



Commentary on “Microanisotropy imaging: quantification of microscopic diffusion anisotropy and orientation of order parameter by diffusion MRI with magic-angle spinning of the q-vector”

Sune N. Jespersen^{1,2*}, Henrik Lundell³, Casper K. Sønderby³ and Tim B. Dyrby³

¹ CFIN/MINDLab, Department of Clinical Medicine, Aarhus University, Aarhus, Denmark

² Department of Physics and Astronomy, Aarhus University, Aarhus, Denmark

³ Danish Research Centre for Magnetic Resonance, Copenhagen University Hospital, Hvidovre, Denmark

*Correspondence: sunen@gmail.com

Edited by:

Mario Nicodemi, Università di Napoli “Federico II,” Italy

Reviewed by:

Indika Rajapakse, University of Michigan, USA

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A commentary on

Microanisotropy imaging: quantification of microscopic diffusion anisotropy and orientation of order parameter by diffusion MRI with magic-angle spinning of the q-vector

by Lasič, S., Szczepankiewicz, F., Eriksson, S., Nilsson, M., and Topgaard, D. (2014). *Front. Phys.* 2:11. doi: 10.3389/fphy.2014.00011

In their recent paper, Lasič et al. describe a parameter termed μ FA (microscopic fractional anisotropy) that quantifies microscopic anisotropy independently of macroscopic anisotropy [1]. Specifically such a microstructural parameter makes it possible to detect and characterize anisotropic domains even if they are organized in a macroscopically (i.e., at the level of the voxel) isotropic way—essentially decoupling macroscopic and microscopic anisotropy. Their method is based on the combination of two types of diffusion measurements, a powder average experiment and magic angle spinning of the q vector: The powder average experiment uses a traditional single pulsed field gradient or PGSE acquisition, where the signal along a large number of diffusion directions is averaged, thus emulating an isotropic preparation of the sample. The magic angle spinning of the q vector, the so-called q-MAS, is an approach for isotropic diffusion weighting recently introduced by the same group [2].

A similar parameter of microscopic anisotropy, termed fractional eccentricity (FE), but relying on double pulsed field gradient (dPFG) diffusion experiments was introduced by us recently in Jespersen et al. [3]. In it we extended previous work on indices of microscopic anisotropy in the long diffusion time limit proposed by Lawrenz et al. [4]. The FE terminology was motivated by the existing nomenclature in the dPFG field. However, a simple argument shows that the two metrics μ FA and FE are in fact identical in systems consisting of identical pores. First, when all domains are coherently aligned along one direction, it was shown in Jespersen et al. [3] that $FE=FA$, and similarly in Lasič et al. [1] that $\mu FA=FA$: thus $FE=\mu FA$ in such a system. Secondly, both metrics are independent of the pore orientation distribution function, so both FE and μ FA are unaffected when reorganizing the domains to match any anisotropic distribution. Hence the identity $FE=\mu FA$ is conserved. Nevertheless, a number of observations concerning differences and similarities must be made.

Clearly, both approaches presuppose the existence of compartments (pores), in which the bulk of the spins will remain during the relevant time of observation. For the q-MAS approach, this is the duration of the q-MAS modulation, 40 ms in Lasič et al. [1]. For the dPFG approach, the relevant time is the sum of diffusion and exchange times from the onset of the first field pulse to the end of the last field

pulse, which was 43 ms in Jespersen et al. [3]. These (comparable) numbers put constraints on the exchange time/permeability of the compartments. Moreover, both approaches involve non-conventional diffusion sequences, requiring programming of gradient modulation waveforms. The q-MAS approach requires the combination of two different types of diffusion experiments, and both approaches use data acquired along several diffusion directions. The dPFG experiment can be used to extract also the diffusion tensor.

The q-MAS approach assumes that diffusion in the individual pores is Gaussian. This can be a good approximation for example when diffusion weighting is not too strong and diffusion times are large. However, another requirement of the q-MAS analysis approach is that the diffusion coefficients in the individual pores are time independent, a condition which may be challenging to balance against the necessity for the spins to experience the pore boundaries, the very source of the μ FA. On the other hand, this is presumably a good approximation for the extracellular space in the long diffusion time limit, still assuming no exchange between the intra- and extracellular space. The Gaussian approximation can be accurate also when diffusion times are very small, but in this regime μ FA will be vanishing as the effect of the confinement is negligible.

The dPFG approach to microscopic anisotropy requires long mixing times,

more specifically it should be long enough that spin displacements separated by the mixing time are statistically independent. This can happen not only for Gaussian diffusion, but also when the diffusion length over the mixing time is comparable to the pore size (or the disorder length scale). Another condition of the dPFG approach is that terms beyond b^2 in the cumulant expansion of the signal must be negligible. This can be difficult to establish in practice, and would require the dPFG experiment to be repeated for a number of different b -values for verification.

Finally, a disadvantage of the μ FA/FE parameter is that it is not additive over pore populations, a property that complicates interpretation. However, this could be circumvented by adopting instead the parameters $\Delta\bar{\mu}_2$ [1] or ε [3], which are both additive, but unnormalized. In fact, these two parameters are likewise identical in multi-Gaussian systems, and their estimations are characterized by the same constraints and assumptions described above for μ FA and FE.

In conclusion, we argued that the indices μ FA and FE are in fact the same parameter of microscopic diffusion anisotropy. The name μ FA is arguably a better name, as it more directly reflects the connection to FA of individual pores

and emphasizes its microstructural nature. The two indices were estimated from two different acquisition strategies, q-MAS [1] and dPFG [3] with each of their advantages and disadvantages, and detailed considerations of pros and cons should be made on a case-by-case level when choosing one or the other. To better inform such decision-making, it would be very interesting to see a detailed comparison of the two approaches on the same system, perhaps a well-characterized model system.

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