DraMS

DraMS specific pages from the archive wiki.

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DraMS Thumbnail

Download

Updated on 2021-10-25:

momadataviewZ.app.zip

Chromatogram Instructions

1. Load a MOMA GCMS run
2. Under "Data Viewers" menu, select "Chromatogram Viewer"
3. From Chromatogram viewer, click "Thumbnail" checkbox (calculation takes time, so there will be a period of unresponsiveness)
4. Create a ZIC or cZIC trace with UI at bottom of window

The 'Z' denotes the thumbnail data, which keeps only the detected peaks that fit within the data volume estimate. If a SIC or cSIC is duplicated with the '+' and the duplicate is changed to a ZIC or cZIC it will stay linked to the original SIC or cSIC when changing m/z. **NOTE:** the linking is only one way ZIC --> SIC, not SIC --> ZIC

Calculation Notes:

- Each summed histogram from the GCMS has a stripped down thumbnail counterpart, which is at most 74 detected peaks
- If a detected peak has a FWHM < 1.5 or > 5.5 bins, it is rejected

Mass Scan Viewer Instructions

1. Under "Data Viewers" menu, select "Mass Scan Viewer"
2. Select a mass scan in the list on the left side of window
3. Click the "Math" popup menu, and select the "Fit All" checkbox
   - This plots the fitted peaks over the raw data
4. To list the details of all the peaks, click "Peaks" popup menu and select the "Show List" checkbox
   - The cutoff can be altered from the default value of 74 peaks with the "Peak Number Cutoff" field
   - The red horizontal line indicates the y-axis value that corresponds to the cutoff

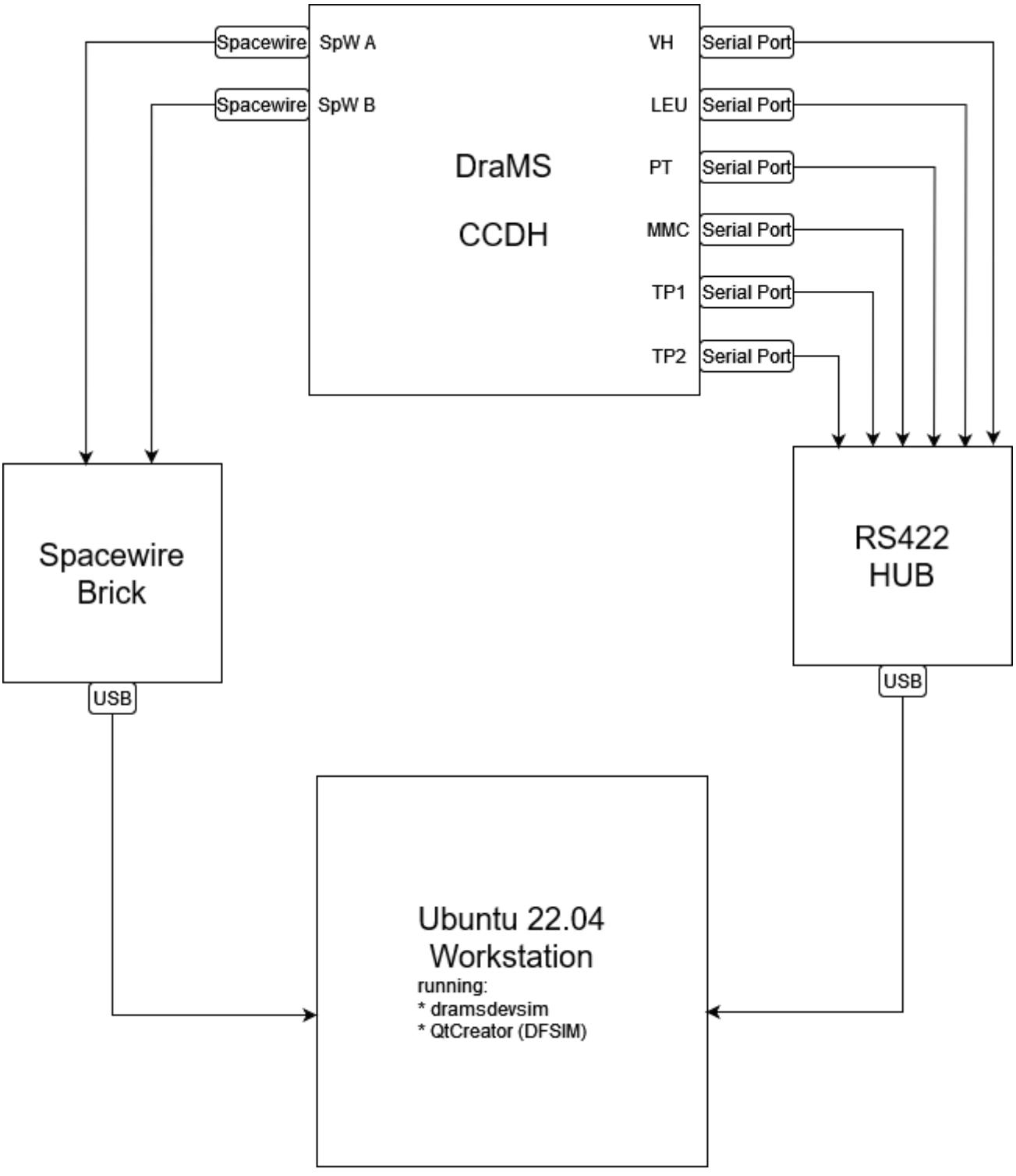
Release History

2021-09-27: Initial release of modified momadataview app for assessing thumbnail product

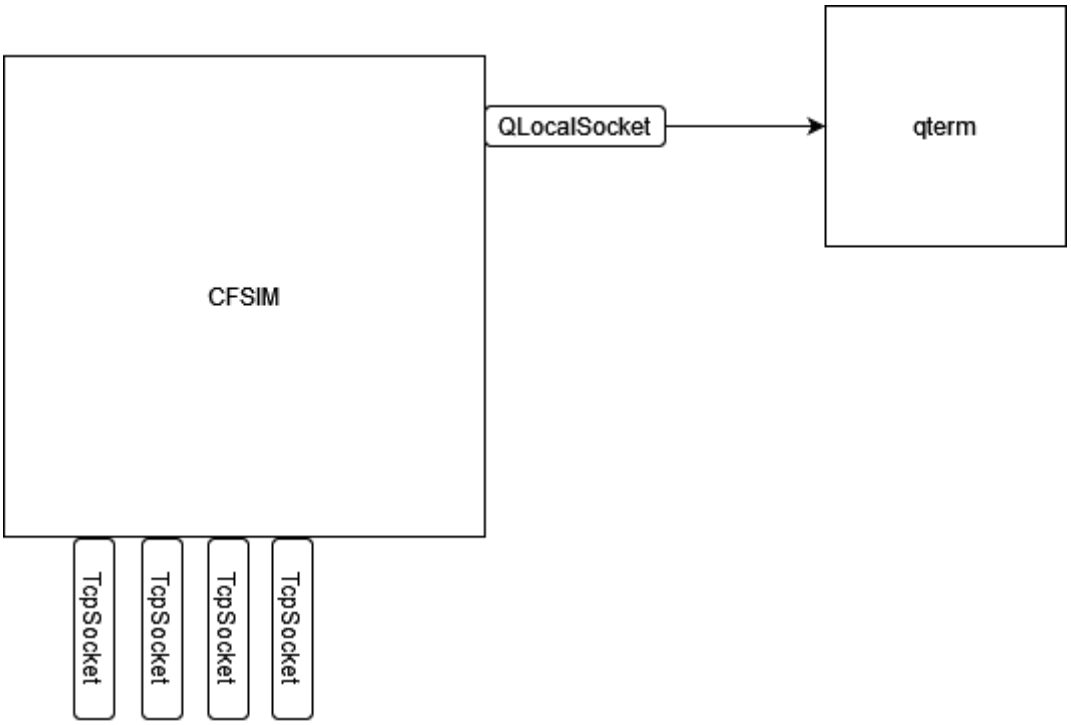
2021-10-15: [316f106] Feature refinement before wider release (includes dynamic peak cutoff line)

2021-10-25: [bc44147] Update mass scan viewer to reflect thumbnail data

DraMS Testing (CCDH Layout)



DraMS Testing (DFSIM Layout)



GSE Setup

Instructions for setting up the GSE computers in the DraMS lab (B37/S118)

GSE Setup

DraMS Lab Getting Started

This document shows you how to get started using the computer in the NASA GSFC Building 37, Room S118 lab.

CLick here for Getting Started Guide

DraMS New User Setup

XINA Setup

XINA (XINA Is Not an Acronym) is a website that provices data visualizations for DraMS telemetry.

1. Open a NAMS request for "GSFC DraMS XINA" at https://idmax.nasa.gov/nams
2. Once access has been granted, visit XINA at https://drams.xina.io

SED GitLab Setup

SED Gitlab hosts several projects needed for DraMS.

1. Open a NAMS request for "GSFC SED GitLab (Code 600)" at https://idmax.nasa.gov/nams
2. Once access has been granted, ask a Maintainer for access to

- https://sed-gitlab.gsfc.nasa.gov/drams (operators, developers)
- https://sed-gitlab.gsfc.nasa.gov/699 (developers)

3. Visit SED GitLab at https://sed-gitlab.gsfc.nasa.gov

DRAMSIOC Setup

DRAMSIOC is a general use VM that has been set up for use by the DraMS GSW team. We will be using DRAMSIOC to host the Subversion (SVN) repository containing the telemetry files captured in the lab.

DRAMSIOC can only be reached by setting up an SSH tunnel. This requires your NASA badge and a computer with a badge reader.

1. From outside the lab, set up an SSH tunnel to DRAMSIOC. VM SSH Tunnel Setup
2. Create an RSA public/private key
   TODO
3. Copy your public key to DRAMSIOC
   TODO
4. Create an SSH config file in C:/Users/dramsops/.ssh/ named "config". Replace YOUR_USERNAME below with your NASA username (e.g., mrburkh1)

   ```
   Host dramsioc
       Hostname dramsioc.gsfc.nasa.gov
       PubKeyAuthentication yes
       User YOUR_USERNAME
       LocalForward 6994 localhost:3690
       TCPKeepAlive yes
   ```

5. Open the SSH: In a Command Prompt type `ssh dramsioc`
6. Checkout (or Update) the "dramsdata" SVN repository. Using TortoiseSVN, right click on a location in the Windows Explorer and select "SVN Checkout". For the "URL of repository" put "svn://localhost:6994/dramsdata".

Secure Lab Enclave (SLE) Setup

The Secure Lab Enclave (SLE) is a private network accessible from the lab (B37/S118 for DraMS). GSE computers in the lab can be accessed remotely through the SLE.

1. Log into the SLE website with your NASA credentials: https://sleaccess.sci.gsfc.nasa.gov/
2. On Windows, open Remote Desktop Connection and enter the IP for the GSE computer you want to access:

- GSE-1 - 10.171.37.130
- GSE-2 - 10.171.37.131
- GSE-3 - 10.171.37.132 (not currently accessible - it's located in the B11/E212 Electrical Lab)

Using SVN with Scripts

Scripts ready for flight will be committed to the Subversion (SVN) located on dramsioc.gsfc.nasa.gov, a virtual machine on the 600 Virtual Machine Environment (VME). There is another Wiki entry on this.

By convention, the scripts should have keywords enabled and use the keywords in the header. We use the keyword "$Id".

Using SVN commandline
Putting a script in SVN the first time: **svn add script.bas**
Adding Keywords to scripts: **svn propset svn:keywords Id script.bas**
Committing scripts: **svn commit -m "Description and reason for commit"**
Retreive scripts: **svn update**

DraMS Consumables

Post processing softare measures consumable items such as WRP run time, HCV cycles, etc. How each of the DraMS consummables is tracked.

WRP

WRP run-time

Run-time is calculated by measuring from the time the WRP speed exceeds 5400 RPM until it returns below 5400 RPM.

WRP Cycles

A cycle is an Start/Stop pair. A start is anytime the WRP RPM reaches at leat 5400 RPM. A stop is each time the WRP RPM crosses below 5400 RPM.

HCV

HCV Cycles

One cycle of the hCV include an HCV open and an HCV close. An HCV open is defined by completing at least 50 positive raw hall counts by monitoring the mnemominc HCV1_HALL_POSITION_COUNTS. An HCV close is counted when the HCV changes by at leat 100 negative counts.

In the event that the HCV is left open when a TID ends, the algorithm should assume the HCV is in the state the previous TID left it.

Filaments

DraMS has two filaments, filament A and filament B.

On Time

Filament A and Filament B on time are determined by measuring the amount of time that HFB_FIL_ON_A or HFB_FIL_ON_B are 1.

Cycles

Filament A and Filament B cycles are determined by counting the number of times the filaments transition from off to on. A few notes about the algorithm:

- if the digital status packet indicates that the SEB is off, then the state of the filaments is considered to be off.
- a filament is considered to be on if if its on "on bit" is set to 1, and if the FIL_VMON is above 2.5V. Otherwise, it is assumed to be off.
- if the FIL_VMON is not being sampled, then only the "on bits" are used to determine if the filaments are on.

Detectors (aka EMs)

On Time

EM A and EM B on times are determined by summing the on times for all scans, and then looking for any time when the EMs were constantly on outside of scanning.

CTL sequences are examined to determine the on time for individual scans. In order to avoid double-counting scans, only sum packet scans are examined when in EI mode, and only science packet scans are examined when in LDI mode.

Additionally, outside of science scans, the total time that the EMs are on are summed. This is determined by summing the amount of time that EM A and EM B are below -1900 V.

Bradley Tse pointed out a flaw in this algorithm:

> There is a corner case where that may introduce its own problems. If the user stops the script after the Sequence was dumped but before scanning started (maybe because they noticed one of the parameters was incorrect), then that means the SebSequences will be duplicated.
>
> And so EM on time for all scans after that (until the next Sequence Dump) will have 2x the amount (or however many times the script was stopped before scans occurred)

Full Cycles and Soft Cycles

EM Cycles are determined through two passes of the data.

The first pass of EM Cycles are counted from the scan status packets. The cycles are calculated differently depending on the type of mode the test is in.

If in LDI mode [1], if HKID 222 (SCN_EM1) or HKID 223 (SCN_EM2) is below the -1900V threshold, then a full cycle is added to the corresponding detector's count. If in Dark Counts mode [2], no full cycles are added here, as typically a Dark Counts run contains only 1 full cycle total. If in EI mode [3], soft counts are added to EM1 if HKID17 (IS_EMON_A) is greater than 9, and the same procedure for EM2 and HKID18 (EMON_B).

The timestamps of the scan packets are used to determine gaps in time when scans are not occurring during the test. A second pass through but looking specifically in the gaps and the binned HK data is necessary to avoid missing any full or soft cycles.

Here, HKID47 (SEB: EM_1_DAC0_SET) and HKID48 (SEB: EM_2_DAC1_SET) are looked through individually. If the HK value is > -50V, the detector is OFF. If the HK value is < -1900 the detector is ON. Full cycles are added for each occurrence where a detector changes from the OFF state to the ON state within a gap.

[1] - LDI Mode is when Filaments are OFF ([HKIDs 17/18] < 9), and the RF (HKID 235) is ON (End Amplitude >= 500A)

[2] - Dark Counts Mode is when Filaments are OFF ([HKIDs 17/18] < 9), and the RF (HKID 235) is OFF (End Amplitude < 500A)

[3] - EI Mode is when a Filament is ON ([HKIDs 17 or 18] > 9)

EM Counts

EM 1 and EM 2 counts are calculated according to the logic below. If the most recent DAC value (HKIDs 222 and 223) is zero, then ions are not counted against the multiplier.

```
    # dummy variable to help when counting ions in science packet (packet 26) scans
    temp_counts = 0
    #
    for each packet in the tm.drams file:
        if the packet indicates that filament A or filament B is on (HKIDs 105 and 102):
            set the current scan type to EI
        else:
            set the current scan type to LDI
        #
        else if the packet type is a scan status packet (type 25):
          if we're in LDI mode:
              count temp_counts against whichever EM is on (or both, if they're both on)
              set temp_counts back to 0
        #
        else if the current mode is LDI mode and the current packet type is a science packet (type 26):
            temp_counts += packet.total_ion_count()
        #
        else if the current mode is EI mode and the current packet type is a sum packet (type 27):
            count packet.total_ion_count() against whichever EM is on (or both, if they're both on)
        #
        # special-case code for handling dark count scans:
        else if the current mode is LDI, and the current packet is a sum packet (type 27), and the packet's RF DAC v
alue (HKID 405) < 50:
            count packet.total_ion_count() against whichver EM is on (or both, if they're both on)
```

Laser

Laser Shots

Laser shots are determined by summing the number of pulses in the LEU.MAX_HKHS packets and LEU.HKHS packets. Each of these packets is generated for each laser shot. Whether we receive the MAX_HKHS packet or the HKHS packet depends on the LEU setting. But the packets are mutually exclusive. We should never get both packet types for the same laser shot.

GPS Valves

GPS Valve Cycles

GPS valves are the microvalves and GC valves in the manifolds. The high- conductance valve (HCV) and the multi-function valve (MFV) are documented in another entry.

Valve cycles are determined by examining the message log and counting the number of times a valve transitions from closed to opened. When counting valve cycles for a TID, the state of the valve cycles in the previous TID is accounted for. The exact regexes used (as of Feb 22) are:

```
VALVE_OPENED_REGEX = r'.*valve \d opened$'
VALVE_CLOSED_REGEX = r'.*valve \d closed$'
```

Multifunction Valves

MFV Cycles

Counts the number of times the Multifuntion Valve (MFV) has been opened. A cycle consists of an open and close. The valve transitions from open to closed when the MFV temperature transistion above 100C (TBC). It is considered closed when it transition from about 100C to below 100C (TBC)

MFV On Time

This is the total powered time of the MFV. This is determined by calculating the duration of time when the MFV temperature is above 100C (TBC).