

## Computational MR imaging

### Laboratory 6: k-space parallel imaging

Report is due on Wednesday the week after the lab session at 23:59. Send your report by email to Bruno Riemenschneider (bruno.riemenschneider@fau.de) and Florian Knoll (florian.knoll@fau.de).

#### Learning objectives

- Reconstruct regularly undersampled data using the GRAPPA algorithm
1. Simple GRAPPA reconstruction: The Matlab and Python functions `grappaR2K2x3` (in the lab folder) implement a GRAPPA reconstruction using a  $2 \times 3$  kernel for accelerated data acquired with  $R_y=2$ . Load the `8coil.mat` data set from the previous lab, simulate  $R_y=2$  and reconstruct the undersampled data using the simple GRAPPA code using the central 24 lines as autocalibration data
  2. Modify the GRAPPA reconstruction algorithm from function `grappaR2K2x3` to replace the  $2 \times 3$  kernel by a  $4 \times 3$  kernel and to reconstruct 2D data with arbitrary acceleration factor along the phase-encoding dimension ( $R_y$ ).

```
function krecon=grappa4x3(kdata,acs,R,flag_acs)
% R: acceleration factor
```

Reconstruct the 8-coil data with simulated  $R = 2, 3$ , and  $4$ , compute the RMSE with respect to the fully-sampled matched-filter combination. For each acceleration factor, plot the reconstructed image and error image. Comment on the image quality with these results and how they compare to your SENSE results from lab 4.

Note: There is a small inconsistency in the GRAPPA functions in comparison to the SENSE example from lab 4. They treat the column (y) dimension as the undersampled phase encoding dimension. In lab 4, we treated the row (x) dimension as the undersampled dimension. In order to keep the results consistent between the labs, please take the transpose of the data before doing the reconstruction, and then again when plotting the image.