Weekend Education Course - Cardiac MRI: Function, Perfusion & Viability

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Research Promises: Parametric Mapping

HIGHLIGHTS:

- Parametric imaging offer the potential to *quantify* tissue characteristics without the need for a reference signal (as is required with conventional T1-weightied imaging such as with late gadolinium enhancement (replacement fibrosis, scar), or T2-weighted imaging (inflammation)).
- Parameter maps enable healthy or baseline values to be defined and global (diffuse) pathology to be identified, and potentially for degrees of disease severity to be assigned.
- Focusing on parametric mapping of the longitudinal relaxation time constant (T1) and derived extra-cellular volume fraction (ECV), the field is rapidly progressing[1-9]:
  - many sources of systematic error have been characterized[3, 10-16] (e.g. complex method dependence, partial volume errors) and are increasingly acknowledged
  - increased focus on method reproducibly (precision) over accuracy (reflecting *unavoidable* systematic errors)
  - potential errors for the ECV have not been addressed

TARGET AUDIENCE: MR Scientists and clinicians who are interested in quantitative imaging of myocardial T_1 relaxation times.

OBJECTIVES/PURPOSE: Participants will have an increased understanding of the complexity of sources of accuracy and precision with quantitative myocardial T_1 imaging and the challenges that still exist for the promise of a T1 and derived ECV as biomarkers of pathology.

TOPICS:

- What makes a good biomarker (of fibrosis)?
- Currently used T1 mapping methods
- T1 accuracy and precision (review)
- Errors in the derived ECV parameter
- Limitations of T1 and ECV as markers of myocardial pathology

CONCLUSION: T1 mapping has been shown to effectively differentiate patient populations in numerous studies and is being widely adopted in clinical research as a novel biomarker of myocardial pathology. However, many pathologies have been associated with relatively small changes in T1 or derived ECV values, changes that are often smaller than known systematic errors and of the same order of magnitude as the variability of current methods. Ongoing work will continue to address concerns and will move towards the goal of patient-specific disease characterization.

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