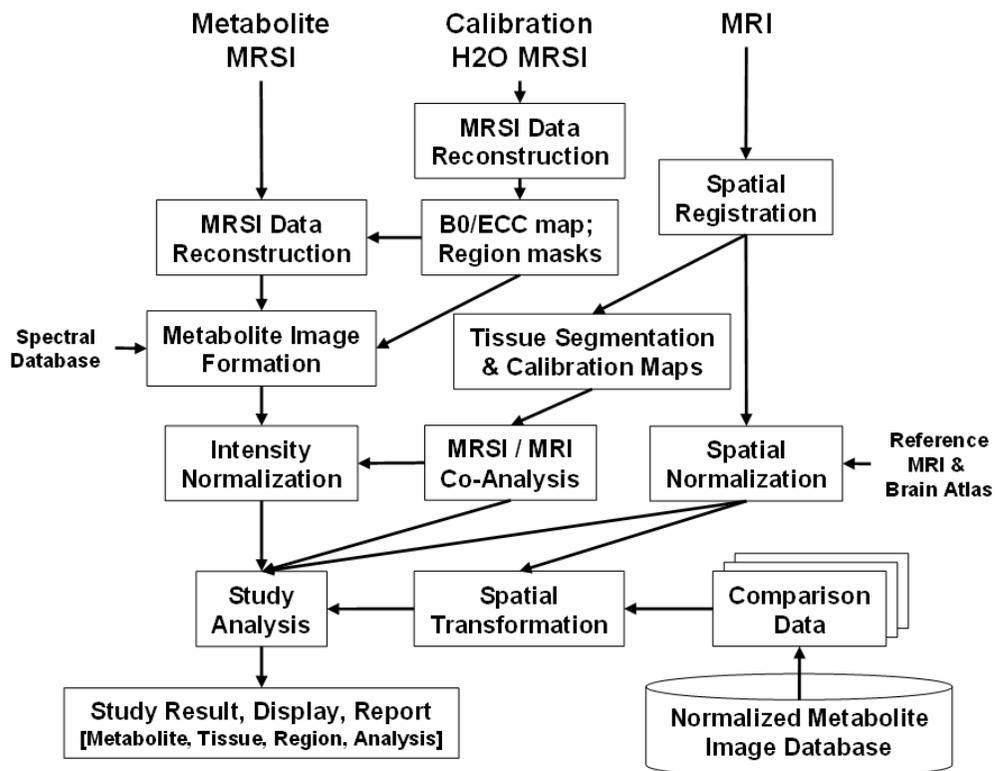


# MIDAS

## A Brief Overview of the MIDAS Project

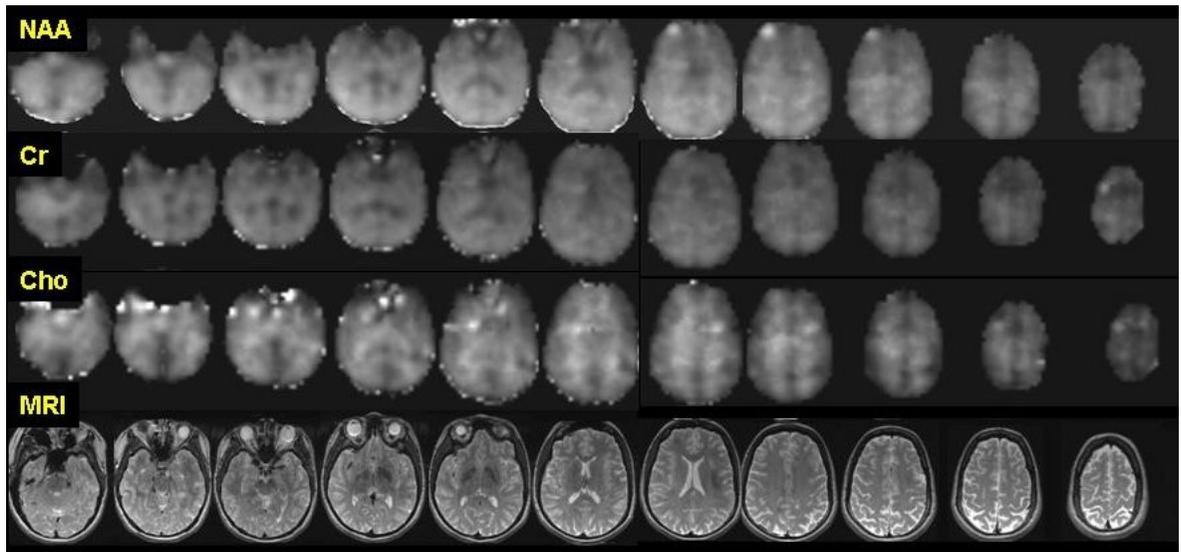
The MIDAS project consists of two main components: software development and MRSI data acquisition. The MIDAS software package provides an integrated set of functions for MRSI and MRI data processing. Each program may be run independently, typically using a GUI to select the data and parameters, or in a completely automated manner using predefined processing protocols. In addition to providing data processing functions, the MIDAS system also provides a framework for managing large numbers and different types of data files, and for keeping track of the processing used.

A complete MRI and MRSI processing protocol can involve many steps, as for example shown in the following flow diagram:



In addition to providing metabolite image reconstruction using automated spectral analysis of MRSI data, this example includes some features that are not generally available for metabolite images, including: signal normalization; spatial transformations to a standard image reference frame (spatial normalization); and statistical analysis functions of group or single subject analyses.

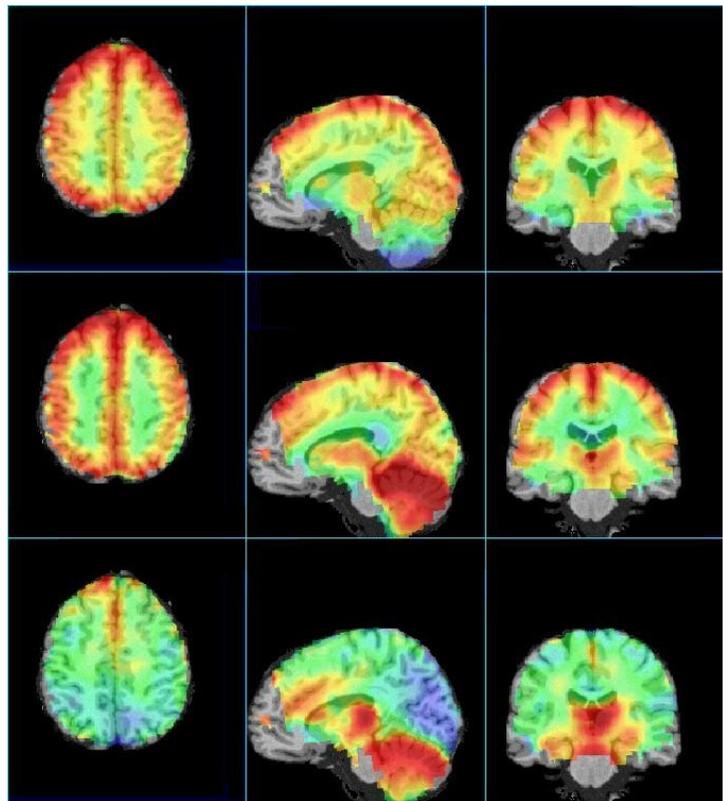
An example of a volumetric MRSI dataset of human brain that was reconstructed with the MIDAS software is shown below:



This  $^1\text{H}$  MRSI data was obtained using a volumetric EPSI sequence on the Siemens Trio using phased-array detection. Once the raw MRSI data was transferred off of the MR scanner and imported into the MIDAS environment, all processing was done automatically, and includes B0 correction and signal normalization.

The MIDAS package also includes MRI tissue segmentation functions. These results can be converted to the spatial resolution of the MRSI data and then used for signal normalization, or included in statistical analysis procedures, for example to perform a tissue regression of metabolite concentrations as a function of tissue type.

Additional functionality in MIDAS includes spatial transformations. Using parameters determined from high-resolution MRI data the metabolite images can be transformed into a common spatial frame of reference. Shown here is an example where metabolite images obtained from 14 volumetric MRSI datasets have been spatially normalized and average metabolite signals determined.



This figure shows average normalized metabolite signals for NAA (top), Creatine (middle) and Choline (bottom). This data was obtained at 1.5T and is displayed using the Rview program (Courtesy C. Studholme, and available independently of the MIDAS package). The color scale indicates higher concentrations in red, and the metabolite images are superimposed on the reference MRI shown in grey. Regions shown in grey indicate where MRSI data quality in any one of the data sets was not suitable.

The additional component of the MIDAS project is the development of a brain metabolite database. Data from normal subjects is currently being acquired at 1.5 T and at 3.0 T that will provide normative data for analysis of individual subject MRSI scans. By expanding the number of collaborators in this project it is hoped that a comprehensive database can be developed that will provide detailed normative information for MRSI in adults.

At the current time a preliminary release of the software is being made available to research sites using in vivo MRS for studies of the human brain. This project also makes available the MRSI data acquired under the project and the volumetric EPSI sequence, which is available for Siemens MR scanners only.

An introduction to the processing functions in the MIDAS package can be viewed at:  
[http://midas.med.miami.edu/Documents/MIDAS\\_Processing\\_Overview.pdf](http://midas.med.miami.edu/Documents/MIDAS_Processing_Overview.pdf)

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Portions of the MIDAS package are written in IDL (<http://www.rsinc.com/>) and Java (<http://java.sun.com>). The programs also make use of the following external packages and data:

FSL: See <http://www.fmrib.ox.ac.uk/fsl/>

“R”: See <http://www.r-project.org/>

Data from the Montreal Neurological Institute: <http://www.bic.mni.mcgill.ca/brainweb>