A Tour Through AVT2EXT

From AVTWiki

After you have installed AVT, you are ready to take this guided tour of AVT, which also serves as an acceptance test to see that the basic functions of AVT are working properly.

Each of these sections should work independently, in any order, but do depend on which data you have loaded.

New users should attempt them in the order listed.

Bug Reporting Note: if at any time you feel that AVT is taking too long to respond to your action, look for a **cmd.exe** window that may be reporting an exception. If an exception has been thrown, copying the contents of this window into your bug report will speed up the process of isolating and correcting the bug. If no exception has been thrown, then this may be another place where a progress indicator is needed.

Testers: use AVTWiki:Test AVT 2 Extension to more thoroughly test AVT.

Requirements Tracing Analysis --Bob 21:19, 26 February 2010 (UTC) As of this writing, this script, together with the scripts it refers to, covers the requirements specified in RS r0.3, except those that are deferred.

Contents

1 Abbreviations used to describe user actions with the mouse

Term	Meaning
Left-click	Click the left mouse button
Click	Left-click
Left-drag	Press and hold the left mouse button while moving the mouse
Drag	Left-drag
Middle-X	Like Left-X except with middle button/wheel of mouse
Right-X	Like Left-X except with right button of mouse

2 Helping to Improve AVT

We appreciate your willingness to try out AVT. If you find any problems with this script or with AVT itself, we want your feedback!

- Best place for short comments is directly in the script. Please
  - be sure you have logged in,
  - use the Signature button in the editor to identify yourself,
  - give the revision number (e.g. R491) where you found the problem, and
  - be bold!
  - If you believe you know how the script should be corrected, go ahead and correct it!
    We ***watch*** these pages, so if what you write seems a litle awkward, we will fix it.
- Second choice is to put your comments on the discussion/talk page associated with this page.
  1. Click the **discussion** tab at the top of the window.
     - *The Talk page will open.*
  2. (Optional) Click the + tab to start a new subsection with your topic.
  3. Say what you want to.
  4. Put a short comment in the main script referencing the longer discussion.
- For items where you don't want to identify yourself to more people than necessary, you can send e-mail to robert.schwanke@siemens.com.

3 A tour of MVT Thoracic Phantom Data Analysis

3.1 Install AVT

1. Follow instructions in AVT Installation or in Installation Guide (downloaded from GForge or as directed by your AVT contact person) to configure and install AVT and ...

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INSTALL_installation_procedure
INSTALL_release_notes
INSTALL_binary_code
INSTALL_source_code
INSTALL_end_user_scenario_documentation
INSTALL_end_user_feature_documentation
XIPHost_default_working_directories

3.1.1 Import DICOM Series into AD

1. Follow instructions in Load Example Data or Installation Guide to download the CDRH Pilot data and install it in the Annotation Database.
   - *Several sets of sample data are available on the SCR GForge site for those with access credentials.*

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MISC_grid_connectivity (deferred)
DATA_DICOM_image_types (deferred)
DATA_thoracic_phantom_images
AD_multiple_collections (Deferred)
AD_curation_operations (Deferred)

3.1.2 Import Ground Truth and Seed Data as AIM

Converting Ground Truth Data, Seed Data, and pre-existing markup data into AIM is outside the scope of the AVT software, but has been done with *ad hoc* scripts for the CDRH data as part of AVT2EXT.

The CDRH ground truth and seed data were loaded into AD as part of **loadCDRH** script described in the installation guide.

3.2 Start Up MVT with CDRH Data

MVT_SoV_case_study

1. Set your primary monitor to one with a resolution of 1600x1200, 1600x1050 or 1280x1024.
   - *Some screen layouts have not been fine-tuned for 1280x1024, although they are functional.* (Bug 2486)
2. Start **XIPHost**
3. (Optional) If you are using a machine with two monitors, drag XIPHost's cmd.exe window to the secondary monitor, so you can watch it for activity.
4. Read the disclaimer that covers the splash screen. If you agree with it, click **OK**, otherwise, click **Cancel** and go find something else to do!

3.3 Query Cases to Analyze

HOST_query_all_experimental_variables
HOST_query_exclude_series
MVT_CDRH_case_capacity
MVT_CDRH_annotation_capacity

Steps

1. Select **AVT AD** tabcard
2. Fill in **PatientID** field of the query form with the value ***** (asterisk)
3. Click **Search AD**
4. When the search results appear, expand the tree by clicking on each Patient or Study line, until you see check-boxes grouped beneath them. Do not click on the Series line unless you want to see all the individual Image and AIM objects associated with that series.
5. Select all six of the series under patient "Yamamoto-51:
6. Check the **AIM plus SEG** check box at the lower right for retrieving the AIMs and segmentation info. Do not check **DICOM**
7. Click **Retrieve**
8. Wait until all the database items have been listed in the left half of a pop-up window.
9. Click **MVT**
   - *When the MVT application starts up successfully, which can take more than a minute, a **subject** list is visible in the main body, and a tool panel is in the right side.*
10. Click on one of the rows in the **Subject** table
    - *The annotations associated with that case are listed in the **Annotation** table below.*

3.4 Manually Select Cases to Exclude

MVT_exclude_individual_cases

1. (Optional) Uncheck boxes next to individual cases to exclude
   - For the CDRH case study, leave all boxes checked the first time you go through this script.

3.5 Choose Sources of Variation Analysis

1. Select **Performance/Sources of Variation** from **Analysis Type** pull-down list

3.6 Designate Nominal Ground Truth Annotations

Ground truth is designated by the "name" of the annotator, collected from the "user.name" attribute in the selected cases.

MVT_ground_truth_reader

1. Select **ITK_1** from the **Nominated Ground Truth** pull-down list.
   This reader's annotations will be used as Nominal Ground Truth, and excluded from the experimental annotations. In this way, the ITK annotations will be compared to all other annotations for the same series and tumor.

3.7 Calculate Measurements

MVT_error_difference_measures
MVT_null_calculation_warning
MVT_list_original_measurements

Available measures include

- RECIST
- RECIST Difference (error)
- WHO
- WHO Difference (error)
- Volume
- Volume Difference (error)
- Relative Volume Difference (error)
- Volume Overlap (percentage)
- Avg Surface Distance (error)
- RMS Surface Distance (error)
- Max Surface Distance (error)

For Performance/Sources of Variation analysis, these measures are computed by comparing experimental markup to ground truth, and are hence errors. For Reader Variability (which currently is available only without ground truth), these measures compare markups from different readers, as peers, and hence are differences.

Deferred measures include

- Maximal slice error *(boolean)*

Use these procedures to select which measures appear in the table of calculations on the next screen:

1. (Optional) Select a comparison in the right column and Click << to remove the selected comparision
2. (Optional) Select a comparison in the left column and Click >> to add the comparision to be computed
   - If you select more than one comparison to add or remove, clicking the button will only move one of them, but repeated clicking will move the rest of them.

- For CDRH Pilot example, deselect **WHO**, **WHO Difference**, **Surface Distance (Average)** and **Surface Distance (Maximum)**

3. Click **RUN**
   *The UI is changed to **Computation Results**.*
   In main body, there are 3 areas,
   - The top one is **Computation Results** list,
   - The middle one is for **Statistics**, **Outliers**, and **Plotting**,
   - The bottom one is the **Visualization** area, with a 3D orthogonal MPR viewer displaying selected markups in different colors.

   The calculated items appear in the Computation Results list one by one as they are calculated.
   When the progress bar in the GUI stops moving, the calculation is done.

3.8 Calculate Summary Statistics

MVT_existing_summary_statistics
MVT_statistics_selector_panel (deferred)

The table of configured summary statistics starts out pre-populated with the means of several measures.

To add a Standard Deviation calculation:

1. Click Methods: **Add**
   The Statistic Designer dialog will open.
2. Under "Statistic Methods", pull down list and select SD.
3. Under Data Selection, move one or more measures from the Unselected column to the Selected Column.
4. Click **Done**

To add a custom R script operating on each of the columns of data:

1. Click Methods: **Custom**
2. Follow instructions in section **Customize Summary Statistic** to create an example.

To remove a custom or built-in statistic,

1. select the calculation you want to remove
2. click **Del**

Then

1. Click **Run**
   - *These types of statistics appear as additional rows in the **Computation Results** table.*

3.9 Multiple Regression Analysis

--Bob 23:05, 14 December 2009 (UTC) **TODO** *Grace Kim tells us that the multiple regression calculation does depend on some choices the user must make. This section needs to be reworked in the next generation of AVT to account for inclusion/exclusion of repeat reads, repeat nodules, and repeat exposures, and for options to use mixed-effect and randome-effect models.*

MVT_multiple_regression
MVT_mixed_effects (deferred)
MVT_independent_variables
MVT_partitioning_by_values
MVT_variable_selection
MVT_suppress_irrelevant_variables

1. Click Methods: **Add**
   The Statistic Designer dialog opens.
2. Select Statistic Methods --> **Multiple Regression**
3. Select a Dependent Variable from the pull-down list.
   - Recommend choosing **Volume Difference**.

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3.9.1 Select Independent Variables

1. Select independent variables from the pull-down lists provided.
   - Recommend **Gender**, **Slice Thickness**, and **Reconstruction Kernel**

1. Click **Done**.
2. Click **Run**
   - *The output of the R multiple regression package appears on the **Statistics** pane.*
     --Bob 17:54, 20 April 2010 (UTC) Many combinations of dependent and independent variables will crash R on this dataset. *Caveat emptor!*

3.10 Factorial ANOVA Analysis

MVT_one_way_ANOVA_methods (deferred)
MVT_factorial_ANOVA_methods

N-way ANOVA Analysis is a synonym for *Factorial ANOVA Analysis*

1. Click Methods: **Add**
   The Statistic Designer dialog opens.
2. Select Statistic Methods --> **N-way ANOVA**
3. Select a Dependent Variable from the pull-down list.
   - Recommend **Volume Difference**

3.10.1 Select Independent Variables

1. Select independent variables from the pull-down lists provided.

- Recommend **NominalGT RECIST**, **NominalGT WHO**, and **NominalGT Volume**

2. Click **Done**.
3. Click **Run**
   - *The output of the R N-Way ANOVA package appears on the **Statistics** pane.*
   - *This routine might crash R, depending on the data.*

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3.11 t-test

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Deferred

#Same as above, select 1 independent variable that has only two possible values.
#Click "Calculate t-test"
#*A table is displayed showing the results of the t-test
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MVT_t_test (deferred)

3.12 Specify Outliers

Table of outlier criteria is initialized with some example outlier specifications.

MVT_highlight_outliers

1. Click **Add** next to **Threshold**
2. Follow instruction in section **Outlier Designer dialog** to add an outlier analysis using Volume Overlap and Bottom 25%.
3. Select Volume Overlap, Top 50% in Threshold table.
4. Click **Del** next to **Threshold**
   Deletes the selected outlier criterion in the list

```
Deferred

#(Optional) Select an outlier criterion and click Edit in "Outlier Analysis"
#:Outlier Designer dialog is opened, initialized with the details of a selected outlier criterion.
```

3.13 Run statistical analysis

1. Click **RUN**
   - *The statistical analysis results are added to the end of "Computation Results" list.*
   - *The outlier analysis results are output in the "Outliers" tab.*

```
Deferred
#*The outlier values are highlighted in the data table.
```

3.14 Mixed Effects Analysis

Deferred

MVT_Mixed_effects (deferred)

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3.15 Levene Test

Deferred

MVT_Levene_test (deferred)

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3.16 Visually Compare Segmentations

MVT_viewport_layout (deferred)
VIEW_multiple_read_only_markups
MVT_MPR_markup_comparisons

1. Double-click one of the rows in the **Computation Results** list
   *the 3D-MPR window displays the image and contours associated with the selected row. Blue contours depict the **Nominal Ground Truth** segmentation, and red contours depict the **Annotation** segmentation.*
   Large series can take several minutes to load.
2. set cross-hairs on tumor in red pane
3. Pan and zoom in all three panes to inspect the contours.
4. Click the dog-ear control in the left pane to flip through the contours on different slices.
   - *--Bob 22:42, 3 April 2010 (UTC) As of build 515 and earlier, clicking on the dog-ear control in the red pane changes the vertical position by only 1/n-th of a slice, instead of a whole slice (Bug 3289). Therefore, the same contours will appear in that window for n clicks before the next set of contours appears.*

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3.17 Statistical plotting

The table of charts is pre-populated with two example plots.

MVT_histogram_charts
MVT_box_and_whisker_charts

1. Click **Add** in "Plotting"
2. Follow instruction in section **"Plotting Designer" dialog** to add an example plot.
3. Select a plot in the Charts list to delete.
4. Click **Del** in "Plotting"
   Delete a selected chart in the list
5. Click **PLOT**
   *The charts are displayed in the **Plotting** tabcard.*
6. The **Plotting** tabcard displays three plots per row. If you have requested more than three, a scroll bar should appear.
   *If the scroll bar does not appear (Bug 3072), click the **Statistics** or **Outliers** tab, then click the **Plotting** tab.*
7. Double-clicking one of the charts will enlarge it in a pop-up window.

```
Deferred

#Click Edit in "Plotting"
#:"Plotting Designer" dialog is opened, initialized to the definition of the selected chart.
```

3.18 Generate Statistics Reports

1. Right-click in a plot pop-up window to show a pop-up menu
   - "Copy" to copy the chart to clipboard
   - "Save as BMP" to export the chart in .bmp format
   - "Save as JPEG" to export the chart in .jpg format
   - "Save as PNG" to export the chart in .png format

MVT_statistic_analysis_report (deferred)
MVT_export_documents (deferred)
MVT_export_data (deferred)
MVT_export_plots

```
Deferred

#Right-click in the data table window to show a pop-up menu
#*"Save as R" to export all data in R format.
#*"Save as CSV" to export all data as comma-separated values.
#*"Save as Excel" to export all data as an Excel worksheet.
#Right-click in the statistical results window to show a pop-up menu
#*"Save as R" to export all results in R format.
#*"Save as txt" to export all results as plain txt file.
```

3.19 Reader Variation

1. If **Subject** tab is not showing in main window, click **Back**
2. Select **Reader Variability** from **Analysis Type** pull-down list
3. Click **Run**
   A table is displayed showing inter-reader and intra-reader meaurements.
   The same statistics, outlier analysis, plotting, and drill-down capabilities are available for the reader variation data.

MVT_inter_reader_variation
MVT_intra_reader_variation

3.20 Box plot of Reader Variation

```
Deferred

#Add a plot
#Specify "Box" as the plot type
#Specify "Reader" as the independent variable.
#Specify "Volume Error" (for example) as the dependent variable.
#:When you click "Plot", a box plot should appear, comparing the distributions of volume error across different readers.
```

MVT_box_and_whisker_charts

3.21 Visualize Reader Variation

1. Select row in data table
   Image, reader's contour, and ground truth contour appear in 3D-MPR panel

MVT_MPR_markup_comparisons

```
Deferred

#Click "All contours by same reader"
#:Other contours by same reader are added to 3D-MPR panel
#Click "All contours of same tumor"
#:Contours by other readers of same tumor are added to 3D-MPR panel
#:If more than four contours are available to view, a selection panel will appear, allowing the user to choose which readers' contours to view."
```

3.22 Exit MVT

1. Click **Exit** in the upper-right corner to shut down MVT
   - *You should now see the XIPHost GUI.*

4 A tour of IA for RECIST, WHO, and Volumetric Markup

Note: The tour of MVT comes first in this tour of AVT2EXT so that you can complete the MVT tour before doing things that will change the contents of the database. We suggest that you avoid useing AE and avoid saving any of your Image Annotations until you are familiar with MVT.

IA_SoV_case_study

However, you can use these notes to decide which series to mark up. We suggest you start with series marked with a green **O**, which are small and have not been annotated by Byrne or Kaplan.

4.1 Load Series into Image Reader

Loading Sample Thoracic Phantom Lung Tumor Data

After following the instructions in the Installation Guide to download the CDRH Pilot data and load it into AD,

DATA_DICOM_image_types (deferred)
DATA_thoracic_phantom_images

1. Run XIPHost
2. In the AD tab-card, enter ***51*** in the **Patient ID** field
3. Click **Search AD**
4. Click on the search results row ending with **Yamamoto-00051**
5. click on the **Study** row that appears below it.
6. Check the checkbox for the first series that appears below it (ending with **CT**).
7. Check the **Series** box above the **Retrieve** button
8. Click **Retrieve**.
9. After the files have all been listed in the left pane of window, click **IA**
   - Launching IA may take up to a minute. If it takes much longer, look for the most recent "**cmd.exe**" window on your desktop and check whether an exception has

been thrown. If so, please copy the transcript into your bug report.
- *If IA appears to start correctly, with cross-hairs in 3 of the viewing panes, but the image appears to be all black, you probably had a space in the absolute path name of your data folder.* (Bug 2841)

4.2 Acknowledge Terms-of-use

This step was handled in the XIPHost log-in and the installer license pane.

MISC_IA_clinical_use_disclaimer

4.3 Read Annotation Instructions

Deferred. For a "real" experiment, IA would present the user with a list of instructions that supplement the guidance built into the software.

4.4 Input User Information for Audit Trail

Deferred. Temporarily, this step is incorporated in the XIPHost login screen.

AUDIT_user_role

4.5 View 3D-MPR Image

Description

- Three of the four image panes initially displayed comprise a double-oblique, 3D-MPR viewer of the series you loaded.
- The red-bordered pane shows the axial view of the 3D image, i.e. the actual slices of the CT image.
- The green-bordered and blue-bordered panes contain reconstructed images in two other planes of the 3D image, initially orthogonal to the slice plane and to each other.
- The colored crosshairs in each pane show where the panes bordered by the corresponding colors intersect that pane.
- The white-bordered pane displays a 3D volume rendering of series, fused with an opaque rendering of the currently-selected volume segmentation of the tumor, (if any).

VIEW_text_overlay
VIEW_orientation_cube
VIEW_scale (deferred)
VIEW_CT_window_and_level_settings
VIEW_double_oblique_MPR_viewing

- Each pane displays an orientation box, marked with single letters denoting the **A**nterior, **P**osterior, **L**eft, **R**ight, **H**ead, and **F**oot sides of the image.
- Two lines of text in the upper-left corner of each pane displays identify the series.
- Three lines of text in the upper right corner identify the scanner and the modality (CT)

- Five lines of text in the lower left corner display certain acquisition parameters, the Slice Position (SP) and the Slice Thickness (ST).
- Two lines of text in the lower right corner display the "width" (W) and "level" (L) of the conversion from image densities to screen brightness.

One additional line of text in the upper-left corner of the red pane gives the slice location, or slice number, of the image that is currently showing in that pane.

- The 'window/level' gradient graphic on the left of each pane depicts TODO.

4.5.1 Begin the tour

1. Click the button labelled **WL/Lung**.
   *The contrast and brightness (**W**indow and **L**evel) of the images should change to a more comfortable combination for marking up images of the lung phantoms.*
2. Click in the red-bordered pane.
   The border will become wider, appearing brighter, to show that you have selected this pane.
   Due to a pernicious event-queue bug (Bug 3218), the change may not appear until you move your mouse around a bit.

4.5.2 Brightness and contrast

1. **Right-drag** the mouse in the same window
   TODO describe how the gradient bar on the left should look, based on the W and L values.
   This controls **brightness** *and* **contrast** *(also called* **Level** *and* '**Window**) of the image.
   Moving left and right controls contrast
   Moving up and down controls brightness
   The rate of change in proportion to movement should be moderate, so that the brightness and contrast are easy to adjust.
   There is an open feature request (#759) to change the cursor to show that you are controlling brightness and contrast.
2. Click the **W/L Lung** button
   This adjusts Window and Level values to preset settings suitable for reading lung images.

VIEW_window_and_level_presets
VIEW_phantom_presets (deferred)
VIEW_window_and_level_adjustment
VIEW_mouse_cursor_feedback_on_adjustment_tools

4.5.3 Pan and Zoom

1. Click **Pan/Zoom**
2. **Left-drag** the ***center of the spinal cord*** in a small circle.
   The image should move with it ('***panning***')
   There is an open feature request (#759) to change the cursor to a hand shape when the mouse is in the portion of the window that controls panning.
3. Release the mouse button.
4. **Left-drag**, starting near any edge of that pane, moving the mouse up and down several times.
   The image should **zoom out** *as the mouse moves down and* **zoom in** as the mouse moves up.
   There is an open feature request (#759) to change the cursor to a magnifying glass or other appropriate icon when the mouse is in the portion of the window that controls zooming

VIEW_pan_zoom
VIEW_mouse_cursor_feedback_on_adjustment_tools

4.5.4 Rotate

1. Click anywhere in the blue pane
2. Click **Rotate**
3. Drag in the pane.
   The image will rotate around the intersection point of the crosshairs
4. Click **Reset**
   The image will return to its original position (but not orientation -- see Bug 3293).

- Restore the original rotational position by hand, using the orientation box as an approximate guide.

5. Click somewhere in the red pane.
6. Note the slice position displayed in the upper-left corner.
7. Click in one of the triangles in the upper right corner of the red-bordered pane (called the **dogEar control**).
   This displays the next slice of the image, above or below the one previously displayed in the pane.
   Note the new slice position.
   Note that the red cross hairs move up and down in the other two panes. Clicking on these triangles is like flipping through a stack of pages, each containing an image slice.
8. Point to a green crosshair near a border in the red pane. Drag the green crosshair left and right.
   The green crosshair should pivot around the intersection with the blue crosshair.
   The image in the green-bordered pane should change, reflecting the changing position of the green plane in the 3D image.

4.6 View Volume Rendering

This will be more interesting after the tumor is segmented, but we list it here with the other general navigation functions.

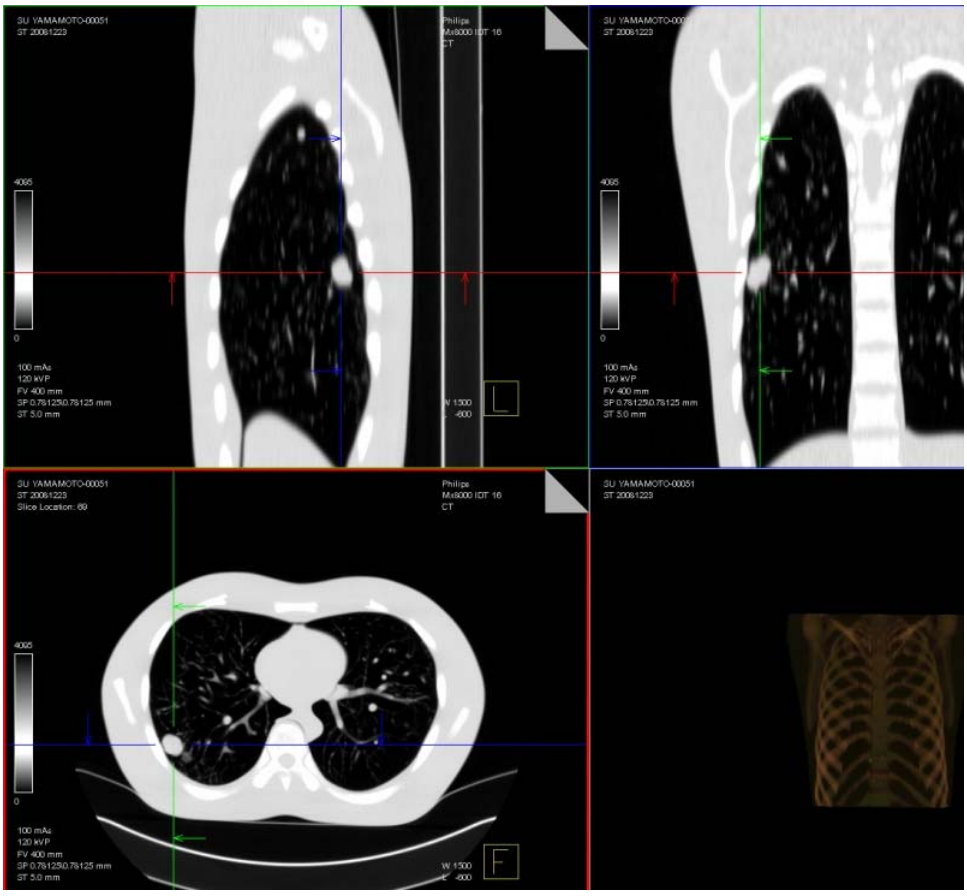
VIEW_fused_volume_rendering

1. Click **Pan/Zoom**
2. Click anywhere in the white-bordered pane.
3. Drag the mouse in the white-bordered pane.
   The volume rendering image will pan and zoom in the same fashion as in the other three panes.
4. Click **Rotate**
5. Drag the mouse in the white-bordered pane.
   The image should turn as if the mouse had grabbed onto the image and were turning it.
6. click **Reset**

4.7 Navigate to Tumor

VIEW_double_oblique_MPR_viewing

1. Use the dog-ear control in the red pane to navicate to **Slice Location: 69**.
2. Using the picture below as a guide, center the cross-hairs on the tumor in the red pane.



4.8 Change the Pane Arrangement

IA_dynamic_viewport_layout

1. Click on the **Setting** tab.
2. Click in the blue pane
3. Click the **3+1 Layout** button.
   TODO rename the button from "Layout 3x1" to "3+1 Layout"
   The image display will change to 3 small panes on the left and a large blue-bordered pane on the right.
4. Click in the red pane
5. Click the **1x1 Layout** button.

TODO rename button "1x1 Layout"
The screen layout will change to a single, red-bordered pane.

6. Click the **2x2 Layout** button

4.9 Create an Observation

1. Click **New**
   A new row will appear in the table of Image Observations

IA_multiple_AIM_annotations_per_image_reader_session

4.10 Classify Nodule characteristics

1. select a value in the **Shape** pull-down list to describe the tumor.

IA_label_confidence_scale_from_RadLex

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4.11 Rate User's Confidence in Annotation

1. select a value in the **Certainty** pull-down list to describe the tumor.

IA_label_confidence_scale_from_RadLex

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4.12 Add Audit Trail Comment

1. Scroll all the way to the right in the **Image Observations** table.
2. Click in the **comment** field of the currently selected observation.
3. Type a brief comment.

AUDIT_comments

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4.13 Add a Seed Line

1. Pan and zoom until the tumor fills most of each of the three MPR panes.
2. Click **Add Seed**
3. Click in the red pane
4. Drag in the interior of the tumor in the red pane.
   A yellow line segment will appear, denoting a set of points interior to a tumor.
5. Release the mouse button.
6. If the yellow line is hard to see, click on the **Setting** tab and click **W/L Liver**

DATA_seed_AIM_object
SEG_IA_mark_tumor_with_seed

*Do **not** click save.*

4.14 Automatically Segment the Tumor

1. Click **Semi-Seg**.
   A contour with the new observation's color will appear on the image, in all three MPR panes, near the edge of the tumor.
   A filled-in contour will appear in the volume rendering pane.
2. Rotate the volume rendering window to visualize the 3-D location of the tumor
3. Use the dog-ear controls in the red pane to look at the other contours.
4. Stop at a slice where there is a noticeable distance between the contour and the edge of the tumor.

SEG_automatic_3D_volume_segmentation
SEG_ITK_volume_segmentation_algorithm
SEG_IA_invoke_automatic_volume_segmentation
VIEW_volume_segmentation_display_as_contours_on_slices
VIEW_volume_segmentation_display_on_alternate_planes
VIEW_fused_volume_rendering

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4.15 Expand a contour manually

1. Click **Punch IN**
2. Draw a free-hand, closed contour that is mostly outside the one currently displayed, and mostly inside the edge of the tumor. However, let it stray inside the current contour at one point, and let it stray outside the tumor at another point.
3. Release the mouse button.
   The two contours will be replaced by a single contour marking the result of adding the interior of the new contour to the interior of the existing contour.

SEG_IA_edit_volume_segmentation_contours

4.16 Reduce a contour manually

1. Click **Punch OUT**
2. Draw a free-hand, closed contour that intersects the existing contour where its edge strays outside the tumor.
3. Release the mouse button.
   The two contours will be replaced by a single contour marking the result of subtracting the interior of the new contour from the interior of the existing contour.

SEG_IA_edit_volume_segmentation_contours

4.17 Manually Segment Tumor

1. Click the **Free-hand** button.
2. Drag the mouse along the edge of the tumor in a complete, closed curve (returning to the starting point).
   A line will appear tracing the path of the mouse cursor.
3. Release the mouse button.
4. *The trace line will be replaced by a line matching the Image Observation color, following a similar path, but consisting of straight line segments connecting vertices of a grid.*
5. Click one of the dog-ear controls once, to move to an adjacent slice.
6. Draw another contour as above.
   It will appear in the same color as the first one, because it is part of the same image observation.
7. Continue drawing contours on slices until you have segmented the whole tumor.

SEG_IA_manual_3D_volume_segmentation

4.18 Manually Mark RECIST Diameter

SEG_IA_manual_diameter_on_a_2D_slice

1. Navigate to the slice where tumor appears to have the longest diameter.
2. Click the **RECIST** button
3. Drag the mouse from one edge of the tumor to the opposite edge, along what you estimate to be the longest diameter.
   A line will appear denoting the measurement you are making.
   The line will have a label reporting its length.
4. Release the mouse button to complete the measurement.

4.19 Manually Mark WHO Diameters

SEG_IA_manual_orthogonal_diameters_on_a_2D_slice

1. Click the **WHO** button.
2. Drag the mouse to mark the longest diameter, similar to marking the RECIST diameter.
   Two perpendicular lines are now displayed, with a label giving the product of their lengths.
3. Drag the ends of the perpendicular diameter to fit the tumor.
4. Release mouse button to complete the measurement.
5. Click **Done** when you have completed both RECIST and WHO.
6. Scroll right in the Image Observations table to see the RECIST, WHO and Volume calculations.

4.20 Mark Annotation as Seed Annotation

DATA_seed_AIM_object

For AVT2EXT, creating a Seed markup causes IA to create a **Tumor Seed Annotation** containing that markup.

4.21 Save Annotation as AIM Object

IA_store_annotations
AUDIT_image_reader
DATA_meaningful_AIM_file_name
AUDIT_create_annotation
AUDIT_AVT_version_date_and_time
IA_save_warnings
DATA_thoracic_phantom_tumor_AIM_object
IA_store_seed_annotations
IA_store_pan_zoom_window_level

1. Click **Done** if you have not already done so.
2. Enter a name in the **Name** field. This will be stored both as **AIM::Annotation.name** and as **AIM::User.name**
3. Select a **Location** (e.g. Thorax) to indicate the location of the lesion.
4. Click **Save**
   - 'Examine the folder **C:\temp**, navigating to the most recently modified sub-folder. In that folder, you will find 4 **.xml** files and a **.dcm** files, containing the SEED, Volume, WHO, and RECIST AIMs and the DICOM segmentation object that you just saved. These files are also saved to the Annotation Database.
5. Copy these five files to a more permanent folder for use later in this Tour.

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4.22 Delete an Observation

IA_multiple_AIM_annotations_per_image_reader_session

1. Create another observation
2. Click **Delete**
   The table entry will disappear.

4.23 Exit the Image Reader

1. Click on the Host tab in the upper right corner.
   The XIPHost window should appear, but there should still be an IA tab next to the Host tab.
2. Click the IA tab in the upper right corner
   The IA application should reappear.
3. Click Exit
   The IA application should disappear, and the IA tab should also disappear.

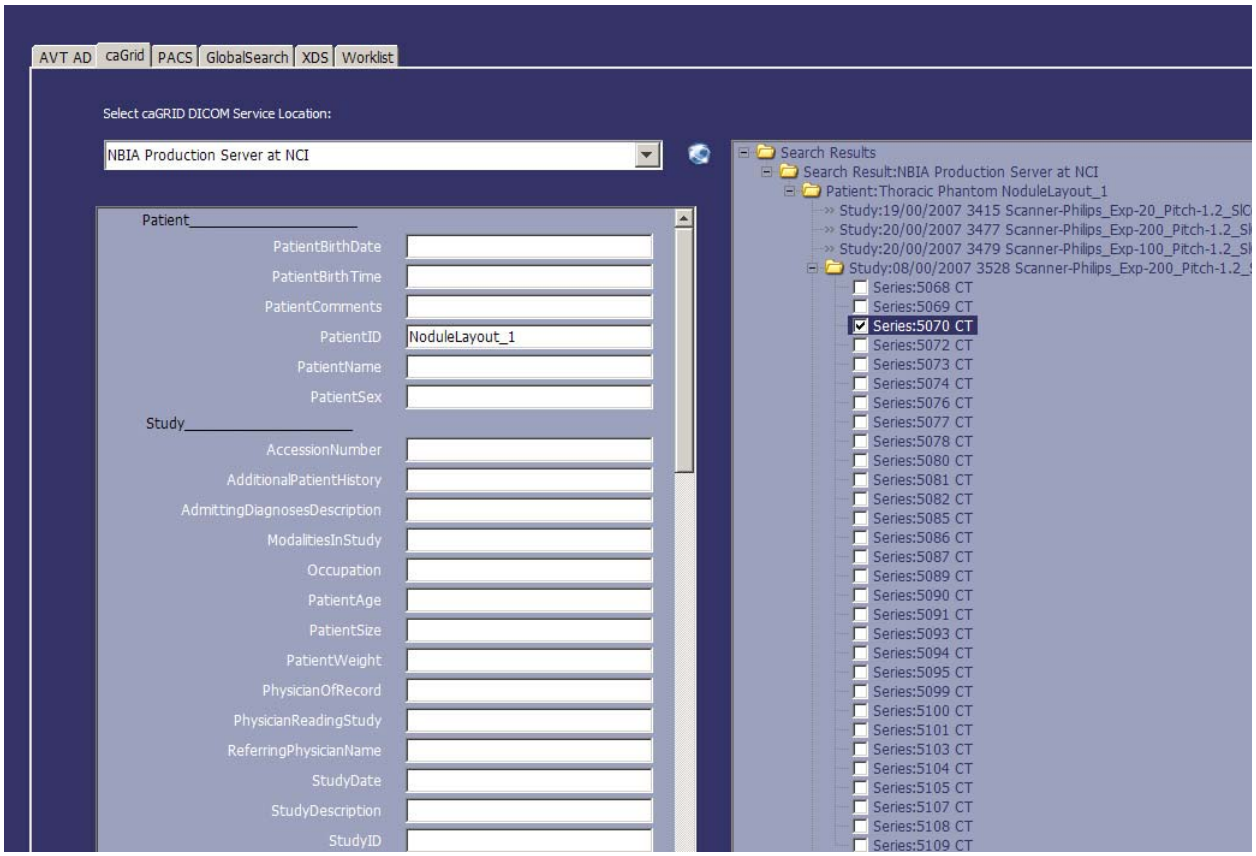
4.24 Load AIM Annotation

DATA_load_and_display_AIM_annotations
IA_navigate_to_markup

1. Follow the instructions in #Load Series into Image Reader, skipping over those that you don't need, to Retrieve the Yamamoto-51 series and start up IA.
2. Click **Load**
3. Navigate to the folder containing the XML and DCM files you saved in section #Save Annotation as AIM Object.
4. Select all of the files and click **Open**.
   IA will navigate to a slice that includes the tumor, displaying the volume contour, RECIST, and WHO markups if provided. The Image Observations table will include the shape, certainty, RECIST, WHO, and Comment values that were stored before.
5. Place all three cross-hairs on the tumor. Pan and zoom for convenient viewing.
   - *The 3D-MPR image display will adjust to display the volume, RECIST, and/or WHO markups associated with the selected tumor.*

4.25 Load NBIA Image Into Image Reader

1. Run XIPHost
2. Click **caGrid** tab
3. For **Patient ID** enter **NoduleLayout_1**
4. Click **Search**
5. When search results appear, expand Study **3528** and select Series **5070**, as shown in the following picture:



6. Clear the **with annotations** box.
7. Click **Retrieve**
8. Click **IA**
9. Click **W/L Lung** to see the image.

- *Alternatively, you can locate a series or image of interest in the NBIA Query web page, then copy a **StudyInstanceUID** or **SeriesInstanceUID** into the XIPHost caGrid query page and **Search**.*

4.26 Load AIM Object From AIME

- *Deferred.*

4.27 Under Construction

The following subsections are in rework.

4.27.1 Describe GBM Tumor – Vasari Protocol

This task is not described here because it is not part of AVT2EXT. It will eventually be documented.

5 A Tour of Algorithm Execution

(For instructions on plugging in a new algorithm as a scene graph, see the AVT Programmer's Guide.)

AE_algorithm_plug_in_interface

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5.1 Select Seed AIM Objects

AE can use either Seed annotations or RECIST annotations as the input to the segmentation algorithm.

AE_input_cases
DATA_seed_AIM_object
XIPHOST_query_seeds

1. In the AVT AD query panel, for Annotation Type, enter **Tumor RECIST Annotation**.
   - The sample database contains no **Tumor Seed Annotation**s, but later, when you create them, you can also search for them.
2. (Optional, but recommended first time) For **Reader Identity**, enter **Byrne_2**
3. Click **Search AD**
4. When the **Search Results** appear, expand them to find the series of interest
5. Check the boxes next to the series you want to segment
   - For a first try, pick the small series.
6. Check **AIM plus SEG**, but do not check **Series**
7. Click **Retrieve**

5.2 Submit Batch to AE

1. Click **AE**
   - *An **Annotation** panel will appear, listing one seed annotation on each line*
   - *The panel below it will eventually display one line for each completed segmentation*
   - *Below that,* **Start** *and* **Cancel** *buttons should be displayed, as well as an activity bar*
2. Change the name in the upper left text box to the reader name you wish to attach to the results.
   - The name should end with **_D**, where **D** is a single digit, if you wish to specify a "reading" session number.
3. Click **Start**

5.3 Monitor AE Progress

AE_progress_indicator

- *Watch the AE cmd.exe window to convince yourself that it is doing something. Currently, loading the image takes much longer than segmenting it.*
- *When each segmentation completes, a line will appear in the progress window reporting that fact.*

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5.4 Cancel Batch Execution

1. After at least one progress line has appeared, but while there are still two seeds that have not completed processing, click **Cancel**
   - *When the current segmentation case completes, AE will skip the remaining cases and terminate the batch.*

AE_cancellation

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5.5 Review AE Results Summary

1. After all segementations are complete or have been cancelled, double-click on a result line to see a sample slice of the segmented series, with the contour overlaid.

AE_results_summary

6 Database Miscellaneous

AVT has not yet developed a comprehensive set of database curation tools. However, many curation operations are possible by clever use of existing capabilities. Here are some of them.

6.1 Deleting from the Database

No deletion capabilities exist yet. However, you could write your own SQL scripts to do what is needed.

6.2 Inspecting and Copying Objects Out of the Database

Whenever XIPHost prepares a set of arguments for an application, it copies them temporarily to a working folder, somewhere within TmpXIP, and lists the absolute path name of each temporary file in the pop-up dialog, **Input dataset description**. To **inspect** an object,

1. Create an XIPHost query that will match the object (and possibly others), and click **SearchDB**
2. Select checkboxes to refine the selection and click **Retrieve**
3. Copy the file path name of an object out of **Input dataset description** and paste it into the tool of your choice.
   - For XML, try **Internet Explorer**

To copy one or more objects,

1. Copy *one of* the path names out of **Input dataset description** and paste it into the Windows Explorer address bar.
2. Delete the file name itself, leaving the folder name, and inspect that folder.
3. Copy and rename the file(s) as needed.

6.3 Patient ID vs. Patient Name

Technically, **PatientName** should be the usual, human-recognizable name of the patient, and PatientID should be the institution's unique ID for the patient. However, in clinical trials, these fields get abused. So, for example, in the CDRH pilot data, the **PatientID** is **Yamamoto-000NN**, and the **PatientName** encodes several acquisition parameters, such as exposure and collimator settings.

6.4 Adding Objects to the Database

To add objects to the database without reloading it from scratch

1. copy the objects into a pair of folders named **annotations** and **images**, structured like **C:\AVT\examples\CDRH**
2. Edit the script **loadCDRH.bat**
3. Save it as a new name
4. Change it to make **dir** point to the folder containing your pair of folders.
5. Delete the two lines ending with **...\connections.properties**
6. Save the file and execute it.

6.5 Examining Objects Returned by Applications

By convention, each of the applications stores the objects it is returning to XIPHost in a working directory somewhere.

1. For IA, look in **C:\temp**
2. For other applications, try **C:\temp**, then try **OutXIP**

3. If all else fails, use #Inspecting and Copying objects out of the Database to see if you found what you wanted.