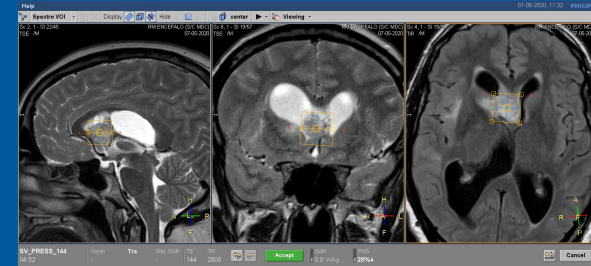


Tutorial



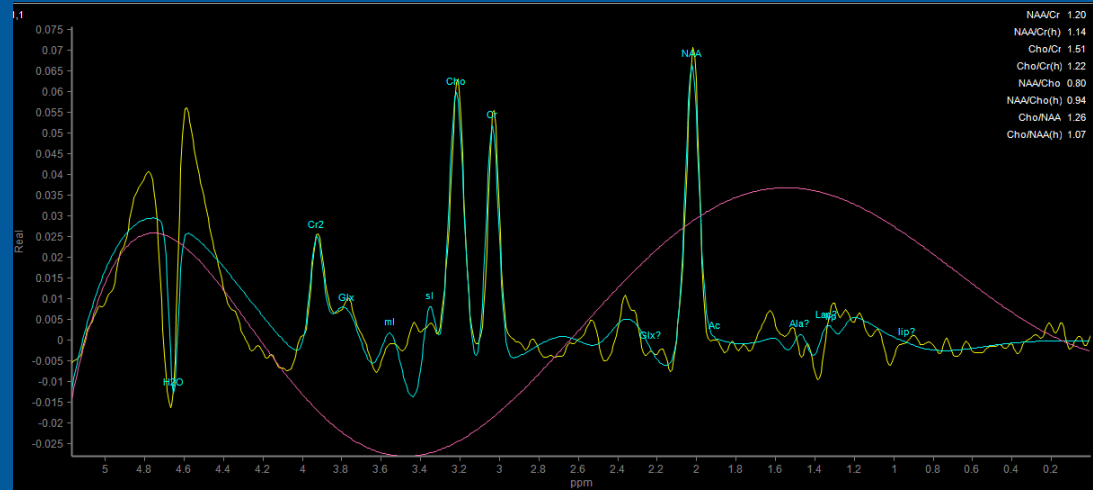
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feb. '21

UPDATE 5 febbraio 2021



Gemelli



SPETTROSCOPIA SINGLE VOXEL



Fondazione Policlinico Universitario Agostino Gemelli IRCCS
Università Cattolica del Sacro Cuore



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TSRM Marino Gentile
Radiographer

Gemelli



+39 3280077833

✉ marino.gentile@outlook.com

✉ marino.gentile@policlinicogemelli.it

🌐 www.variodyne.it

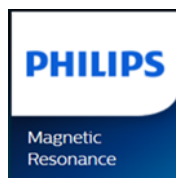
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feb. '21

Apparecchiature utilizzate

PHILIPS

sense and simplicity



MR Systems Ingenia

Ingenia (2017-09-19)



Philips Medical Systems Nederland B.V.
Veenpluis 4-6, 5684 PC Best, The Netherlands.

RM Ingenia 1.5T

MR Systems Ingenia

SRN: 70750

Nominal Main Magnetic Field (B0) 1.5T

Maximum Gradient of the static Magnetic Field [View details...](#)

Main Operation Frequency for 1H 63.87 MHz

Frequency range 1H 63.57 MHz - 64.18 MHz

Frequency range Multi Nuclei Option not available

Maximum Gradient Output	20.0 cm	40.0 cm	60.0 cm
	91.0 T/s	119.0 T/s	180.0 T/s

[View technical details...](#)

IEC/EN 60601-2-33 Ed. 2 Am. 2 (2007)

CE 0344

PHILIPS

Healthcare

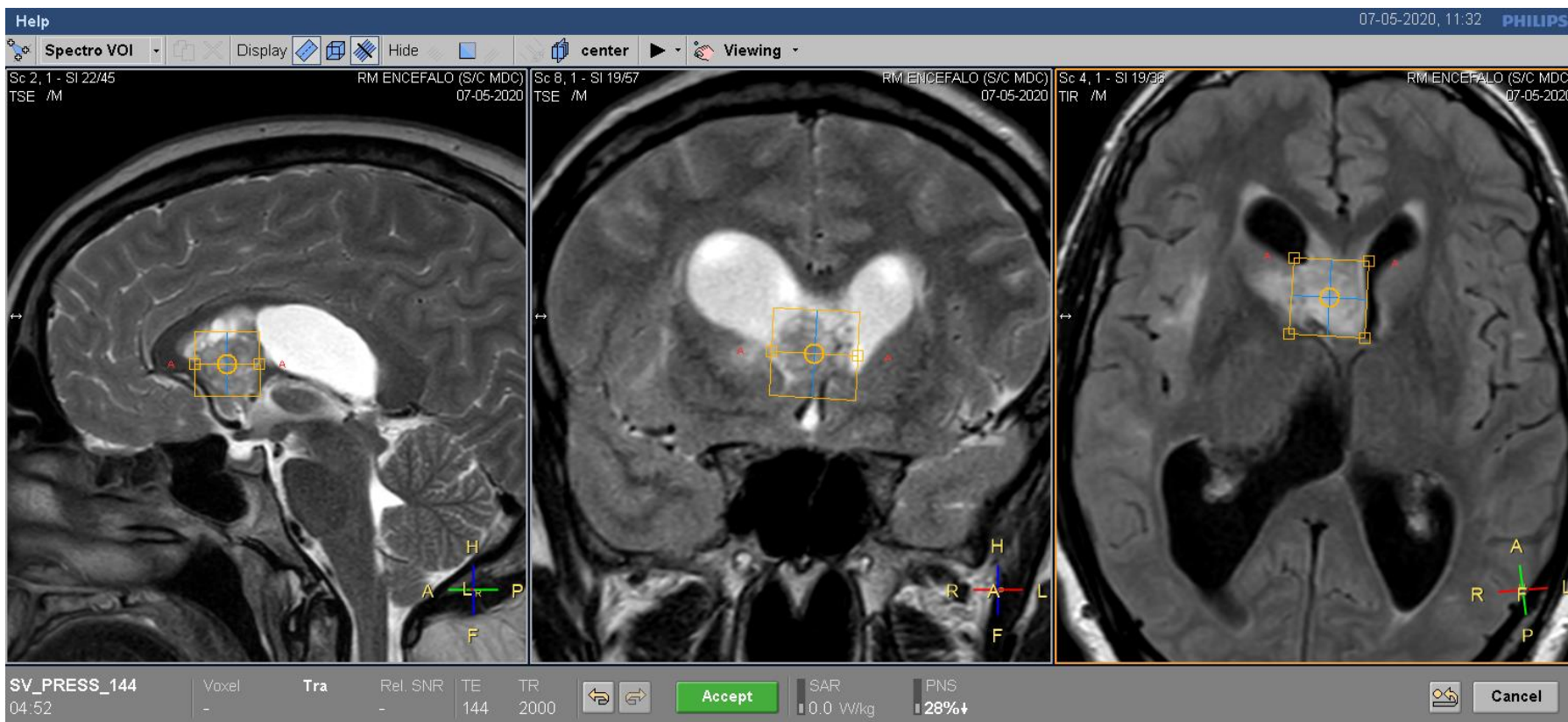
Apparecchiature utilizzate



PHILIPS

dStream

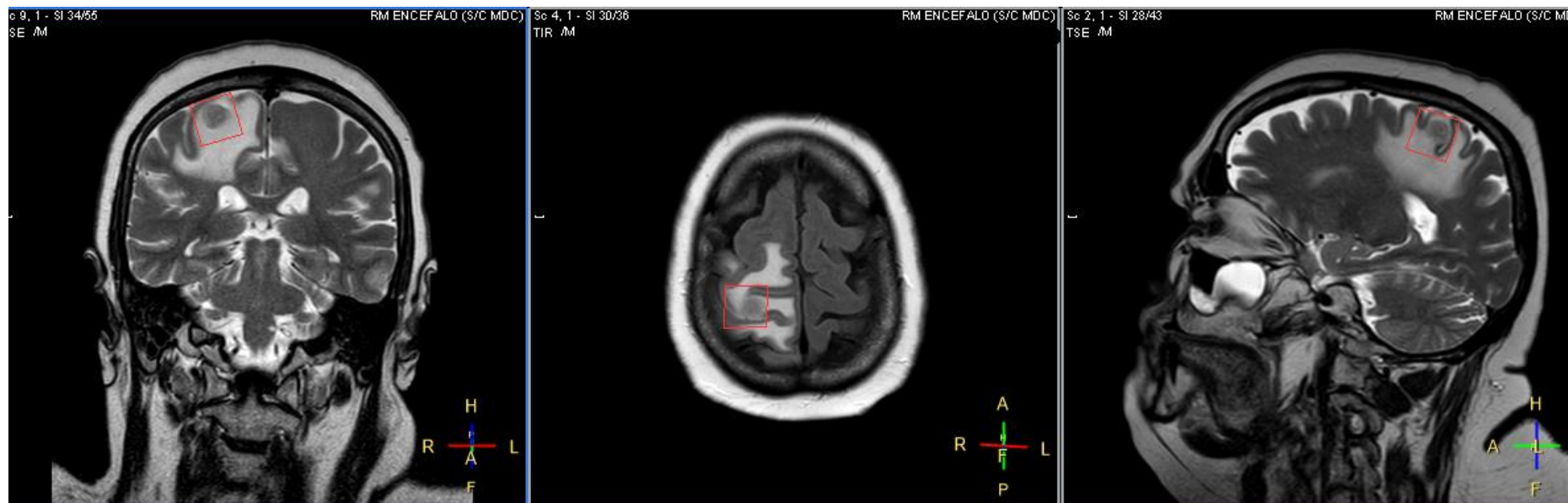
Spettroscopia SV



Esempio d'impostazione di spettroscopia «**Single Voxel**»

Ricostruzione spettroscopia SV

Esempio d'impostazione della sequenza Spettroscopia «Single Voxel»



Spettroscopia SV

SV_PRESS_144		Voxel	Tra	Rel. SNR	TE	TR			Accept
04:52		-	-	-	144	2000			
Initial	Geometry	Contrast	Motion	Dyn/Ang	Postproc	Offc/Ang	Coils	Conflicts	<<
TE	user defined		Total scan duration		04:52.0				
(ms)	144	Act. TR/TE (ms)		2000 / 144					
TR	user defined		Min. TR/TE (ms)		1437 / 46				
(ms)	2000	Spectral resolution (Hz/p...)		0.98					
NSA	128	Readout duration (ms)		1024					
Preparation phases	auto	Head SAR		< 5%					
		Whole body SAR / level		0.0 W/kg / normal					
		SED		0.0 kJ/kg					
		Max B1+rms		1.10 uT					
		PNS / level		28% / normal					
		dB/dt		14.3 T/s					
		Sound Pressure Level (dB)		-11.9					

Esempio di parametri - spettroscopia «**Single Voxel**»

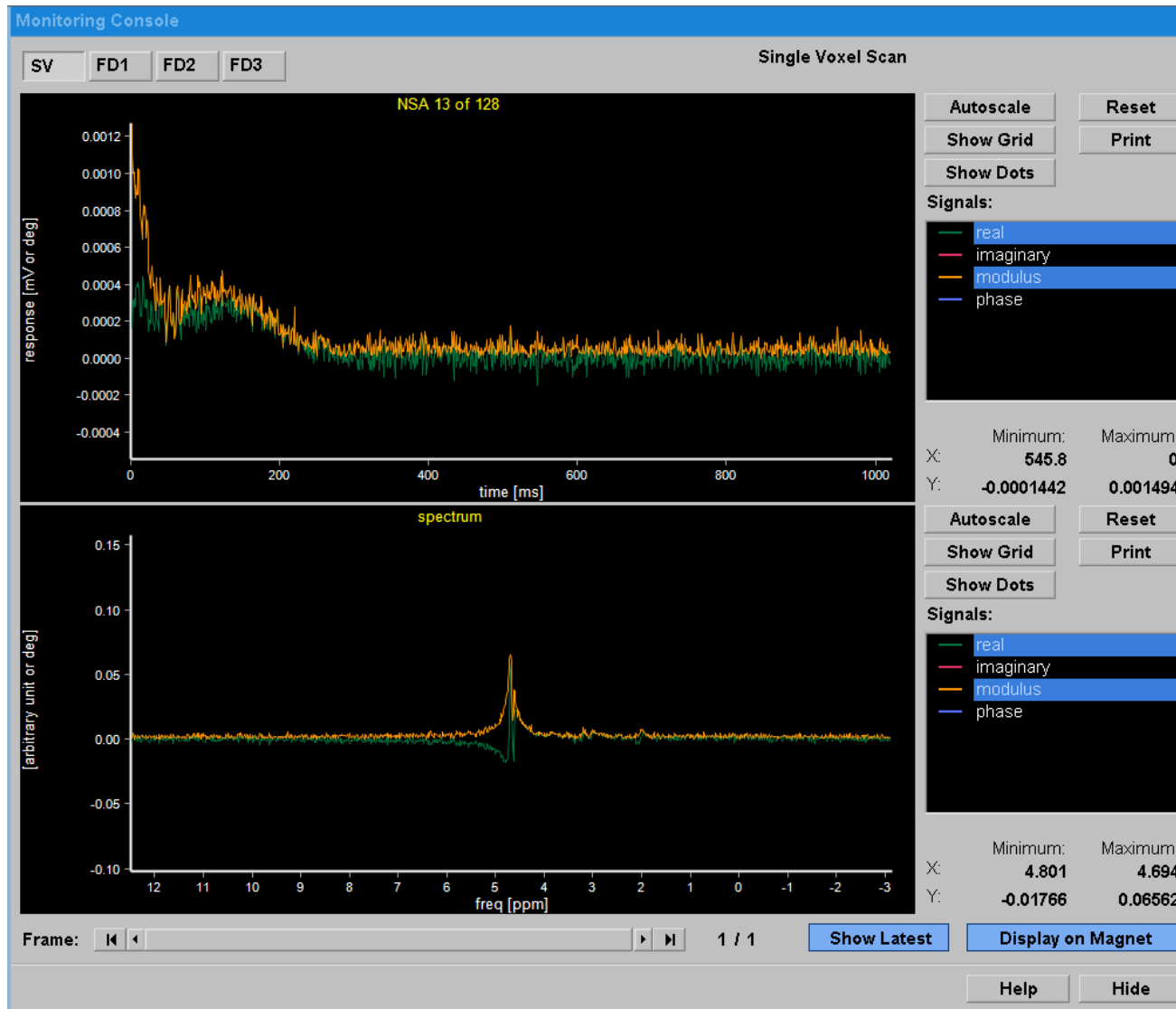
Spettroscopia SV

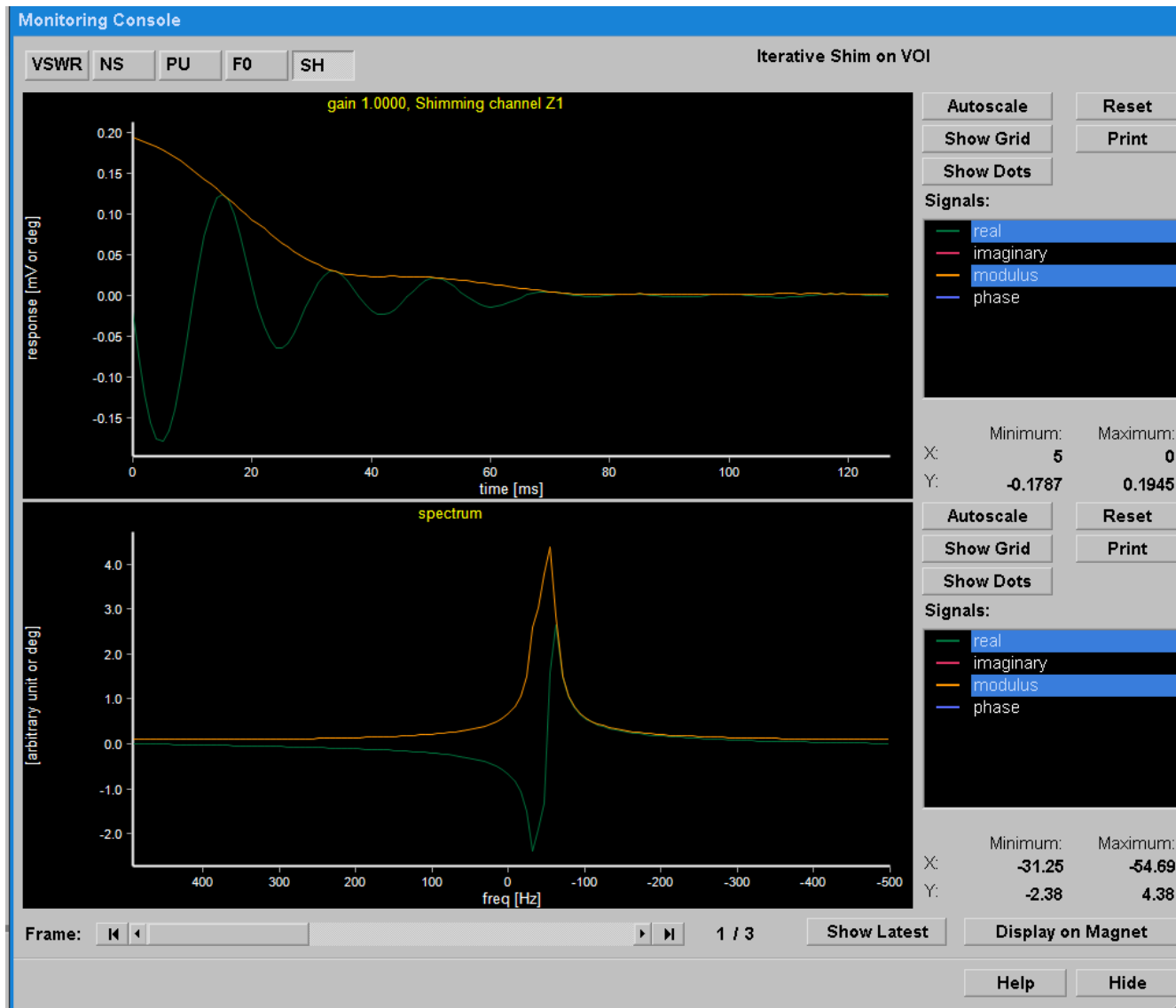
SV_PRESS_144		Voxel	Tra	
04:52		-		
Initial	Geometry	Contrast	Motion	Dyn/Ang
VOI orientation			transverse	
VOI size AP (mm)			20	
RL (mm)			20	
FH (mm)			20	
Samples			1024	
Spectral BW (Hz)			1000	
Chem. shift Dir AP			A	
Chem. shift Dir LR			L	
Chem. shift Dir FH			F	
REST slabs			0	

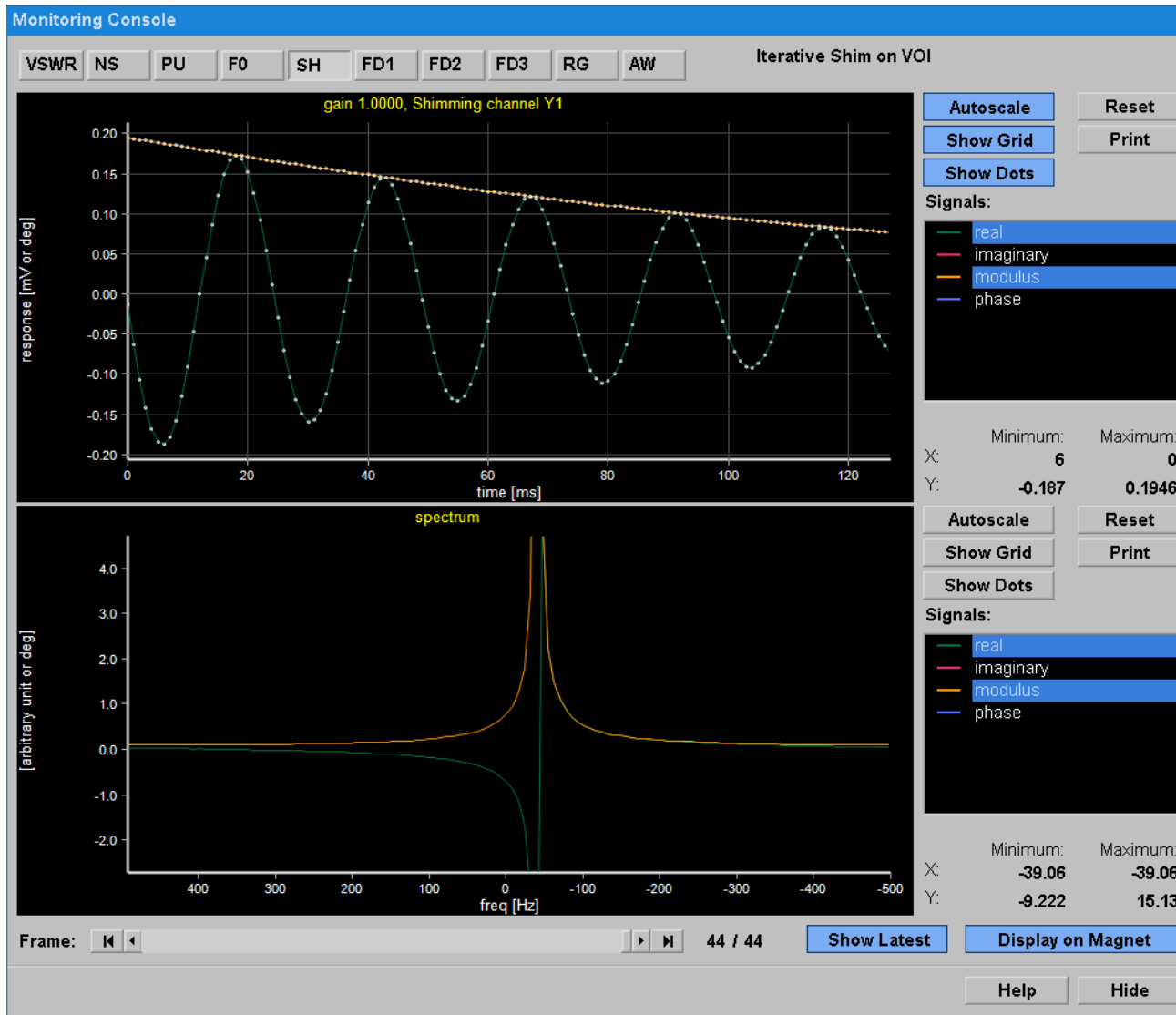
Il Voxel può essere sicuramente ridotto, in caso di necessità, a $15*15*15$

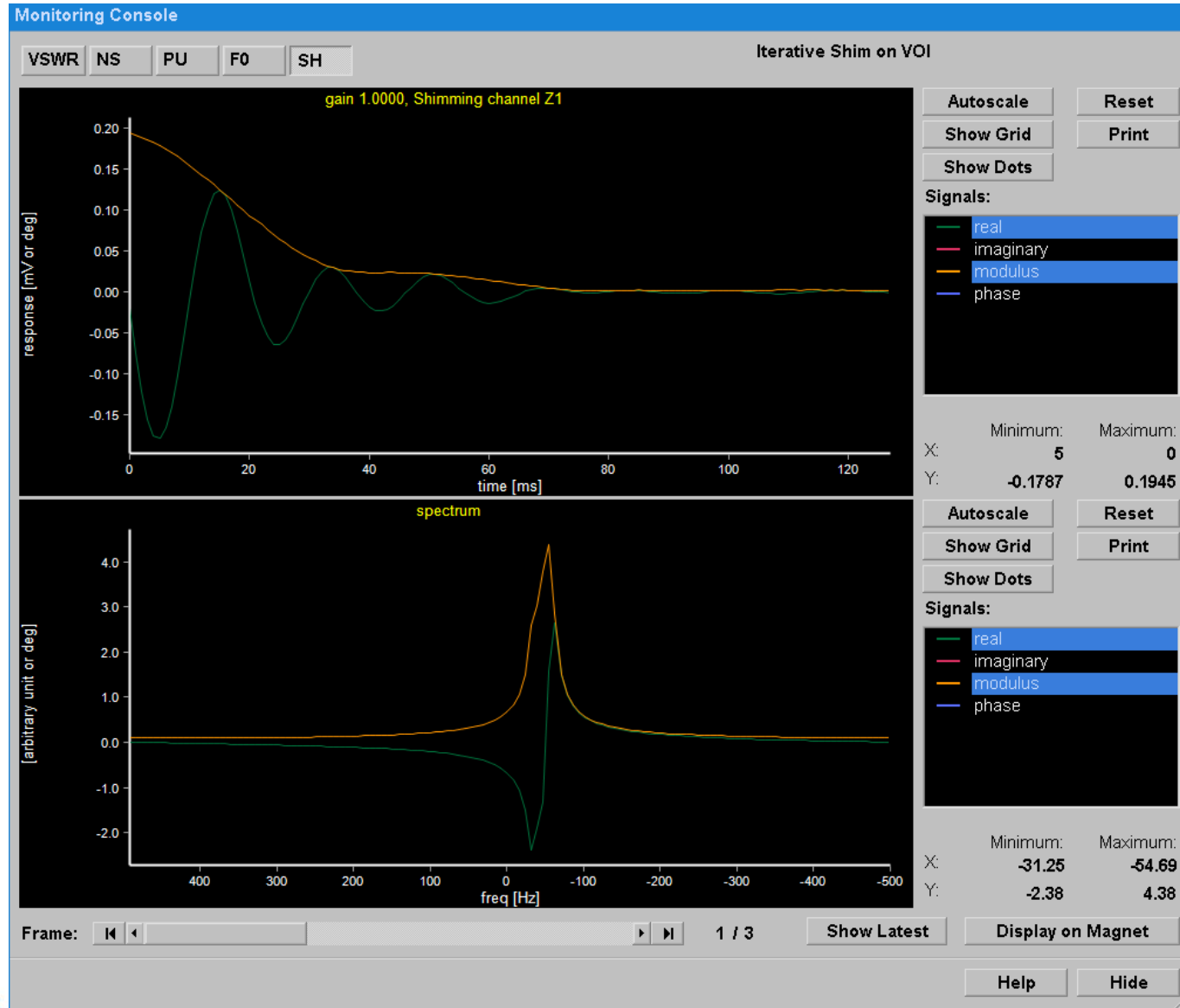
Sulla parte inferiore del monitor è possibile seguire i vari passaggi di preparazione all'esecuzione vera e propria della sequenza...

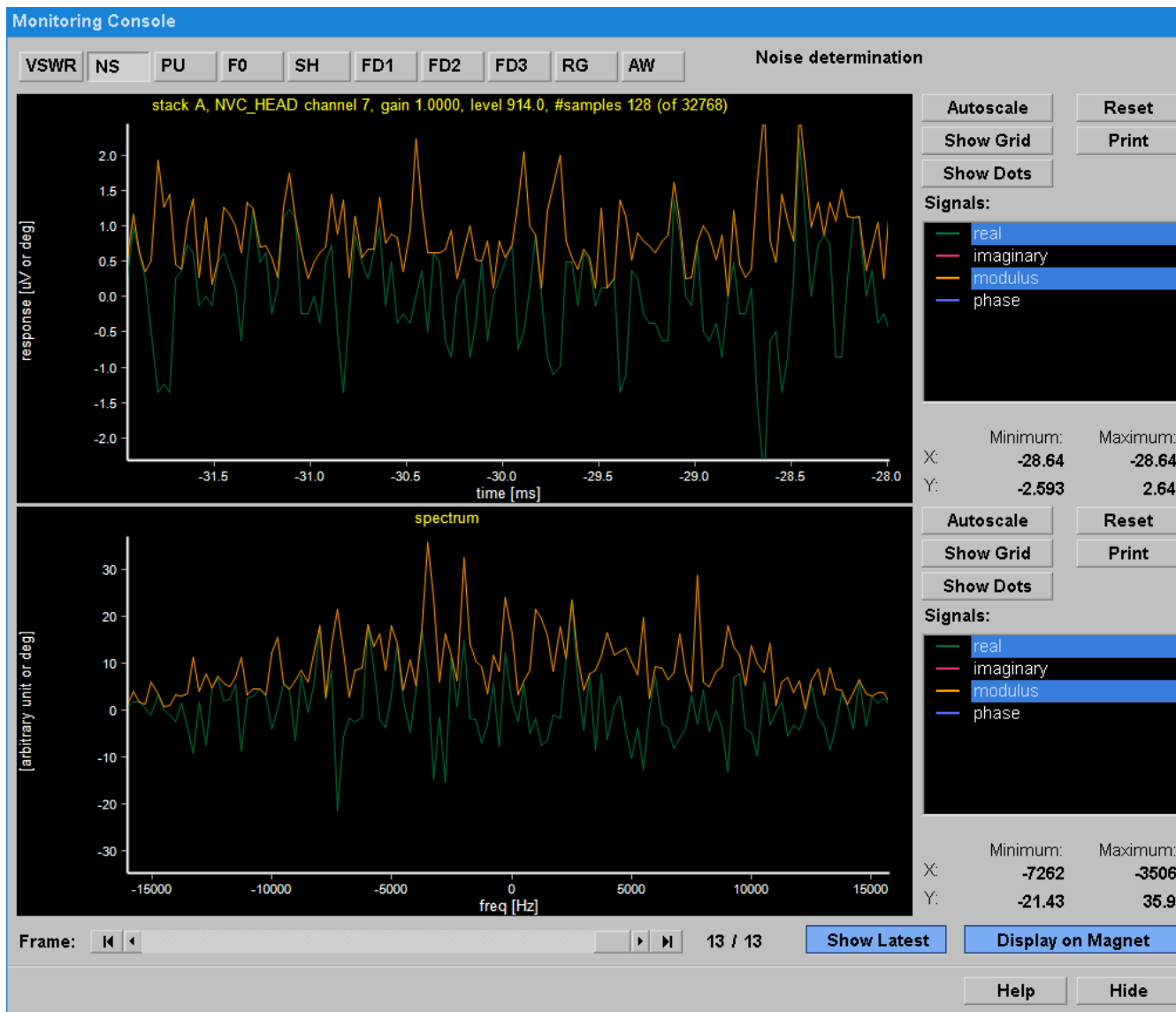
```
16:02 Optimal water suppression final value: 342.8 (deg)
16:01 Performing automatic water suppression optimization...
16:01 FWHM of peak 5.9 Hz
16:00 Iterative shimming on VOI procedure finished
15:59 Performing iterative shimming...
```









Ricostruzione spettroscopia SV

The screenshot shows the Philips MRI software interface. The top menu bar includes 'Patients', 'Examination', 'Review', 'Analysis', 'System', and 'Help'. The left sidebar displays patient information (Registration ID, Date of Birth, Gender) and a list of scan items under the heading 'Cranio tumori'. The list includes various sequences such as SmartBrain, MPR, T2W, FLAIR, T1W, SWIp, DWI, Perfusion, and SV_PRESS_144. The 'SV_PRESS_144' sequence is highlighted in blue. A context menu is open over this sequence, with 'SpectroView' selected and highlighted in blue. A large green arrow points from the text on the right towards the 'SpectroView' option in the menu.

Selezionare la sequenza
SV_PRESS_144 e fare clic con
il tasto dx.
Selezionare «**SpectroView**»



Ricostruzione spettroscopia SV

The screenshot shows the Philips SpectroView software interface. On the left, there is a list of MRI series for a patient. The series are:

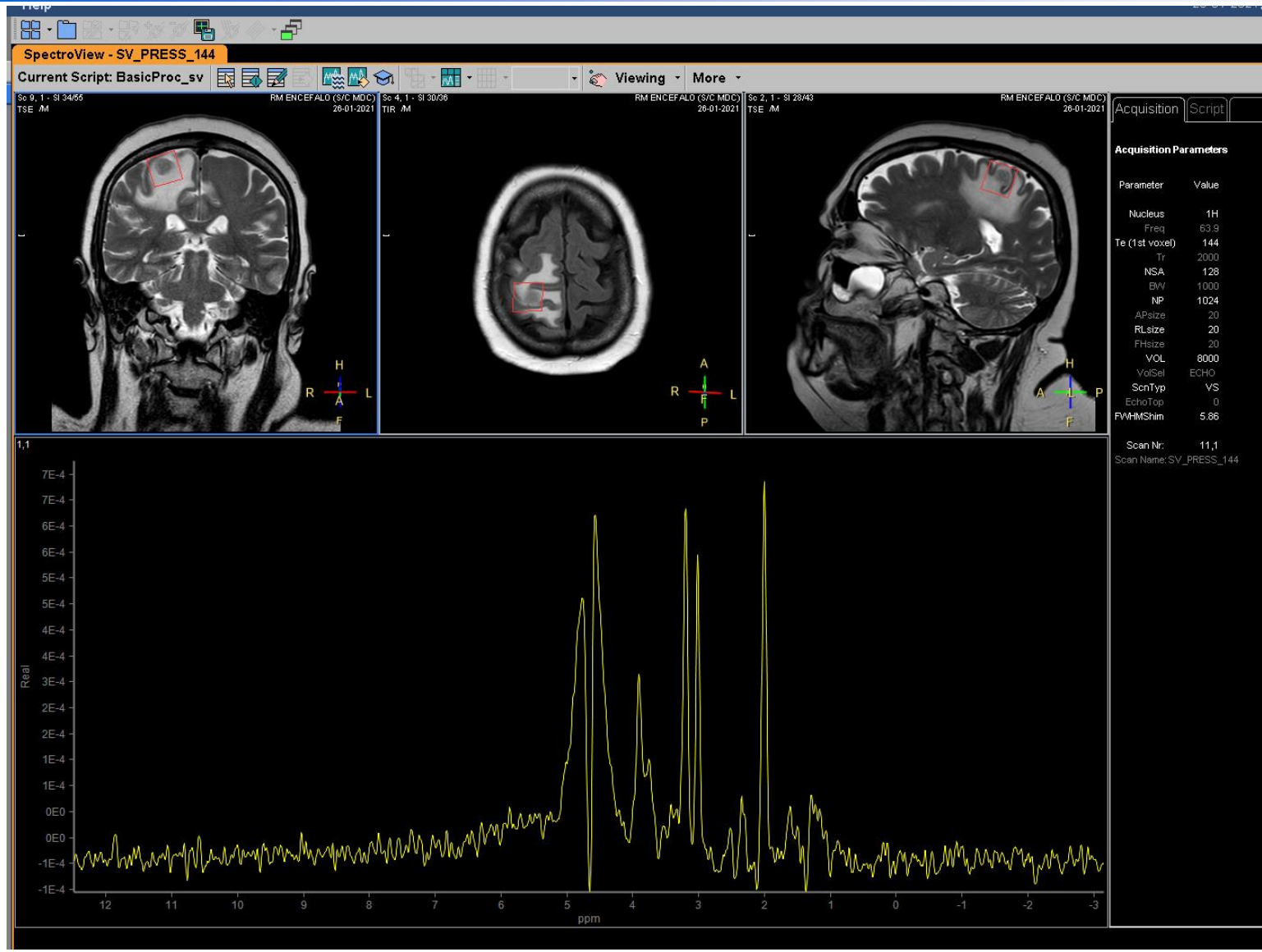
Series ID	Series Name	Series Type
1,1	SmartBrain	☆
1,2	MPR - SmartBrain	
2,1	T2W_TSE_SA...	☆ SAG
3,1	T2W_TSE_AX	AX
4,1	FLAIR_longTR	☆ AX
5,1	T1W_AX TSE	☆ AX
6,1	SWIp_	☆ AX
7,1	DWI	☆ AX
8,1	Perfusione_T2	
	2D_PRESS_14...	DFS
9,1	T2W_TSE_CO...	☆ cor
10,1	sT1W_3D_WATS	☆ AX
11,1	SV_PRESS_144	SV

On the right, the 'SpectroView - SV_PRESS_144' window is open. A dialog box titled 'Unknown Anatomy' is displayed, with the message: 'Anatomy is not yet defined for this series. Please specify the anatomy for this study.' The dropdown menu is set to 'Brain', and the 'OK' button is circled in red with a green arrow pointing to it.



Apparirà questa schermata...
fare clic su OK

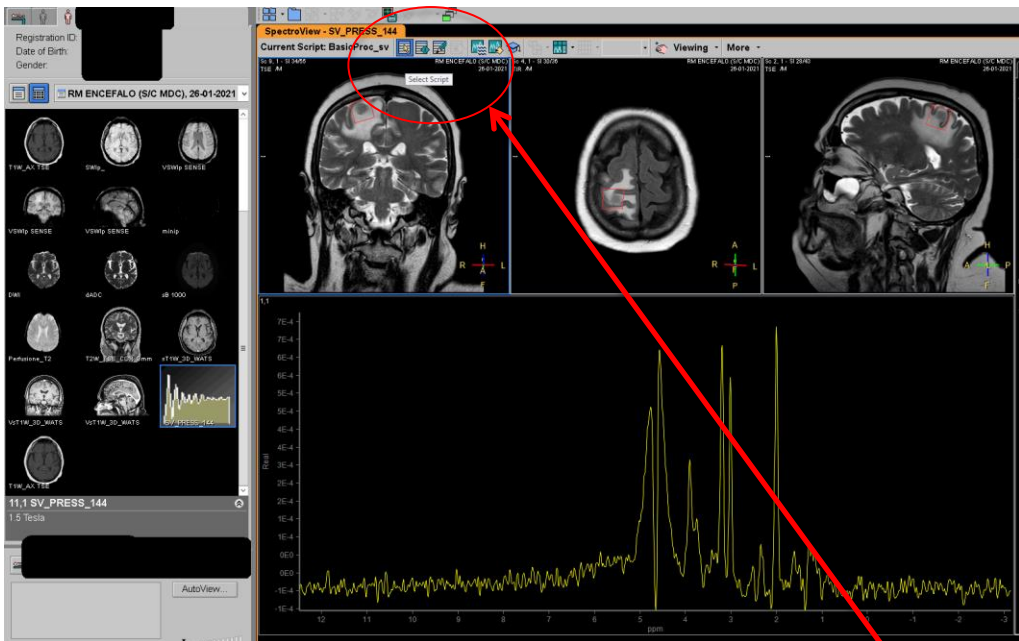
Ricostruzione spettroscopia SV



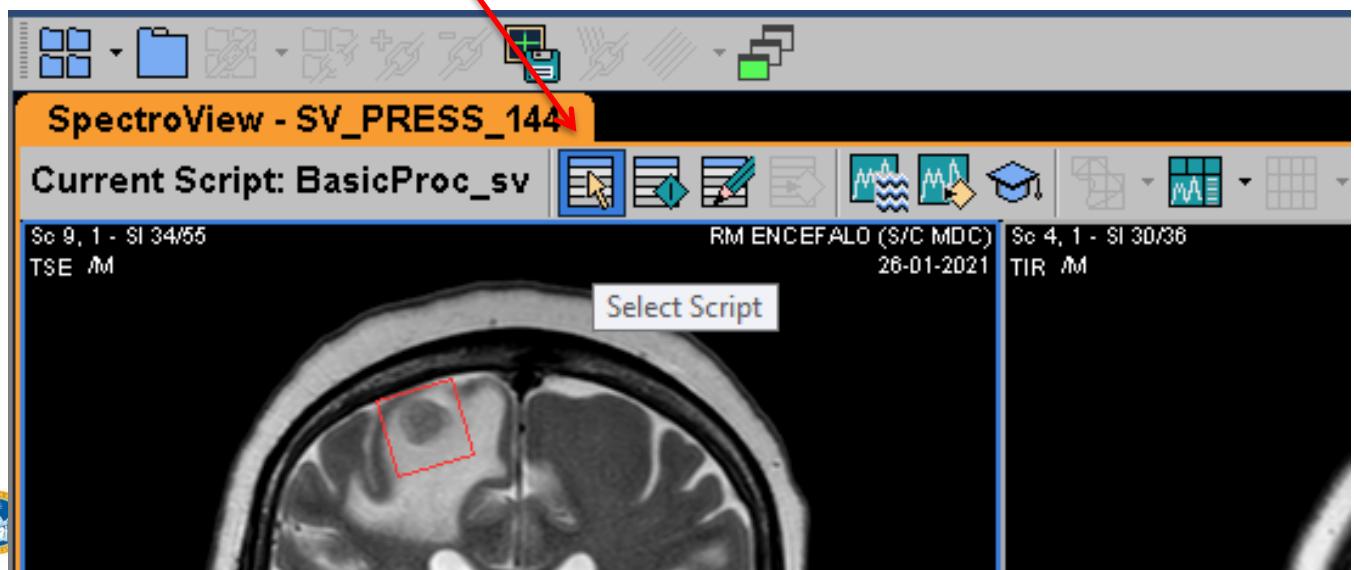
Apparirà
questo...



Ricostruzione spettroscopia SV



Selezionare
«Select Script»



Ricostruzione spettroscopia SV

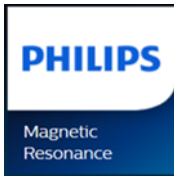


Selezionare: «**Long-TE Brain (1H SV)**» come indicato nella figura...

E fare clic su **OK**

Name	Description	Nucleus	Anatomy	Field	TE
<unnamed>-20191121-113639	Based on Long-TE Brain (1H SV)	1H	Brain	1.5T	long
<unnamed>-20191121-113732	Based on Long-TE Brain (1H SV)	1H	Brain	1.5T	long
<unnamed>-20200601-123550	Based on Long-TE Brain (1H SV)	1H	Brain	1.5T	long
<unnamed>-20200613-172043	Based on Long-TE Brain (1H SV)	1H	Brain	1.5T	long
<unnamed>-20200804-153316	Based on Basic Processing (1H SV)	1H	Brain	1.5T	long
<unnamed>-20200804-153350	Based on Long-TE Brain (1H SV)	1H	Brain	1.5T	long
<unnamed>-20201216-152808	Based on Long-TE Brain (1H SV)	1H	Brain	1.5T	long
<unnamed>-20201216-172039	Based on Long-TE Brain (1H SV)	1H	Brain	1.0T, 1.5T, 3.0T, 7.0T	long
BasicProc_sv	Basic Processing (1H SV)	1H	Brain	1.0T, 1.5T, 3.0T, 7.0T	short
LongTeBrain_sv	Long-TE Brain (1H SV)	1H	Brain	1.0T, 1.5T, 3.0T, 7.0T	long

Ricostruzione spettroscopia SV



The screenshot shows the 'Script Parameters' dialog box in the SpectroView software. The window title is 'SpectroView - SV_PRESS_144'. The current script is 'LongTeBrain_sv'. The parameters are as follows:

- Name: <unnamed>-20210126-170148
- Description: Based on Long-TE Brain (1H SV)
- Anatomy: Brain
- Nucleus: 1H
- Echo Time: Long (selected)
- Processing Step: Initial Baseline Subtraction
- Supported Field Strengths: 1.0T, 1.5T (checked), 3.0T, 7.0T
- Baseline Terms: 7

The 'Initial Baseline Subtraction' checkbox is checked, and a list of other options is visible:

- Dual Volume Decode
- Spectrum Phase Adjustment
- Initial Baseline Subtraction
- Shift Peak Frequency
- Select Peaks
- Peak Fitting
- Results Table
- Graph Display

Buttons at the bottom: Run, OK, Cancel.

Apparirà la
seguente
schermata ...

Ricostruzione spettroscopia SV



SpectroView - SV_PRESS_144

Current Script: LongTeBrain_sv

Script Parameters

Name: <unnamed>-20210126-170148

Description: Based on Long-TE Brain (1H SV)

Anatomy: Brain

Nucleus: 1H

Supported Field Strengths: 1.0T 1.5T 3.0T 7.0T

Echo Time: Short Long

Processing Step: Select Peaks

Dual Volume Decode

Spectrum Phase Adjustment

Initial Baseline Subtraction

Shift Peak Frequency

Select Peaks

Peak Fitting

Results Table

Graph Display

All None

Ac
Ala
Cho
Cr
Cr2
Glx
H2O
Lac
lip
ml
NAA
sl

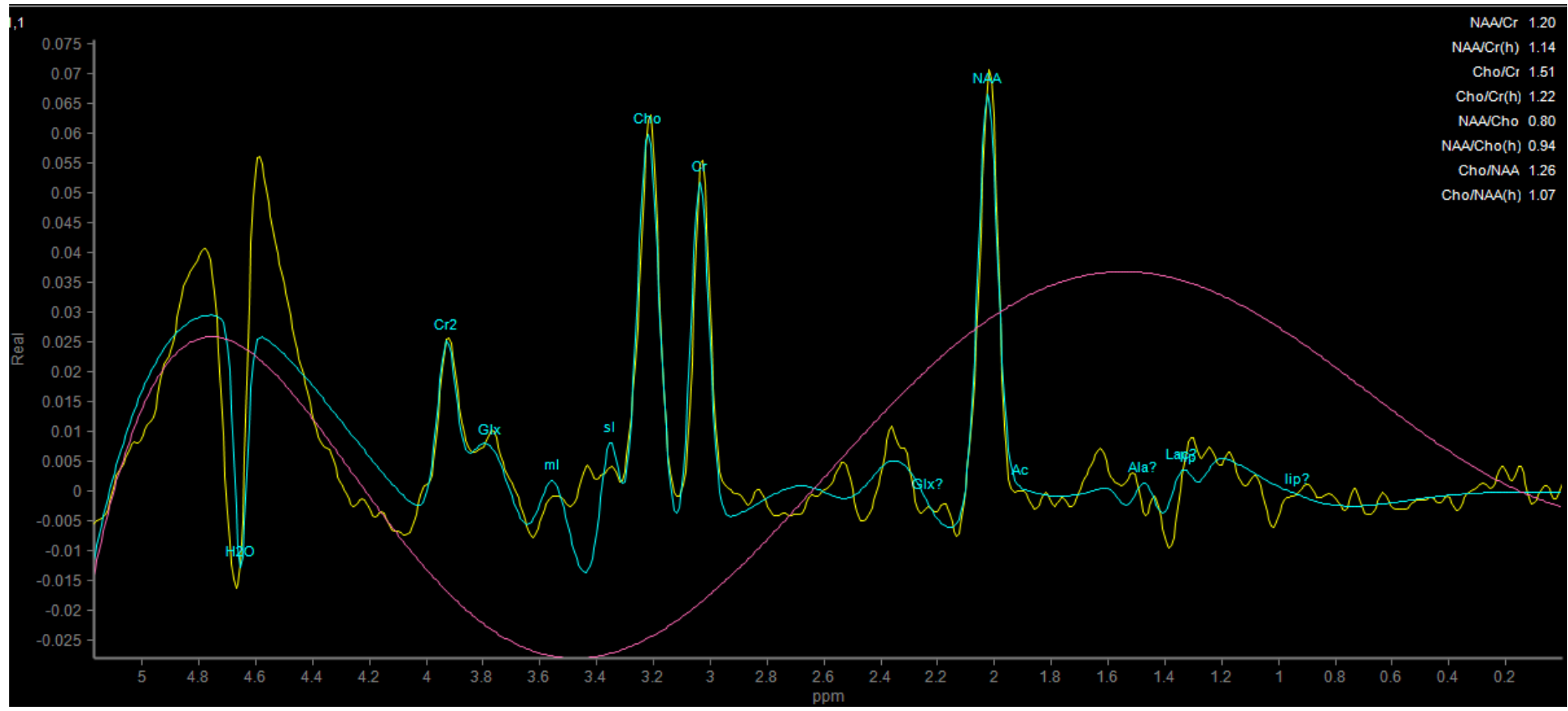
Run OK Cancel

Controllare che sia selezionato 1.5T e siano selezionati (in blu) i metaboliti di interesse

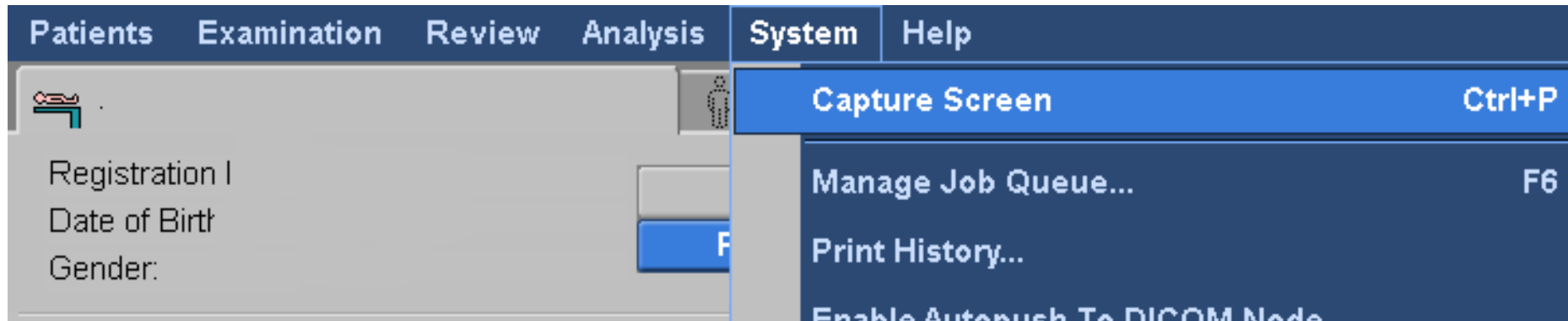
Fare quindi clic su «**RUN**»

Ricostruzione spettroscopia SV

Ecco il risultato finale!



Ricostruzione spettroscopia SV



L'ultimo passaggio è salvare il risultato ...

Fare «**Capture Screen**» e ricordarsi di inviare in archivio l'immagine salvata ...

