Correction of Fat-Water Swaps in Dixon MRI

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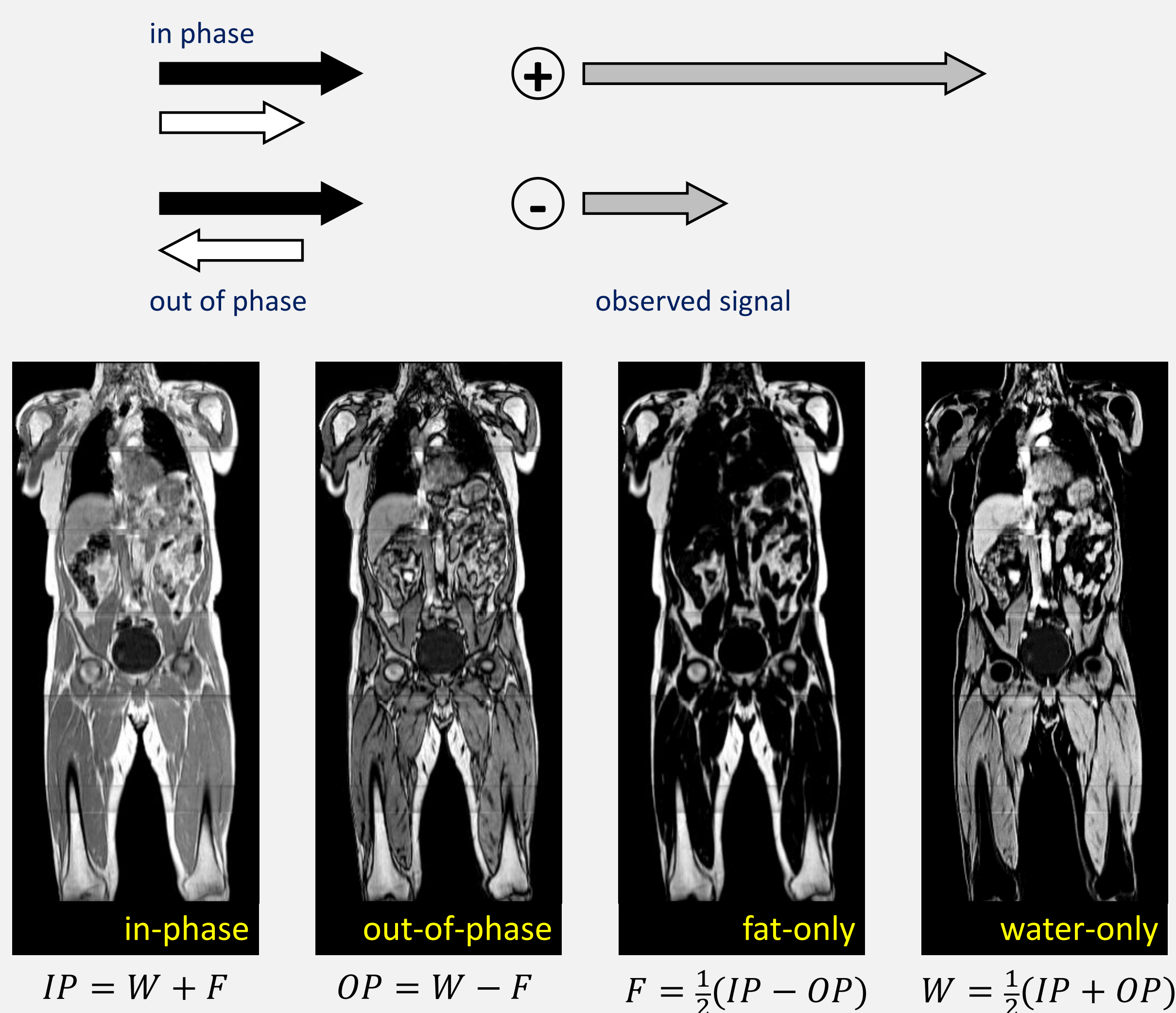
BioMedIA

Fat-Water Imaging

Separation of fat important in diagnostic imaging

- Fat signal obscures patterns of oedema, inflammation, and tumours
- Fat signal can highlight pathologies, e.g., fatty tumours
- Enables quantification of the amount of visceral adipose tissue

Chemical shift based fat-water separation

- Commonly known as **Dixon** fat-water separation
- Two images acquired at different echo times

in phase / out of phase / observed signal

in-phase   out-of-phase   fat-only   water-only

$IP = W + F$ $OP = W - F$ $F = \frac{1}{2}(IP - OP)$ $W = \frac{1}{2}(IP + OP)$
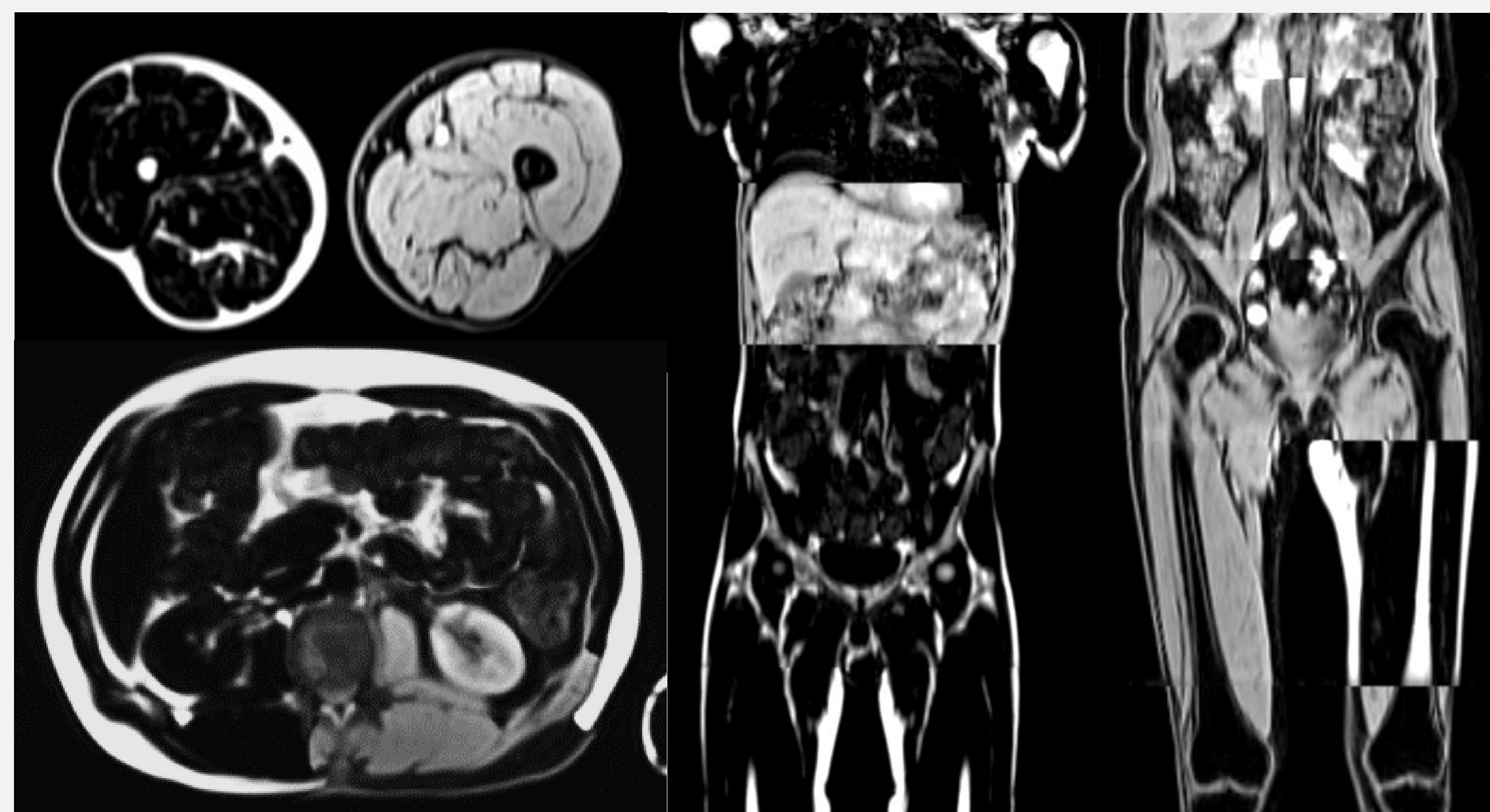
Fat-Water Swaps

Tissue inversion is well known in Dixon MRI

- Inherent to all Dixon fat-water separation methods
- Natural ambiguity in phase encoding
  a voxel containing only water 'looks' like fat that is off-resonance by -210 Hz (+210 Hz) at 1.5T
- Optimization methods such as IDEAL can converge to wrong substance

Relevance

- 5-10% of Dixon MRIs contain some sort of fat-water swap; leading to
- Errors in radiological reading
- Incorrect quantification, e.g., in body fat measurements
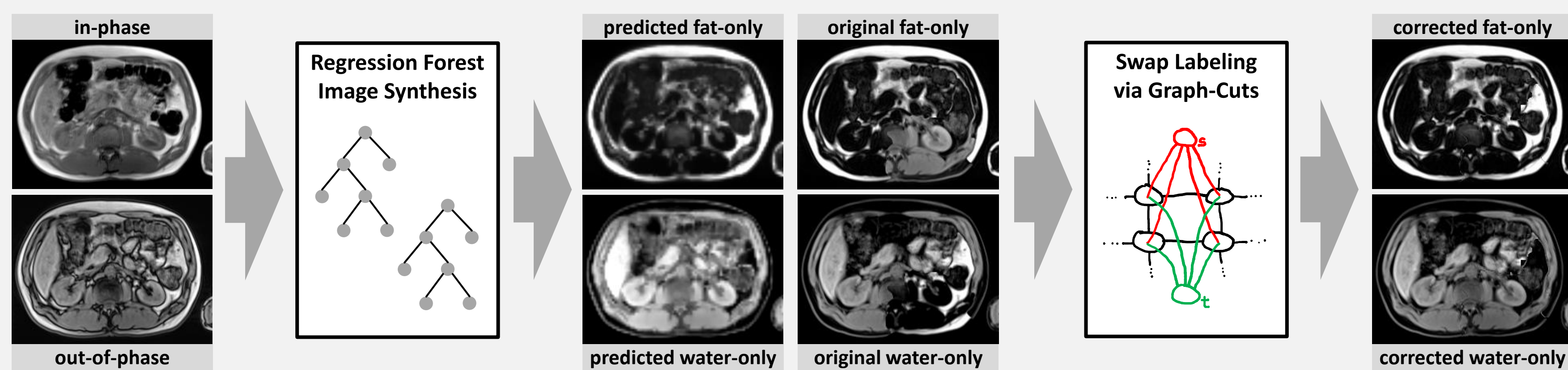- Invalid attenuation correction for PET/MR

Examples

Our Solution: Dixon-Fix

First method for 'repairing' fat-water images retrospectively

STEP 1: Predicting swap-free fat-water images from in- and out-of-phase images

STEP 2: Computing globally optimal swap labelling using graph cuts

in-phase / out-of-phase → Regression Forest Image Synthesis → predicted fat-only / original fat-only / predicted water-only / original water-only → Swap Labeling via Graph-Cuts → corrected fat-only / corrected water-only

original fat-only / original water-only / swap labeling / corrected fat-only / corrected water-only
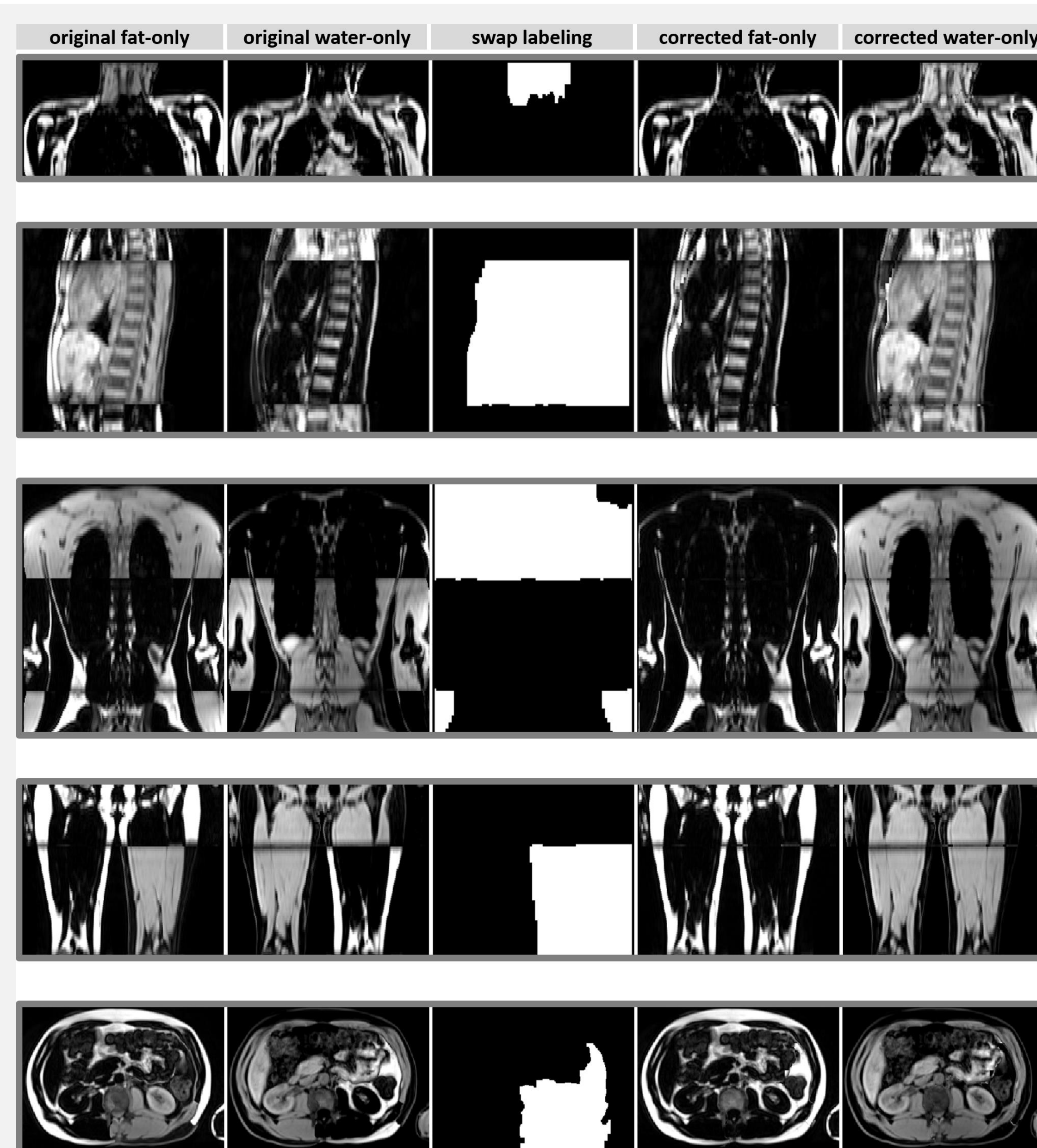
Experimental Evaluation

- 46 subjects with whole-body Dixon MRI
- 10 subjects show various types of fat-water swaps
- 23 swap-free subjects used for training the regression forest

Results

- Fat-water swaps in all 10 subjects were successfully corrected
- In all 13 swap-free images some voxels were incorrectly swapped

Runtime

- Step 1 of image synthesis takes about 10 minutes
- Step 2 of multi-resolution graph-cuts takes about 5 seconds

Limitations

False-positives
- The current approach cannot be used to identify swap-free scans
- Incorporation of more sophisticated priors could help

No quantitative evaluation (yet)
- Synthetic experiments possible, but may be unrealistic
- Manual swap annotations required, but tedious to obtain

Source code available

http://biomedia.doc.ic.ac.uk/software/dixonfix/

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NHS National Institute for Health Research

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