



# Experiences with Moving Averages Monitoring in Real Time

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# Quality Control?

*Dr. James Westgard at 2011 AACCC meeting:*

Quality Control regulations are actually  
Quality Compliance regulations!

They specify the minimum frequency and don't  
reflect what may really be needed to ensure  
the system is in control.



# Problems with Standard QC

- Snapshot in time, usually performed post maintenance and calibration (when system is optimized)
- Expensive and time-consuming, multiple bottles of QC material and “hits” of reagent used
- Matrix Effects
- Best solution is continuous monitoring-but how?



# Moving Averages

- Also known as Running Average or Average of Normals
- Continuous process rather than snapshot
- Extremely cost effective
- Allows comparison of analyzers and modules on the same graph
- Roche/Data Innovations have moved MA from theoretical to reality!



# Background Material

**Assessment of “Average of Normals” Quality Control procedures and Guidelines for Implementation**, Cembrowski, Chandler, and Westgard, The American Journal of Clinical Pathology 81:4 pp.492-497 (1984)

**Evaluation of the Average of Patients Application: Application to Endocrine Assays**, Douville, Cembrowski, and Strauss. Clinica Chimica Acta 167 pp.173-185 (1987)

**Design and Assessment of Average of Normals (AON) Patient Data Algorithms to maximize run lengths for automatic Process Control**, Westgard, Smith, Mountain, and Boss. Clinical Chemistry 42:10 pp.1683-1688 (1996)



# So Where to start?

**Goal is to monitor process not the patients!**

*Dr. Mark Cervinski, Ph.D, DHMC*

## ➤ **Identify “Marker” Chemistries**

- Monitor all analytical systems: Chemistry, ISE and Immunoassay

## ➤ **Want a 360 View**

- Module to Module on same instrument
- All Modules, all instruments (Modular PPE vs. Cobas CCE)
- All Modules against an average of “all” line

## ➤ **Three Bears Theory**

- Detection flags need to be appropriate, not too hot or too cold



# Marker Chemistries

Mark Simmons, PhD suggestions of medium to high potential candidates based on Average of Normals, Westgard et. al.

- **Alkaline Phosphatase:** *chance of drift*
- **Aspartate aminotransferase (AST) and Bicarbonate (CO<sub>2</sub>):** *sample issues*
- **Calcium:** *chance of drift, problem chemistry for many users*
- **Blood Urea Nitrogen (BUN) Creatinine and Glucose:** *small sample size*
- **Sodium and Chloride:** *monitor possible reference electrode issues*
- **Free Thyroxine (FT<sub>4</sub>) and Thyroid Stimulating Hormone (TSH):** *for IA (E-mod)*



# Initial Chemistries selected

Based on daily total volume, minimum of 20 tests:

ALB, **ALKP**, ALT, AMY, **AST**, **BUN**, **CA**, CHOL, **CL**,  
**CO<sub>2</sub>**, CPK, **CRE**, DBIL, FE, **FT4**, GGT, **GLU**, HDL,  
HSCRP, K, LDH, LIP, MG, **NA**, PHOS, PSA, TBIL,  
TP, TROPT, **TSH**, TRIG, URIC, VIT B12



# Calculate Mean and SD

- Use MA protocol function to automatically calculate mean and SD
- 500 results used for most, low volume 100
- Must set truncation limits (filters), used +/- 4 SD of Reference Range
- Looking for “normal” population so excluded pediatric, hematology/oncology, dialysis, ICU and ED (trauma) patients
- Are you excluding Quality Control samples?

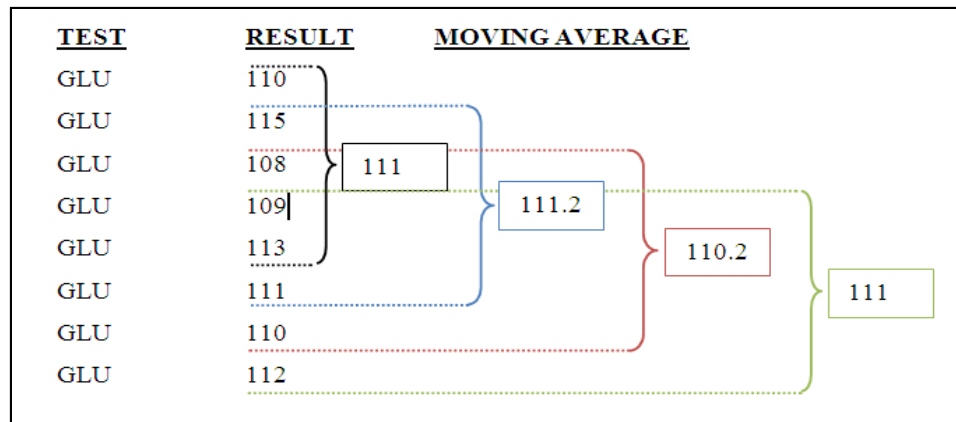


# Determining the “N”

- Need to determine “N” or number of results used in MA data point graph calculation
  - Used Cembrowski and Parvin articles
  - Calculated  $S_p$  (SD of population)/ $S_a$  (SD of analytic method) used Cembrowski Nomogram,  $S_a$  based on QC values
  
- More is better right, so why not just set it high (>50)?
  - Increasing N too high decreases sensitivity and increases number of affected samples prior to detection (may take too long to flag shift)

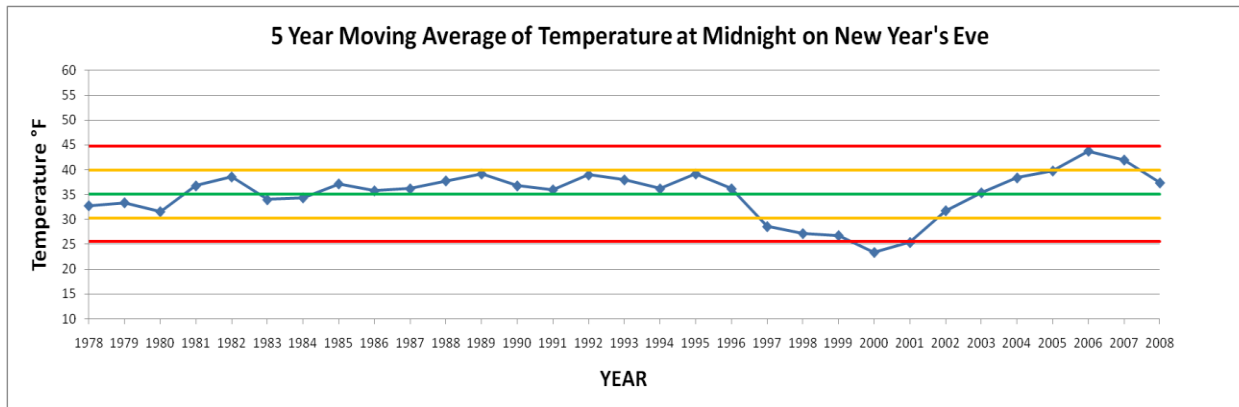
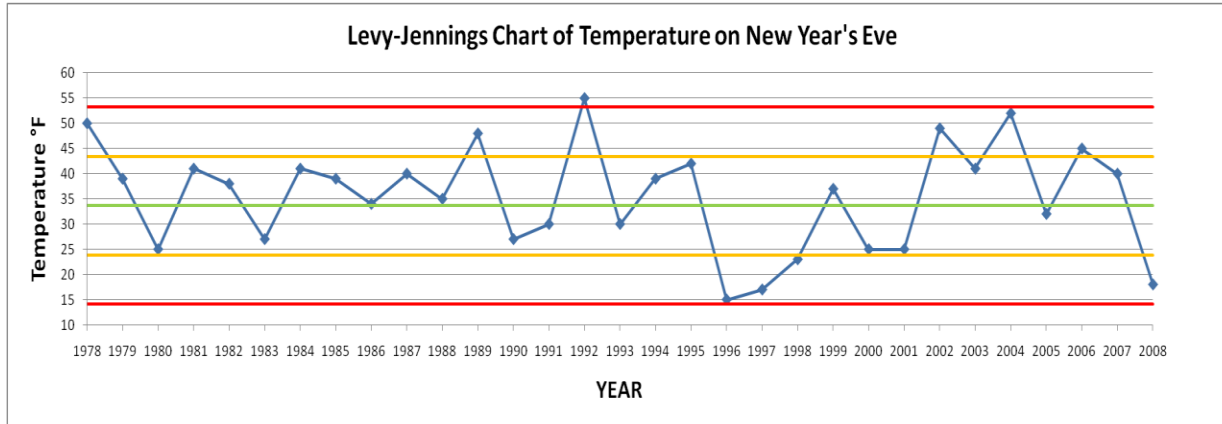
# Initial Trial: Simple Moving Average

- Each graph data point is comprised of multiple test results
- Can set exclusion criteria based on SD (ex. exclude 4SD above and below mean)
- Set warning and error thresholds (flags)
  - Straight SD limits, based on calculated average
  - SD Prime limits, using the Standard Error of the Mean (SEM) =  $SD/\sqrt{N}$ , where 2SD' represents 95% of confidence interval
  - Absolute Value limits, useful if using CLIA Total Allowable Error (TEa) limits
- Observations are weighted equally
- Allows the smoothing of data to account for scatter about the mean





# Simple Moving Average: Smoothing Effect

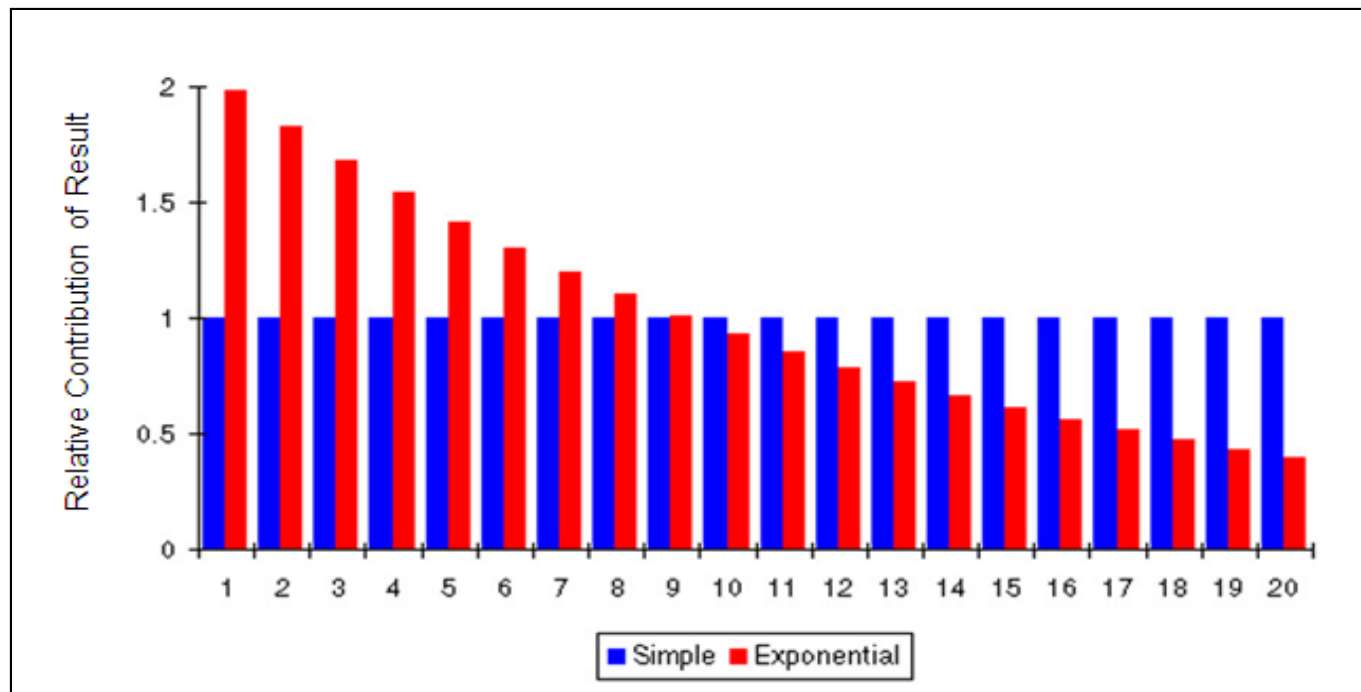


Source: Data Innovations Moving Averages participant's Guide, 2010



# Exponential (Weighted) Moving Average

- Also know the exponentially weighted moving average (EWMA)
- Exponential smoothing assigns exponentially decreasing weights over time to each data point.

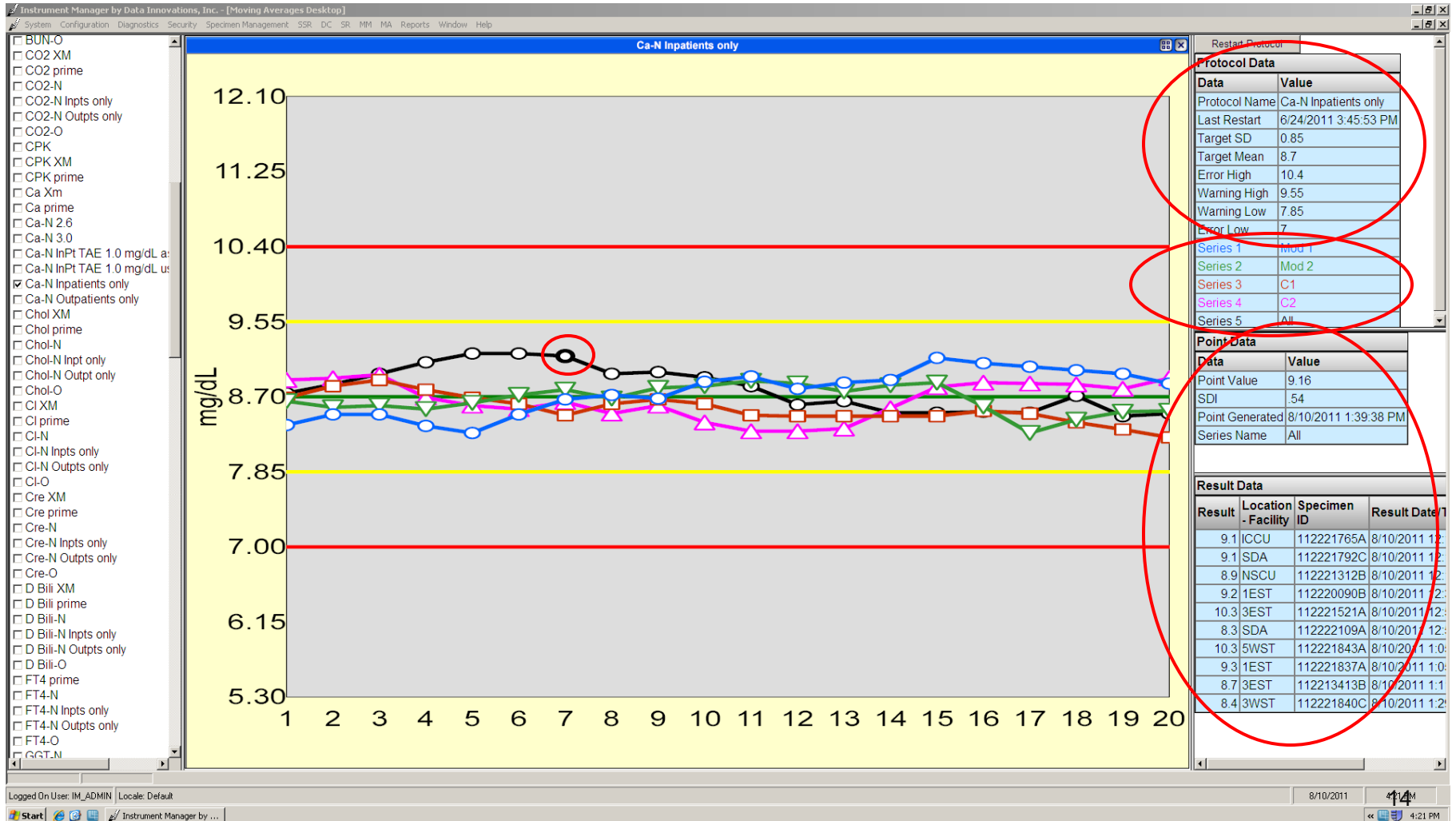




# Initial Findings

- Simple MA SD thresholds may be too broad and SD' may be too restrictive
- Exponential MA too sensitive to single fluctuations, need to refine methodology and revisit
- Some assays are not good candidates for MA because of volume and patient population (cardiac markers, uric, etc).
- Different Inpatient vs. Outpatient means causing issues with “All Patient” warning limits

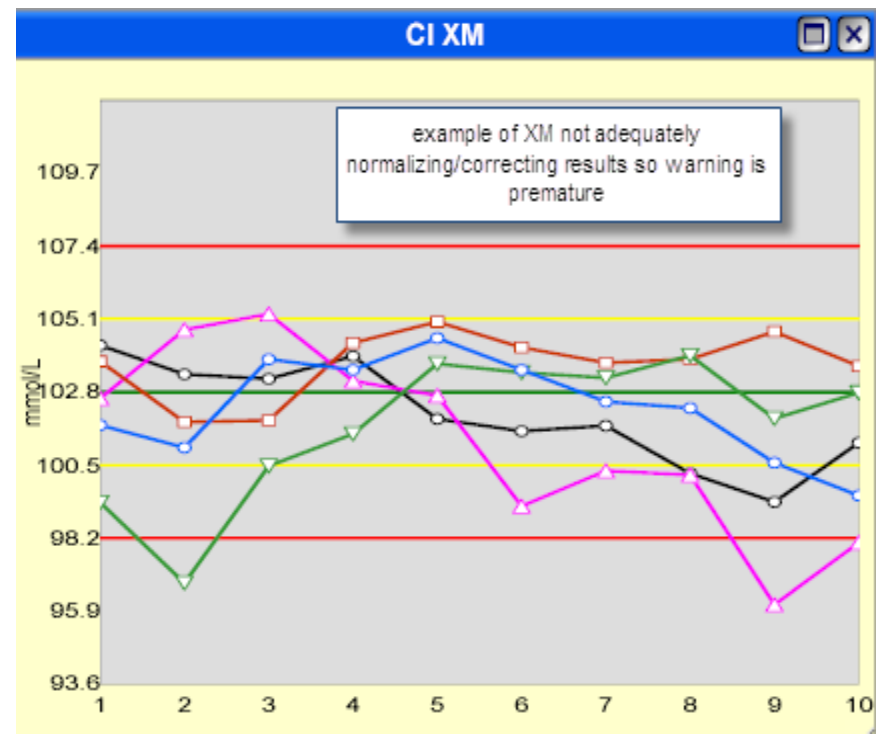
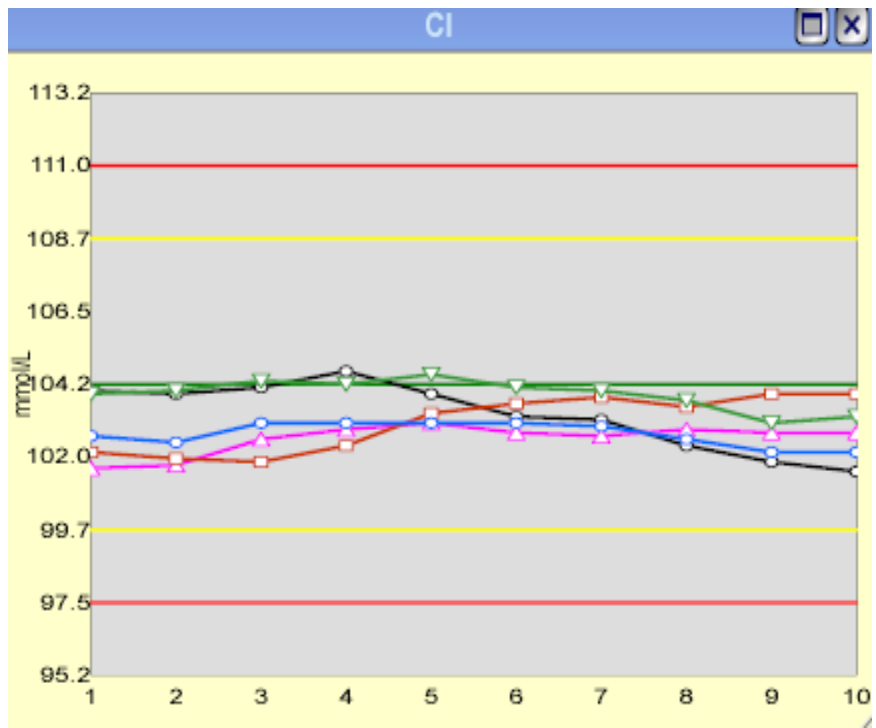
# MA Screen Basics





# SD vs. XM: Chloride

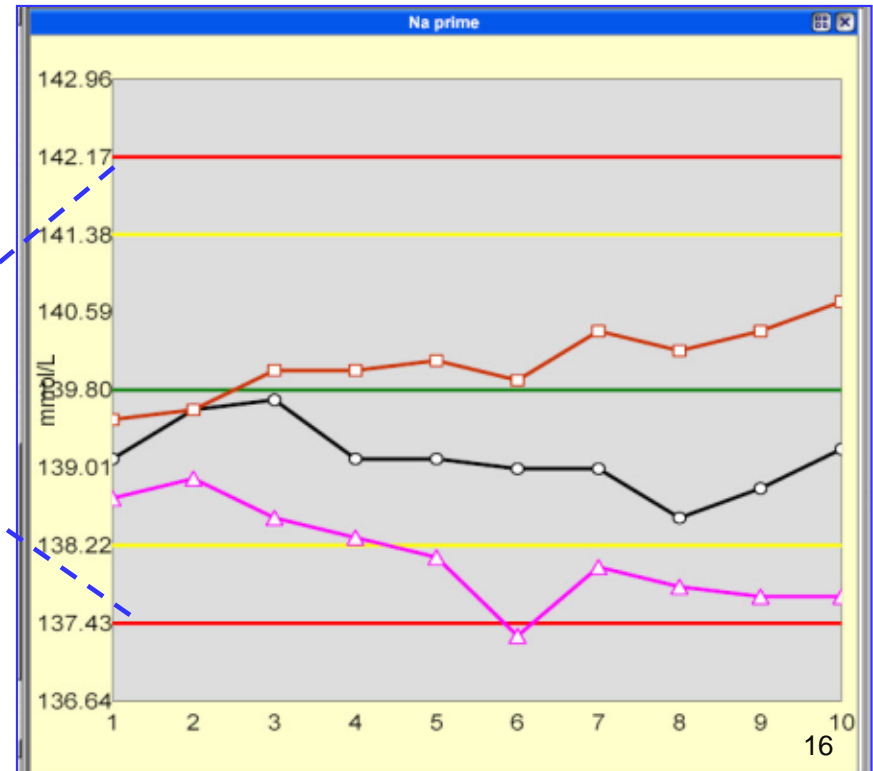
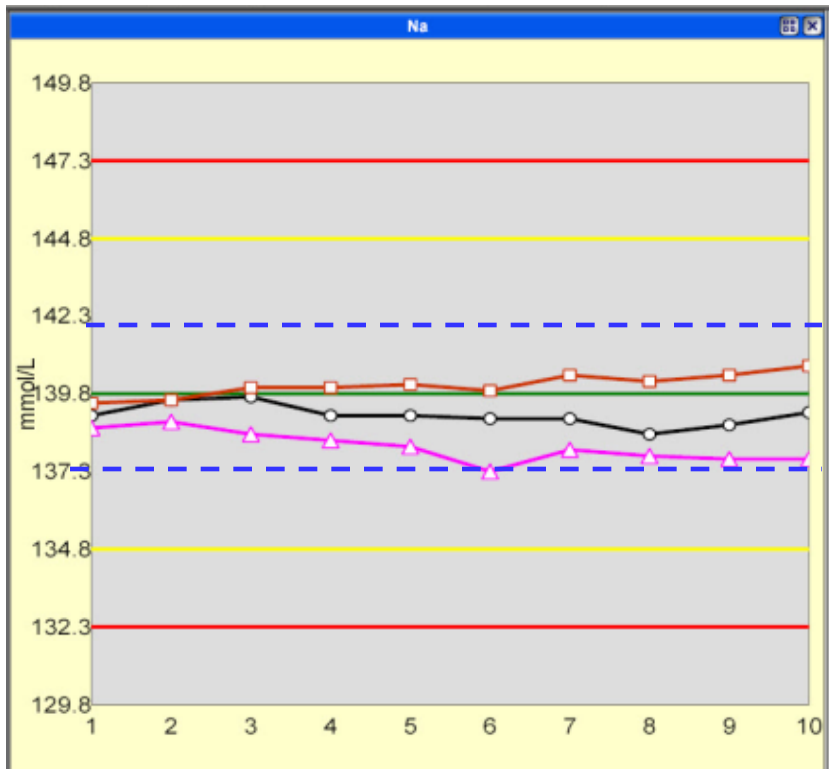
## Example of Running Average versus Weighted Average





# SD vs. SD Prime: Sodium

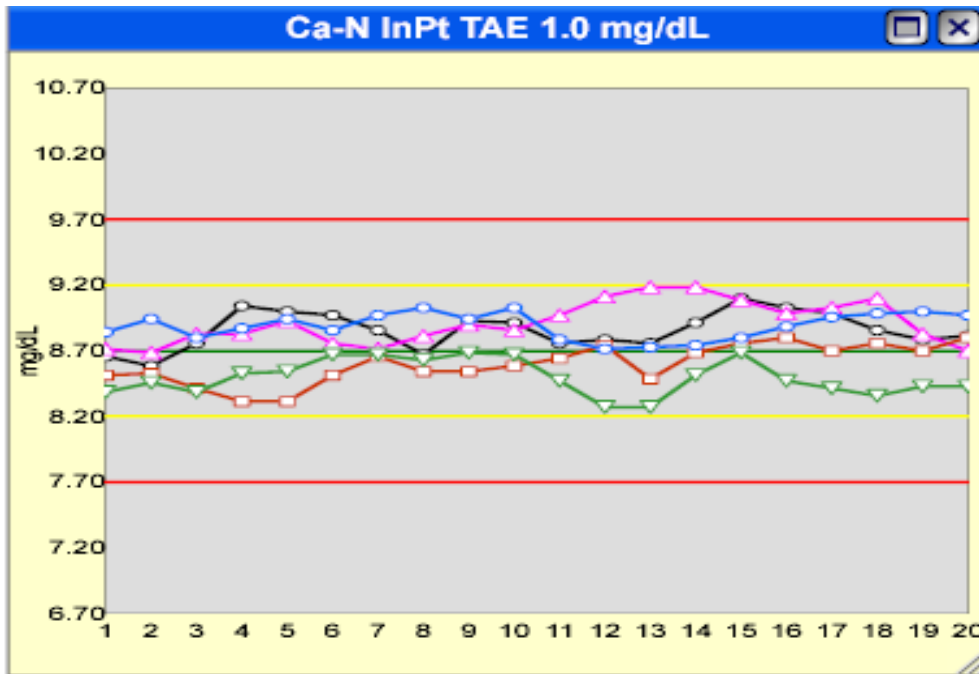
- Shift of +/- 3 mmol/L is this an error?
- Are filters set correctly?
- Are the SD warning and error limits too lenient?





# Using Absolute Values to Set Error Limits

- Can use SD or absolute value to set warning and error flags
- TEa for calcium is 1.0 so we didn't want to exceed this

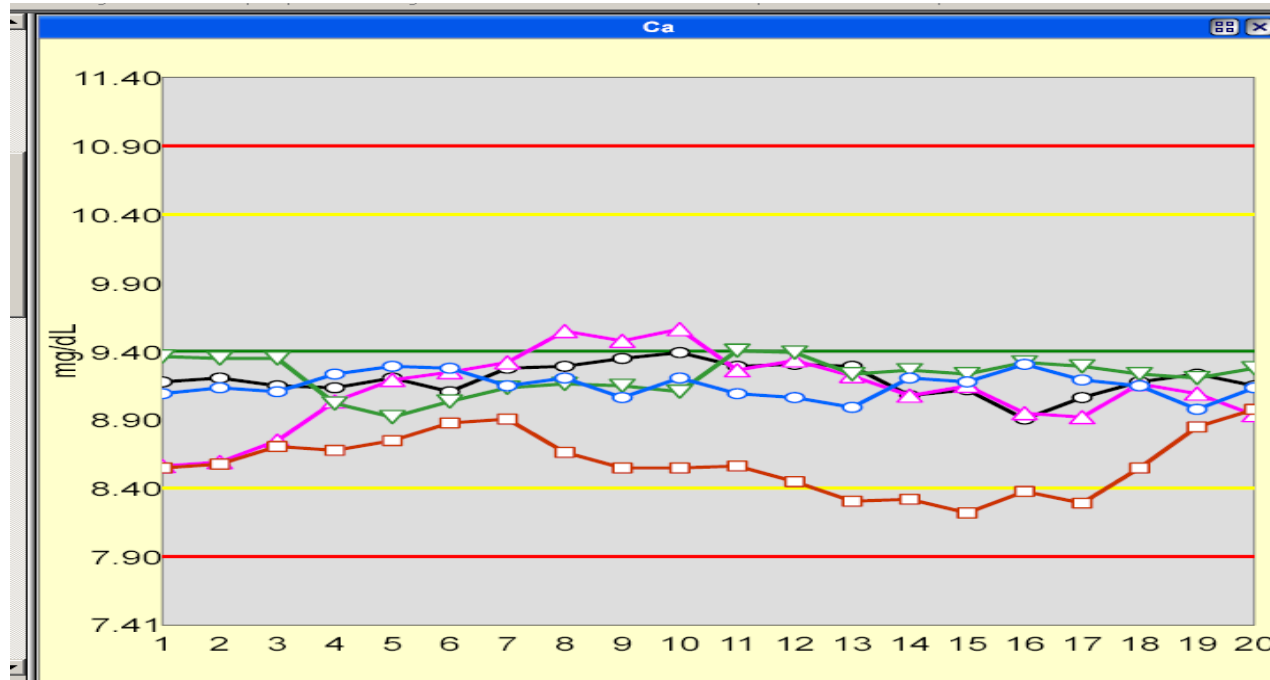


Warnings and Errors	
Error Low	
Threshold Value	2 (Standard Deviations Below mean)
Notifier Event	- None -
Start Holding for Verification	Do not hold tests
Mark out of service	No
Warning Low	
Threshold Value	1 (Standard Deviations Below mean)
Notifier Event	- None -
Start Holding for Verification	Do not hold tests
Mark out of service	No
Warning High	
Threshold Value	1 (Standard Deviations Above mean)
Notifier Event	- None -
Start Holding for Verification	Do not hold tests
Mark out of service	No
Error High	
Threshold Value	2 (Standard Deviations Above mean)
Notifier Event	- None -
Start Holding for Verification	Hold this test
Mark out of service	No
Error Low	
Threshold Value	7.7 (Absolute Value)
Notifier Event	- None -
Start Holding for Verification	Do not hold tests
Mark out of service	No
Warning Low	
Threshold Value	8.2 (Absolute Value)
Notifier Event	- None -
Start Holding for Verification	Do not hold tests
Mark out of service	No
Warning High	
Threshold Value	9.2 (Absolute Value)
Notifier Event	- None -
Start Holding for Verification	Do not hold tests
Mark out of service	No
Error High	
Threshold Value	9.7 (Absolute Value)
Notifier Event	- None -
Start Holding for Verification	Hold this test
Mark out of service	No



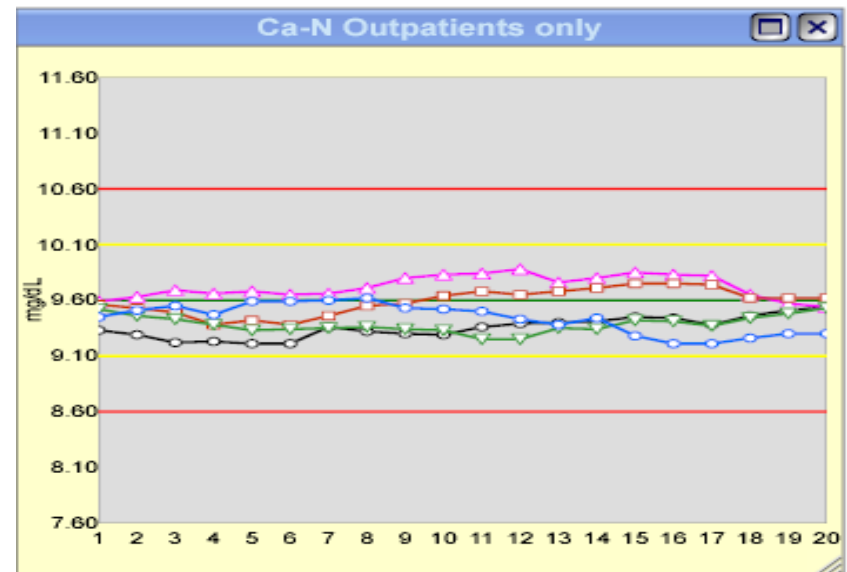
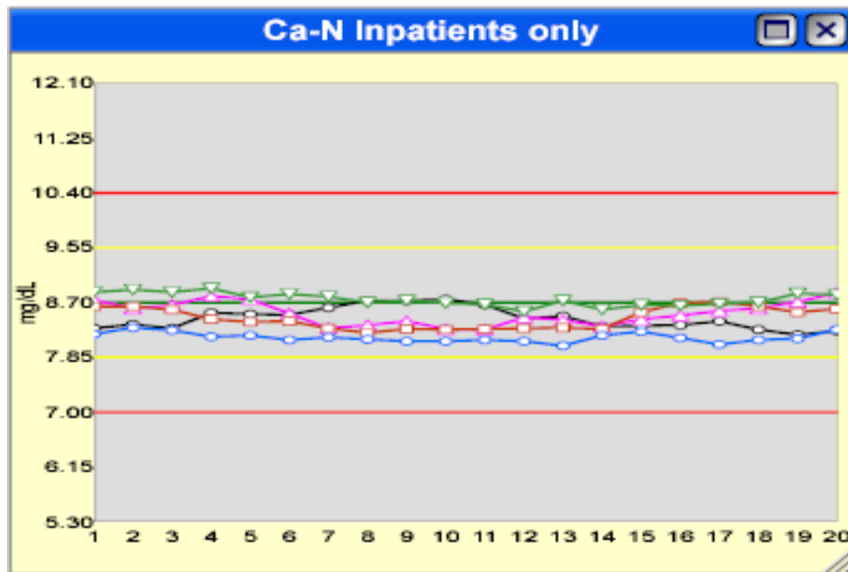
# Patient Population Effect?

Repeated daily pattern observed from 4-7am, already excluded ICU and HemOnc patients!



# Inpatient vs. Outpatient: Calcium

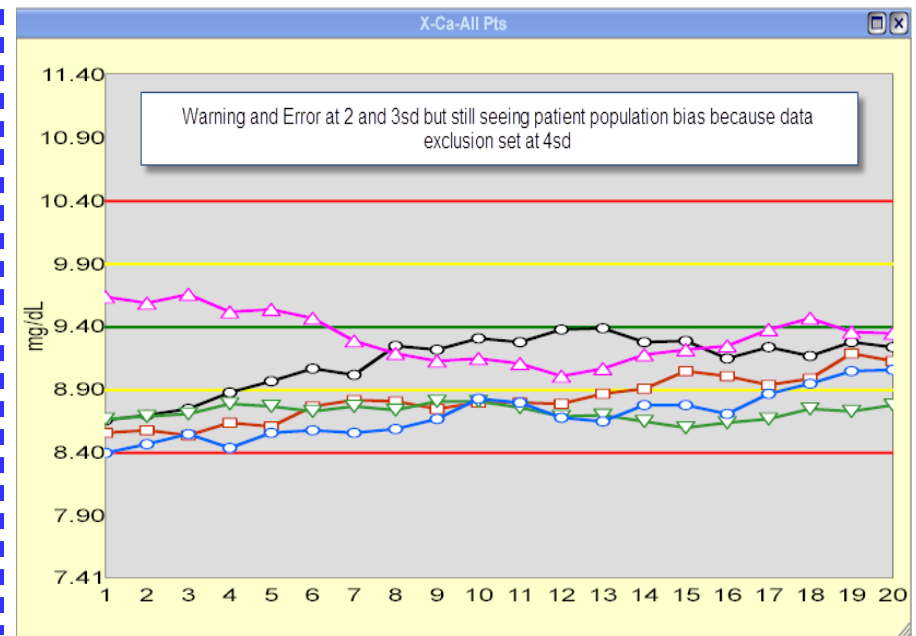
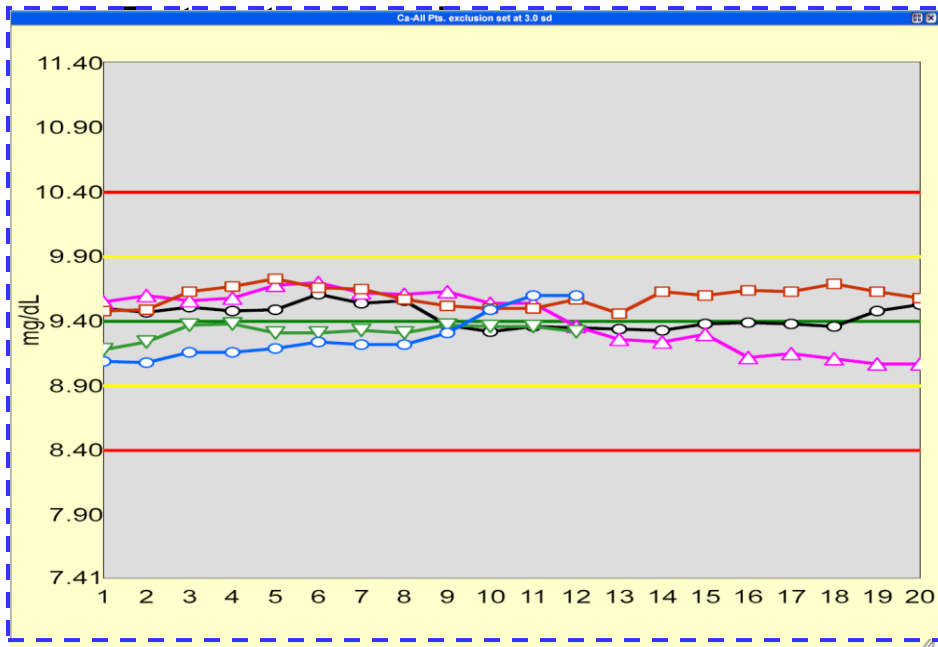
Certain chemistries (Alb, Ca, TP) with significantly different patient means, calcium inpatient 8.7 while outpatient 9.6





# Fine Tuning Protocols

- For most assays we changed the 2 SD warning and 3 SD error to 1 and 2 SD
- In this scenario 3 SD error limit exceeds TEa of 1.0 by 0.5
- For tests with different Inpatient vs. Outpatient (Alb, Ca, TP) means we changed the exclusion from 4 SD to 3 or 2.6 SD to normalize the “All





# Real Time Notification

**Using Notifier Function to set customized user defined event:**

- Status Screen
- Pop on designated PC work stations
- E-Mail
- Can set to hold flagged tests or all tests in SM Workspace for Tech review

# Status Screen Alerts-Passive Notification

Status Display

Data Innovations, LLC  
License #: IH-100001

Connection	Status	In Service	In	InQ	SendQ	Sent	Errors
Purge	On						0
Qmgr	On (2/2)						0
Quality Control	On						0
Specimen Routing	Off						0
Moving Averages	On	Yes	1059	0	0	0	1

Start Selected Connections   Stop Selected Connections   Det

Status Detail

Driver: Data Innovations Inc. Inter-IM Interface v8.00.0006

Configuration: Inter-IM for MA Calcs

Status: On @ 8/9/2011 1:44:53 PM

Device: TCP/IP:10001:Server

Last Message Sent:

Last Message Received: 8/9/2011 1:44:53 PM

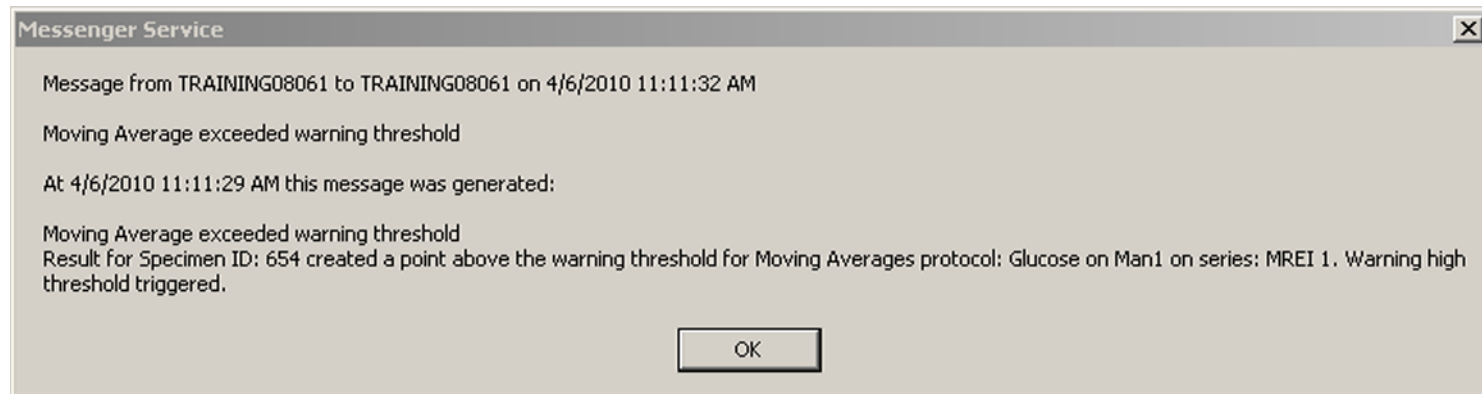
Last Date/Time	Qty	Error
8/9/2011 08:25:34	1	Result for Specimen ID: 112210211B created a point above the error threshold for Moving Averages protocol: TP-N Inpt Prime on series: C1. Error high threshold triggered.

Resend Messages   Clear SendQ   Clear Errors   Other   Mark Out of Service   Close



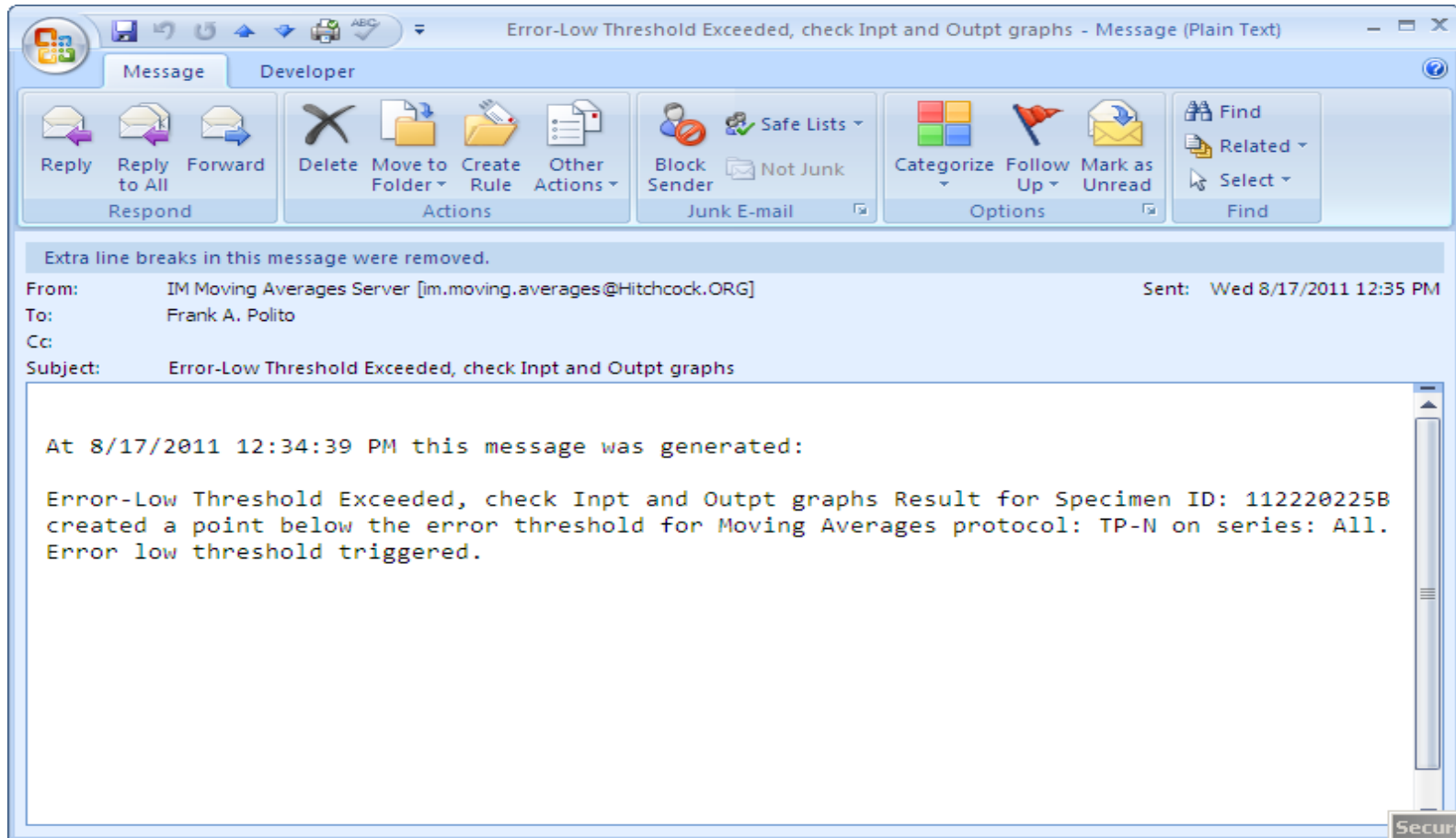
# Pop Up Notification-Active

Can have pop message on specific and multiple PCs





# E-Mail Notification-Active





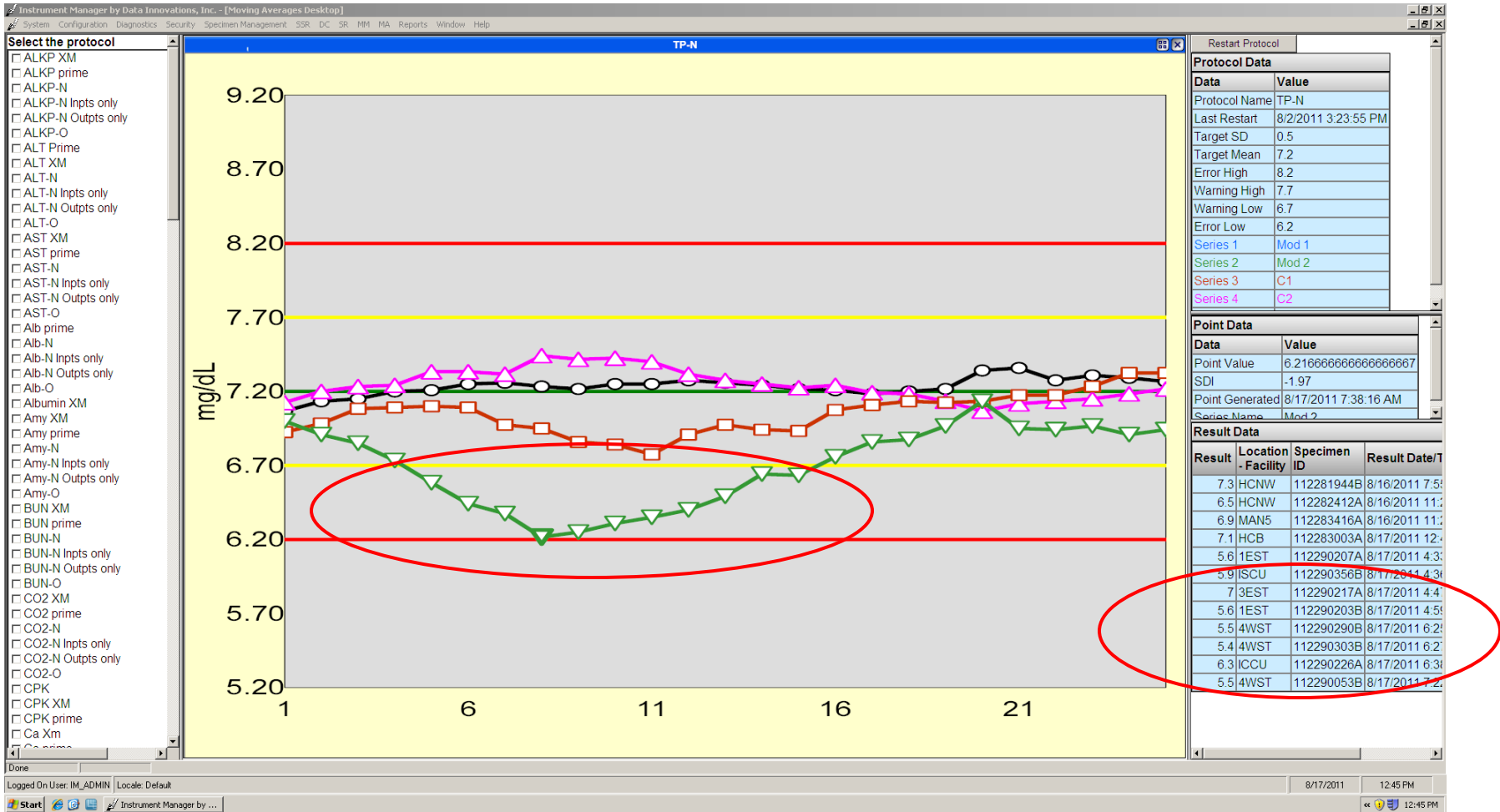
# Triggered Events

- **Can be set to resend at set intervals until events cleared**
- **Can be customized with instructions, prompts**
- **Protocols can be set to hold results if certain events triggered such as error versus warning (high or low) alerts**

System Configuration Diagnostics Security Specimen Management SSR DC SR MM MA Reports Window Help	
Title	Text
▶ Error Low check Inpt and Outpt graphs	Result for Specimen ID: 112391308A created a point below the error threshold for Moving Averages protocol: Na-All Pts on series: C1. Error low threshold triggered.
Error Low	Result for Specimen ID: 112391446A created a point below the error threshold for Moving Averages protocol: Na-Inpts only on series: All. Error low threshold triggered.
Error Low	Result for Specimen ID: 112391369A created a point below the error threshold for Moving Averages protocol: Na-Inpts only on series: All. Error low threshold triggered.
Error Low	Result for Specimen ID: 112391642A created a point below the error threshold for Moving Averages protocol: Na-Inpts only on series: All. Error low threshold triggered.
Error Low	Result for Specimen ID: 112400025A created a point below the error threshold for Moving Averages protocol: Na-Inpts only on series: All. Error low threshold triggered.



# E-Mail from Day Off





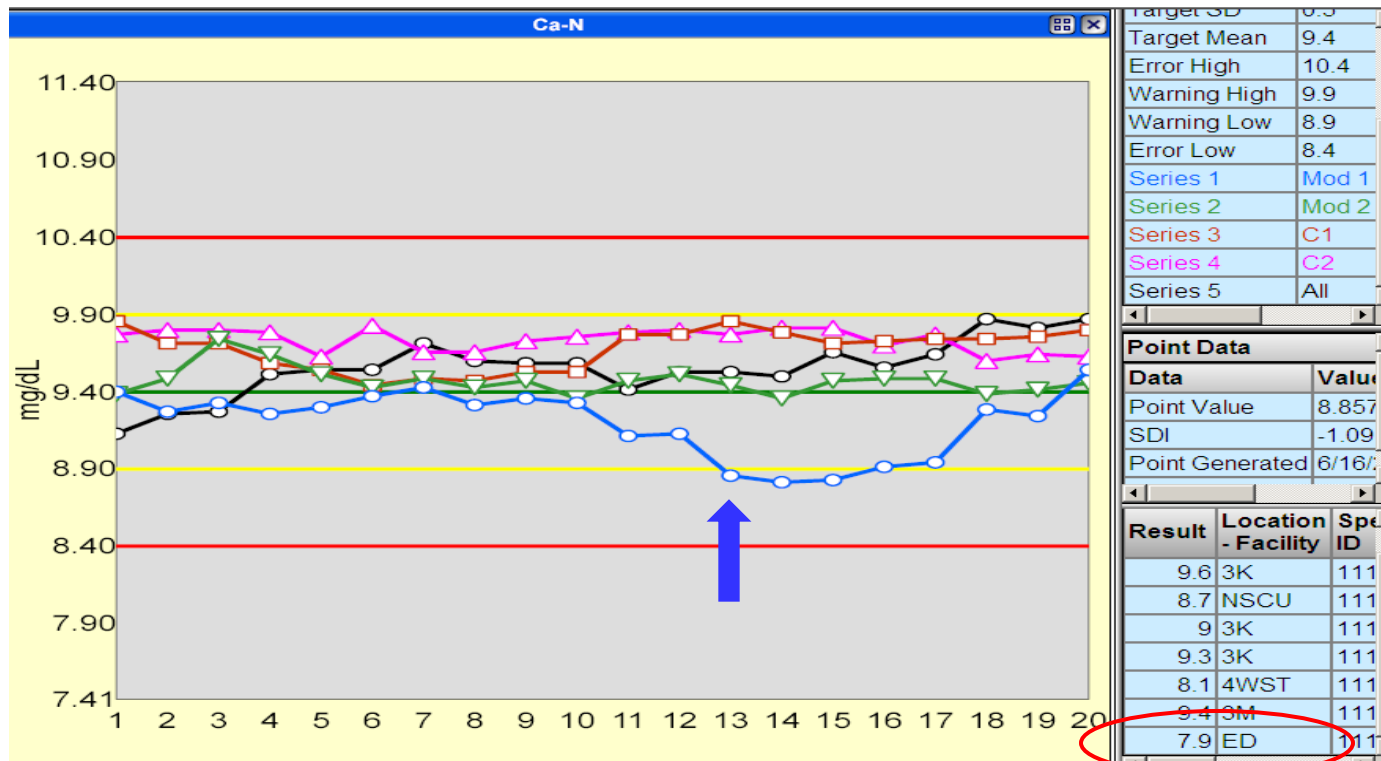
# Is it working?

- Use proactively post QC rounds daily
- All warning notifications are examined for trends and action taken
- Ability to look across modules and analyzers to troubleshoot
- Ability to look at total or All population vs. Inpatient and Outpatient
- Goal is to catch drift/changes so acting on warnings is crucial



# Continue to Fine Tune Protocols

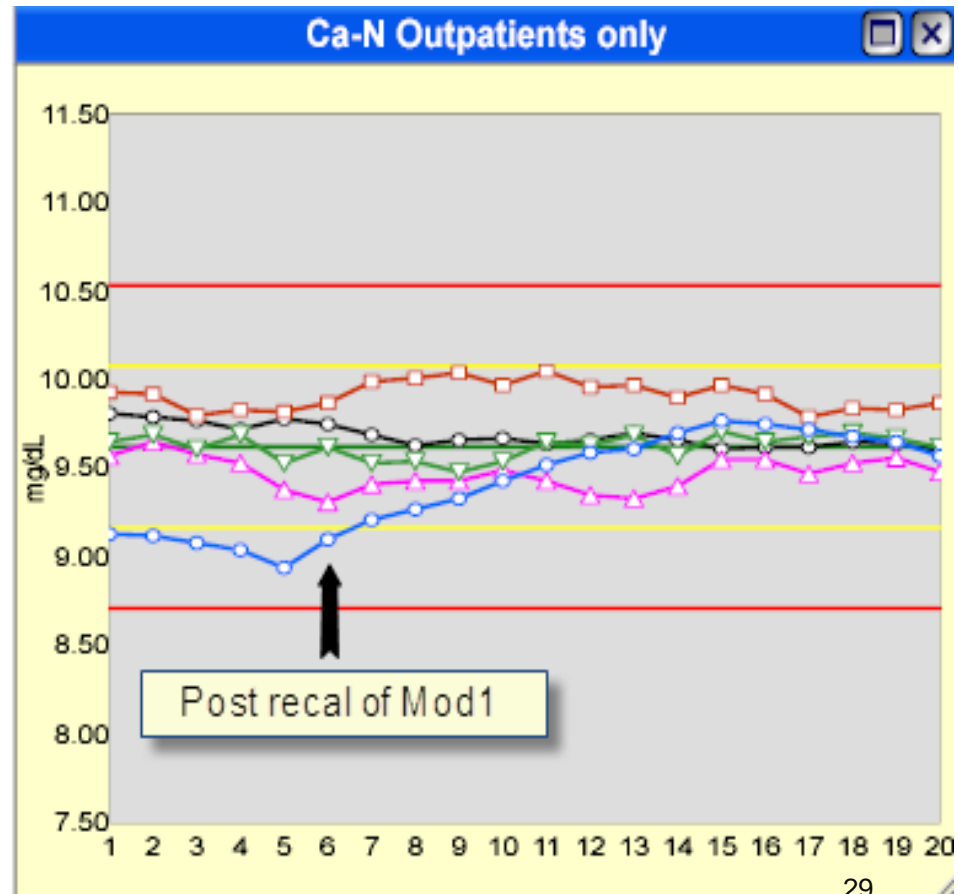
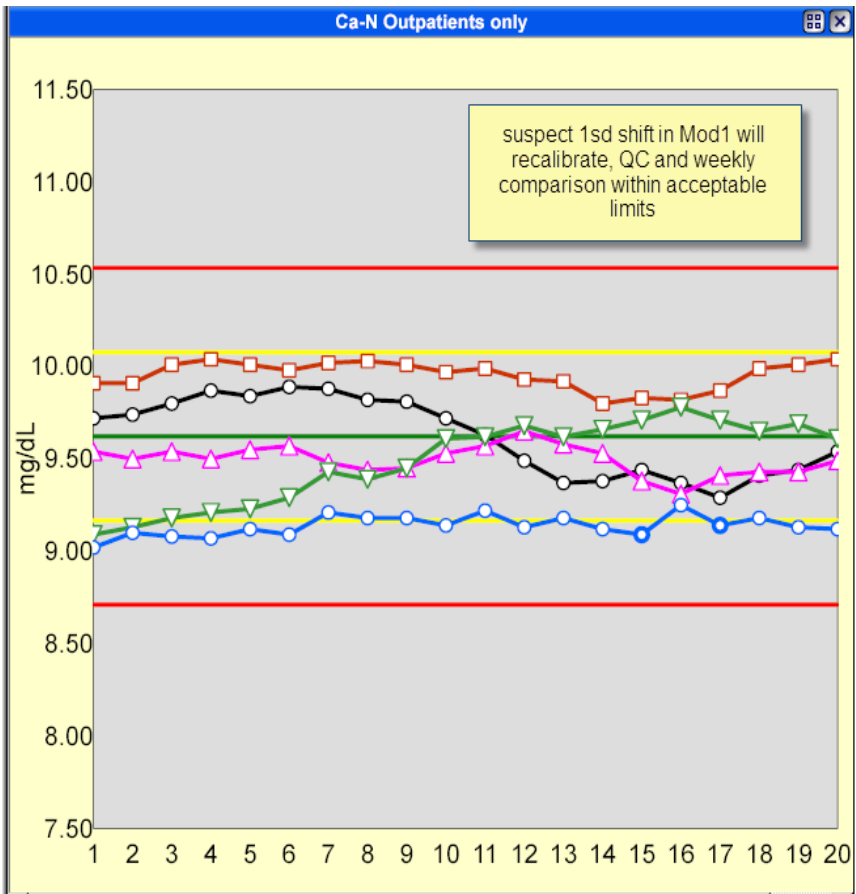
- Must ensure exclusion filters are set correctly
- Fine tune SD warning/error flags and exclusion limits





# Shift on One Module Only?

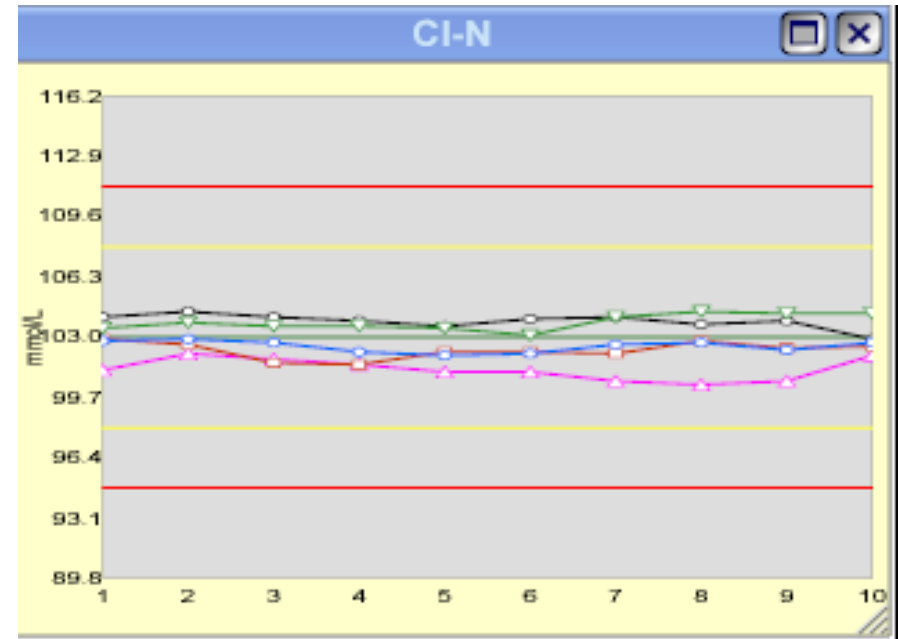
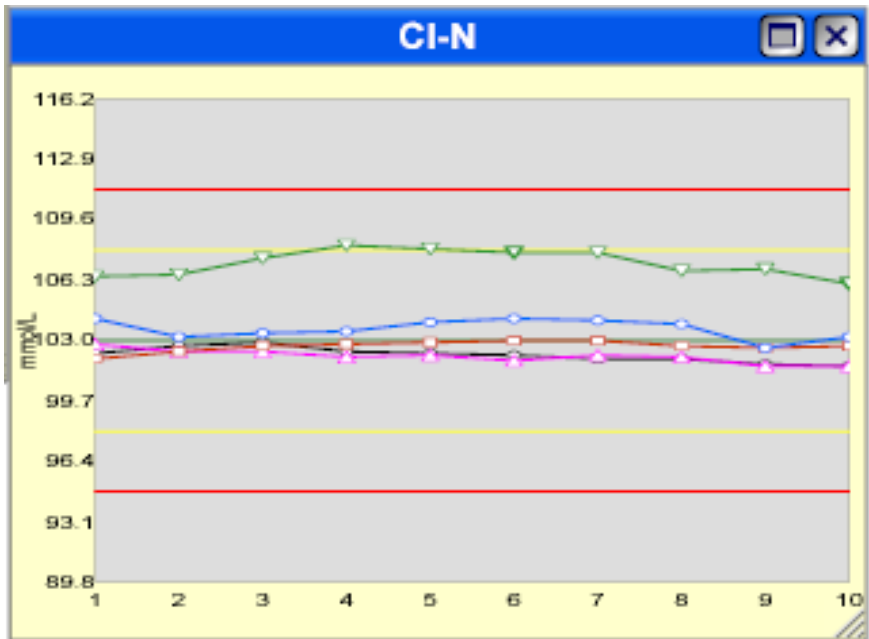
Change only half of CLIA Total Allowable Error (TEa) of 1.0 mg/dL





# Observed Possible Shift Prior to Daily PM

- To calibrate or not?
- CLIA TEa is 5% or approximately 5, already at 3
- QC within range but shift seen in All Pts, Inpt and Outpt graphs





# Problem?

From: IM Moving Averages Server [im.moving.averages@Hitchcock.ORG] Sent: Wed 11/16/2011 12:20 PM  
To: Frank A. Polito  
Cc:  
Subject: Error-High Threshold Exceeded, check Inpt and Outpt graphs

At 11/16/2011 12:20:23 PM this message was generated:

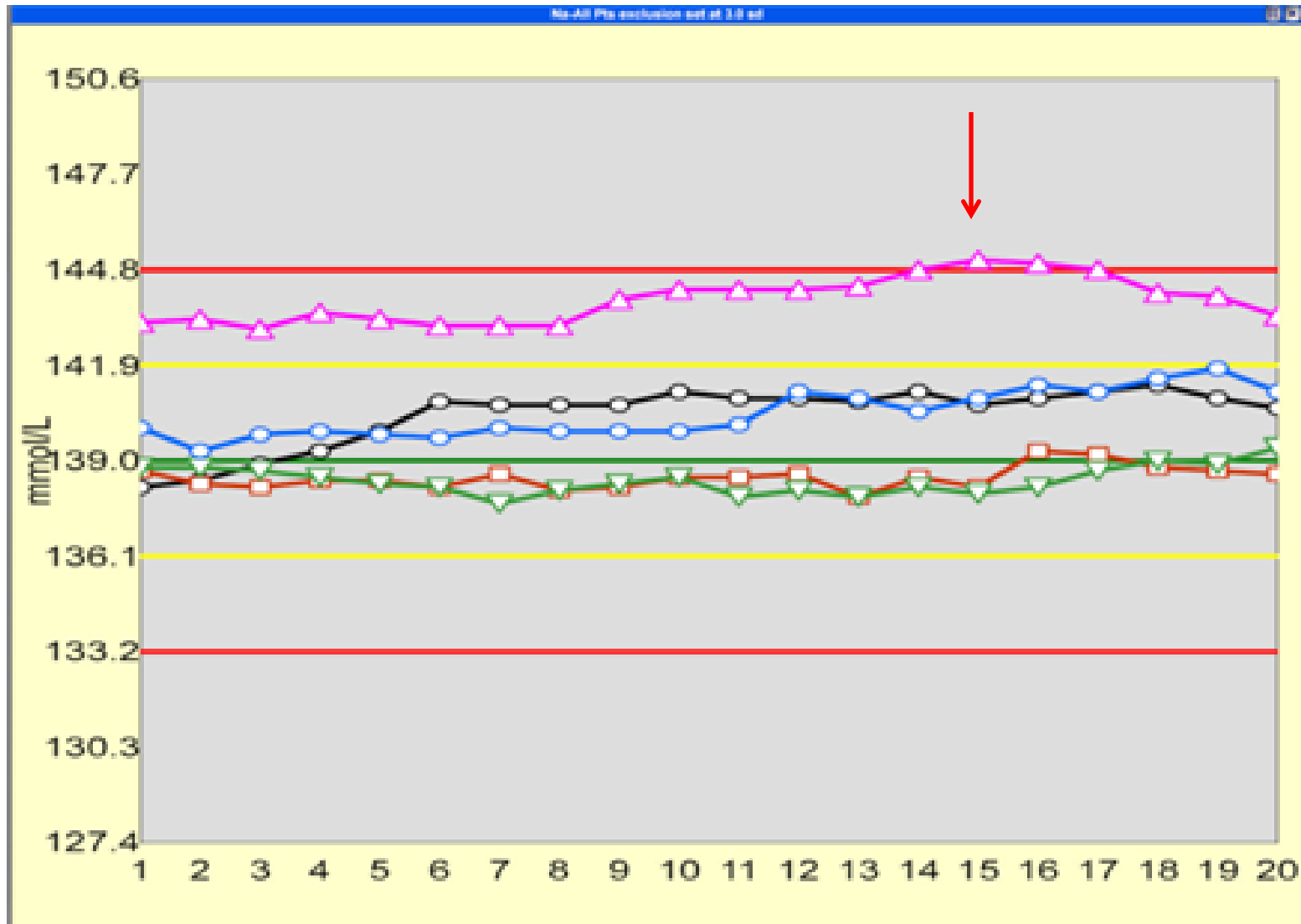
Error-High Threshold Exceeded, check Inpt and Outpt graphs Result for Specimen ID: 113201230C created a point above the error threshold for Moving Averages protocol: Na-All Pts exclusion set at 3.0 sd on series: C2. Error high threshold triggered.

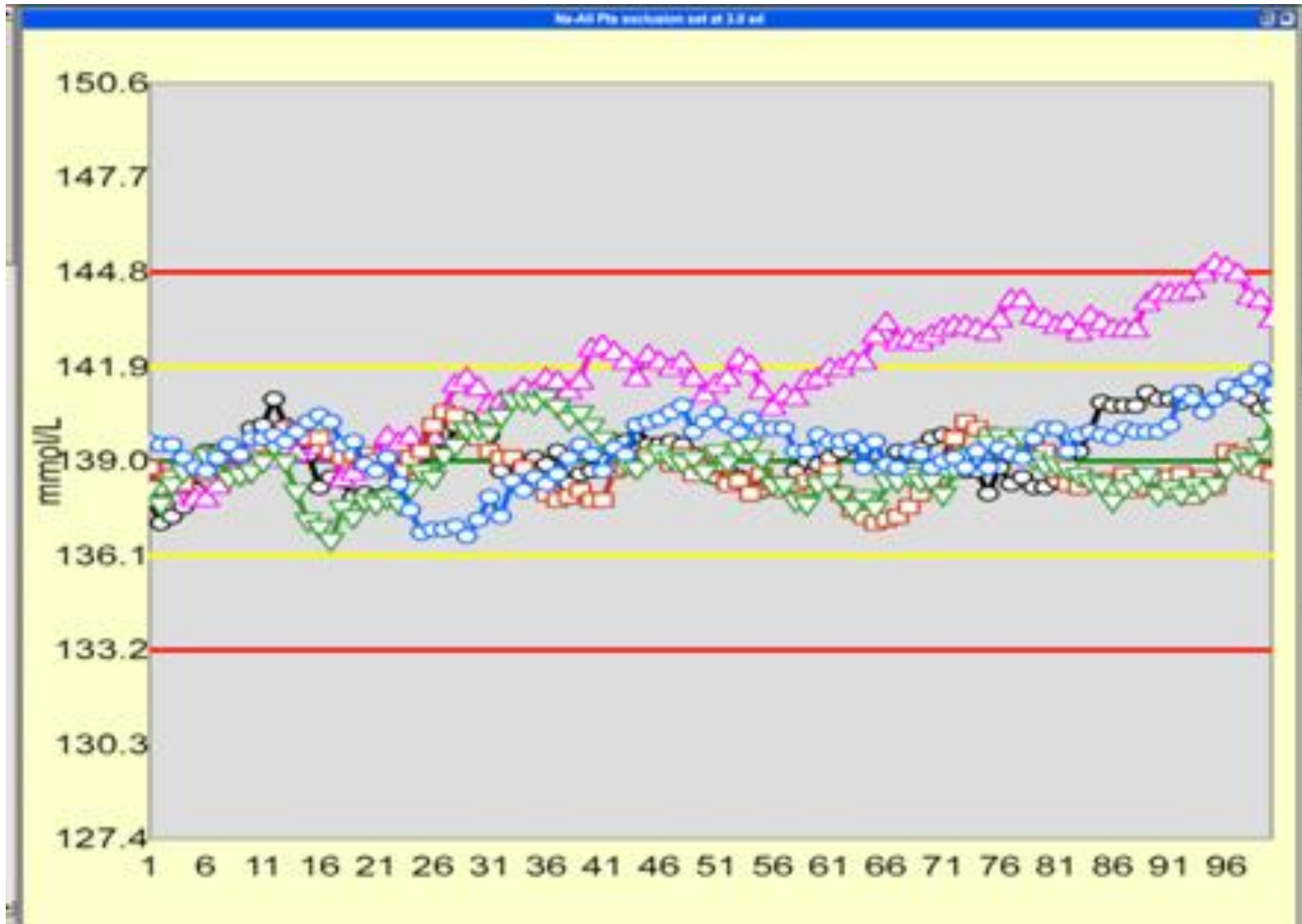
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**From:** Timothy  
**Sent:** Wednesday, November 16, 2011 12:49 PM  
**To:** Frank A. Polito;  
**Subject:** C502 Na issue

C502 ISE's were shut off just after rounds today because we began to see the ISE issue again. Diane had seen a couple repeat Na's by that time that she couldn't feel good about.

We actually turned the ISE's on on C501 (doesn't use the affected R2 probe system), and have contacted Dave . He will be here by 1500, and did conform what we had done was "okay".







# Next Steps

- Adjust exclusion rates on “all Pt” graphs from 4.0 SD to 3.0 or 2.6 for those assays where Inpt vs. Outpt are different
- Remove those tests that don’t seem to work Uric Acid (Pts on Uricase) CPK and LDH (population really not normal).
- Adding assay Protocols: Urine Microalbumin, Thyroxine/T4 and Ferritin
- Refine Protocols further- go from better to best “N” for earlier detection
- Work with Roche/DI to improve product:
  - Rather than points on MA graph X-axis have date/time
  - Allow MA graph to scroll forward and backward rather than changing number of display points

