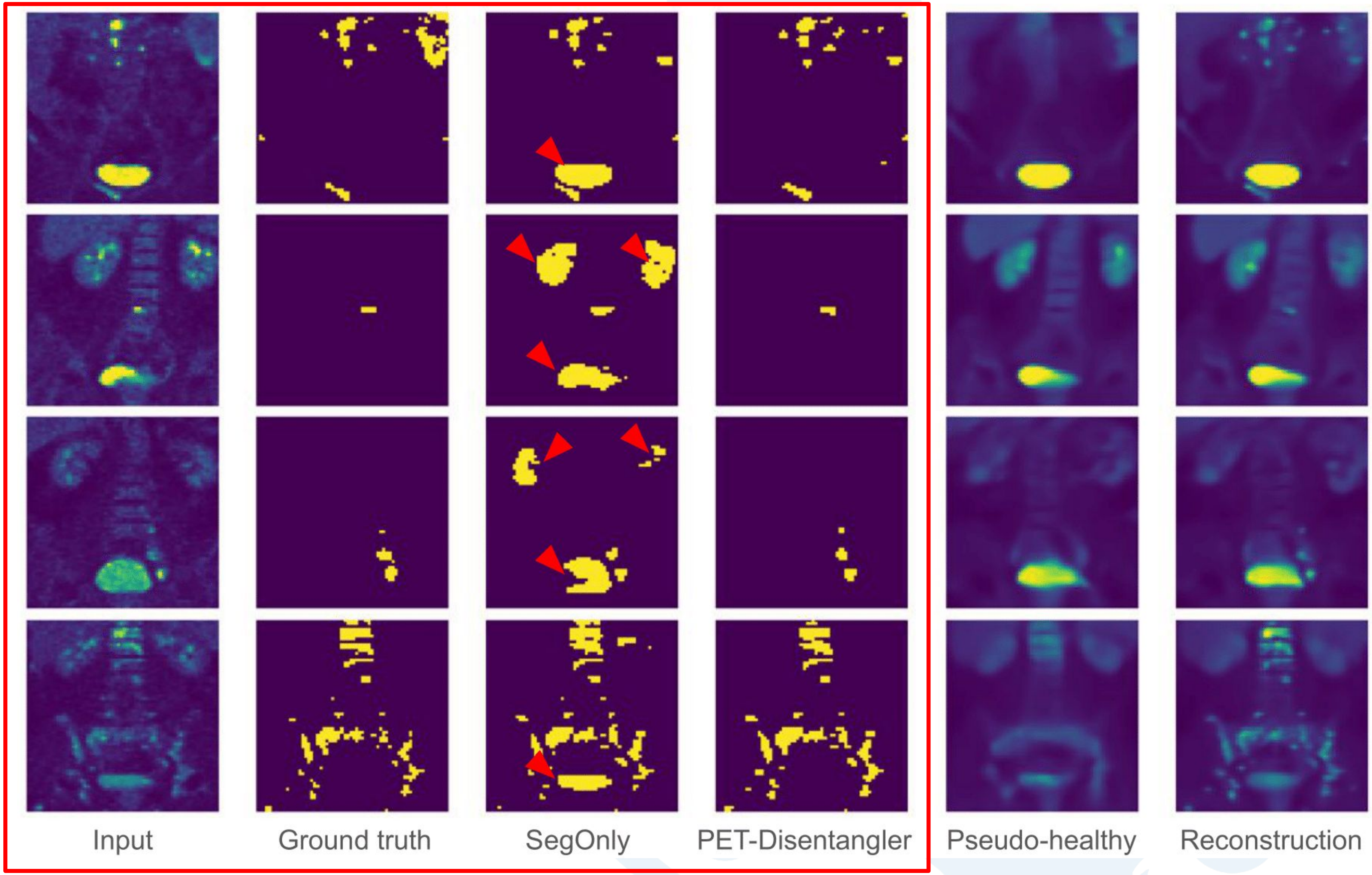
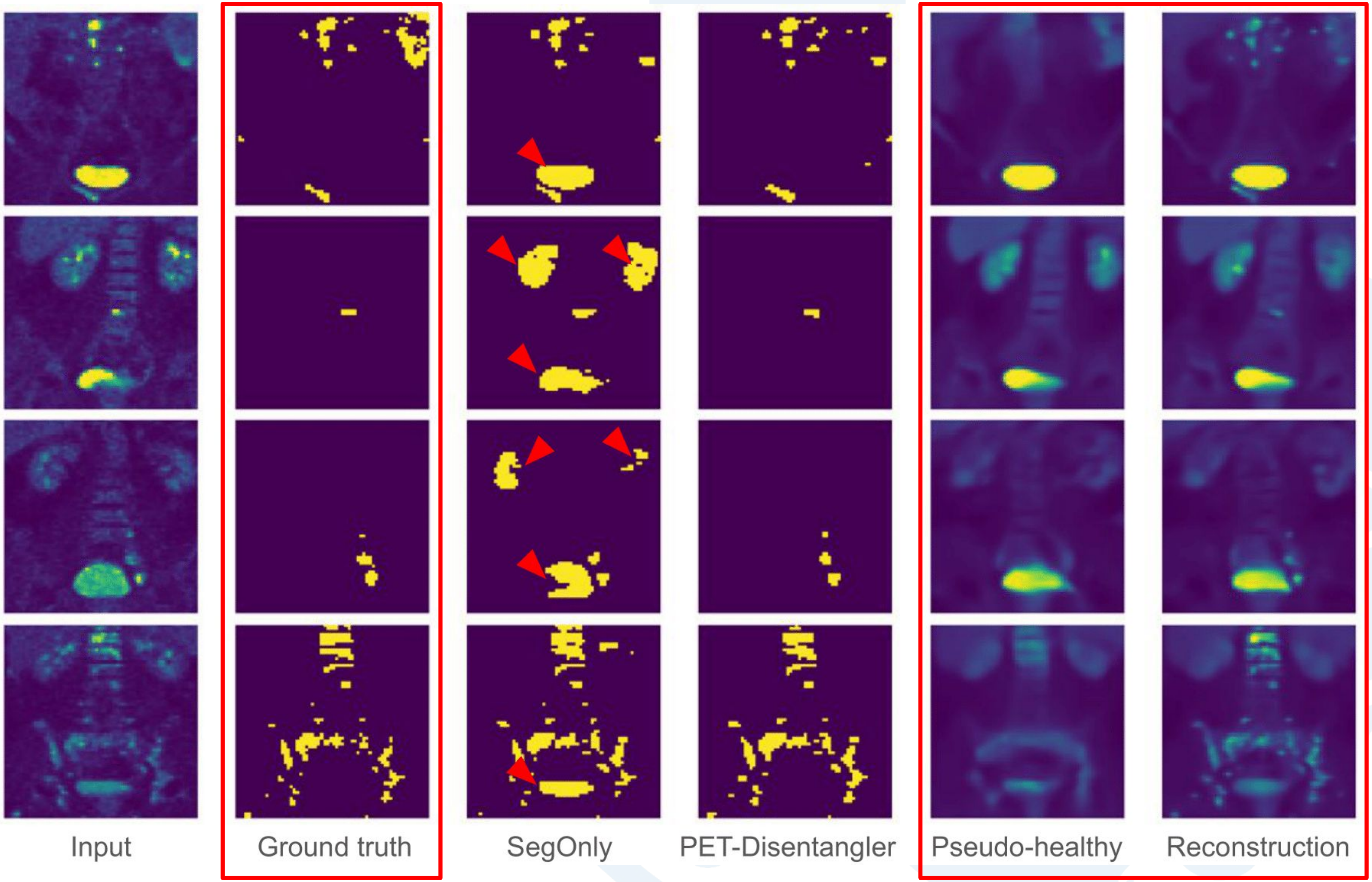


Table 1. Lesion segmentation Dice on lower torso

Method	Healthy (71)	Disease (31)	Overall (102)
SegOnly	0.0007 ± 0.0026	0.1864 ± 0.2474	0.0572 ± 0.1598
SegRecon	0.0013 ± 0.0048	0.1847 ± 0.2474	0.0570 ± 0.1593
SegReconHealthy	0.0008 ± 0.0012	0.1791 ± 0.2403	0.0550 ± 0.1547
PET-Disentangler	**0.7174 ± 0.4200**	**0.5153 ± 0.2843**	**0.6560 ± 0.3937**


Input
Ground truth
SegOnly
PET-Disentangler
Pseudo-healthy
Reconstruction


Input
Ground truth
SegOnly
PET-Disentangler
Pseudo-healthy
Reconstruction

Conclusions

PET-Disentangler, a lesion segmentation model that disentangles 3D PET into healthy and disease features.

PET-Disentangler greatly reduces false positives of healthy uptake compared to non-disentanglement methods.

Future work: investigate using an additional modality (i.e., CT, MRI) with corresponding PET.

Acknowledgements

NSERC
CRSNG

NIH

NVIDIA

CIHR IRSC

BC Cancer Agency
CARE + RESEARCH

BC
CAN
CER
FOUNDATION

Digital Research
Alliance of Canada

Alliance de recherche
numérique du Canada

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2. S. Gatidis, T. Hepp, M. Früh, C. La Fougère, K. Nikolaou, C. Pfannenberg, B. Schölkopf, T. Küstner, C. Cyran, and D. Rubin, “A whole-body FDG-PET/CT Dataset with manually annotated Tumor Lesions,” Scientific Data, vol. 9, no. 1, p. 601, 2022.

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Thank you!