MARVEL: MR Fingerprinting with Additional micRoVascular Estimates using bidirectional LSTMs

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1 · MR Fingerprinting

Some MRI sequences are sensitive to several physiological tissue parameters. **MR Fingerprinting** [4] consists in using these sequences to simultaneously reconstruct parameter maps, allowing to reduce the examination time.

To estimate the voxel parameters, large dictionaries of signals, associated to known parameters, are numerically simulated for the sequence under consideration. The time signal (the **fingerprint**) of the acquired voxel can then be compared with the signal dictionary: by identifying the dictionary signal closest to the fingerprint, parameters are associated with the considered voxel: this is the **matching** method.

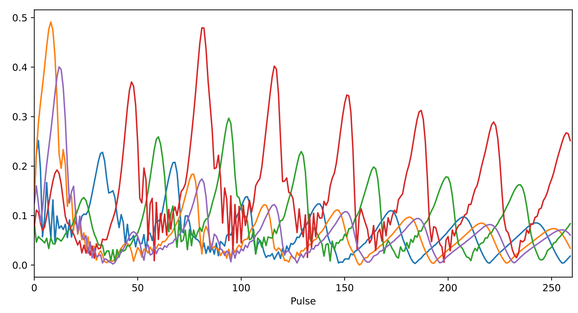

Figure 1: Simulation of 5 fingerprints for a bSSFP-type sequence

Considering microvascular parameters

To date, simple sequences (Spoil-type) have been used to estimate the relaxometry parameters T_1 and T_2 as well as the magnetic field B_1. The use of sequences sensitive to more parameters (*e.g.*, **bSSFP**-type) could enable the estimation of additional parameters such as **microvascular parameters** cerebral blood volume CBV and mean vessel radius R **without the need for contrast agent injection**.

Problems caused by considering vascular parameters CBV and R

- How to simulate associated signals?
- How to manage the size explosion of signal dictionaries?

2 · Matching *versus* Deep Learning

Once the MRI acquisition has been performed, the challenge of MR Fingerprinting is to estimate all parameter maps as accurately and as quickly as possible, which is done by various strategies.

Matching limitations

Matching reconstruction with a signal dictionary has many limitations, which become very constraining as the number of parameters to be estimated increases and make matching unsuitable for clinical applications.

- ✓ **Reliable estimation of parameters**
- ✗ **Significant reconstruction time**
- ✗ **Discretize parameter maps**
- ✗ **Storage of large dictionaries**
- ✗ **Poor scalability with the number of parameters**

Deep Learning Deep learning methods have been proposed to improve reconstructions while overcoming the limitations of matching.

- ✓ **Fast reconstruction time**
- ✓ **Continuous maps as the network interpolates parameters**
- ✓ **No dictionary storage after training**
- ✗ **Only works with a limited number of parameters**

Solutions for taking into account vascular parameters CBV and R

- Piecewise simulation of vascular signal dictionaries
  ✓ quickly generated by batch during network training
- Use of a bidirectional network structure
  ✓ adaptation to the increasing complexity of the task (both in size and variety of parameters to be estimated)

3 · Fast Simulation of Vascular Dictionaries

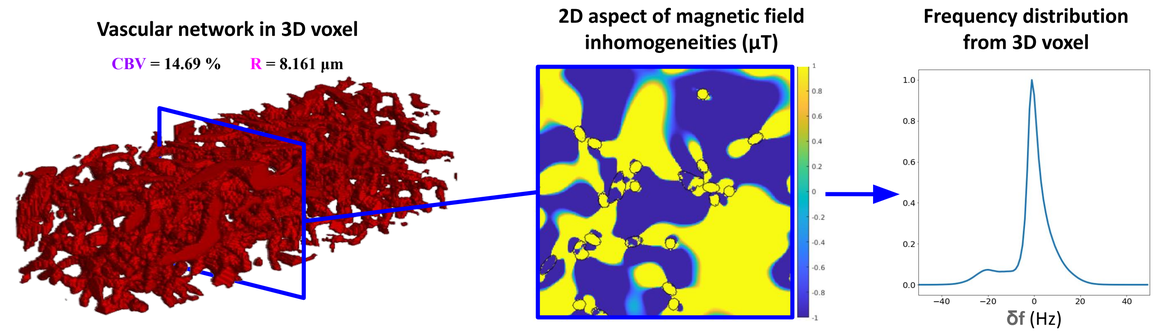

Figure 2: Simulation of an intra-voxel frequency distribution

Two-step simulation of vascular signal dictionaries:

1. A **base dictionary** is generated to store signals satisfying Bloch equations. Those signals depend on 4 parameters T_1, T_2, B_1 and δ_f.
2. **Tissue microvascular structures** induce magnetic frequency δ_f inhomogeneities at the voxel scale. Thanks to simulations of these inhomogeneities for numerous structures associated with parameters CBV and R [2], a **vascular dictionary** can be generated by convolving the base dictionary, similarly to [5].
   ✓ During a network training, the vascular dictionary could be generated by pieces in a quick way, only by storing the base dictionary.

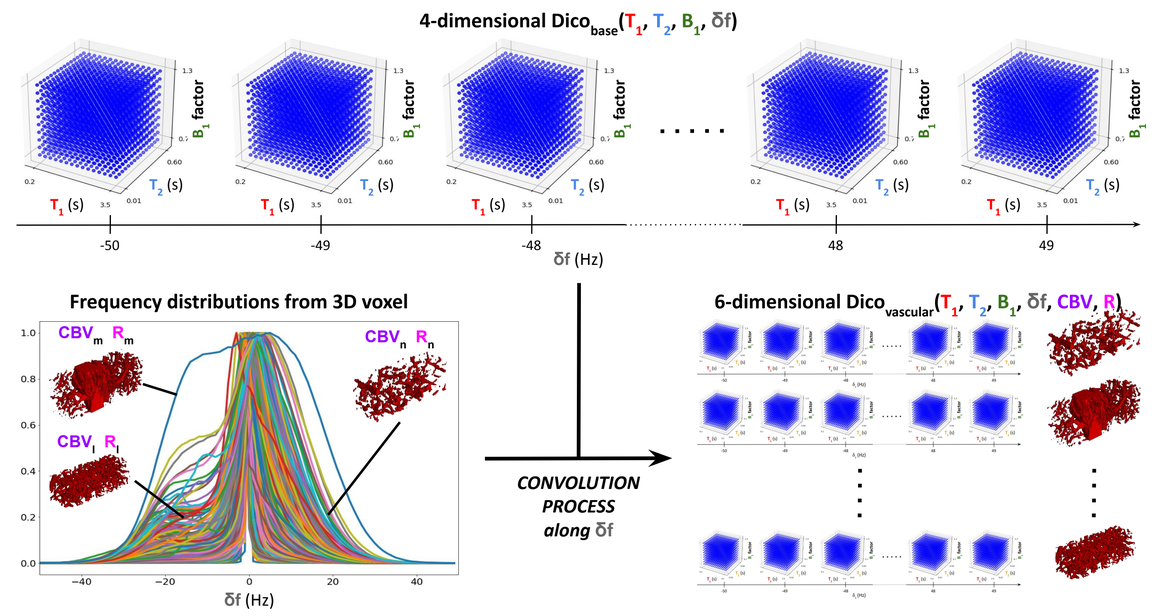

Figure 3: Creation of a vascular MRF dictionary with 6 parameters using a base dictionary with 4 parameters and frequency distributions.

4 · Use of a Neural Network with a Bidirectional Structure

The dense [1] or unidirectional recurrent [3] structures considered by previous works for reconstruction do not seem suitable for the dimensional increase of the problem.

We propose to use a **bidirectional LSTM** network (BiLSTM), which allows better retrieval of the information stored in the different parts of the signal.

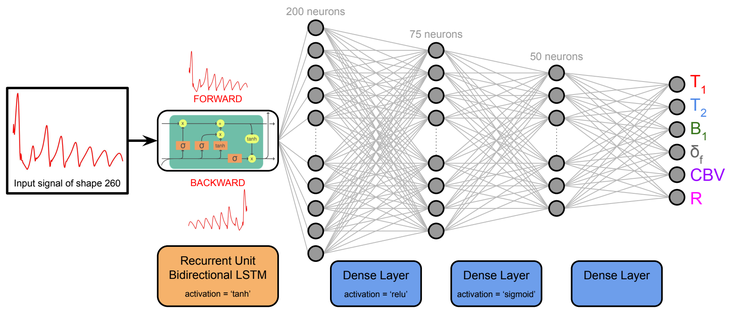

Figure 4: Structure of the bidirectional LSTM network

Training

To avoid storing large dictionaries, the network is trained from a base dictionary of 1 000 000 signals, used to batch-simulate vascular dictionaries of the same size (for each batch, each signal is convolved with one random vascular structure among 3 000). Gaussian noise at various SNR levels is then added to signals. Alltogether, with about 20 batches, around 20 000 000 signals are generated.

5 · Benefits of the Bidirectional Structure for Reconstruction

Matching

- ✓ Parameters T_1, T_2, B_1 and δ_f: good reconstruction contrasts
- ✗ Reconstruction time (> 20 min)
- ✗ Vascular parameters CBV and R: reconstruction quality limitated by the size and the storage of the dictionary ($\simeq$ 7 000 000 signals: 43 000 base signals $\times$ 300 vascular structures)

Unidirectional LSTM networks

- ✓ Great reconstruction with a weak number of parameters
- ✗ Inefficient networks when the number of parameters increases

Bidirectional LSTM networks

- ✓ Reconstruction time ($\simeq 3.5$ s)
- ✓ Map reconstruction in lines with matching for parameters T_1, T_2, B_1 and δ_f
- ✓ Map contrasts of CBV and R
- ✓ Observed values in different brain areas in lines with literature

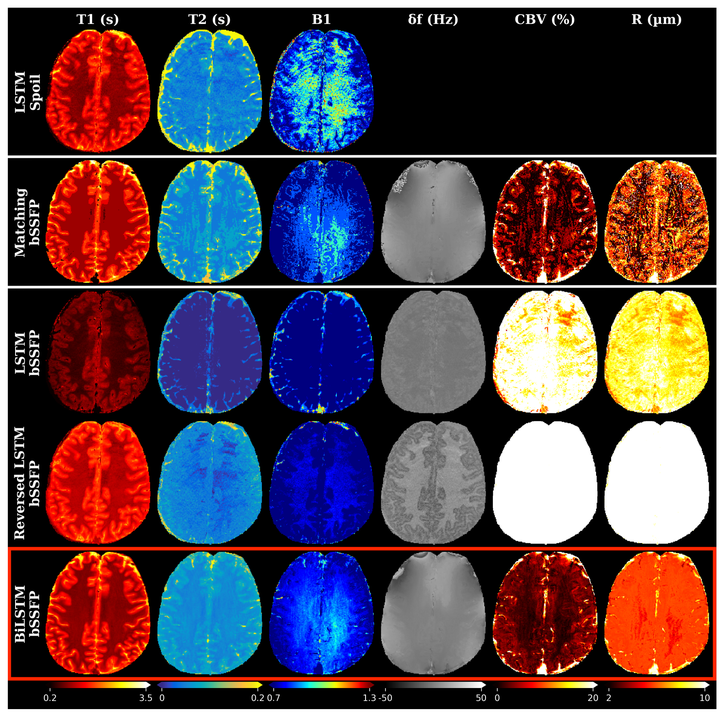

Figure 5: Reconstructed parameter maps of a healthy volunteer obtained by matching and various neural networks from Cartesian acquisitions

Table 1: Mean and standard deviation of parameter values reconstructed in white matter (WM), grey matter (GM) and sagittal sinus (SS)

Parameter	Tissue	LSTM	Rev. LSTM	BiLSTM	Matching	Literature
T_1 (ms)	WM	538 ± 121	1119 ± 177	$\mathbf{823 \pm 55}$	931 ± 46	$\sim 690 - 1100$
	GM	674 ± 202	1440 ± 261	$\mathbf{1320 \pm 339}$	1381 ± 380	$\sim 1286 - 1393$
T_2 (ms)	WM	0.5 ± 6	37 ± 15	$\mathbf{54 \pm 5}$	50 ± 13	$\sim 56 - 80$
	GM	8 ± 22	53 ± 21	69 ± 21	$\mathbf{80 \pm 70}$	$\sim 78 - 117$
CBV (%)	WM	19.8 ± 4.5	40.0 ± 0.4	$\mathbf{2.0 \pm 0.9}$	2.0 ± 5.0	$\sim 1.7 - 3.6$
	GM	22.2 ± 5.3	39.8 ± 1.2	$\mathbf{3.9 \pm 3.4}$	1.49 ± 1.9	$\sim 3 - 8$
	SS	19.5 ± 8.5	37.3 ± 4.2	21.2 ± 7.3	28.2 ± 8.8	
R (µm)	WM	8.2 ± 0.8	10.0 ± 0.0	$\mathbf{5.6 \pm 0.3}$	4.2 ± 2.3	6.8 ± 0.3
	GM	8.5 ± 0.9	10.0 ± 0.0	$\mathbf{5.8 \pm 0.5}$	5.4 ± 2.2	7.3 ± 0.3
	SS	7.8 ± 1.3	10.0 ± 0.2	8.8 ± 1.5	10.1 ± 2.2	

Best values compared to literature are in **orange**.

6 · Undersampled Reconstruction

Reconstructing **undersampled spiral acquisitions** shows the robustness to various noise levels and acquisition types. Subsampling significantly reduces examination time.

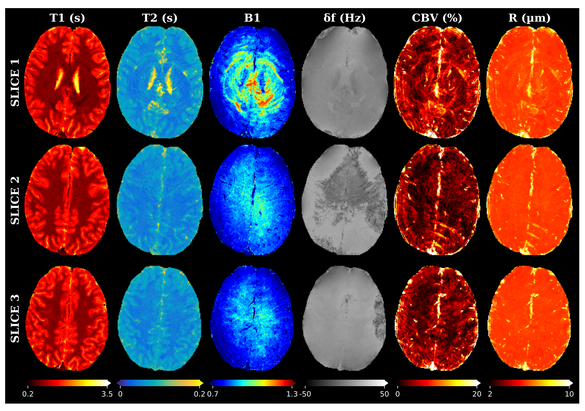

Figure 6: Reconstructed parameter maps of a healthy volunteer obtained with our bidirectional LSTM from a bSSFP spiral acquisition

7 · Conclusion & Limitations

Conclusions of our study

- ✓ **Quick** analysis of MRF data containing **multiple dimensions** including microvascular properties, using a **BiLSTM network** trained with fast and realistic simulations
- ✓ Encouraging results on healthy volunteers, with nice WM/GM contrast for CBV maps

Future work

- Conduct further (quantitative) analyses and comparisons with reference methods in **patients** to validate the whole approach
- Improve sequence sensitivity to vascular parameters using automatic procedures in order to improve the network reconstruction (avoiding smoothness effects)
- Improve signal simulations using more realistic frequency distributions and adding other sources of magnetic susceptibility to our model (such as myelin fiber)

References

1. Cohen *et al.* in Magnetic Resonance in Medicine (2018)
2. Delphin *et al.* in ISMRM & ISMRT Annual Meeting & Exhibition (2023)
3. Hoppe *et al.* in International Conference on Medical Image Computing and Computer-Assisted Intervention (2019)
4. Ma *et al.* in Nature (2013)
5. Wang *et al.* in Magnetic Resonance in Medicine (2019)