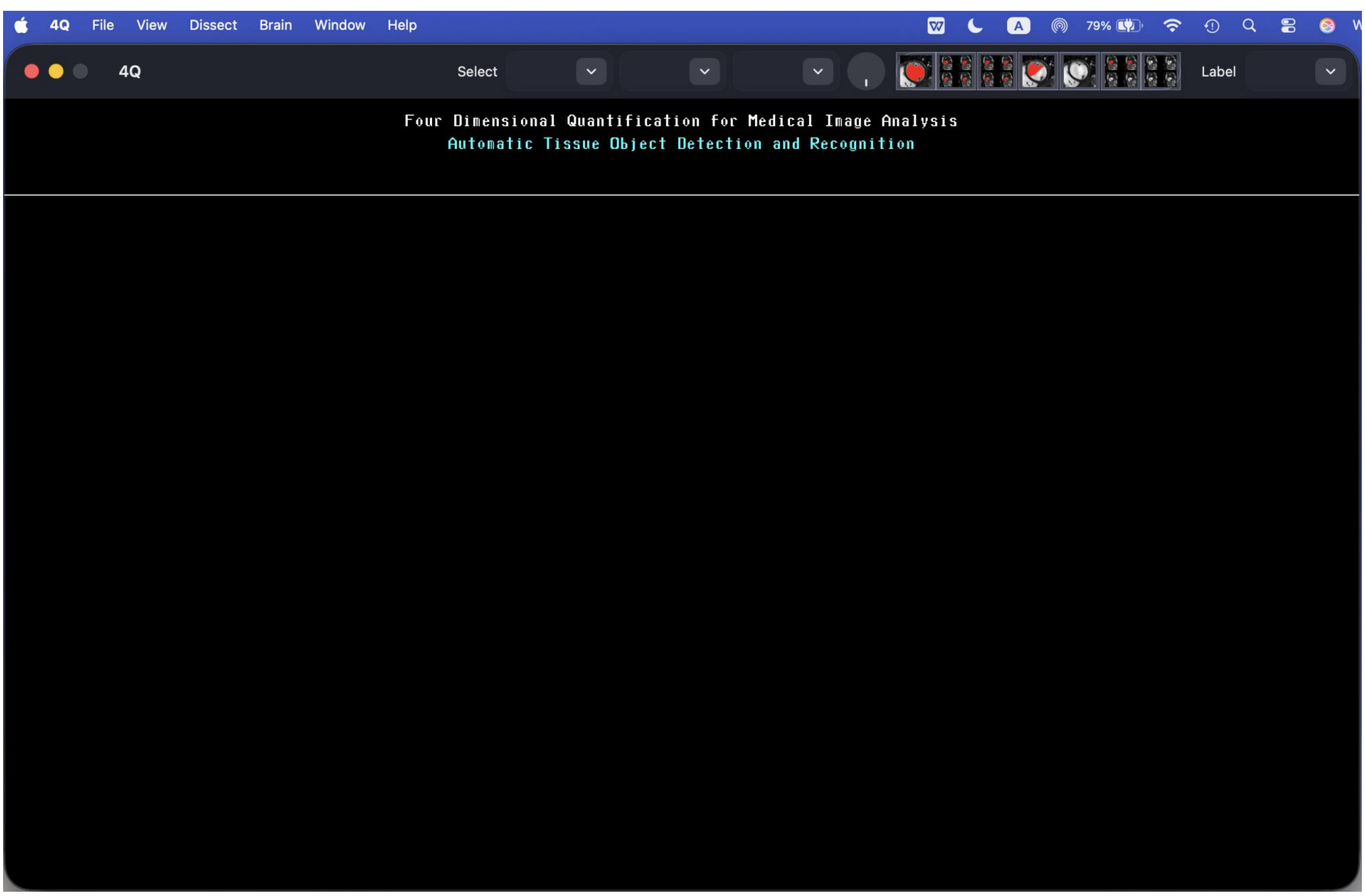
4Q User Guide

Introduction

Load cardiac MRI studies and view them in 2D, 3D and movie formats. Segment tissue objects in an initial image and automatically propagate results from there to all images. Volumetric analysis results are automatically calculated and presented in a curve display format. Examine tissue objects and assign your own labels. After multiple examinations, objects will be recognized automatically and given your assigned labels. Observations are kept in separate recordings for recall.

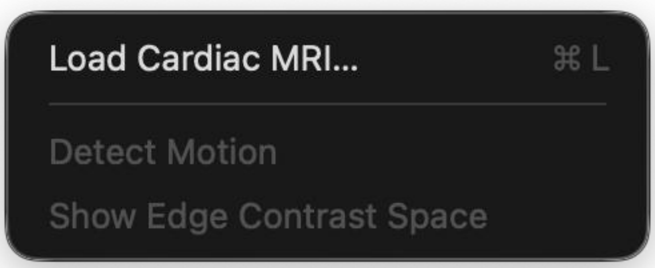
The Interface



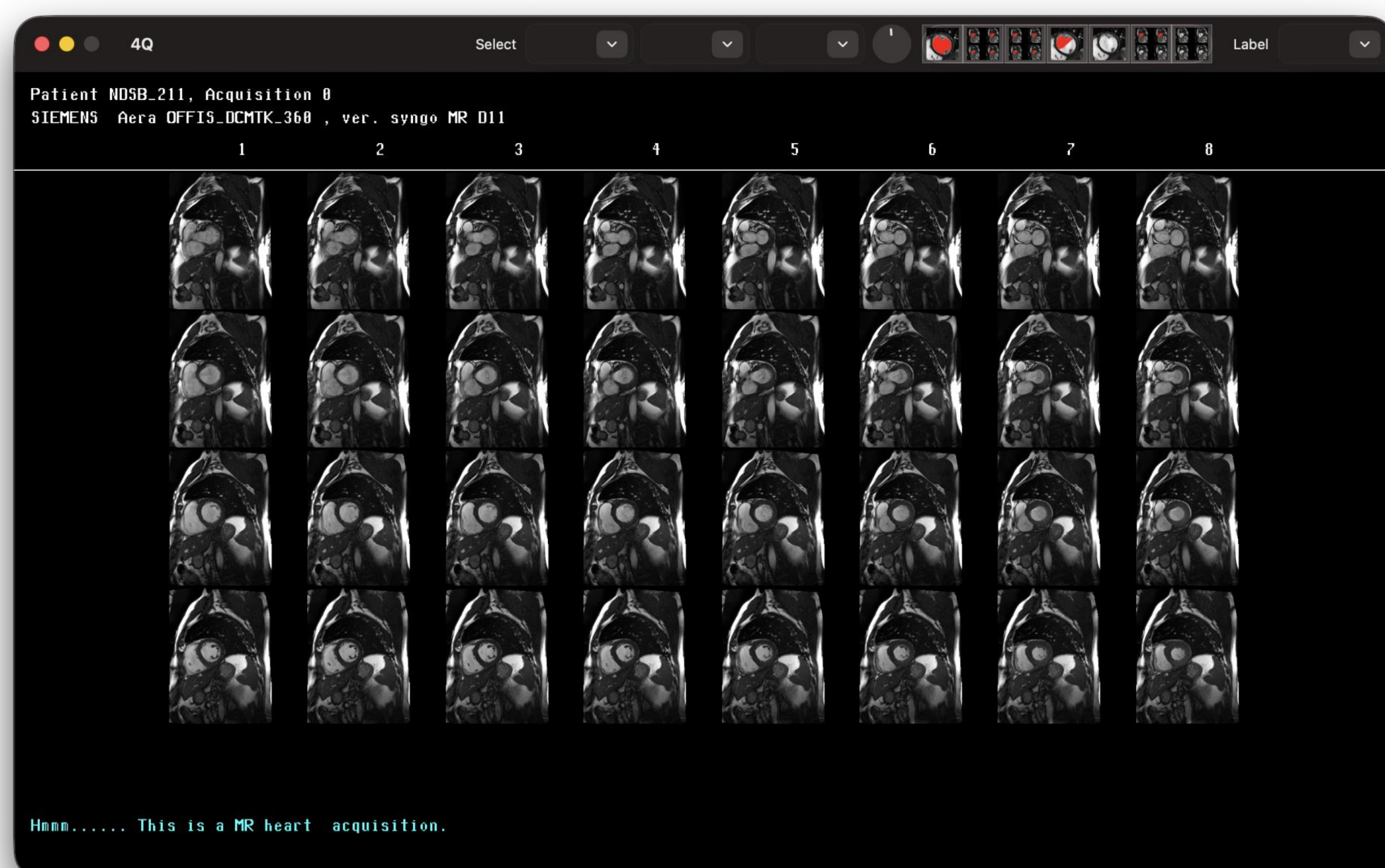
A dissection paradigm is used to guide the placement of menus, windows, toolbar buttons, and toolbar text selections. The single window with a black background is a dissection pan. Mouse and cursor clicks and drags are used to rotate 3D tissue objects, including movie displays and “dissect” segmented 2D tissue objects.

A “brain” is capable of learning, recognizing, and labeling tissue objects. Training observations or “lessons” are accumulated and “remembered” in user-defined files.

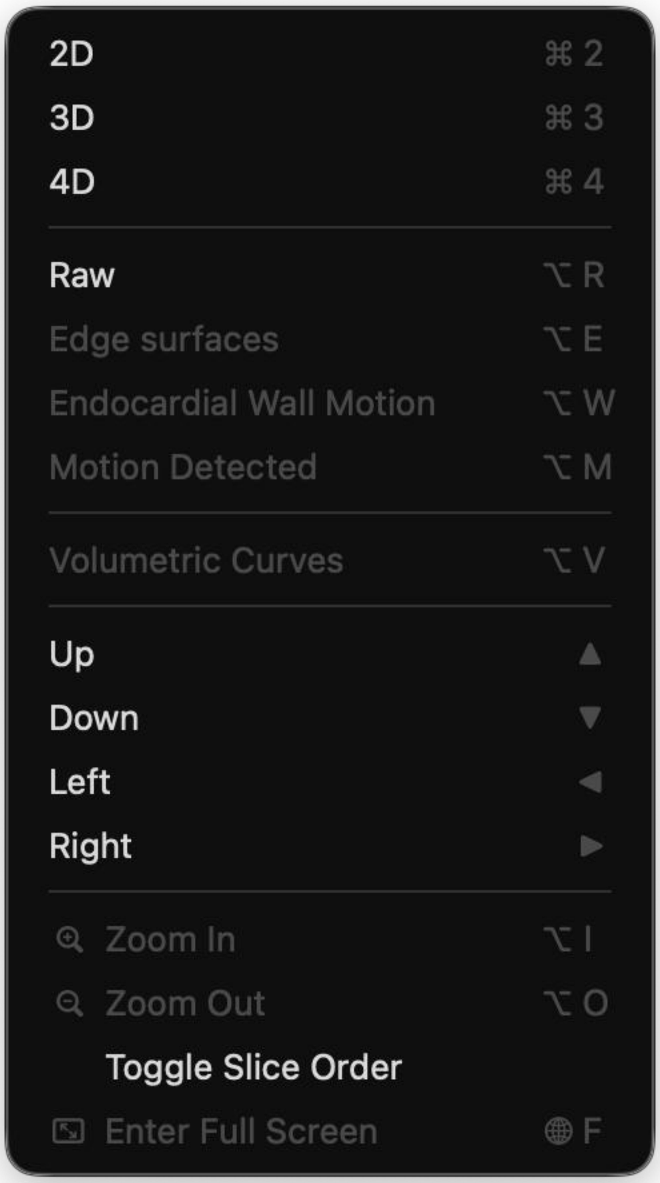
File Menu



Load DICOM-formatted study acquisition image sets. Images are displayed immediately in the dissection pan for viewing and segmentation.

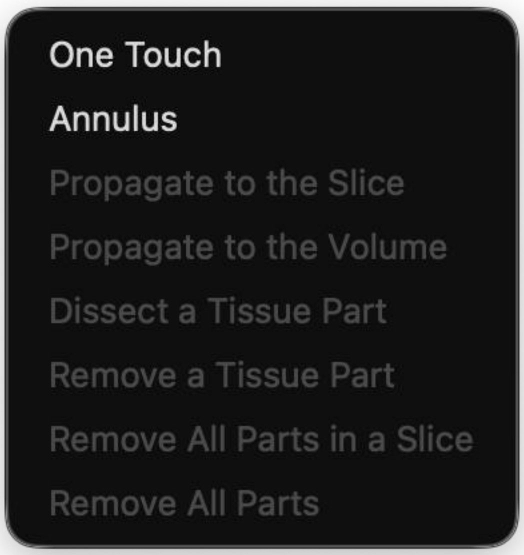


View Menu



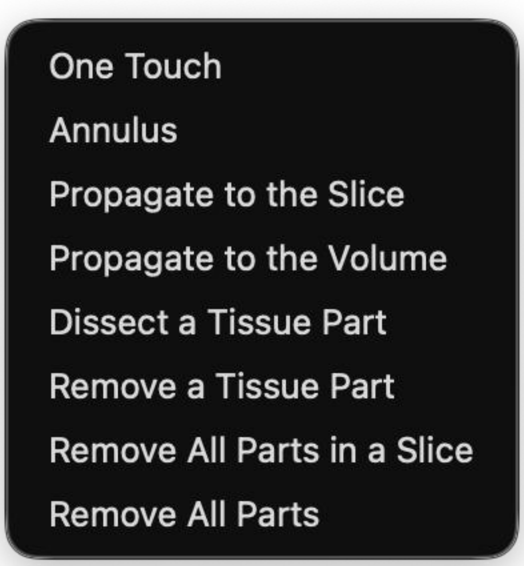
Display defaults to the original RAW 2D format after loading. The 3D format displays slice images in a stack that can be rotated manually in the vertical dimension. 3D can be zoomed in or out with the designated keyboard keys. 4D displays 2D or 3D as a movie. Move the image display up, down, left, or right with the arrow keys. Toggle the slice order in any multi-slice format.

Dissection Menue



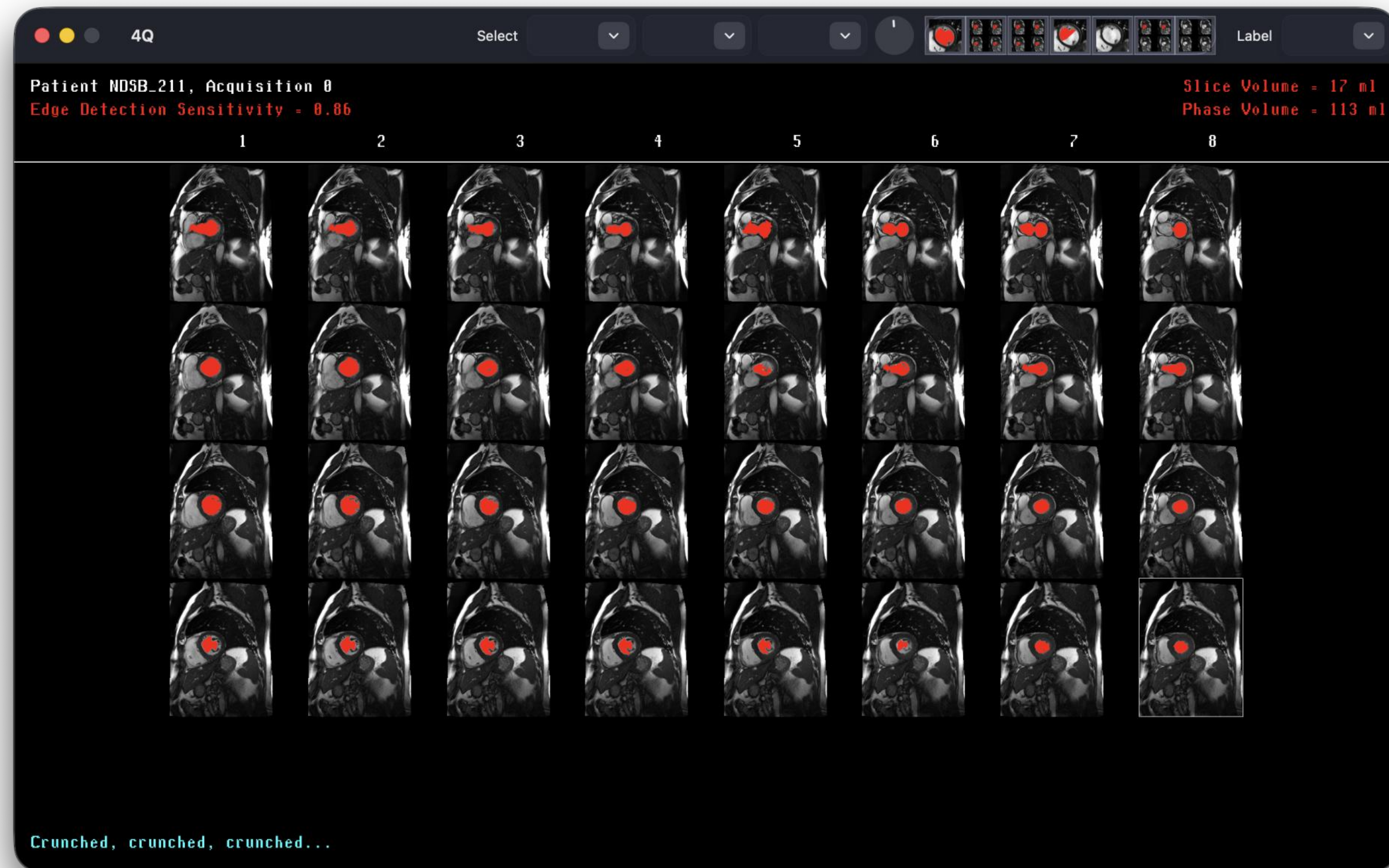
One Touch means you can “touch” any tissue part you see by positioning the cursor over the part and clicking the mouse. A color-coded region is created by expanding from the one-touch location to the surrounding edge pixels and displayed over the part area. This defines segmentation of a tissue part and creation of a tissue object in the computer. Tissue objects can be disjoint because multiple parts of the same tissue may be visible. Segment each disjoint part separately using one touch.

Use Annulus to segment the myocardium. This is a work in progress.



Propagate a segmentation to a single slice through all multiphase volumes or all slices in all volumes. Do not do both. You’ll get additional disjoint tissue objects.

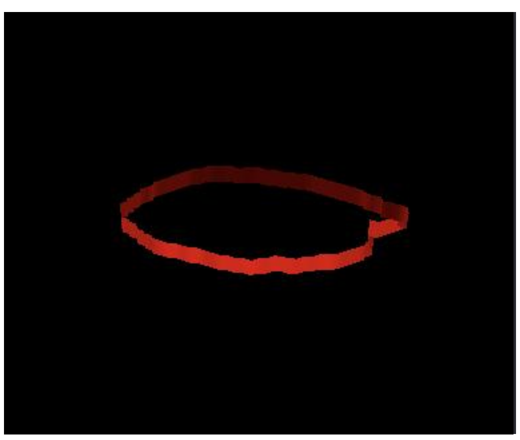
Dissect a tissue part by clicking and dragging the cursor through the object on the screen. Select any piece with the mouse and cursor to remove it. Button counterparts are in the toolbar for easy access. All slice or volume objects can be removed as desired. The tissue objects shown here do not require any dissection. Be careful what you dissect. Segmentation might be trying to tell you something. Only remove obvious defects.



Volumetrics

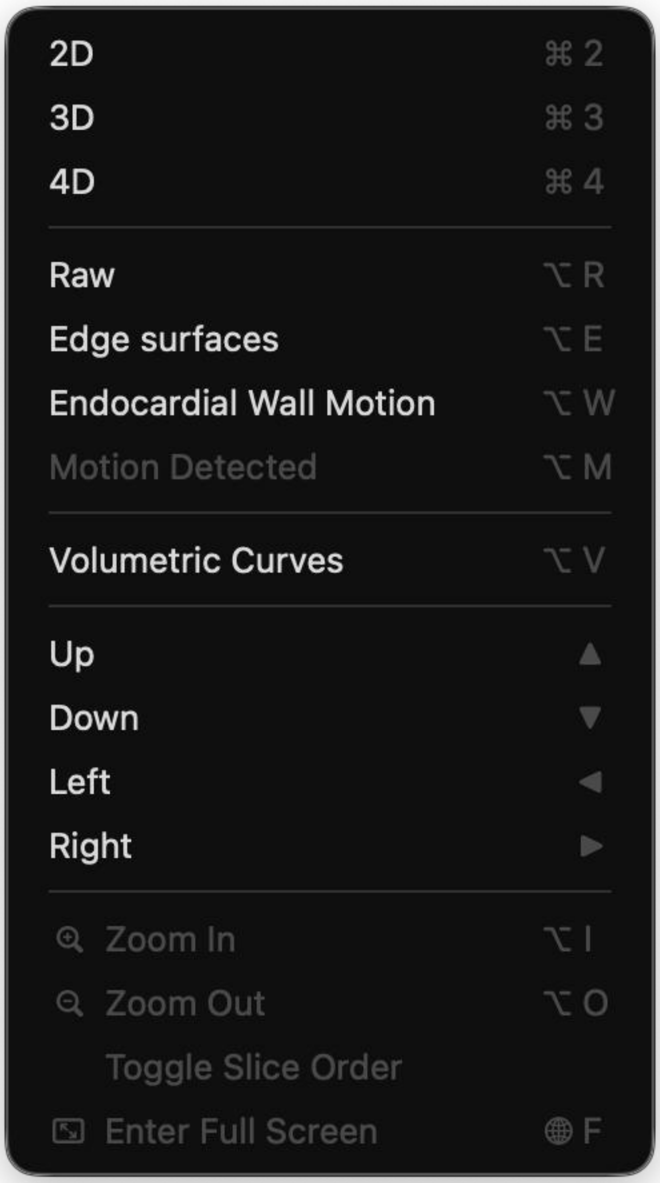
Image slices displayed in 2D ignore the thickness and spacing of the slices. Each “pixel” in the slice is actually a voxel. A voxel volume is the pixel area times slice thickness or slice spacing. Total object volume is the sum over the stack of slices. Here is the voxel volume calculation code. Slice thickness, slice spacing, and pixel spacing are taken from the DICOM metadata.

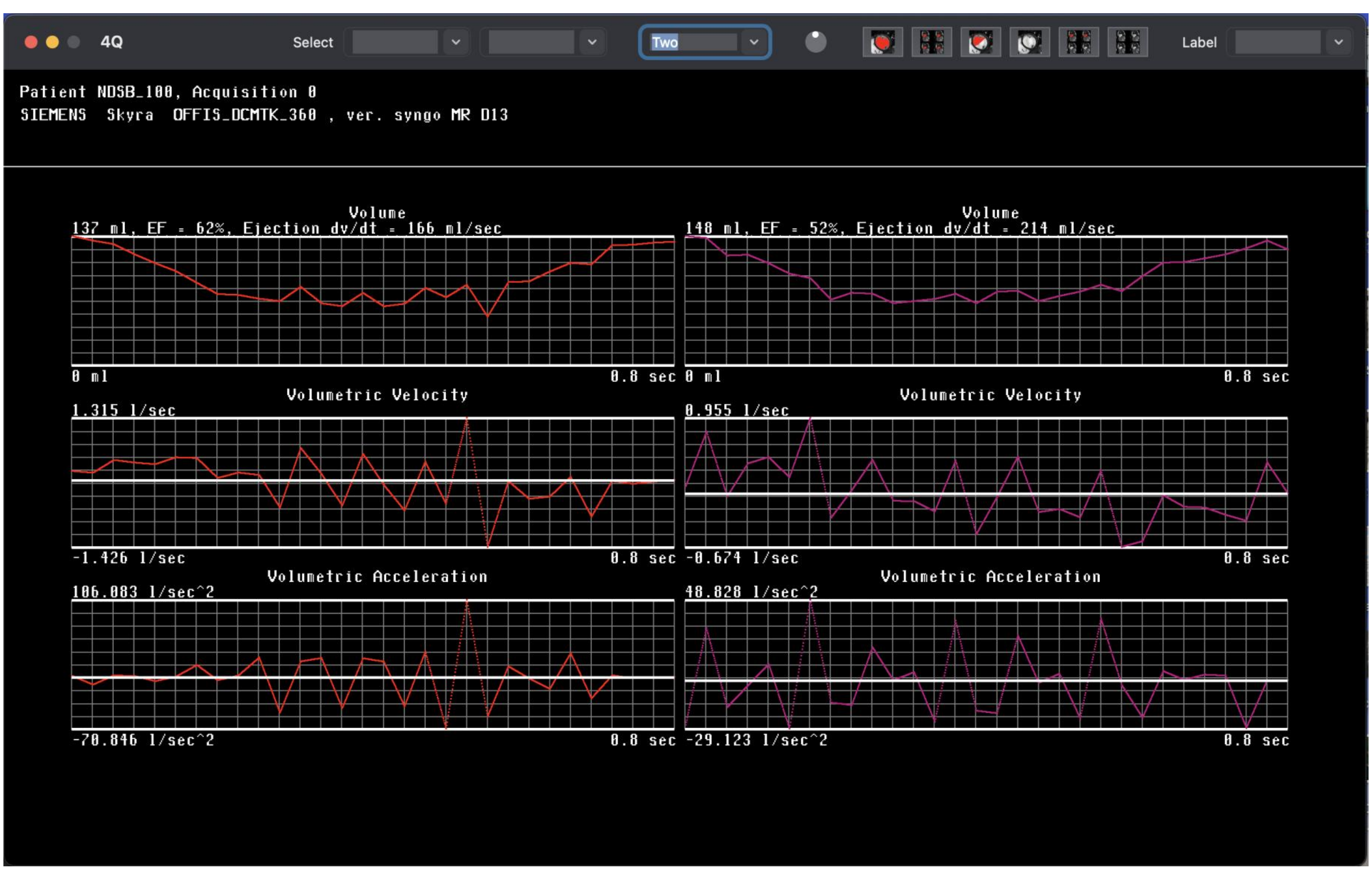
```
/// Compute voxel depth and volume
func computeVoxelVolume() {
    if slices.count == 1 {
        voxelDepth = slices[0].thickness
    } else if sliceSpacing != 0 {
        voxelDepth = sliceSpacing
    } else if sortedSlices[0].scaledLocation != 0 {
        voxelDepth = abs(sortedSlices[1].location - sortedSlices[0].location)
    } else {
        voxelDepth = 0
    }
    voxelVolume = slices[0].pixelSpacing1 * slices[0].pixelSpacing2 * voxelDepth / 1000.0
}
```



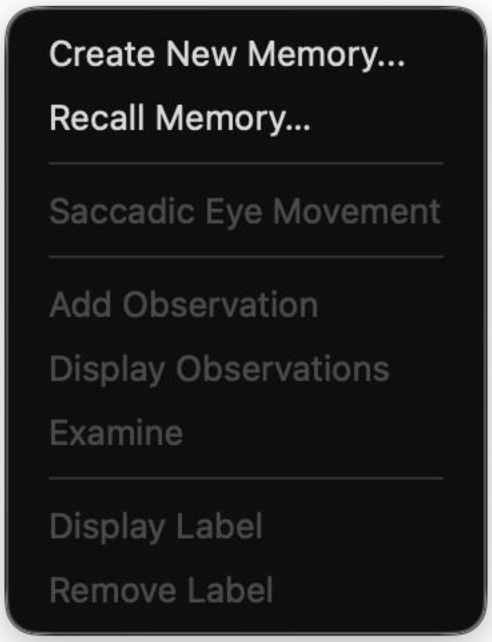
This is what a slice edge looks like.

Use Volumetric Curves in the View Menue to display curves and volumetric parameters.


2D ⌘ 2
3D ⌘ 3
4D ⌘ 4
Raw ⌥ R
Edge surfaces ⌥ E
Endocardial Wall Motion ⌥ W
Motion Detected ⌥ M
Volumetric Curves ⌥ V
Up
Down
Left
Right
Zoom In ⌥ I
Zoom Out ⌥ O
Toggle Slice Order
Enter Full Screen F


4Q
Select
Two
Label
Patient NDSB_100, Acquisition 0
SIEMENS Skyra OFFIS_DCMTK_360 , ver. syngo MR D13
Volume
137 ml, EF = 62%, Ejection dv/dt = 166 ml/sec
0 ml
0.8 sec
Volume
148 ml, EF = 52%, Ejection dv/dt = 214 ml/sec
0 ml
0.8 sec
Volumetric Velocity
1.315 1/sec
-1.426 1/sec
0.8 sec
Volumetric Velocity
0.955 1/sec
-0.674 1/sec
0.8 sec
Volumetric Acceleration
106.083 1/sec^2
-70.846 1/sec^2
0.8 sec
Volumetric Acceleration
48.828 1/sec^2
-29.123 1/sec^2
0.8 sec

Brain Menu

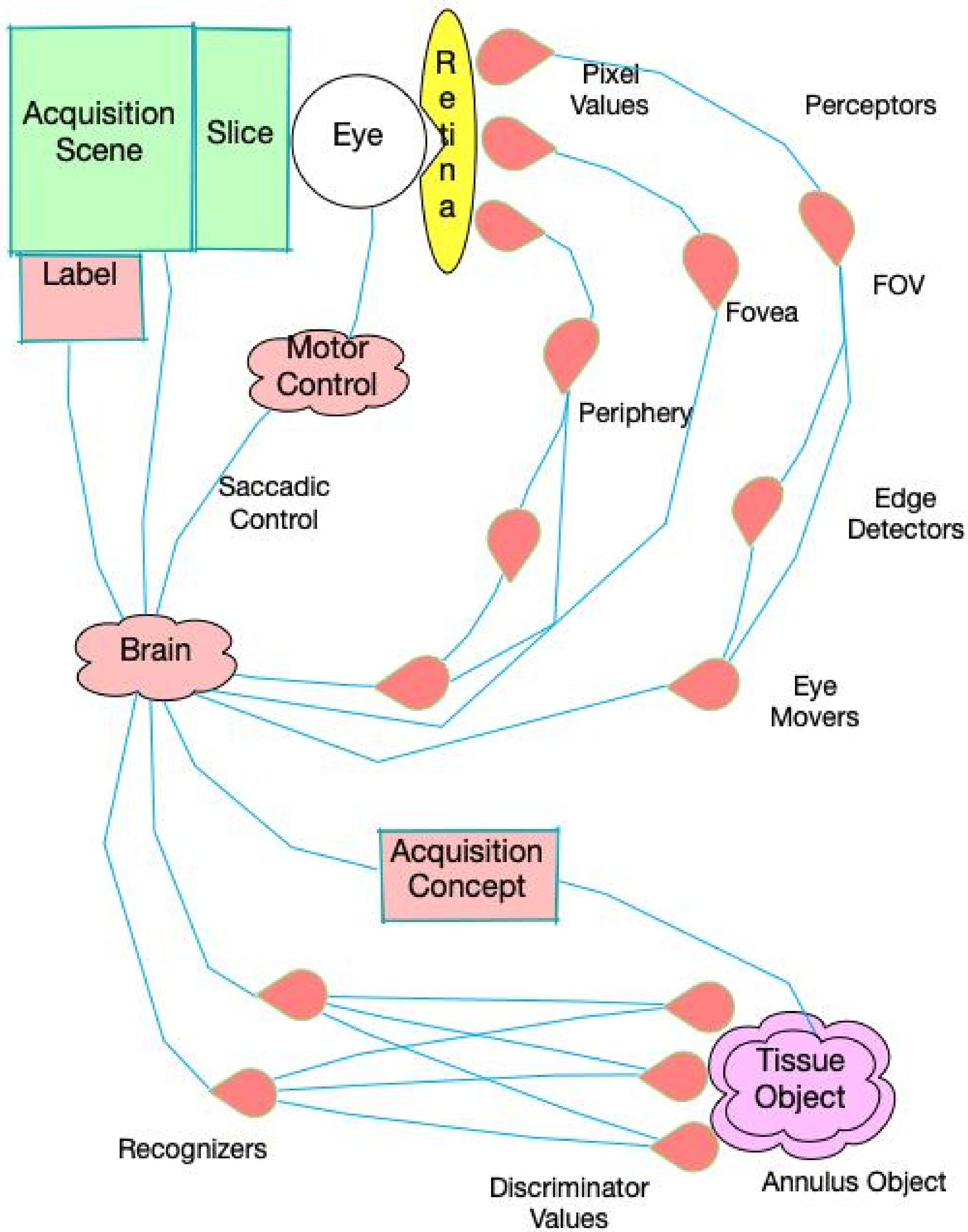


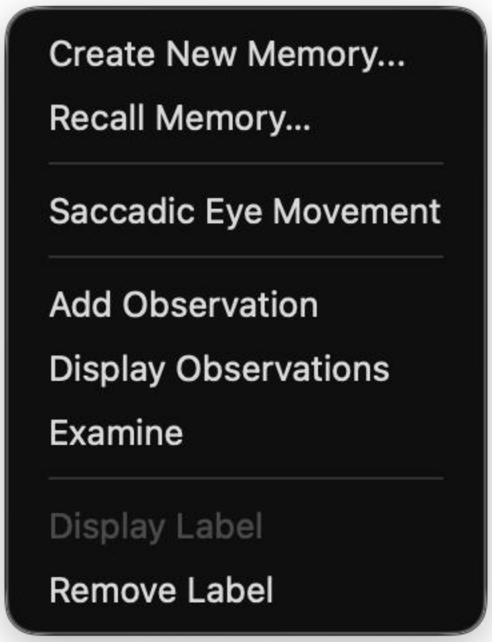
The brain in the computer (I call him/her Clyde/Claudette) is capable of perceiving tissue parts and creating tissue objects. It has way more than the 200 nerve cells a tardigrade has (~200) but about half that of the brainy fruit fly (139,255 neurons). A single eye has a retina with a fixed visual field of view (FOV) and no lens. Receptor neurons cover the entire field. Fovea receptors are in the center, and peripheral receptors surround FOV receptors.

Each neuron has a number of dendrites for input and a single axon for output. Neurons perform simple analyses of dendritic input and fire pulses out of their single axon to other neurons. A receptor neuron has a single dendrite that receives a pixel intensity value, which it transmits to perceptor neurons. Perceptor neurons collect these values and distribute them to edge detection and eye movement neurons for final or looping forms of processing.

The brain has to be taught to recognize tissue parts. Once a tissue object is created, the user selects the object with the mouse and cursor and activates receptor neurons that sense the object discriminator values. A set of discriminator values is transmitted to the recognizer neurons as an observation. Recognizer neurons are accessed, labeled, and taught with a number of observations determined by you. Recognizer neuron observation data are stored in memory in user-defined memory files. Memory files are automatically updated.

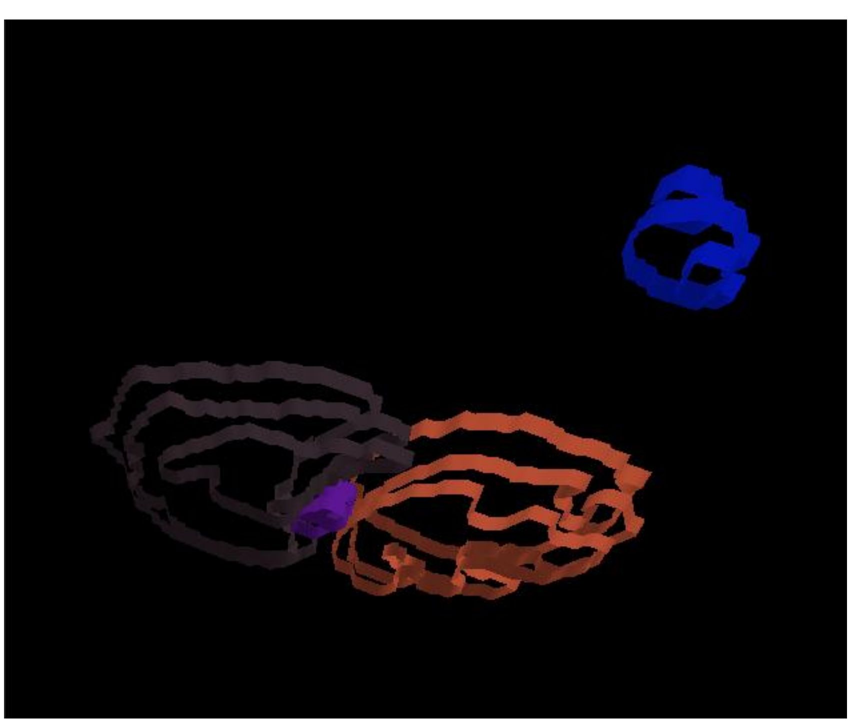
4Q Tissue Segmentation and Object Recognition Neuron Network

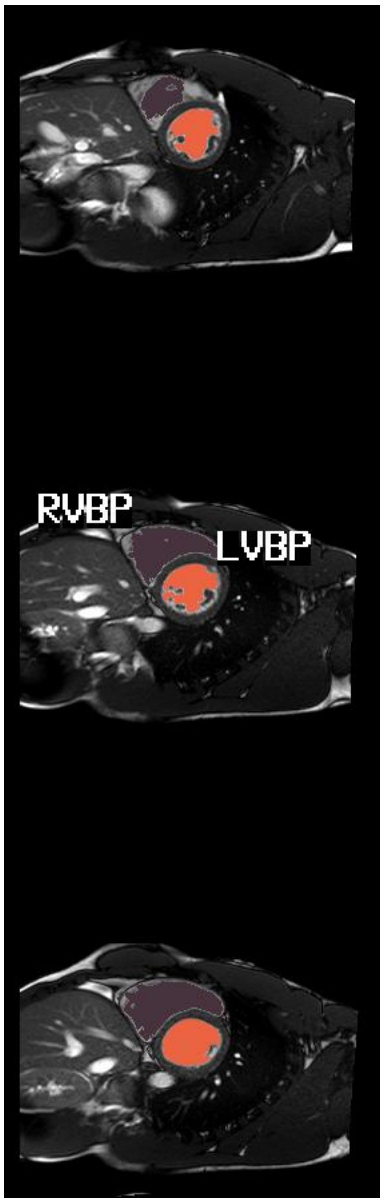




Create a new memory file or recall an existing one. Memory files have a .4qm file extension. To add an observation, first select a tissue object with the mouse and cursor. Use the menu item to access a recognizer and add the observation. The user can select an existing recognizer or label a new one. A set of tissue object discriminator values is sensed and written to memory as a recognizer observation. The statistical distribution of these values can then be displayed. At least 3 observations are required to attempt recognition of a tissue object. Select and examine any other object. If it is recognized, the recognizer label will be displayed. The observation used to examine can be added to a new or existing recognizer.

The brain is capable of sensing tissue parts and creating tissue objects using a saccadic eye movement model. The starting location is the center of a selected image. The brain will sense the periphery for a part's location, create a tissue object, and step from there. Each object is automatically recognized and labeled. Here are some results from early development.





The two blood pools in this three-slice volume were recognized and labeled automatically. Saccadic eye movement took 4 steps and recognized the left and right blood pools. The other two tissue objects were not recognized. The brain was taught to recognize only the left or right blood pools.

About the Author

H. Ross Singleton has a twenty-year history in medical imaging. He graduated from Purdue University with a BS in Engineering Sciences Engineering later renamed Aero Astro & Mechanical Engineering. He left the university with a commission as an Ensign in the USNR and served in the Supply Corp as a Disbursing Officer, the civilian equivalent of a financial manager for approximately 500 sailors. He is a Vietnam veteran, having spent two back to back nine-month tours aboard a guided missile frigate in and around North Vietnam and North Korea. Upon discharge, he entered the University of Michigan and graduated with an MS in Bioengineering. He was recruited by Medical Data Systems, a startup office in Ann Arbor, Michigan. There, he became deeply involved in Nuclear Cardiology. He developed Serial Mode that led to the first commercial scintillation camera multiple gated acquisition software termed MUGA. After leaving the office, he was recruited by the University of Alabama at Birmingham Cardiology Division to do research in Cardiac Nuclear MRI. Work in this technology led to numerous publications on edge detection and related applications. Upon leaving the university, he became a professional software and systems engineer (CSEP), working with BellSouth, SAIC (Ford Motor Company), SAIC (Army), CSC (IRS) and TASC (FAA). Ross is now happily retired in Bloomfield Hills, MI, as Owner/Developer of medical imaging computer vision software.