MOMA Data Viewer

- User Guide
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User Guide

MOMA Data View is an application built with the Qt framework that is used to interpret, display, and analyze MOMA data. It can be used for both real time and post processing purposes. At this time we only support Macs.
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Installation

Prerequisites

- A NASA AUID (agency user id)
- Access to the momaioc server. This will require your AUID account to be setup with the momaioc server. Please contact Bradley Tse if you do not have access.
- A functioning RSA token that is attached to your AUID which will be used when creating a tunnel to the momaioc server. The tunnel is used to gain access to the supplementary files and data.
- Either the `svn` command line tool or a working Subversion GUI client. See the instructions for installing Subversion. `svn` is used to download MOMA Data View, all required supplementary files, and MOMA data.
- You need to either be logged into the NASA network (not NASA guest) or VPNed in

Tunneling into momaioc

This step creates a "tunnel" to the momaioc server, which basically gives you access to all of the files on the server. The momaioc server contains our Subversion repository which is where we store all of the data, apps, and files.

1. Open up a terminal and paste this command into the terminal, replacing AUID with your actual AUID:

```
ssh AUID@momaioc.gsfc.nasa.gov -L 6994:localhost:3690
```

If that command complains about an unknown hostname, then use this command instead:

```
ssh AUID@128.183.20.207 -L 6994:localhost:3690
```

2. You should now be prompted for your password. Your password will have the following format (omitting the carrots when you actually enter it): <RSA_PIN><RSA Generated Numbers> Be careful about entering your password because after 3 consecutive unsuccessful attempts you will be locked out.

3. You have now successfully created a tunnel to the momaioc server, which means we can now access the data and files! You do not need to do anything else with this terminal tab. It should be left open for the duration of your work session. All other terminal work should be done in a different tab.

Downloading momagse

The momagse directory contains various configuration files and all of our apps, including MOMA Data View.

1. Open a new terminal tab

2. Change to your home directory:

```
cd ~
```

3. Download/checkout the momagse directory:

`svn co` svn://localhost:6994/momagse

4. You should now have the momagse directory!

Installing MOMA Data View

1. Mount the MOMA Data View dmg

```
open ~/momagse/Apps/momadataview.dmg
```

2. A Finder window should have opened with the MOMA Data View application in it. Drag and drop the application to your Applications directory.

3. Unmount the MOMA Data View dmg

4. You now have MOMA Data View installed!

Updating to a newer version

Note: The following instructions assume you have met all of the prerequisites.

1. Create your momaioc tunnel

2. Open a new terminal tab or window.

3. Update your momagse directory:

```
svn up ~/momagse
```

4. Follow the same steps in Installing MOMA Data View except this time replace the pre-existing app.

Getting the data

1. Create your momaioc tunnel

2. **Open a new tab or terminal window.** If it does not already exist, create a momadata directory in your home folder and change into it.

```
mkdir ~/momadata
cd ~/momadata
```

3. If you do not have any data, then use the following commands to check out the data:

`svn co` svn://localhost:6994/momadata/etu `etu`
`svn co` svn://localhost:6994/momadata/fm `fm`
`svn co` svn://localhost:6994/momadata/qsm `qsm`

If you already have data, then you can update your working copy as follows:

```
svn up ~/momadata/etu ~/momadata/fm ~/momadata/qsm
```

Build Environment

The following configuration is used to build MOMA Data View:

- Qt 4.8.7
- Apple LLVM version 7.0.2 (clang-700.1.81) 64bit

Windows Build/Deployment

1. Open the gsw-cpp project in QtCreator

2. Select 'release' mode and build the project

3. Open a Git Bash prompt at root of the project

4. Run: ./scripts/windeployqt.sh missions/moma/momadataview "libgenericdecoders.dll,libgenerictransferfuncs.dll"

5. Copy (or zip up) all of the files and folders in ./appimages/staging/missions/moma/momadataview/

Changelog

5.2.0

Revision: 9728

Release Date: 2021-04-02

5.1.0

Revision: 9588

Release Date: 2020-12-18

5.0.2

Revision: 9531

Release Date: 2020-11-23

5.0.1

Revision: 9300

Release Date: 2020-10-08

5.0.0

Revision: 8994

Release Date: 2020-07-29

4.25.0

Revision: 5528

Release Date: 2017-06-28

4.24.4

Revision: 5425

Release Date: 2017-06-02

4.24.3

Revision: 5351

Release Date: 2017-05-22

4.24.2

Revision: 5328

Release Date: 2017-05-12

4.24.1

Revision: 5249

Release Date: 2017-05-1

4.24.0

Revision: 5113

Release Date: 2017-04-19

- General
  - Supported packet types are now defined in an external config file: TMDef/tm_packet_types.txt. As a result, this version of MDV can now support the new LITMS packet types.
  - The 699config.ini dialog is now scrollable to avoid issues with it being too big and the edges being off the screen

- Limit Monitor
  - Added buttons to "Clear All" triggered limits, and "Enable/Disable All Limits"
  - Disabling all limits now automatically clears any triggered limits

- HK Viewers
  - Decreased padding around the edges

- Raw Packet Viewer
  - Horizontal scroll bar position is now restored when the selected packet changes

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4.23.6

Revision: 5013

Release Date: 2017-04-10

- Fixed bug where if the min mass in the SIC range was less than the scan's min mass, the calculated ion count was incorrect. This impacted the DAC Scan and Chromatogram Viewer.
- Increased the max allowed mass to 2000 in the Chromatogram Viewer's SIC range
- Changed order of the splash page fields
- Added a packet count to the splash page
- Chart closest point tooltip calculations are now performed in a separate thread. This should help improve performance for high rate samples.

4.23.5

Revision: 4985

Release Date: 2017-03-28

- Mass Scan Viewer
  - Fixed values of DACs 8-12 in the Scan Info area

4.23.4

Revision: 4976

Release Date: 2017-03-24

- Sequence Viewer
  - Now correctly uses the SET_BIN_TIME command to calculate ramp durations

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4.23.3

Revision: 4939

Release Date: 2017-03-15

- Data Rate Viewer
  - Fixed the TVAC GSE packet being included in the data rate calculation
  - Added a checkbox to toggle the inclusion of GSE packets. Unchecked by default.
  - Added a new data size series (base 10)

4.23.2

Revision: 4870

Release Date: 2017-03-02

- Performance improvements. TIDs now load ~2-4x faster.

4.23.1

Revision: 4776

Release Date: 2017-02-14

- Science Settings
  - Added new Summed Scan Timestamp Mode: Average first and last
  - Added new Scan Info Display Format Mode: Succinct

4.23.0

Revision: 4762

Release Date: 2017-02-10

- General
  - Added support for the calibrated laser pulse energy conversion. HKID 1087 will use it.
  - Added support for 4 new laser pulse energy HK items: AVG (1089), MIN (1090), MAX (1091), and STD_DEV (1092)
  - Added model and DAC table to the splash page
  - Other minor tweaks, bug fixes, and optimizations

- All Charts
  - Added ability to change a series' axes via its legend item's right-click menu. This is not currently saved between sessions.
  - Added ability to choose your own series colors from the Setup menu. This will impact all charts. Reload of viewers is required to reflect changes.
  - Tweaks to the axis settings dialog

- HK Charts
  - Added option to display the journal.txt with the message log. This feature is currently not available in the Message Log Viewer.

- Science Settings
  - Added a new "Average Summed Scan Timestamps" option, which uses the Scan Status packet timestamps
  - Improvements to the setting's status indicator that is shown on each science viewer

- Mass Scan Viewer

    - Added laser energy stats to the scan info display
    - Split up the info into two panes
    - Added a “Animate Scan Changes” chart right-click option, which is off by default.

- DAC Scan Viewer
    - Added support for science packets

- Raw Packet Viewer
    - Added ability to export the packet list’s columns
    - Added a local datetime display at the top
    - The timestamp column’s tooltip is now the raw timestamp converted to seconds

- TID Explorer
    - The selected TID now stays in sync with the open TID

4.22.7

Revision: 4676

Release Date: 2017-01-26

- All
    - The Settings button has been removed from the science viewers. It can now be accessed from the Setup menu
    - Plots that are opened through an HK Viewer's right-click menu are now added to the Data Viewer menu's open viewers list
    - Closing an HK Viewer no longer closes the plots that were opened through it
    - Fixed negative timestamps when raw FSW Ticks > ((2^32) / 2)

- Energy Viewer
    - New Energy Viewer to calculate and display the energy used by the instrument
    - Data Viewers-->Open-->rsim_energy.grf
    - OR Data Viewers-->Viewer Finder-->search "energy"

- Charts
    - Added in support for exporting the series data, accessible through the chart's right-click menu

- Mass Scan Viewer
    - If the "Average" setting is enabled, the selected scans will also be averaged

- Chromatogram Viewer
    - Fixed bug where the scan indicator line would be hidden if the TIC series was hidden

- DAC Scan Viewer
    - Fixed a crash when using the Opt+Left-Click feature for certain data sets

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4.22.6

Revision: 4625

Release Date: 2017-01-14

- Fixed crash caused by the chart's line items (messages, markers, limits, etc)

4.22.5

Revision: 4623

Release Date: 2017-01-13

- Added new Duty Cycle Viewer
- Small tweaks to Mass Scan Viewer's auto-scale logic

4.22.4

Revision: 4596

Release Date: 2017-01-06

- Added support for the TVAC Packet

4.22.3

Revision: 4563

Release Date: 2016-12-02

- Bug fixes
  - Fixed crash when opening DAC Scan Viewer while summed scans are being filtered out

- Mass Scan Viewer
  - The cFactor for each scan is now applied before summing multiple scans

- Data Rate Viewer
  - Added a new Data Rate Viewer to plot the TID's data rate
  - Data Viewers->Open->data_rate.grf
  - OR Data Viewers->Viewer Finder->search "data"

- TID Explorer
  - Searching now uses the same fuzzy filtering algorithm that everything else uses
  - Cmd+E now always shows the TID Explorer and highlights the search text. Use Cmd+W to close it.
  - Now supports Down/Tab and Up/Back-tab keys to navigate the tree
  - Added more right-click options

- General
  - Minor tweak to HK graph's auto-scale logic

4.22.2

Revision: 4482

Release Date: 2016-11-04

4.22.1

Revision: 4475

Release Date: 2016-11-03

4.22.0

Revision: 4426

Release Date: 2016-10-27

- New Annotation feature

- DAC Scan Viewer
  - Fixed bug that was causing the series to be labeled in reverse order

- Message Log Viewer
  - Fixed the font not being properly saved/restored
  - Fixed bug that was adding a blank line for messages that were filtered out

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4.21.1/2

Revision: 4391

Release Date: 2016-10-18

- Science Data
  - Fixed the incorrect parsing of summed packets with an odd number of scans. It was causing the bins to be shifted by one to the right. This affected data that was generated with FSW v3.4.6 and above.
  - Fixed some rounding inconsistencies

- Mass Scan Viewer
  - Sum region is now saved/restored

- Chart
  - Closest X tooltip is now displayed even when crosshair is visible

- General
  - Fixed problems with the SWTS packet timestamps

4.21.0

Revision: 4355

Release Date: 2016-10-12

- Charts
  - Mouse wheel now zooms in and out -- doing it over a specific axis will modify only that axis
  - Shift key now enables "Panning" mode -- doing it over a specific axis will pan only that axis
  - Added a new Zoom Mode: X Only, Scale Y -- This zooms in an x-window, but auto scales the y-axis to fit the data.
  - Zoom mode is now displayed in the bottom right corner
  - Zoom stack size is displayed in the top right corner. Clicking on it will reset the zoom.
  - Added ability to cycle the chart's zoom mode with Cmd+Ctrl+Z shortcut
  - Added shortcut text in the chart menu for the ToolTip Mode
  - Changes to an axis's settings are now immediately shown
  - Fixed some edge case bugs with the cursor shape
  - Zoom stack popping is now disabled while the mouse crosshair is visible
  - Minor fixes to the Quick Graph's search algorithm
  - Fixed a minor memory leak with the menu
  - Hovering over the legend items now changes the cursor to a pointing hand

- General
  - Timestamp resolution is now correct for TIDs with resets (Big thanks to Mark!)
  - Added in the option to average the counts of the Summed scans - accessible from either the Mass Scan Viewer's or Chromatogram Viewer's "Settings" dialog
  - All "Latest" checkboxes are now auto-unchecked when the window is scrolled up
  - Tweaks to viewer default sizes
  - Added ability to plot a HK Items conversion to the Database Info window

- Mass Scan Viewer
  - Added a "Sum" mode that allows you to sum the counts in a range
  - You can now remove individual "Kept" series
  - Auto-grow/auto-shrink now only accounts for the data in the current x-axis range
  - Closest point ToolTip now correctly updates when the scan changes
  - Minor visual tweak to the filter popup

- Chromatogram Viewer
  - Added cTIC and cFactor AGC series
  - AGC series can now be individually toggled
  - Updated the how the "Integrate" mode works
  - Added new min and max inputs for the SIC functionality
  - Fixed bug where it would be difficult to manually input values into the "Integrate" widgets
  - Fixed bug where sometimes it would not load properly the first time
  - Now remembers its zoom mode and tooltip mode

- DAC Scan Viewer
  - You can now use the chart crosshair (option+left-click) to select the closest scan in the Mass Scan Viewer!
  - Added in an auto-scale option -- mainly relevant to auto-scale when the SIC range changes
  - Fixed bug where the current scan's tooltip would be in the wrong place if a SIC range is applied
  - Fixed data point visiblity being off
  - SIC range better validates its input
  - SIC range is now saved between sessions

    - SIC range is colored green when it is valid and being used

- HK Viewers
    - Added in right-click options to change all HK items to a specific value mode

- HK Graphs
    - Added a new "Real-time" tooltip option that displays the most recent values for each series
    - When adding new series, the new series is scaled to the current zoom window
    - Fixed bug where sometimes the auto-scaling would not work when opening an active TID until you manually reset the zoom
    - Fixed bug where the selected marker's ID was not being displayed on the chart indicator
    - Fixed bug where messages and markers were already selected the first time the panel is displayed
    - Decreased the font size of the message and markers
    - Replaced the row column from the messages and markers with a label at the bottom

- Raw Viewer
    - Added in HKID and Science value columns
    - All HK items are now displayed, but some are still incorrect
    - You can now right-click on an HK item to access its database info
    - You can now click on the address area in the hex display to toggle between Hex and Decimal
    - Fixed bug where sometimes selecting the first packet would not update the display
    - Fixed bug where sometimes the display would not be cleared when no packet is selected

- Message Log Viewer
    - Fixed extremely long load times
    - Redesigned the search feature

4.20.0

Revision: 4023

Release Date: 2016-08-16

- All Charts
    - Double clicking on a y-axis now scales to only the data contained in the current x-axis range - no longer pops a range off the axis' zoom stack
    - Double clicking on a x-axis now sets its range to fit all data - no longer pops a range off the axis' zoom stack
    - Replaced the mouse coordinates in the bottom left corner with an indicator directly on the axis - this has the added benefit of showing the coordinates for all axes instead of only one
    - A "closest point" tooltip is now on by default
    - Added a new "Closest X" tooltip mode which displays a combined tooltip for all series
    - Zooming can now be initiated outside of the axis rectangle
    - Delta x and y are now displayed along the zoom rectangle
    - Slight tweaks to the Cyan and Orange series colors
    - Changed the "All series data points visible" options to hopefully make it more intuitive

- Mass Scan Viewer
    - Default zoom mode is now x-axis only -- zoom mode is saved between sessions
    - Added in a right-click menu option to control the chart's anti-aliasing
    - The zoom level is no longer auto reset when the mass cal is changed or the cFactor option is applied

- Chromatogram Viewer
  - Added an "Interpolate" option to the integration functionality that will interpolate between points to calculate the area of the full window
  - Added an "AGC" option that will show series for the AGC parameters - the series are also available to export
  - You can now export the visible HK series - this required a separate "Time" column for each exported series since their times differ
  - Changed it's real-time auto scaling logic to match the HK Graphs
  - When series are checked/unchecked, their axis is automatically scaled now
  - Fixed bug where adding a HK series for the first time would cause the graph's zoom level to be reset
  - Minor changes to hover tooltips
  - Integration functionality's area is now rounded to the nearest whole number
  - Added ability to copy the area's value with Cmd+C; the selection must have focus since the chart also uses Cmd+C

- Message log Viewer
  - Remembers its font between sessions

- HK Graphs
  - Using the mouse crosshair will automatically open the msg/marker panel

- General
  - The list of open viewers in the "Data Viewers" menu is now sorted alphabetically to make it easier to find a viewer
  - Fixed the J2k epoch - this shifts the UTC time of data by 64 seconds, relative time is unchanged
  - Minor tweaks to the "HK Selection" dialog

4.19.1

Revision: 3859

Release Date: 2016-07-15

- Chromatogram Viewer
  - Fixed the area calculation
  - Improved the functionality of the integration feature

4.19.0

Revision: 3845

Release Date: 2016-07-14

- Chromatogram Viewer
  - Added new integration functionality. You can toggle it by using the "Integrate" checkbox. The chart crosshair (option+click or middle-click) can be used to move the integration region. The "Move Mode" determines which part of the region is moved.

- Mass Scan Viewer
  - Added support for 2nd order polynomial curve fits

- Improved the auto shrink/grow functionality
- The Mass Cal Dialog's curve fit now has a range that makes sense for the control mode
- Fixed a bug where the MIC series was getting reloaded as a SIC series when the Mass Cal changed

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4.18.6

Revision: 3822

Release Date: 2016-07-08

- Fixed the checked markers not being displayed

4.18.5

Revision: 3818

Release Date: 2016-07-07

- Fixed TICs not being extracted from the new sum packet format
- Fixed bugs caused by Tom's 4-byte padding
- Added sum of TICs

4.18.4

Revision: 3812

Release Date: 2016-07-05

- Added support for the new sum packet format that contains the cTIC factor and MBC/SIC for each scan (added in FSW 3.4.6)
- Added display of the new sum packet fields for each scan to the Mass Scan Viewer
- cTIC factor calculation now properly accounts for the TIC weight of each scan
- The text of the currently selected message or marker is now auto displayed on the chart
- Fixed bug where Laser Pulse Packets with no pulses were being dropped
- HK Viewers now save/restore their font size
- Minor changes to tooltips

4.18.3

Revision: 3773

Release Date: 2016-06-22

- Reverted accidental change to RF Mon and RF Dac conversions - this slightly shifted RF Mon and RF Dac conversions by ~0.001V.

4.18.2

Revision: 3765

Release Date: 2016-06-20

- Added ability to export visible series in Mass Scan Viewer - useful to export kept and averaged series
- Added plot of mass cal curve fit in mass cal dialog
- Fixes/improvements to real-time auto-scaling logic

4.18.1

Revision: 3726

Release Date: 2016-06-06

- General
  - New app icon to easily differentiate between MOMA applications
  - Fixed bug where MDV would pop up if hidden
  - All GSE created packets are never used for t0 now - impacts old ETU TIDs < 7300

- Charts
  - All charts now support animations. Can be disabled/enabled from Setup->Chart Animations. Requires a restart of the application.
  - Double-click on an axis to rescale only that axis
  - Axes now display the attached series' legend
  - Changed the default series colors
  - Added ability to select zoom mode in the right-click menu
  - Slight tweak to the default title padding

- HK Graphs
  - Added in Central Moving Average option when selecting HK items
  - Axes are no longer rescaled when modifying/adding HK items
  - Improved auto-scale logic. Now only auto-scales the currently visible series
  - Existing HK series' visibility and data point visibility are not reset when modifying/adding HK items
  - Message and Markers now have basic filtering functionality

- Mass Scan Viewer
  - Ported to the new chart library, which adds a legend, and copy/save functionality
  - Added averaging option
  - Fixed bug where using the "View Sequence" right-click option would not display the sequence with the correct scan data if the Sequence Viewer had never been opened
  - No longer resets zoom when changing graph modes

- DAC Scan Viewer
  - Now has chart copy/save functionality

- Raw Packet Viewer
  - Added in relative time column
  - Attempts to reselect the previous HK item when changing the selected packet

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4.17.3

Revision: 3540

Release Date: 2016-04-27

- Chromatogram Viewer
  - Fixed the crashing when enabling the cTIC and MIC after adding a HK item
  - Fixed the incorrect calculation of the cTIC. Now uses the Src A Focus A register readback value instead of the last set DAC value

- DAC Scan Viewer
  - Ported to the new chart library
  - Added in an "auto-select" option that will automatically display the DAC Scan of the selected scan in the Mass Scan Viewer - NOTE: This does not work in real-time yet

- HK Selection Dialog
  - Fixed the Tab and Backtab functionality to scroll through the filtered HK items
  - Changed the shortcut to graph from Shift+Return to Cmd+Return (Shift+Return still works for now)

- TID Explorer
  - Fixed the expanded and selection state not being properly restored between sessions

- DAC Scan
  - Fixed the averaged DAC Scan values being truncated to an int

- Other
  - Quick Graphs are now centered when created

4.17.2

Revision: 3442

Release Date: 2016-04-7

- Fixed TID Explorer crashing when opened
- You can now double-click on files in the TID Explorer to open them in their default application
- When saving or copying a chart's image, the TID is now displayed in the bottom right corner instead of the top left to avoid overlapping the legend or title

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4.17.1

Revision: 3434

Release Date: 2016-04-7

- New charts now have the right-click option to copy directly to the clipboard
- Added option to TID Explorer to use instead of the Open File dialog

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4.17.0

Revision: 3403

Release Date: 2016-04-4

- Sequence Viewer:
  - Fixed the Sequence Timeline not properly updating when the selected scan changes
  - Fixed the hex display not automatically scrolling to the selected cmd
  - When you select multiple cmds, only each cmd's region will be highlighted. Before it would highlight everything from the start of the first cmd to the last one.
  - You can now zoom with the mouse - double-click to reset zoom
  - DACs that are set outside of the sequence now use the closest scan status packet's values
  - Different cmds have different colors
  - Added in support for SEB_RAMP
  - Option+Click or middle button click on the Sequence Timeline to automatically go to the closest scan
  - Fixed the RAMP_IMM so that it now uses the scan status packet's bin time. Before it was hard coded to 10us
  - Visible DACs can now be toggled via the right-click menu
  - Added in option to auto-select the selected scan's sequence
  - Other minor visual changes

- Chromatogram Viewer:
  - Beta version is now the default version
  - Now properly saves and restores any HK series that were added

- Graph's Message and Markers:
  - Added in a "Latest" checkbox that sticks to the end
  - Added in useful right-click menu options
  - Added in ability to filter out 0-id markers

- Graphs:
  - Added in a menu option to save the graphs
  - Graph window titles and menu names are properly updated when HK series are added or removed
  - When saving the windows, the added HK series are now properly saved
  - Added in the ability to plot moving averages of the data
  - Redesigned the HK selection dialog
  - Fixed the issue with the series disappearing when zooming in on unordered data such as resets

- TID Explorer Beta:
  - Accessed through the File menu
  - Provides an easier way of quickly navigating through TIDs

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4.16.0

Revision: 3295

Release Date: 2016-03-22

- Sequence Viewer:
  - Sequences now use the selected scan in the Mass Scan Viewer to extract register values for the SET_DAC and PAUSE SEB commands.
  - Still unsupported:
    - RAMP command that uses the register values
    - No SET_*_REG commands within the sequence are being used. Right now it only uses the Scan's scan status packet values.
  - A green line is now used to indicate the beginning of a segment (i.e when pause or ramp commands are selected)
  - General visual improvements to the sequence timeline
  - Fixed the rollover issue when the sequence's timestamp is greater than t0
  - Uses the new hex display

- New and improved raw packet viewer
- Minor changes to the "About" dialog and menu ordering

4.15.3

Revision: 3265

Release Date: 2016-03-19

- Added in support for FSW v3.4.2 which changes how sum packets are timestamped. They are now timestamped when the last scan's science data ack is received, as opposed to being timestamped when the first science packet is received. The significant difference is that the sum packet's timestamp is now greater than the last corresponding scan status packet's timestamp. Before the sum packet's timestamp was less than the first corresponding scan status packet's timestamp.
- Chart axis grids are now gray for better visibility

4.15.2

Revision: 3254

Release Date: 2016-03-15

- Bug fix for very large science data timestamps

4.15.1

Revision: 3250

Release Date: 2016-03-15

- Added in a slight margin for sides with no axis

- Fixed how MAIF sample timestamps were being calculated for old packets with no timestamp

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4.15.0

Revision: 3235

Release Date: 2016-03-10

- Added in display of the TID to the menu bar so you can easily tell which TID is opened
- Changed the limit monitor's popup dialog to only tell how many HKIDs were triggered instead of how many values
- Decreased the size of the point indicator so that it matches the size of the series points
- Optimizations to the plot times for large series
- Axis settings are now accessed through right-clicks instead of double clicking
- Added back in limit monitor's limit value indicator and point indcator
- Added in the ability to disable the limit monitor popup for 5 minutes
- Slightly increased the minimum zoom rect size
- When creating quick graphs using only the HKID, the graph's title now displays the key instead of just the HKID
- Added in shift functionality to graph that will now display a point indicator for each series

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4.14.0

Revision: 3187

Release Date: 2016-02-29

4.13.5

Revision: 3158

Release Date: 2016-02-25

- Minor change to SWTS packet size

4.13.4

Revision: 3147

Release Date: 2016-02-24

- When adding a new housekeeping item to the Chromatogram Viewer, there is a little icon on the right side that has search tips
- Added in ability to toggle the legend
- Added in ability to show only the selected series

- Added in ability to display message log and marker text on the charts
- Added in ability to display the "max ion counts" on the Chromatogram viewer

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4.13.3

Revision: 3122

Release Date: 2016-02-22

- This version contains a pretty stable version of the new Chromatogram Viewer. After some more usage in the lab, the old one will be fully replaced with the new one.
- New features:
  - Uses the brand new charting library that adds a lot of nice functionality:
    - Full multi-axis support
    - Series using anti-aliasing to make them look nicer
    - Ability to display data point labels
    - Legend is displayed above the chart and allows the visibility of series to be toggled
  - All cSIC and cTIC traces now have their own axis
  - Added ability to plot housekeeping items on their own axis
  - All SIC traces are now saved between sessions

4.13.2

Revision: 3097

Release Date: 2016-02-18

- See changelog for v4.13.3 for a full feature list of the new Chromatogram Viewer Beta
- Bug fixes to Chromatogram Viewer Beta
  - Fixed the zoom not being properly set to full scale if the series min value was greater than 0.
  - If a series has no data or the series has all the same y values, the axis now keeps a range that makes sense instead of setting the min and max of range to the same value
  - Corrected counts axis is now correctly hidden on startup
  - Fixed SIC widgets enabled state on startup
  - Scan indicator is now shown properly on first open
  - Gave it its own settings key so it doesn't conflict with the regular Chromatogram Viewer

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4.13.1

Revision: 3090

Release Date: 2016-02-18

- Fixed the Chromatogram Viewer Beta not being properly reloaded when new TIDs are opened and also not properly updated when used in real-time

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4.13.0

Revision: 3088

Release Date: 2016-02-18

- If the tm file indicated in the metadata file does not exist, it falls back on the old logic of searching the current TID directory for any file containing "tm.mom".

- ChromViewer Beta!
  - Uses the brand new graph library with lots of changes and new features
  - See changelog for v4.13.3 for a full feature list

4.12.0

Revision: 3083

Release Date: 2016-02-17

- Mass Scan Viewer
  - Added display of filament state for each scan

- Miscellaneous
  - Fixed restoration of saved quick graphs
  - Updated splash page to include info about the status of the metadata file
  - Still attempts to parse and use unsupported metadata file versions (i.e. newer versions that momdataview doesn't explicitly support yet)
  - Fixed skipping of packets larger than 41k bytes. Now supports the max size of 65k.
  - Added in support for EIS packet type 40
  - Added in support for SWTS status packet type 45

4.11.2

Revision: 2980

Release Date: 2016-01-19

- Corrected the J2k offset

4.11.1

Revision: 2937

Release Date: 2016-01-05

- Science data

    - Scan's are no longer sorted by time (reverted from a previous version) and instead are again in the order they exist in the TID. This was causing issues in real-time.

- Mass Scan Viewer
    - Added in graph options to auto grow and shrink the y-axis when viewing scans

- Sequence Viewer
    - Fixed a crash when multiple sequences are selected at once

- Chromatogram Viewer
    - Now uses the same auto-scaling implementation as the HK Graphs

- DAC Scan Viewer
    - Fixed the axis not being automatically updated
    - Empty scan's are now skipped which fixes some scaling issues if a DAC Scan has empty scans. A DAC Scan may have empty scans if the required "END" marker is missing.

- HK Graphs
    - Fixed the static x-window implementation. Before the window would slowly increase on each refresh.

4.11.0

Revision: 2888

Release Date: 2015-12-17

Updated to support version 2 of the tm.meta

- Graphing
    - Optimization to graph zooming. Now zooming should always be smooth, even for very large data sets like the Bus 1 current sample.

- Decoding
    - Added in support for decode type 217 which calculates the laser UV energy

- Mass Calibration
    - Fixed loss of precision when saving and loading the mcal file
    - Now determines the mass cal to use from the tm.meta file
    - Saving the mcal to the TID updates the tm.meta's default mcal field
    - Prompts the user that they're overwriting a file

- Science
    - Added in some extra error handling for corrupted science data
    - Fixed a few corner cases for cTIC calculation

- Marker Viewer
    - Now remembers its "show zero marker" state

4.10.0

Revision: 2823

Release Date: 2015-12-3

- Scan data
  - Added in option in the global science settings to select which science packet types are used
  - Scan's are now ordered by time instead of their index in the telemetry file

- Mass Calibration
  - The mass cal dialog now works directly with the global mass cal. This means that any changes you make to the mass calibration are reflected right away. When closing the dialog, you will be prompted to save the changes. If you do not save, then the mass cal will be reverted back to the original one.
  - Fixed bug where negative intercepts were being rounded to an integer
  - Fixed the m/z -> RF DAC transformation
  - The mass cal dialog's is automatically updated to reflect the currently selected scan's phase cycle
  - Added option to save using the current mass cal's filename

- Sequence timeline
  - The DAC values are cut off at 3 decimal places for now. Eventually an option to set the number of decimal places will be added.

4.9.3

Revision: 2809

Release Date: 2015-11-23

- Beta version of the new sequence viewer timeline view

4.9.2

Revision: 2786

Release Date: 2015-11-17

Bug Fixes

- Fixed the message missing whitespace in the message log
- Fixed how the "sci from eng" column in the database was being applied by patch files

---

4.9.1

Revision: 2768

Release Date: 2015-11-11

Bug Fixes

- Made the Preferences dialog smaller so it fits on the screen better

- DAC Scan Viewer
  - Fixed the DAC scan counts being less than the expected TIC - This was fixed by hardcoding it to only use Summed packets
  - Fixed the number of traces for a DAC Scan changing by switching to a different Scan type and then back - This was due to the "End" marker missing for some data; added in some extra logic to handle these cases
  - Fixed the mass range functionality so that it properly uses each scan's unique transform when calculating the counts

---

4.9.0

Revision: 2749

Release Date: 2015-11-5

Bug Fixes

- Fixed divide by zeros that were occurring when calculating the cTIC

New Features

- Now supports the ability to differentiate between models!
  - This was achieved by adding in full support for the tm.meta file, which details which model a tm file was created with
  - This allows you to select different default paths and files for the different models via the 699config.INI file
  - If you attempt to open a tm file that has a model that does not currently exist in the 699config.INI file, you will be prompted with a dialog to set the key-value pairs
  - This dialog can be opened at any time from the momadataview->Preferences menu (or use the shortcut CMD+,)

Removed

- SciTmViewer
- Open archive file menu option

4.8.1

Revision: 2744

Release Date: 2015-11-5

Bug Fixes

- Now correctly handles Scan Status packets that are out of order with respect to their corresponding sum packet

- No longer incorrectly associates Scan Status packets to scans that are not related
- Using the slider in the Mass Scan Viewer now properly remembers the Scan list's horizontal scroll position

New Features

- Added a "# SS" column to the Scan list, which is the number of scan status packets associated with this scan
- Added the packet indexes for the Scan Status and Science/Sum packets at the bottom of the Scan Info display

---

4.8.0

Revision: 2732

Release Date: 2015-11-3

Bug Fixes

- Mass Scan Viewer:
  - Fixed the "cmd" key causing the latest scan to be deselected
  - Fixed the total scan count not updating if "latest" isn't checked
  - Fixed the packet type filtering capability
  - When summing multiple scans, the "latest" checkbox will be automatically unchecked

- Chromatogram Viewer:
  - The Mass option when using the SIC functionality now works as expected. Before this did not exactly work correctly. It performed a conversion from mass -> bin once, and then used that corresponding bin to determine the ion counts. However, this was wrong because the conversion from mass -> bin is scan dependent! Furthermore, it previously did not support the two step conversion that was required if the MassCal was done with either RF MON or RF DAC.

- DAC Scan Viewer:
  - The scan indicator is now only drawn if the selected scan is currently displayed
  - The scan indicator is now properly shown when using the "View DAC Scan" functionality from the Mass Scan Viewer

New Features

- Added in basic support for the new tm.meta file
  - Now searches for the tm.meta file to determine the name of the tm.mom file
  - Full support of all other features coming in the next release

- Added in new Science Settings feature
  - Control the GC AGC parameters from this new settings dialog

- Mass Scan Viewer:
  - Added in a cTIC column to the scan list
  - Added in an Average TIC (TIC/#Sum) column to the scan list
  - Added in option to apply the cTIC factor to the spectrum
  - The phase cycle and beta value are now displayed at the top of the scan's info display

- Mass Calibration:

    - The Mass Calibration dialog now inserts the correct control value irregardless of what the Mass Scan Viewer's current display mode is
    - If a phase cycle does not exist, the user will now be automatically prompted to create a new entry

- Chromatogram Viewer:
    - Improved the Export functionality, now lets you choose which traces to export
    - Added in support for cSIC traces
    - Added in support to have multiple cSIC/SIC traces displayed at once
    - Switching between the Mass and Bin option no longer attempts to do a conversion - The reason for this is because the mass <-> bin conversion is scan dependent
    - Improved the scan indicator

- DAC Scan Viewer:
    - Improved the scan indicator
    - Added in the "Show Data Points" option

- Message Log Viewer:
    - Now automatically fixes messages that were separated between packets, i.e. no more partial messages on their own line

- Graphs:
    - When the graph is set to full scale, the scale stack is automatically cleared now
    - Added in option to display an indicator of the scale stack - useful to know how far zoomed in you are
    - Multiple value graphs now initially load much faster

- Quick graph:
    - Greatly improved its functionality
    - Now supports fuzzy searching of the HK Items in the search bar. For instance, in order to plot MAIF:MAIN_IMON, you can simply start typing "mainim" and the option should pop up. Very useful!
    - Can now be opened via CMD+G shortcut
    - Now defaults to Sci mode
    - Remembers its state between sessions

- Raw Packet Viewer:
    - Editing the current packet index field now pauses the viewer automatically

- Marker Viewer:
    - Columns are now properly sorted by their double value instead of their string representation

- Data interpretation:
    - Equation type 9 now uses the Science K Constants to apply a polynomial to the converted value

- General:
    - Now prompts the user about which TM File to open if a TID has more than one
    - When opening viewers, you can now select more than one at a time
    - When re-opening the TID that is currently opened the tm file will actually be re-opened and parsed

---

4.7.0

Revision: 2584

Release Date: 2015-09-24

Bug Fixes

- Fixed issue where HK graph did not properly rescale itself when initially blank and then data arrives at a later time
- Fixed graph "blinking" that occurs in the Mass Scan Viewer when the "latest" checkbox is checked and the Command key is held down
- Fixed/improved how the scan summing functionality works. Now the first selected scan is always the one that scans get summed on top of and also the mass calibration that is used
- Fixed crash that occurs when you have 1 or more trace "kept" and then open a new TID

New Features

- Completely redesigned how auto scaling works for HK graphs
  - When zoomed in on data, it will no longer automatically zoom you back out
  - If data exists outside of the current window, then the appropriate axis side will be bolded
  - If new data arrives while zoomed in, the right axis will be colored green to indicate this
  - Added capability to "freeze" the current x axis window
- Added shortcuts for the graph right-click options
- The slider in the Mass Scan Viewer now reflects the currently selected scan

---

4.6.3

Revision: 2555

Release Date: 2015-09-18

Bug Fixes

- Fixed crashing when the Scan Status data does not exist for a scan
- Fixed timestamp calculation for various decoders

New Features

- Added cTIC column to Mass Scan Viewer

4.6.2

Revision: 2491

Release Date: 2015-09-03

Bug Fixes

- Actually fixed the cTIC this time
- Fixed decoder 223, upirani pressure low

New Features

- Added in capability to filter by packet type in the Raw Packet Viewer

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4.6.1

Revision: 2477

Release Date: 2015-09-02

Bug Fixes

- cTIC now works for Science Packets
- The Mass Calibration Dialog now opens with the phase cycle of the currently selected scan (if one exists)

4.6.0

Revision: 2473

Release Date: 2015-09-01

Significant changes

- New v2 mass calibration format that supports different mass calibrations for different phase cycles and also calibration via the RF values

New Features

- Chromatograph Viewer :
  - now supports displaying the cTIC
  - improved SIC functionality
  - graph crosshair now displays the closest mass spec in the Mass Scan Viewer
  - you can now display the messages and markers on the graph
  - "scan indicator" is now a straight line instead
  - improved export capabilities
- Raw Packet Viewer index input is slightly modified to save space
- Added in a "Load Global" button to the Mass Calibration Dialog
- You can now remove multiple Mass Calibration data points at once
- DAC Scan Viewer scan list is now ordered by the order of the scantypeinfo.json config file
- Mass Scan Viewer's Scan Info now uses the scantypeinfo.json config file for the Scan Id and Scan Value interpretations
- Slightly changed the format of the scantypeinfo.json file and also the default location of it
- Graph crosshair is now triggered via option+left-click instead of the previous shift+left-click because the shift modifier was causing issues with other widgets
- Supports the new Science Summed Packet structure that includes the TIC for each summed scan
- All graphs now support Adaptive Sampling and the ability to display the data points
- "AS" is now drawn to the top left corner to indicate that Adaptive Sampling is being used
- Tooltips in the message and markers left panel are now immediately shown on hover

Bug fixes

- Fixed the incorrect RF Monitor conversion for the last bin segment

Bug fixes

- Fixed the Scan Status packet data being associated with the wrong scan (only for single scans).

4.5.1

Revision: 2321

Release Date: 2015-07-30

Bug fixes

- Fixed the Scan Status packet data being associated with the wrong scan (only for single scans).

4.5.0

Revision: 2303

Release Date: 2015-07-21

Significant change

- Added in support for Equation Type 12: Lookup tables! This means that data conversions can now be done via lookup tables. All lookup tables should exist in the "momagse/TMDef/lookupTables" directory.

Bug fixes

- Changed the name of the "Limit Viewer" to "Expected Value Viewer"
- Fixed a crash when the science data packets have no actual science data. The culprit was the Mass Scan Viewer, and an example TID was 01277.

4.4.1

Revision: 2288

Release Date: 2015-07-16

Bug fixes

- No longer crashes on close

4.4.0

Revision: 2275

Release Date: 2015-07-13

Significant change

- Added in a new Limit Monitor that is constantly watching incoming values.

New Features

- Added in tooltips to all items on the splash page
- Turned off auto coloring of old traces

Bug fixes

- Made a fix to how markers were being extracted by the old limit viewer (which is really the expected values viewer) so that it actually works now

---

4.3.0

Revision: 2238

Release Date: 2015-06-23

Significant change

- v1.0 of the database patch file spec detailed here has been fully implemented. This means that the HKID (data id) is now the unique identifier. One immediate impact this has is that HK Viewers will automatically update to display the names in a patch file. For example, there is no longer a need for a separate QSM MAIF housekeeping viewer because the regular one will automatically replace it's names with the QSM naming as detailed in the QSM patch file.

New Features

- Added in option to color old graph traces a different color.
- Added in t0 in seconds to the splash page display. This is the value that is used to calculate all relative times throughout the application.
- The "Get Info" display now displays the "Mux Channel #" field
- The "Get Info" display now displays the equation type name and also the equation
- The HK Graph's now have a much more useful initial size

Bug fixes

- In the DAC Scan Viewer, when a scan is selected that now has scan data, the icon indicator will now be shown in the scan type drop-down list
- Fixed a memory leak - the viewer's we're not properly destroying their TelemetryFile instance
- The Marker Viewer now initially loads significantly faster for large amounts of markers

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4.2.3

Revision: 2218

Release Date: 2015-06-15

Bug fixes

- Fixed the DAC Scan viewer not being properly reset between TIDs
- Added back in the accidental removal of the more descriptive DAC Scan trace labels

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4.2.2

Revision: 2189

Release Date: 2015-06-04

Bug fixes

- Fixed the "Conversion calculator" not converting sci or eng values to the correct raw value when there should be an exact conversion. This was a result of comparing two doubles for equality, and was fixed by doing a fuzzy comparison.

4.2.1

Revision: 2181

Release Date: 2015-06-03

Bug fixes

- Fixed the crashes when plots had no data. The cause was the formatting of very large axis values.
- Fixed the graph marker list rows not updating their tooltips properly

---

4.2.0

Revision: 2178

Release Date: 2015-06-02

New Features

- **Housekeeping Graphing**
  - Added in the ability to display a plot's data points with a circular indicator. This can be accessed by right clicking on a graph and selecting "Show data points"
  - Graph cursor position in lower left corner now always has 4 decimal points
  - You can now plot data of any size, including the 100Hz data, and even the 1000Hz RSIM Bus1 current
  - Added in the ability to display both the message log and markers on a graph. This can be access by right clicking on a graph and selecting "Messages and Markers".
    - You can find the closest message or marker on the graph by either middle clicking or shift clicking on the graph

    - You can select a range of messages or markers to highlight a portion of the graph
- **Other**
    - The Sequence Viewer now fully supports loading a sequence from a file (given it's in the correct format). This can currently be accessed by going to the "File" menu, and then "Open Sequence".
    - The Sequence Viewer now prompts for a sequence ID when saving a sequence to a file
    - Added in a "Converter Calculator" to Hk Item's "Get Info" menu. This allows you to easily convert between raw, eng, and sci values.
    - Changed the MOMA msg log viewer to use "Menlo", a monospace font, by default to help with viewing hex values and tables. "Menlo" is similar to Deja Vu Sans Mono and is shipped with all Macs
    - Minor visual modifications to the Raw Packet viewer
    - Added in a relative time column to the Marker Viewer so that it can be correlated to the other data

Bug fixes

- Added in proper handling of the pre-boot RSIM packets, i.e. now it never uses the pre-boot RSIM packet's timestamp as t0 since that timestamp can be very incorrect, causing all other timestamps to be wacky.
- Fixed bug where a scan's total ion count was not being calculated correctly when it was larger than 65535 per 100 bins (including summed scan data)
- Fixed the seconds counter that is displayed in the toolbar so that it displays the correct seconds even if the packet's timestamp is before the time sync's tick counts.
- Made the Marker Viewer's pause functionality more sane
- Fixed a bug where raw values were not being displayed correctly in the Hk Viewer if they were greater than a signed int's max value
- Fixed the MAIF decoders so that they use the MAIF 1-sec timestamp and they now also account for the ADC sample rate
- "Copy Raw/Eng/Sci" functionality now correctly converts time to relative seconds
- Fixed a bug where using either "Make Hk" or "Quick Graph" was wiping out any loaded patch files
- Fixed the RSIM current decoders so that they properly (or as close as possible) calculate the first sample's timestamp

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4.1.1

Revision: 2021

Release Date: 2015-04-02

- Added in handling of the pre-boot RSIM packet
- Fixed bug with sequence viewer sometimes displaying the packet #s in the packet count column

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4.1.0

Revision: 2021

Release Date: 2015-03-31

- Added in the ability to view the spectrum using RF Amp Monitor and RF Amp DAC
- Added in the ability to select multiple scans to view their summed spectrum
- Added in exporting capability for the selected scans

- You can now view a scan's related DAC Scan by right clicking on the scan and also display the scan's indicator on the DAC Scan plot
- I added in a slider to the Mass Scan Viewer in order to quickly scroll through the scans. It's important to note that this purposely does not update when selecting a scan in the list.
- Added in the option to "Verify before saving" a mass cal
- Removed "Journal" functionality in Mass Scan Viewer because it should no longer be needed
- More minor improvements and bug fixes to the scan info display
- Other minor bug fixes
- Tweaks to how the msg log is highlighted when viewing a scan's related msg log

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4.0.2

Revision: 1931

Release Date: 2015-03-12

- The related portion of the message log is now highlighted
- Added in the RF/Aux start and end values
- Fixed the rod bias DAC not being properly extracted and displayed
- Fixed the pause register values not being properly extracted
- Improved the accuracy of the "Counter per second" value
- Changed the DDS Stats values to be the "science" conversion
- The Scan Info scroll bar now stays at its previous position
- Now properly indicates that a corresponding Scan Status packet was not found, and also properly clears the previous Scan Status state when a new TID is opened
- Other general improvements and more accurate information in the scan info display
- The mass cal is properly handled when a new TID is opened, particularly when the dialog is still open
- Added in usage of a status bar in the mass cal dialog
- Removed "Modify Viewer Params" from the menus

4.0.1

Revision: 1931

Release Date: 2015-03-11

- Fixed a bug that was causing some scans to not display properly. It wasn't interpreting the custom scan values (aux phase, ramp time, etc.) correctly which was resulting in an exception.

4.0.0

Revision: 1929

Release Date: 2015-03-10

- The auto switching of TIDs when a new TID is created will only work with momagse v3.8.3 and up. Communication with the GSE app is now accomplished using a local socket instead of shared memory. This will hopefully fix the issue where sometimes the data viewer doesn’t change when a new TID is

created.
- Improved the Mass calibration functionality and made it easier to use
- I changed the config file format, so this change will break backwards compatibility with the mass cal files we currently have, which is like 2 I think
- Mass Cal's will be copied from the global directory (momagse/mcals) if none exist. Otherwise, the most recent mass cal file will be automatically loaded.
- Saving a mass cal automatically timestamps it, so you never have to worry about overwriting an old mass cal
- The default masses are now configurable in a file called default-masses.amu which can also be found in momagse/mcal.
- This was really the most important change out of all the changes, so please provide as much feedback on this as possible.
- The Science Data Cache now uses the 0x86 Science Packet ACK ID. This fixes the delay of the Mass Scan Viewer when displaying Science packets
- Added in decode type 210 for the MAIF 1-min packet
- Added in decode type 226 for the RF Frequency
- Added in decode type 203 which can be used to extract the RF/AUX values from the sum and combined packet
- Added in a display of all Scans to the mass scan viewer. This allows you to also view things related to the scan, along with display the currently selected scan on the other custom viewers.
- You can now view a scan's related message logs by right clicking on the scan
- Changed the mass scan viewer to display which mass cal file is loaded.
- Added in an equation type to convert the RF Step and AUX Step sizes
- You can now resize the HK Viewer's font size using cmd- +,-,0
- You can now view HK value's meta data info in the HK Viewer by right clicking
- When a HK View's value is being displayed as raw, the tooltip will now display an integer conversion. I figured we might as well make it used for something instead of displaying "raw"
- Added in the ability to save a sequence to a file.
- Added in ability to close the current window with cmd-w
- TextEdit's search dialogs can now be triggered with ctrl-f and "wrap" is also checked by default
- Reverted Message Log viewer font and font size to the default one
- The splash page now correctly displays if the patch file is not actually found
- Filtered messages in the Message log viewer now correctly display the relative timestamp
- Quick Graph's can now be properly saved and restored, including ones with multiple HKIDs
- Fixed the Marker Viewer slowing down the application when more than ~5000 markers exist
- Minor tweaks to the Config699Dialog
- Moved change log into the 699wiki and added a link to the About Dialog
- The custom viewers can now be properly saved and restored
- Changed the loading of new tm files. It's now smoother and properly displays which step is actually occurring.
- The hex bytes of the selecting sequence's command are now highlighted
- Better usage of the status bar to indicate any events
- Added a slider to the raw packet viewer
- Almost every "text area" now has the search capability which is really useful if you're interested in a specific value or perhaps a sequence of bytes.
- Better time resolution since we have 4 decimals
- Changed indicator of a scan in the DAC Scan viewer to a plot icon
- Everything save's their state much better now between sessions
- Added mass cal file to the splash page

3.3.0

Revision: 1792

Release Date: 2015-02-06

- When an error occurs while opening a viewer, an informative dialog is displayed instead of silently failing
- Added in ability to copy raw values to clipboard
- Added in ability to export DAC scan data to a file
- Added in ability to toggle auto scaling of individual HK graphs (including quick graphs) by right clicking on the graph
- ChromViewer now has a default file name when exporting data
- ChromViewer fat lines are fixed
- ChromViewer has better performance
- ChromViewer now always updates but has same auto scaling toggling as the HK graphs by right clicking on graph
- New spiffy icons

3.2.2

Revision: 1776

Release Date: 2015-02-03

- Added in ability to convert message log timestamps to relative time. The relative time is the same relative time that all other viewers use.

3.2.1

Revision: 1770

Release Date: 2015-02-02

- Fixed the sequence viewer not correctly converting the RF_AMP DAC value
- Minor improvements to the Config699Dialog
- Improved "Make Hk Viewer" and "Quick Graph" initial size, position, and resizing of columns
- Updated versioning to use ... Versioning now follows the conventions detailed here
- Minor naming changes to the menus

3.2.0

Revision: 1736

Release Date: 2015-01-26

- Sequence Viewer is now fully functioning. It has a config file that determines how the various values are extracted and interpreted
- The open file dialog now uses the native dialog. The native dialog has a few annoying quirks, but it does allow searching which is a very useful feature, particularly to filter TIDs based upon their name.
- Slight visual changes to the splash page

3.1.0

Revision: 1684

Release Date: 2015-01-07

- The TICs is the default trace in the Chromatogram Viewer, and the range trace is off by default but can be toggled on
- Added in the ability to export the TICs trace of the Chromatogram Viewer
- Added in the ability to update the Chromatogram Viewer during realtime data
- Chromatogram Viewer now auto scales and refreshes the plot when a new Telemetry File is opened
- Chromatogram Viewer now has a total scan count indicator
- Reworked the interface of the ChromatogramViewer so it's a little more user friendly
- Fixed the bug where the Mass Scan viewer wouldn't show the first scan if only 1 existed
- DAC Scan viewer now supports science conversions, and is fully configurable from a config file located at momagse/viewerConfigs/dacscanviewer.json. New scan values can be added this way, and labels, default conversions, etc, can be configured from this file
- DAC Scan viewer now displays the first DAC trace (if one exists) when a new Telemetry File is opened
- Fixed crashes in both the Chromatogram and DAC Scan viewer
- Science Viewer defaults to line mode
- Moved the y axis label slightly off the edge because it made it hard to read
- Fixed the RSIM bus 1 current sample decoding. Previously it was not calculating the timestamp for each sample correctly.
- SequenceViewer exists but is not fully functioning

3.0.0

Revision: 1629

Release Date: 2014-12-09

- Telemetry files now load *significantly* faster. Files that used to take 5 or more minutes now load in under 30 seconds.
- The splash page now displays some useful meta data about the currently open telemetry file
- A progress dialog pops up when opening a new telemetry file
- The database patches are now correctly loaded when required by the telemetry file, as indicated by the telemetry file extensions
- The Housekeeping Viewers now contain a "latest" checkbox that will make the viewer display the latest value on each update interval. This is now controllable on a per viewer basis and is automatically unchecked when viewing previous data.
- The Housekeeping Viewers now contain a packet index indicator. Note that the total is the total number of all packet types, but the index will only stay on the packet types that are relevant for that specific viewer.
- No more random whitespace in the Message Log viewer! You may still see some messages continued on a new line with no timestamp, but this has to do with the fact that some messages are split up between packets.
- The Raw Packet Viewer now uses a monospace font! A bunch of other changes to it. Also now contains the ability to seek to any index.
- All viewers now probably reset their state when a new telemetry file is opened and also provide better indicators that no relevant data exists.
- Fixed some corner case crashes
- Mass Scan Viewer now contains a "latest" capability!