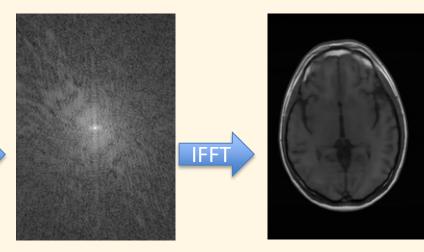


Towards multi-sequence MR image recovery from undersampled k-space data

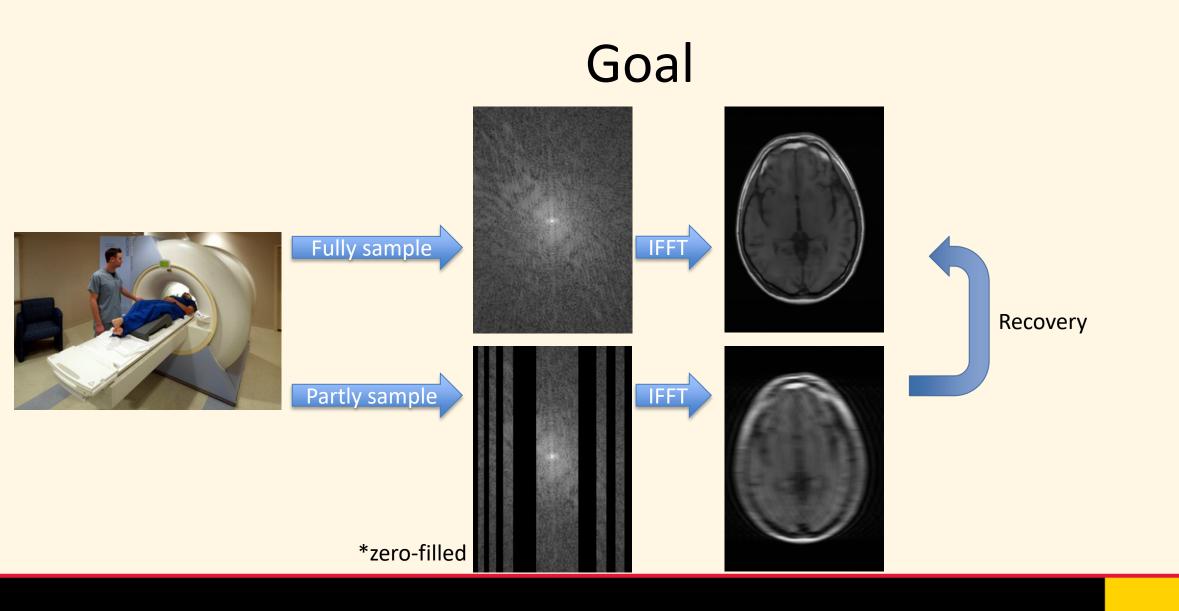
Cheng Peng, Wei-An Lin, Rama Chellappa, S. Kevin Zhou

Problem setting



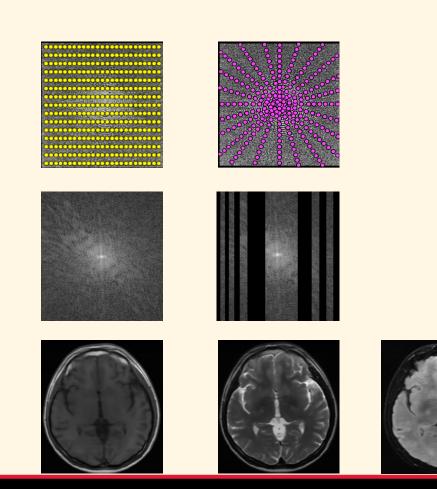


Slow, high definition



Factors in MR acquisition time

- Sampling trajectory (Cartesian, Radial, etc.)
- Sampling resolution

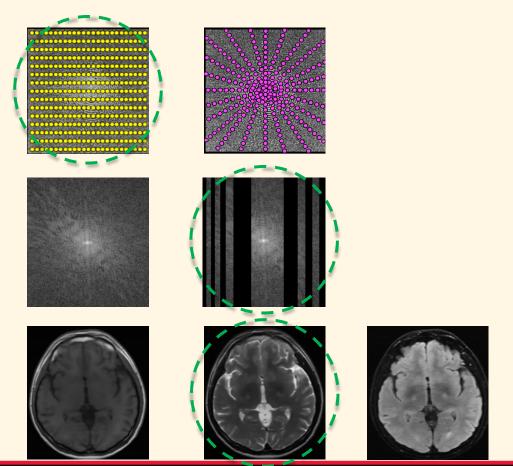


• Sampling sequences (T1, T2, FLAIR, etc.)

Factors in MR acquisition time

- Sampling trajectory (Cartesian, Radial, etc.)
- Sampling resolution

• Sampling sequences (T1, T2, FLAIR, etc.)

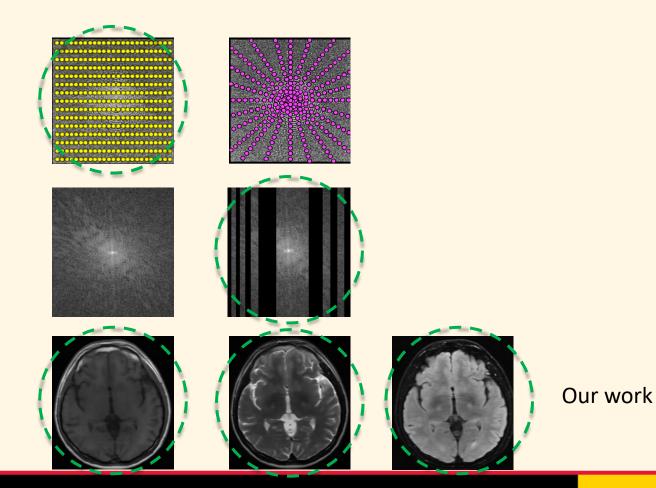


Most previous work focuses on single sequence recovery

Factors in MR acquisition time

- Sampling trajectory (Cartesian, Radial, etc.)
- Sampling resolution

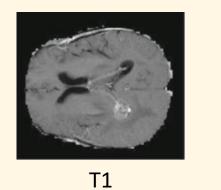
Sampling sequences
(T1, T2, FLAIR, etc.)



Questions

- How much does the shared information help multi-sequence reconstruction/recovery?
- How should one determine what sequence to undersample, and by how much ("the undersampling strategy")?
- Factors: sequence acquisition time, information entropy (uniqueness), measurement system

T1 VS FLAIR



FLAIR

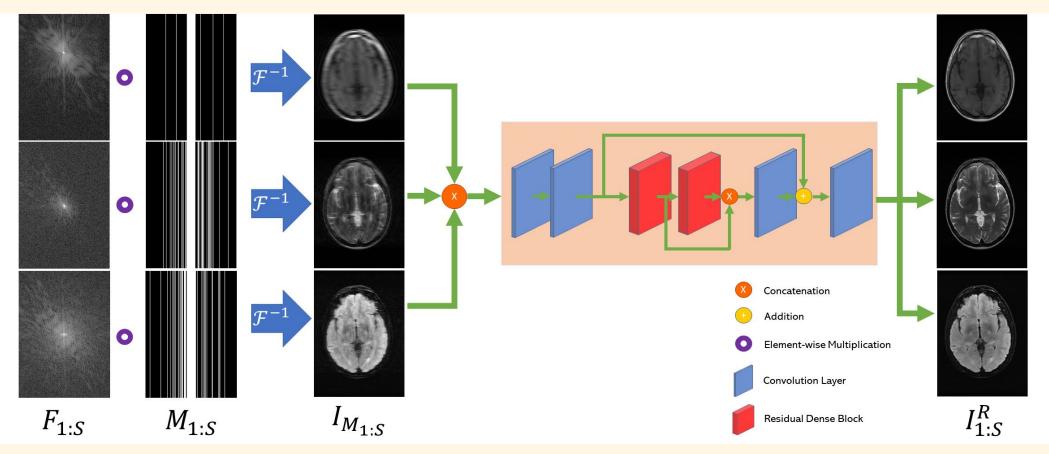
BraTS dataset

*	TR (msec)	• • • • • •	
T1-Weighted (short TR and TE)	500	14	
T2-Weighted (long TR and TE)	4000	90	
Flair (very long TR and TE	9000	114	

*School of Medicine, Case Western Reserve,

https://casemed.case.edu/clerkships/neurology/Web%20Neurorad/MRI%20Basics.htm

Residual DenseNet (RDN)



Ways to find undersampling strategies

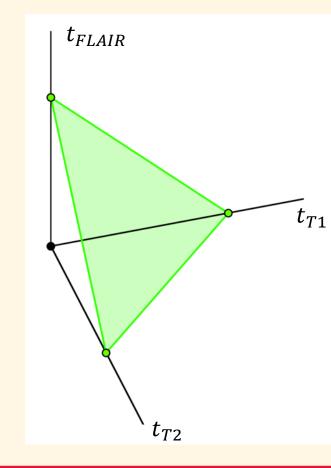
- Strategy 1: Same undersampling factors for all sequences.
- Strategy 2: Exhaustively search by training dedicated CNNs for every possible undersampling strategies.
- Strategy 3: Base on the PSNR of observed undersampled MRsequences vs. the ground truth.

Blink Recovery Model

- We propose to use a guide RDN, called BRM, trained to recover sequences from all possible undersampling strategies through L1/L2 constraints.
- Assumption: PSNR measures recovery quality well
- PSNRs are calculated for recovered sequences of different undersampling strategies.

BRM training

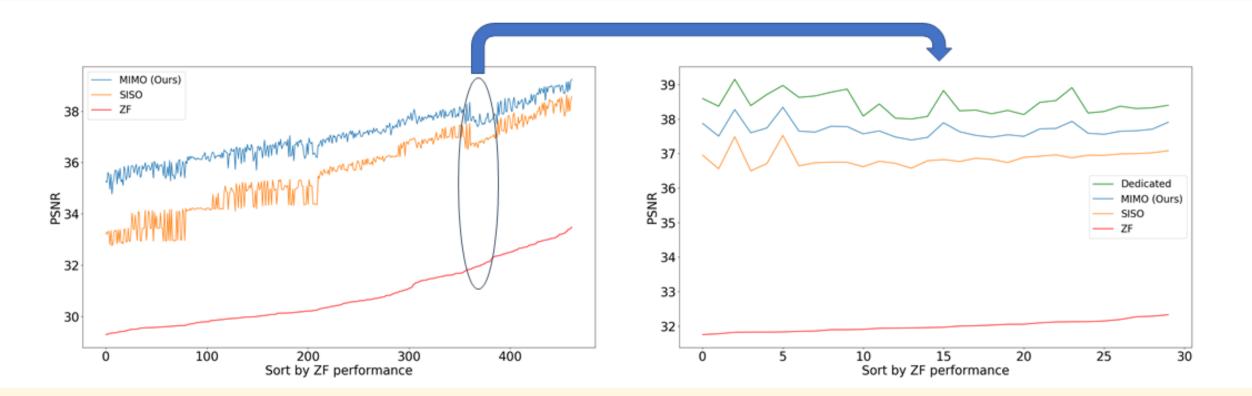
- The undersampling strategies are randomly generated based on: $\sum_{s=1}^{S} \frac{t_s}{\lambda_s} = T_{max}$
- t_s is the time cost of fully sampling sequence s.
- λ_s is the undersampling factor of sequence s.
- T_{max} is the total time constraint.
- The undersampling process is done online.

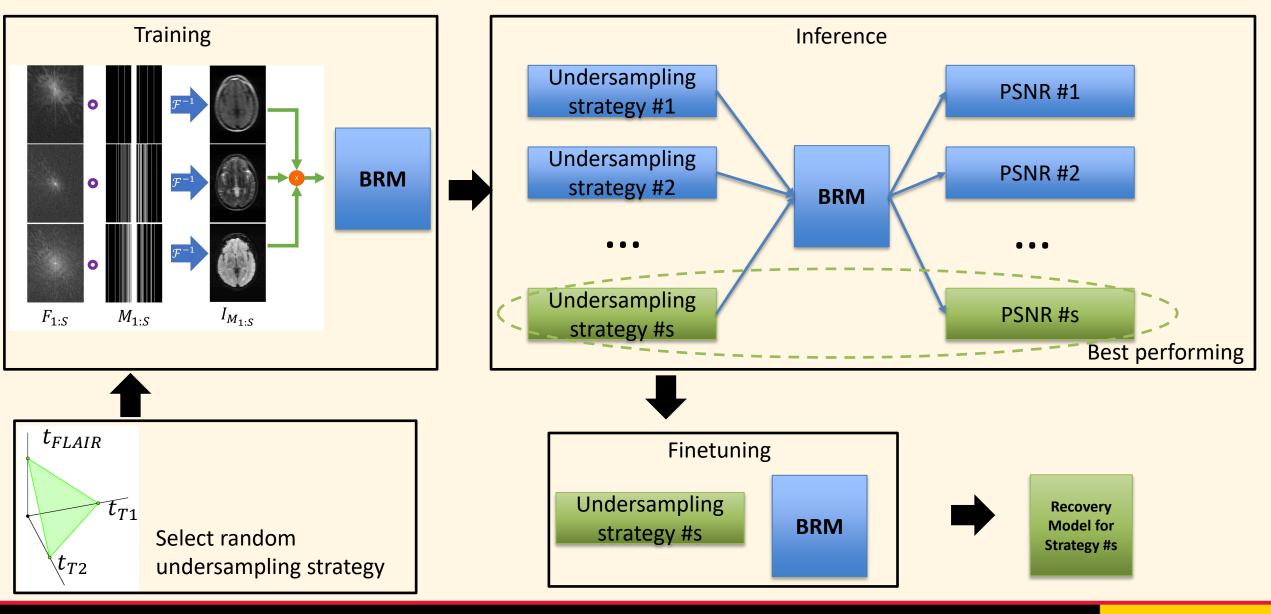


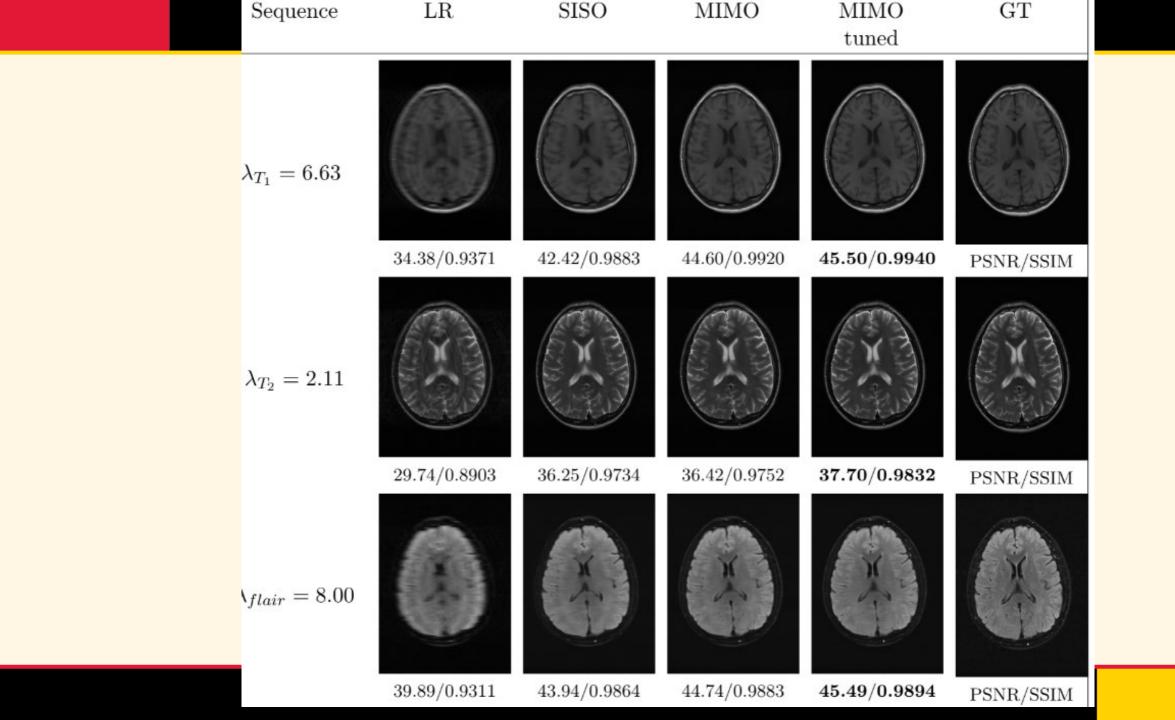
Evaluation Dataset

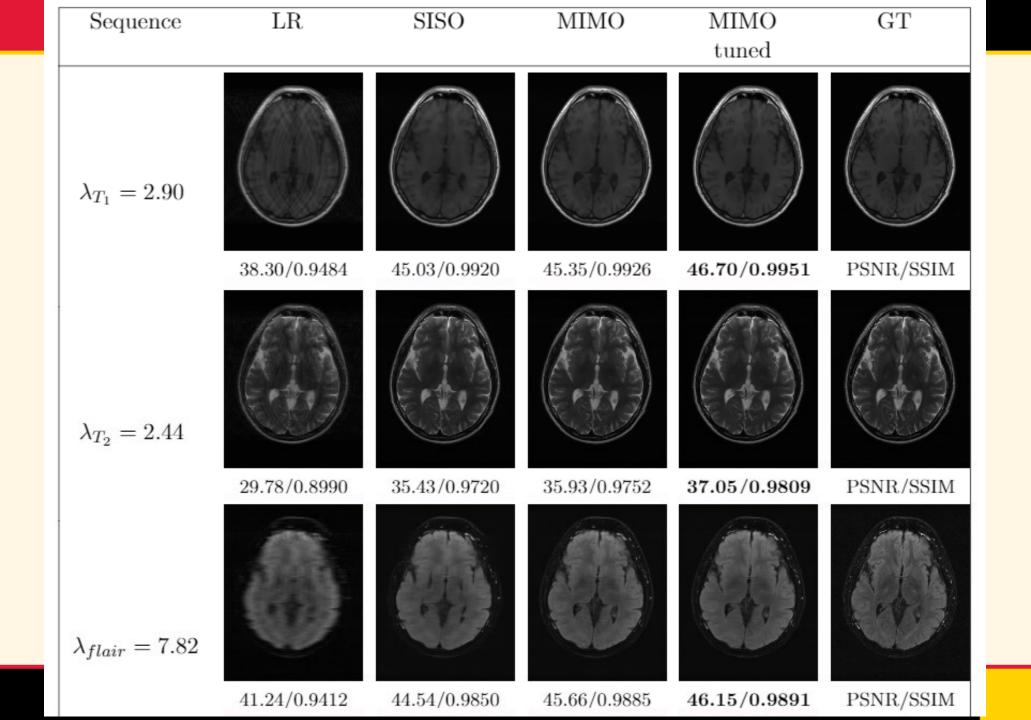
- We acquired the k-space data of three sequences (T1, T2, FLAIR) from 20 patients, in total 2880 three-sequence images.
- To expand on the dataset, we simulated k-space data from the BraTS dataset and selected 167 scans, which are co-registered in T1, T2, and FLAIR.
- Note that simulated k-space data is conjugate symmetric, unlike real k-space measurements.

Empirical results









$t_{T_1}:t_{T_2}:t_{flair}$	$\lambda_{T_1}, \lambda_{T_2}, \lambda_{flair}$	ZF	SISO	MIMO	MIMO
					(tuned)
1:1:1	6.6, 2.1, 8.0	33.48/0.918	38.57/0.980	39.24/0.984	40.00/0.987
Real	8.00, 2.11, 6.63	33.43/0.920	38.36/0.979	39.16/0.984	40.07/0.987
	7.25, 2.11, 7.25	33.39/0.918	38.50/0.980	39.15/0.984	40.07/0.986
1:4:6	2.90, 2.44, 7.82	33.81/0.926	38.85/0.983	39.33/0.985	40.28/0.988
Real	3.01, 2.44, 7.69	33.60/0.924	38.83/0.983	39.32/0.985	40.37/0.987
	3.93, 2.44, 6.99	33.58/0.925	38.81/0.983	39.31/0.986	40.13/0.987
1:1:1	5.66, 3.14, 3.93	32.21/0.887	37.69/0.974	38.32/0.978	38.99/0.980
Simulated	5.27, 3.41, 3.74	32.31/0.889	37.88/0.975	38.31/0.979	38.98/0.980
	6.10, 3.14, 3.74	32.21/0.887	37.51/0.973	38.31/0.978	38.99/0.980
2:3:6	2.61, 3.74, 5.16	32.87/0.899	38.01/0.976	38.67/0.980	39.37/0.982
Simulated	2.44, 3.74, 5.40	32.84/0.899	37.87/0.975	38.66/0.980	39.35/0.982
	2.61, 3.41, 5.66	32.82/0.899	37.80/0.975	38.65/0.980	39.33/0.982

Figure 3: Quantitative evaluations for the top performing $\lambda_{1:S}$ under different acquisition time assumption. The performance numbers presented here are PSNR (dB) and SSIM.

Conclusion

- Multi-sequence recovery achieves much better results than individual sequence recovery
- BRM is
 - 1. much faster than exhaustive search through training dedicated CNNs;
 - 2. much more reliable than zero-filled sequence PSNR;
 - 3. adaptive to different sequence time costs