QUANTIFICATION OF MR SPECTRA

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PhD course 2023

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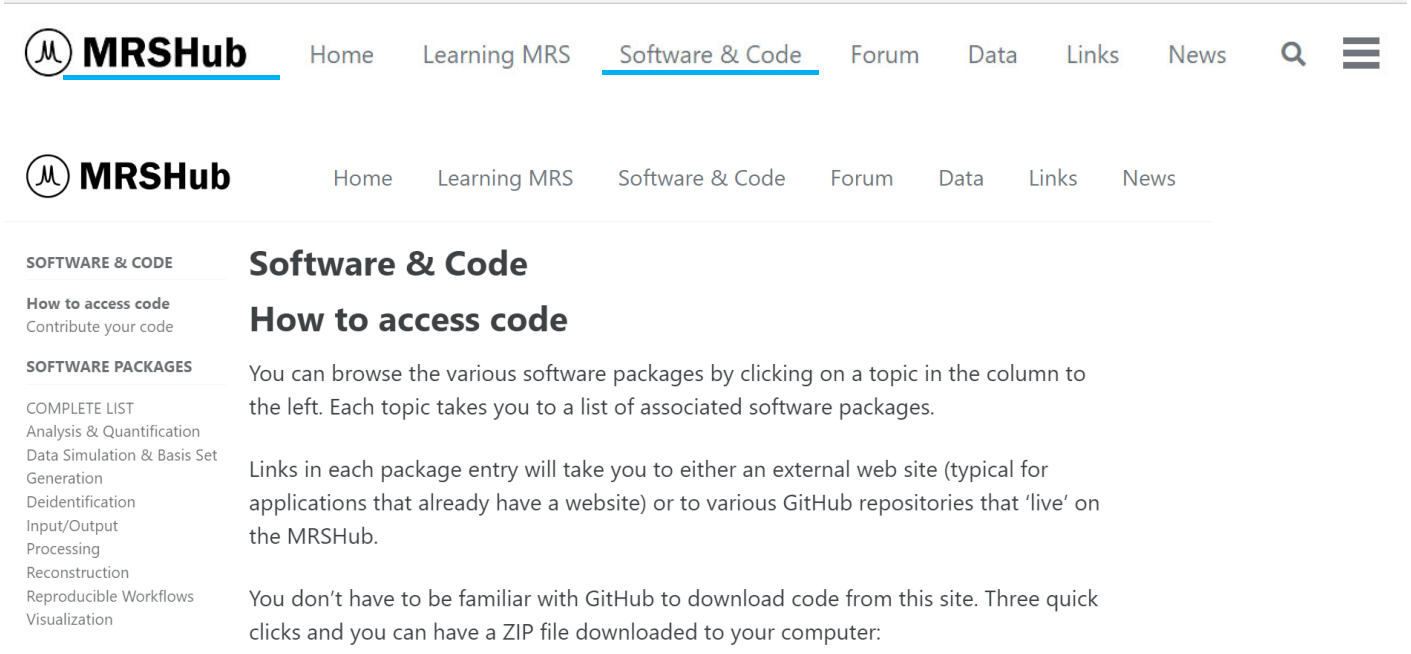
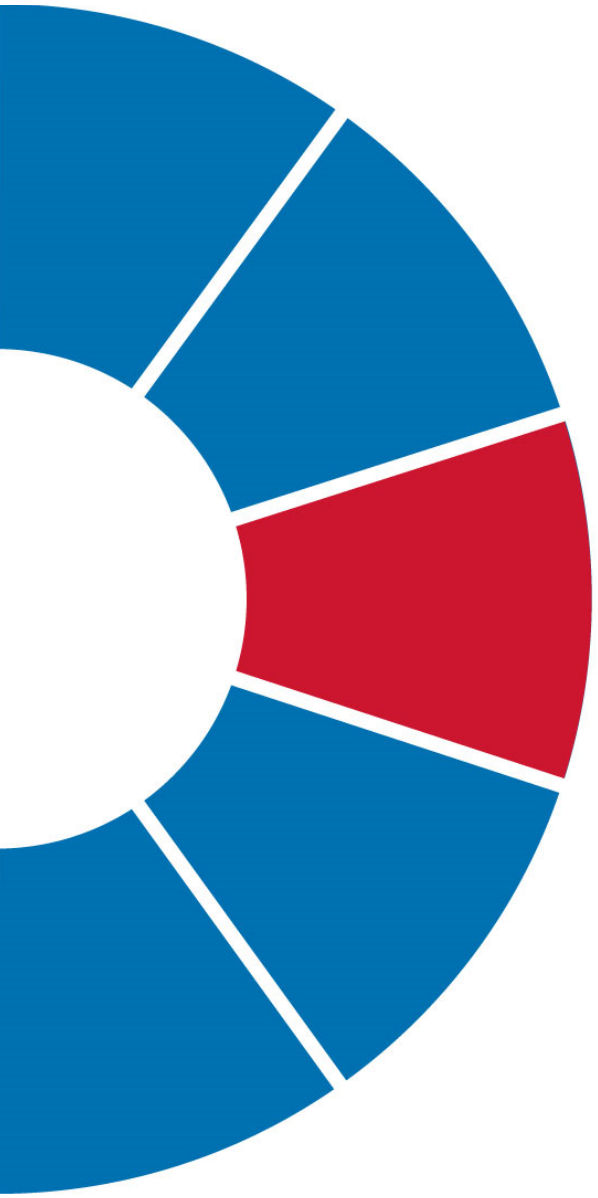
FURTHER READING



OUTLINE

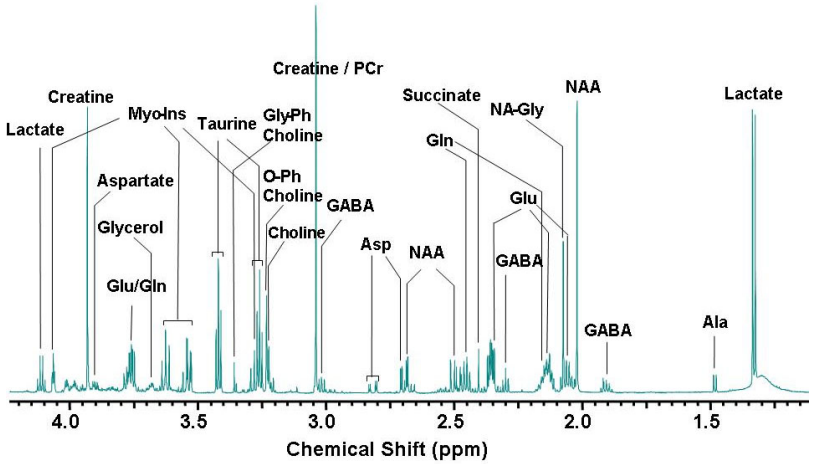
- ☺ Quantification
- ☺ Clinical vs preclinical data
- ☺ Artifacts in ^{1}H MRS
- ☺ Quality Management – Quality control
- ☺ Prepocessing steps
- ☺ Quantification - software



QUANTIFICATION

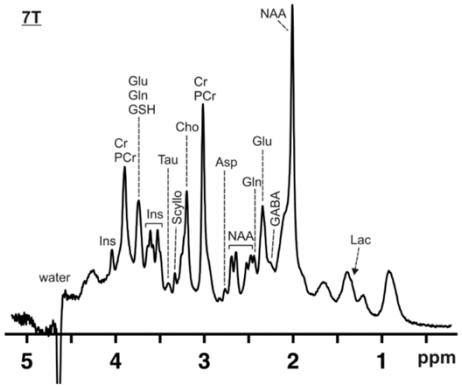
MAGNETIC RESONANCE SPECTROSCOPY

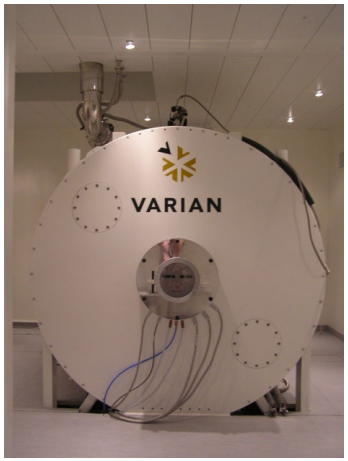
- NMR Spectroscopy



MAGNETIC RESONANCE SPECTROSCOPY

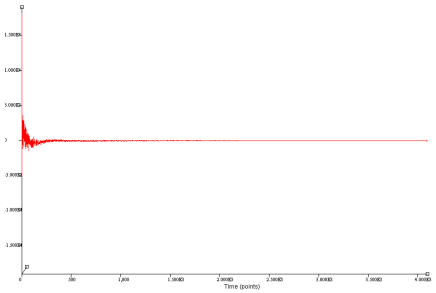
- In Vivo MR spectroscopy (MRS)
  - Measurement of different metabolites- metabolism
  - Different organs
  - Different nuclei: 1H, 13C, 31P, 15N, ..
  - Different magnetic fields
  - Different acquisition parameters



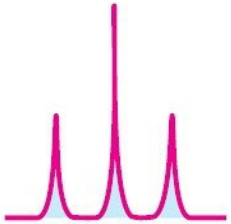


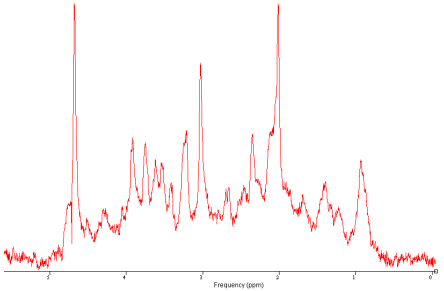
QUANTIFICATION

- MRS – principal goal – quantification of changes in concentration of known metabolites



- Frequencies
- Amplitudes
- Damping factor
- Phase
- Beginning time





- Frequencies
- Surface
- Linewidths
- Zero order phase.
- first order phase

WHY IN VIVO 1H MR SPECTROSCOPY ?

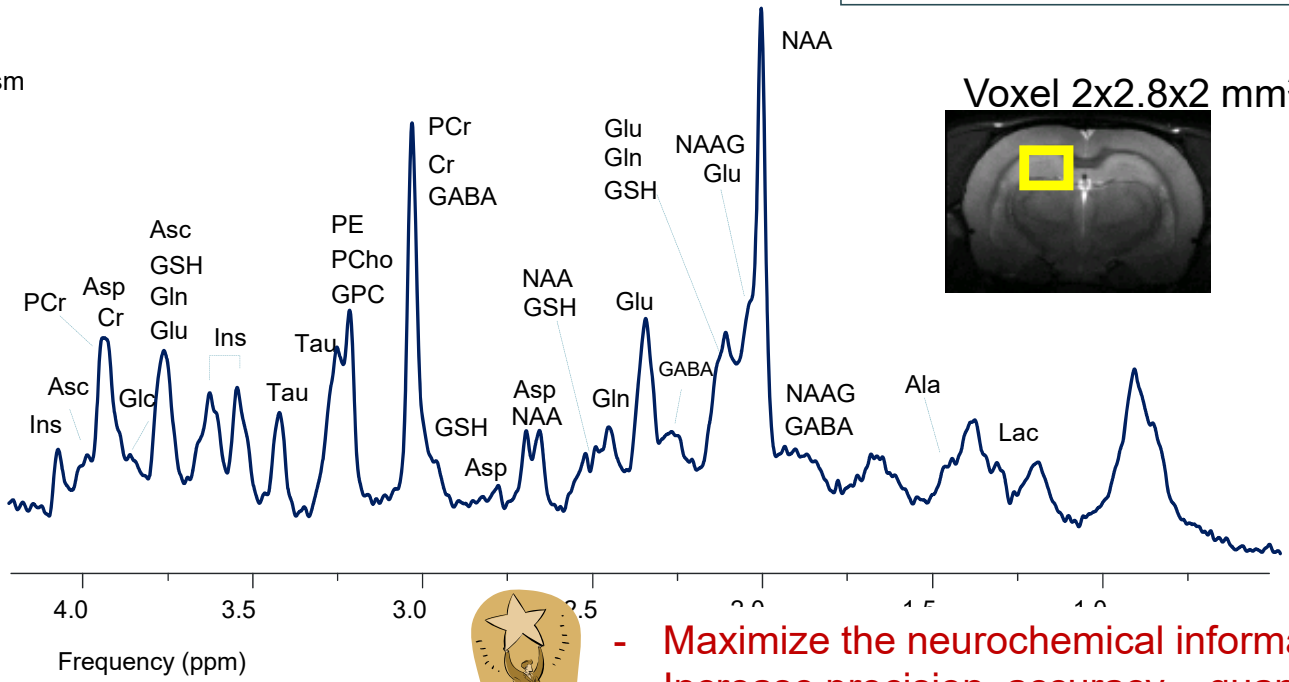
Neurochemical Profile at 9.4T

>18 Markers of :

Myelination/Cell proliferation
Energy metabolism
Osmoregulation
Neurotransmitter metabolism
Antioxidants

- **at high magnetic field (9.4T)**
- **ultra short TE (2.8ms)**

- ***in vivo***
- **non invasively**
- **localized in hippocampus**



Voxel 2x2.8x2 mm^3

- Maximize the neurochemical information
- Increase precision, accuracy – quantification
- Increase the reliability of obtained concentrations

CD Rae et al, Anal Biochem. 2017; CD Rae .Neurochem Res. 2014; V Račkayová et al 2017; JMN Duarte 2012

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SPECIAL ISSUE REVIEW ARTICLE

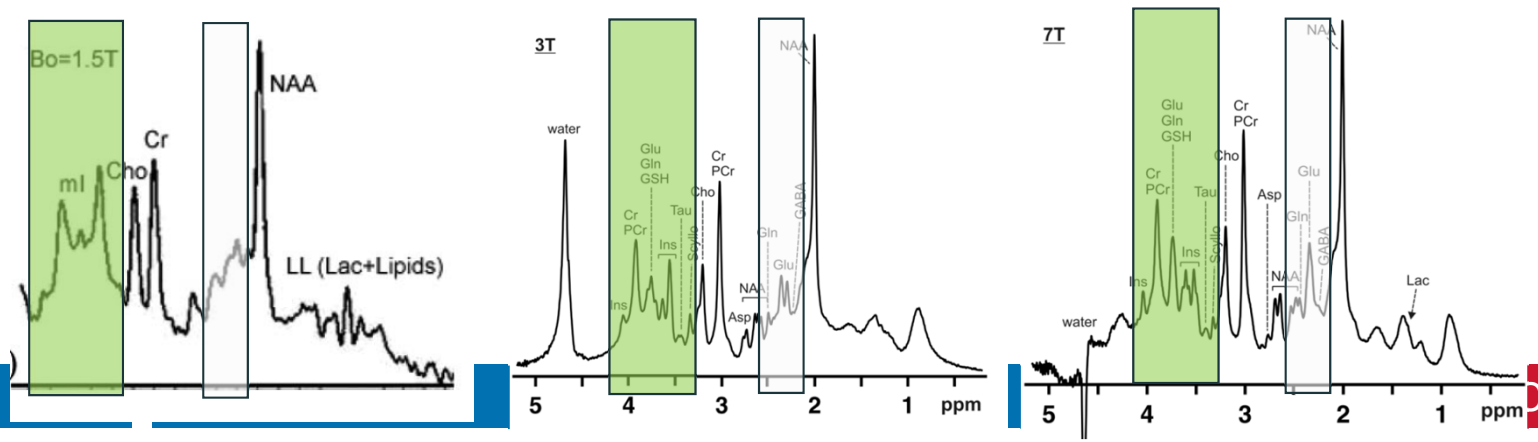
NMR IN BIOMEDICINE WILEY

Terminology and concepts for the characterization of in vivo MR spectroscopy methods and MR spectra: Background and experts' consensus recommendations

Roland Kreis[1] | Vincent Boer[2] | In-Young Choi[3] | Cristina Cudalbu[4] | Robin A. de Graaf[5] | Charles Gasparovic[6] | Arend Heerschap[7] | Martin Kršňák[8] | Bernard Lanz[9,10] | Andrew A. Maudsley[11] | Martin Meyerspeer[12,13] | Jamie Near[14] | Gülin Öz[15] | Stefan Posse[16] | Johannes Slotboom[17] | Melissa Terpstra[15] | Ivan Tkáč[15] | Martin Wilson[18] | Wolfgang Bogner[19] | Experts' Working Group on Terminology for MR Spectroscopy

WHY HIGH MAGNETIC FIELD ?

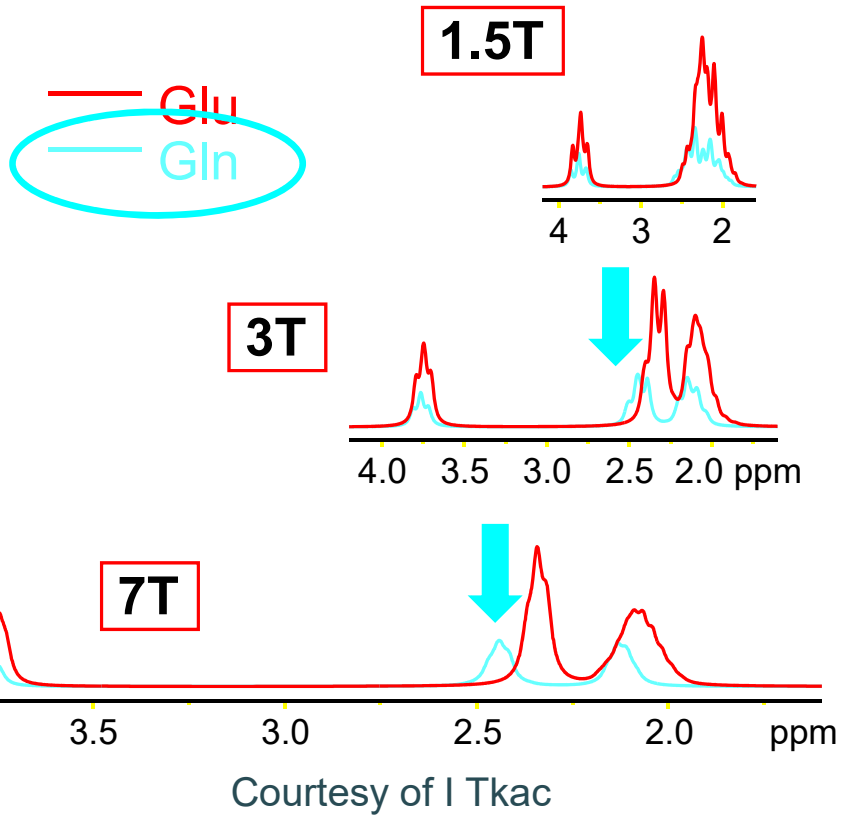
- More signal
- More spectral resolution
- And more sensitivity



Ralf Mekle et al, (2009) MRM 50: 1279

WHY HIGH B_0?

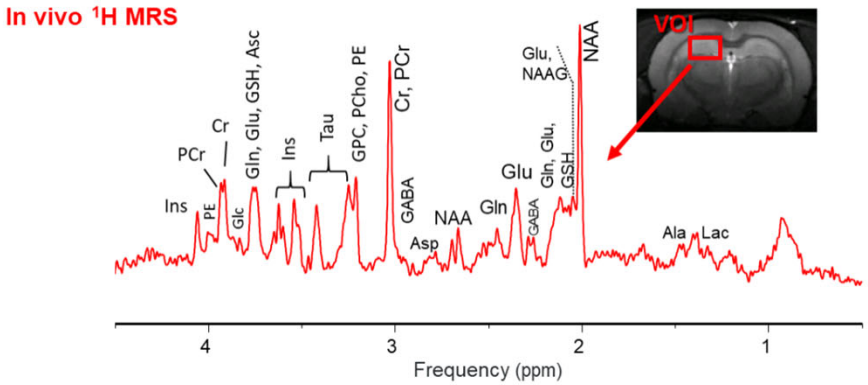
- Enormous progress
  - ↑ SNR
  - ↑ chemical shift dispersion – ↑ resolution
  - decreased strong J-coupling effects
  - Improve quantification precision and accuracy
  - ↓ T_2* - ↑ spectral lw in Hz

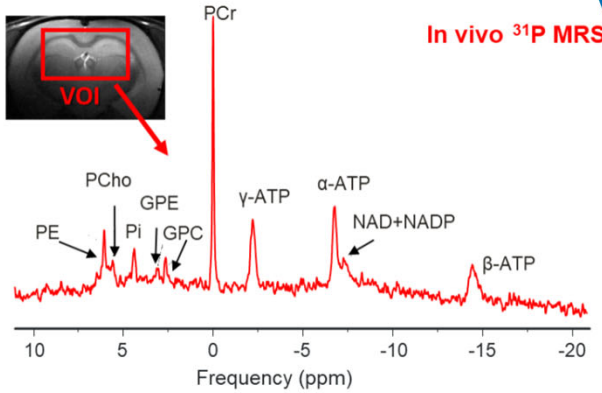


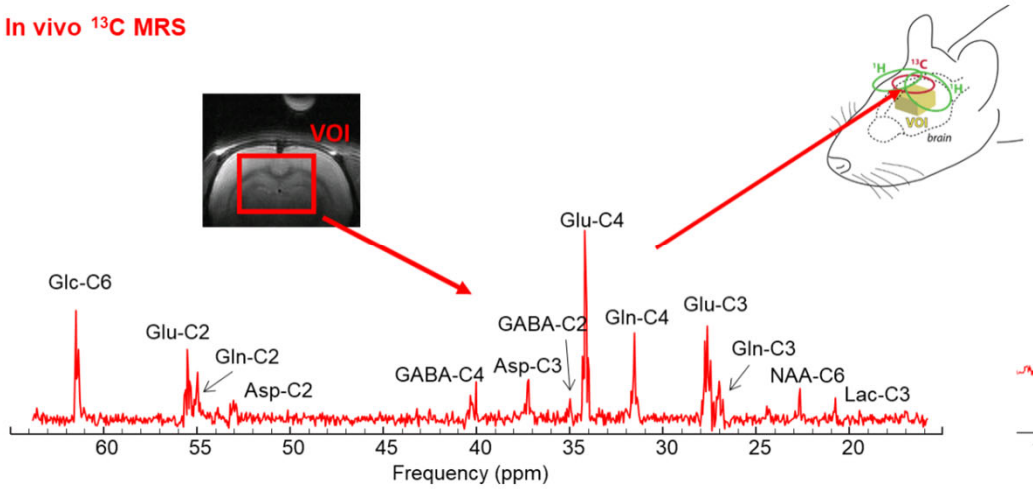
Courtesy of I Tkac

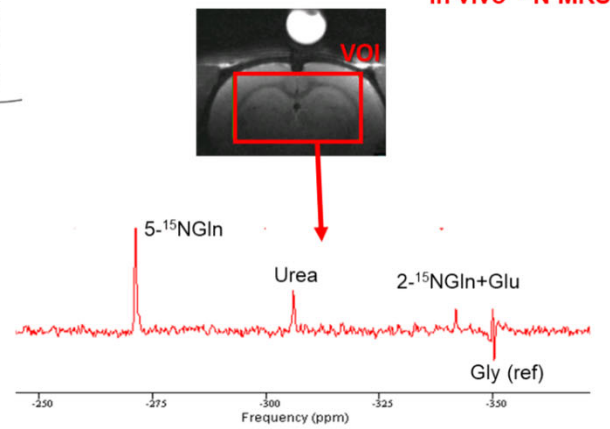
Oz G, et al., Clinical proton MR spectroscopy in central nervous system disorders. Radiology. 2014
Wilson M, et al., Methodological consensus on clinical proton MRS of the brain: Review and recommendations. Magn Reson Med. 2019

X NUCLEI MRS – 9.4T

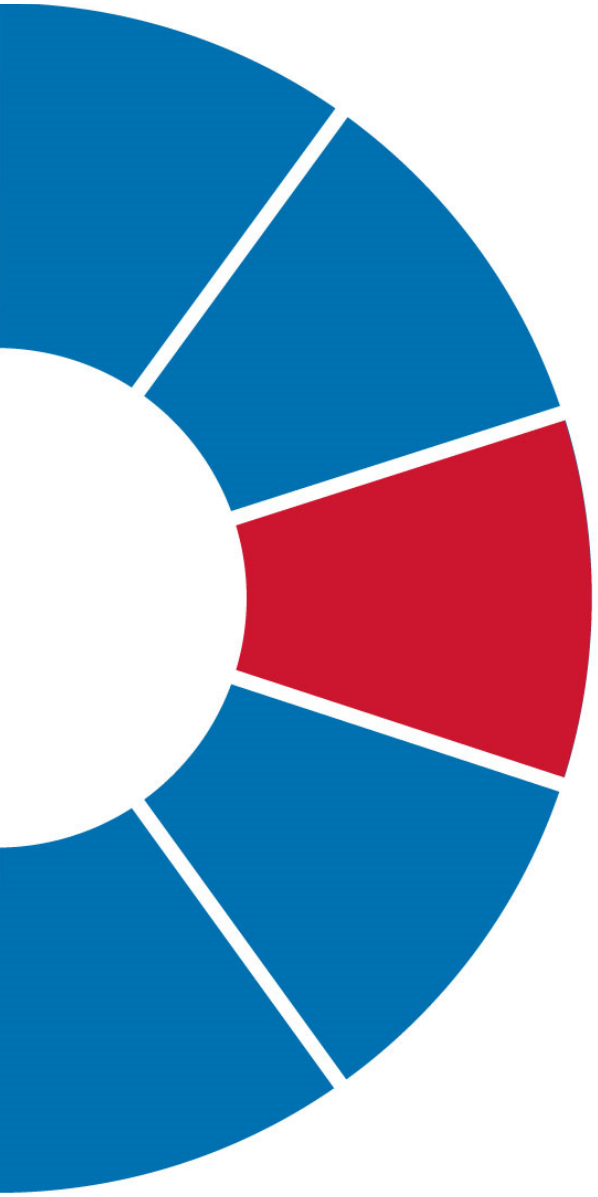








Lanz et al, 2017, 2020; Cudalbu et al 2021;



CLINICAL VS PRECLINICAL MRS

CLINICAL VS PRECLINICAL DATA

	Preclinical	Clinical
Subjects	Animal (rat/mouse) - anesthesia	Human – no anesthesia
Motion	☺	? ☹
Time for scanning	☺ Shim, WS, OVS, …	☹
@scanner	MRS experts	Not necessary MRS experts
Amount of data	+++	+++++++

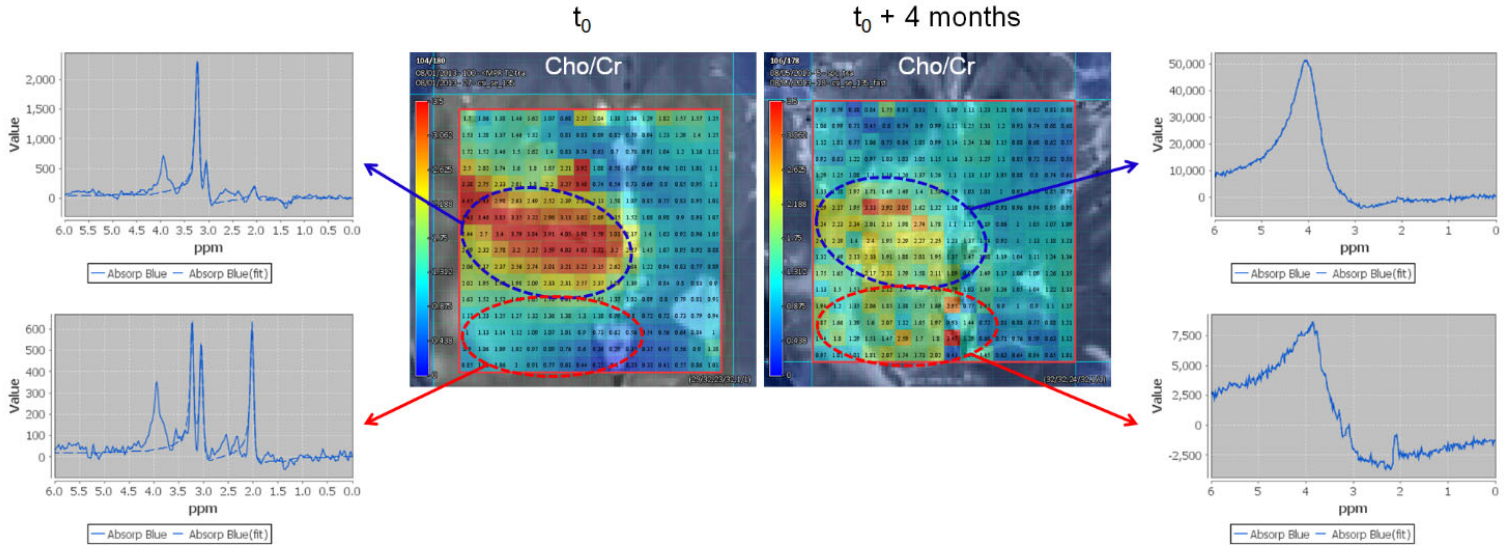
(Lots) Data with sometimes artifacts

- Need to be identified
- Corrected or data discarded
- Preprocessed
- Quantified

Clinicians

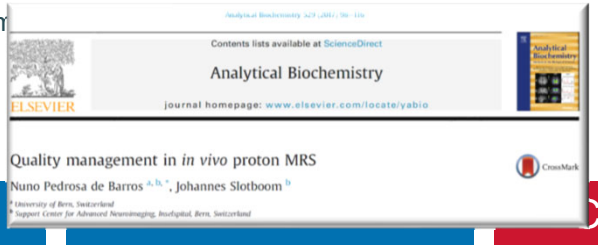
☹ Draw incorrect decisions
☹ Standard quantification software – NO quality check
☹ CRLB …..

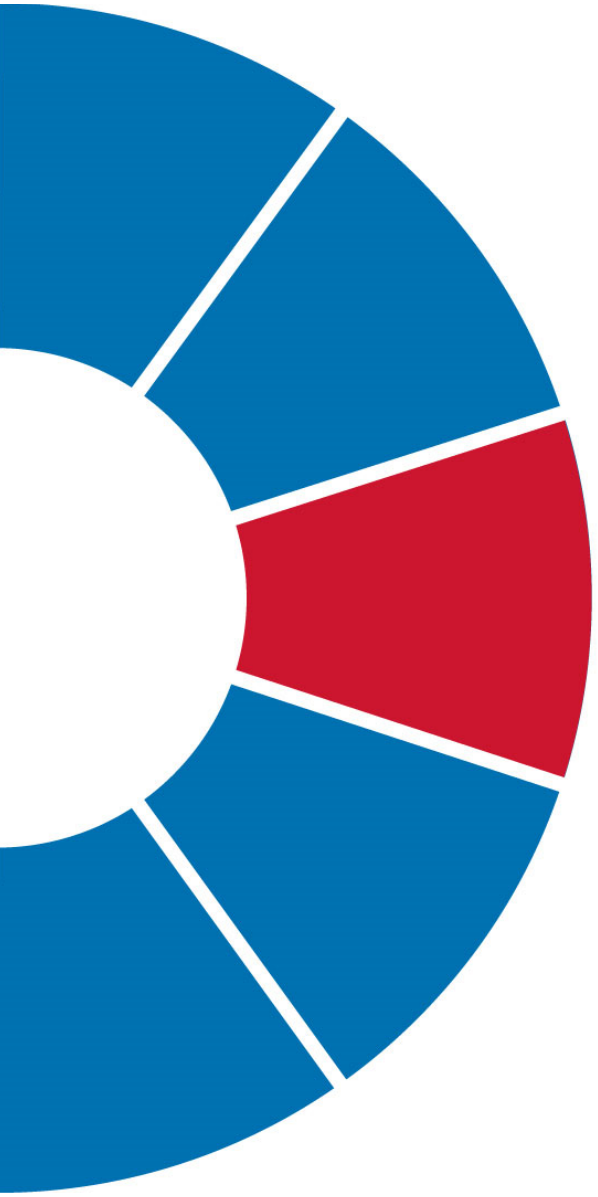
CLINICAL VS PRECLINICAL DATA



Example showing two Cho/Cr maps of a Glioma patient acquired 4 months apart.
Siemens Aera 1.5 T, 2D-PRESS, 12x12 interpolated to 32x32, TE/TR 135/1500m

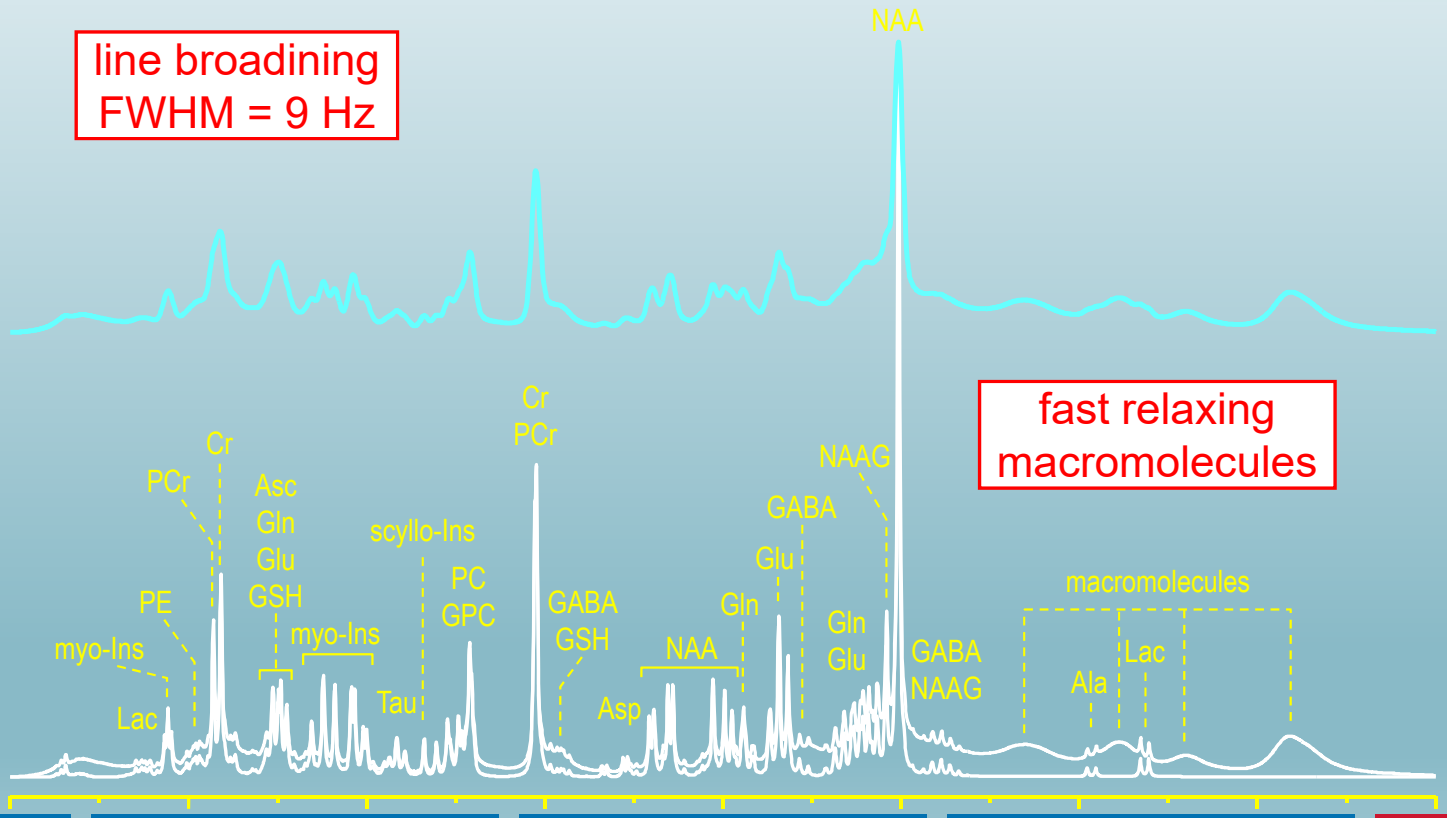
From N Barros et al, Analytical Biochemistry, 2017



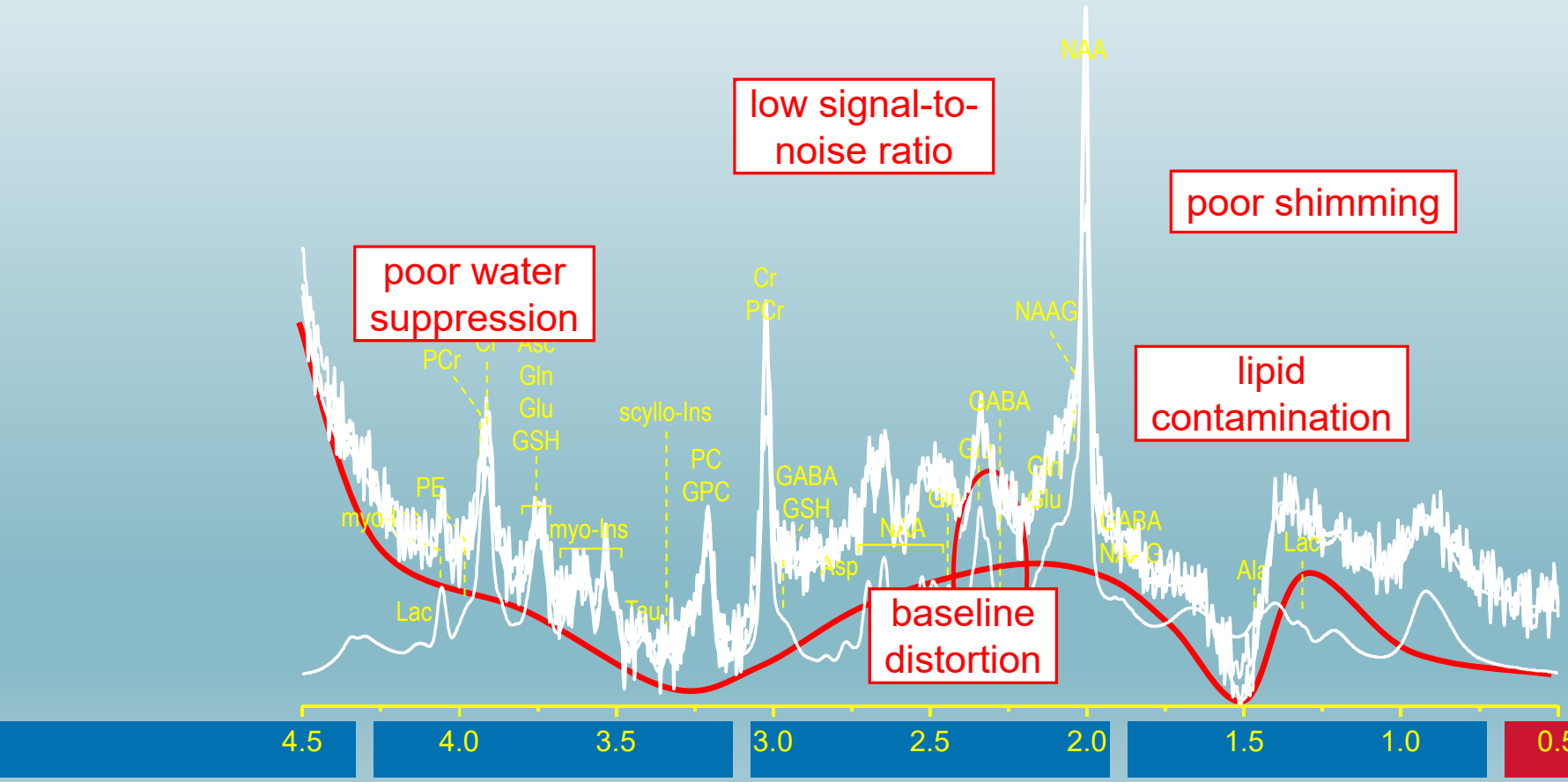


ARTIFACTS IN 1H MRS

SIMULATED HIGH-RESOLUTION 1H NMR SPECTRUM OF THE HUMAN BRAIN AT 7T



DISTORTIONS OF 1H NMR SPECTRUM OF THE HUMAN BRAIN AT 7T



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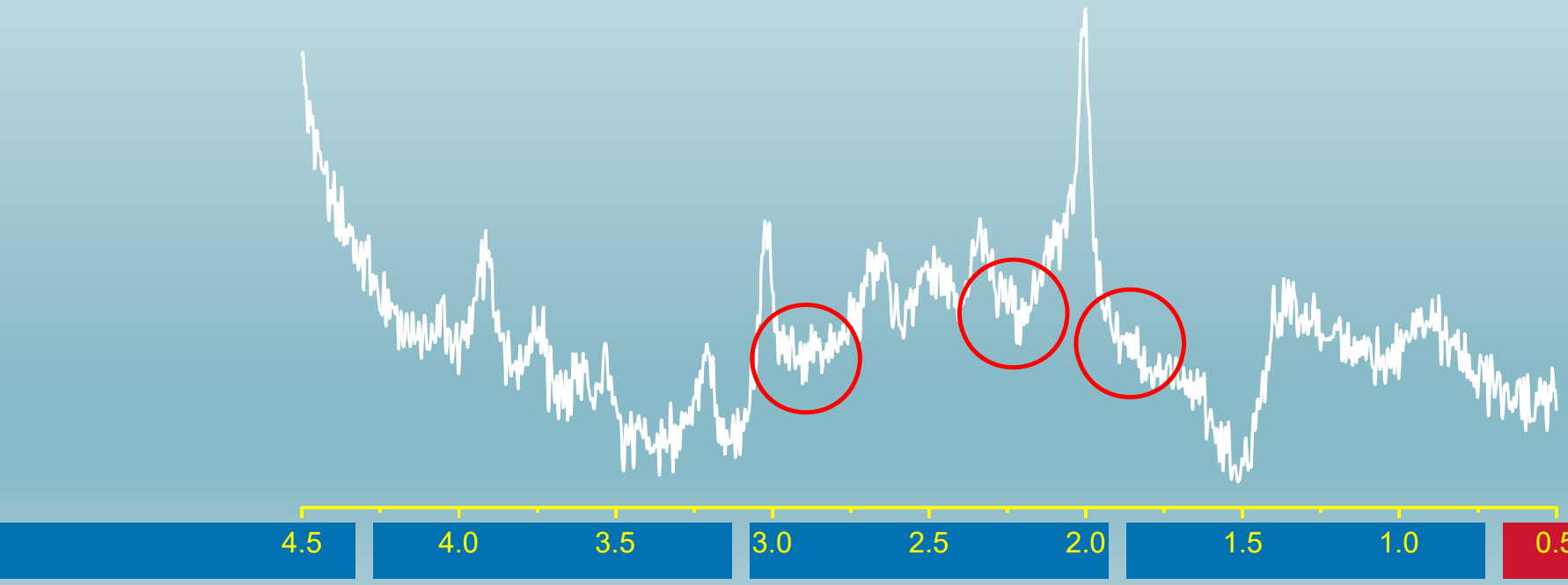
IS RELIABLE QUANTIFICATION OF GABA AND GLU POSSIBLE?

GLUTAMATE? DIFFICULT, LIMITED PRECISION

GABA? IMPOSSIBLE FROM THIS TYPE OF SPECTRA!!



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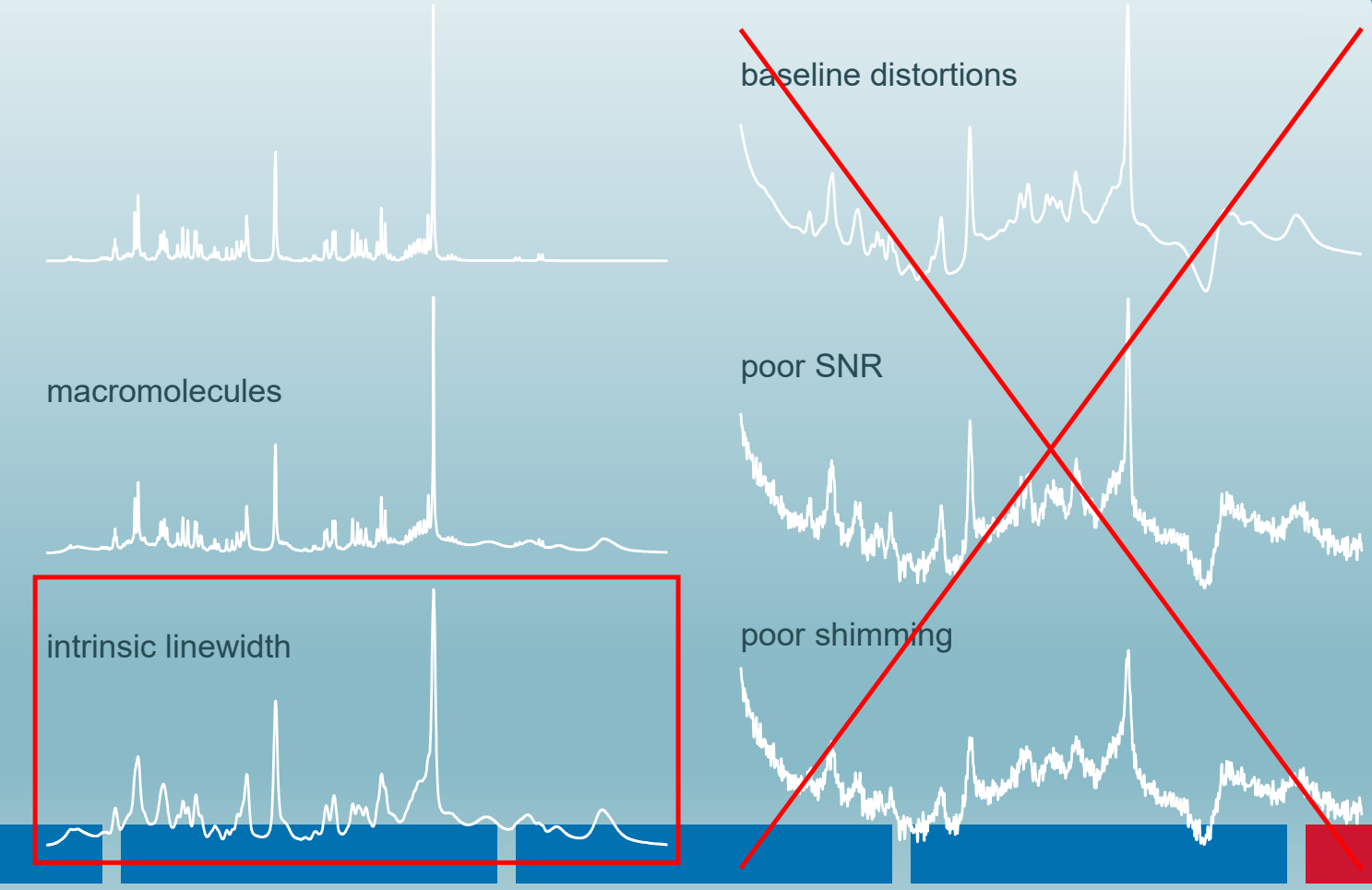
EFFECTS INFLUENCING SPECTRAL QUALITY



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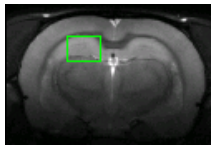
GOOD QUALITY DATA AT SHORT TE

- **Shimming: e.g. FASTMAP, MAPSHIM**
- **Pulse sequence at short TE**

Provide undistorted multiplets and no T_2 weighting

Increased no of metabolites

Improved quantification



- **Mouse MRS:**
  - ✓ **Small organ size (low SNR)**
  - ✓ **Susceptibility (artifacts)**
  - ✓ **Field inhomoheneities**

R Kreis 2004; C Cudalbu 2013 (450) Quality of MRS/MRSI – YouTube - I Tkac

ACQUISITION SEQUENCES

- Reduced CSDE
- Good localization :
  - double : OVS+Seq or LASER
- Strong crusher gradients
- Good WS

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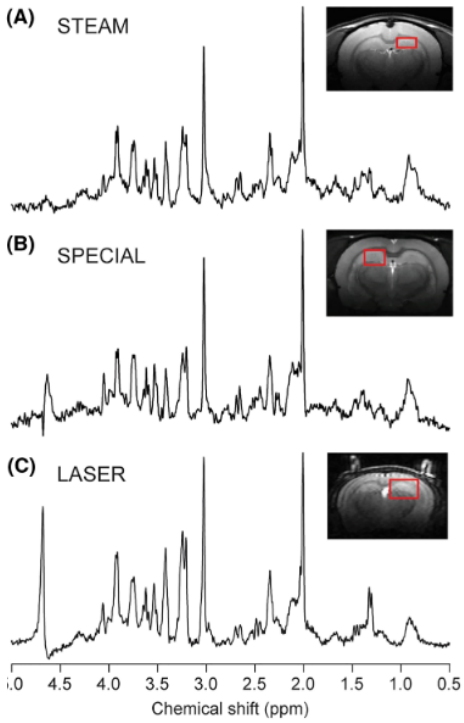
DOI: 10.1002/nbm.4325

SPECIAL ISSUE REVIEW ARTICLE

NMR IN BIOMEDICINE WILEY

Magnetic resonance spectroscopy in the rodent brain: Experts' consensus recommendations

FIGURE 3 Example ^{1}H MR spectra obtained in rodent brains at 9.4 T with STEAM (A), SPECIAL (B) and LASER (C) sequences. A, STEAM spectrum: rat brain, 2.3 × 1.3 × 2.5 mm^3 voxel placed in the hippocampus, TR = 5 s, TE = 2 ms, TM = 20 ms, number of averages = 448. Spectrum is shown with Gaussian factor = 0.15. B, SPECIAL spectrum: rat brain, 2 × 2.8 × 2 mm^3 voxel placed in the hippocampus, TR = 4, TE = 2.8 ms, number of averages = 160. C, LASER spectrum: mouse brain, 1.7 × 2.25 × 2.25 mm^3 voxel placed in hippocampus, TR = 4 s, TE = 27 ms, number of averages = 384. The STEAM spectrum was provided by Ivan Tkáč



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DOI: 10.1002/nbm.4459

SPECIAL ISSUE REVIEW ARTICLE

NMR IN BIOMEDICINE WILEY

Water and lipid suppression techniques for advanced ^{1}H MRS and MRSI of the human brain: Experts' consensus recommendations

Ivan Tkáč[1] | Dinesh Deelchand[1] | Wolfgang Dreher[2] | Hoby Hetherington[3] | Roland Kreis[4] | Chathura Kumaragamage[5] | Michal Považan[6] | Daniel M. Spielman[7] | Bernhard Strasser[8] | Robin A. de Graaf[5]

Received: 15 March 2019 | Revised: 29 October 2019 | Accepted: 7 November 2019
DOI: 10.1002/nbm.4236

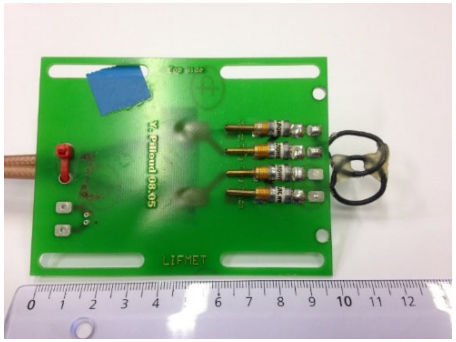
SPECIAL ISSUE REVIEW ARTICLE

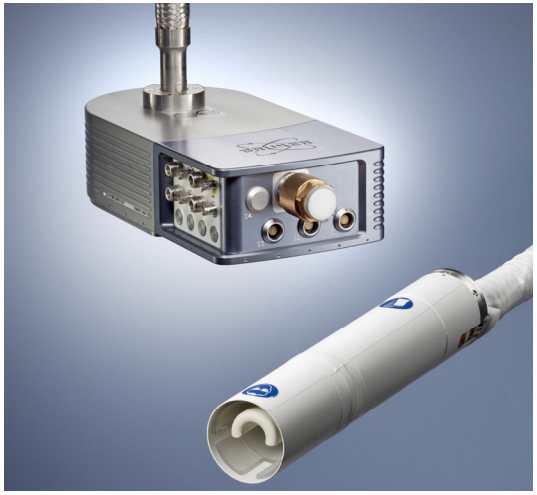
WILEY NMR IN BIOMEDICINE

Advanced single voxel ^{1}H magnetic resonance spectroscopy techniques in humans: Experts' consensus recommendations

Gülin Öz[1] | Dinesh K. Deelchand[1] | Jannie P. Wijnen[2] | Vladimír Mlynárik[3] | Lijing Xin[4] | Ralf Mekle[5] | Ralph Noeske[6] | Tom W.J. Scheenen[7,8] | Ivan Tkáč[1] | the Experts' Working Group on Advanced Single Voxel ^{1}H MRS

RF COILS





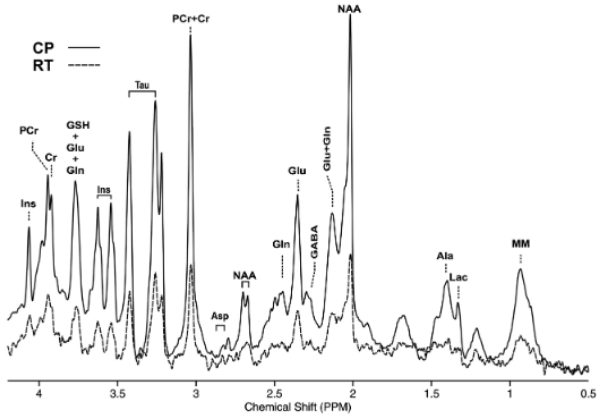


FIGURE 1 Spectra acquired with the STEAM sequence (TR/TE = 5000/3.5 ms, 384 averages) in a 2.0 × 1.1 × 2.0 mm^3 VOI located in the mouse frontal cortex. A cryogenically cooled ^1H two-element phased-array transmit/receive coil was employed for excitation and signal reception (solid line). As a comparison, a 72 mm diameter birdcage quadrature volume resonator was used for excitation and a ^1H receive-only 2 × 2 surface array coil was used for signal reception (dotted line). A 5.2-fold higher SNR was obtained with the cryoprobe (CP) compared with the room-temperature probe (RT)

Received: 11 November 2019 | Revised: 29 March 2020 | Accepted: 30 April 2020
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SPECIAL ISSUE REVIEW ARTICLE

NMR IN BIOMEDICINE WILEY

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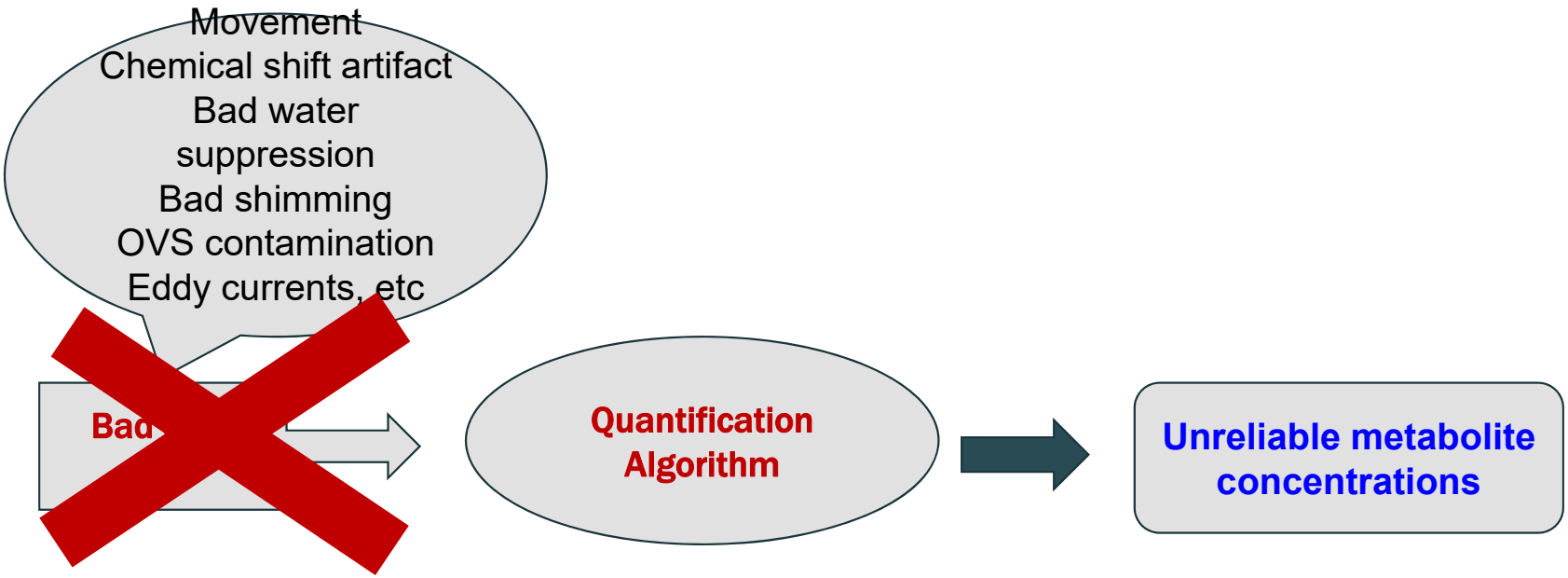
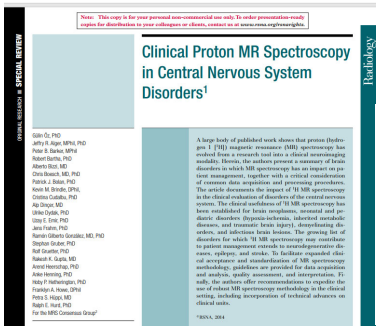
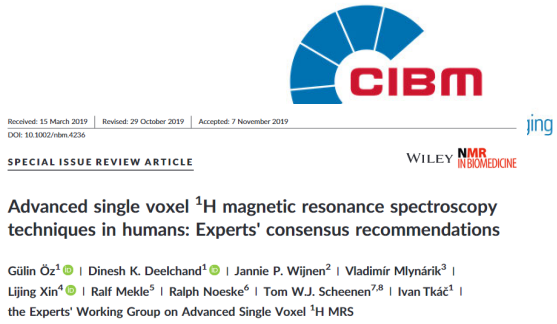


ISMRM 2010, Potentials and Challenges at High Field MRS
R Kreis, NMR Biomed 2004, 17:361
Tkáč I, et al, Appl Magn Reson. 2005 29:139.

MINIMUM QUALITY CRITERIA





Signal

- SNR >3 for major resonances
- Linewidth - shimming
- Lineshape – symmetric
- WS
- No lipid contamination
- No other visible artifacts
  - Not so obvious artifacts (Chemical shift artifact, localization inaccuracies, signal cancellation, etc)
- CRBs
- Residuals with unexplained features

Quantification

ISMRM 2010, Potentials and Challenges at High Field MRS
R Kreis, NMR Biomed 2004, 17:361
Tkáč I, et al, Appl Magn Reson. 2005 29:139.
http://www.ismrm.org/workshops/Spectroscopy16/program.htm
2nd TRANSACT Workshop, University Bern: Quality Issues in Clinical MRS 2014
The MRS Consensus Group. (2014), Radiology, 270(3):658-79.

OVERALL NEEDS

1. Acquisition part:

- ***The MRS Consensus Group.*** **(2014) Clinical Proton MR Spectroscopy in Central Nervous System Disorders, *Radiology*, 270(3):658-79.**
  - Facilitate the wider use of MRS for brain diseases
  - Highlight the clinical benefits of using MRS as a part of a standard MR exam
  - Spectral quality standards
  - Encourage across-vendors standardization
  - Clos the gap between standard MRS and optimized methodology used in research centers
  - Recommendations : Standardization of data acquisition, analysis and reporting of results
    Automation of preparation phases for MRS acquisition and processing

- ***Methodological consensus on clinical proton MRS of the brain: Review and recommendations*****, Magn Reson Med. 2019 Aug;82(2):527-550.**
  - Guidance on the best practices for clinical MRS
  - Highlight the shortcomings of current commercially available MRS sequences
  - Highlight research efforts to improve these shortcomings

OVERALL NEEDS

1. Acquisition part:

Received: 15 March 2019 | Revised: 29 October 2019 | Accepted: 7 November 2019
DOI: 10.1002/nbm.4236

SPECIAL ISSUE REVIEW ARTICLE

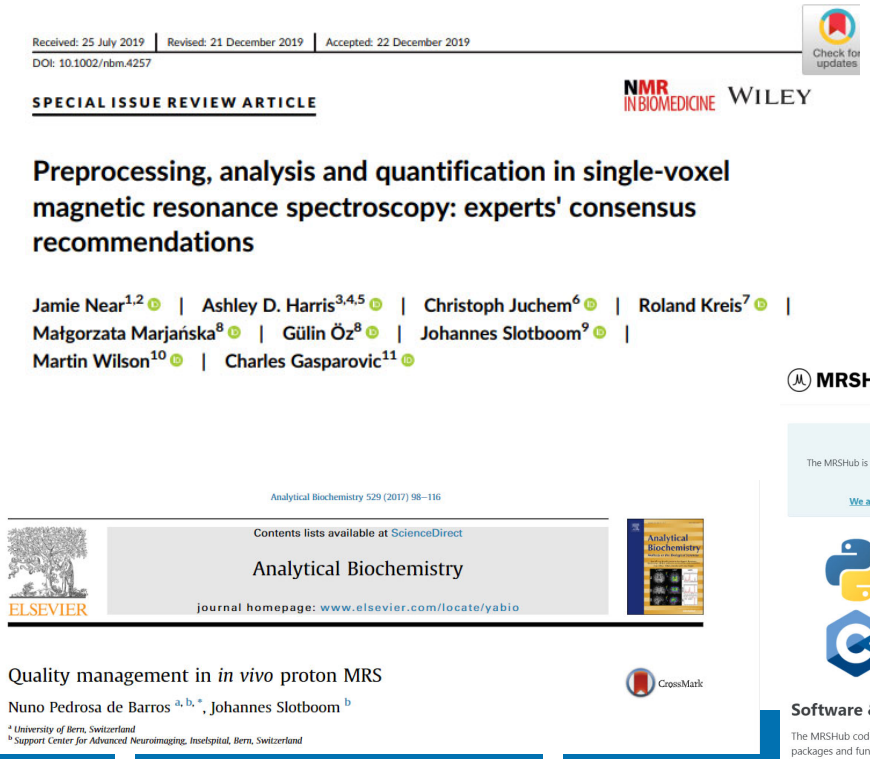
WILEY NMR IN BIOMEDICINE

Advanced single voxel ^{1}H magnetic resonance spectroscopy techniques in humans: Experts' consensus recommendations

Gülin Öz[1] | Dinesh K. Deelchand[1] | Jannie P. Wijnen[2] | Vladimír Mlynárik[3] | Lijing Xin[4] | Ralf Mekle[5] | Ralph Noeske[6] | Tom W.J. Scheenen[7,8] | Ivan Tkáč[1] | the Experts' Working Group on Advanced Single Voxel ^{1}H MRS

OVERALL NEEDS

2. Processing part:



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SPECIAL ISSUE REVIEW ARTICLE

NMR IN BIOMEDICINE WILEY

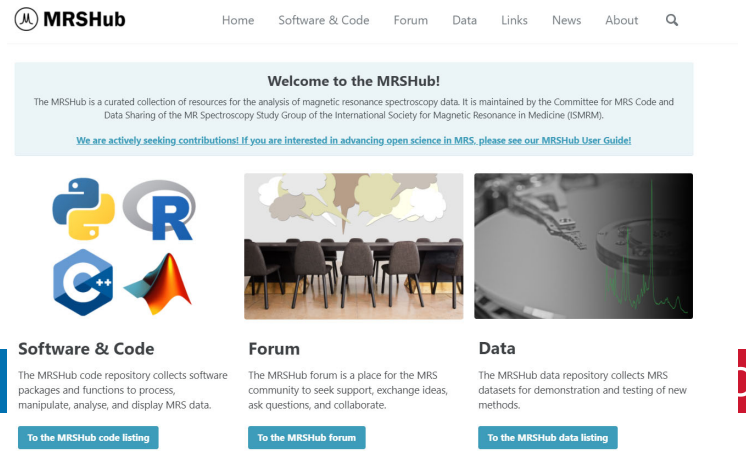
Preprocessing, analysis and quantification in single-voxel magnetic resonance spectroscopy: experts' consensus recommendations

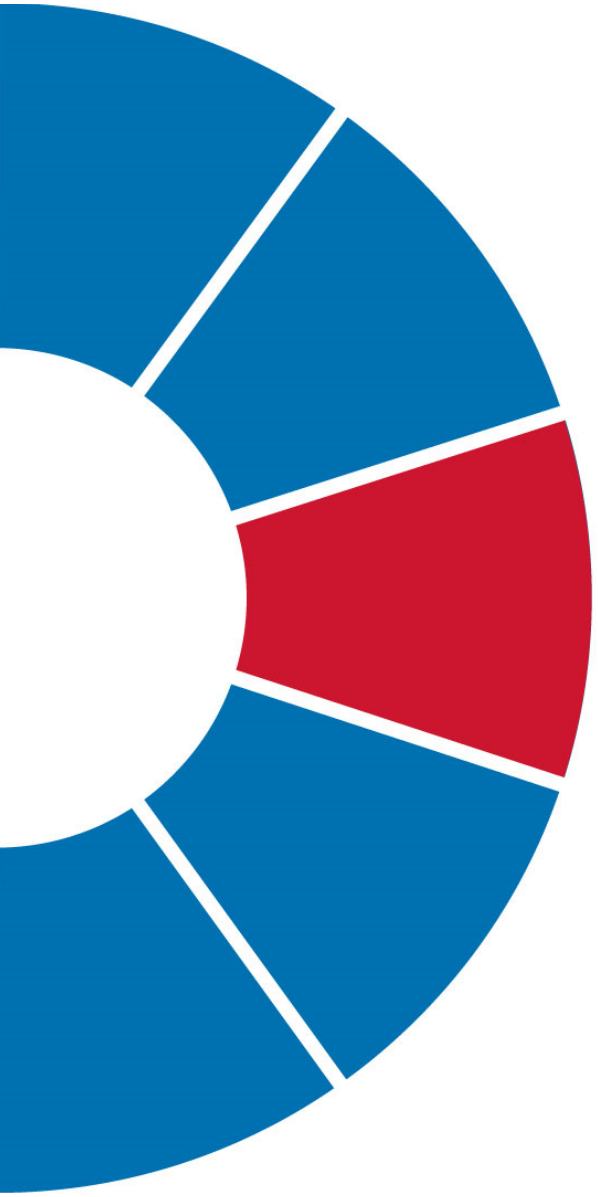
Jamie Near[1,2] | Ashley D. Harris[3,4,5] | Christoph Juchem[6] | Roland Kreis[7] | Małgorzata Marjańska[8] | Gülin Öz[8] | Johannes Slotboom[9] | Martin Wilson[10] | Charles Gasparovic[11]

Analytical Biochemistry 529 (2017) 98–116
Contents lists available at ScienceDirect
Analytical Biochemistry
journal homepage: www.elsevier.com/locate/yabio

Quality management in *in vivo* proton MRS

Nuno Pedrosa de Barros [a, b, *], Johannes Slotboom [b]
[a] University of Bern, Switzerland
[b] Support Center for Advanced Neuroimaging, Inselspital, Bern, Switzerland





QUALITY MANAGEMENT-QUALITY CONTROL

OVERALL NEEDS

2. Quality control (Quality Management)

3. Preprocessing

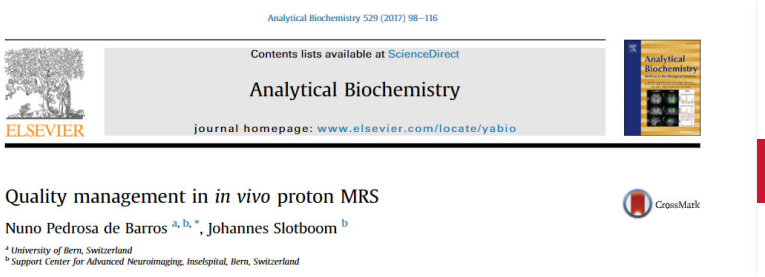
4. Quantification

5. Results display

AUTOMATED

QUALITY MANAGEMENT

- Quality Planning – quality targets
- Quality Assurance – identification of what might go wrong – battery of tests on well defined phantoms - identify the not so obvious artifacts
- **Quality Control – detection of artifacts (rejection or correction)**
  - **Signal Quality Control**
  - **Quantification Quality Control**
- Quality Improvement



N Barros et al, Analytical Biochemistry, 2017

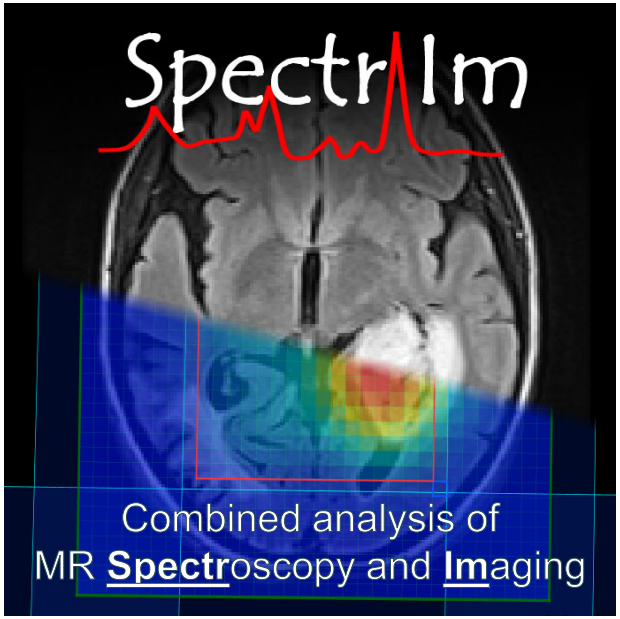
QUALITY CONTROL

- Manual quality control - not an option
  - Time demanding
  - Needs MRS experts
  - Subjective
- Automatic quality control
  - Semi-automatic – INTERPRET project[1]
  - Automatic - several published – pattern recognition algorithms
    - A.J. Wright, et al Magn. Reson. Med. 59 (2008) 1274–1281.
      - ICA (features) + LS support vector machine (classification)
    - Kyathanahally SP et al, ISMRM (2016).
      - More features (30) and classifier handles imbalanced data

[1] M. van der Graaf, et al, NMR Biomed. 21 (2008) 148–158.

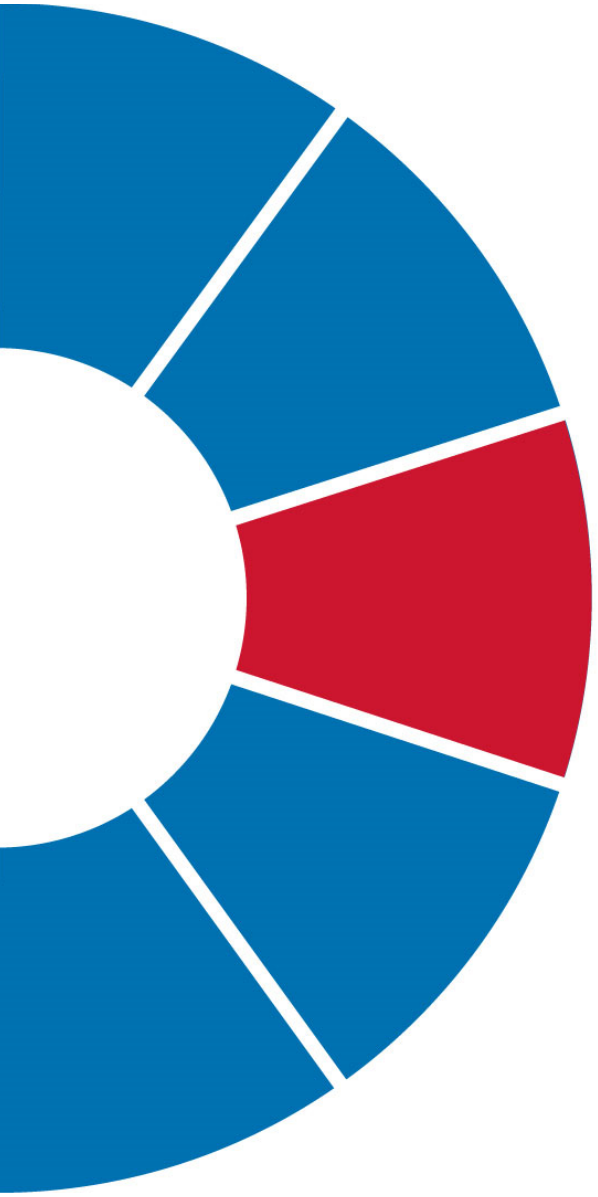
QUALITY CONTROL

- Allow the combined exploration of MRI and MRS data
- Features:
  - For researcher/programmer
  - For the clinician
- Works as an "artifact/low SNR detector", so it doesn't substitute CRLB or the fit quality number.



- New random forest based method for automatic quality assessment
- New set of MRS features - 47 of them (time and frequency domain)
- Trained of spectra from 40 MRSI grids

Pedrosa de Barros N, et al, NMR Biomed. 2016 May;29(5):563-75.



PREPROCESSING STEPS

PREPROCESSING STEPS

- Phase offsets (0 and 1st order)
- Subject motion
- Scanner drift
- Eddy currents
- Alignment of spectra that need to be added/subtracted
- Water contamination
- …..

PREPROCESSING STEPS

- Why ?
  - quantification algorithms do not account for all of them
  - Lead to errors in the quantification process

- Requirements:
  - Automated methods
  - Included in the quantification software

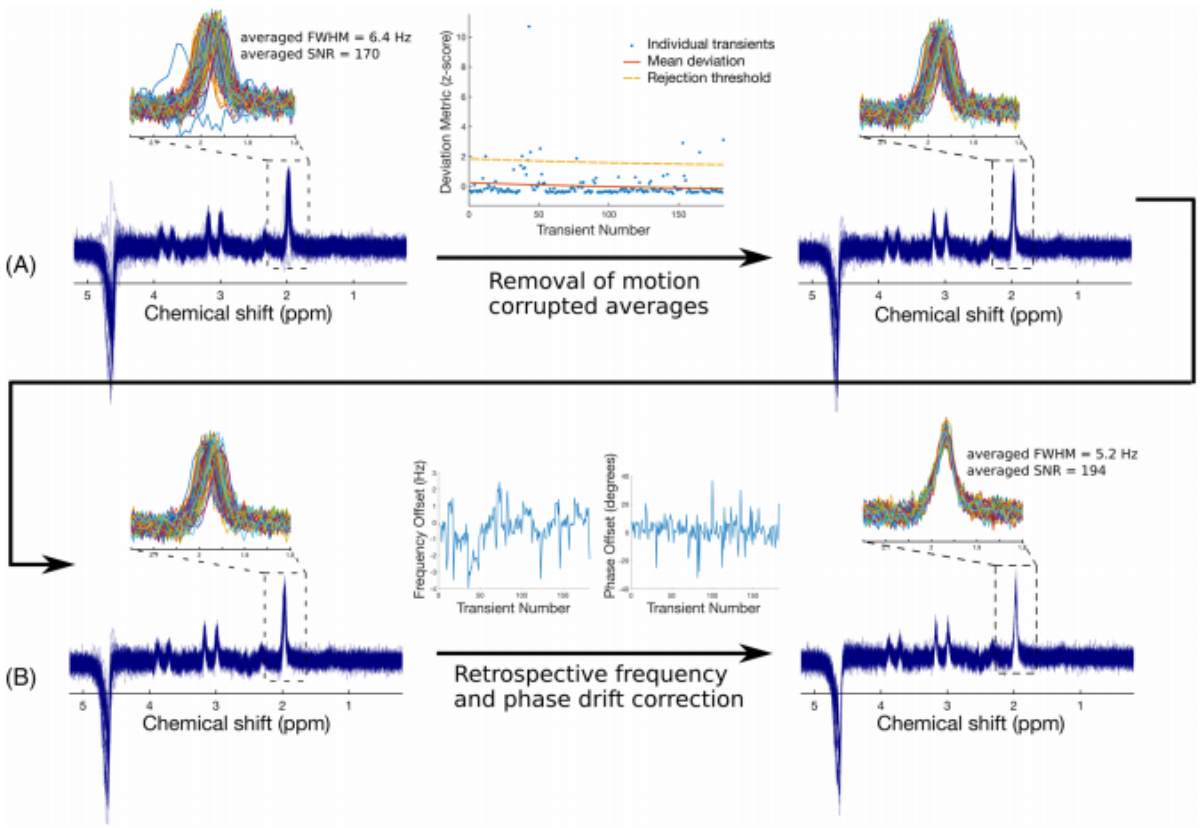
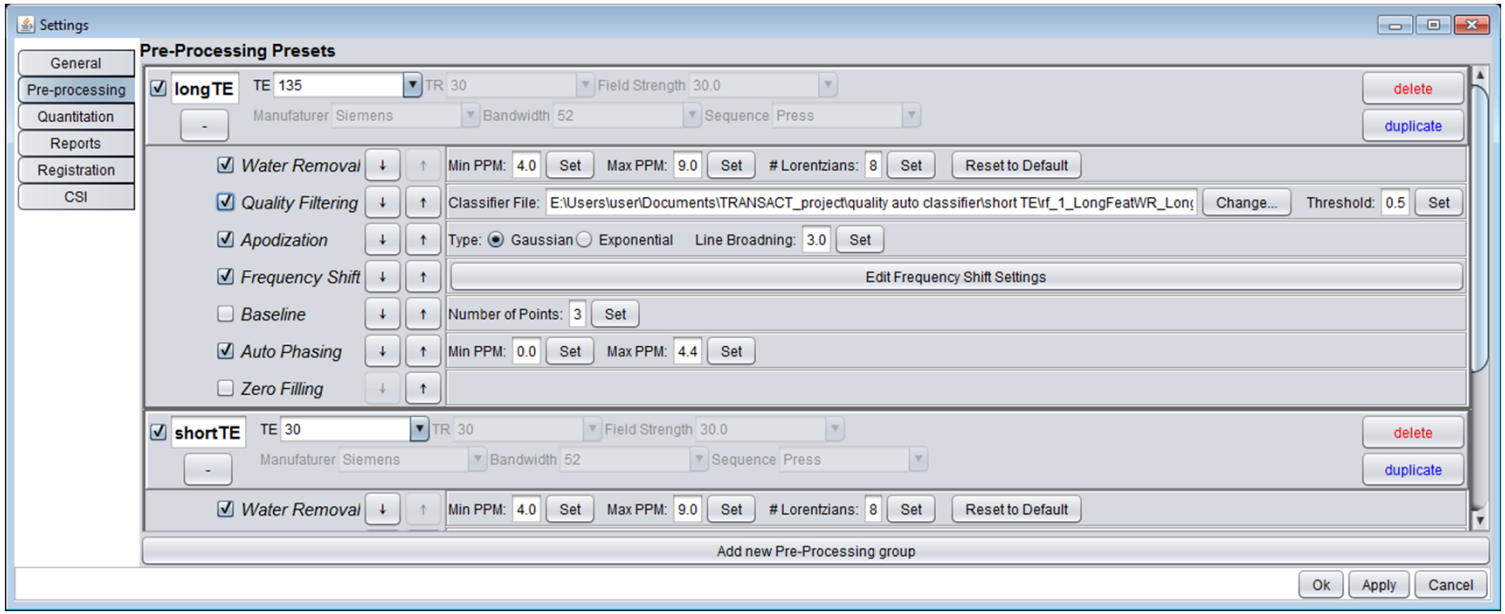


FIGURE 2 Removal of corrupted transients and retrospective frequency and phase drift correction from a 3 T human brain PRESS acquisition with T_E = 270 ms. A, Removal of motion-corrupted transients. Corrupted transients stand out as noticeably different from the others, and are effectively removed using an unsupervised outlier removal procedure (see reference 15). B, subsequent retrospective frequency and phase drift correction. Following drift correction using spectral registration, the individual transients have improved coherence and can now be averaged. These processing steps yield a marked improvement in both the full-width at half-maximum (FWHM) and SNR of the final averaged spectrum

PREPROCESSING

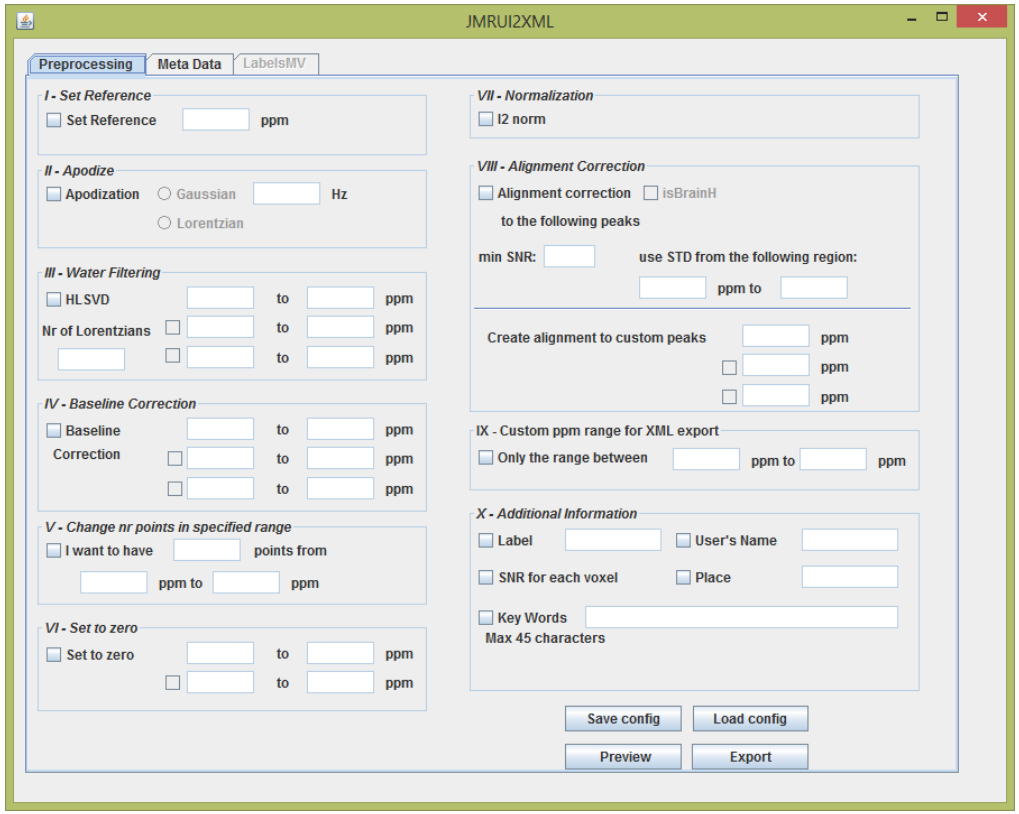
SpectrIm

CIBM Center for Biomedical Imaging



Pedrosa de Barros N, et al, NMR Biomed. 2016 May;29(5):563-75.

PREPROCESSING: JMRUI2XML



Mocioiu V, et al, BMC Bioinformatics. 2015 Nov 9;16:378.

1) automates magnetic resonance spectroscopy preprocessing
2) platform for outputting exchangeable MRS data.

CIBM.CH

PREPROCESSING

Practical aspects

- Recently released software capable of all preprocessing routines just described (and many more): The FID Appliance (FID-A) [5].
  - Free, open source, MATLAB-based
  - github.com/CIC-methods/FID-A

5. Simpson R et al. MRM, in press.

http://www.ismrm.org/workshops/Spectroscopy16/program.htm

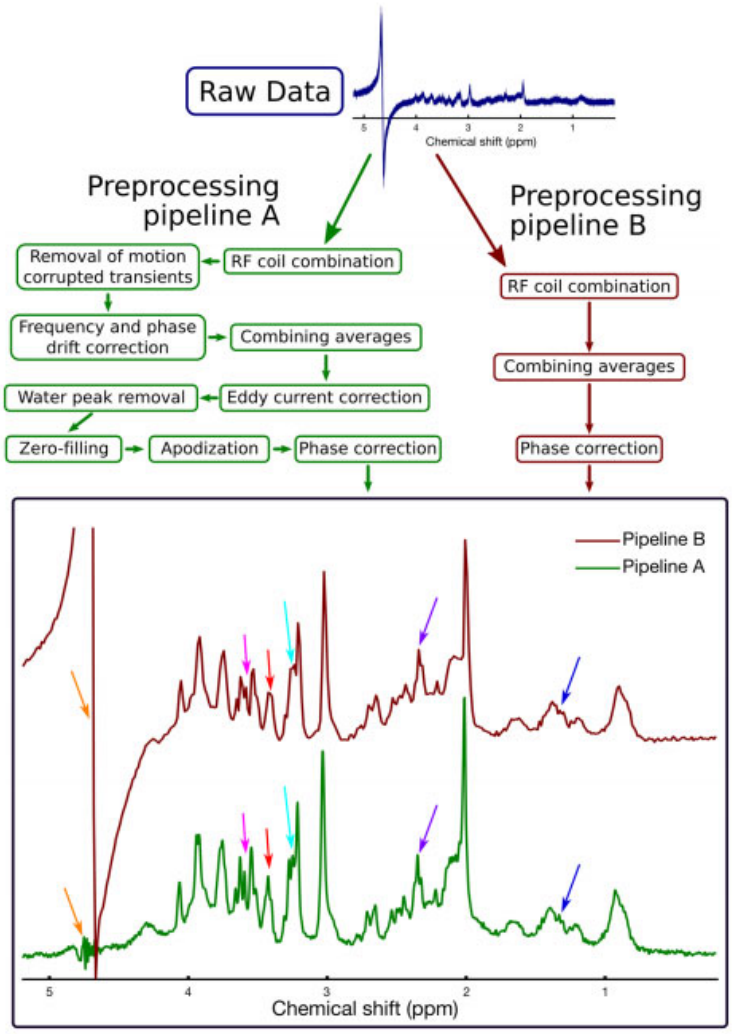
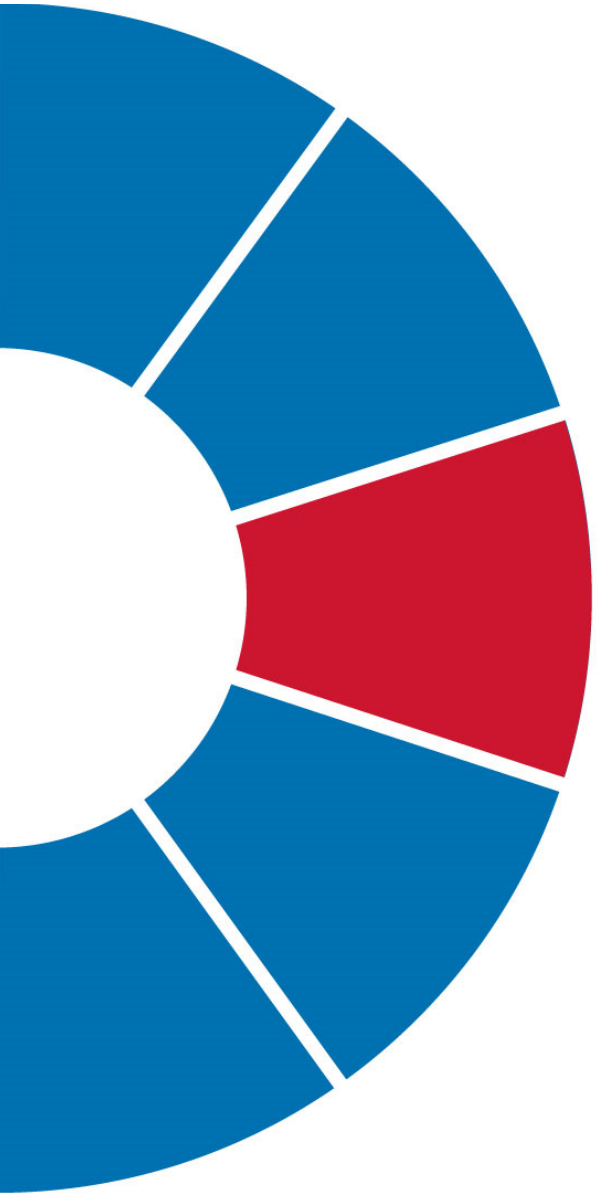


FIGURE 4 Illustration of two example processing pipelines, applied to the same raw data. The dataset was obtained from a rat brain using the PRESS sequence at 7 T with T_E = 11 ms. Processing pipeline B (dark red boxes, right-hand side) includes only basic steps to combine the coils and transients (similar to the standard processing pipeline provided by clinical scanner vendors). Processing pipeline A (green boxes, left-hand side) involves additional steps to remove motion-corrupted averages, to retrospectively correct frequency and phase drift, and to remove eddy current artefacts. Pipeline A resulted in several noticeable improvements in spectral quality, including reduced water contamination (orange arrows), and improved visual definition of most spectral peaks, including lactate (1.3 ppm, dark blue arrows), glutamate-H4 (2.3 ppm, purple arrows), tCho (3.2 ppm, light blue arrows), taurine (3.4 ppm, red arrows) and *myo*-inositol (3.5 ppm, pink arrows). These improvements highlight the importance of using an appropriate processing pipeline. Note that, as stated in the recommendation tables, zero-filling and apodization may be used to improve the visual appearance of the spectrum, but should not be performed prior to spectral analysis

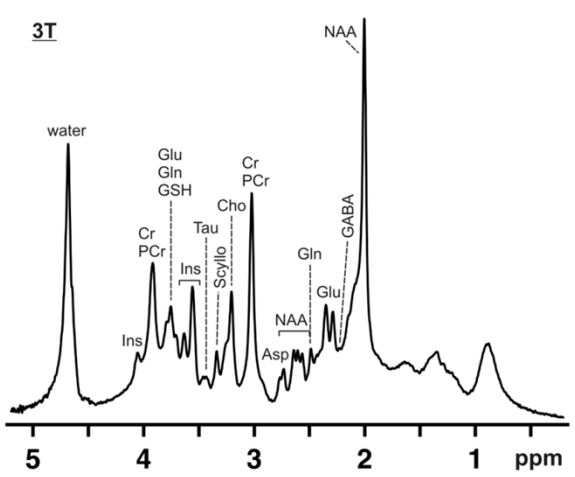


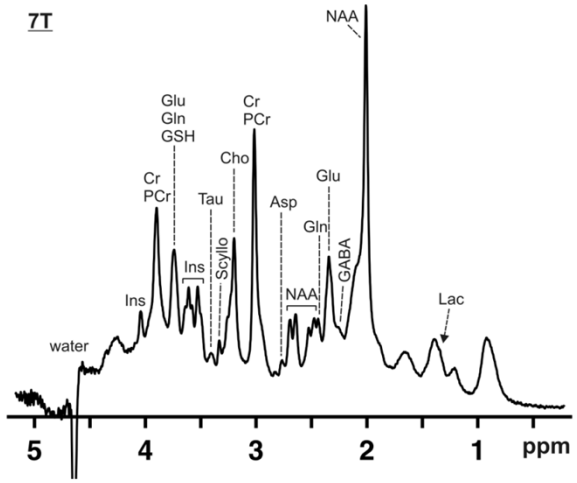
QUANTIFICATION SOFTWARE

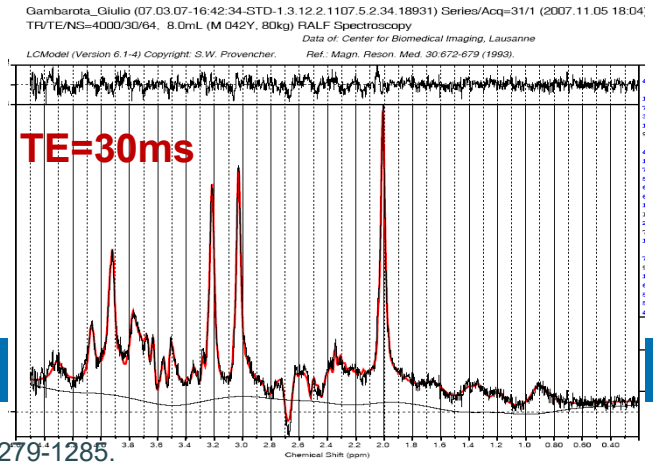
QUANTIFICATION

- MRS – principal goal – quantification of changes in concentration of known metabolites
- Accurate and precise quantification:
  - Signal quality
    - Hardware performance
    - Pulse sequence design & adjustment
  - Data (pre)processing (estimate the signal amplitude or peak area)
  - Quantification strategies (→ tissue content)
- Final Goal:
  - Maximize the neurochemical information
  - Increase the precision and accuracy of quantification
  - Maximize the reliability of neurochemical data

QUANTIFICATION







Merkle R, et al. Magn Reson Med 61, 1279-1285.

QUANTIFICATION

Signals are different (acq param, Bo, nucleus, etc)

– quantification is also different

THE ALGORITHMS ARE AUTOMATIC
BUT NOT FULLY PUSH-BUTTON
NEED TO BE ADAPTED

QUANTIFICATION

In vivo spectra - high B_0

- short TE

→ Increased - sensitivity
- spectral resolution

is difficult:

- Complexity of the spectra:
  - many resonances
  - peak overlap
  - contribution of macromolecules and residual water
- Unpredictable lineshape :
  - residual eddy currents
  - field inhomogeneity
- Unpredictable baseline:
  - macromolecules
  - lipid signals
  - partially suppressed water

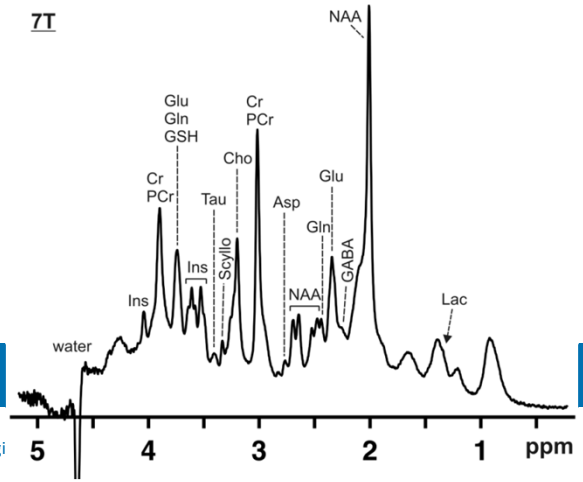
QUANTIFICATION

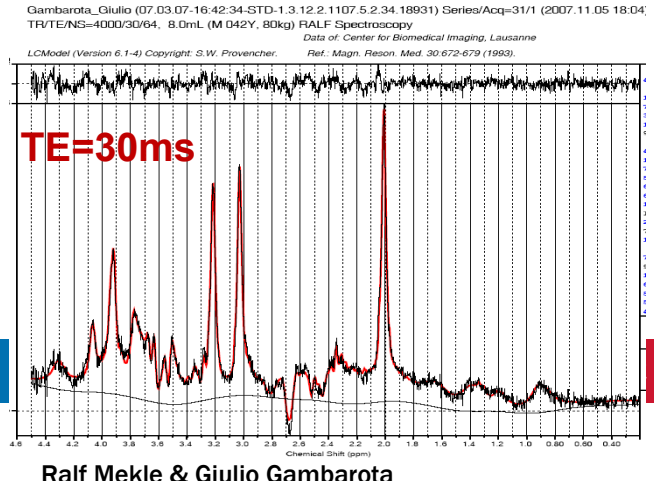
In vivo spectra - high B_0

- short TE

→ Increased - sensitivity

- spectral resolution





Ralf Mekle & Giulio Gambarota

IBM.CH

QUANTIFICATION

☹Vendors software - visualization of spectra

☹Peak fitting - !!!! Overlapping peaks ☹

☺X nuclei

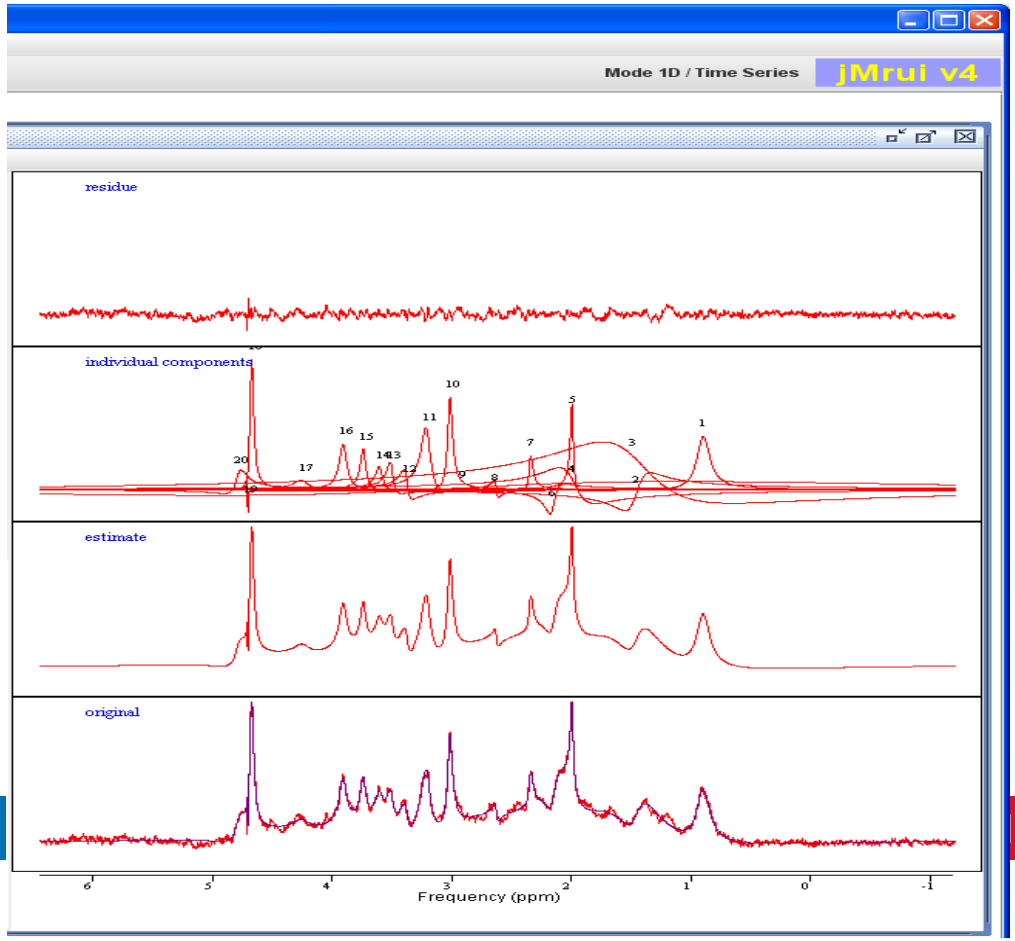
☺"Basis-set" fitting – In vivo MRS spectrum is modelled as a linear combination of individual metabolite basis spectra

- Experimentally
- Simulated
  - User-friendly software packages: NMRScopeB, Vespa, GAMMA, GAVA, ….
- Macromolecules contribution
- Lipids contribution (i.e. malignant brain tumors)

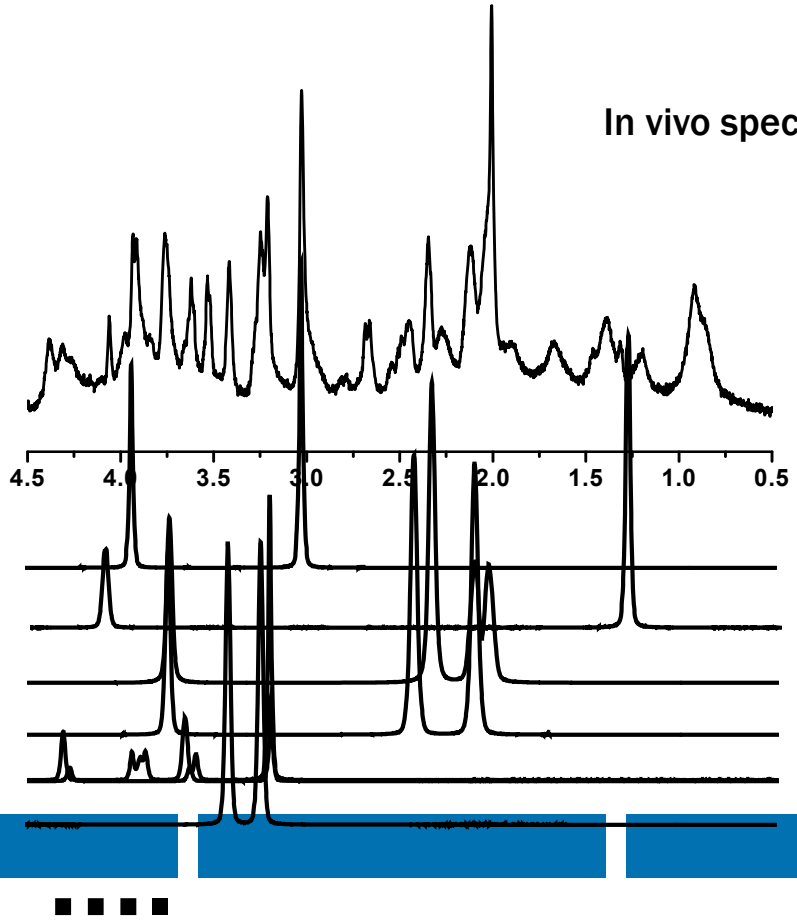
SHORT DESCRIPTION OF THE ALGORITHMS

HLSVD quantification

Amplitude	sd. Amp.
666.88	0.2707
676.74	0.1729
333.53	2.40
140.71	0.6707
1.971E4	0.9626
1.111E3	3.45
1.455E3	2.14
479.78	138.56
475.13	34.35
420.84	46.61
551.35	18.94
837.73	11.91
351.08	226.13
1.112E3	0.2797
33.12	0.0265
614.40	0.0191



QUANTIFICATION WITH A BASIS SET



QUANTIFICATION SOFTWARE

	Cost	Type of data	Preprocessing	Simulations	Lineshape model	MM
Vespa	free	all	yes	yes	yes	yes
TARQUIN	free	all	yes	Yes – basic	Voigt	Baseline –TD Add
jMRUI	free	all	yes	yes	Lorentzian	Add TD
LCModel	Yes	all	yes	No Basis sets	estimated	Splines

Anke Henning. eMagRes, 2016, Vol 5: 981–994. DOI 10.1002/9780470034590.emrstm1472
Dirk van Ormondt, et al, eMagRes, 2015, Vol 4: 651–662. DOI 10.1002/9780470034590.emrstm1427
Jamie Near, Magnetic Resonance Spectrscopy Elsevier 2014
Jamie Near, et al, NMR Biomed, 2020 **https://doi.org/10.1002/nbm.4257**

MACROMOLECULES

Received: 21 November 2019 | Revised: 8 July 2020 | Accepted: 13 July 2020

DOI: 10.1002/nbm.4393

SPECIAL ISSUE REVIEW ARTICLE

NMR IN BIOMEDICINE WILEY

Contribution of macromolecules to brain ^{1}H MR spectra: Experts' consensus recommendations

Cristina Cudalbu[1] | Kevin L. Behar[2] | Pallab K. Bhattacharyya[3] | Wolfgang Bogner[4,5] | Tamas Borbath[6,7] | Robin A. de Graaf[8] | Rolf Gruetter[9] | Anke Henning[10,6] | Christoph Juchem[11] | Roland Kreis[12] | Phil Lee[13] | Hongxia Lei[1] | Małgorzata Marjańska[14] | Ralf Mekle[15] | Saipavitra Murali-Manohar[6,7] | Michal Považan[16] | Veronika Rackayová[1,9] | Dunja Simicic[1,9] | Johannes Slotboom[17] | Brian J. Soher[18] | Zenon Starčuk Jr.[19] | Jana Starčuková[19] | Ivan Tkáč[14] | Stephen Williams[20] | Martin Wilson[21] | Andrew Martin Wright[6,22] | Lijing Xin[1] | Vladimír Mlynárik[4,5]

Received: 27 January 2021 | Revised: 25 May 2021 | Accepted: 11 June 2021

DOI: 10.1002/mrm.28910

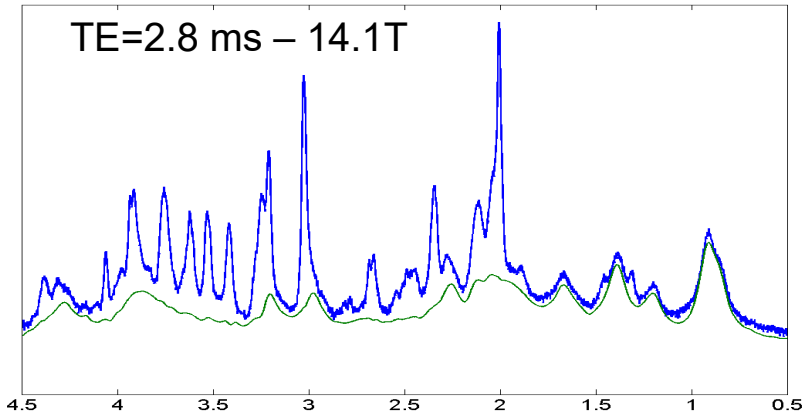
FULL PAPER

Magnetic Resonance in Medicine

In vivo macromolecule signals in rat brain ^{1}H-MR spectra at 9.4T: Parametrization, spline baseline estimation, and T_2 relaxation times

Dunja Simicic[1,2,3] | Veronika Rackayova[1,2] | Lijing Xin[1,2] | Ivan Tkáč[4] | Tamas Borbath[5,6] | Zenon Starcuk Jr[7] | Jana Starcukova[7] | Bernard Lanz[3] | Cristina Cudalbu[1,2]

MACROMOLECULES



Low molecular weight metabolites

High molecular weight macromolecules

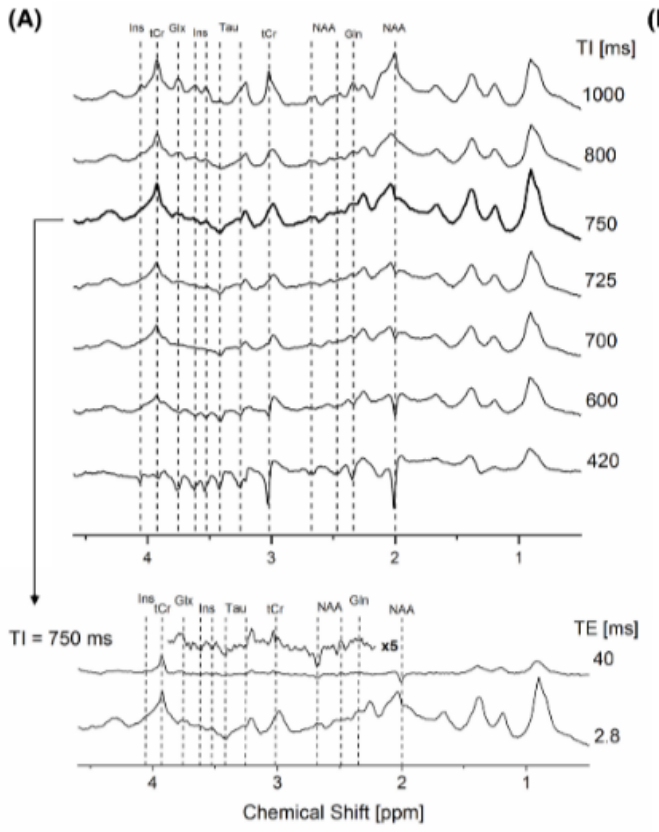
- ^{1}H MRS brain signals (short TE) - complicated – macromolecules
- Error in macromolecule estimation – error in metabolite concentrations
- two types of the MM signals
  - nuclei of backbones of macromolecules having severely restricted mobility – very short T_2
  - nuclei of outer parts of macromolecules or those of smaller macromolecules having higher mobility – useful clinical information

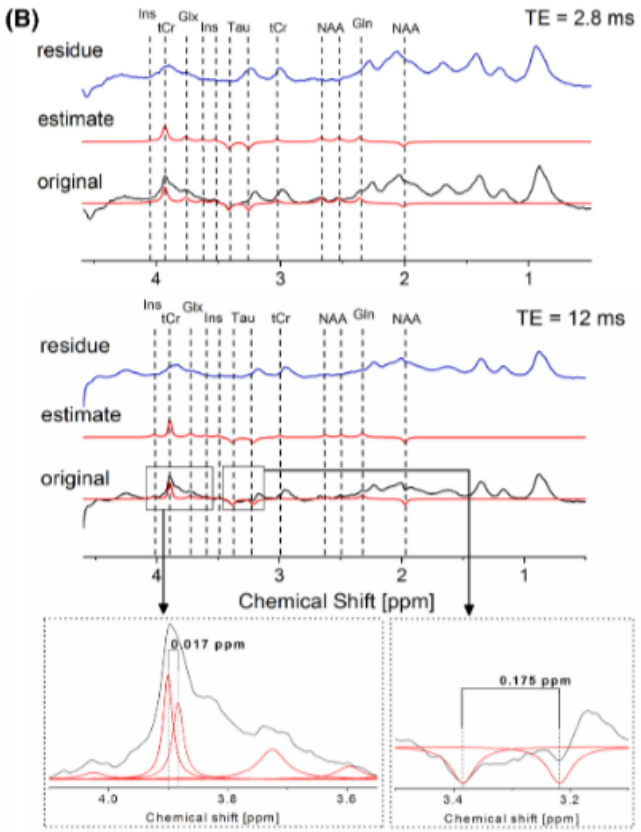
MACROMOLECULES

- In the normal brain, MM signals arise mainly from the protons of amino acids within cytosolic proteins primarily in regions undergoing rapid motions on the time scale of NMR.
- MM resonances have physical properties different from those of metabolites

  - The longitudinal (T_1) and transverse (T_2) relaxation times of MM are shorter than those of metabolites
  - MM are also characterized by increased linewidths compared to those of metabolites
  - The MM are further characterized by a more hindered mobility as well as diffusivity
    - apparent diffusion coefficient (ADC) 10–20 times lower than that of metabolites

  - MM have extensive scalar coupling patterns among the resonances (~7Hz), which can affect the detection of GABA





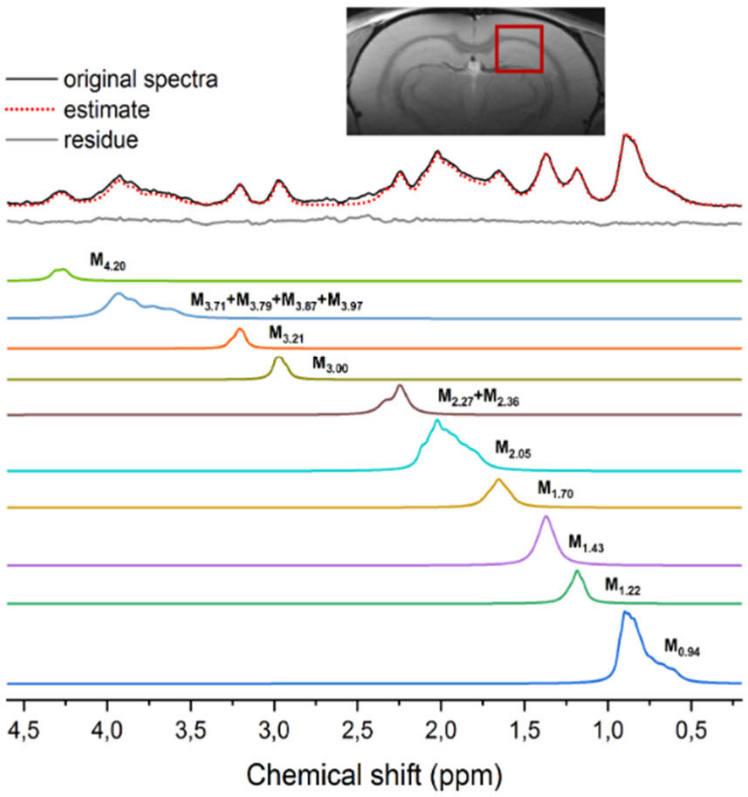
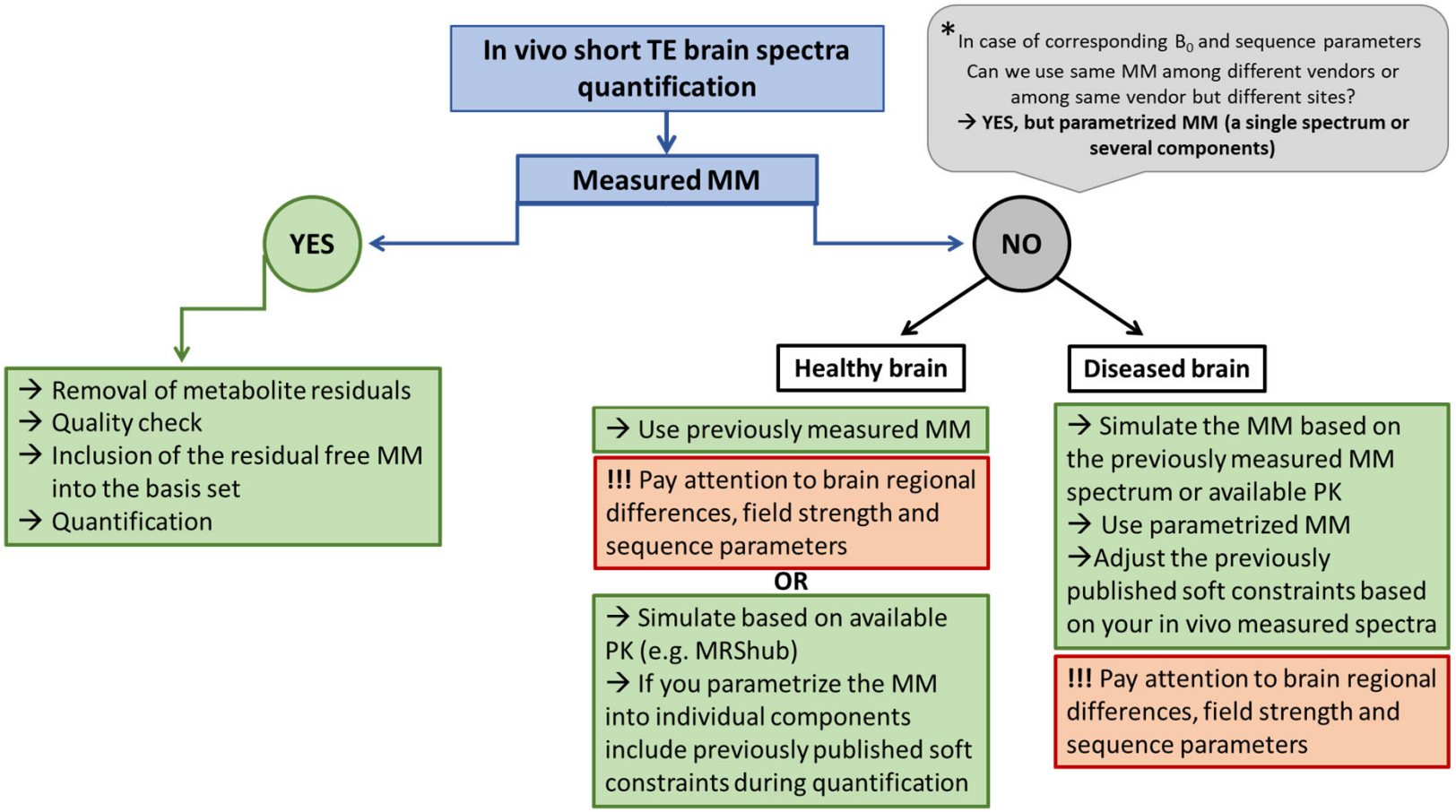


FIGURE 2 MM spectrum parametrized into 10 individual components using AMARES. The original spectrum was fitted using AMARES and the fits of individual components were saved separately to form a parametrized basis-set (in color). The insert image shows the VOI = 3 × 3 × 3 mm^3 centered on the rat hippocampus (all MM spectra were acquired from VOI positioned in this location)



Quantification - Lipids

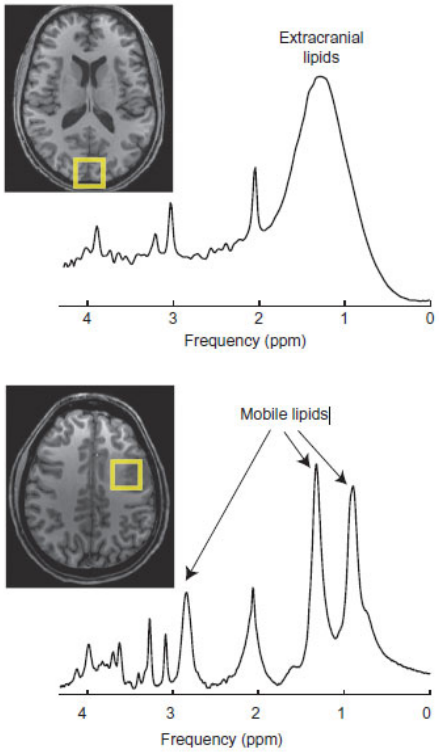


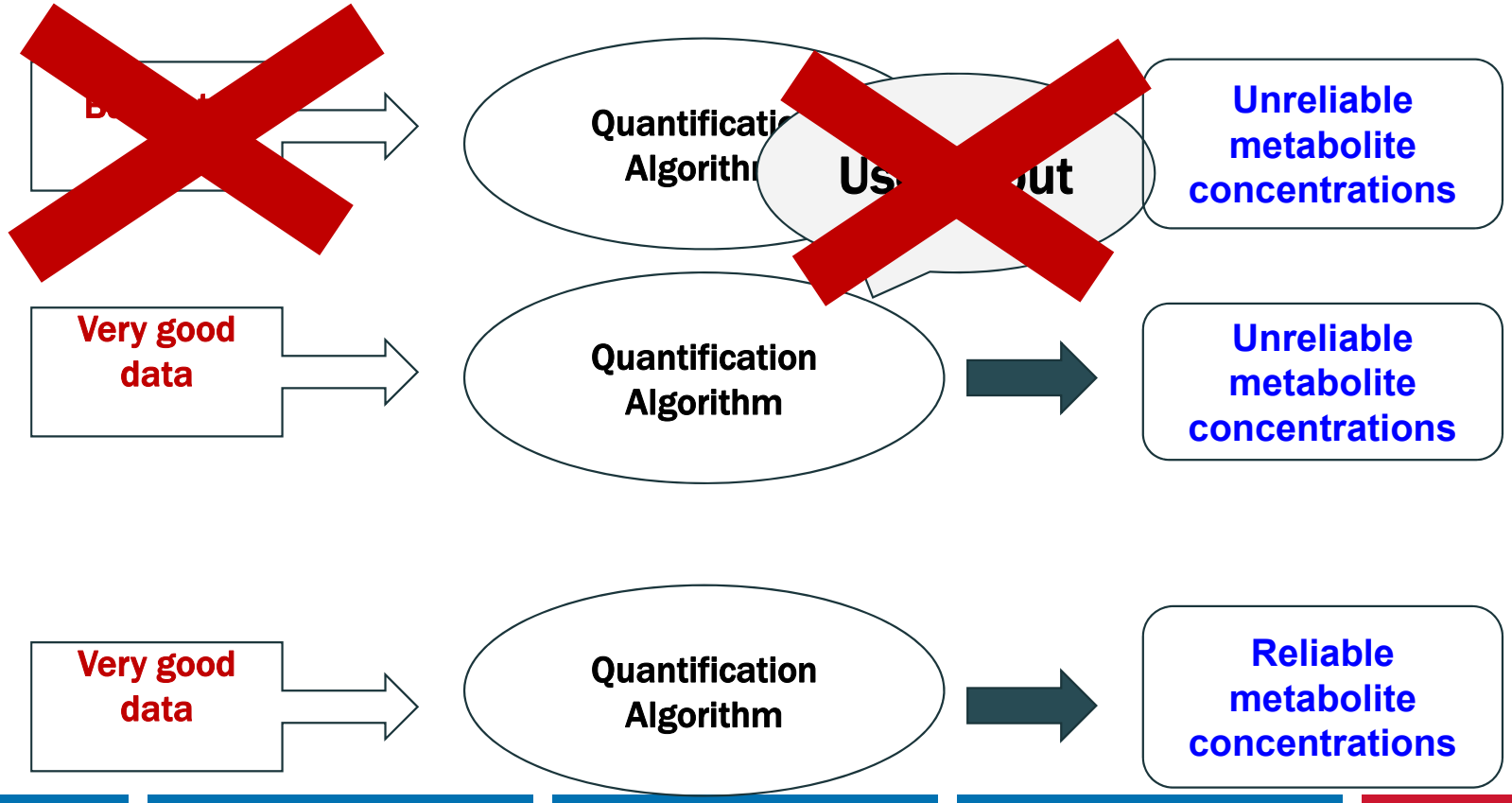
FIGURE 1.5.9 Lipid resonances in the human brain. Top, extracranial lipids are observed if the volume of interest (yellow box) is placed too close to the scalp. Bottom, prominent resonance from mobile lipid are often observed in malignant brain tumors, as shown in this example.

Jamie Near, Magnetic Resonance Spectroscopy Elsevier 2014

CHAPTER
1.5

Spectral Quantification and Pitfalls in Interpreting Magnetic Resonance Spectroscopic Data: What To Look Out For

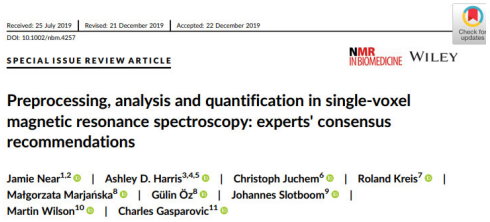
Jamie Near
Department of Psychiatry, McGill University, and the Centre d'Imagerie du Cerveau, Douglas Mental Health University Institute, Montreal, QC, Canada



QUANTIFICATION (ABSOLUTE)

Signal amplitudes
Peak area → **Concentrations**
mmol/kg$_{ww}$

- External concentration reference
- Internal concentration reference
  - Ratios to tCr or NAA or Cho - They might change – disease
  - Water internal reference
    - Corrections for T1, T2 and water content
    - Very short TE – T2 correction could be neglected
    - Fully relaxed signals – long TR – T1 neglected
    - MT


Received: 25 July 2019 | Revised: 21 December 2019 | Accepted: 22 December 2019
DOI: 10.1002/nbm.4257
SPECIAL ISSUE REVIEW ARTICLE
NMR IN BIOMEDICINE WILEY

Preprocessing, analysis and quantification in single-voxel magnetic resonance spectroscopy: experts' consensus recommendations

Jamie Near[1,2] | Ashley D. Harris[3,4,5] | Christoph Juchem[6] | Roland Kreis[7] | Małgorzata Marjańska[8] | Gülin Öz[8] | Johannes Slotboom[9] | Martin Wilson[10] | Charles Gasparovic[11]

http://www.ismrm.org/workshops/Spectroscopy16/program.htm
2nd TRANSACT Workshop, University Bern: Quality Issues in Clinical MRS 2014
The MRS Consensus Group, (2014), Radiology, 270(3):658-79.

$$metabolite.abs = \frac{signal_{met}}{signal_{H2O}} \times WCONC_{GM_{H2O}} \times \frac{(exp^{-TE/T2_{H2O}}) \cdot (1-exp^{-TR/T1_{H2O}})}{(exp^{-TE/T2_{met}}) \cdot (1-exp^{-TR/T1_{met}})} \quad , \qquad (2)$$

where *metabolite.abs* is the absolute concentration of a given metabolite.
$signal_{met}/signal_{H2O}$ is the ratio of metabolite signal to water signal, as determined using LCmodel. This value is returned by LCModel when the parameters WCONC, ATTH2O, and ATTMET are all set to 1, and water scaling is on.
$WCONC_{GMH2O}$ is the LCModel parameter specifying the tissue water concentration in grey matter (43300 mM) (Ernst, Kreis, and Ross 1993).
TE is the echo time of the experiment (TE = 11.12 ms)
TR is the repetition time of the experiment (TR = 3000 ms)
$T2_{H2O}$ is the measured water T2 relaxation time at 7T (49.13 ms)
$T2_{met}$ is the projected metabolite T2 relaxation time at 7T (**Supplementary Table 3**)
$T1_{H2O}$ is the measured water T1 relaxation time at 7T (1491 ms)
$T1_{met}$ is projected metabolite T2 relaxation time at 7T (**Supplementary Table 3**)

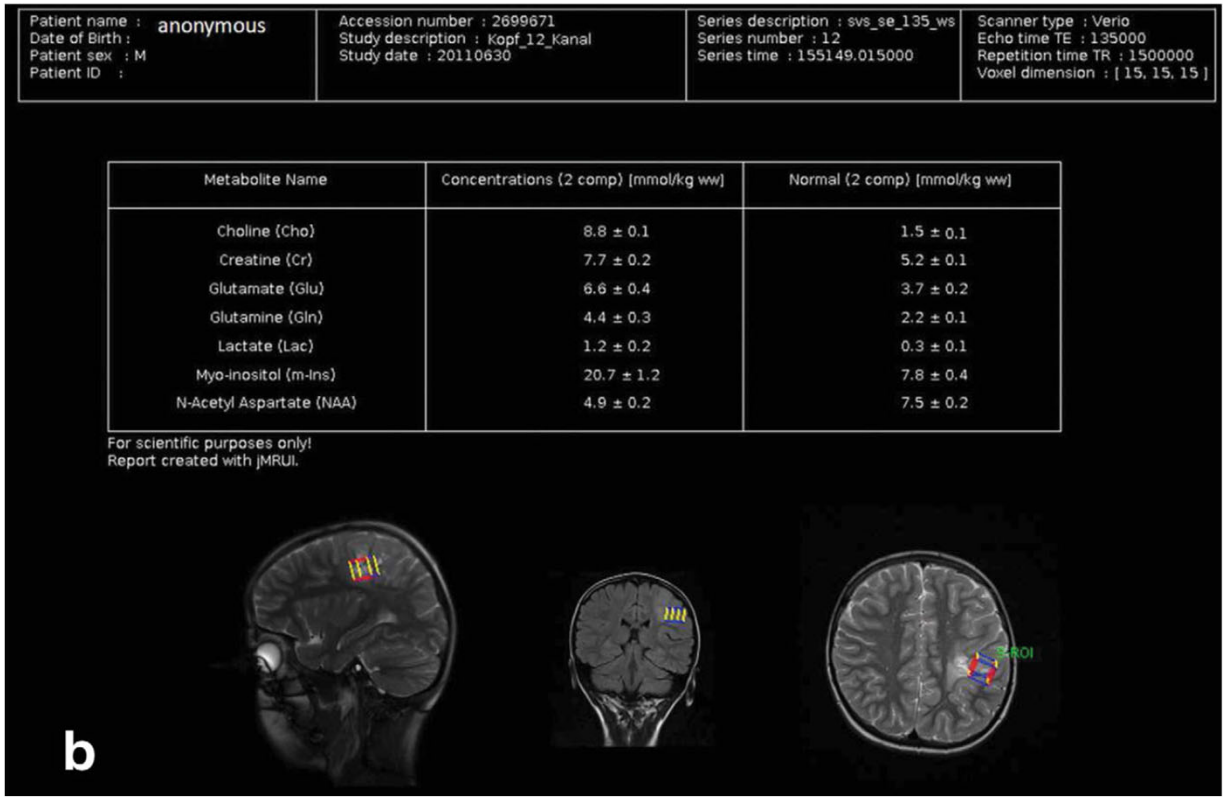
Microsoft Word - WT_AgingPaper_Supplementary_edit_6Oct20.docx (els-cdn.com)

QUANTIFICATION QUALITY CONTROL

- CRLB – theoretical estimation
  - Assumes that the model is perfect
  - R Kreis, MRM 75, 2016 – CRLB % !!! – low conc metabolites
    - CRLB vs mean CRLB in normal cohort

- Fit residuals

QUANTIFICATION: RESULTS DISPLAY



Patient name : anonymous Date of Birth : Patient sex : M Patient ID :	Accession number : 2699671 Study description : Kopf_12_Kanal Study date : 20110630	Series description : svs_se_135_ws Series number : 12 Series time : 155149.015000	Scanner type : Verio Echo time TE : 135000 Repetition time TR : 1500000 Voxel dimension : [15, 15, 15]

Metabolite Name	Concentrations (2 comp) [mmol/kg ww]	Normal (2 comp) [mmol/kg ww]
Choline (Cho)	8.8 ± 0.1	1.5 ± 0.1
Creatine (Cr)	7.7 ± 0.2	5.2 ± 0.1
Glutamate (Glu)	6.6 ± 0.4	3.7 ± 0.2
Glutamine (Gln)	4.4 ± 0.3	2.2 ± 0.1
Lactate (Lac)	1.2 ± 0.2	0.3 ± 0.1
Myo-inositol (m-Ins)	20.7 ± 1.2	7.8 ± 0.4
N-Acetyl Aspartate (NAA)	4.9 ± 0.2	7.5 ± 0.2

For scientific purposes only!
Report created with jMRUI.

Olivier Scheidegger et al, MRM 70:25–32 (2013)

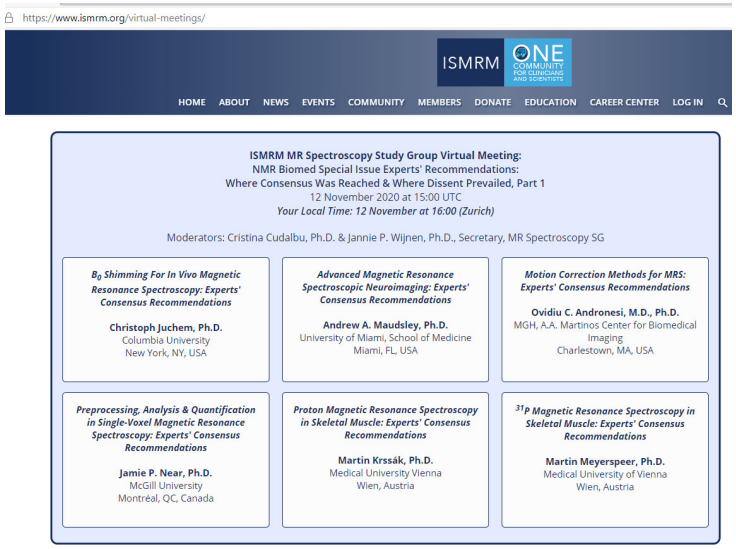
SUMMARY

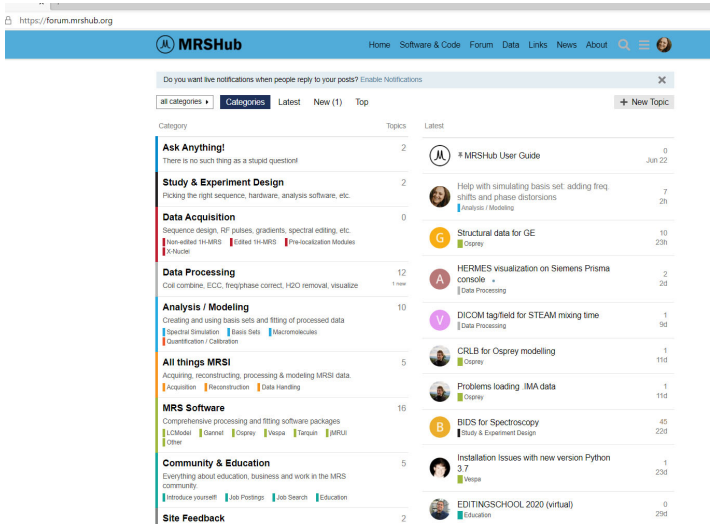
- ***Software "X"***
  - ***Data are sent/loaded***
  - ***Automatic QC***
  - ***Preprocessing –list: saved, shared …***
  - ***Quantification – extreme care – reliable and accurate***
  - ***Display results***
  - ***CE labelled or FDA approved***

AUTOMATED

SUMMARY

- ***MRS Study Group @ISMRM – Virtual meetings***





- ***The MRS Consensus Group: push-button processing and quantification of clinical MR spectra***

NEW APPROACHES

Machine Learning /Deep learning
Automatic Classification Strategies

frontiers in Oncology

ORIGINAL RESEARCH
published: 09 October 2019
doi: 10.3389/fonc.2019.01010

Super-Resolution ^{1}H Magnetic Resonance Spectroscopic Imaging Utilizing Deep Learning

*Zohaib Iqbal[1], Dan Nguyen[1], Gilbert Hangel[2], Stanislav Motyka[2], Wolfgang Bogner[2] and Steve Jiang[1]**

[1] Medical Artificial Intelligence and Automation Laboratory, Department of Radiation Oncology, University of Texas Southwestern Medical Center, Dallas, TX, United States, [2] Christian Doppler Laboratory for Clinical Molecular MR Imaging, Department of Biomedical Imaging and Image-guided Therapy, High Field MR Center, Medical University of Vienna, Vienna, Austria

Received: 15 December 2017 | Revised: 12 February 2018 | Accepted: 12 February 2018
DOI: 10.1002/mrm.27166

SPECTROSCOPIC METHODOLOGY
FULL PAPER

Magnetic Resonance in Medicine

A convolutional neural network to filter artifacts in spectroscopic MRI

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RESEARCH ARTICLE

Magnetic Resonance in Medicine

Quantification of MR spectra by deep learning in an idealized setting: Investigation of forms of input, network architectures, optimization by ensembles of networks, and training bias

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NEW APPROACHES- MR FINGERPRINTING

MRF extracts parameter maps from signals generated using non-steady-state pulse sequences in conjunction with Bloch simulations and pattern matching.

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WILEY NMR IN BIOMEDICINE

RESEARCH ARTICLE

^{31}P magnetic resonance fingerprinting for rapid quantification of creatine kinase reaction rate *in vivo*

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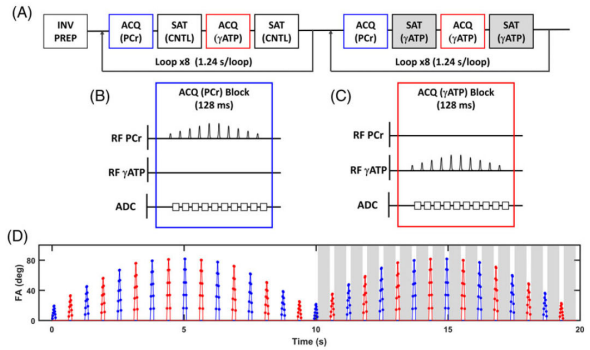
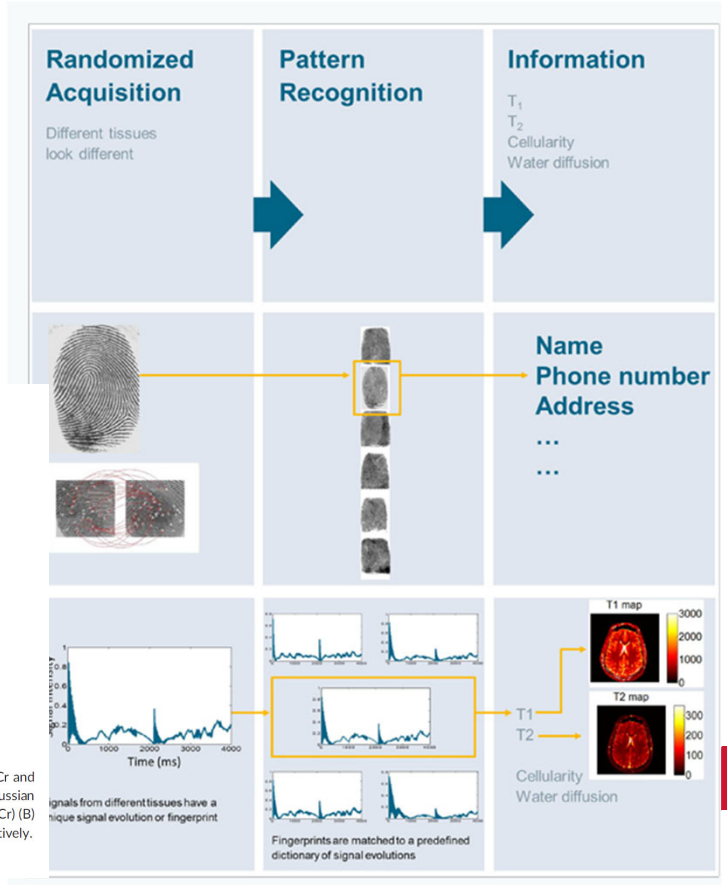


FIGURE 1 Sequence design. A, schematic diagram of the CK-MRF pulse sequence. ACQ(PCr) and ACQ(γATP) are acquisition blocks for PCr and γATP, respectively. SAT(CNTL) and SAT(γATP) are contralateral and γATP saturation blocks, respectively. ACQ(PCr) and ACQ(γATP) used Gaussian excitation pulses, while SAT(CNTL) and SAT(γATP) used continuous wave RF pulses. B,C, pulse sequence diagrams for one block of ACQ(PCr) (B) and ACQ(γATP) (C). D, timing and nominal flip angles of all excitation pulses. Blue and red colors indicate PCr and γATP excitation, respectively. Grey shaded areas indicate γATP saturation



NEW APPROACHES- DENOISING

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Denoising of diffusion MRI using random matrix theory

Jelle Veraart[a,b,*], Dmitry S. Novikov[b], Daan Christiaens[c], Benjamin Ades-aron[b], Jan Sijbers[a], Els Fieremans[b]

NeuroImage 263 (2022) 119634

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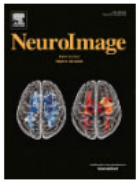

MP-PCA denoising for diffusion MRS data: promises and pitfalls

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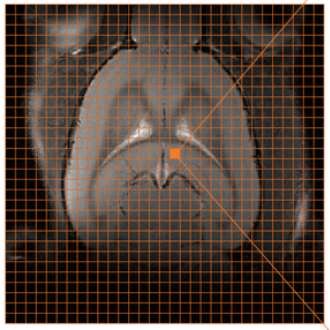
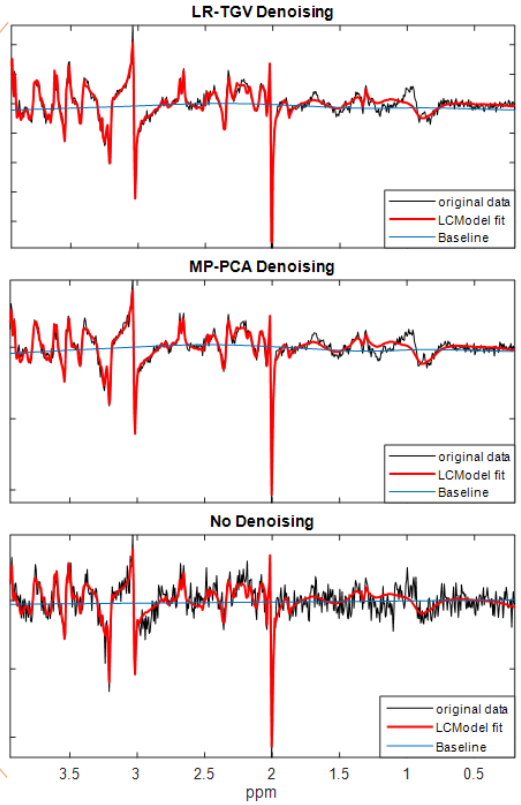
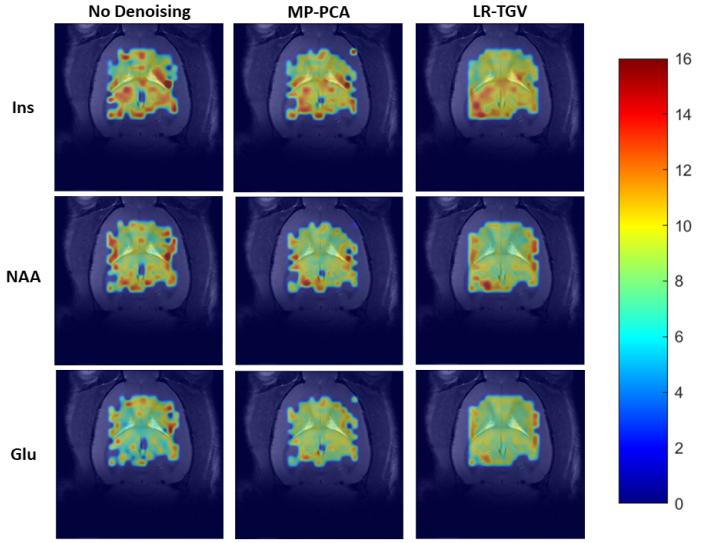
NEW APPROACHES- DENOISING







B Alves

SUMMARY & ACKNOWLEDGMENTS

MRS & MRSI is incredibly rich & versatile ☺

Thank you for listening! Questions?

For any question yon might have later on, please write me an email:

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THANK YOU FOR YOUR ATTENTION

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