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Pharmacokinetic analysis of dynamic contrast-enhanced (DCE) MR breast images

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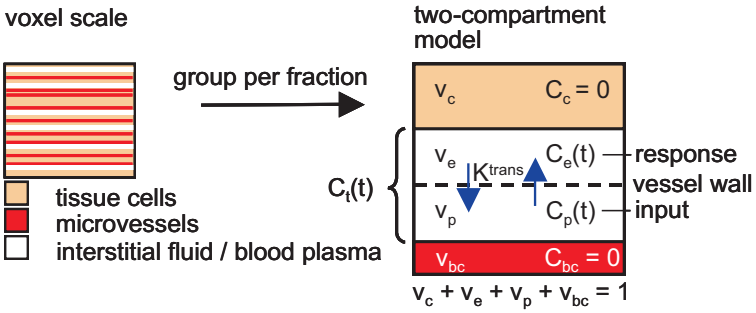
ABSTRACT

DCE-MR breast imaging is becoming an important modality as a problem-solving tool and in screening of high-risk patients. In DCE-MR a T_1-weighted time series is recorded during the uptake of a contrast agent (CA: Gd-DTPA) that enables the assessment of voxel-specific dynamic tissue properties.
Tumor malignancy often goes hand in hand with high vascularity and high vessel wall permeability because of angiogenesis; i.e. a large number of new vessels is formed at such a rate that their walls are not properly constructed and therefore highly permeable. These 'malignant' tissue characteristics affect the shape of the CA-uptake curve. The goal is to investigate the use of a pharmacokinetic two-compartment model (extended Kety [1]) in the context of dynamic analysis of CA-uptake curves as a contribution to automatic detection and characterization of breast cancer.



The equations: $v_e \frac{dC_e(t)}{dt} = K^{trans}(C_p(t) - C_e(t))$ and $C_t(t) = v_p \cdot C_p(t) + v_e \cdot C_e(t)$ describe the model. K^{trans} = volume transfer constant $[min^{-1}]$, v_c = cell fraction [-], v_e = extravascular, extracellular fraction [-] (EES), v_p = blood plasma fraction [-], v_{bc} = blood cell fraction [-]. C_t / C_p / C_e = tissue / blood plasma / EES concentration CA [mM].

However, the models that are currently dominating the clinical practice are 'heuristic shape models' such as Kuhl's model [2] and the Three-Time-Point (3TP) model [3]. These models classify the shape of the CA-uptake curves into three categories: (1) persistent uptake (benign), (2) plateau uptake in the intermediate to late phase (suspicious), and (3) washout in the late to intermediate phase (malignant). This type of classification is based on clinical experience and statistics supported by biopsy-proven data. One of our aims is to uncover the limitations of these shape models and to investigate if two-compartment modeling can lead to a better, i.e. physiology-based, tissue classification.

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