

Claims

1. A method of analysing the magnitude of Magnetic Resonance Imaging (MRI) data from acquired MRI images to determine the relative signal contributions of at least two species to each voxel of the images, the method comprising the steps of:
 - using the magnitude of the multi-echo MRI data of images from the subject, where the images are acquired at arbitrarily timed echoes including at least one echo time where water and fat are not substantially in-phase with each other;
 - fitting the magnitude of said acquired multi-echo MRI data to a single signal model to produce a plurality of potential solutions for the relative signal contributions for each of the at least two species from the model, by using a plurality of different starting conditions to generate a particular cost function value for each of the plurality of starting conditions, where said cost function values are independent of a field map term for the MRI data; and
 - analysing said cost function values to calculate the relative signal separation contribution for each species at each voxel of the images.
2. A method according to claim 1 wherein said analysis of said cost function values comprises the step of:
 - comparing the generated cost function values to determine which is the correct solution for said signal separation.
3. A method according to claim 2 wherein the lowest cost function value of said species is determined to be the correct solution for said signal.
4. A method according to any preceding claim wherein said magnitude of said multi-echo MRI data is fitted to said single signal model using a model fitting algorithm.
5. A method according to claim 4 wherein said model fitting algorithm is an instance of at least one of the following: least squares estimation, iteratively reweighted least

squares, least trimmed squares, or other robust approaches using m-estimators or s-estimators.

6. A method according to claim 4 wherein said model fitting algorithm is combined with at least one regularisation term.
7. A method according to any preceding claim in which the single signal model includes a spectral model of one of the at least two species with more than one spectral component.
8. A method according to any preceding claim wherein said single signal model includes at least one of the relaxation time quantities (T_1 , T_2 , T_2^*) to correct for signal decay.
9. A method according to claim 7 wherein the starting condition values of the relaxation time quantities are in the physically observable range.
10. A method according to claim 8 wherein the starting condition values of the relaxation time quantity T_2^* are between 1 and 100ms.
11. A method according to claim 9 wherein the starting condition values of the relaxation time quantity T_2^* are between 10 and 30ms.
12. A method according to any preceding claim further comprising the step of using said species signal contribution to generate separate images showing the results for each species.
13. A method according to claim 12 in which one or more of the resulting images are post-processed.
14. The method according to any preceding claim wherein the separated species contributions are used to estimate a field heterogeneity ('fieldmap') term.
15. The method according to any of claims 8 to 10 wherein the estimated relaxation time quantities are used to estimate a field heterogeneity ('fieldmap') term.

16. The method according to any preceding claim wherein the at least two species include at least two of water, fat, hyperpolarized contrast elements or metabolites of such elements, markers for the presence of cancerous cells.
17. The method according to any preceding claim wherein the subject includes a phantom model or animal or human tissue comprising at least one of the following organs: liver, pancreas, kidney, spleen, heart, muscle or adipose tissue.
18. The method of any preceding claim in which cost function values in a certain voxel are used to update a likelihood map of the presence of at least one species in the voxel.
19. An image processing system arranged to analyse the magnitude of Magnetic Resonance Imaging (MRI) data from acquired MRI images to determine the relative signal contributions of at least two species to each voxel of the images, the image processing system comprising at least one processing device arranged to:
- use the magnitude of the multi-echo MRI data of images from the subject, where the images are acquired at arbitrarily timed echoes including at least one echo time where water and fat are not substantially in-phase with each other;
 - fit the magnitude of said multi-echo MRI data to a single signal model to produce a plurality of potential solutions for the relative signal contributions for each of the at least two species from the model, by using a plurality of different starting conditions to generate a particular cost function value for each of the plurality of starting conditions, where said cost function values are independent of a field map term for the MRI data; and
 - analyse said cost function values to calculate the relative signal separation contribution for each species at each voxel of the images.
20. A non-transitory computer program product having executable program code stored therein, the program code operable for analysing the magnitude of magnetic resonance imaging (MRI) data in accordance with the method of any of claims 1-16.
21. The non-transitory computer program product of Claim 20, wherein the non-transitory

computer program product comprises at least one from a group including: a hard disk, a CD-ROM, an optical storage device, a magnetic storage device, a Read Only Memory, ROM, a Programmable Read Only Memory, PROM, an Erasable Programmable Read Only Memory, EPROM, an Electrically Erasable Programmable Read Only Memory, EEPROM, and a Flash memory.