FETMRQC: AUTOMATED QUALITY CONTROL FOR FETAL BRAIN MRI

Thomas Sanchez, Oscar Esteban , Yvan Gomez , Elisenda Eixarch , and Meritxell Bach Cuadra

PROBLEMATIC

- Fetal Brain MRI quality control is hard to automate:
 - Most automated QC have invalid prior (Adult brain)
 - Quality standard is different from adult brain MRI (ex: fetal motion)
- Fetal Brain Imaging often use on SSR
 - Construct 3D isotropic, high resolution, volumes with differently oriented 2D stacks
 - Rely on manual selection of stack
- => This study propose a QC tool on 2D low resolution stacks

DATA

- T2w stacks from 146 subjects
- 2 databases from 2 different institutions
 - CHUV:61 subjects
 - BCNatal: 85 subjects
- 1010 LR series
- Two raters, 100 stacks in common.
 - Score between I and 4 for regression task
 - Pass/Fail label for classification

FEATURE EXTRACTION

Selected relevant IQM from MRIQC and implemented specific IQMs

Ex:

- mask volume, mask centroid
- Deep learning base score from other paper: dl_slice_iqa and dl_stack_iqa
- Propose new feature

Table 3. Detailed description of the metrics proposed for FetMRQC.

Intensity-based metrics						
slice_loss	Use metrics commonly used for outlier rejection [13,14,18] to compute the difference between slices in the volume. We consider (normalized) mean averaged error, (normalized) mutual information, normalized cross correlation, (normalized) root mean squared error, peak signal-to-noise ration, structural similarity and joint entropy					
sstats [8]	Compute the mean, median, standard deviation, percentiles 5% and 95%, coefficient of variation and kurtosis on brain ROI					
entropy [8]	Measure the overall entropy of the image					
bias	Level of bias estimated using N4 bias field correction [28]					
$filter_image$	Estimate the sharpness by using Laplace and Sobel filters (commonly used for edge detection)					
SHAPED-BASED	SHAPED-BASED METRICS					
closing_mask	Morphological closing of the brain mask in the through-plane direction, to detect inter-slice motion. Report the average difference with the original mask					
filter_mask	Estimate the sharpness of the brain mask using Laplace and Sobel filtering. In an ideal case, the brain mask would be smoothly varying, especially in the through-plane direction					

MODEL

- 2 Model for 2 tasks: classification and regression
- 3 variants:
 - Individual feature (best performing one is dl_stack_iqa)
 - Base: use a subset of feature (rank error, rank error full mask volume, centroid, centroid full, dl slice iqa and dl stack iqa)
 - FetMRQC : use every feature (including the one proposed)
- 2 Training setting:
 - in-domain for generalization on new subjects
 - out-of-domain for generalization on new sites

MODEL

Table 6. Selected hyperparameters for the different nested cross validation procedures. The in-domain experiment uses 5-fold nested cross-validation, while the out-of-domain experiment splits data by site (CHUV and BCNatal) and as a result has only two folds. The list of possible parameters is provided in Table 5.

In-domain –	omain – Regression				In-domain – Classification						
	Remove feat.	Scaling	Winnow	PCA	Model		Remove feat.	Scaling	Winnow	PCA	Model
Base	x	Standard	1	1	Random Forest	Base	0.8	Robust	1	1	Random Forest
	0.9	Standard	1	X	Random Forest		x	None	✓	1	Random Forest
	0.8	Standard	1	X	Random Forest		x	${\bf Standard}$	✓	X	Random Forest
	0.8	Standard	/	X	Gradient Boosting		0.8	${\bf Standard}$	✓	X	Random Forest
	0.8	Standard	✓	X	Random Forest		X	${\bf Standard}$	✓	X	Random Forest
FETMRQC	×	Robust	/	1	Random Forest	FETMRQC	X	Standard	/	1	Gradient Boosting
	x	Robust	/	/	Gradient Boosting		0.9	Robust	✓	1	Random Forest
	0.8	None	/	X	Random Forest		0.8	Robust	✓	X	Gradient Boosting
	0.9	Robust	1	X	Gradient Boosting		0.9	${\bf Standard}$	✓	1	Lin. Regression
	x	None	/	X	Random Forest		x	${\bf Standard}$	✓	X	Gradient Boosting
Out-of-doma	Out-of-domain - Regression					Out-of-domain - Classification					
	Remove feat.	Scaling	Winnow	PCA	Model		Remove feat.	Scaling	Winnow	PCA	Model
Base	0.9	Robust	1	X	Gradient Boosting	Base	0.8	Standard	✓	X	Random Forest
	x	None	/	1	Random Forest		0.8	${\bf Standard}$	✓	1	Random Forest
FeTMRQC	0.9	None	1	1	Lin. Regression	FETMRQC	0.9	Standard	✓	X	Random Forest
	x	Robust	1	X	Random Forest		0.8	Standard	/	X	Random Forest

Table 1. In-domain evaluation

	Regression		Classification			
	MAE (↓)	Spearman (†)	F1 (†)	AUC (↑)		
dl_stack_iqa	0.72 ± 0.05	0.37 ± 0.11	0.85 ± 0.02	0.53 ± 0.02		
Base	0.58 ± 0.05	0.60 ± 0.03	0.88 ± 0.02	0.71 ± 0.06		
FetMRQC	$\boldsymbol{0.53 \pm 0.09}$	$\textbf{0.71} \pm \textbf{0.05}$	$\boldsymbol{0.90 \pm 0.02}$	$\textbf{0.77} \pm \textbf{0.07}$		

Table 2. Out of domain evaluation

	Regression		Classification			
	MAE (↓)	Spearman (†)	F1 (†)	AUC (†)		
dl_stack_iqa	0.75 ± 0.03	0.42 ± 0.10	0.83 ± 0.04	0.57 ± 0.07		
Base	0.75 ± 0.01	0.38 ± 0.03	0.85 ± 0.02	0.67 ± 0.06		
FetMRQC	0.68 ± 0.06	0.50 ± 0.08	$\boldsymbol{0.89 \pm 0.01}$	$\boldsymbol{0.77 \pm 0.05}$		

RESULTS

IMPACT ON SRR

 NiftyMIC and NeSVoR are two super resolution reconstruction techniques

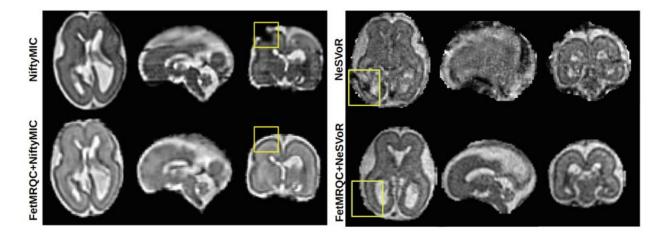


Fig. 7. Illustration of usefulness of QC on the SR reconstruction, using NiftyMIC [18], and NeSVoR [17]. FetMRQC+NiftyMIC successfully removes 6 series out of the 13 available, and FetMRQC+NeSVoR removes 2 out of 5. FetMRQC leads to a substantially greater image quality.

CONCLUSION

- The paper claim that :
 - QA and QC for T2w fetal brain MRI can be automated
 - Classical machine learning help to have interpretable decision and good generalization
- Issue :
 - No specific "winning" architecture mentioned
 - Deep Learning based feature seems to really important, even more for classification, in which measure are they interpretable.