PBTC Acquisition of MR Spectroscopy Data

The MRS acquisition will be integrated with MR imaging and performed using a standard single-voxel PRESS (point-resolved spectroscopy) sequence.

1. REGIONS OF INTEREST (ROI)

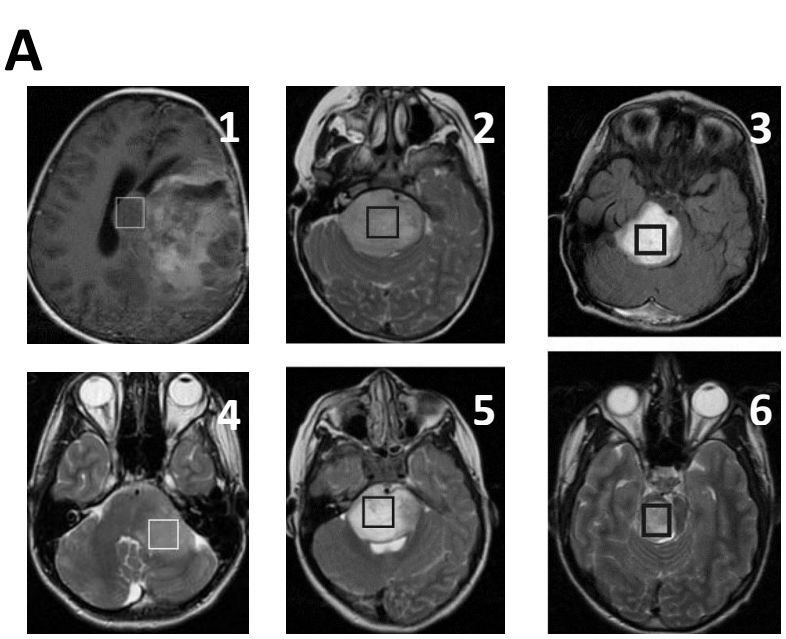
INSTRUCTIONS FOR DATA ACQUISITION

- Documentation: An MR spectroscopy study must be traced back to the region of interest. The ROI needs to be documented on at least one MR image. Any format that will allow a user to review the selected ROI for the MR study is okay (i.e., JPG, BMP, TIF, PFD, Postscript, etc). It needs to be possible to link the MRS study and the MRI + ROI by i.e. choosing unique file names.
- Select ROI to cover tumor tissue only (to the extent possible) - avoiding surrounding normal appearing tissue.
- Always review all images that show the ROI used for MRS. The slice thickness for MRI is typically 5mm whereas the slice thickness for MRS is typically 20 mm.
- Areas of blood and calcification within the lesion should be avoided or minimized because this results in degradation of spectral quality.
- Fluid that is bright on T2 weighted MR does not pose a problem. However, metabolites are intracellular and an excessive fraction of fluid (i.e. >50%) will reduce the effective volume of tissue and result in a proportional reduction of the signal-to-noise ratio.
- Tumors are often necrotic in the center. If the size of the lesion allows, then place ROI at the edge of the solid component.
- The volume of the ROI should not be below $3cm^3$ (1.5T) or 2 cm^3 (3T) to ensure adequate signal-to-noise ratio.
- Note that sampling from ROIs larger than ≈ 16cc might be compromised by poorer magnetic field homogeneity resulting in less well-defined peaks and non-uniform water suppression.
- The specificity of lipid signal is compromised when the ROI is close to structures that contain fat such as the scalp or skull. Lipid signal from the skull can be misinterpreted as signal from the lesion.
- With each spectrum also acquire the water signal for internal referencing. On GE and Philips

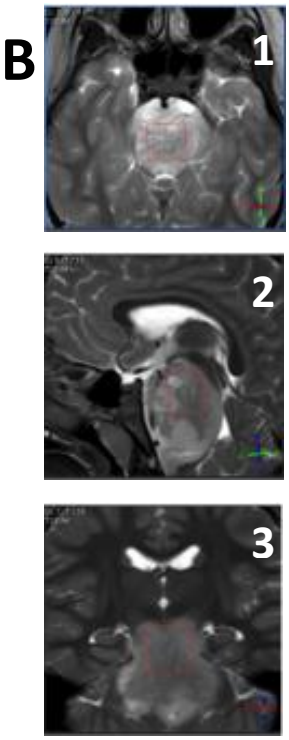
systems this is done automatically. Some system may require an additional scan with “Water suppression” switched off. This scan can be much shorter because the water concentration is high. The shape of the water peak can be used to correct the line-shape of metabolites and the intensity can be used as an internal concentration reference. Include an example of the water peak.

- Troubleshooting at the scanner: If a first spectrum acquired does only show random noise signal, repeat scan with larger ROI. If the second spectrum also shows random noise, check the lesion for blood products, and determine whether an adequate shim was achieved. Scanners generally display the achieved homogeneity. The shim should be better than ≈ 0.12 ppm. If there is no apparent technical problem, the MRS indicates that there is little viable tissue, which might be valuable information. Do not discard.

Examples for ROIs



A: Examples for positioning/sizes of ROIs. MR spectra should be obtained from suspicious tissue avoiding partial volume with surrounding normal tissue to the extent possible.



B: The ROIs should be documented on MRI for quality control.

2. SEQUENCE AND SEQUENCE PARAMETERS

For both locations, two spectra will be acquired:

- A metabolite spectrum, which contains the information about the metabolites (=*metabolite scan*)
- A water reference scan that will be used for absolute quantitation (=*water scan*)

General Electric and Phillips systems always acquire both spectra automatically and no separate measurement is required. Newer Siemens systems (Skyra) also acquire both spectra automatically once the "button" to generate an unsuppressed water reference scan is checked. For Siemens systems where the water scan is not automatically obtained, follow instructions provided below in

Sequence parameters

All spectra will be acquired with a standard single-voxel SV-PRESS sequence with a short echo time (TE) of 35ms.

MR Scanner	General Electric, Philips, Siemens
Field strength	1.5T and 3.0T
Coils	T/R or SENSE Head coil.
Sequence:	SV-PRESS
Repetition time (TR):	1.5 s (1.5T) and 2.0 s (3T)
Echo time (TE):	35 ms (*metabolite scan* and *water scan*)
FOV:	n.a. (default)
Phase encoding:	1 × 1 (= single-voxel mode)
Dimensions of ROI	
AP direction	14.5-25mm (1.5T) 13-25mm (3T)
SI direction	14.5-25mm (1.5T) 13-25mm (3T)
LR direction	14.5-25mm (1.5T) 13-25mm (3T)
Averages for metabolite spectrum:	128
Averages for water spectrum:	≥ 8
Outer volume suppression/ saturation bands	No.

1.2.2 Instructions for data acquisition

- Review/display images with axial, sagittal, and coronal orientation for accurate voxel placement.
- Documentation: Albeit spectra will be acquired from highly standardized ROIs, the actual area scanned should be documented. The manufacturers provided software to generate screenshots should be used. Screenshots should then be saved together with MR images.
- With each spectrum also acquire the water signal for internal referencing. On GE, Philips, and Siemens "Skyra" systems this is done automatically.
- For other Siemens scanners where the *water scan* is not automatically obtained
    - Append the SVS sequence once it starts to run (so the voxel is in the exact same location) and open it
    - Change the water suppression to "none"
    - Change the # of averages to 16
    - Right click on properties, change the sequence name to "SVS reference"
    - Apply and run the sequence (no additional shimming is necessary)

Vendor specific instructions for MRS data access and extraction

Spectra will be processed centrally with LCModel software (LCModel©, Stephen Provencher Inc., Ontario, Canada). In order for the LCModel software to process spectra the following guidelines need to be followed (adapted from LCModel & LCMgui User's Manual, June 15, 2014, LCModel version 6.3-1J). The LCModel User's Manual is accessible at http://s-provencher.com/pub/LCModel/manual/manual.pdf (accessed 05/05/2015).

Note that below instruction may need to be updated when manufacturers update their scanner software.

General Electric: On GE scanners, metabolite and water spectra are acquired automatically and the data are stored in one file (P-file). No extra scan is required. P-files are stored in the directory "/usr/g/mrraw".

IMPORTANT! GE uses a limited number of file names and there is the danger that files will be overwritten if not saved in a timely fashion. Therefore, the file should be renamed and the data copied to a separate directory immediately after the completion of a study:

- On the MR scanner console go to the Browser
- Right-Click on Background
- Select Service tools and Command Window in scroll-down window (a command terminal will pop-up)
- Go to command window and type:
    - cd /usr/g/mrraw
    - mkdir PBTC_MRS_DATA (generates a backup directory – needs to be done only once!)
    - cp Pxxxxx.7 PBTC_MRS_DATA (copies the pfile into the PBTC folder)
    - cd PBTC_MRS_DATA (switch to directory PBTC_MRS_DATA)
    - mv Pxxxxx.7 StudyID.date.ROI.Pxxxxx.7 (rename file with unique file name)
    -

Copy the file "StudyID.date.Pxxxxx.7.anon" to a Linux/Unix/PC platform, using FTP with "binary mode". "ASCII" or "text" mode will corrupt files.

The x's represent the 5 digit code for the pfile that is being saved. "StudyID" is your identifier for this patient and study also used when anonymizing MR images. "ROI" is the region of interest and could contain information such as "center_tumor", "enhancing", "non-enhancing", "partial_volume", etc. "Date" is the date of the examination.

Philips: On scanners with up-to-date software metabolite and water spectra are always acquired and no separate scan is required. Extract the *.SPAR and *.SDAT data. This is done by going to "System -> Advanced Tools -> Research" and starting the process "dbimexp". Under the patient select the spectroscopy study to be extracted. The *.SPAR and *.SDAT files are being extracted to "cygdrive/e/Export" where they can be accessed remotely. Copy the data to a Linux/Unix/PC platform, using FTP with "binary mode". "ASCII" or "text" mode will corrupt files.

On a Philips system four files are generated for each ROI (you will have a total of eight files for two ROIs):

A file containing the data of the *metabolite scan*: xxxPID_act.SDAT
A file containing the data of the reference *water scan* : xxxPID_ref.SDAT
A file containing patient information and scan parameters for the *metabolite scan* : xxxPID_act.SPAR
A file containing patient information and scan parameters for the *water scan* : xxxPID_ref.SPAR

Siemens: Generate .rda files via selecting in the spectroscopy card “option -> export raw data”. This will generate two files: the *metabolite scan* and the *water scan* for each ROI. You will have a total of four files for two ROIs. Copy the data to a Linux/Unix/PC platform, using FTP with “binary mode”. “ASCII” or “text” mode will corrupt files. All patient information is stored in the header of the *.RDA files. The header is in ASCII format and can be directly edited in any editor.

PatientName: LAST^FIRST^^^
PatientID: 121212121212
PatientSex: F
PatientBirthDate: 20140101
StudyDate: 20140106
StudyTime: 183605.981000
StudyDescription: HEAD^ROUTINE BRAIN
PatientAge: 005D
PatientWeight: 5.000000

The file names should be

StudyID.date.ROI_NWS.rda

StudyID.date.ROI_WS.rda

Where StudyID is your identifier for this study that also links the MR spectroscopy with the MR imaging portion of the examination. ROI is the region of interest and could contain information such as “center_tumor”, “enhancing”, “non-enhancing”, “partial_volume”, etc. “Date” is the date of the examination.

Submitting MRS data for central processing

MR spectroscopy files are small. MRS data will be submitted to the PBTC ODMC and anonymized.

Quality control

We will use the above values for FWHM (=full width at half maximum – a measure of the magnetic field homogeneity) and SNR (signal-to-noise ratio) to exclude MR spectra of poor quality. The position of the ROI will be reviewed to ensure that the MRS is representative for tumor tissue.