that Fis is always associated with DNA. The results were consistent with our recent work on the in vitro single-molecule imaging of Fis [2] and CRP (unpublished).

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Study of Breast Cancer Metabolism by MRI and in-vivo MR Spectroscopy

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During malignancy metabolic alterations occur in cells and tissues and thus the study of cancer metabolism involves identification, characterization and quantification of metabolites using advanced technologies like magnetic resonance (MR). Various MR methodologies like routine, diffusion, perfusion and dynamic contrast MRI monitors the tumor morphology and various physiological functions during progression of cancer as well as during therapy in vivo. Tumor volume, apparent diffusion coefficient, kinetic parameters like volume transfer coefficient, etc are estimated and these provide information on the tumor microstructure, microenvironment, abnormal vasculature etc. Such changes are associated with the alterations in the tumor metabolism, leading to changes in the cell architecture. While in vivo MR spectroscopy is used to study and monitor cancer metabolism by detection of various biochemicals or metabolites involved in various metabolic pathways. Several in vivo NMR studies using 1H and 31P MRS have demonstrated increased levels of total choline containing compounds, phosphomonoesters and phosphodiesters in human breast cancer. These are indicative of altered choline and pohopsholipid metabolism. These levels get reversed on successful treatment. This talk will highlight the role of in vivo MR methodologies in breast cancer metabolism.

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Precision Medicine Approaches in Metabolic Disease

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The future in diabetes care promises to move from a more generic form of care to treatment that is better tailored toward the individual. To achieve this it is essential to begin to define the principles that govern individual responsiveness to the environment (i.e. food and exercise) as well as to drugs so that health practitioners can better match optimized treatments with improved long term health. This will require analysis of multiple layers of metabolic systems such as the genome, the transcriptome, the proteome and the environment using a range of model systems as well as interdisciplinary approaches to define the underlying features that determine key biological outcomes. These novel approaches will be aided by advances in accurate data acquisition, better ways of integrating data from different labs/centres and across different omic platforms and advances in data analysis and visualization. I will describe our efforts to map individual diversity in response to diet using different genetic strains of flies, mice and humans. I will describe omics analysis in both Drosophila and mice of different genetic backgrounds that clearly highlight the immense complexity of the gene-diet interaction. By marrying these data with longitudinal analysis of humans it should be feasible to develop a suite of biomarkers that predict future health outcomes and optimal prevention strategies for individuals. Such a venture will necessitate a move toward 'big data' medical care where individuals are empowered with personalized data that provides them with better options for long term health.