Specialty area: Perfusion Imaging: ASL, DCE & DSC
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Highlights:
- Visualise the data to decide whether fitting a model is appropriate
- Choose an appropriate model (family) based on the tissue type
- Use the data to inform model selection

Title: DCE Post-Processing: What Model to Use?

Target audience: This course is aimed at basic research scientists and clinicians

OUTCOME/Objectives: To provide a practical understanding of the issues to consider when selecting a model for analysis of DCE-MRI data

PURPOSE: The complexity and number of models for DCE-MRI data analysis has been steadily increasing. System hardware improvements have resulted in better-quality data, which allows models with increasing numbers of parameters to be fitted, in order to better reflect the underlying physiology. However, choosing the most appropriate model for a given dataset remains difficult (1).

METHODS: Data quality in DCE-MRI can vary wildly between patients and within different tissues and tumours. If the data are suitable for model fitting, (acquired with a good temporal resolution and contrast-to-noise ratio), model choice should start with the tissue being imaged. Normal kidney tissue and liver tissue, for example, require models that take account of the tracer extraction (kidney) or dual blood supply to the tissue (liver). Most other tissues can be described using any of the models described in this perfusion imaging course. Simulation studies (2) can assist by defining situations where a model is invalid, but often there is no clear physiological reason to favour one model family over another. In this case, model selection should be data-driven.

Choosing a model requires a metric to decide whether a particular model is a better fit to the data than an alternative. The F-test and the Akaike information criterion have been used by several authors for model selection. For example, (3) a Patlak model usually includes no consideration of backflux from the extravascular-extracellular space into the vasculature, but the model can be extended to include backflux by adding an extra parameter. Both models can be fitted to the data, using an F-test to decide whether there is enough information in the data to estimate the extra parameter. In this way, the data itself drives the model selection.

Taking this approach a step further, a systematic method can be used where progressively more complex models (i.e with more free parameters) are fitted to the data until a statistical test indicates that the inclusion of additional parameters cannot be justified.

RESULTS: A recent simulation study (2) found that the Tofts model only provides proper parameter estimates in the case of a weakly vascularised or highly perfused tissue. This highlights the importance of selecting a model based on prior knowledge of the tissue or, if no prior knowledge is available, selecting a model suitable for a wide range of tissue parameters. In a study of glioblastoma (3), an F-test was used for model selection from a small family of nested models, showing that using an objective measure to select a model on a voxel-by-voxel basis is feasible.

DISCUSSION: In the vast majority of DCE-MRI studies, a model is chosen *a priori* and applied without considering whether there is enough information in the curves to fit the chosen number of free parameters. Recently, statistical tests have been used to choose an appropriate model from a nested model family. This approach requires extra computation time but should lead to more robust parameter estimates.

CONCLUSION: DCE-MRI model selection should be data-driven

REFERENCES: 1. Sourbron SP, Buckley DL. Tracer kinetic modelling in MRI: estimating perfusion and capillary permeability. Phys Med Biol. 2012;57(2):R1–33. 2. Sourbron SP, Buckley DL. On the scope and interpretation of the Tofts models for DCE-MRI. Magn Reson Med. 2011;66(3):735–45. 3. Bagher-Ebadian H, Jain R, Nejad-Davarani SP, et al. Model selection for DCE-T1 studies in glioblastoma. Magn Reson Med. 2012;68(1):241–51.