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Quest Towards Alternative Partial Alignment of DNA

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Abstract: Dipolar couplings between magnetic nuclei are important parameters in NMR that imbibe orientational information and also pico-millisecond dynamics.¹ This crucial information is lost due to isotropic tumbling of molecules in solution, where these are averaged out to zero. Fortunately, partial anisotropy introduced by alignment medium provides scaled (~0.1%) dipolar couplings as residual dipolar couplings (RDCs). Complete description of structure and dynamics require multiple orthogonal datasets (alignments).² Different alignment media which work on steric, electrostatics or both have been used to get orthogonal alignments for proteins. However, difficulty arises for nucleic acids because uniformly charged back bone resulting in similar alignments in different media, necessitating alternative strategies. Domain elongation,^{3a} protein binding site incorporation,^{3b} and kink modulation methodologies were developed to study RNA dynamics atomistic level.⁴ We propose an approach, where flanking domain changes the overall tumbling and could result in orthogonal alignment. I will present the progress we have made in developing this methodology and the results we have so far.

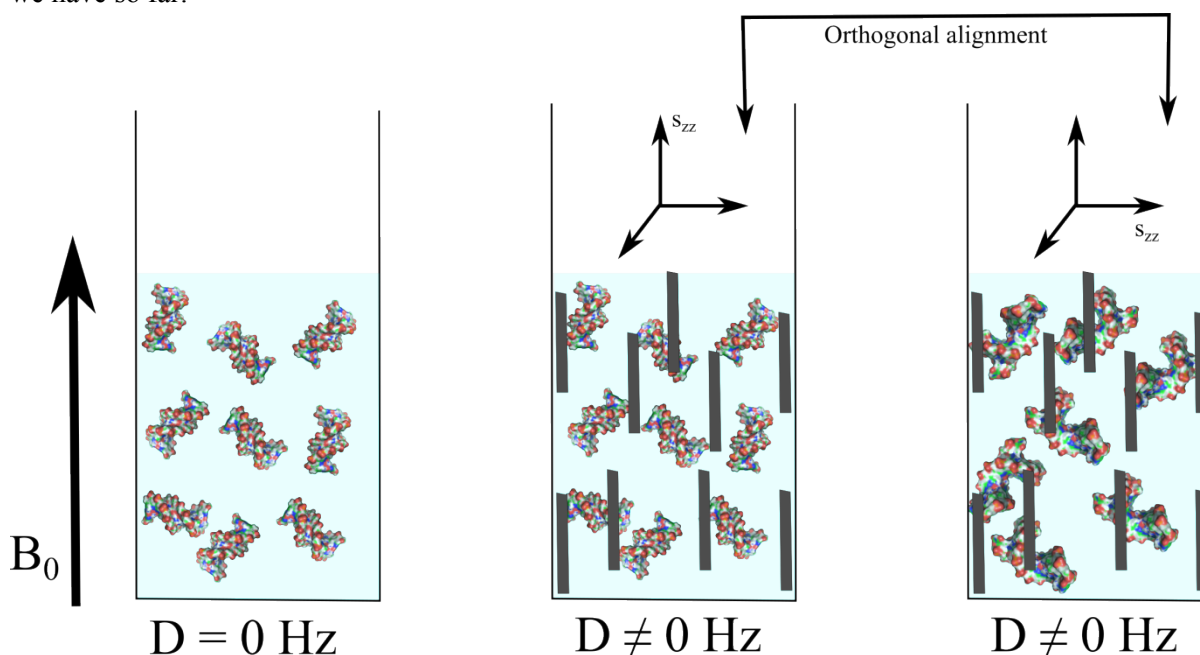


Figure: Alternative alignment due to change in tumbling

References and Notes:

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