Breaking Speed Limits with Simultaneous Ultra-Fast MRI Reconstruction and Tissue Segmentation

Paper #239

MIDL
Montréal 2020

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Disclosure

I have no financial interests or relationships to disclose with regard to the subject matter of this presentation.

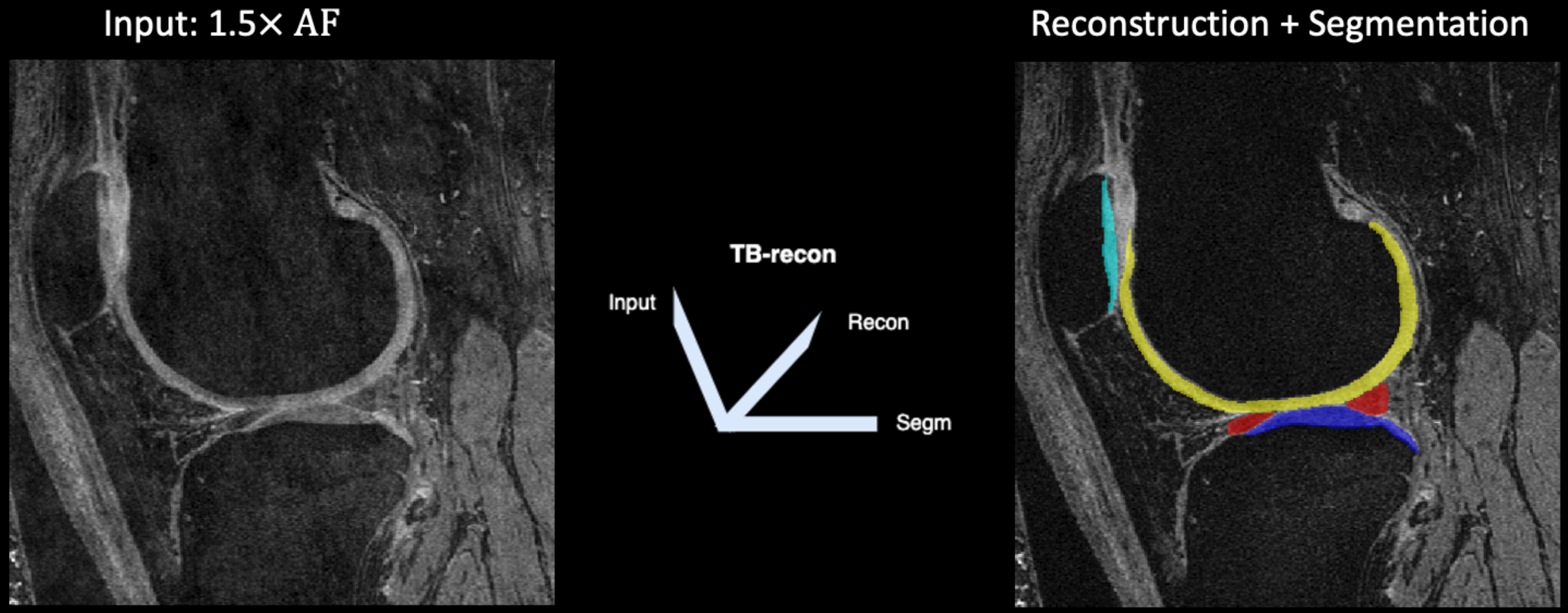
Funding source

This project was supported by R00AR070902 from the National Institute of Arthritis and Musculoskeletal and Skin Diseases, National Institutes of Health, (NIH-NIAMS).

National Institute of Arthritis and Musculoskeletal and Skin Diseases

Deep Learning in Magnetic Resonance Imaging (MRI)

- Long scanning time is the **main** limitation of MRI
- We devised a DL framework for **MRI reconstruction and segmentation** from highly undersampled MRIs
- We bridged image reconstruction and analysis by proposing a **task-based** reconstruction approach



Hypotheses:

- Reconstruction in the image-domain provides higher data **interpretability** over k-space

- Reconstruction and segmentation are similar and related tasks

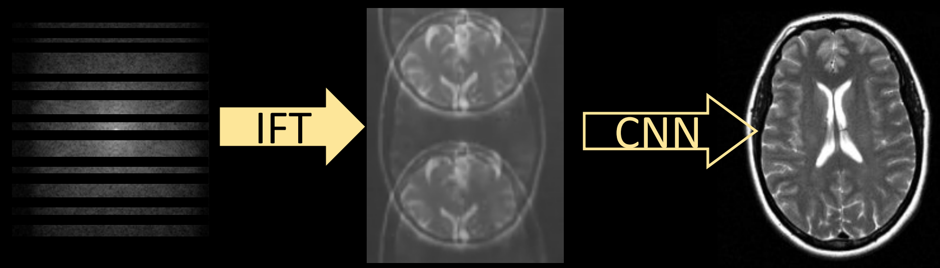
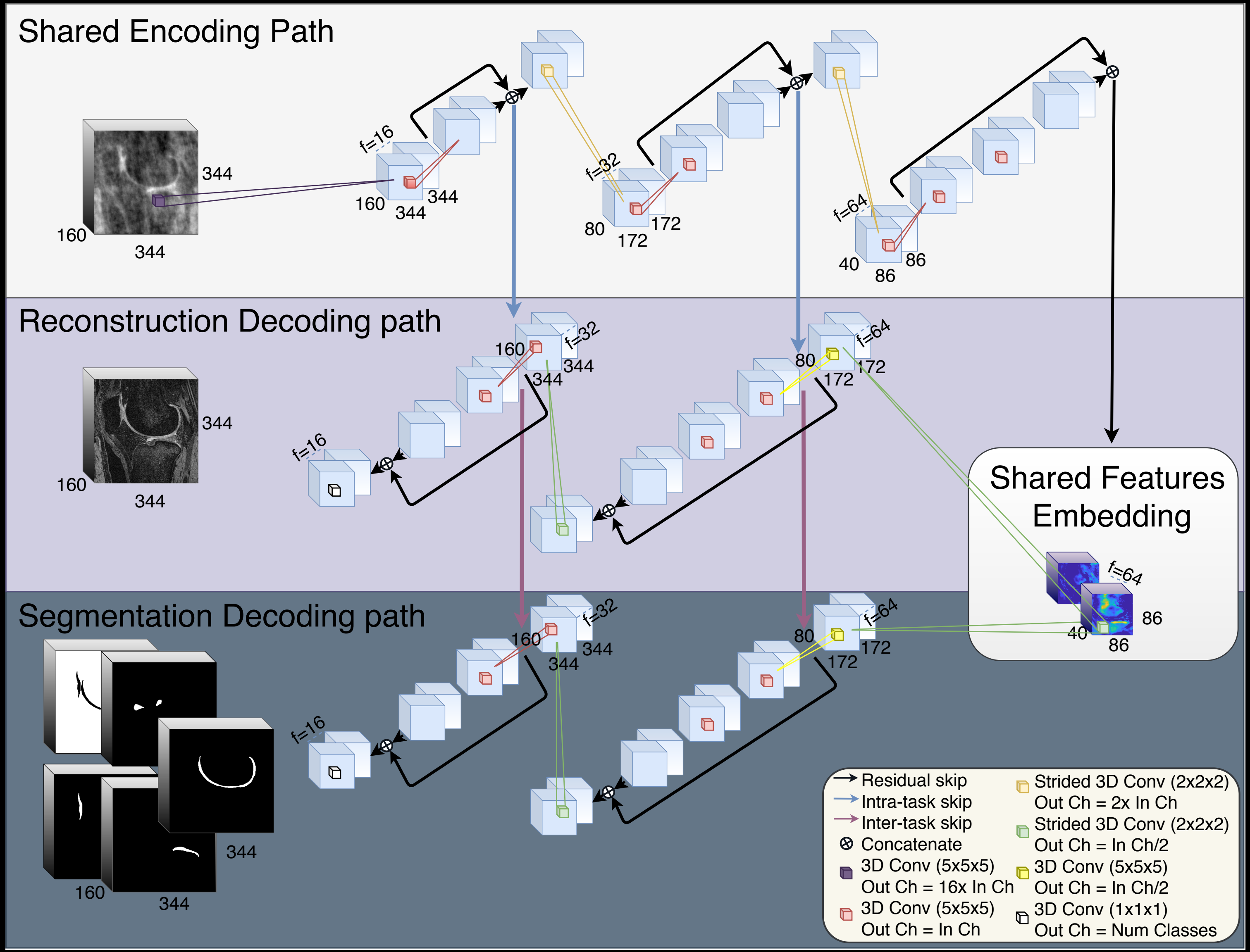


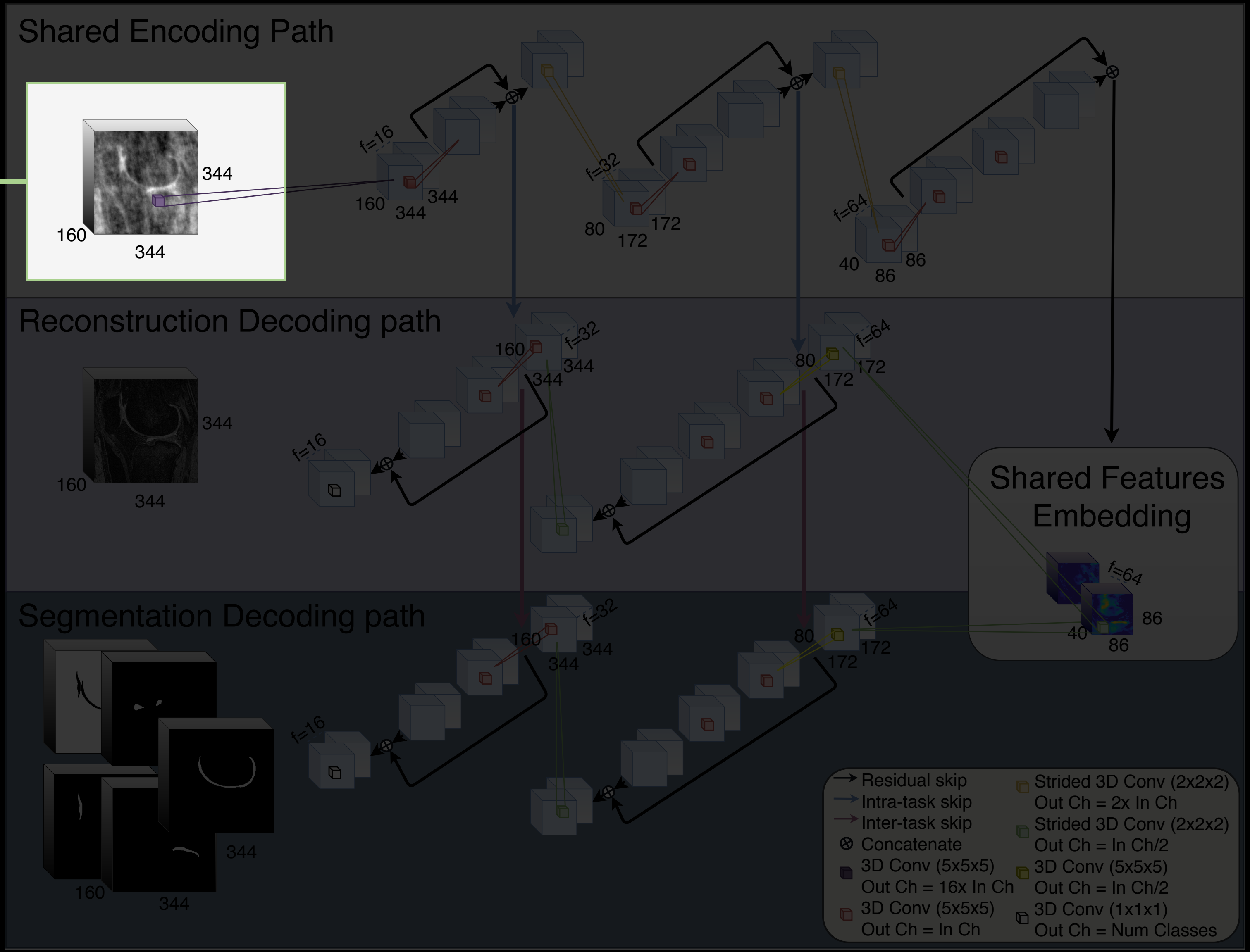
Image-Domain Learning

Simultaneous segmentation and image reconstruction

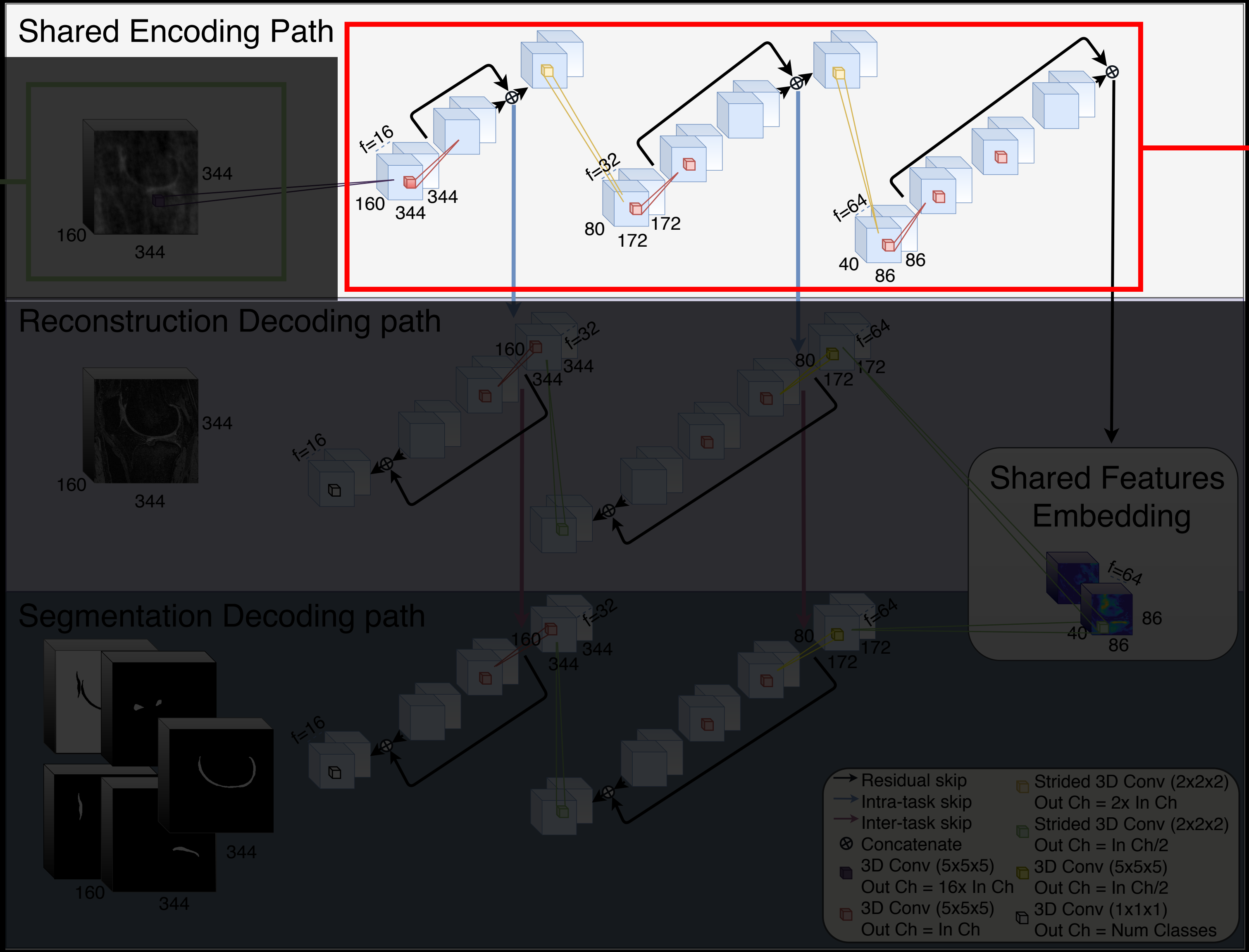
Proposed approach: Task-based image reconstruction: TB-recon



Input:
zero-filled MRI

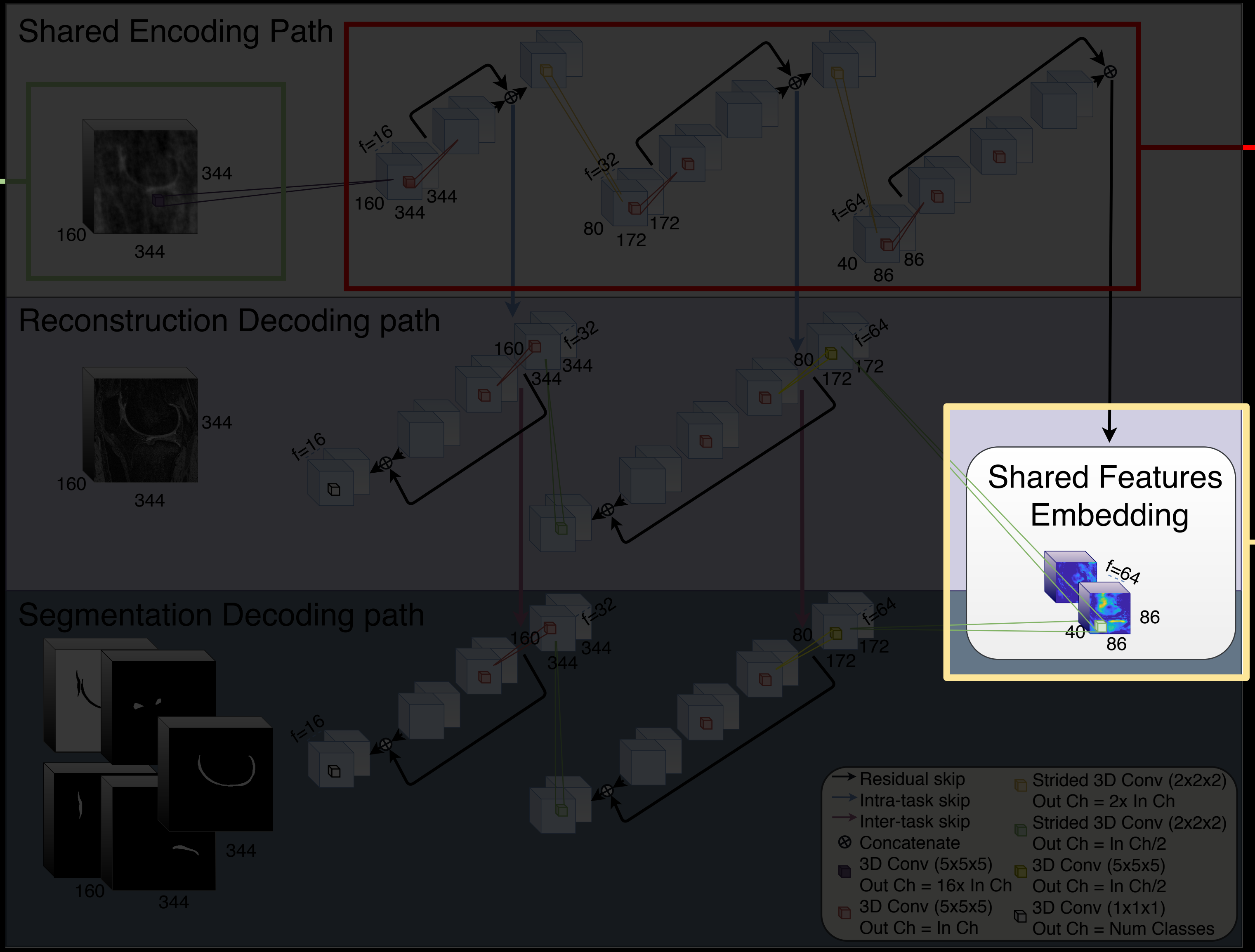


Input:
zero-filled MRI



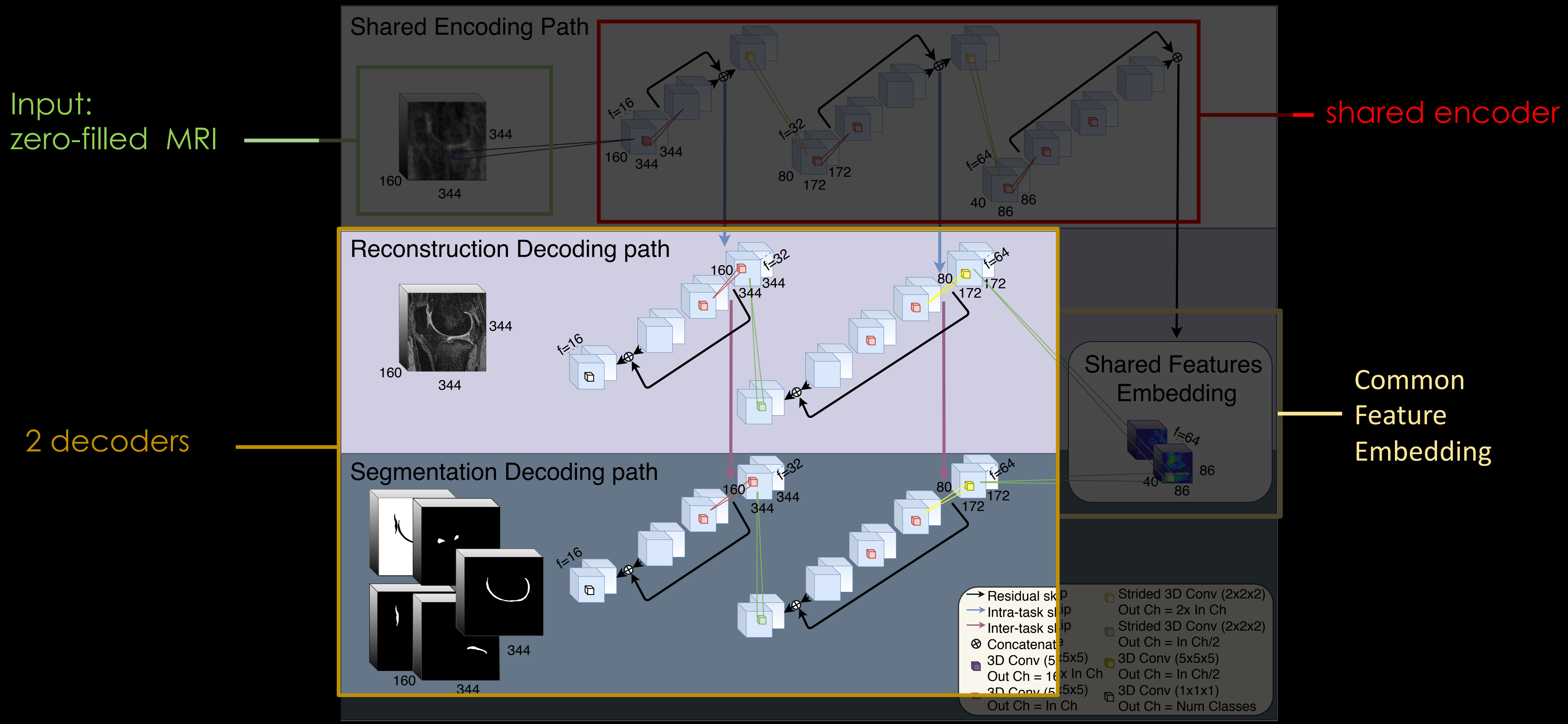
shared encoder

Input:
zero-filled MRI



shared encoder

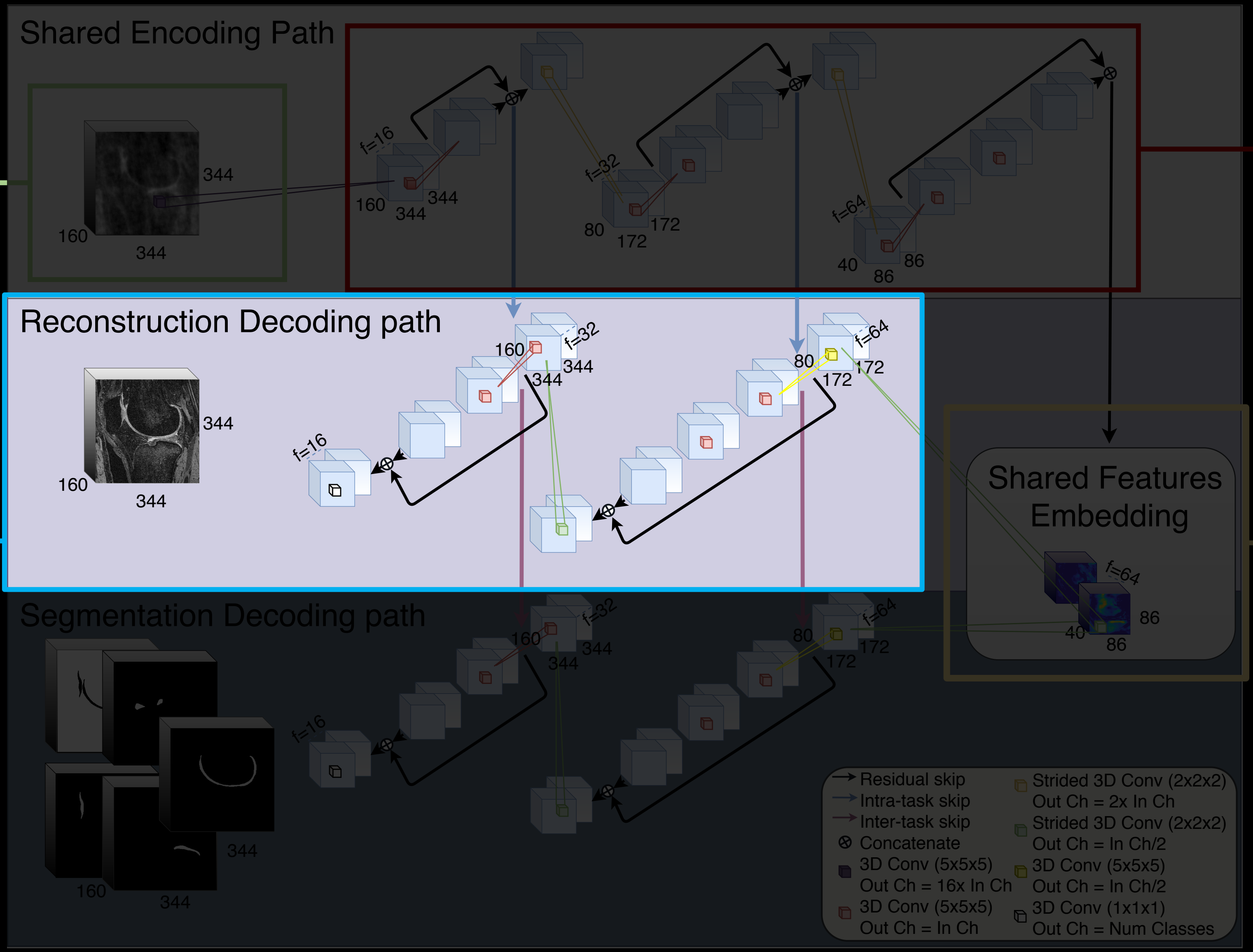
Common Feature Embedding



Input:
zero-filled MRI
2 decoders
shared encoder
Common
Feature
Embedding
Shared Encoding Path
Reconstruction Decoding path
Segmentation Decoding path
Shared Features
Embedding
f=16
f=32
f=64
Residual skip
Intra-task skip
Inter-task skip
Concatenate
Strided 3D Conv (2x2x2)
Out Ch = 2x In Ch
Strided 3D Conv (2x2x2)
Out Ch = In Ch/2
3D Conv (5x5x5)
Out Ch = In Ch/2
3D Conv (1x1x1)
Out Ch = Num Classes
Out Ch = In Ch

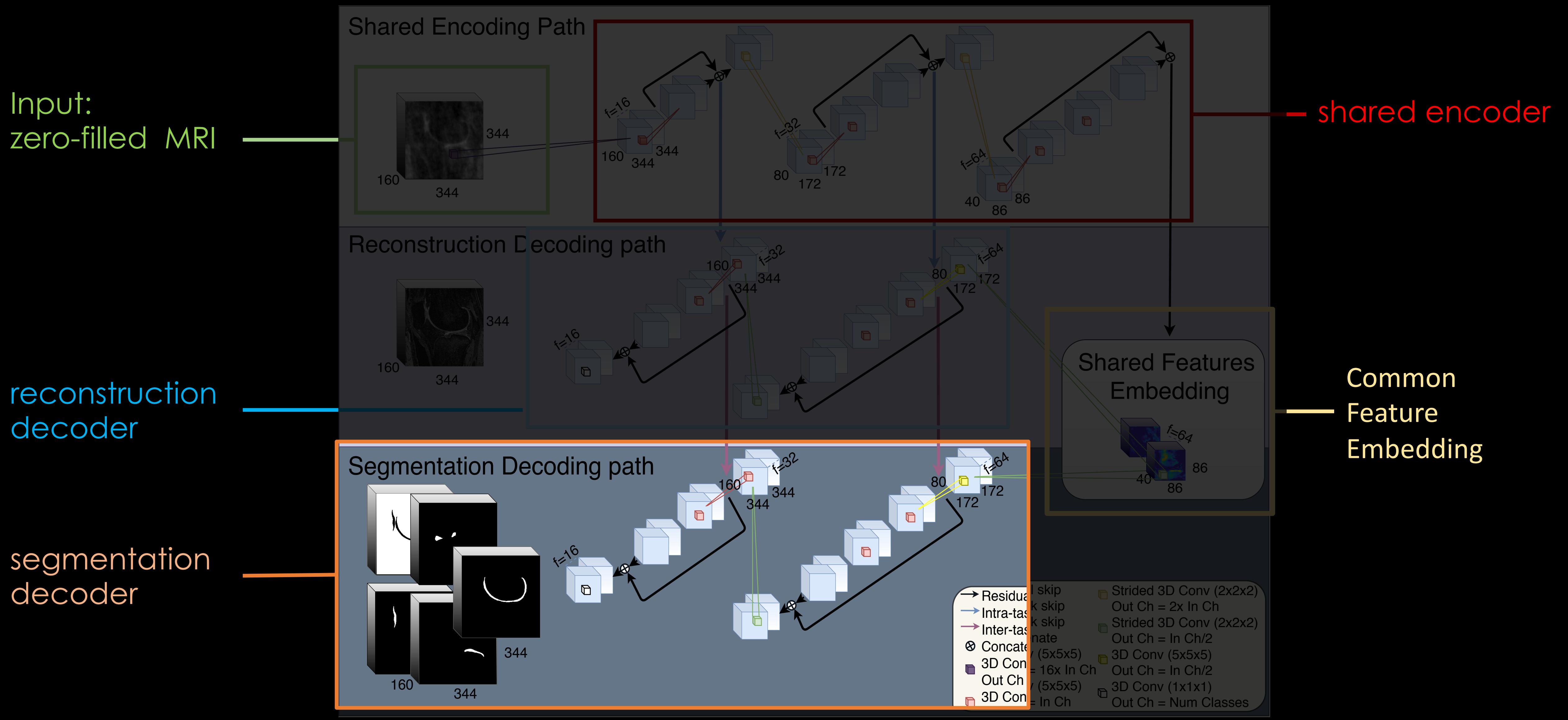
Input:
zero-filled MRI

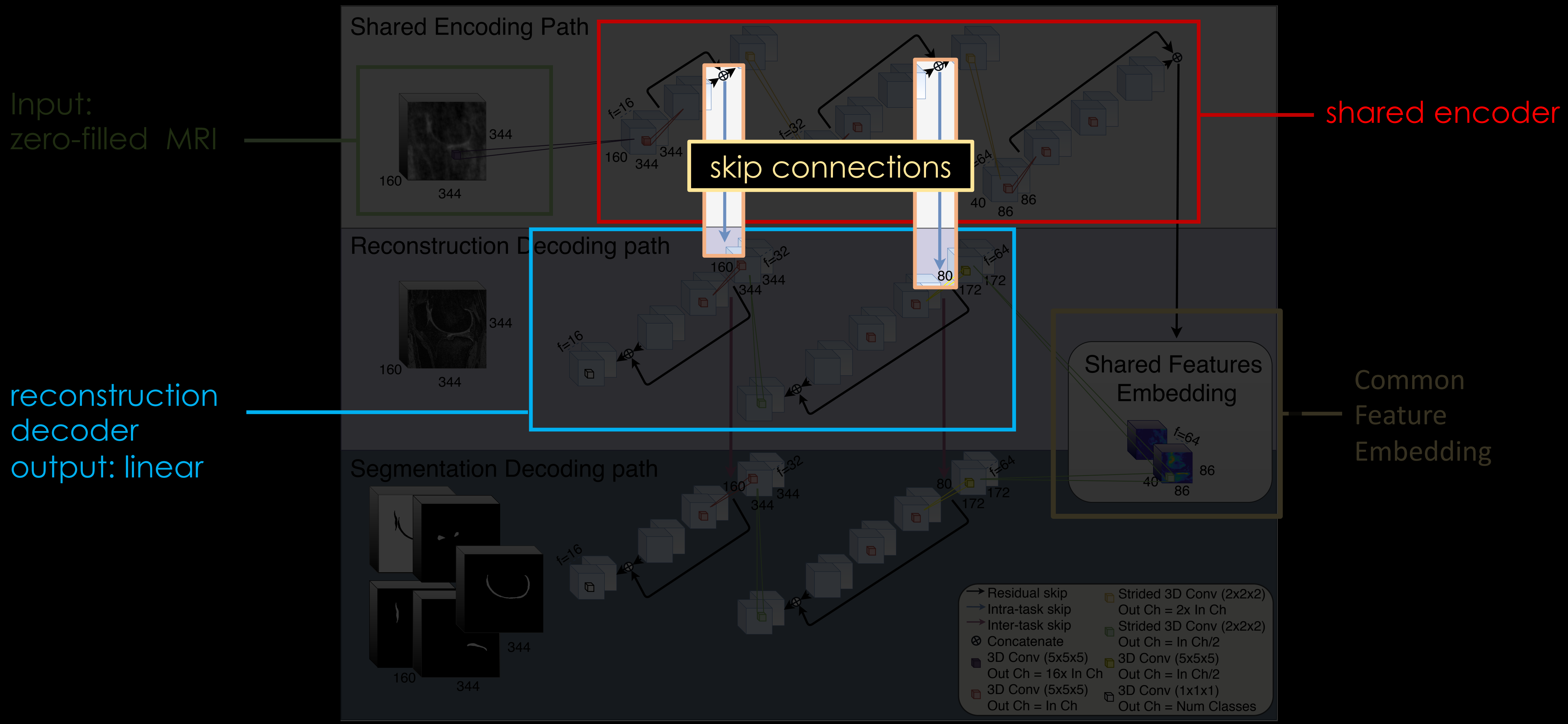
shared encoder



reconstruction
decoder

Common
Feature
Embedding


Input:
zero-filled MRI
reconstruction decoder
segmentation decoder
shared encoder
Common Feature Embedding
Shared Encoding Path
Reconstruction Decoding path
Segmentation Decoding path
Shared Features Embedding



Input:
zero-filled MRI
Shared Encoding Path
shared encoder
skip connections
Reconstruction Decoding path
reconstruction
decoder
output: linear
Segmentation Decoding path
Shared Features Embedding
Common
Feature
Embedding
Residual skip
Intra-task skip
Inter-task skip
Concatenate
3D Conv (5x5x5)
Out Ch = 16x In Ch
3D Conv (5x5x5)
Out Ch = In Ch
Strided 3D Conv (2x2x2)
Out Ch = 2x In Ch
Strided 3D Conv (2x2x2)
Out Ch = In Ch/2
3D Conv (5x5x5)
Out Ch = In Ch/2
3D Conv (1x1x1)
Out Ch = Num Classes

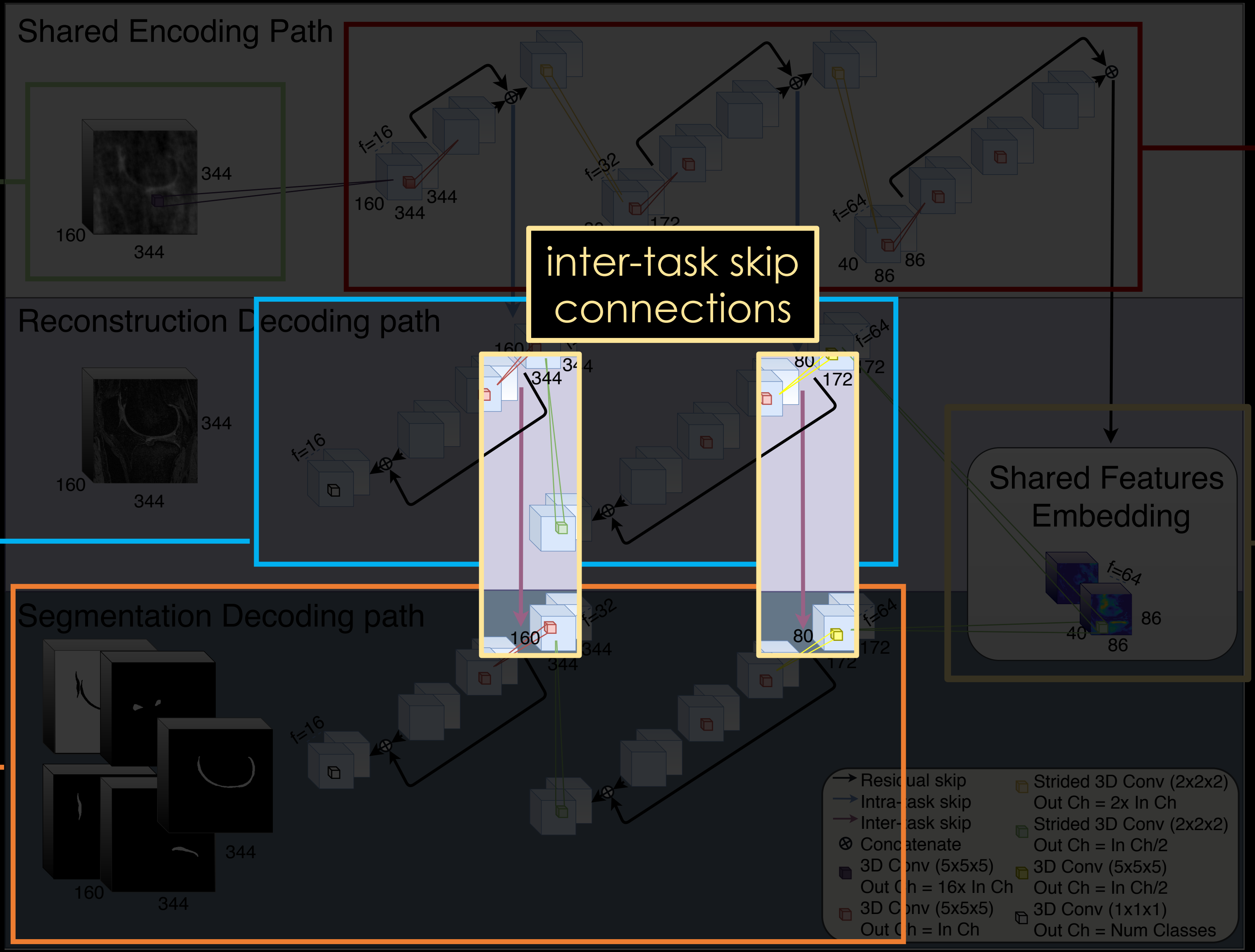
Input:
zero-filled MRI

shared encoder

reconstruction decoder

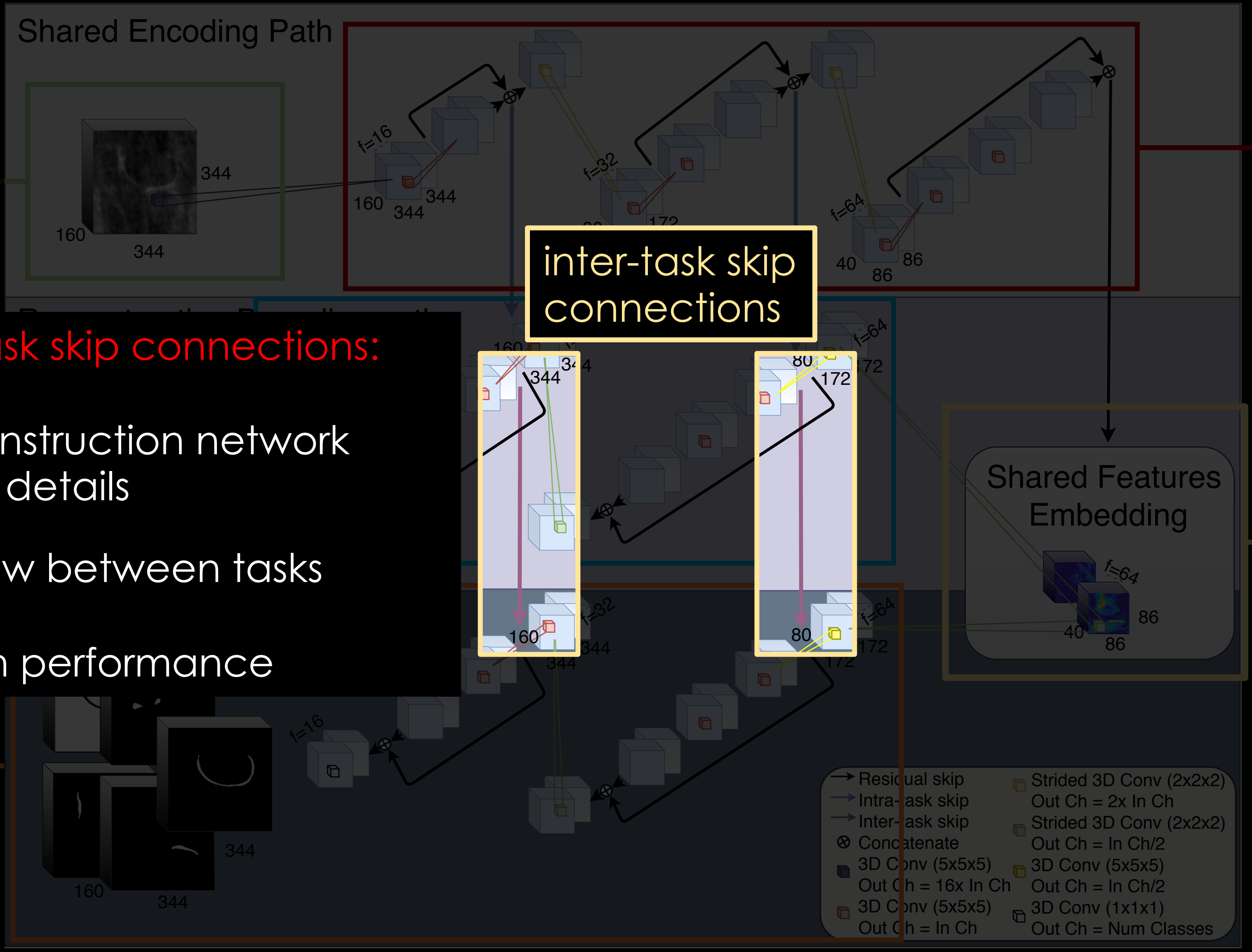
Common Feature Embedding

segmentation decoder
output: softmax activation



Advantages of inter-task skip connections:

- Features in the reconstruction network better describe fine details
- Facilitate feature flow between tasks
- Better segmentation performance



End-to-end network training

- Undersampled zero-filled MRI denoising and tissue segmentation

- A multi-task loss is minimized

$$\boxed{\begin{gathered}\boldsymbol{\mathcal{L}_{TB-recon} = \mathcal{L}_{recon} + \alpha \cdot \mathcal{L}_{segm}} \\ \boldsymbol{\mathcal{L}_{recon} = 1 - SSIM(\hat{y}_{recon}, y_{recon}) + \beta \cdot MAE(\hat{y}_{recon}, y_{recon})} \\ \boldsymbol{\mathcal{L}_{segm} = 1 - DICE(\hat{y}_{segm}, y_{segm}) + \gamma \cdot NLL(\hat{y}_{segm}, y_{segm})}\end{gathered}}$$

with α, β and ɣ empirically set to 1, 6.67[2] and 0.01 respectively

- Monitored metric: Dice Similarity Coefficient (DSC)

[1] *Milletari, F., et al."V-net: Fully convolutional neural networks for volumetric medical image segmentation." Fourth International Conference on 3DV. IEEE, 2016.*
[2] Zhao, H., Gallo, O., Frosio, I., & Kautz, J. (2016). Loss functions for image restoration with neural networks. *IEEE Transactions on computational imaging*, 3(1), 47-57.

Network trained end-to-end

- The network is trained for 500k iterations
- 20 epochs early-stopping
- 5% dropout rate[3]
- Adam optimizer[4] (learning rate = 1E-5)
- NVIDIA V100 32GB GPU
- Python 3.6.5 and Tensorflow 1.12

[3] Srivastava, N., Hinton, G., Krizhevsky, A., Sutskever, I., & Salakhutdinov, R. (2014). Dropout: a simple way to prevent neural networks from overfitting. The journal of machine learning research, 15(1), 1929-1958.
[4] Kingma, D. P., & Ba, J. (2014). Adam: A method for stochastic optimization. arXiv preprint arXiv:1412.6980.

Imaging data

- *174 knees from 87 participants to the Osteoarthritis Initiative study (OAI)[5]*
- *3D sagittal double-echo steady-state (DESS) MRI scans*
- *Acquisition parameters:*
    - *3.0T Siemens Trio at two time points.*
    - *TR 16.2ms*
    - *TE 4.7ms*
    - *FOV 14cm*
    - *Readout bandwidth 185kHz*
    - *Matrix size 384x384x160*
    - *Resolution 0.364x0.364x0.7mm*

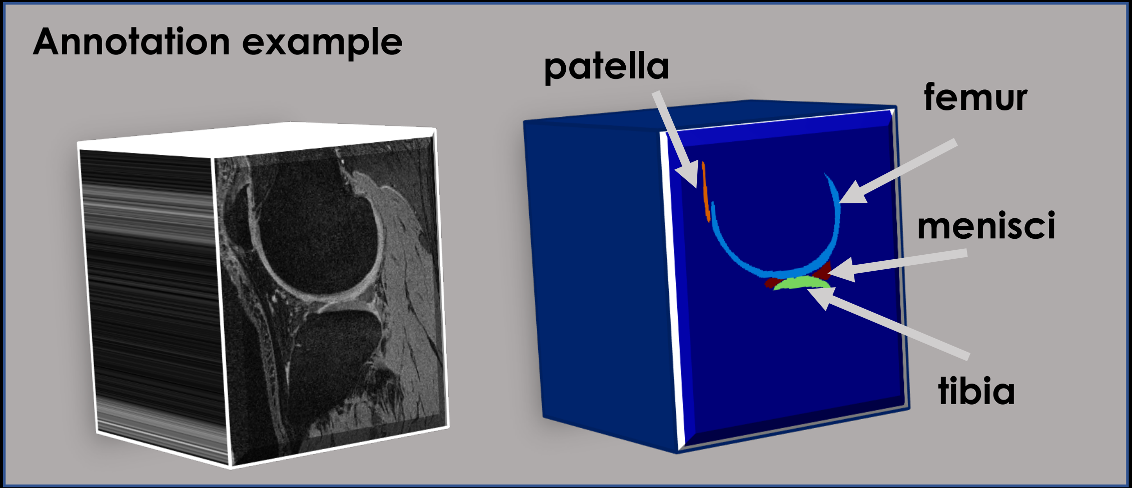


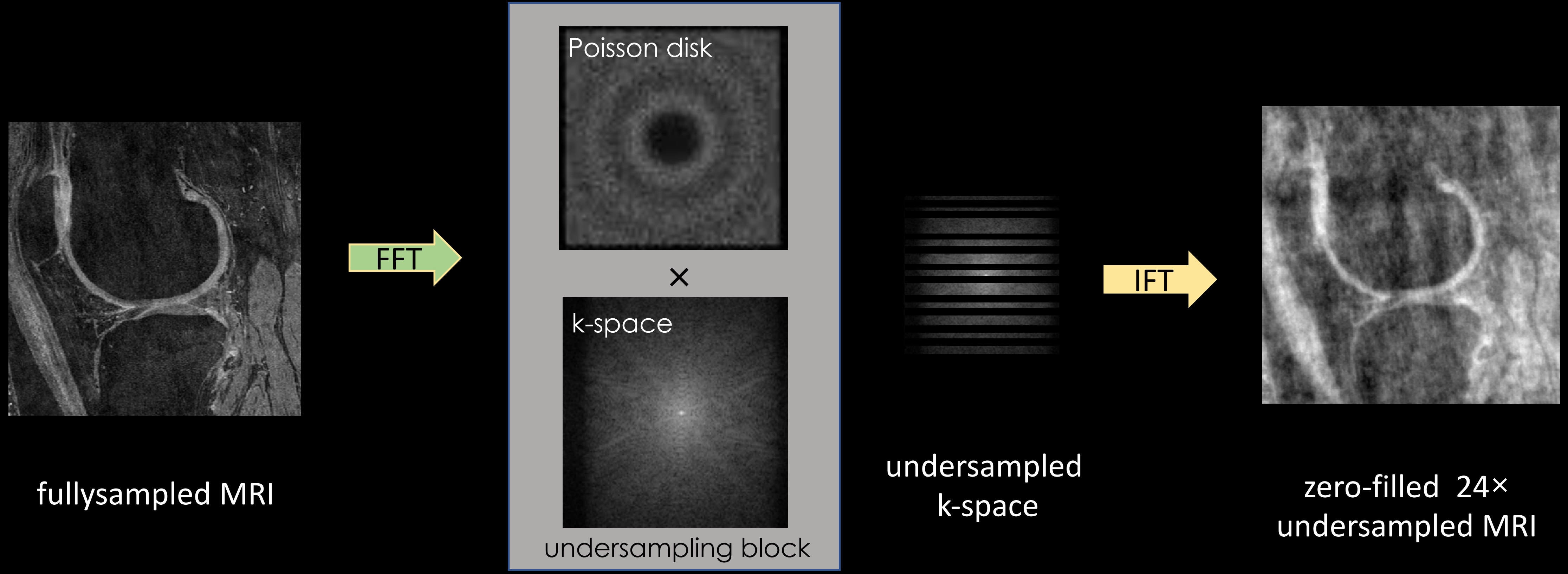
Table 1 Population attributes distribution in training validation and test splits. Race is reported in non-White/White or Caucasian/Black or African American/Asian order; sex in male/female order.

	Training	Validation	Test
Age	59.37±9.09	58.57±9.51	70.86±7.40
BMI [kg/m^2]	30.49±4.21	33.30±6.01	31.23±3.90
Race	1/47/11/0	0/8/6/0	1/13/0/0
Sex	28/31	8/6	9/5

[5] Peterfy, C. G., Schneider, E., & Nevitt, M. (2008). The osteoarthritis initiative: report on the design rationale for the magnetic resonance imaging protocol for the knee. Osteoarthritis and cartilage, 16(12), 1433-1441.

Retrospective undersampling

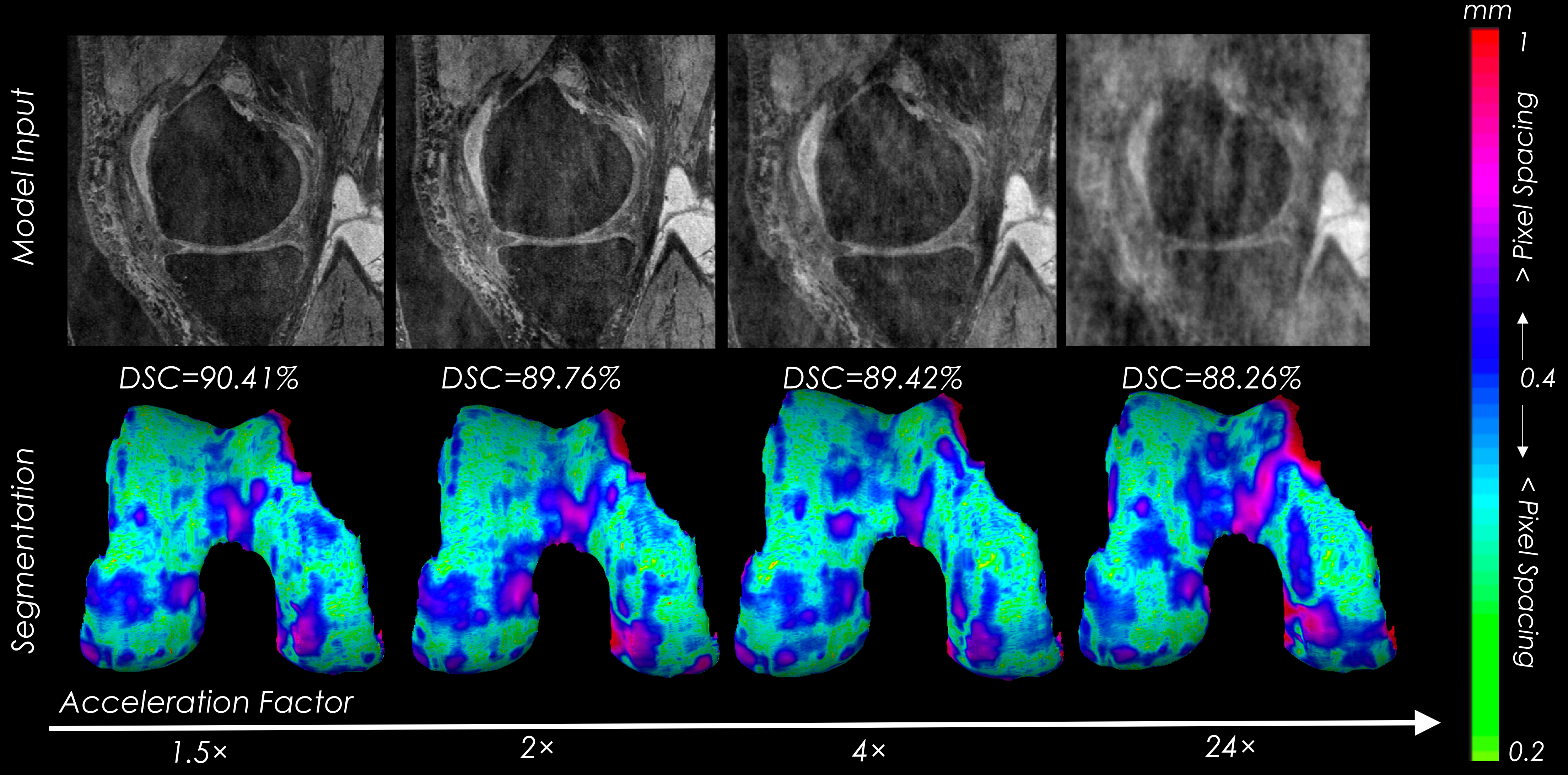
- Variable-density Poisson disk undersampling mask[6]
- 5 acceleration factors (AF) 2x, 4x, 6x, 12x, 24x
- Retrospective undersampling performed using the SigPy software[7]



[6] Bridson, R.. "Fast Poisson disk sampling in arbitrary dimensions." SIGGRAPH sketches. 2007.
[7] http://indexsmart.mirasmart.com/ISMRM2019/PDFfiles/4819.html

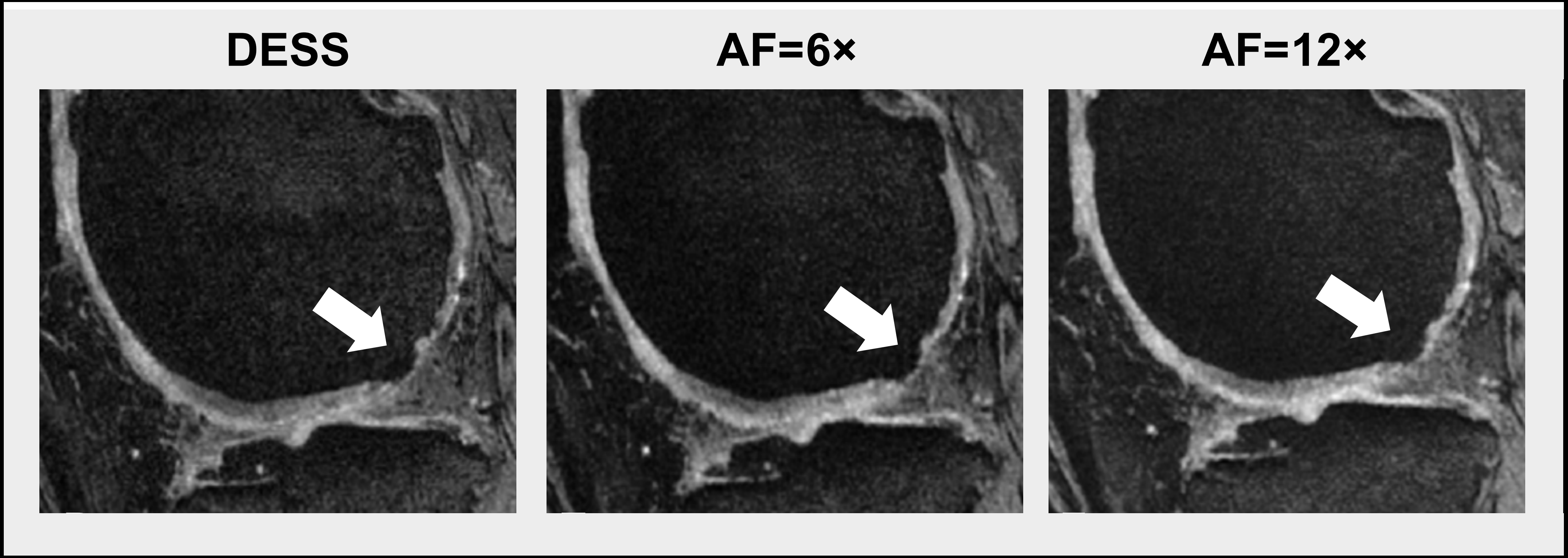
Results – TB-recon's femural cartilage segmentation

Point by Point distance between automatic and manual segmentation



Results – TB-recon Reconstruction

Bone marrow edema visible in a sagittal DESS (A), is well observed at 6× (B) and 12× (B) AFs reconstructed MRIs



Results – Ablation study

Investigated importance of:

- MRI reconstruction
- Inter-task skip connections

Femur - DSC	4×	6×	24×
TB-recon	**87.33±1.93**	**87.58±1.79**	**85.63±2.56**

Tibia - DSC	4×	6×	24×
TB-recon	**85.12±3.85**	**86.18±3.59**	**85.84±3.51**

Patella - DSC	4×	6×	24×
TB-recon	**82.10±6.83**	**81.76±7.82**	**77.65±7.96**

Menisci - DSC	4×	6×	24×
TB-recon	**84.91±2.79**	**83.78±3.06**	**82.28±2.64**

Results – Ablation study

No MRI reconstruction

Femur - DSC	4×	6×	24×
TB-recon	**87.33±1.93**	**87.58±1.79**	**85.63±2.56**
zero-filled	82.27±2.75	81.79±2.73	16.27±0.91

Tibia - DSC	4×	6×	24×
TB-recon	**85.12±3.85**	**86.18±3.59**	**85.84±3.51**
zero-filled	83.32±4.53	81.26±5.20	29.75±1.80

Patella - DSC	4×	6×	24×
TB-recon	**82.10±6.83**	**81.76±7.82**	**77.65±7.96**
zero-filled	78.10±7.17	77.37±6.47	70.88±10.59

Menisci - DSC	4×	6×	24×
TB-recon	**84.91±2.79**	**83.78±3.06**	**82.28±2.64**
zero-filled	81.87±2.99	81.61±3.15	16.69±0.93

bold = significant outperformance

Results – Ablation study

Femur - DSC	4×	6×	24×
TB-recon	**87.33±1.93**	**87.58±1.79**	**85.63±2.56**
zero-filled	82.27±2.75	81.79±2.73	16.27±0.91
naïve	84.97±2.69	82.94±2.99	83.71±2.82

Tibia - DSC	4×	6×	24×
TB-recon	**85.12±3.85**	**86.18±3.59**	**85.84±3.51**
zero-filled	83.32±4.53	81.26±5.20	29.75±1.80
naïve	84.09±3.86	83.26±4.20	56.15±2.38

Patella - DSC	4×	6×	24×
TB-recon	**82.10±6.83**	**81.76±7.82**	**77.65±7.96**
zero-filled	78.10±7.17	77.37±6.47	70.88±10.59
naïve	53.74±4.36	77.62±7.61	32.45±2.24

Menisci - DSC	4×	6×	24×
TB-recon	**84.91±2.79**	**83.78±3.06**	**82.28±2.64**
zero-filled	81.87±2.99	81.61±3.15	16.69±0.93
naïve	82.35±2.69	81.47±3.31	54.59±2.24

No MRI reconstruction

No inter-task skip connections

bold = significant outperformance

Femur - DSC	4×	6×	24×
TB-recon	**87.33±1.93**	**87.58±1.79**	**85.63±2.56**
zero-filled	82.27±2.75	81.79±2.73	16.27±0.91

No MRI recon

task skip
ctions

For more details on our work, including additional experiments
please refer to our paper #239

Caliva, F. Leynes, A., Shah, R., Bharadwaj, U. U., Majumdar, S., Larson, P., & Pedoia, V. (2020, January). Breaking Speed Limits with Simultaneous Ultra-Fast MRI Reconstruction and Tissue Segmentation. In Medical Imaging with Deep Learning

[illegible]	[illegible]	[illegible]	[illegible]
zero-filled	81.87±2.99	81.61±3.15	16.69±0.93
naïve	82.35±2.69	81.47±3.31	54.59±2.24

bold = significant outperformance

Contributions

- **TB-recon** for task-based MRI reconstruction
- Segmentation at **ultra-high acceleration factors** is possible
- The proposed **shared encoder** + **inter-task** skip connections facilitate segmentation

Broader impact

Task-based reconstruction can break speed limits, which have hampered the application of magnetic resonance imaging

Potential applications:

- disease and abnormality identification
- organ volume estimation
- lesion size and counting (e.g. multiple sclerosis and micro-bleeds)

We hope this paper further stimulates research community's interest on task-based fast MRI

Acknowledgements

Valentina Pedoia's Lab
Rutwik Shah
Kaiyang (Victor) Cheng
Alejandro Morales Martinez
Adam Noworolski

Peder E. Z. Larson's Lab
Andrew P. Leynes
Xucheng Zhu

Sharmila Majumdar's Lab
Upasana Upadhyay Bharadwaj
Claudia Iriondo

Funding source

This project was supported by R00AR070902 (VP), R61AR073552 (SM/VP) from the National Institute of Arthritis and Musculoskeletal and Skin Diseases, National Institutes of Health, (NIH-NIAMS).

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