

This paper describes a realistic cardiac MR perfusion simulator; both the kinematic model of the perfusion process as well as breathing effects are described and a novel model for the AIF is proposed. Additionally the most common degradation factors involved in the MR image formation, such as those derived from parallel acquisition protocols, the presence of thermal noise and its correlation, the partial volume effect, the field inhomogeneity and the image saturation, are also incorporated into the simulation. Resulting images show a strong resemblance with natural images and perfusion curves obtained seem parallel to those that could be observed in a real setting.

## Perfusion model

We assume the following differential equation for perfusion:

$$\frac{dc(t)}{dt} = K_T c_a(t) - K_e c(t) \Rightarrow c(t) = c_a(t) * r(t) \quad (1)$$

where  $c_a(t)$  is the concentration of Gadolinium in the blood (the so-called AIF),  $c(t)$  is the concentration of Gadolinium in the tissue, and  $K_T$  and  $K_e$  are constants, the values of which depend on the tissue itself.  $r(t)$  is the impulse response of the tissue:

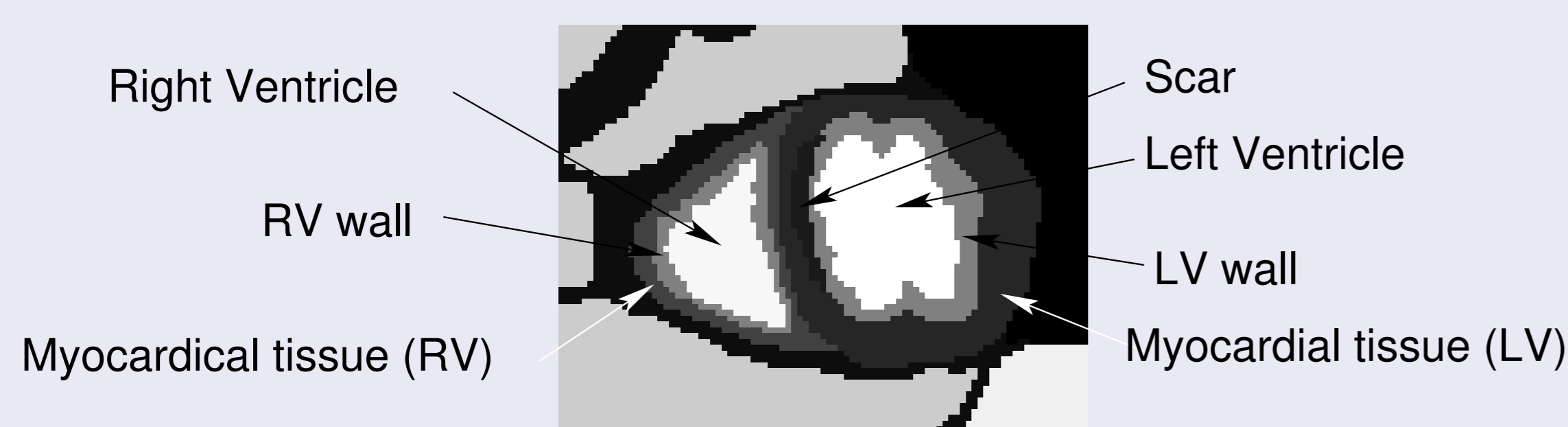
$$r(t) = K_T e^{-K_e t} u(t).$$

For the sake of an underlying continuous model, the AIF has been modeled as a Gamma distribution

$$c_a(t) = M_1 \cdot \frac{t^{a-1} e^{-t/b}}{\Gamma(a)b^a} u(t) \Rightarrow c(t) = M_1 \cdot r(t) \cdot \frac{\gamma_i(a, t(\frac{1}{b} - K_e))}{(1 - K_e \cdot b)^a} \quad (2)$$

with  $M_1$  a normalization constant and  $a$  and  $b$  the shape and amplitude parameters. More involved models may be used, such as a linear combination of Normal or Gamma distributions. The concentration of blood and tissue in each point will be given by the discrete sampling of the continuous values, i.e.  $c_a(n\Delta t)$ ,  $c(n\Delta t)$ .

## Areas of interest



As a seed point, a segmented cardiac image from a real acquisition is considered. The main areas considered are the left and right ventricles, where the wall and the tissues are differentiated. A scar is also defined in the myocardial tissue. This initial image can be changed if needed.

To further simulate the perfusion, each tissue is assigned a different initial gray level, taken the average values found in these kind of sequences: assuming a dynamic range between [0-255], the myocardial tissue is initially set to 32, blood to 240 and air to 0.

## Simulation Example

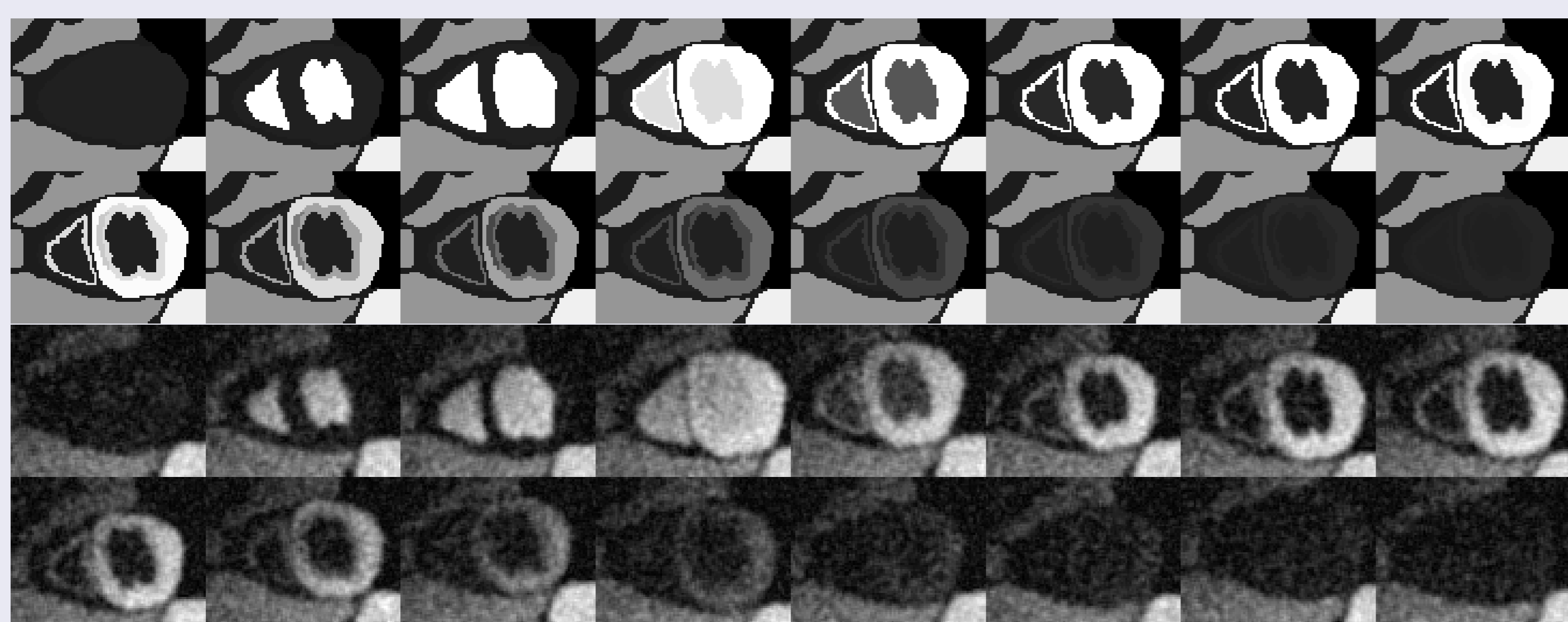


Figure: Simulation of the perfusion with MR acquisition.  $N = 16$ ,  $\Delta t = 2.5$  sec.,  $K_T = 0.8$  (tissue),  $K_T = 0.5$  (scar),  $K_e = 0.3$  (tissue),  $K_e = 0.4$  (scar). Top: No degradation of the image. Bottom: MR simulation, single coil acquisition, Rician noise ( $\sigma_n = 15$ ), PVE, spatial correlation, inhomogeneous field and respiration movement.

## Acknowledgements

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## Simulation of the MR acquisition

**Perfusion in the tissue:**  $K_T$  and  $K_e$  for each area. Only right and left ventricles, blood and scar affected by perfusion. Total number of scans  $N_t$  and the sampling time  $\Delta t$ . The concentration of Gadolinium in each point of the image is calculated using eq (2).

**Perfusion sequence scans:** From the concentration the T1 maps are created

$$\frac{1}{T_1} = \frac{1}{T_{10}} + c_n \cdot r_1 \quad (3)$$

with  $T_{10}$  the  $T_1$  value before the contrast injection and  $r_1$  a relaxivity parameter; then the signal images are obtained assuming the following model

$$I_n(\mathbf{x}) = M_0 \left( 1 - e^{-\frac{T_R}{T_1(\mathbf{x})}} \right), \quad n = 0, \dots, N. \quad (4)$$

**Acquisition coils:** Single coil or multiple coil heads option. Single coil: Rician-distributed. Multiple coil: a simulated sensitivity map is defined for each coil. Reconstruction is done using Sum of Squares. Covariance matrix defined for coils (correlation assumed).

**Parallel imaging:** When multiple coils, SENSE and GRAPPA are available for simulation.

**Spatially correlated noise:** The noise added in the single and multiple coil simulation can also be spatially correlated.

**Partial Volume Effect (PVE):** Due to the resolution in MR scans, there are voxels in which different tissues are mixed up. Simulated by a convolution with a Gaussian kernel.

**Breathing movement:** One of the main problems when analyzing heart MR data is the mismatch of the different images due to the breathing movement (as well as the heart movement itself). Simulated by a random affine transformation.

**Field inhomogeneity:** Image is multiplied by a non uniform illumination  $F(\mathbf{x})$ .

**Saturation:** Some acquisition schemes saturate the signal in the image. Image cropped using a maximum;  $M_n^s(\mathbf{x}) = \min \{M_n(\mathbf{x}), S_{\max}\}$ .

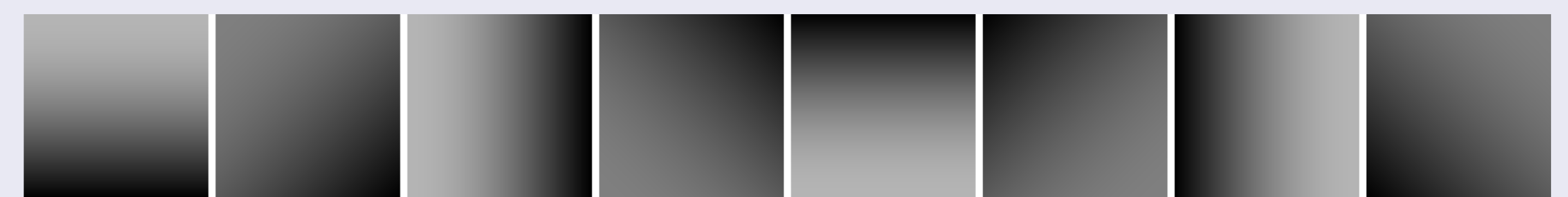


Figure: Synthetic sensitivity map for an 8-coil system.

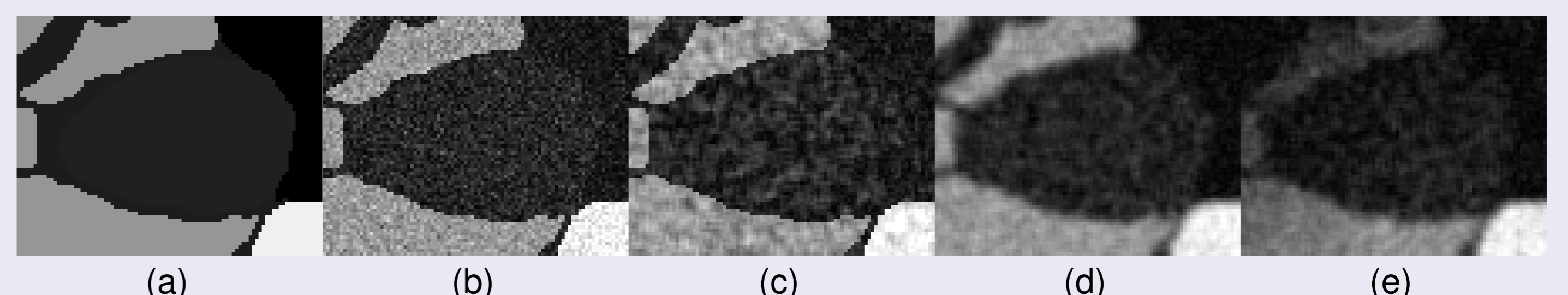


Figure: Noise corruption for a single coil acquisition. (a) Original synthetic image. (b) Rician noise,  $\sigma_n = 20$ . (c) Rician noise spatially correlated,  $\sigma_n = 20$ . (d) Rician noise spatially correlated ( $\sigma_n = 10$ ) and PVE ( $\sigma_g = 1.5$ ). (e) Rician noise spatially correlated ( $\sigma_n = 10$ ), PVE ( $\sigma_g = 1.5$ ) and an inhomogeneous field.

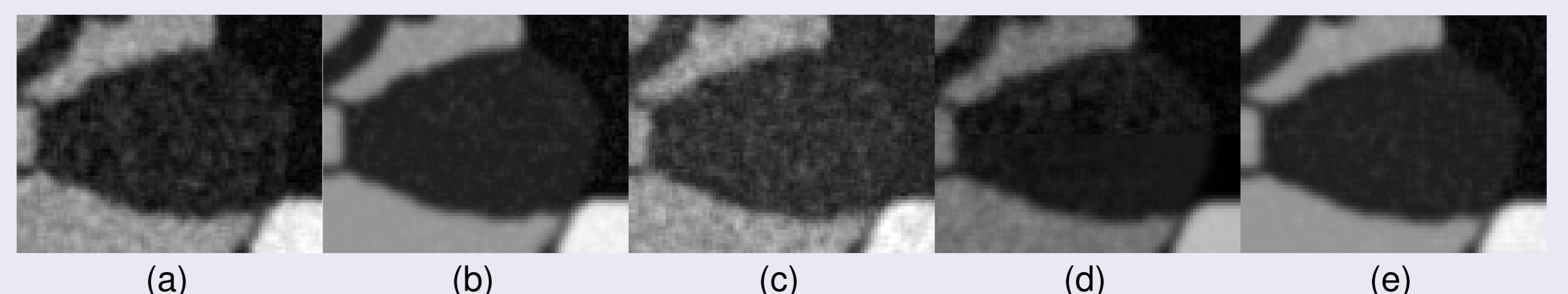


Figure: Multiple coil acquisition (spatially correlated, PVE and  $\sigma_n = 10$  in each coil). (a) Single coil acquisition. (b) 8-coil, no correlation between coils. (c) 8-coil, coefficient of correlation between coils  $\rho^2 = 0.1$ . (d) 8-coil,  $\rho^2 = 0.1$ , 2x subsampling and SENSE. (e) 8-coil,  $\rho^2 = 0.1$ , 2x subsampling and GRAPPA.

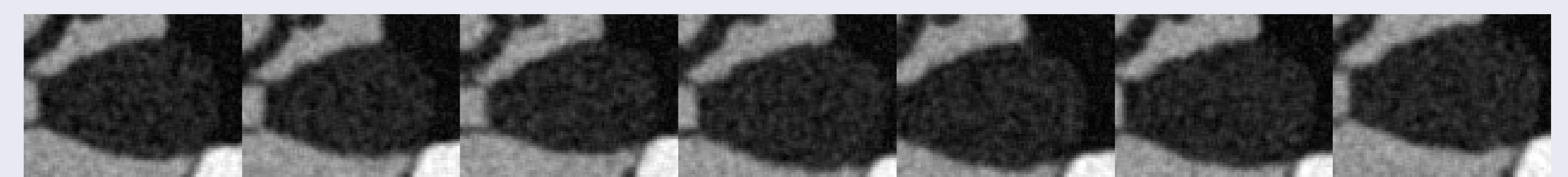
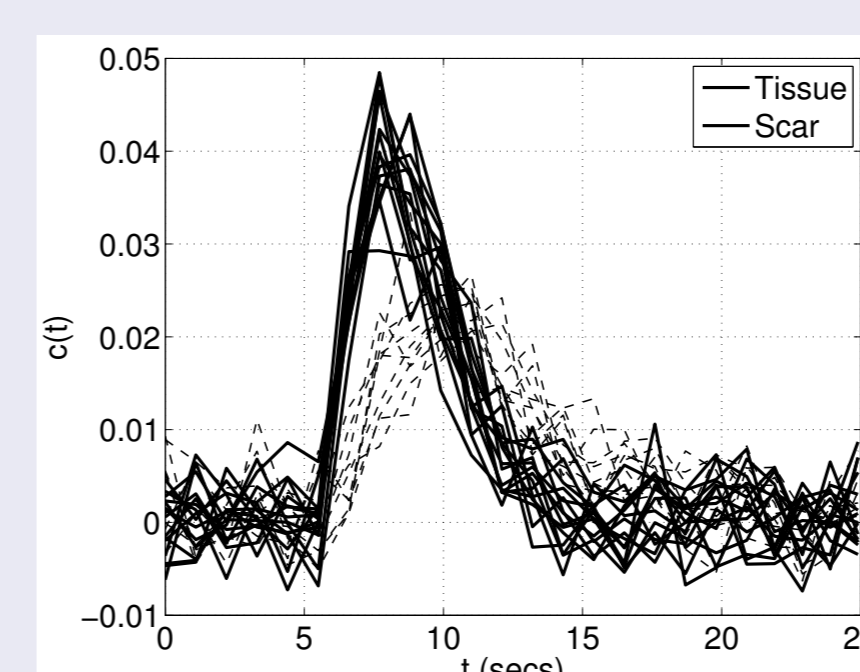
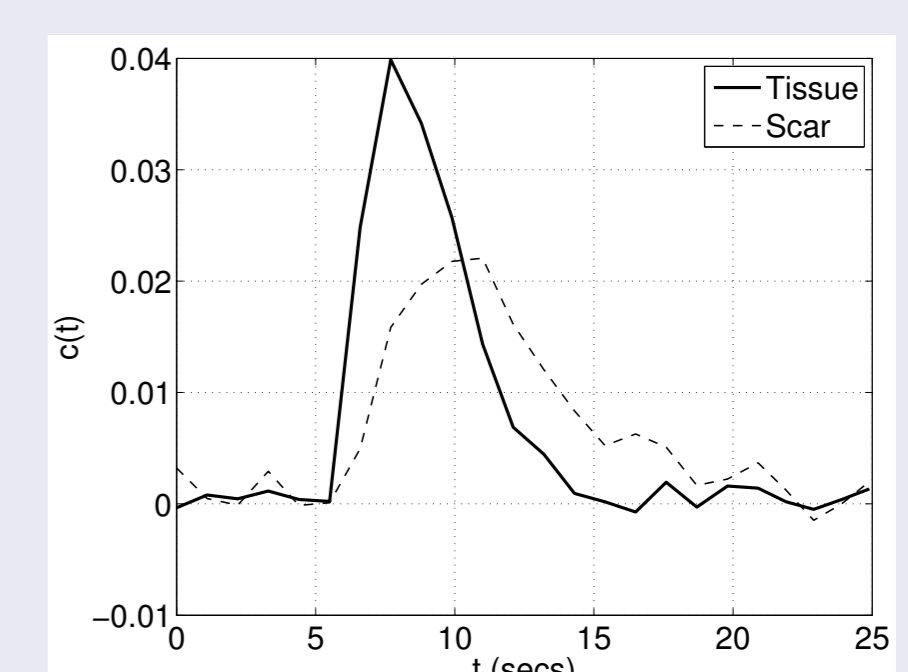


Figure: Simulation of the breathing movement in a single slice.



(a) Individual points



(b) Averaged

Figure: Simulation of the perfusion: estimated concentration of Gadolinium in tissue. Estimated from simulated MR single coil acquisition with  $\sigma_n = 10$ . (a) Selection of points (b) Average for all the points in each tissue (obtained by clustering).