

SIEMENS

Applications Guide

Spectral Editing with SVS

(Works-in-Progress)

MAGNETOM TaTs and Verio Systems (3T)

syngo MR Numaris 4 VB17A

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Version 1.1

WIP #529

Important Note

This document provides a description of techniques developed by Siemens. Siemens has tested the software provided with this works-in-progress package in combination with the proposed clinical application. However, each user should be aware of the fact that incorrect use of this software may produce unknown results.

The sequences contained in this software package do not exceed the FDA safety performance parameter guidelines for MRI exams. Specifically, there is no change to patient risk as compared to routine operation of the MAGNETOM with regard to: static magnetic field; the time rate of change of the gradient magnetic fields; the rate at which RF power is deposited into the body (SAR); or the acoustic noise created by the MAGNETOM.

The software has been tested internally but not yet in a clinical environment. For routine applications, its functionality may not be complete, and use of this software will remain investigational.

In general, the clinical user will, in its sole responsibility, decide on the use of this application package or on subsequent therapeutic or diagnostic techniques and shall apply such techniques in its sole responsibility.

Siemens will not take responsibility for the correct application of, or consequences arising from use of, this applications package.

The software in this package may change in the future, or may not be available in future software versions. Siemens has the right to remove this software at any point. In case of any questions that are related to the use of this package please contact one of the WIP authors listed on the next page.

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Introduction

This SVS spin-echo sequence for detecting GABA is provided by the MR application development spectroscopy group. It has no product status. It is designed for detecting the GABA 1H MRS signal at 3.0 ppm in brain. GABA being an inhibitory neuro-transmitter might be down-regulated in diseases such as epilepsy.

The technical challenge of detecting tiny *in vivo* GABA signals lies in reliably suppressing much larger overlying creatine signals. The preliminary results generated with this WIP package suggest that there is hope that this might be possible. Together with your help we hopefully come to a conclusion whether GABA detection by *J*-coupled difference editing is at all feasible.

In the US, usage of the sequence requires an IRB to the best of our knowledge. In other countries, similar procedures might be necessary. It is the user's responsibility to comply with local regulatory requirements. Furthermore it is currently open whether or not Siemens Medical Solutions will provide a sequence of this type with further SW releases.

We at Siemens Medical Solutions hope that we provide you with a useful tool for your purpose. We are very much interested in your feedback on the results obtained. Please send your feedback, e.g. by using the questionnaire in section 9, directly to either of the authors or your collaboration management partner. Especially if you consider publishing data acquired with this package, please feel free to contact us for obtaining additional information.

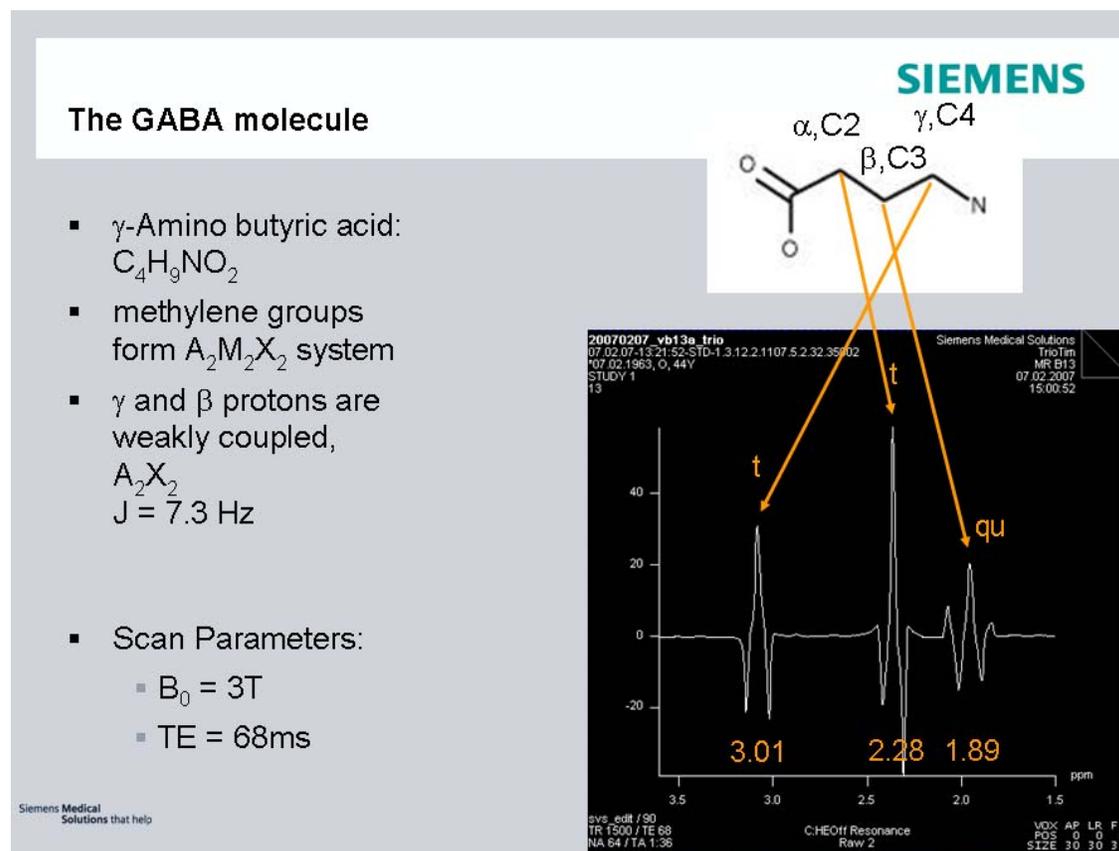
Prerequisites

Usage of the editing SVS sequence requires SVS and spectroscopy post-processing licenses. The editing sequence is only released for the 3T systems – TaTs and Verio.

Furthermore it is assumed that you are familiar with running and evaluating brain spectroscopy examinations.

Sequence Description

The implemented method is a spin-echo variant of a J -difference editing method, nearly identical to the one described by Mescher et al. [1,2]. It is based on the following principle:



The γ -protons of GABA showing a signal at 3.0 ppm, and β -protons showing a signal at 1.9 ppm are weakly coupled, forming approximately a A_2X_2 system ($J = 7.3$ Hz). During odd-numbered acquisitions (1, 3, 5 ...) a frequency selective, refocusing Gauss pulse is irradiated to the β -protons at 1.9 ppm. This pulse refocuses the J evolution of the triplet peak at 3.0 ppm. The data acquired during the odd acquisitions is stored in the dataset named "raw1" respectively "On Resonance". During even-numbered acquisitions (2, 4, 6 ...) the same pulse is applied to the opposite side of the spectrum, i.e. at $4.7 + (4.7 - 1.9) = 7.5$ ppm. During these acquisitions, the triplet signal at 3.0 ppm remains unaffected, and the outer signals from the triplet are inverted at $TE = 1/(2J) = 68$ ms. The data of the even acquisitions are stored in "raw2" respectively "Off Resonance". The difference spectrum (labeled with

“Difference”) raw3 = raw1 – raw2 shows at 3.0 ppm only the signal contributions of opposite sign of both acquisitions, resulting in a doublet 14.6 Hz between the two signals, while the overlapping creatine singlet signal, being identical during both acquisitions, should be suppressed.

While the sequence described in [1] uses the same editing mechanism to also suppress the water signal, this WIP sequence resorts to CHESS water suppression. With this WIP package the usage of array coils is possible. To have a proper signal for the phase sensitive signal combination with array coils the “Weak Water Suppression” is recommended.

Updates:

- Compared to a previous version of this WIP (for VA25A) the spoiling is improved.
- Additionally the regional saturation pulses are now available with this sequence.
- In order to suppress the coupled MM resonances coedited with GABA, the special card provides a field to specify the location to mirror the control pulse. Please see Ref. 3 for details
- Verio support
- 32 channel support

Installation Instructions

Installation of this package should be performed by an experienced user. For installation you need to access the file-system of the scanner (“Advanced User” functionality), which requires a password. Please contact the local application support for this information.

Installation can be executed with the following steps:

- Copy the installation ZIP file to the scanner C:\temp
- Click on it with the right mouse button & select “Extract all” - Select „Next“
- Enter c:\ for the target path and click on “Next”
- open Explorer and double-click ‘Install_WIP.bat’:

Read the output carefully and check for error-messages.

A log file will be written to C:\MedCom\log

- Reboot scanner to get all changes into effect.

The following files will automatically be copied to the system:

C:\MedCom\MriCustomer\seq\svs_edit_529.dll
C:\MedCom\MriCustomer\seq\svs_edit_529.i86
C:\MedCom\MriCustomer\IceConfigurators\IcePrgSpecEdit.evp
C:\MedCom\bin\IceSpecEdit.evp
C:\MedCom\bin\IceSpecEdit.dll
C:\MedCom\MCIR\Med\lib\libIceSpecEdit.so

For a custom protocol, create a new measurement protocol using the Exam-Explorer for the new sequence sv_s_edit_529. The new protocols can be inserted into an existing exam by the “insert sequence” functionality from the “User Sequences” tree.

The measurement protocol

contrast card, TE:

Since the sequence disguises itself as a triple echo sequence in order to span up memory for raw1 ... raw3, three TE values are offered. However, only the first TE entry is relevant and should be changed.

While the described GABA editing works at $TE = 1/2J = 68$ ms and $TE = 1/J = 136$ ms, we obtained so far the better results for $TE = 68$ ms. When editing pulses of a minimum bandwidth of 40 Hz are used (recommended setting), then the shortest available echo time might be only $TE = 69$ ms, the precise value still depending on coil loading (due to variable duration spin-echo refocusing pulses). If the echo time of 68 ms is not possible increase the bandwidth of the editing pulses until this TE can be realized.

contrast card, water suppression ...

... should be switched on. Use water suppression bandwidth as usually (35 Hz at 1.5T, 50 at 3T), or consider to use even slightly larger values when larger voxels are used

geometry card, voxel size ...

... we tend to use voxel up to 3 x 3 x 3 cc in order to be able to detect the tiny GABA signals.

system card, adjustments ...

... make sure that the Advanced Shim Mode and adjustment of the water suppression pulses are switched on. Consider to improve shimming interactively.

sequence card, bandwidth ...

... use the usual acquisitions bandwidths, e.g. 1000 Hz at 1.5T and 1200 Hz at 3T.

sequence card, delta frequency ...

... consider to use a delta frequency of -1.7 ppm, suitable for localizing a resonance at 3 ppm in vivo.

sequence card, phase cycling ...

Use regular 'Auto' phase cycling mode and a multiple of 16 as the number of averages. In this implementation, the phase cycling only covers the three slice-selective pulses of the regular spin-echo sequence

sequence special card, editing frequency ...

Provide the centre frequency of the editing Gaussian pulses being effective on the right hand side of the water signal, e.g. `editing_frequency = 1.9 ppm` in the case of **in vivo GABA** editing. As internally the frequency offset is computed by "`4.7 – editing_frequency`", you have to input a `editing_frequency = 1.7 ppm` in the case of room temperature **phantom** experiments, to account for the temperature dependence of the water signal resonating then at 4.9 ppm.

sequence special card, editing bandwidth ...

Choose the smallest possible bandwidth for the editing pulses to achieve a TE of 68 ms.

Post-Processing

Evoke the post-processing SW from the patient menu within the exam task card. Since each series generated by the editing sequence contains three raw data sets, the data has to be loaded from the patient browser. Generate a post-processing protocol matching your acquisition protocol, consisting of approximately the following steps:

MRS postprocessing protocol

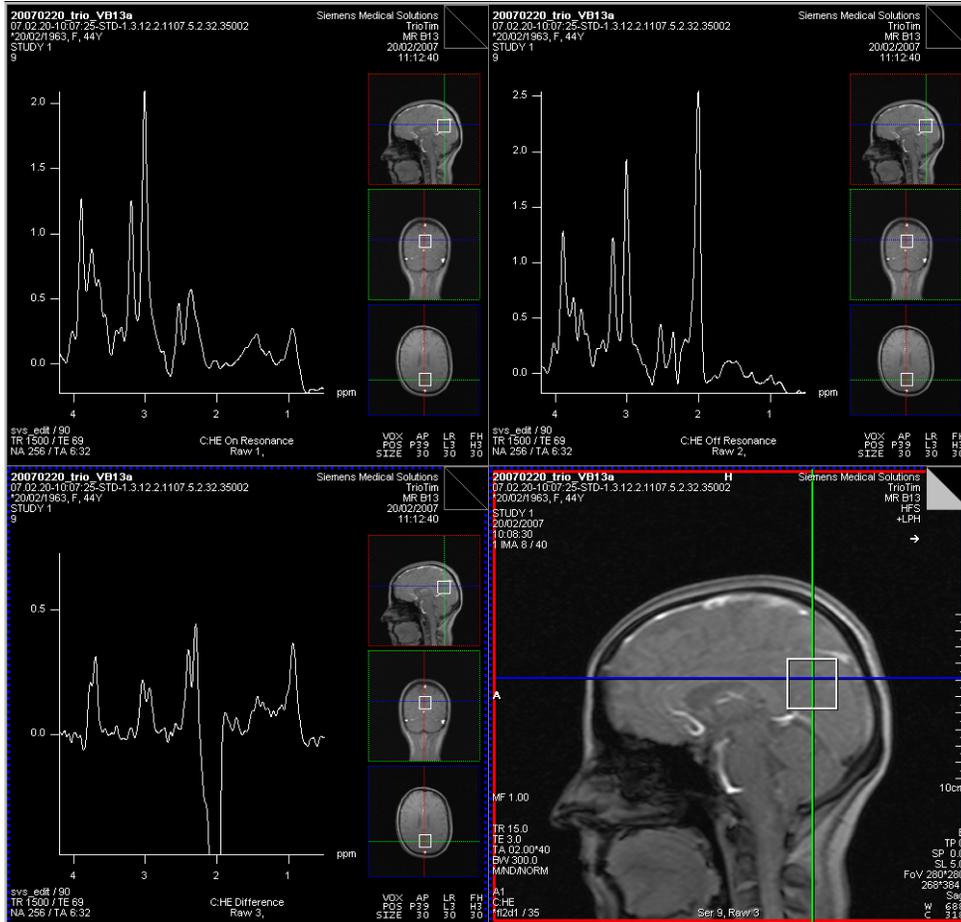
Water reference processing:	ON, 20 average points signal subtraction and frequency correction selected
Filter:	Hanning, width 400 ms
Zero filling:	optional, 2048
FT	ON
Baseline: polynom.order:	optional, consider to use a 1st or 2 nd order polynomial only close about 3 ppm
Phase correction	manually, as described below
Curve fitting:	optional fitting of the edited GABA signal singlet or dublett, Gaussian line-shape calc.range: 2.5–3.5 ppm

One advantage of this J-coupling editing technique is that the phase of the GABA signal can be pre-determined (this is a more robust procedure than trying to interactively phase-correct the usually tiny GABA signal). The following method for finding the correct phase of the edited spectra has been established experimentally using a creatine / GABA phantom:

- first load the un-edited spectrum raw2 and the GABA post-processing protocol
- interactively phase the creatine signal at 3 ppm, using only zero order phasing
- copy the post-processing protocol (Protocols/Copy)
- then load the edited spectrum raw3
- then copy the zero-order phase found for the creatine signal, e.g. by pasting the protocol (Protocols/Copy)

Preliminary Results

Examples of GABA detection in the brain of a healthy volunteer, acquired on a MAGNETOM Trio, voxelsize = 27cc, TA = 12 min.s., are shown below:



In the edited spectrum (Raw 3) the residual singlet contributions of the choline-signal at 3.2 and the CH₂ creatine signal at 3.9 ppm appear to be negligible. A resonance at 3.0 ppm which could be ascribed to GABA is depicted.

The residual lipid contaminations have no effect in the interesting spectral range at 3 ppm.

Questions to the User

Please return this section to the address provided in the introduction.

The following feedback is based on _____ attempts to detect GABA.

GABA was detected in

____ % of the cases unambiguously

____ % of the cases possibly

____ % of the cases it was unexpectedly NOT detected.

Can failure be ascribed to a certain cause? Please comment:

In vivo detection of GABA is important in order to

References

1. Mescher, M., Tannus, A., Johnson, M.O. and Garwood, M. Solvent suppression using selective echo dephasing. J Magn Reson A 123 (2), 226-229 (1996)
2. Mescher, M., Merkle, H., Kirsch, J., Garwood, M., Gruetter, R. Simultaneous in vivo spectral editing and water suppression NMR in Biomedicine 11, 266-272 (1998)
3. Henry, P.G., Dautry, C., Hantraye, P., Bloch, G. Brain GABA Editing without Macromolecule Contamination. ISMRM 1999 #1581