

# Enhanced DICOM MR for spectroscopy, structural and functional imaging

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# Acknowledgments

- *Mark Day, UCSF*
- *Kees Verduin, Philips Medical Systems*
- *Robert Haworth, GE Healthcare*
- *Elmar Seeberger, Siemens Medical Solutions*
- *Bradley J Erickson, Mayo Clinic*
- *Danielle Graveron-Demilly, Lyon*

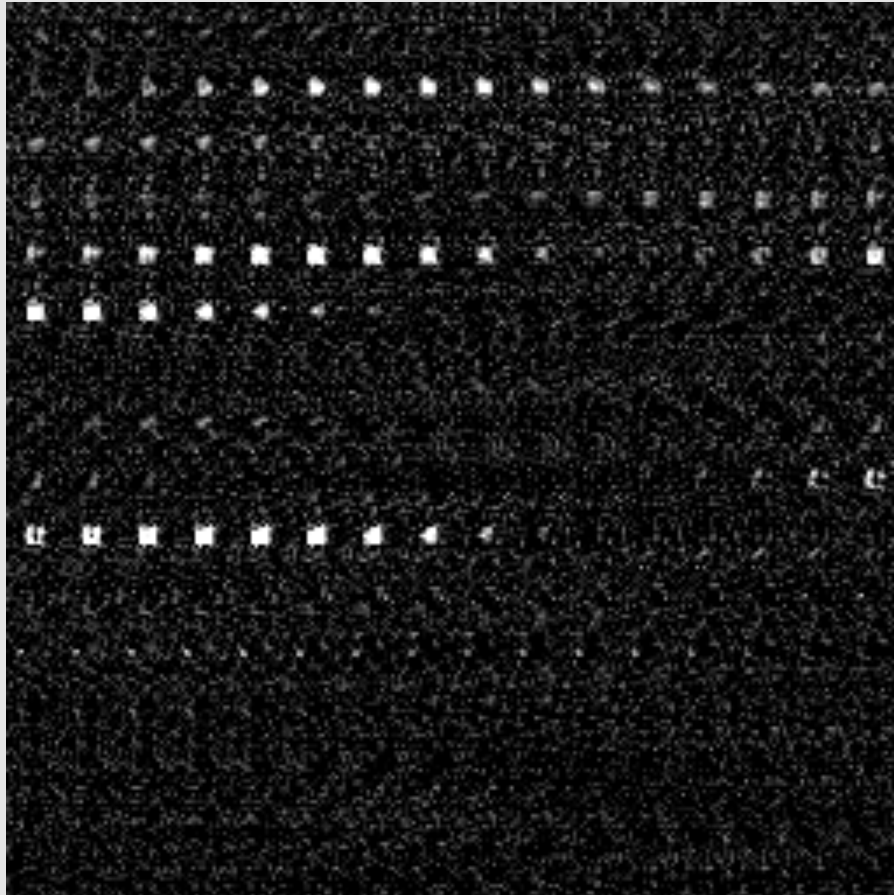
# DICOM & Spectroscopy

- Two primary problems to be addressed ...
- Spectroscopy acquisition datasets from different vendors and software releases are incompatible and in a proprietary format -> requires customized analysis software
- Results of analysis can only be distributed to clinical users as “screen shots” -> cannot interact with them or interrogate them for meaning

# Proprietary data formats

- Completely incompatible with DICOM - cannot be transferred with DICOM network services, unlike images, no embedded demographic (identity and date) information - need to manually ftp, archive, and track - does not scale to clinical setting
- Buried inside a pseudo-DICOM file - private elements or non-standard pixel data - can transfer and hide in PACS, but need proprietary software to analyse

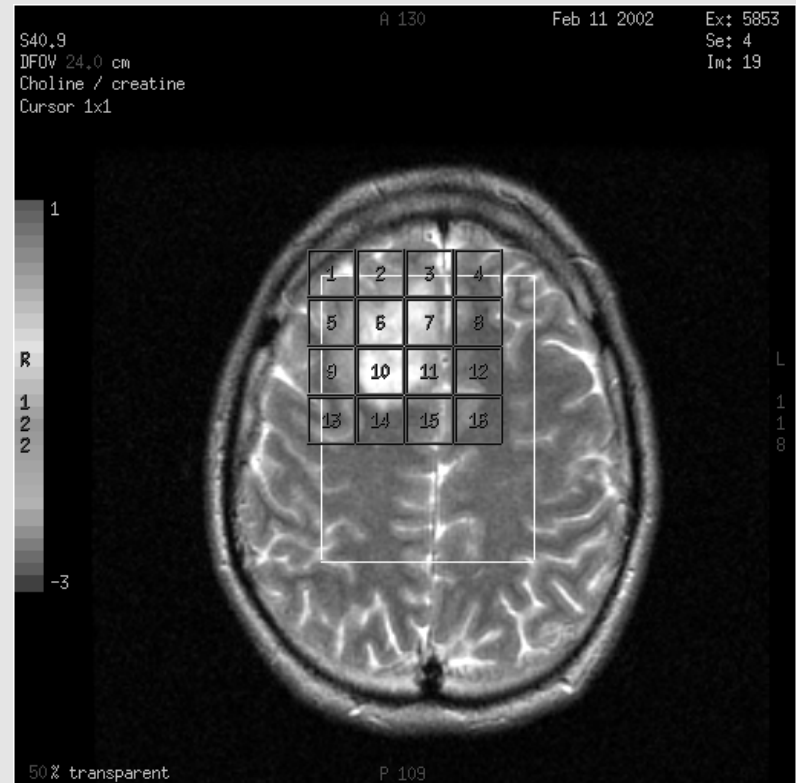
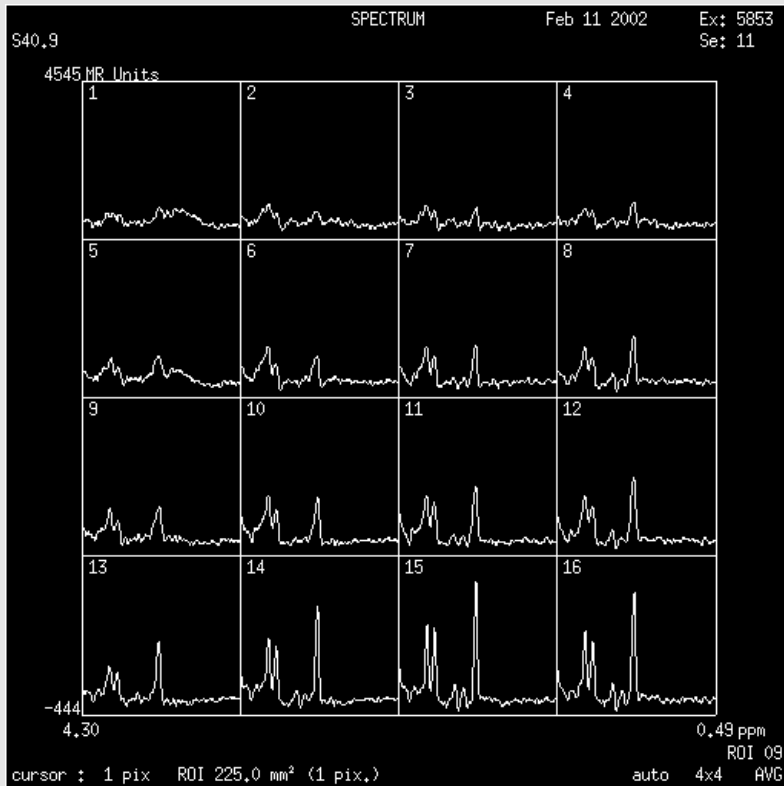
# “Pretend” DICOM files



# Screen shots

- No representation of spectra (whether processed or not) - visually graphed as an image loses ability to quantify peaks retrospectively, etc.
- No correlation of localization information (voxel selection and sat) unless rendered and captured
- Pre-rendered overlays on top of structural image - “underlying” image cannot be windowed
- Metabolite maps can only be pre-windowed with one grayscale or pseudo-color setting and not adjusted
- Metabolite maps cannot be correlated with corresponding spectra

# Screenshots



# Goal

- Encode acquired spectroscopy data in a standard, interoperable format that can be stored in and retrieved from the PACS
- Encode results of processing in a standard, interoperable format such that the PACS or workstation user can interact with it
- I.e., extend DICOM to provide explicit support for spectroscopy



# Enhanced MR Effort

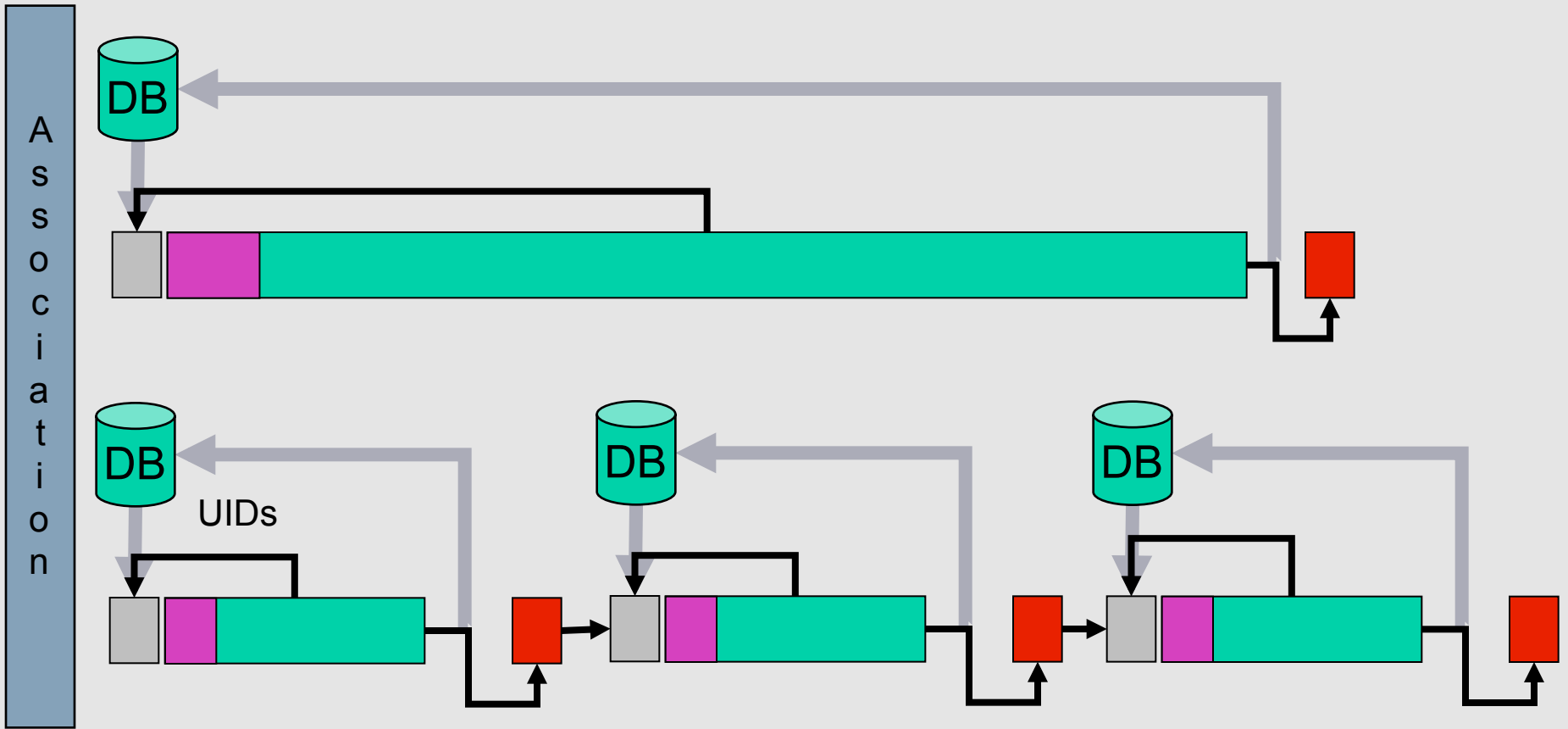
- Original DICOM standard 1993 - included a simple single-frame MR object with a (short) list of pulse sequence related attributes and 16 bit 2D image pixel data
- A decade later, advancing technology had outgrown this simplistic approach
- More complex organization of data required (3D, 4D volumes of space and time and other parameters like diffusion)
- More parameters and descriptions of pulse sequences
- Incorporate lessons learned from a decade of experience

# Enhanced MR Effort

- Scope to include images and spectra
- Scope excluded standardizing encoding of k-space data but allowed storage/retrieval
- Multiple frames (slices) per object rather than single, to simplify handling and improve performance
- Most new pulse sequence attributes mandatory and with fixed sets of values to choose from - improve interoperability by avoiding dependence on private attributes or values

# Multi-frame Performance

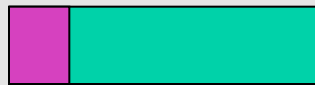
- Exploding data volumes
- Multi-frame encoding is not a panacea
- Avoids replication of common header information
- Reduced latency on high BDP networks
- Reduced database overhead - one entry in the “image” table for entire volume rather than one entry per slice
- Exposes opportunity for 3D and motion-prediction based compression



Store, parse, check



C-Store request

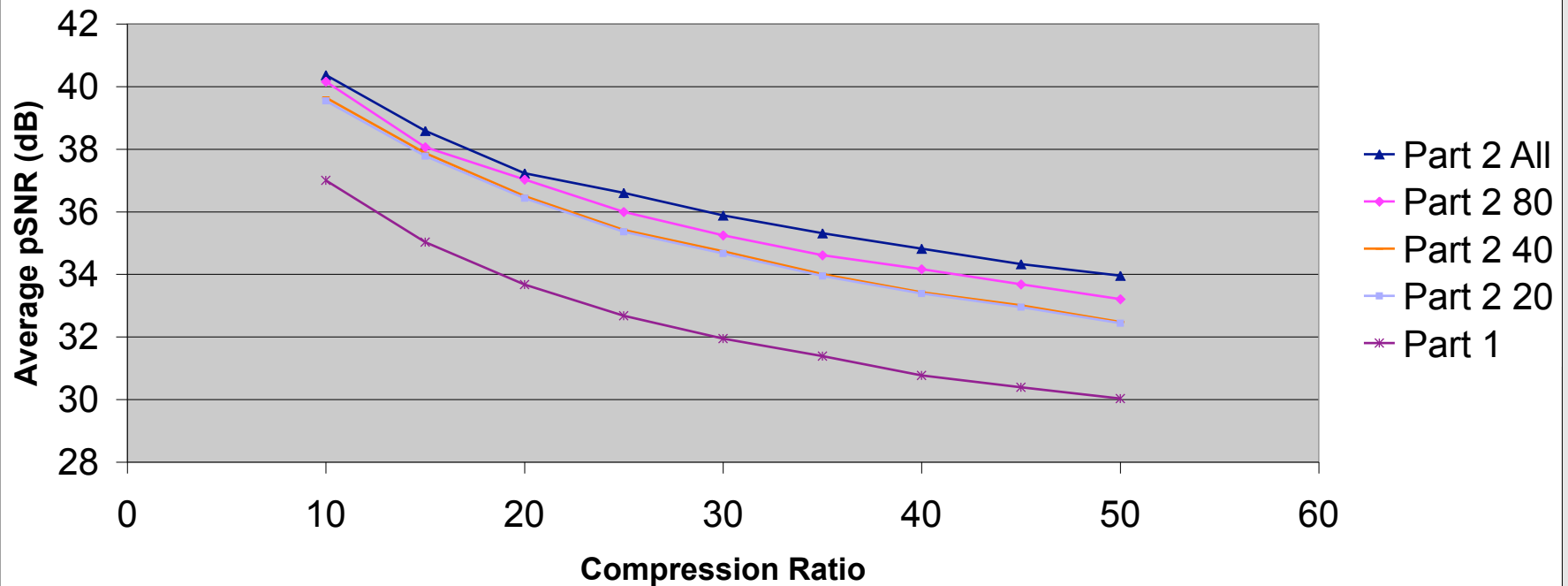


Dataset (attributes+pixels)



C-Store response (acknowledgement)

## Lossy 3D JPEG 2000 Compression (Alexis Tzannes, Aware, 2003)



# Technique Attributes & Terms

	MR	
SOP Class	Original	Enhanced
Attributes (Mandatory)	44 (2)	103 (94)
Terms (Enumerated)	38 (9)	228 (47)

# MR Acquisition Contrast

- Original DICOM SOP Class
  - Guess from echo and repetition time, etc.
- Enhanced DICOM SOP Class
  - New mandatory frame level attribute
  - Acquisition Contrast
    - DIFFUSION, FLOW\_ENCODED, FLUID\_ATTENUATED, PERFUSION, PROTON\_DENSITY, STIR, TAGGING, T1, T2, T2\_STAR, TOF, UNKNOWN

# Greater Inter-functionality

- Cardiac motion - vendor independent applications that handle spatial & temporal (cardiac cycle) MR images
- Diffusion MR - vendor independent applications that handle diffusion B value and direction
- Multi-stack spine - vendor independent applications that recognize stacks of parallel slices through inter-vertebral disk spaces
- Contrast and perfusion - vendor independent applications that recognize timing and phase of enhancement in MR images for display and or quantitative analysis
- *Spectroscopy - vendor independent applications that process and display single-voxel, multi-voxel or multi-slice MR spectra and reference and metabolite map images*



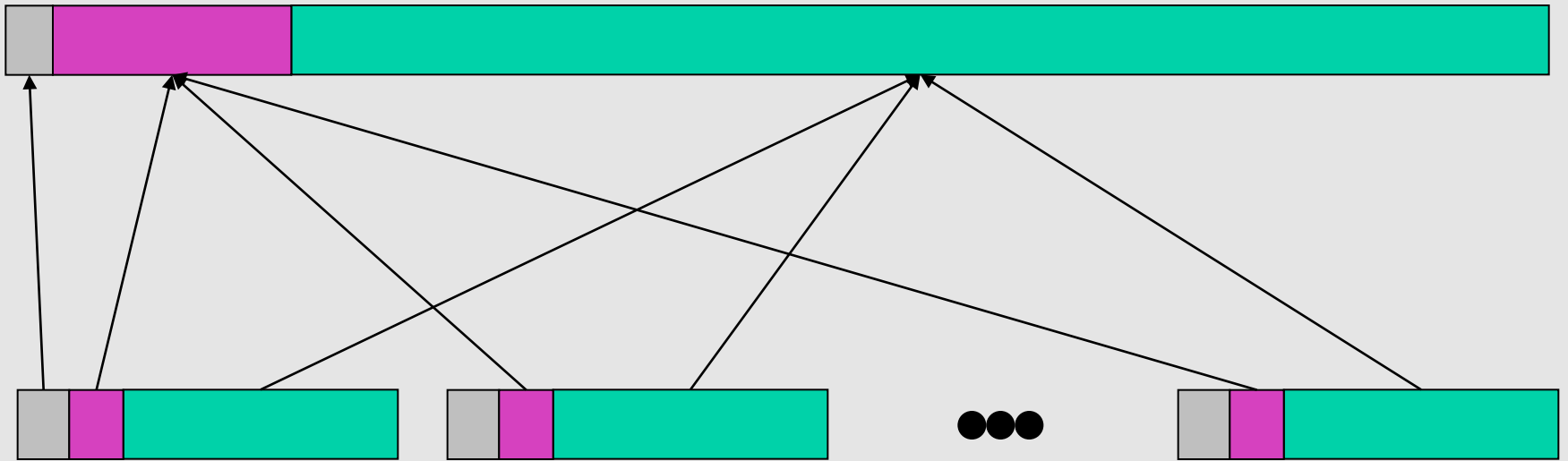
# Geometry unchanged

- Same as in original DICOM MR SOP Class
- Image Position and Orientation (Patient)
- Still need to compute AXIAL, SAGITTAL or CORONAL from orientation vector
- Still need to compute edge labels (A/P etc) from orientation vector
- May still need to compare orientation vectors to determine if slices are parallel - stacks and dimensions can be used to describe this

# Organization of Data

- Goal is to reduce the work that the receiving application has to do to “figure out”
  - How the data is organized
  - Why it is organized that way
- Without preventing use of the data in unanticipated ways
  - E.g. 3D on a dataset not intended as a volume
- Two levels
  - The detailed shared & per-frame attributes
  - The overall dimensions, stacks and temporal positions

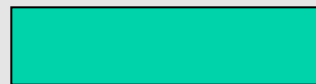
# Multi-frame Functional Groups



Shared attributes

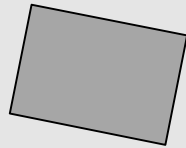


Per-frame attributes



Pixel data

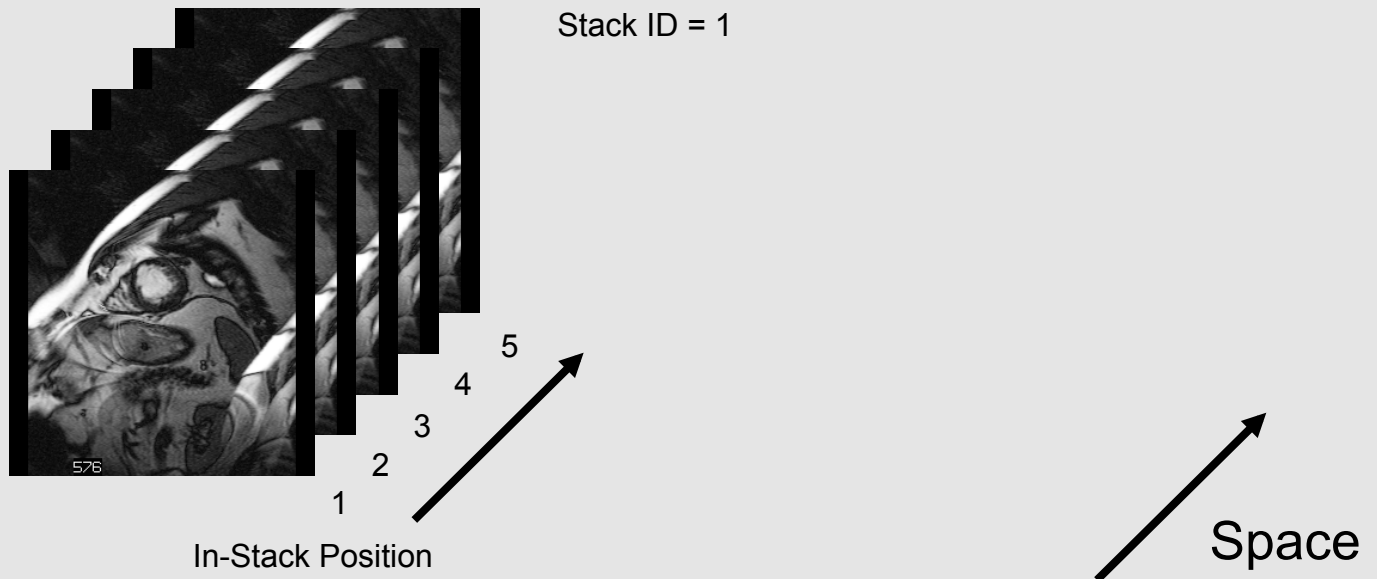
# Stacks



# Dimensions

Start with a dimension of space.

A set of contiguous slices through the heart.

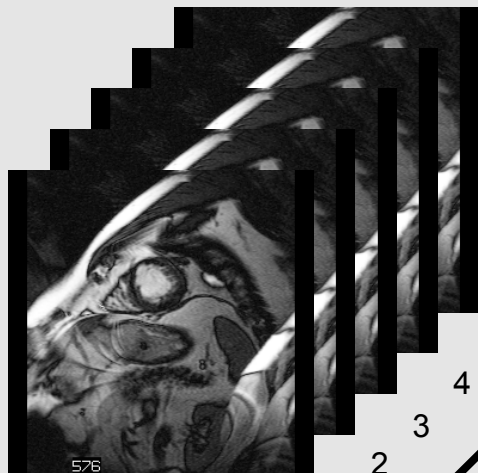


Trigger  
Delay  
Time

Temporal  
Position  
Index

48 ms

2



Stack ID = 1

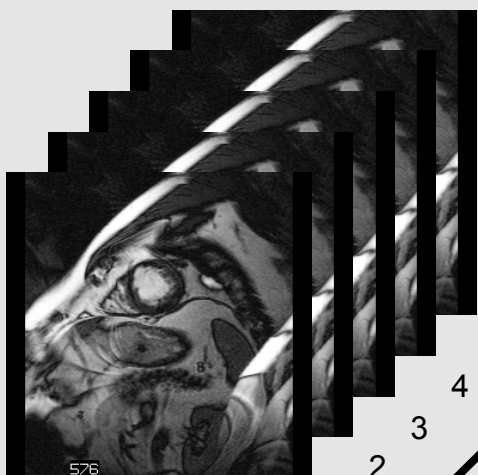
In-Stack Position

Add dimension of time  
(delay time from R-wave).

Sets of contiguous slices  
throughout cardiac cycle.

0 ms

1



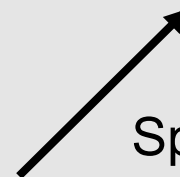
Stack ID = 1

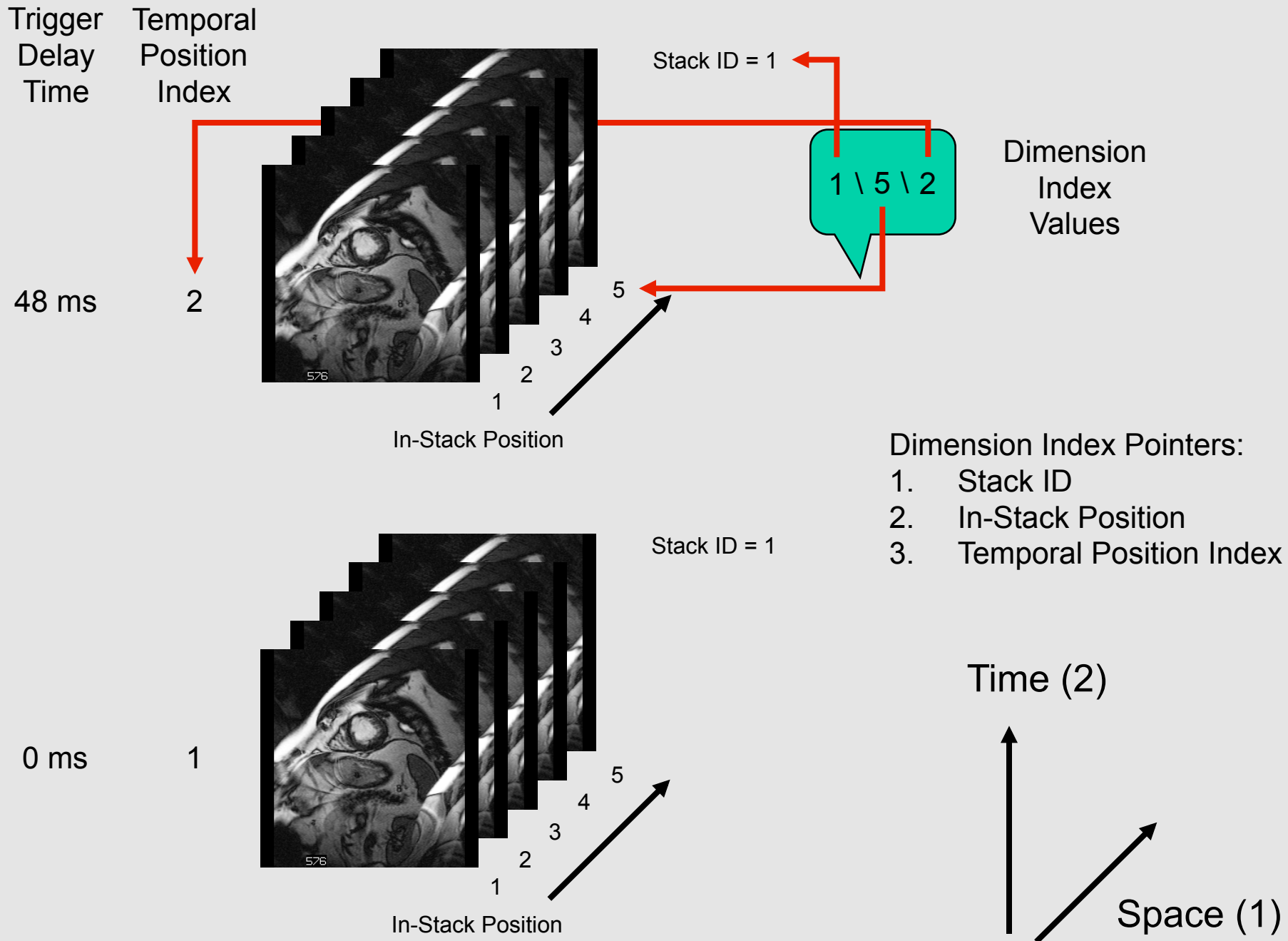
In-Stack Position

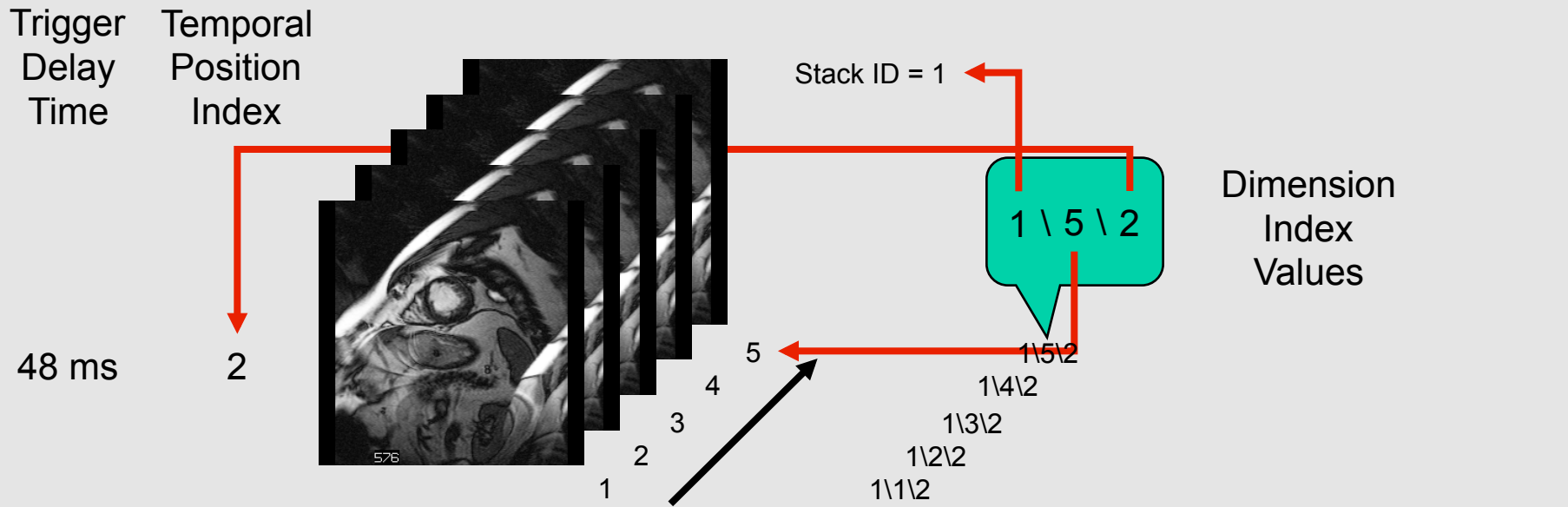
Time



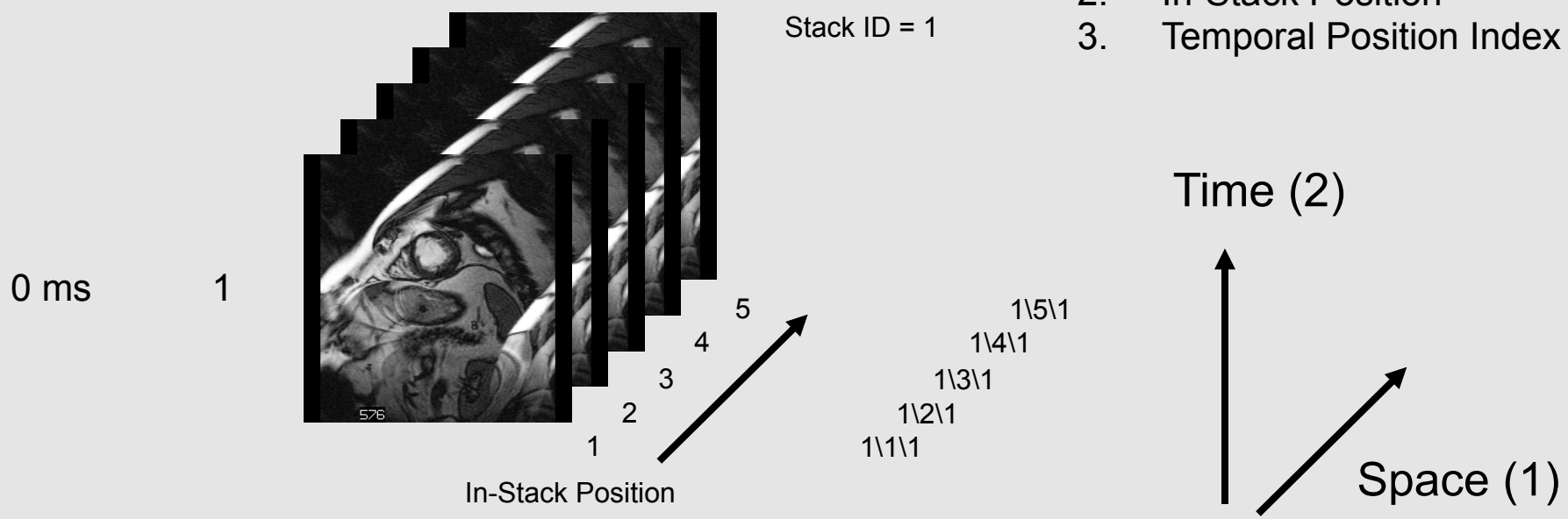
Space



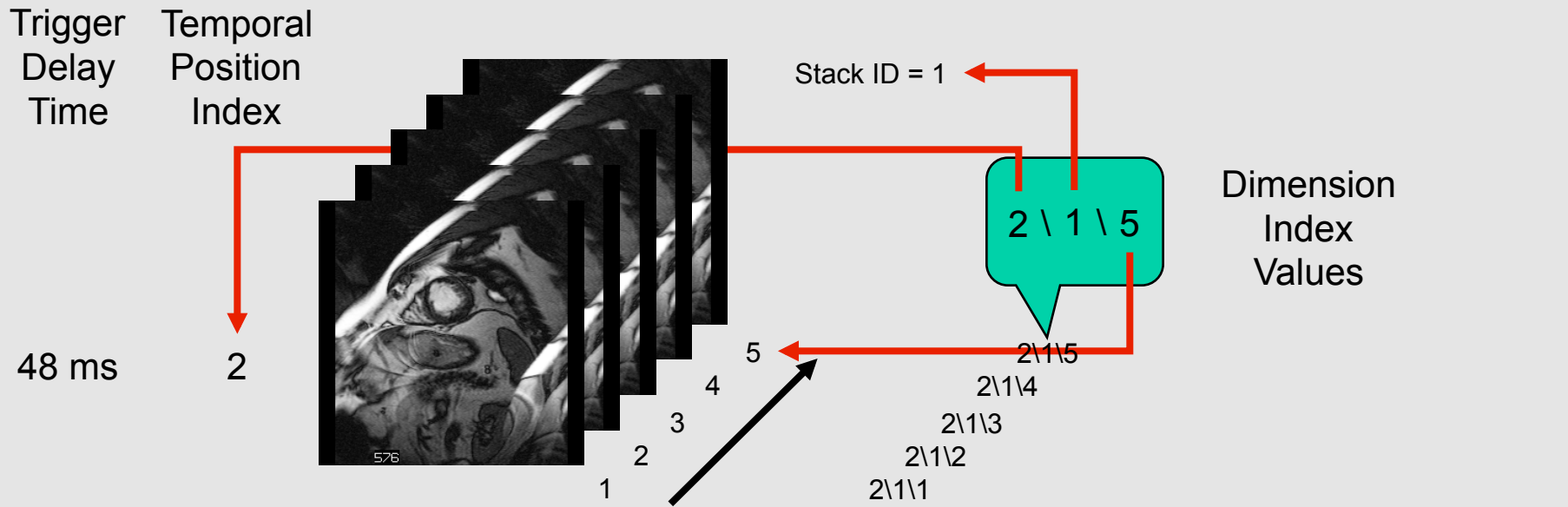




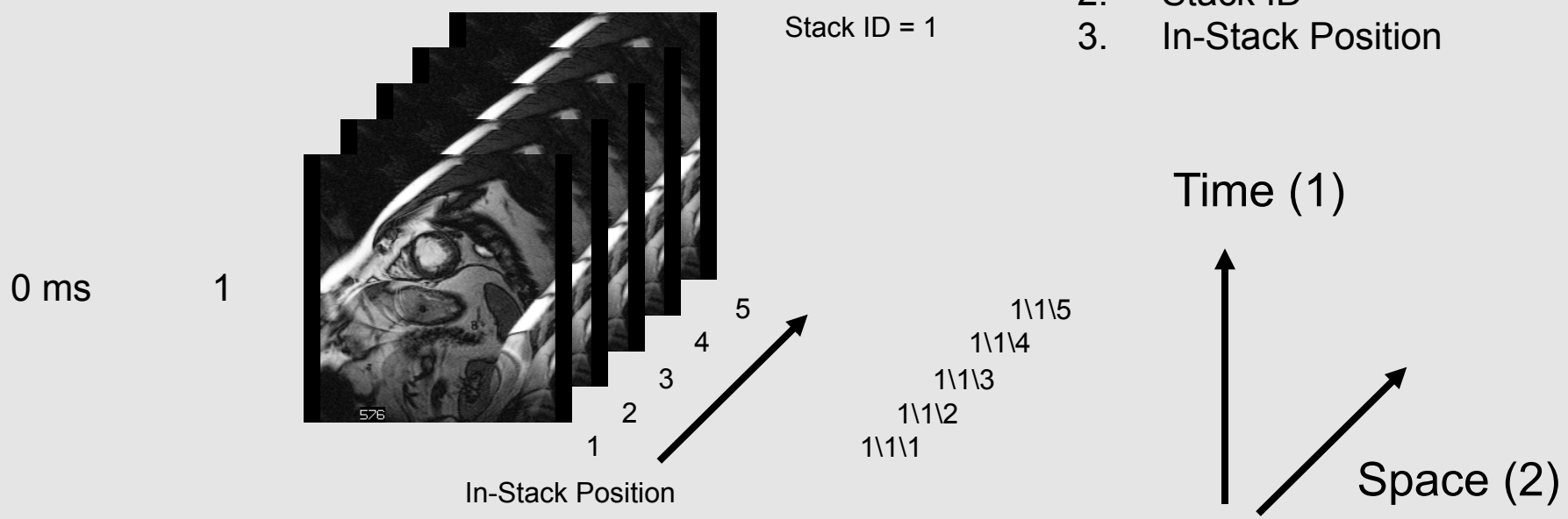
- Dimension Index Pointers:
1. Stack ID
  2. In-Stack Position
  3. Temporal Position Index

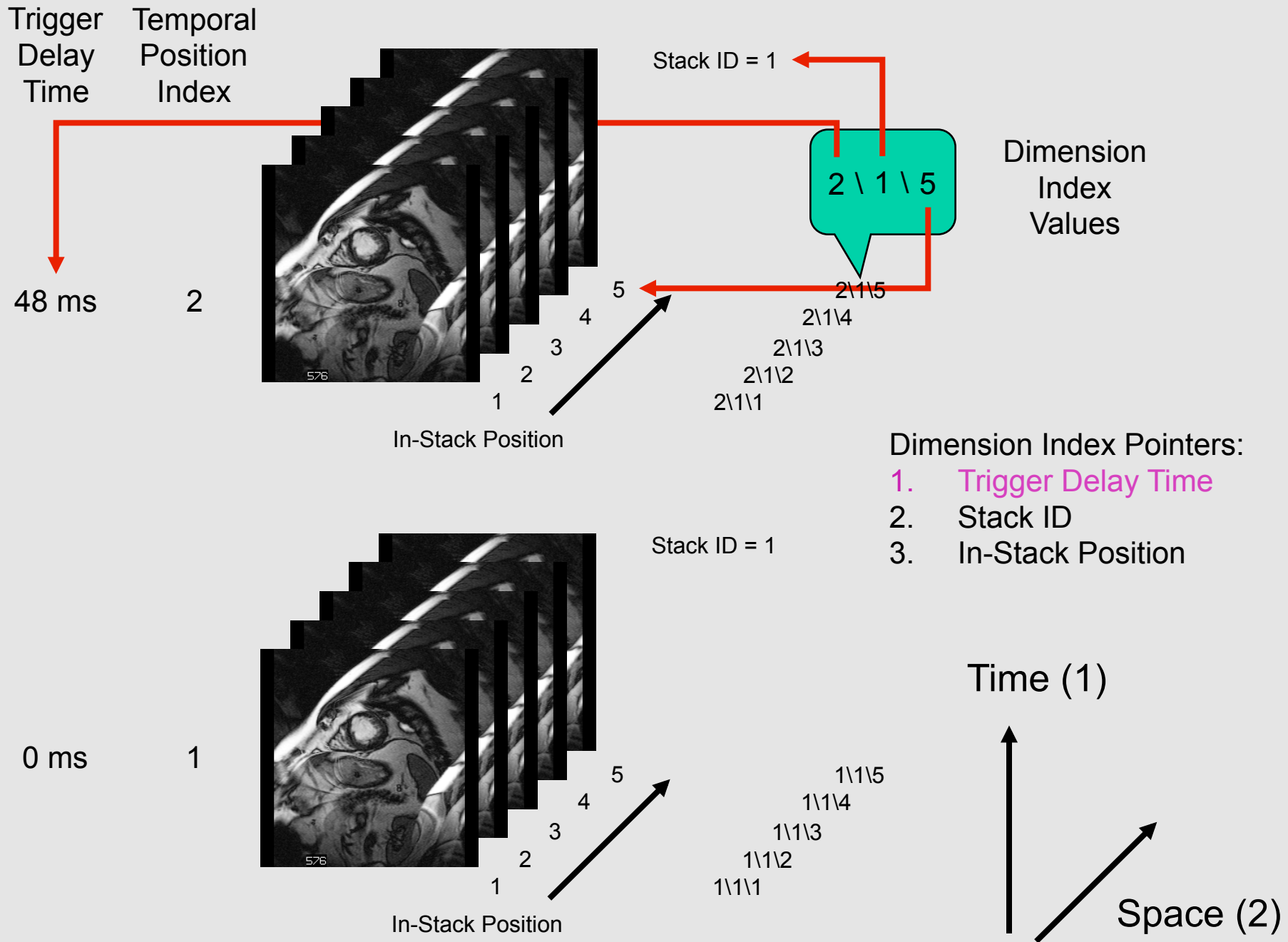






- Dimension Index Pointers:
1. Temporal Position Index
  2. Stack ID
  3. In-Stack Position





# Dimension features

- Description of dimensions separate from their indices
  - Dimensions are described once
  - Indices within dimensions are encoded per-frame
- Receiving application only needs to follow the index values
  - Does NOT need to select or sort by attribute value
  - Dimensions can be entire functional groups
  - Dimensions can be private attributes or functional groups

# Dimension applications

- Selection of sort order for simple viewing
- Partitioning of frames for hanging
- Selection of frames that constitute a
  - volume in space
  - temporal sequence
  - contrast administration phase
  - physiological parameter, e.g. diffusion b value

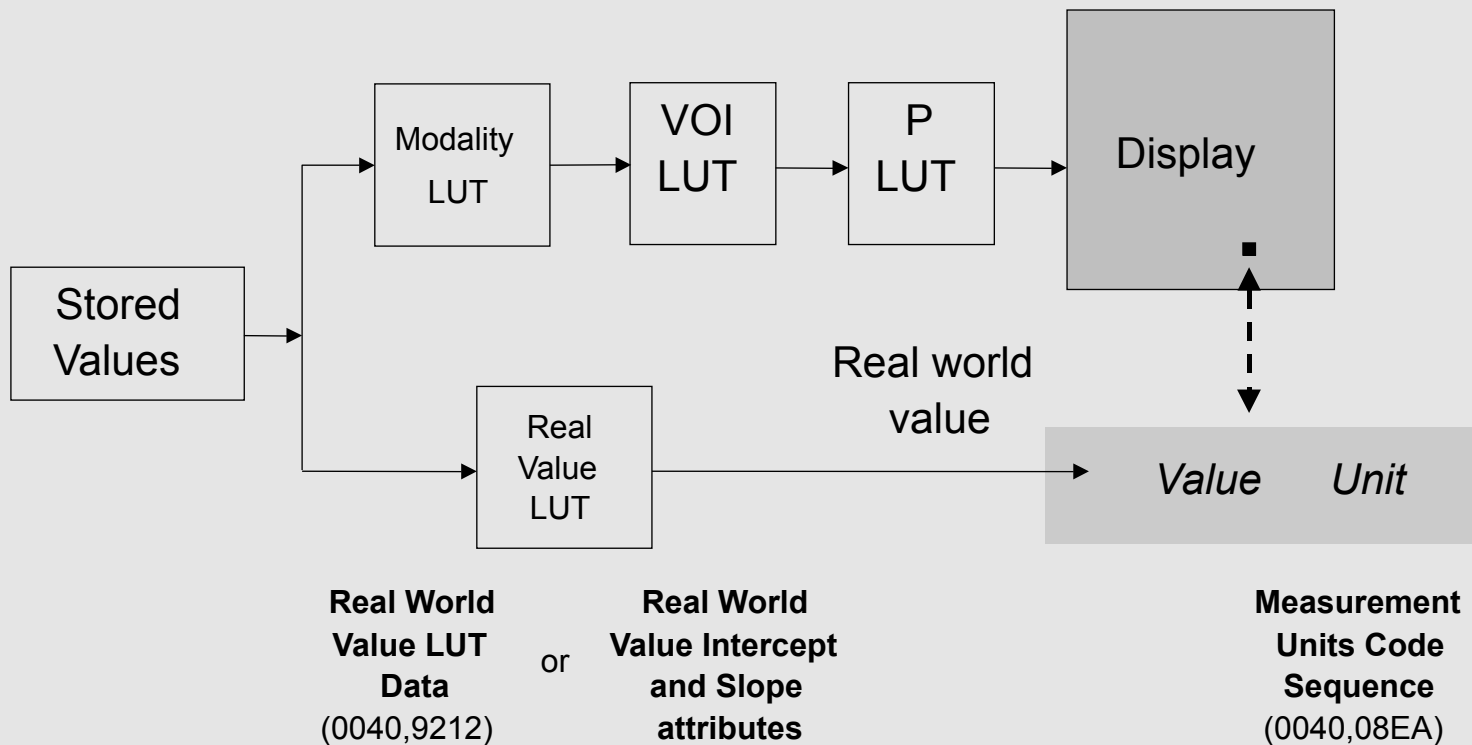
# Enhanced Contrast/Bolus

- Original SOP Class
  - Plain text description
  - Difficult to determine presence/absence
    - E.g., description value of “None”
  - Single agent (did not distinguish oral/iv)
  - Codes optional and never used
- Enhanced SOP Class
  - Mandatory codes only
  - Multiple items with separate coded routes & timing
  - Presence or absence per-frame can be described

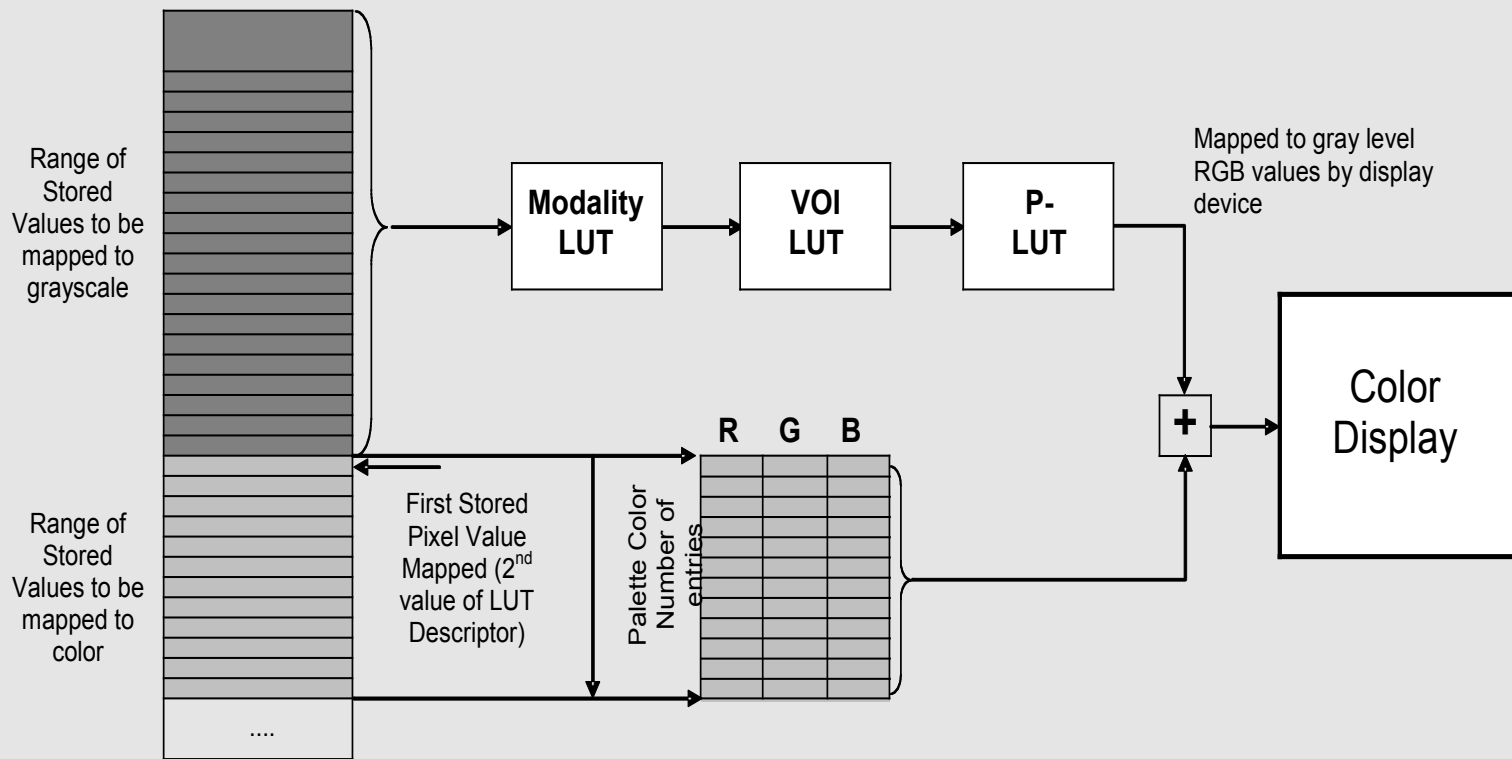
# Coded anatomic regions

- Original SOP Class
  - Incomplete list of optional defined terms
  - Optional laterality
- Enhanced SOP Class
  - Mandatory coded anatomic region
  - Comprehensive & appropriate list of codes
  - Mandatory laterality
  - Per-frame or for entire object

# Quantitation of pixel values - Real World Values



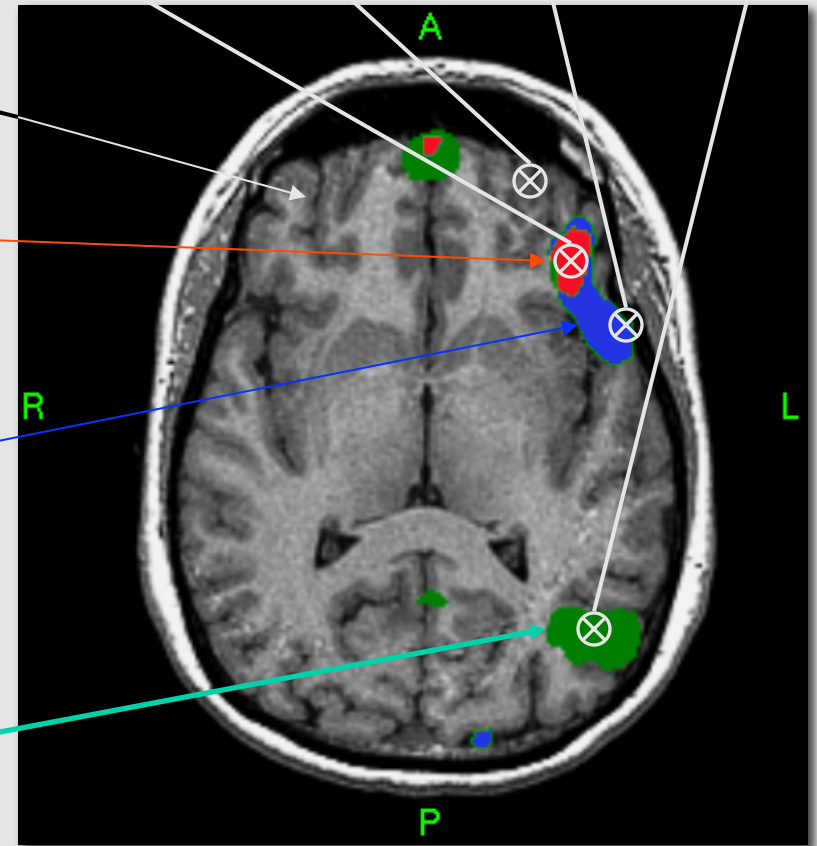
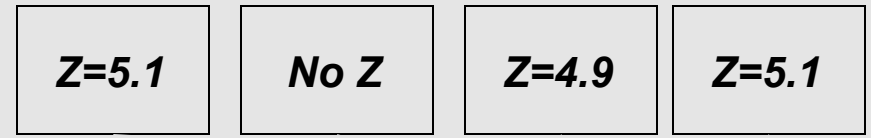
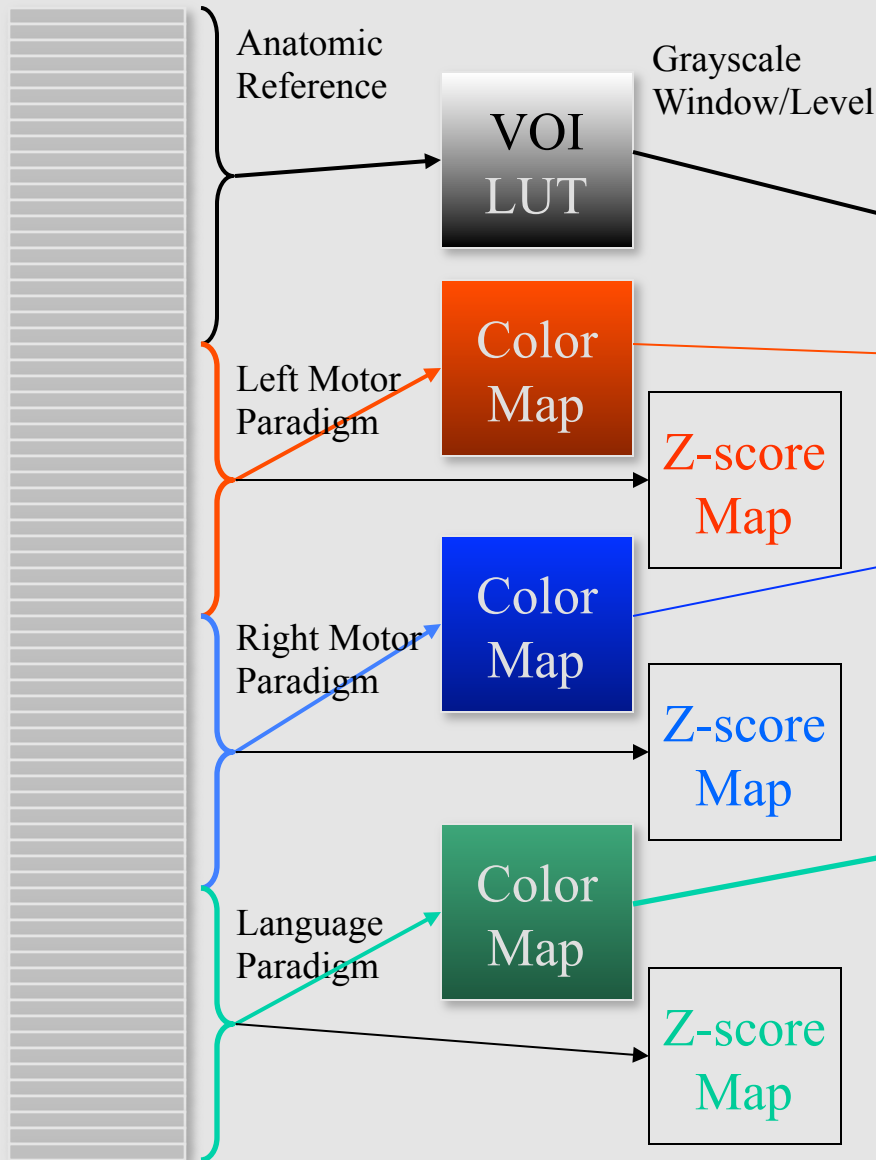
# Color display of functional data





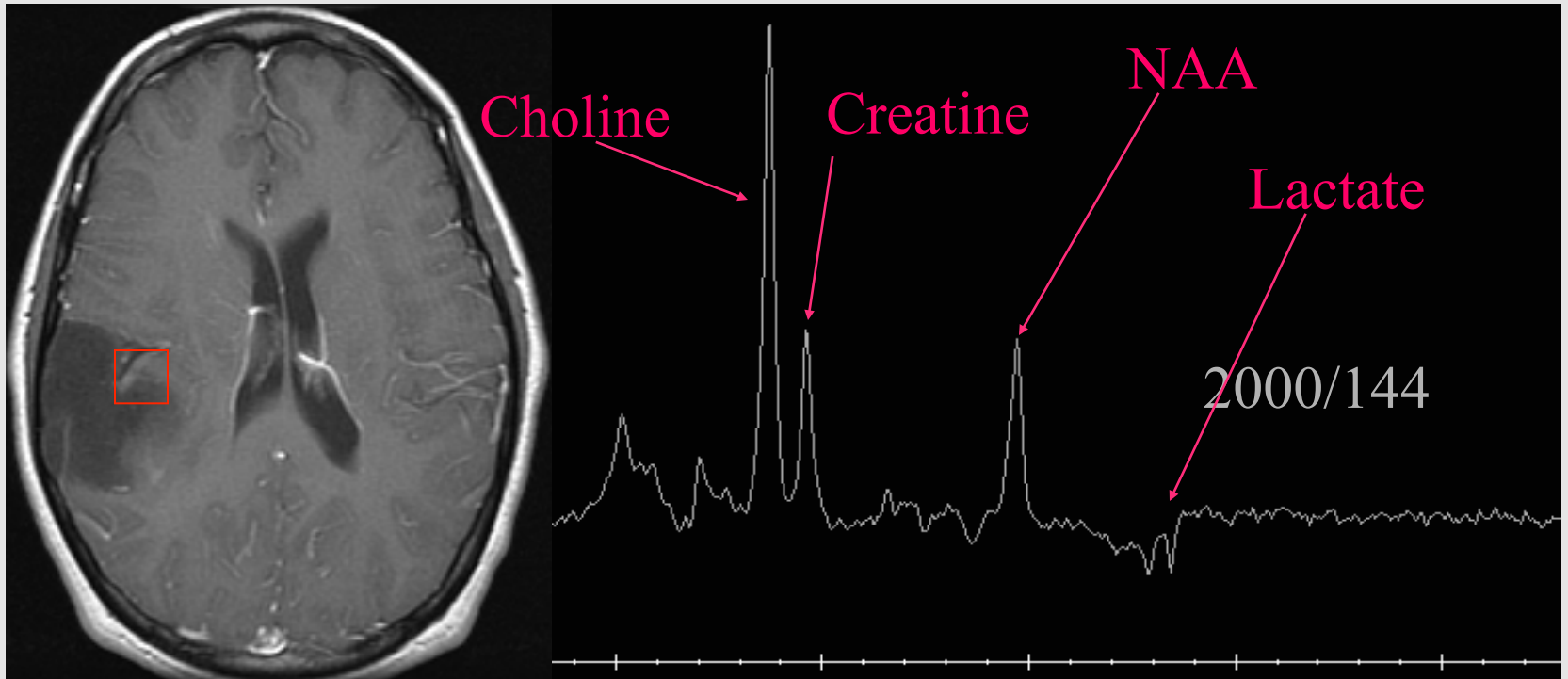
# Color by functional paradigm

Pixel Values

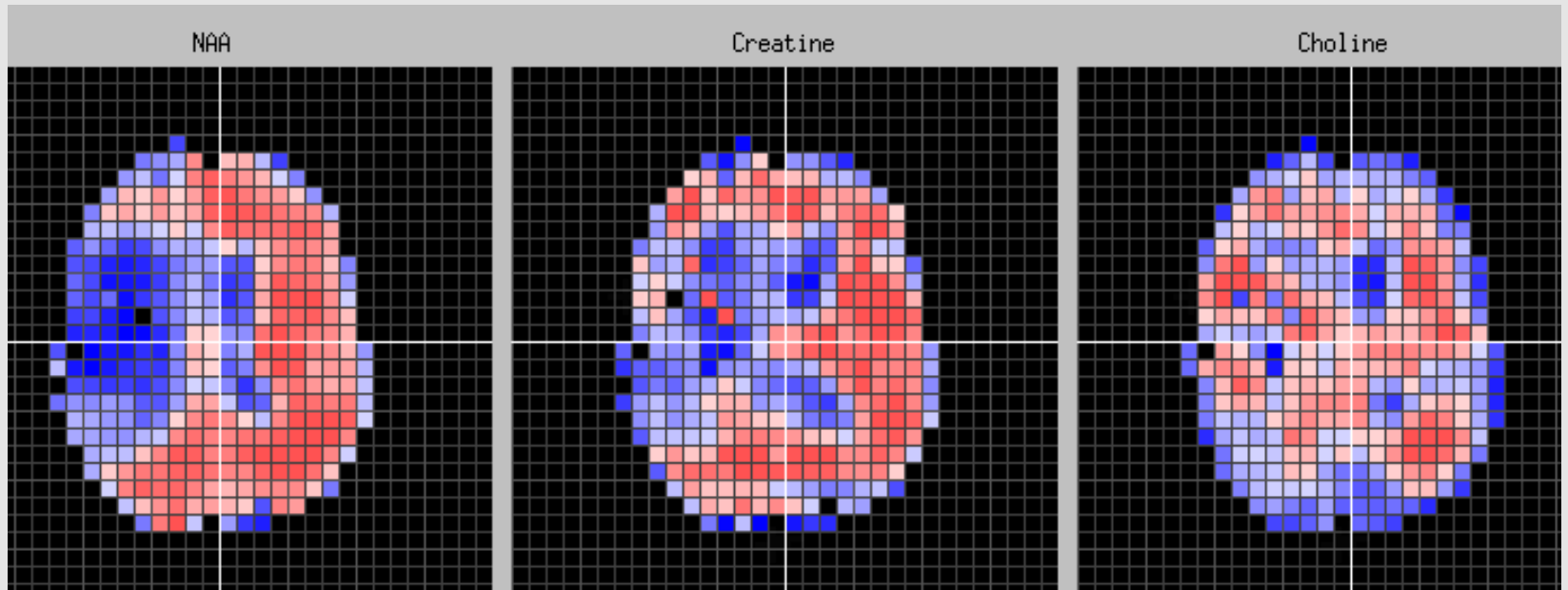


Z Score Real World Value Map

# MR Spectroscopy



# Metabolite Maps



# MR Spectroscopy

- Spatially localized spectra
  - MR Spectroscopy SOP Class
  - signal intensity versus frequency or time
  - not stored as pixel data - new Spectroscopy Data attribute
  - arrays of floating point and/or complex values
  - 1D or 2D data within single or multiple voxels and frames
  - allows for interaction, analysis and quantitation
- Metabolite maps
  - Enhanced MR Image SOP Class
  - images of one particular peak of the spectrum, ratio, etc.
  - are stored as images (in Pixel Data attribute)

# Spectroscopy Data Module

- Rows and Columns
  - Number of voxels vertically and horizontally in frame
  - Single voxel spectroscopy: Rows and Columns == 1
  - Multi-voxel - treated as a “slice” per frame; may be multi-frame
- Data Point Rows and Columns
  - Data Point Rows == 1 for 1D spectra
  - Data Point Rows > 1 for 2D spectra
- Signal Domain Rows and Columns
  - FREQUENCY or TIME
- Data Representation
  - COMPLEX, REAL, IMAGINARY, MAGNITUDE



*The  
Medicine  
Behind the  
Image*

# Spectroscopy Data

○

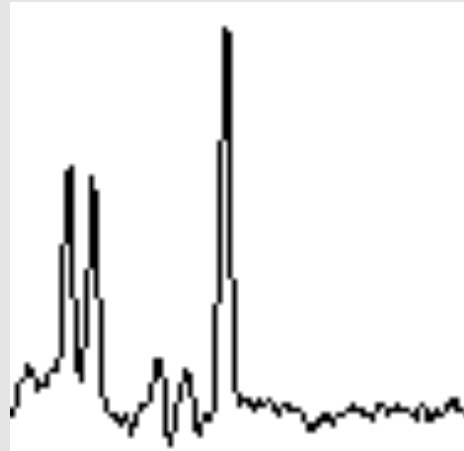


The  
**Medicine**  
Behind the  
**Image**

# Spectroscopy Voxel

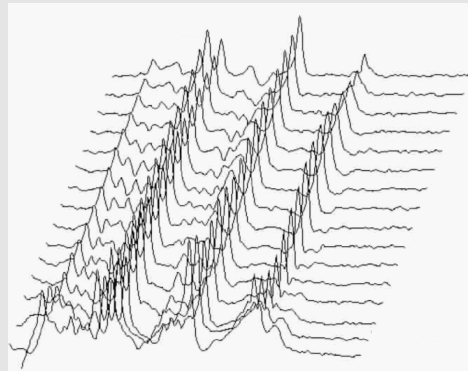


# Spectroscopy Voxel





# Spectroscopy Voxel



# Spatial Localization

- Spectroscopy objects share same patient-relative coordinate space as defined for images
- Each spectroscopy “frame” (whether single or multiple voxels) has same set of position and orientation direction cosines as images do
- Hence any spectroscopy voxel location can be correlated with any images in same spatial frame of reference
- Localization volume and saturation slabs orientation, position and thickness are also described in the same coordinate space
- I.e., the information is provided - application can render and allow user interaction as desired

Dicom Image Viewer

DICOMDIR Image Spectra Attributes Frames

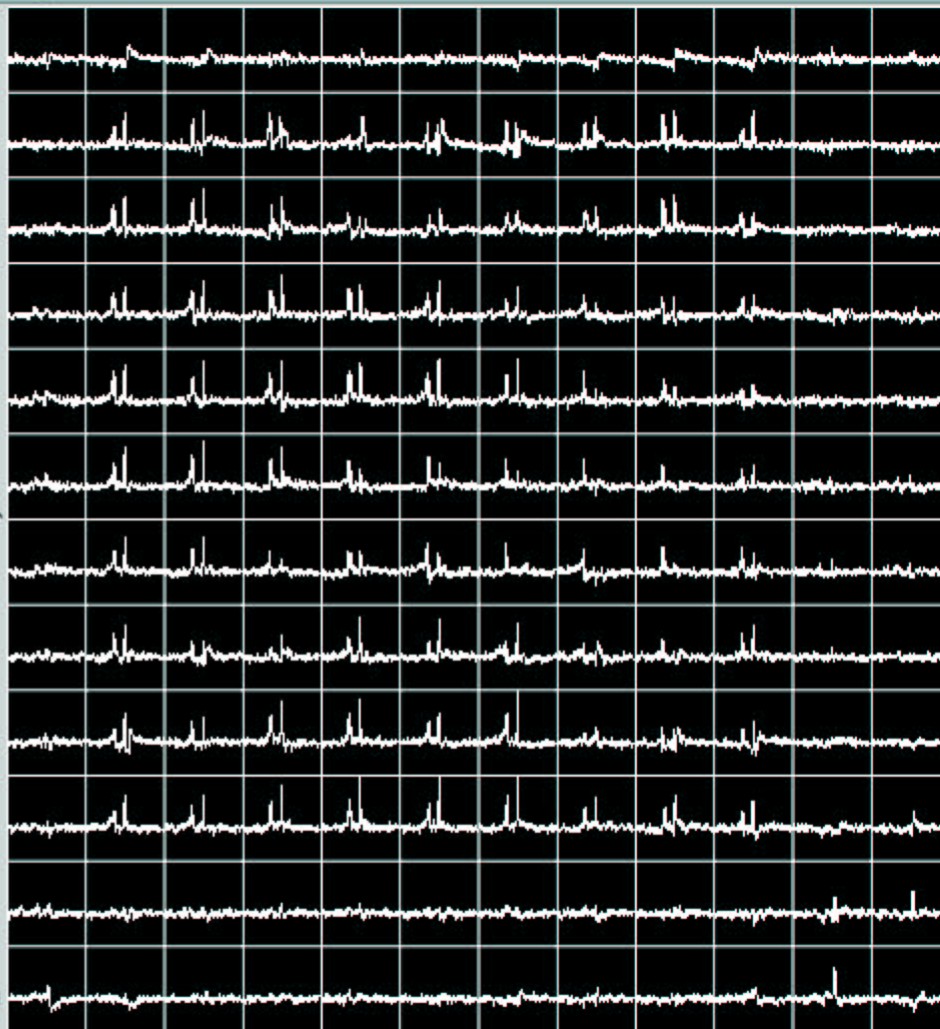
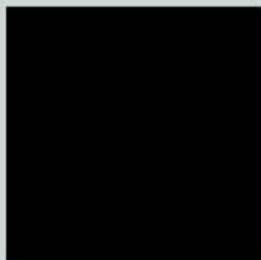
File... Import Send... XML... Validate...

Frame index: 1 8

Sort frames by:  implicit  dimension

1 [124 frames] {MR(MF,T1) <AXIAL L\P>  
1 [32 frames] {MR(MF,FLUID\_ATTENUATED) <AXIAL L\P>

1 [124 frames] {MR(MF,T1) <AXIAL L\P>  
1 [32 frames] {MR(MF,FLUID\_ATTENUATED) <AXIAL L\P>  
2 {MR(MF,DERIVED,T1,RESAMPLED,MPR) <SAGITTAL P\F>



Frame	AccessionNumber	AcquisitionContrast	AcquisitionDateTim	AcquisitionDuration	AcquisitionNumber	ApplicableSafetyStandardAgency	BaselineCorrect
4	9995025	UNKNOWN	20020728125300	600	100	FDA	NONE

(11:68,1)



# Dicom Image Viewer

DICOMDIR Image Spectra Attributes Frames

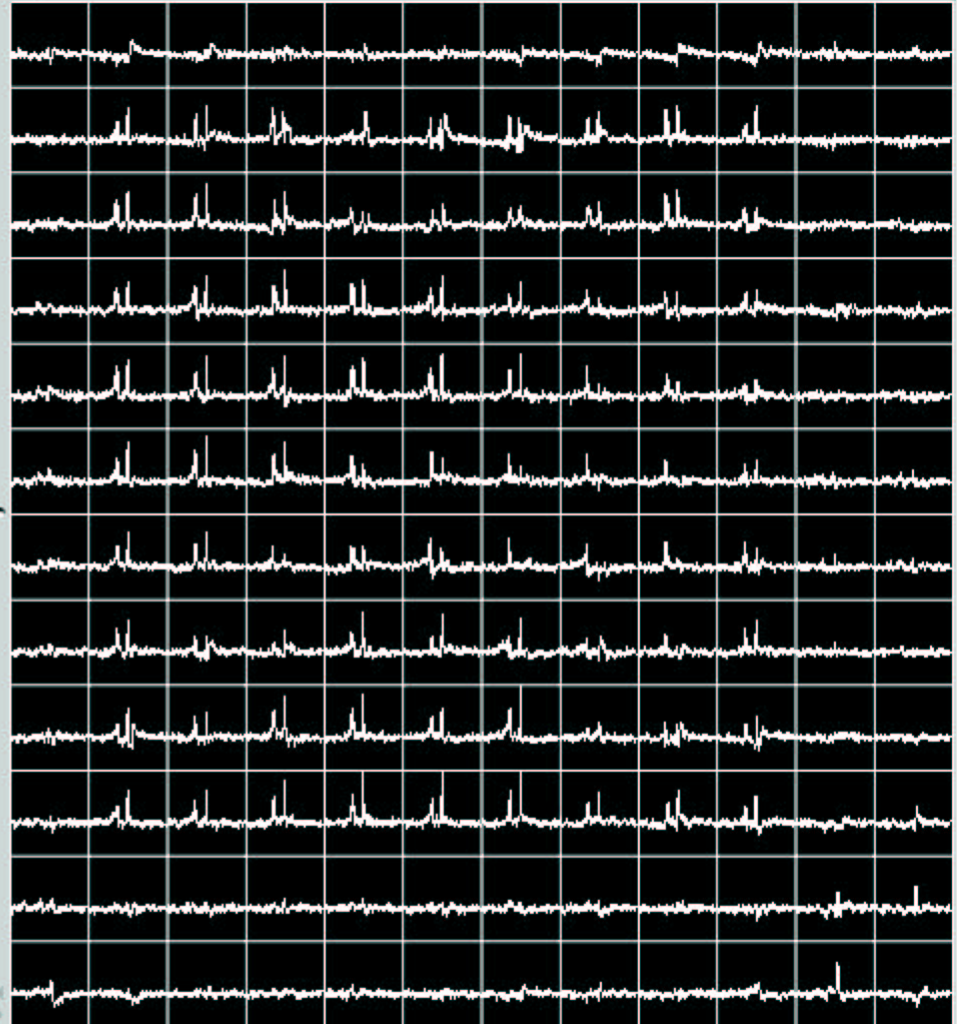
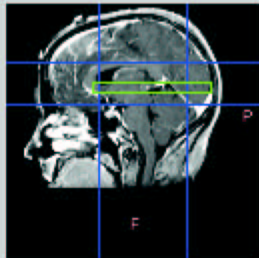
File... Import Send... XML... Validate...

Frame index: 1 8

Sort frames by:  implicit  dimension

1 [124 frames] {MR(MF,T1) <AXIAL L\P>  
1 [32 frames] {MR(MF,FLUID\_ATTENUATED) <AXIAL L\P>

1 [124 frames] {MR(MF,T1) <AXIAL L\P>  
1 [32 frames] {MR(MF,FLUID\_ATTENUATED) <AXIAL L\P>  
2 {MR(MF,DERIVED,T1,RESAMPLED,MPR) <SAGITTAL P\F>



Frame	AccessionNumber	AcquisitionContrast	AcquisitionDateTim	AcquisitionDuration	AcquisitionNumber	ApplicableSafetyStandardAgency	BaselineCorrect
4	9995025	UNKNOWN	20020728125300	600	100	FDA	NONE



Done.



# Dicom Image Viewer

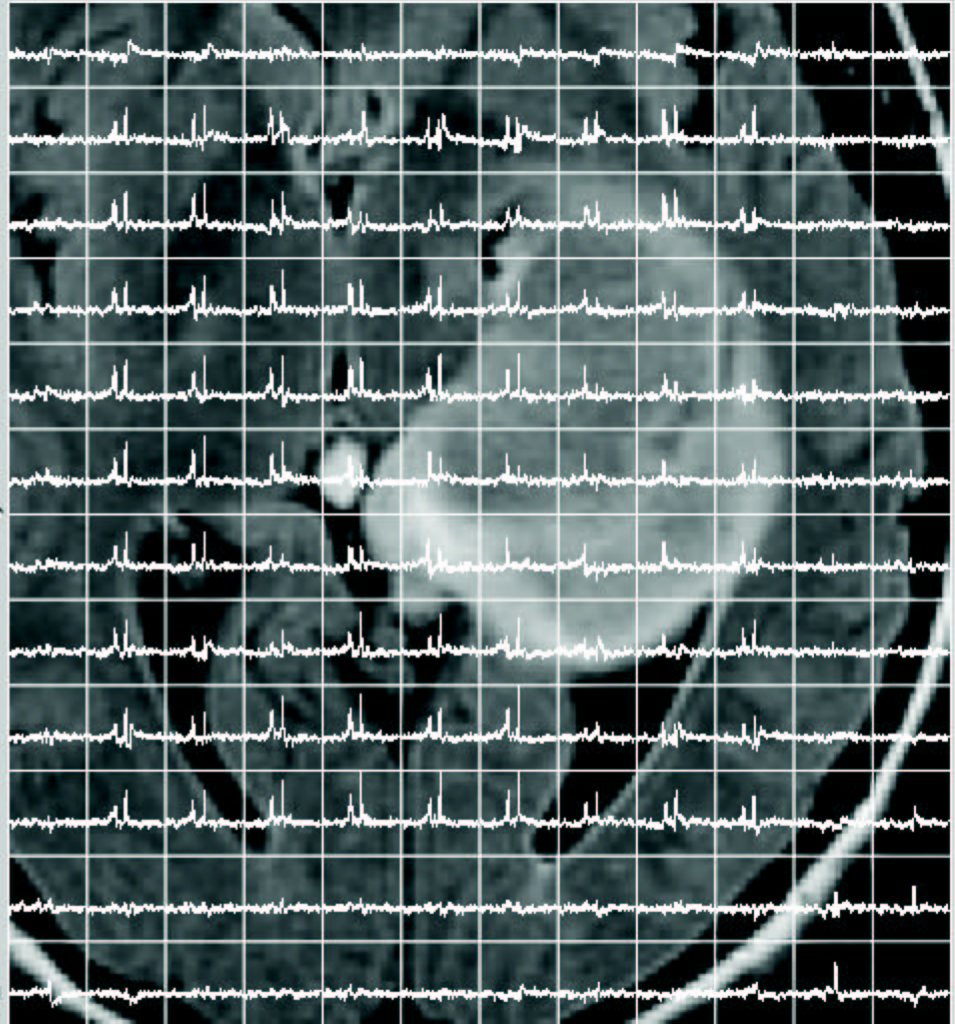
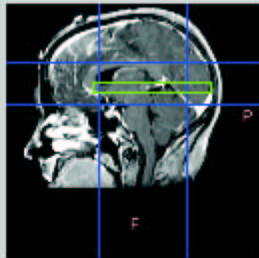
DICOMDIR Image Spectra Attributes Frames

File... Import Send... XML... Validate...

Frame index: 1 8

Sort frames by:  implicit  dimension

- 1 [124 frames] {MR(MF,T1) <AXIAL L\P>
  - 1 [32 frames] {MR(MF,FLUID\_ATTENUATED) <AXIAL L\P>
- 
- 1 [124 frames] {MR(MF,T1) <AXIAL L\P>
  - 1 [32 frames] {MR(MF,FLUID\_ATTENUATED) <AXIAL L\P>
  - 2 {MR(MF,DERIVED,T1,RESAMPLED,MPR) <SAGITTAL P\F>



Frame	AccessionNumber	AcquisitionContrast	AcquisitionDateTim	AcquisitionDuration	AcquisitionNumber	ApplicableSafetyStandardAgency	BaselineCorrect
4	9995025	UNKNOWN	20020728125300	600	100	FDA	NONE



(7:172,4)

# Spectroscopy Attributes

- Transmitter Frequency
- Spectral Width
- Chemical Shift Reference
- Volume Localization Technique
- De-coupling
- De-coupled Nucleus
- De-coupling Frequency
- De-coupling Chemical Shift Reference
- Time Domain Filtering
- Number of Zero Fills
- Baseline Correction
- Frequency Correction
- First Order Phase Correction
- Water Referenced Phase Correction

# Pulse Sequence Attributes

- Pulse Sequence Name
- MR Spectroscopy Acquisition Type
- Echo Pulse Sequence
- Multiple Spin Echo
- Multi-planar Excitation
- Steady State Pulse Sequence
- Echo Planar Pulse Sequence
- Spectrally Selected Suppression
- Geometry of k-Space Traversal
- Rectilinear Phase Encode Reordering
- Segmented k-Space Traversal
- Coverage of k-Space
- Number of k-Space Trajectories

# Metabolite Maps

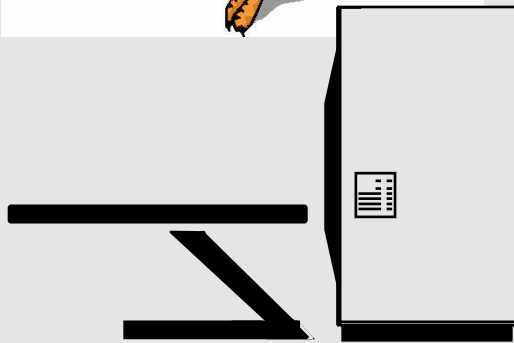
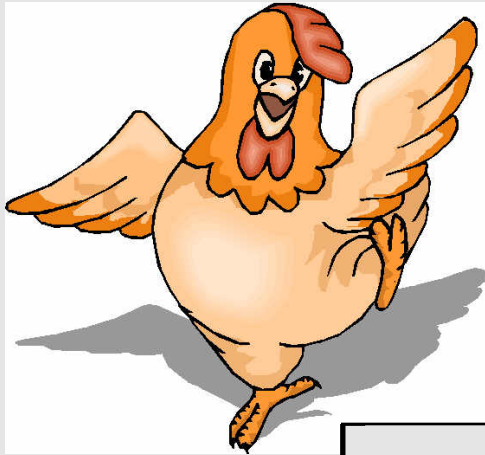
- Stored as Enhanced MR Images like any other
- Pixel data is grayscale but pseudo-color map may be specified
- Specific image type, based on which additional mandatory attributes are present
  - Text description of map required
  - Code describing metabolite may be present, e.g., codes for NAA, Ch/Cr ratio, etc.
  - Chemical Shift Integration Limits in ppm



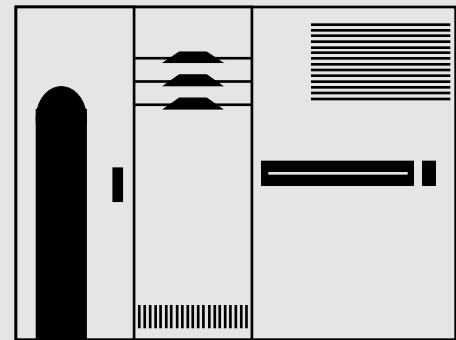
# Raw Data

- Discussion over whether or not to standardize “raw” (k-Space) data in DICOM
- Vendors were reluctant
  - Encoding depends too much on specific sequence and hardware
  - Of limited value to consumers of data
  - No research-orientated champion in DICOM to push the issue or do the work
- Desirability of storing and retrieving raw data to/from PACS recognized
  - New Raw Data SOP Class
  - Same “header” (patient/study/series) as all DICOM objects
  - No payload defined - expected to be in private attributes

# But when ?



*Modality*



*PACS*

# NEMA Initiatives

- MR test tools, images and spectra available
- CT test tools and images developed
- Implementation testing & demonstration
  - June 2005 - SCAR demonstration
  - November 2005 - RSNA InfoRAD demonstration
- After SCAR, CT test tools and images released

# NEMA & SCAR Test & Demonstration

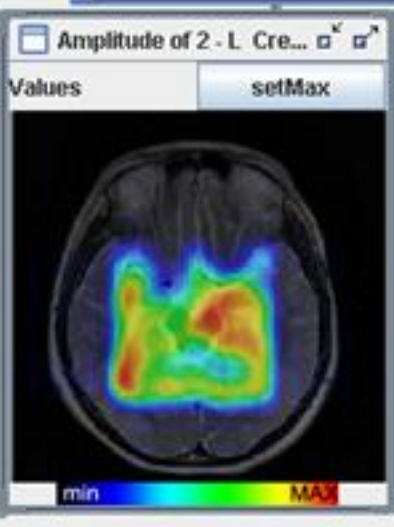
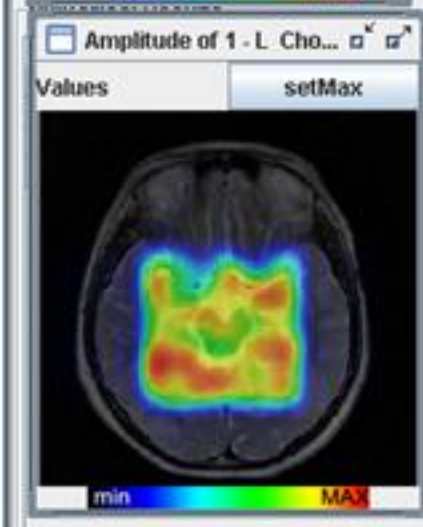
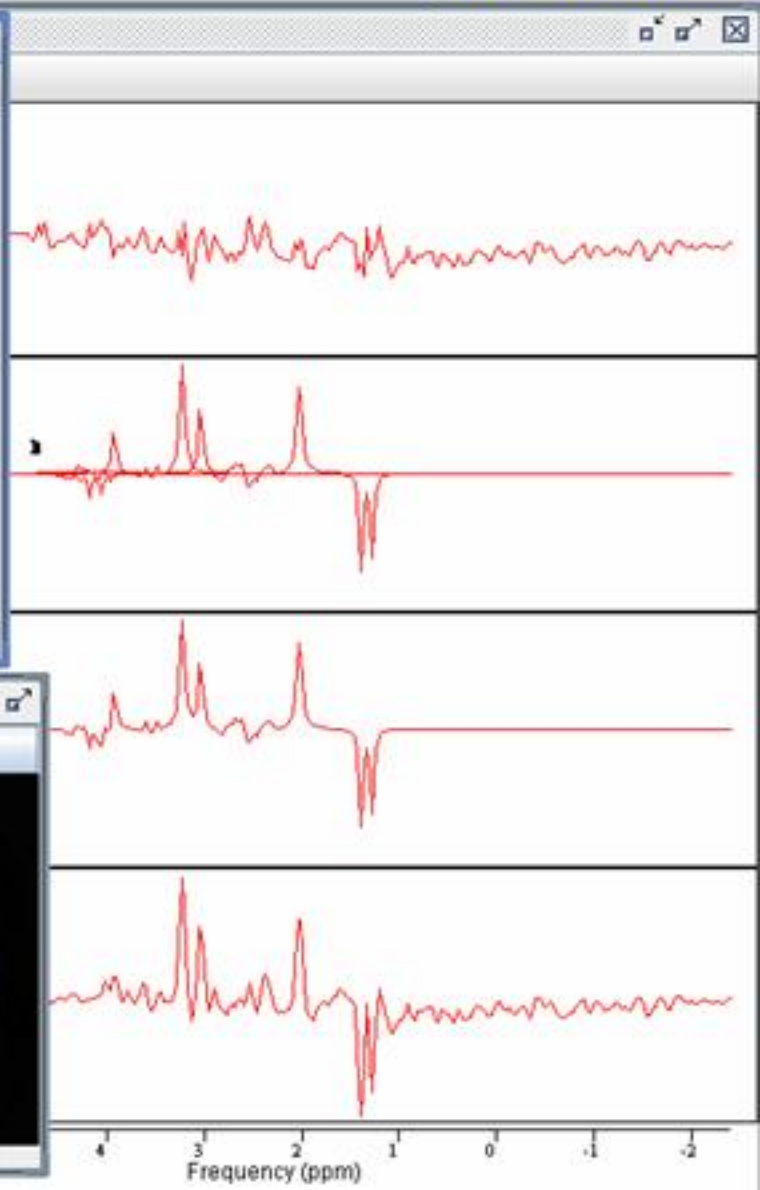
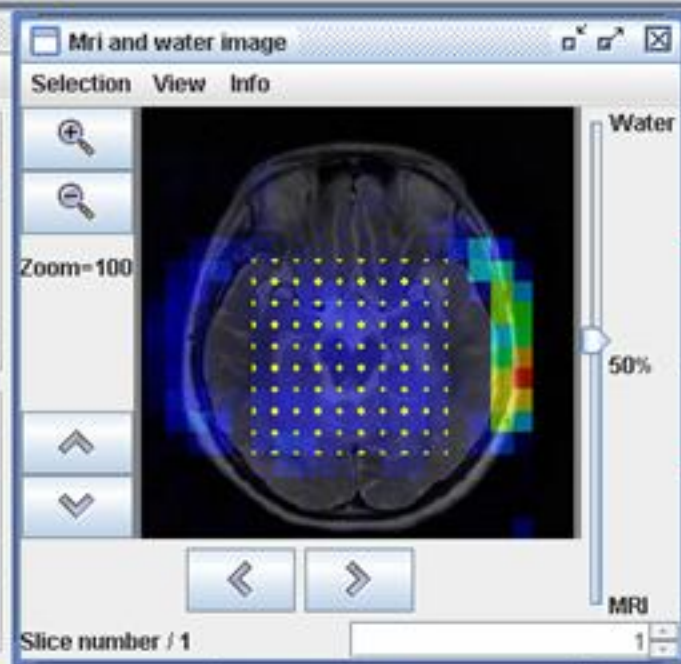
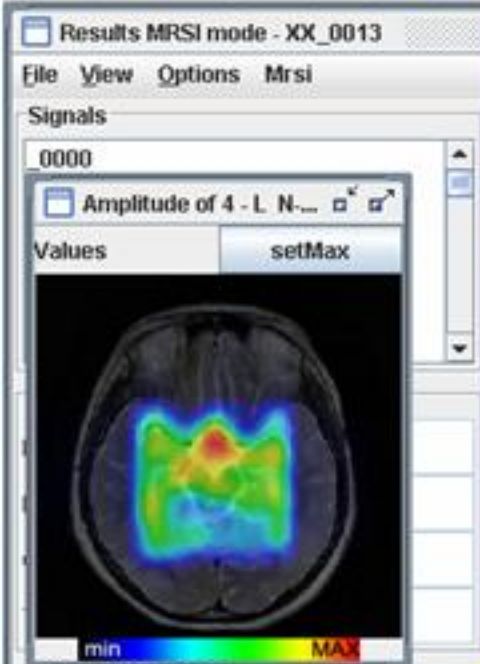


# Purpose of the Test & Demonstration

- Participants
  - Test that it works
  - Identify problems and solutions
- Other vendors
  - Show what work needs to be done
- Users
  - Show that it works
  - Begin to show some of the benefits
    - Performance
    - Interoperability of new attributes, dimensions, applications, spectroscopy ... testing of clinical scenarios

# Enhanced MR in Product

- Philips has released acquisition devices with Enhanced MR, Spectroscopy and Raw Data in current product - have provided sample objects now on NEMA ftp site
- Siemens has stated it has been released in VB13 for Tim systems
- No word from GE yet
- jMRUI has been involved in NEMA demos and can read time-domain spectroscopy data, and write processed data and metabolite maps



# Conclusion

- DICOM Enhanced MR image and spectroscopy objects are intended to raise the level of inter-functionality between different vendors' acquisition devices and applications
- Opportunity for developers of processing and analysis applications to avoid dependence on proprietary formats and tight coupling to vendors and versions
- Opportunity to distribute results to clinical (PACS) applications providing interaction beyond screen shots
- Adoption of DICOM spectroscopy objects is necessary (but not sufficient) for broader clinical utilization of MRS
- Toolkits are freely available and open source - no need to “fear” supposed “complexity” of DICOM