

# Interpretation of diffusion MRI data using a gamma distribution model

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## Introduction:

Although many models have been proposed to interpret non-Gaussian diffusion MRI data in biological tissues, it is often difficult to see the correlation between the MRI data and the histological changes in the tissue. Among these models, so called statistical models, which assume the diffusion coefficient  $D$  is distributed continuously within a voxel, are more suitable for interpreting the data in a histological context. In this work, we examined a statistical model based on the gamma distribution which is expected to reflect biological conditions more realistically than a truncated Gaussian model [1].

## Methods:

The gamma distribution is given by

$$\rho(D) = \frac{1}{\Gamma(k)\theta^k} D^{k-1} \exp\left(-\frac{D}{\theta}\right)$$

where  $\Gamma$  is the gamma function (fig 1). There are two parameters which defines the distribution: the shape parameter  $k$  and the scale parameter  $\theta$ . When  $D$  is distributed according to this function, the corresponding diffusion MR signal becomes

$$S(b) = \int_0^\infty \rho(D) \exp(-bD) dD$$

$$= \frac{1}{(1 + \theta b)^k}$$

where  $b$  is the  $b$ -value, and  $k$  and  $\theta$  are the parameters of gamma distribution [2] (fig 2). These parameters can be estimated by curve-fitting to the MR data taken at multiple  $b$ -values. Using these estimated parameters, the gamma distribution is then evaluated. Since the distribution itself, or the "shape" is not suitable for quantitative evaluation, area fractions of specified  $D$  ranges were evaluated for such a purpose. In this work, the area fraction of  $D < 1.0$  ( $\times 10^{-3} \text{ mm}^2/\text{s}$ ) (frac<1) and the area fraction of  $D > 3.0$  ( $\times 10^{-3} \text{ mm}^2/\text{s}$ ) (frac>3) were tentatively evaluated (fig 3).

## Results and discussion:

A typical fitting result is shown in fig 4. The gamma model was fitted to an actual prostate cancer MR data (single case, no average over subjects), with  $b$ -values of 0, 500, 1000, 1500 and 2000. Since the gamma distribution model has one less parameter than the bi-exponential model, fit is expected to be worse. However, as seen in the figure, the fit is almost as good as the bi-exponential model. Fig 5 shows a scatter plot of frac>3 vs frac<1 of clinical data. Frac<1 represent the tissue component primarily consists of small tumor cells, where restricted diffusion is dominant. Frac>3 is considered to represent perfusion. Histologically proven prostate cancer (ca) and contralateral healthy peripheral zone (PZ) data from previous studies are plotted with two points (ca and PZ) per case. Also, data with  $b$ -value range of 0 - 1000s/mm<sup>2</sup> and 0 - 2000s/mm<sup>2</sup> are plotted together. Cancer / non-cancer data are clearly separated by frac<1, while frac>3 for non-cancer tissue has slightly larger value of frac>3 (perfusion). Also, there is no systematic difference between 0-1000 data and 0-2000 data.

## Conclusion:

A statistical model based on the gamma distribution is proposed. Using this model, the diffusion MR data is well fitted, and histological interpretation of the data is possible.

## References:

1. Yablonskiy AD et al, MRM 50:664-559 (2003).
2. Jensen JH et al, NMR Biomed 23:698-710 (2010).

