

## $k - t$ SLR: MATLAB CODE PACKAGE

### 1. DESCRIPTION OF THE FILES

- **aperiodic\_pincat.mat**: A 2D cross section of the physiologically improved non uniform cardiac torso phantom (PINCAT) [Behzad et al., 07]. The phantom is modified to include realistic perfusion dynamics and non-periodic respiratory motion. The dimensions of the data are  $N_x \times N_y \times t : 128 \times 128 \times 50$ .
- **invivo\_perfusion.mat**: A 2D myocardial perfusion MRI data set acquired using a saturation recovery FLASH sequence with Cartesian sampling. The dimensions of the data are phase encodes  $\times$  frequency encodes  $\times$  time:  $90 \times 190 \times 70$ . The data has significant motion content due to inconsistent gating and/or breathing motion. The data is obtained at the University of Utah, courtesy of Dr. Edward DiBella.
- **A\_fhp3D.m**: The forward Fourier sampling operator.
- **At\_fhp3D.m**: The backward Fourier sampling operator.
- **defDDt.m**: The forward and backward gradient operators.
- **strucrand.m**: Function to generate the  $(k_x, k_y) - t$  radial sampling pattern. The sampling pattern has uniformly spaced radial rays within each frame and small random rotations across frames. The random rotations are essential to achieve incoherent sampling.
- **minSNandTV.m**: This function is the crux of the k-t SLR algorithm. This minimizes the spectrally regularized cost (containing the Schatten p-norm and the TV norms) by iterating between (a) shrinkage of singular values, (b) multi-dimensional total variation shrinkage, (c) conjugate gradient update of the reconstruction and (d) update rules for the Lagrange multipliers.
- **givefastSVD.m**: Function to perform a fast singular value decomposition of a large thin matrix.
- **CG\_solver.m**: A standard conjugate gradient solver.
- **main\_pincat.m**: Main file to be run for the PINCAT data.
- **main\_perf\_invivo.m**: Main file to be run for the in-vivo data.

## 2. USING THE CODES

- Run the **main\_perf\_invivo.m** and/or **main\_pincat.m** files to use k-t SLR for respectively reconstructing the PINCAT and the in-vivo data.
- The different parameters for the k-t SLR algorithm are defined in the **opts** variable in the **main...m** files.
- It is crucial to tune the regularization parameters appropriately to get the best results. The parameters in **opts.mu1** and **opts.mu2** are optimized for the best performance for the two data sets included here.
- The continuation parameters in **opts.beta1** and **opts.beta2** can be randomly set to very low values. The idea is to start with very low values and gradually increment it until convergence. This continuation strategy is crucial when using the non-convex Schatten p-norm to avoid local minimum solutions.