

# An automated tool for fast quality analysis of animal MRI

Aref Kalantari<sup>1</sup>, Markus Aswendt<sup>1</sup>

<sup>1</sup> University of Cologne, Faculty of Medicine and University Hospital Cologne, Department of Neurology, Cologne, Germany

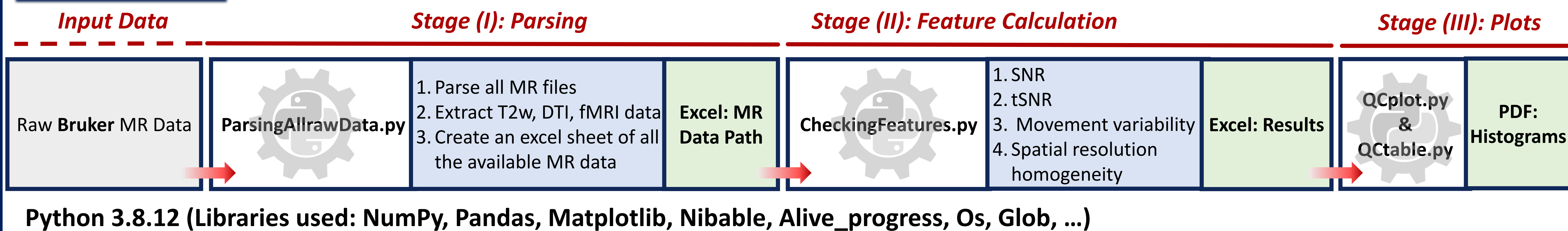
## Objectives

Which dataset is of sufficient quality for further processing?

- **Standardization** of image quality in preclinical, animal MR imaging.
- **Categorization** of good vs. bad quality datasets

## Structure

How is this pipeline structured?

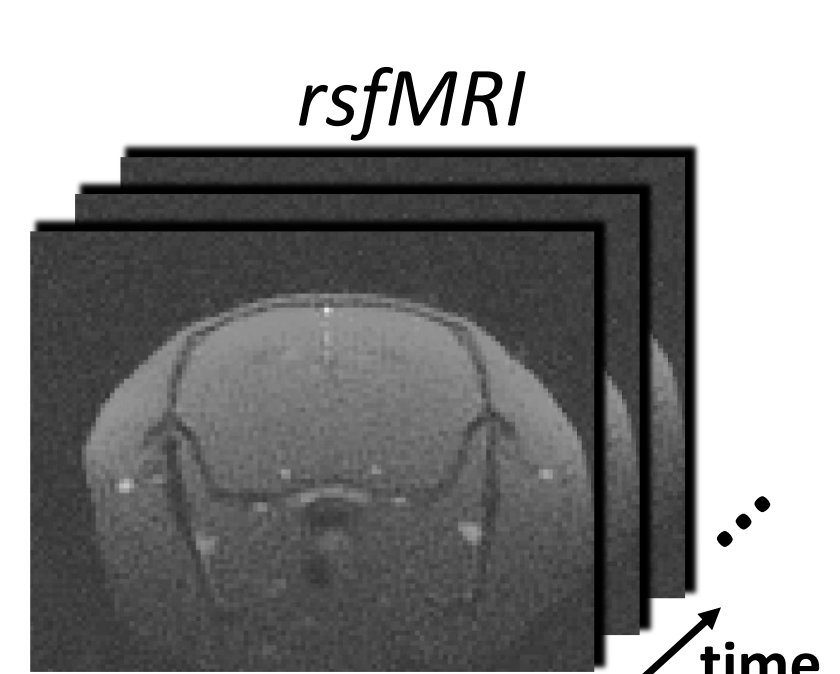


## Methods

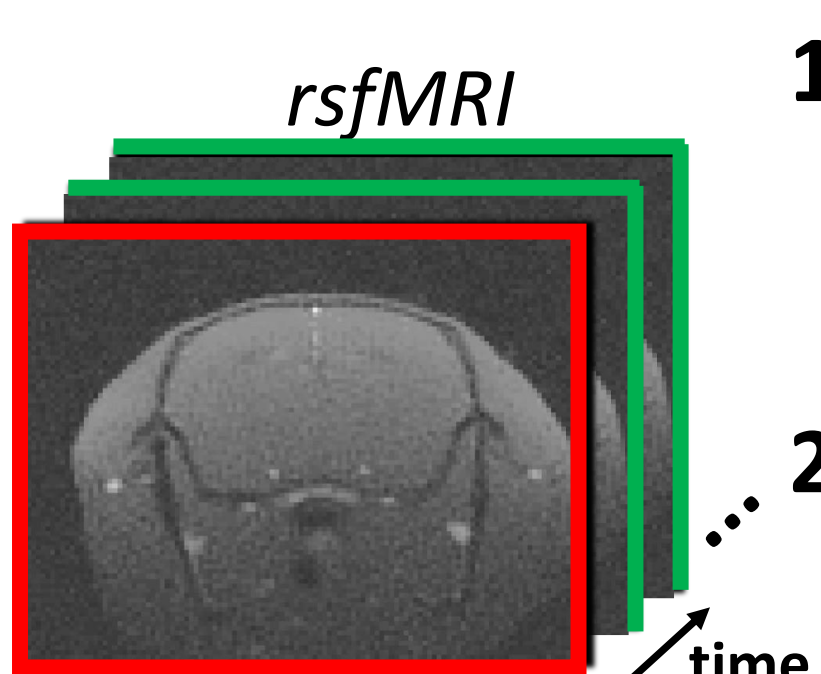
**SNR**: Chang Method (Fully automated approach without the need to define regions of interest)

$$tSNR = \frac{\mu_{SNR}}{\sigma_{SNR}} = \frac{\mu}{\sqrt{\frac{1}{N} \sum_{i=1}^N (I_i - \mu)^2}}$$

### SNR & tSNR



### Movement Severity



1. **Mutual information** between  $I(t_0)$  and  $I(t_0+t)$  for  $t = 1, \dots, t_N$  resulting in  $N$  values or a mutual information vector.
2. **Standard deviation** of the mutual information series is the metric of **movement severity**

### Categorization in good vs. bad quality

Based on the definition of **outliers** via **IQR rule**:

- Lower than  $Q1 - 1.5 \times IQ$
- Higher than  $Q3 + 1.5 \times IQ$

## Results

Exemplary use cases of the pipeline

**Dataset A:** 2.300 total scans with 900 scans of T2w, DTI and rsfMRI

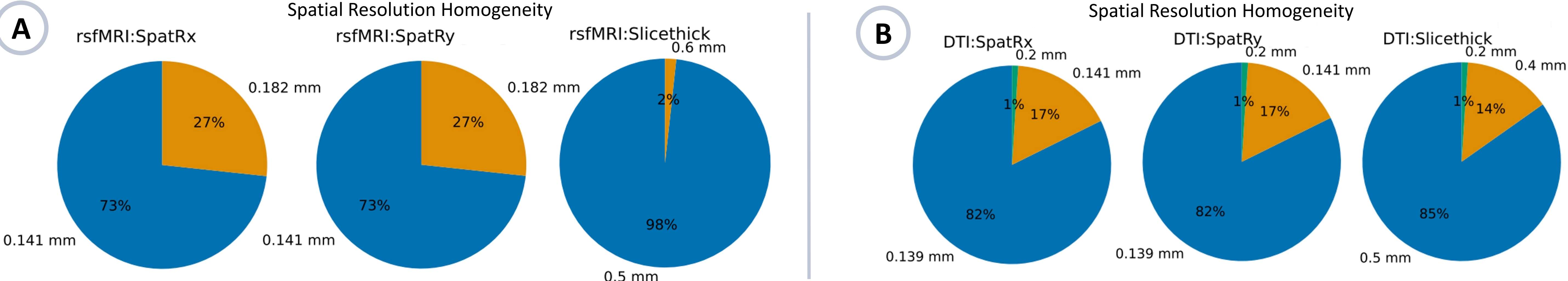
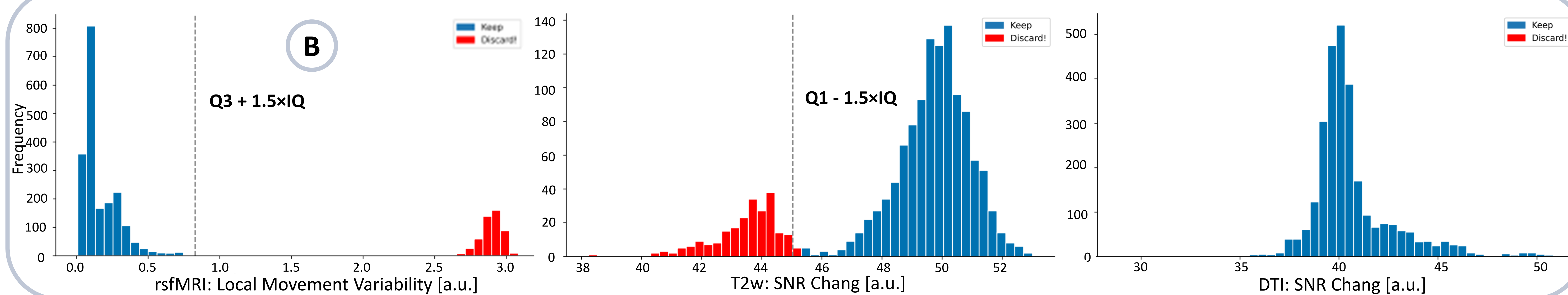
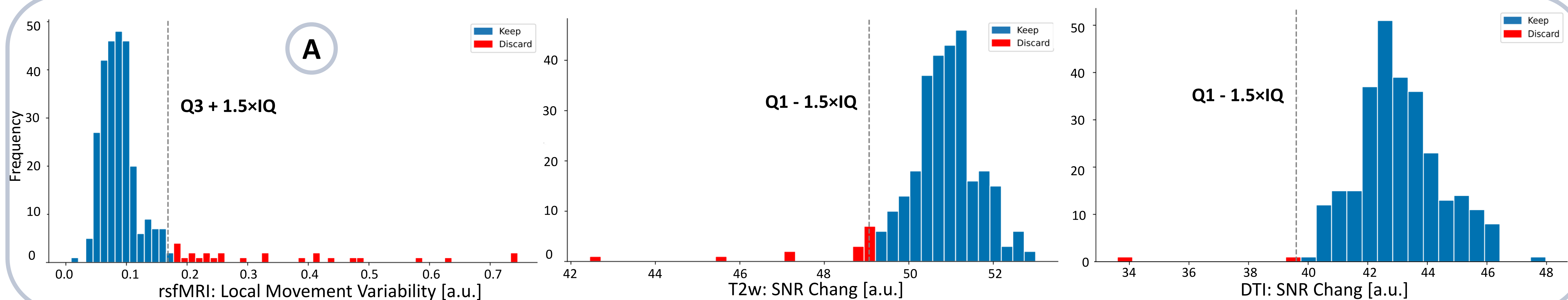
**Study:** Pallast et al., 2020

**Facts:** 10 hours of quality feature calculation, Average of 40 seconds per scan

**Dataset B:** 7.000 total scans with 4.500 scans of T2w, DTI and rsfMRI

**Study:** Complete data storage from our lab

**Facts:** 14 hours of quality feature calculation, Average of 11 seconds per scan



## Outlook

What are some ideas for the future?

- 1) Increasing sequence variety in addition to T2w, DTI, fMRI sequences
- 2) Further improving calculation speed via implementing parallel computing
- 3) Creating compatibility with Bruker's ParaVision software to directly compare quality features of new data with the main data storage

- The pipeline is available on GitHub under: <https://github.com/aswendt/AIDAqc>
- Necessary information on how to install the pipeline is available in addition to some examples and a test dataset



1. Chang et al. " Medical Imaging 2005: Image Processing. Vol. 5747. SPIE, 2005.
2. Maes et al. Proceedings of the IEEE 91.10 (2003): 1699-1722.
4. Pallast N et al. Front Neuroinform. 2019;13: 42.

Aref Kalantari  
Aref.kalantari-sarcheshmeh@uk-koeln.de