On-line Flagging of Anomalies and Adaptive Sequential Hypothesis Testing for Fine-feature Characterization of Geosynchronous Satellites

By

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Abstract

The objective of on-line flagging in this paper is to perform an interactive assessment of geosynchronous satellites anomalies such as cross-tagging of satellites in a cluster, solar panel offset change, etc. This assessment will utilize a Bayesian belief propagation procedure and will include an automated update of the baseline signature data for the satellite, while accounting for the seasonal changes. Its purpose is to enable an ongoing, automated assessment of satellite behavior through its life cycle using the photometry data collected during the synoptic search performed by a ground or space-based sensor as a part of its metrics mission. The change in the satellite features will be reported along with the probabilities of type I and type II errors.

The objective of adaptive sequential hypothesis testing in this paper is to define future sensor tasking for the purpose of characterization of fine features of the satellite. The tasking will be designed in order to maximize new information with the least number of photometry data points to be collected during the synoptic search by a ground or space-based sensor. Its calculation is based on the utilization of information entropy techniques. The tasking is defined by considering a sequence of hypotheses in regard to the fine features of the satellite. The optimal observation conditions are then ordered in order to maximize new information about a chosen fine feature.

The combined objective of on-line flagging and adaptive sequential hypothesis testing is to progressively discover new information about the features of geosynchronous satellites by leveraging the regular but sparse cadence of data collection during the synoptic search performed by a ground or space-based sensor.

1.0 Introduction

This work is a continuation of [1]. The notation in this paper is derived from [1]. It builds upon the various concepts, methods, assumptions and procedures defined in [1]. These include the time slider, the two facet model, Brightness Ratio, Cluster-based evidence, Model-based evidence, Bayesian belief propagation, near-real time assessment of change, Inversion Model, Predictive Model, and Statistics Model. This paper may be viewed as new work on the decision to move the time slider [1], which is required in order to update the baseline signature (brightness) data for a satellite.

Reference 1 describes a Bayesian belief propagation procedure for the detection and resolution of cross-tag between two satellites. Such resolution is necessary in order to correctly associate new data for each satellite. This paper extends this data association procedure to multi-satellite cross-tag detection and resolution, including the probabilities of false positive and false negative.

Fig. 2 - Fig. 4 show a notional baseline and new data for three satellites that comprise a notional cluster. A cluster is a group of satellites that are normally simultaneously captured in a sensor's field of view as shown in Fig. 1. The three satellites are denoted as S_1, S_2 and S_3, respectively. The baseline data is denoted with blue markers and the new data is denoted with red markers. The data has large gaps, which correspond to the daytime gap in data collection. The same data is plotted in Fig. 5 with respect to the orbit angle, which is the same as the longitudinal phase angle except that it is computed with respect to the orbital plane of the satellite instead of the equatorial plane. Note how the brightness data for the three satellites overlaps with each other making it difficult to correctly associate the data on the basis of brightness values alone. If the satellites maneuver during daytime, the new data may be cross-tagged. The data in Fig. 2 - Fig. 4 may present itself in six different ways (e.g. S_1 tagged correctly but S_2-S_3 are cross-tagged, or S_3 tagged correctly but S_1-S_2 are cross-tagged, or S_1 is tagged as S_2, S_2 is tagged as S_3 and S_3 is tagged as S_1, etc.). The specific manner in which the data may present itself is unknown a priori. Accordingly, the methods in this paper are designed to resolve the cross-tag irrespective of how the data presents itself.
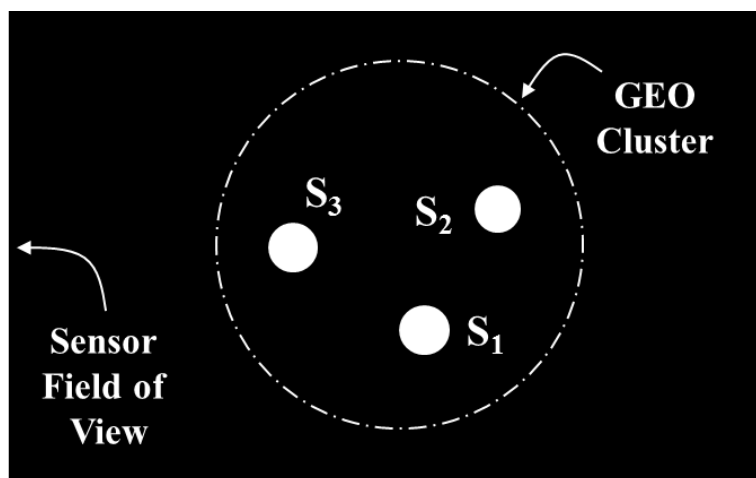
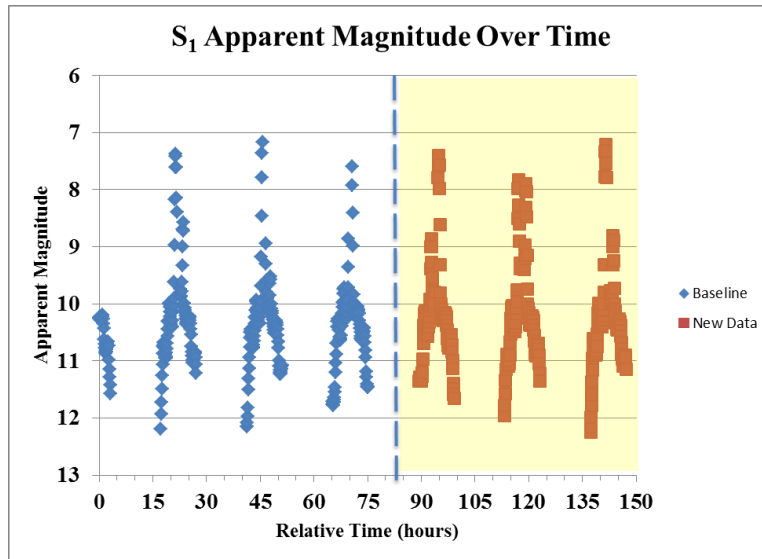

Fig. 1. Sensor Field of View
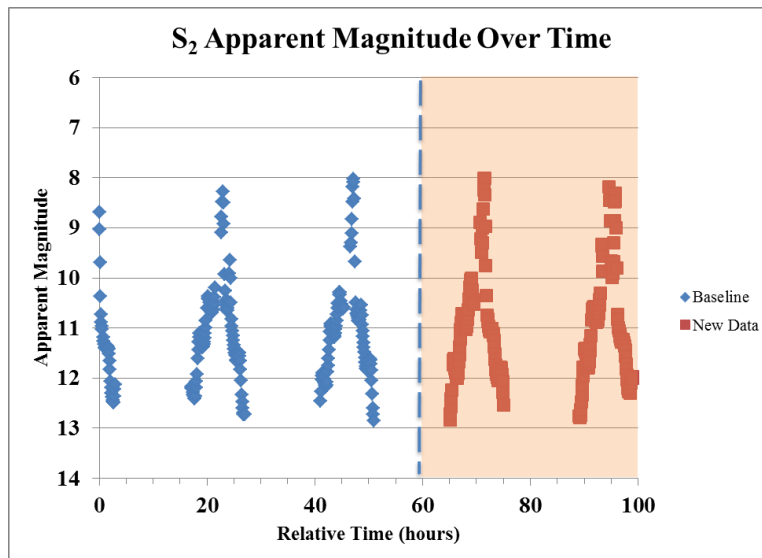
Fig. 2. Satellite S₁ Apparent Magnitude over Time

Fig. 3. Satellite S₂ Apparent Magnitude over Time
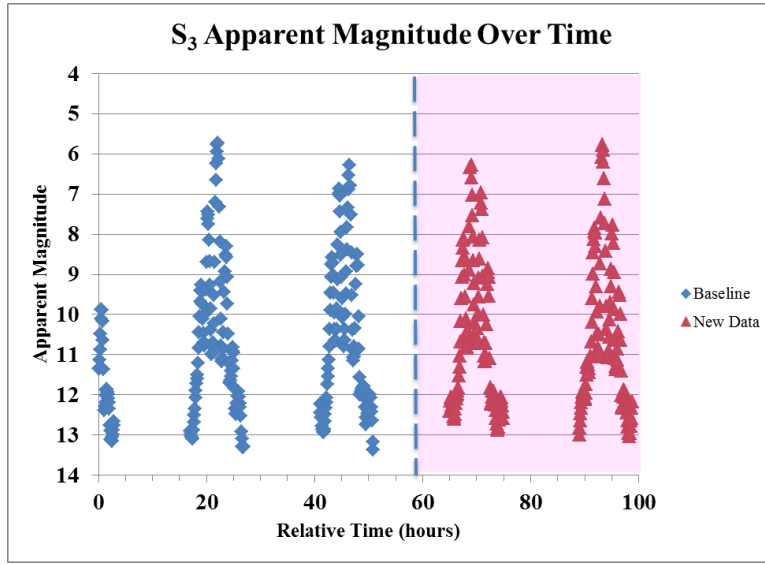
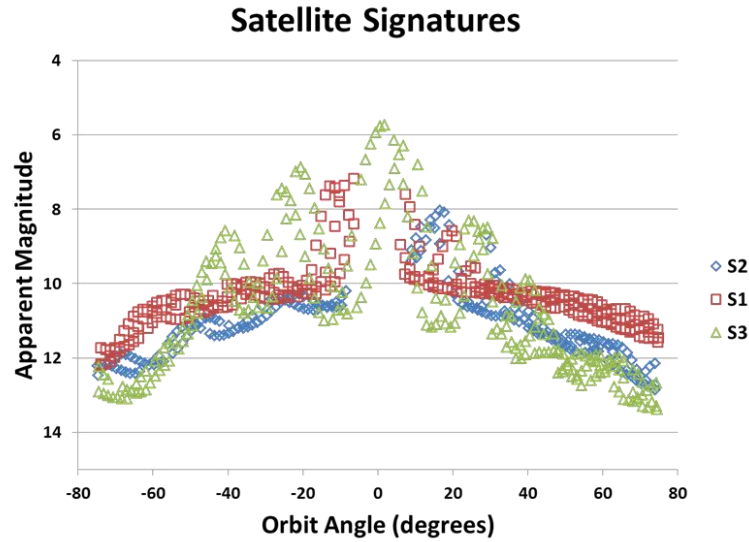**Fig. 4. Satellite S₃ Apparent Magnitude over Time**

Fig. 5. Signatures of the Three Satellites in the Cluster

Reference 1 computes belief in cross-tag resolution using Bayes theorem, cluster-based evidence and model-based evidence. This work resolves cross-tag using three methods (Z-test for dependent data, classical sequential analysis and Brownian motion drift analysis). It analyzes the sequence of values of Brightness Ratio (r_k) and $P(NOM \mid r_k)$ for this purpose. It also makes recursive use of model-base evidence.

2.0   Background

Change is defined as the difference between the observed behavior and the expected behavior. The expected behavior is defined by the user on the basis of prior data. Typical methods utilized in order to determine the expected behavior are a physics-based model, statistical model, or data interpolation. In this work, we use a physics-based model, which is based on the inversion of prior data. The change is expressed in terms of a ratio, r_k, where k is the observation number [1], which is denoted as the Brightness Ratio. Specifically:

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$$r_k = \frac{I_{Ok}}{I_{Mk}} - 1$$

Where I_{Ok} is the observed single point brightness, I_{Mk} is the expected single point brightness. Under ideal, nominal conditions, the ratio of I_{Ok} and I_{Mk} would equal one. The values of $k < 0$ comprise the baseline data and $k \geq 0$ is new data (i.e. the green and yellow markers in Fig. 6, respectively). The time slider is located after $k = -1$, or at the end of the baseline data. Alternately, the time slider separates the baseline data and new data. The definition of r_k includes a subtraction by one so that its expected value, $E(r_k) \approx 0$ under ideal conditions. The methods, assumptions and procedures are defined by considering that $E(r_k) \neq 0$ when change occurs. The nonzero value of $E(r_k)$ is treated as a measure of bias between the expected brightness and observed brightness.
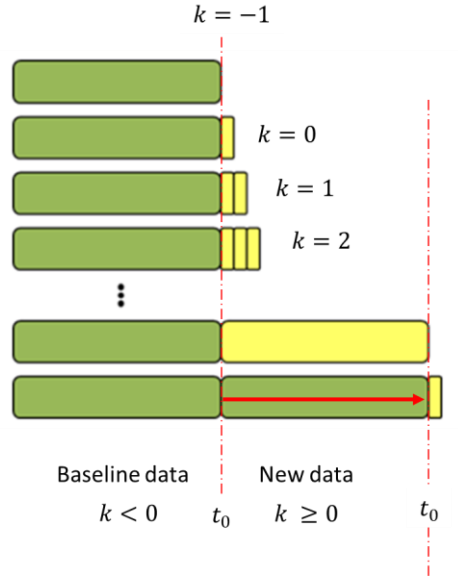

Fig. 6. Schematic of Time Slider Movement

The two-facet model is used as the Inversion Model. It represents a three-axis stabilized satellite as two facets, namely a body facet that points to nadir and a solar panel facet that tracks the sun as seen in Fig. 7. This Inversion Model may be considered a 0th order model that captures basic truth about the satellite, while not explicitly accounting for the fine features of the satellite (e.g. antenna, dishes, self-occlusions). The benefit of this model is that it can be utilized to estimate the body and panel optical behavior for any three-axis stabilized satellite. Its shortcoming is that its accuracy depends on the complexity of the satellite's geometry. Thus, there typically is bias in the values of the Brightness Ratio, depending on the observation conditions as follows in [1], and the analysis is limited to a subset of permissible orbit angle values. Specifically:

- At small phase angles, the solar panel specular behavior dominates and the bias is larger.
- At medium phase angles ($< 75°$), the body diffuse behavior dominates. The bias is small except where there are brightness contributions from features that arise from self-occlusion and body attachments.
- At phase angles close to $90°$, the specular glints from body attachments dominate the character of brightness and the bias can be larger.
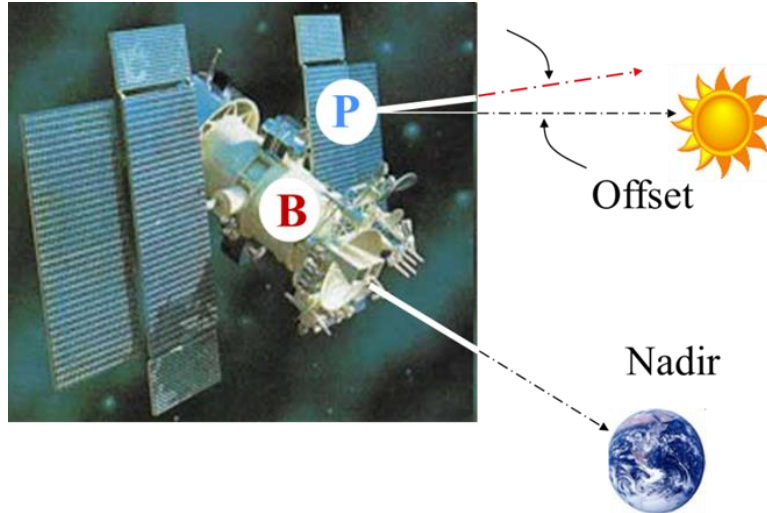- The analysis is not performed for phase angles greater than $90°$.

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Fig. 7. Two-facet model

Thus, the value of $E(r_k)$ is nearly zero for each satellite for most orbit angles. There are regimes of orbit angles where the Brightness Ratio is large. These represent the observation conditions where the Inversion Model needs improvement, which could be attained by adding higher order terms to the basis functions for the two facets in order to represent the fine features or by defining additional facets to represent the satellite geometry. Note that if there was no change in a satellite, sensor orbit, and solar declination, the character of $E(r_k)$ is expected to remain unchanged because the Inversion Model is 'invariant'. If there was change in the satellite, observation conditions, or illumination condition, the value of $E(r_k)$ can change. It is necessary to assess if this change is nominal (NOM) (unchanged from the baseline) or anomalous (ANOM) (changed from the baseline). The value of $E(r_k)$ can become ANOM due to cross-tag. This is because, in the calculation of the brightness ratio, the denominator (or the predicted value of satellite brightness by the Predictive Model) is for a different satellite.

The goal is to detect change, characterize it as NOM or ANOM and provide its resolution as quickly as possible and to be able to provide a measure of confidence for the assessment. In order to detect change, we will use three different methods to analyze the data sets. However, in each method, we will be using hypothesis testing to evaluate our results. Each hypothesis test must have a specified null hypothesis, alternative hypothesis, test statistic, significance level (alpha, or probability of type I error), and when applicable beta (probability of type II error) before beginning. The null hypothesis, denoted as H_o, defines a state where no change has occurred. The alternative hypothesis, denoted as H_a, defines a state where change has occurred. The test statistic used in each of the methods involves the sample mean.

To assign a confidence level to our calculations, we must designate specific values for alpha and beta. The value of alpha is equivalent to the probability of a type I error. A type I error is when the null hypothesis is rejected and the alternative hypothesis is accepted, when in reality the null hypothesis is true. In other words, the test leads the user to assess that the satellite has changed, when the satellite state is still NOM (i.e. unchanged from the baseline). A false positive is the event that the test concludes that a change has occurred, when in reality no change has occurred and the satellite state is NOM. Or, a false positive is a type I error.

$$\alpha = level\ of\ significance\ of\ the\ test = P(Type\ I\ Error)$$
$$= P(\text{rejecting the null hypothesis and accepting the alternative hypothesis,}$$
$$\text{when in reality the null hypothesis is actually true})$$

Beta is defined to be the type II error. A type II error is to accept the null hypothesis and reject the alternate hypothesis, when in reality the alternate hypothesis is true. In other words, this is when the hypothesis test concludes the satellite state to be NOM (i.e. same as the baseline), when in reality a change has occurred. A false negative is

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when the test concludes the satellite state to be NOM or that nothing has changed as compared to the baseline, when in reality the satellite state has changed. Thus, a false negative is a type II error.

$$\beta = P(Type\ II\ Error) = P(\text{accepting the null hypothesis, when in reality the null hypothesis is false})$$

3.0   Composite Hypothesis Testing

In order to detect anomalies, we can utilize multiple methods and then combine their results using a composite hypothesis test to obtain one final resolution. Three different methods will be described in Section 4.0 and any combination of these methods can be combined into a composite hypothesis test. In the examples in Section 8.0, the three methods used in the composite hypothesis test will be the Z-test for dependent data using the r_k values, the Z-test for dependent data using the P(NOM|r_k) values, and the sequential analysis using either the r_k or Δr_k values, where $\Delta r_k = r_k - r_{k-1}$. As described in the next section, the Z-test for dependent data using the r_k values makes no assumptions for the data and provides a value for P(False Positive). This method is derived from the physics based model. The Z-test for dependent data using the P(NOM|r_k) values also makes no assumptions for the data and provides a value for the P(False Positive). However, it is derived from the Bayesian belief propagation. The sequential analysis using either the r_k or Δr_k values assumes independence for successive points of data and provides a value for the P(False Positive) and P(False Negative). This method is also derived from the physics based model.

Once we obtain the results for all three tests for an observation, we compare the results from the different tests. If the sequential analysis method determines we need to continue sampling, then no decision is made, and we wait for the next observation. If the sequential analysis comes to a conclusion of NOM or ANOM and all three tests agree a satellite is NOM or ANOM, then we can make that conclusion as shown in Fig. 8. However, if the tests do not agree, then we can make no conclusion about that satellite. If all satellites in a cluster are determined to be NOM, we can update the time slider as explained in Section 8.9 and continue evaluating observations. If a satellite is concluded to be ANOM, then we will try to resolve what changed in that satellite. One way to do this is by using the cross-tag resolution method described in Section 8.8. Once all cross-tags and changes are resolved, we can continue collecting data.
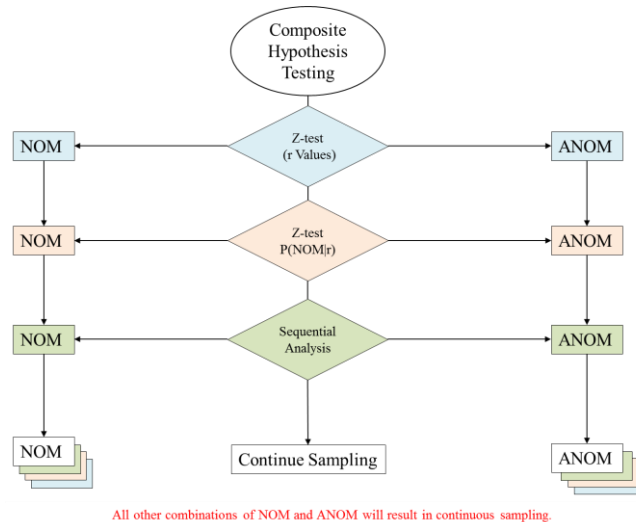

Fig. 8. Composite Hypothesis Testing Flow Chart

Although Fig. 8 only illustrates three possible cases, each method can result in multiple outcomes. If we considered all possible outcomes for each of the three methods, the total number of outcomes would be quite large. For the purpose of this assessment, we are only concerned with the result when all three tests produce the same outcome.

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Thus, Fig. 8 depicts the outcomes this paper will focus on. We must also note that there are two separate methods that can be used for the sequential analysis. If r_k is independent and has an approximately normal distribution then Brownian motion drift analysis is used. If r_k is independent but does not have an approximately normal distribution then the classical sequential analysis method is used. This process is illustrated in Fig. 9.
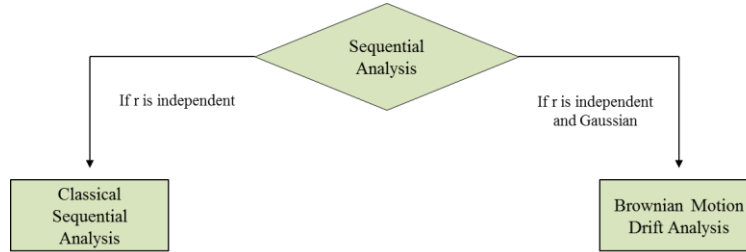

Fig. 9. Sequential Analysis Flow Chart

4.0 Hypothesis Testing Methods

The detection of change is performed using either the value of r_k or Δr_k and by using the results of the Bayes belief calculation (i.e. P(NOM|r_k)). There are three methods:

1. Z-test for dependent data [1]
2. Classical sequential analysis: This is used when r_k is independent of r_{k-1}.
    This provides the ability to stop after enough observations have been taken in order to make a decision about the hypotheses based on the user-defined values of the type I and type II errors [2].
3. Brownian motion drift analysis: This is an application of sequential analysis that is applied to the observed process (r_k) interpreted as a Brownian motion in order to determine whether or not the drift is no longer zero. The procedure is used when Δr_k is independent of Δr_{k-1} and both have a normal distribution. This analysis also provides the ability to stop after a finite number of observations based on the user-defined values of the type I and type II errors [3].

If there is no change, the time slider is moved forward and the prior probability density function (pdf) is updated. This is to enable an ongoing assessment of the satellite state.

4.1 Z-test for Dependent Data

The Z-test for dependent data is a Central Limit Theorem type of statistical method that can be used when the observations are not independent. Thus, this is a general method that can be used for any set of observations. The test statistic can be approximated by a normal distribution under the null hypothesis. Each test statistic is compared to the baseline by defining a z-score measure. The z-score represents the distance between the sample mean after pass k and the baseline mean in terms of the number of standard deviations away from the sample mean. The sample mean, after pass k, may be either less or more than the baseline mean in order for the absolute value of the z-score to remain below a user-defined threshold [1].

4.2 Classical Sequential Analysis

Classical sequential analysis is a statistical method that evaluates data as it is obtained, as it re-computes the test statistics each time a new data point is obtained. By using this method to assess the input data, the test does not require a predetermined sample size before beginning. This characteristic is unique to sequential analysis and allows the user to execute a decision earlier and with fewer observations as compared to the Z-test for dependent data. The process consists of computing a likelihood function and defining a set of bounds based on α and β to use in evaluating the likelihood output [2].

4.3 Brownian Motion Drift Analysis

Brownian motion is a continuous limit of a random walk process. The sequential analysis method can be applied to Brownian motion to test whether or not the drift of the Brownian motion process is zero. This method is useful because it evaluates data as it is collected and allows the user to make a decision once a fixed bound has been reached. The Brownian motion approach, however, has a specific set of requirements that must be verified before being used for testing [3].

5.0 Hypothesis Testing Assumptions

5.1 Z-test for Dependent Data

In order to receive accurate results using the Z-test for dependent data, there are certain conditions that must be true about the data set that will be evaluated:

- Large sample size n for the baseline data.
- The data points are assumed to be sampled from the same population distribution.

5.2 Classical Sequential Analysis

In order to receive accurate results using classical sequential analysis, there are certain conditions that must be true about the data set that will be evaluated:

- r_k is independent of r_{k-1} in the baseline data.
- This method does not require the data set to have a standard normal distribution.

5.3 Brownian Motion Drift Analysis

In order to apply methods applicable to Brownian motion to r_k, there are certain conditions that must be true about the data set that will be evaluated:

- Δr_k is independent of Δr_{k-1} in the baseline data.
- Standard Normal density (pdf) of Δr values
- $r_k(0) = 0$
- $r_k(t)$, $0 \leq t < \infty$ is a continuous function of t (or time). Note that each observation k is associated with its monotonically increasing value of time at which the observation was taken.

6.0 Hypothesis Testing Procedures

6.1 Z-test for Dependent Data

While describing the Z-test for dependent data, the following description considers the r_k values, although the procedure is the same when using the value of P(NOM| r_k).

- In order to perform the Z-test for dependent data, the null hypothesis and alternate hypothesis are defined as follows. The null hypothesis defines a state when no change has occurred. The alternative hypothesis defines a state where change has occurred in the mean of r_k values. The estimated value of the population mean $E(r_k)$ is denoted as μ_k, which is the sample mean. The hypothesis test is defined in order to assess if $\mu_{k \geq 0}$ differs from the baseline mean, $\mu_{k < 0}$:

$$\text{Null hypothesis} = H_o : \mu_{k \geq 0} = \mu_{k < 0}$$

$$\text{Alternative hypothesis} = H_a : \mu_{k \geq 0} \neq \mu_{k<0}$$

- The Z-test for dependent data does require us to pick a significance level α. We will use α = .05. However, the Z-test for dependent data does not allow us to specify β. Therefore, we will not know our type II error for these calculations and cannot accept our null hypothesis at any point for this method with a handle of the probability of doing so in error.

- The Z-test for dependent data algorithm starts with the given baseline data containing n observations, shown as the green segment in Fig. 6. These data points are considered to be before the user-defined reference time, t_0. The mean is calculated for the values of this data set, which provide the baseline against which the new data is compared:

$$\text{Baseline mean} = \mu_{k<0}, \text{ which is estimated by the sample mean } \frac{1}{n}\sum_{k=-n}^{-1} r_k$$

- Since the successive values of r_k can be dependent, the population variance σ^2 is adjusted using what we will call the "dependent variance". This dependent variance reflects the alpha-mixing parameter, α, which specifies how many previous passes on which each value has significant dependence. The dependent variance is comprised of the sample variance and a term that involves covariance, which is calculated using the alpha mixing procedure [4]. Specifically:

$$\text{Dependent variance} = \text{population variance} + 2*(\text{covariance-related term})$$

The covariance-related term is estimated by:

$$(\sigma_{k<0})^2 = S_{k<0}^2 + 2 * \frac{1}{n-\alpha}\sum_{k=-n}^{-1}[\sum_{i=1}^{\alpha}[(r_{ik} - \mu_{k<0})(r_{ik} - \mu_{k<0})]],$$

$$S_{k<0}^2 = Var(X_{k<0}) = \frac{1}{n-1}\sum_{k=-n}^{-1}(r_k - \mu_{k<0})^2, \text{ which estimates the variance of the baseline } r_k \text{ values}$$

- The alpha mixing calculations commence when a sufficient amount of new data is received. The number of passes that constitute sufficient new data may be a fraction of the data size in the baseline (e.g. when new data is collected that spans a full night). When new data is received for passes 0 to k (shown in yellow color in Fig. 6), the data that spans from pass (k-n) to pass (k) is utilized to perform the assessment. The data from passes (k-n) to 0 is from the baseline. This corresponds to the use of a sliding window of the last n observations for the alpha mixing analysis.

- For each new pass k, the value of r_k is computed first and then used for the Z-test for dependent data calculation. The mean is estimated for the r_k for the set of values from passes (n-k) to k:

$$\text{Current sample mean after pass k} = \text{estimate of } \mu_{k \geq 0} = \bar{r}_k = \frac{1}{n}\sum_{i=k-n+1}^{k} r_k$$

- The estimate of the current mean after pass k, $\bar{r}_k$, is compared with the baseline by defining a z-score measure (or standard score measure), which is denoted as η_k [4]:

$$\text{Z-score } \eta_k = \frac{\bar{r}_k - \mu_{k<0}}{\sigma_{k<0}/\sqrt{n}}$$

The z-score represents the distance between the sample mean after pass k and the baseline mean in terms of the number of standard deviations. The sample mean after pass k may be less or more than the baseline mean in order for the absolute value of the z-score to remain below a user-defined threshold.

- Each new observation for which we do not reject the null hypothesis, we continue to assume that the satellite is NOM (i.e., unchanged from the baseline) and continue to evaluate new observations. When there is an observation that does not satisfy the null hypothesis, it implies that the mean has changed in a statistically

significant amount as compared to the baseline, which prompts us to reject the null hypothesis and accept the alternative. Therefore, we can conclude the satellite is different from its state in the baseline data (i.e. the occurrence of change) and the time slider cannot be forwarded up to the current pass k. Once we have obtained n new observations for which we do not reject the null hypothesis, the time slider can be moved forward to the current pass k.
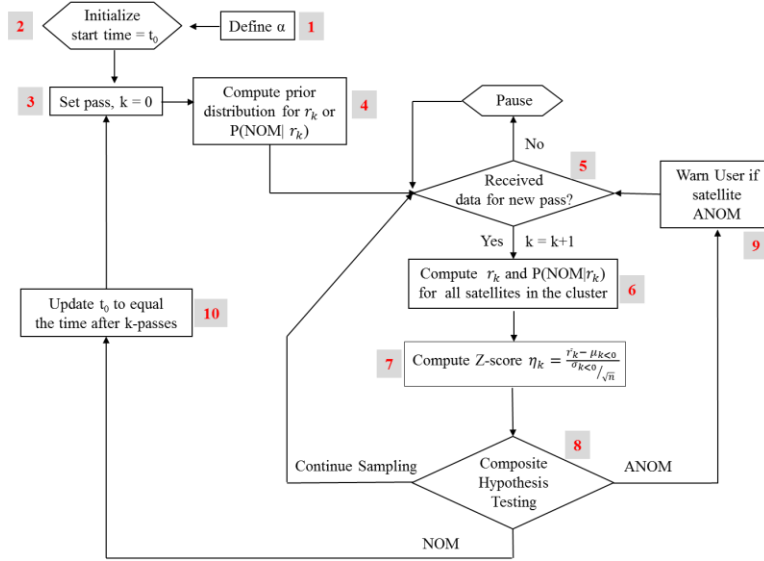

Fig. 10. Z-test for Dependent Data Flow Chart

6.2 Classical Sequential Analysis

The classical sequential analysis method will proceed by using the r_k values; however, other values may also be used as long as they are independent. The classical sequential analysis does not require the data set to have a standard normal distribution.

- As described in Section 6.1, this method also requires the creation of a set of baseline r values. Once the baseline has been defined, the baseline mean and standard deviation must be computed for future calculations.

- The classical sequential analysis method does require a predetermined α and β. The test also requires a predefined δ that is fixed to greater than zero, where delta is the number of standard deviations the sample mean is away from the null hypothesis mean 0. For our examples, α = 0.05, β = 0.05, and δ = 1.0. Because this test allows us to determine α and β, we can quantify the P(type I error), P(type II error) and be able to accept the null hypothesis when necessary.

- To be able to properly use the classical sequential analysis test, a null hypothesis and alternative hypothesis must also be defined. The null hypothesis describes a state where no change has occurred. The alternative hypothesis describes a state where a change has occurred that is larger than the predefined δ. Both hypotheses are defined below.

$$\text{Null hypothesis} = H_o: \mu = \mu_0$$

$$\text{Alternative hypothesis} = H_a: \left| \frac{\mu - \mu_0}{\sigma} \right| > \delta$$

- Before the method can be evaluated, a user-defined bound must be established. The lower bound is denoted as B and is defined by

$$B = \frac{\beta}{1 - \alpha}$$

The upper bound is denoted as A and is defined by

$$A = \frac{1-\beta}{\alpha}$$

- Once a new set of data is received, the classical sequential analysis method uses a likelihood function to evaluate the data set at each observation k. The likelihood function has a closed form expression if r_k is normally distributed; it has to be numerically computed otherwise. In this work, the likelihood function is computed using the following equation, which is valid for normally distributed r_k:

$$L_n = \frac{1}{2} * e^{-\frac{1}{2}k\delta^2}(e^{\frac{\delta}{\sigma}\Sigma(r_k-\mu)} + e^{-\frac{\delta}{\sigma}\Sigma(r_k-\mu)})$$

- After the likelihood function is computed, the output is evaluated according to the prefixed bounds. If the likelihood function $\in$ (B, A) then the process continues sampling. If the likelihood function is less than or equal to B, then the null hypothesis is accepted and thus, we conclude that no change has occurred. If the likelihood function is greater than or equal to A, then the alternative hypothesis is accepted, and thus, we conclude that a change has occurred.
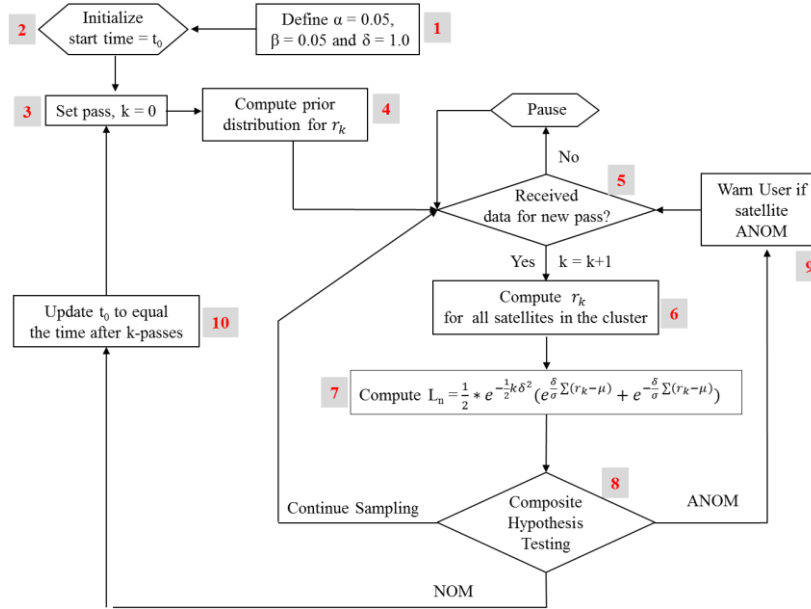

Fig. 11. Classical Sequential Analysis Flow Chart

6.3 Brownian Motion Drift Analysis

As described early, Brownian motion is a specific sequential analysis method, so its process is very similar to that of the classical sequential analysis method. For our examples, the main difference between Brownian motion and the classical sequential analysis is that the Brownian motion baseline is executed using the Δr_k values. The creation of the baseline is identical to that described in Section 6.1.

- Once the r_k baseline has been created, the Δr_k values are computed using the equation listed below.

$$\Delta r_k = r_k - r_{k-1}$$

After the Δr_k baseline is generated, the mean and standard deviation of the baseline is calculated for a later use.

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- Brownian motion does require α, β and δ to be set prior to testing. For this method, delta is defined as the number of standard deviations that mean drift μ is away from null hypothesis mean drift 0. The Brownian motion examples have α = 0.05, β = 0.05 and δ = 1.0.

- A null hypothesis and alternative hypothesis must also be defined in order to proceed with Brownian motion. The null hypothesis describes a state where no change has occurred. The alternative hypothesis describes a state where a change has occurred. Both hypotheses are defined below.

$$\text{Null hypothesis} = H_o: \mu = 0$$

$$\text{Alternative hypothesis} = H_a: |\mu| > \delta * \sigma$$

- Before the method can be evaluated, a user-defined bound must be established. The lower bound is denoted as A and is defined by

$$A = \frac{\beta}{1-\alpha}$$

The upper bound is denoted as B and is defined by

$$B = \frac{1-\beta}{\alpha}$$

- Once a new set of data is received, the Brownian motion drift method standardizes each r_k by subtracting each r_k by the value at observation 0 and then dividing by the standard deviation of the baseline. This adjusted r value is denoted below.

$$\tilde{r}_k = \frac{r_k - r_0}{\sigma_{baseline}}$$

- This method also uses a likelihood function to evaluate the data set at each observation k. This likelihood function is computed using the following equation for two-sided drift analysis as explained in Section 6.3.1:

$$L_n = 0.5 * e^{-\frac{k\delta^2}{2}} * (e^{(\delta * \tilde{r})} + e^{-(\delta * \tilde{r})})$$

- After the likelihood function is computed, the output is evaluated according to the prefixed bounds. If the likelihood function ∈ (A, B) then the process continues sampling. If the likelihood function is less than or equal to A, then the null hypothesis is accepted and thus, we conclude that no change has occurred. If the likelihood function is greater than or equal to B, then the alternative hypothesis is accepted, and thus, we conclude that a change has occurred.
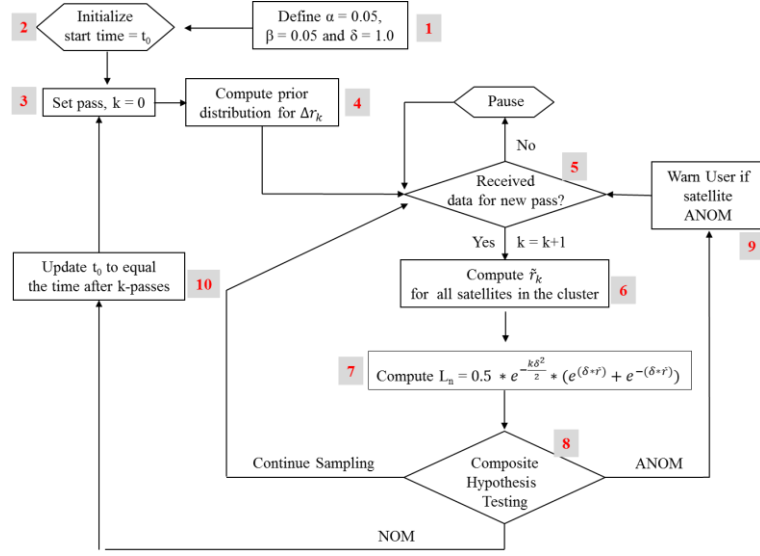
Fig. 12. Brownian Motion Drift Analysis Flow Chart

6.3.1 Two-sided Drift Analysis

Reference 3 presents a hypothesis test to detect change in drift for Brownian motion. If μ_o denotes the drift corresponding to the null hypothesis and μ_1 denotes the drift corresponding to the alternative hypothesis, then the likelihood ratio function

$$L(t, W(t); \mu_0, \mu_1) = e^{\left[(\mu_1 - \mu_0)*W(t) - (\frac{t}{2})*(\mu_1^2 - \mu_0^2)\right]}$$

is used to test H_o: $\mu = \mu_o$ vs. H_a: $\mu = \mu_1$ for values $\mu_o < \mu_1$ [3]. Our process r_k is transformed to the correct scale to be a Brownian motion, and this likelihood ratio $L(t, W(t); \mu_0, \mu_1)$ can be approximated discretely by

$$L_k(\mu_0, \mu_1) = e^{\left[(\mu_1 - \mu_0)* r_k - \frac{k}{2}*(\mu_1^2 - \mu_0^2)\right]}$$

In our case, $\mu_o = 0$, referring to the null hypothesis case of "no drift", which we are equating to the NOM state. However, we are interested in a test for H_o: $\mu = 0$ vs. H_a: $|\mu| \geq \mu_1$ for some value $\mu_1 > 0$.
Note that our process r was normalized to be a Brownian motion (with scale $\sigma = 1$), and we are testing the alternative hypothesis $|\mu| > \delta$.

Following the idea presented in [2] to extend a likelihood ratio test for a 1-sided alternative to a test for a 2-sided alternative, we compute a new likelihood ratio function as follows. The numerator is the sum of the likelihood functions (i.e. joint densities) associated with $\mu = \delta$ and $\mu = -\delta$, each multiplied by probability 0.5. The denominator is the likelihood function associated with $\mu = 0$. Dividing the denominator into both numerators results in the expression being the sum of two likelihood ratio functions corresponding to the alternative hypotheses $\mu = \delta$ and $\mu = -\delta$, respectively.

That is, $L_k(\mu_0, \mu_1)$ for our 2-sided case with $\mu_o = 0$ and $\mu_1 = +/- \delta$ becomes

$$\acute{L}_k(\mu_0, \mu_1) = .5 * L_k(0, \delta) + .5 * L_k(0, -\delta)$$

$$= .5 * e^{\left[(-\delta)* r_k - \frac{k}{2}* \delta^2\right]} + .5 * e^{\left[(\delta)* r_k - \frac{k}{2}* \delta^2\right]}$$

$$= .5 * e^{\left[-\frac{k}{2}* \delta^2\right]} * (e^{[-\delta * r_k]} + e^{[\delta * r_k]})$$

,which is the formula mentioned above.

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6.4 A Note on the Use of the Brightness Ratio during Hypothesis Testing

The Brightness Ratio is defined in Section 2.0. Note r_k is not symmetric. For example, if $I_{Ok} = 5 * I_{Mk}$ then $r_k = 4$ but if $I_{Mk} = 5 * I_{Ok}$, then $r_k = -\frac{4}{5} = -0.8$. The range of values we consider to be acceptable for r_k is (-0.6, 1.5). Although the r values are asymmetric, this characteristic is only of concern during the classical sequential analysis test. This is the case because the Z-test for dependent data has a test statistic that is normal due to the Central Limit Theorem for Dependent Data, irrespective of distribution. Similarly, the Brownian motion drift analysis is computed only on the delta r values, which can be independent and normally distributed regardless of the probability distribution of the r values. Thus, the classical sequential analysis method applied to r is the only method that may be affected by the asymmetry. However, classical sequential analysis does not require the data set to be sampled from a normal distribution. For future work in this case, the likelihood function used in the classical sequential analysis will be derived from the population distribution via an empirical probability density function.

7.0 Cross-tag Resolution Method

7.1 Overview

Once the results from the three methods have been obtained, we can begin analysis. If all three methods determine a satellite is ANOM, then we can conclude the satellite has changed in some way. One way the satellite can change is due to a cross-tag with one of its peer satellites. This means the satellite has been miss identified as another satellite in its cluster. This method helps to resolve those situations.

7.2 Methods

Suppose the three methods have determined at least one of the satellites is ANOM. Then, we must try to determine the change in that satellite. If two satellites are determined to be ANOM by all three tests or one satellite is determined to be ANOM and the other satellite's state cannot be determined, then we can use the cross-tag resolution method to determine if the cause of ANOM is due to a cross-tag. When two satellites are determined to be ANOM by at least one test, we can take the new data from the two satellites and swap them. Thus, the baseline of the first satellite is now paired with the new data of the second satellite, while the baseline of the second satellite is paired with the new data of the first satellite. The three methods can be run again on these new pairs of data to see if this swap resolved the cross-tag.

7.3 Assumptions

The present work assumes if a cross-tag does occur the cross-tag occurred during the daytime gap. Fig. 2 - Fig. 4 illustrate the reason for this assumption. The baseline data for each satellite concludes at the end of a night's observations, and the new day begins at the start of the next night. Therefore, when the three methods are performed, a result is obtained and applied to all the new data since the beginning of that night. Thus, we conclude something changed during the daytime gap.

7.4 Procedures

After the composite hypothesis test has determined at least one satellite to be ANOM, we must try to determine the changes in the satellite. If there is a second satellite which is determined to be ANOM, or no conclusion could be reached, then we can use the two not NOM satellites in this cross-tag resolution method. The procedure's steps are listed in order below.

1. Swap the new observations for the two satellites, S_1 and S_2. Thus, the baseline of satellite S_1 is now paired with the new data of satellite S_2, while the baseline of S_2 is paired with the new data of S_1.
2. Compute the prior distribution for the values being used: r_k, Δr_k, or P(NOM | r_k).
3. Perform the three methods again as described in Sections 6.1 and 6.2.

4. Analyze the new results. If all three tests now conclude NOM for either satellite, say S_1, then there was a cross-tag present. If one of the satellites is still ANOM, say S_2, and there was a third satellite, S_3, in the cluster that was not NOM, then we can perform another swap. We can swap the new data of S_2 after the first swap with the new data of S_3 by completing steps 1 - 4 again. However, if the results still conclude not NOM for both satellites, then we cannot determine if there was a cross-tag and it is likely that the cause could be from a different cross-tag scenario or that a different change had occurred in the satellite.

Once all the possible cross-tag situations have been tested for all satellites in the cluster that were determined to not be NOM by the composite hypothesis test, we have a better understanding of which satellites were cross-tagged and have resolved the cross-tag so we are associating the data to the right object.

7.5 Confidence Assessment

To be able to utilize the cross-tag resolution method described above, the composite hypothesis test used to determine whether or not we believe that a particular satellite has changed from what is believed to be its NOM state must be assigned a level of confidence. Suppose that each hypothesis test is performed at significance level α and that the null hypothesis H_o reflects that the satellite is NOM. Significance level α means that there is only α probability that the test will incorrectly conclude that the satellite is ANOM, when in reality it is NOM; i.e. $\alpha = P$ (test rejects H_o | H_o is true).

Recall that if at least one of the tests concludes that the satellite is ANOM, we will not conclude that the satellite is NOM. It is of interest to know the probability of type I error of this sort of conclusion. To this end, we compute the probability that we will not conclude that the satellite is NOM, when in reality the satellite is NOM as follows:

$P(at\ least\ one\ of\ the\ 3\ tests\ incorrectly\ conludes\ that\ the\ satellite\ is\ ANOM\ |\ satellite\ is\ NOM)$

$$= P(\ null\ hypothesis\ is\ rejected\ in\ at\ least\ one\ of\ the\ 3\ hypothesis\ tests\ |H_0\ is\ true)$$

$$= P\left(\bigcup_i \{test\ i\ rejects\ H_0\}\bigg|\ H_0\ is\ true\right) \le \sum_i P(test\ i\ rejects\ H_0\ |\ H_0\ is\ true)$$

$$= \sum_i (\alpha)$$

$$= 3\,\alpha$$

This means that the composite test for whether or not the satellite is NOM using the group of 3 tests performed individually at level α has an overall significance level of less than or equal to 3α.

For the current case, we perform the 3 tests on a single satellite at level 0.05. Moreover, suppose that at least 1 of the 3 tests results in a rejection of the null hypothesis that the satellite is NOM. If we use this criterion of "at least one rejection" necessary to conclude that the satellite is not NOM, then our method has reached the conclusion: "we cannot conclude that the satellite is NOM". Using the above calculation, we recognize that our method has less than or equal to 0.15 probability of failing to conclude that the satellite is not NOM, when in reality it is NOM.

Additionally, we are interested in knowing the probability that the composite test method correctly concludes that the satellite is NOM, which would be the case if all three tests conclude to not reject the null hypothesis of NOM. In other words, what is the P(all 3 tests correctly result in non-rejection of null hypothesis that satellite is NOM | satellite is NOM)? To compute this number, we use the complement rule and the above computation as follows:

$P(\ all\ 3\ tests\ correctly\ result\ in\ non\ rejection\ of\ the\ null\ hypothesis\ that\ the\ satellite\ is\ NOM\ |\ satellite\ is\ NOM)$

$$= 1 - P(null\ hypothesis\ is\ rejected\ in\ at\ least\ one\ of\ the\ 3\ tests\ of\ H_0\ |H_0\ is\ true)$$

$$= 1 - P\left(\bigcup_i \{test\ i\ rejects\ H_0\} \Big| H_0\ is\ true\right) \geq \sum_i P(test\ i\ rejects\ H_0 \mid H_0\ is\ true)$$

$$= 1 - 3\alpha$$

In other words, we perform the 3 tests on a single satellite at level 0.05. Moreover, suppose that none of the 3 tests results in a rejection of the null hypothesis that the satellite is NOM. Using our composite testing methods, we are led to conclude that the satellite is NOM. By the above computation, we recognize that our method has at least a 0.85 probability of correctly concluding that satellite is NOM.

8.0 Examples
To illustrate the three methods described in Section 4.0, we will consider the three satellite cluster shown previously in Fig. 5. The three satellites denoted as S_1, S_2, and S_3, and their signatures are displayed in Fig. 13 - Fig. 15. This is the same data as in Fig. 2 - Fig. 4. The observations were simulated as taken from a space-based sensor. The observations for S_1 span 7 days, while the observations for S_2 and S_3 only span 5 days. The number of days of observation can be visualized by counting the daytime gaps in Fig. 2 - Fig. 4.

Each data set was divided into two parts. The first portion was used to simulate a set of baseline data. A baseline is data which has been reviewed by a human or passed a collection of statistical tests in order to verify which satellite the observations belong to and that the satellite's state is nominal (i.e., NOM). The second portion of data represents the new incoming observations for that satellite. The baseline is used to determine what results we can expect for a particular satellite, and these expectations can be used to verify the current state of the satellite from the new observations. Fig. 13 - Fig. 15 display the three data sets used for the examples. The blue points in each graph represent the observations used as the baseline for that satellite, while the red points represent the new observations which are being tested with each of the three methods.
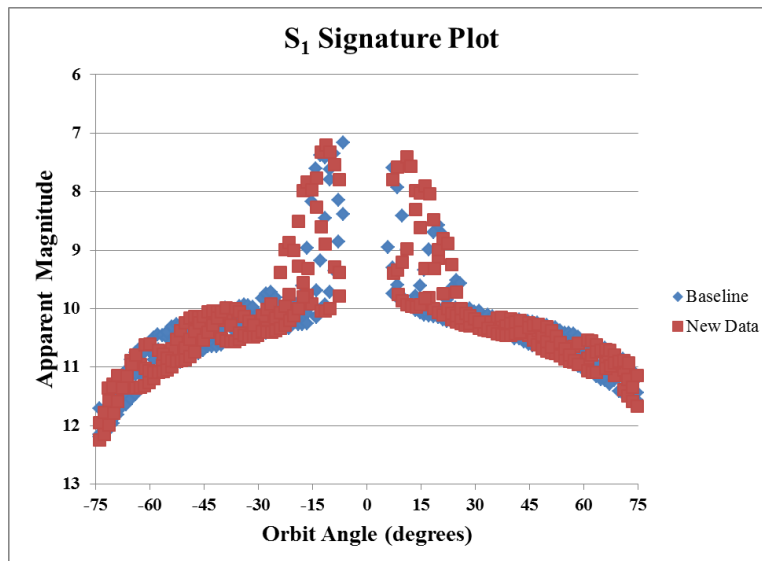
Fig. 13. Satellite S₁ Signature Plot
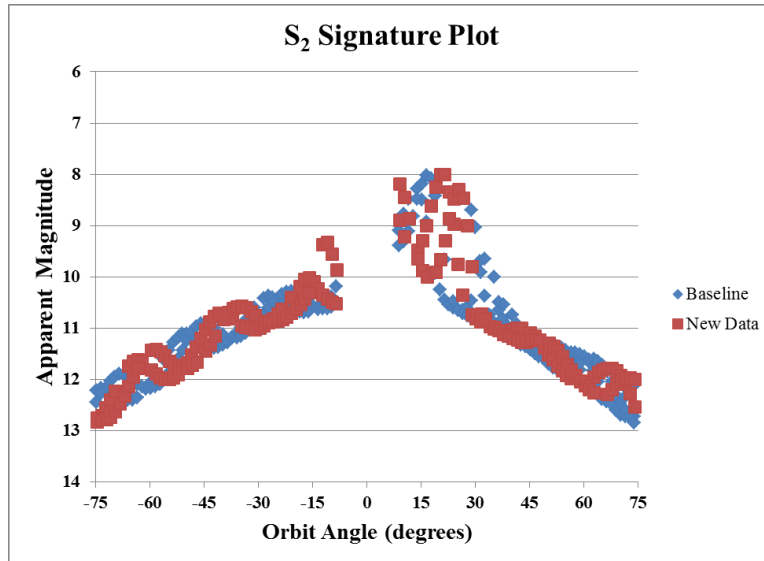
Fig. 14. Satellite S$_2$ Signature Plot
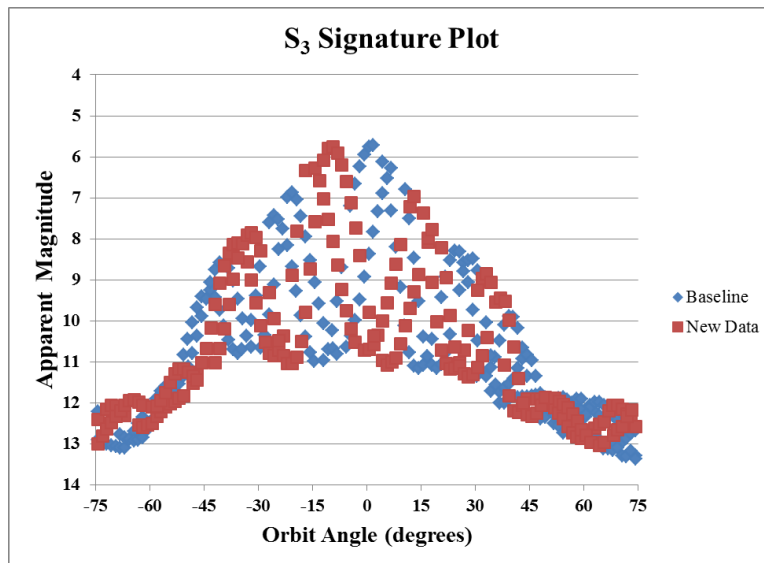
Fig. 15. Satellite S$_3$ Signature Plot

Once the baseline and the new data sets were created for each satellite, the baseline values were further reduced by randomly selecting points from the data. Since there is no guarantee how much data will be provided, we want to use these tests on the minimum amount of data, so we generate sparse baseline data sets of 31 or 32 points. This way, even when using the differences in the r_k values, we will still have 30 points and the Central Limit Theorem for Dependent Data will be valid for the Z-test method. To generate the sparse data, we sorted by orbit angle. We took the total number of points divided by 30 to determine how often to select an observation. Then, we randomly selected a point that frequently to get 31 or 32 observations. The resulting signature graphs for the three satellites are shown in Fig. 16 - Fig. 18. This reduced data was utilized in order to perform the change detection and data association.
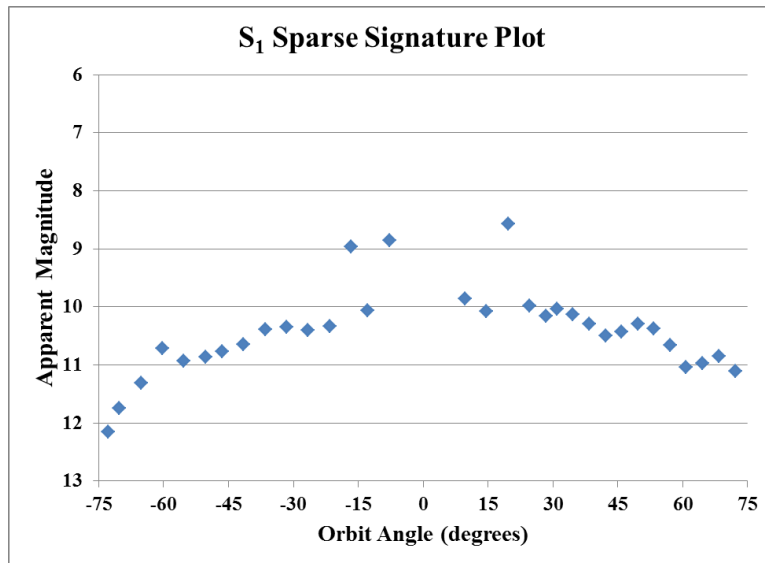
Fig. 16. Satellite S₁ Sparse Signature Plot
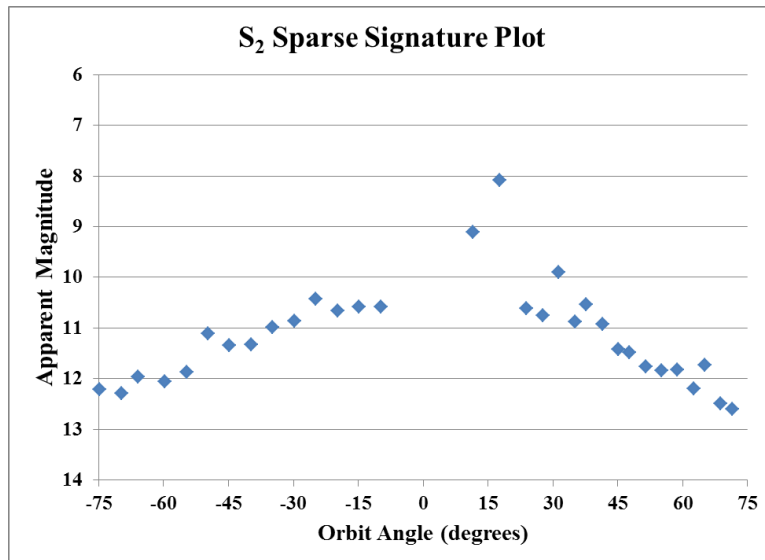
Fig. 17. Satellite S₂ Sparse Signature Plot

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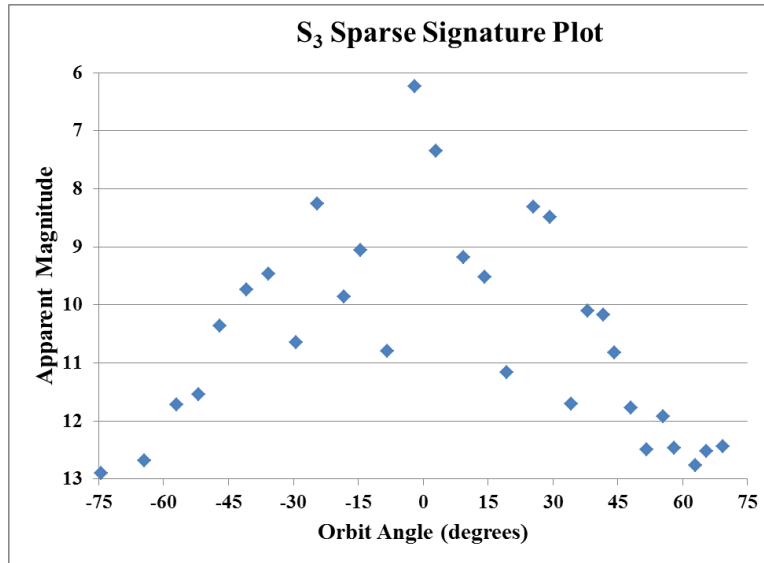
Fig. 18. Satellite S₃ Sparse Signature Plot

From the three data sets, we can construct 6 more data sets. From these 9 data sets, we can create 6 different potential cross-tag situations which are displayed in Table 1. The analysis of these six cases and their resolutions are presented in section 8.0. Each example describes how a cross-tag anomaly is resolved to allow for correct data association. Section 9.0 describes an efficient way to collect data using maximum information entropy.

Table 1. Possible Cross-tag Situations

Example	Satellite S_1:	Satellite S_2:	Satellite S_3:
1	NOM	NOM	NOM
2	Cross-tagged as S_2	Cross-tagged as S_1	NOM
3	Cross-tagged as S_3	NOM	Cross-tagged as S_1
4	NOM	Cross-tagged as S_3	Cross-tagged as S_2
5	Cross-tagged as S_2	Cross-tagged as S_3	Cross-tagged as S_1
6	Cross-tagged as S_3	Cross-tagged as S_1	Cross-tagged as S_2

8.1   Method Parameters

8.1.1   Z-test for Dependent Data

The Z-test used here is based on a Central Limit Theorem for dependent data. There are no population assumptions necessary, but if the sample size is sufficiently large, the sample mean values have an approximately normal distribution from the Central Limit Theorem. Therefore, as long as we have at least 30 values, it is reasonable to apply the Central Limit Theorem for dependent data. For the examples, we will use the Z-test for dependent data on both the r values and the $P(NOM|r_k)$ values.

8.1.2   Classical Sequential Analysis

The classical sequential analysis method has one main assumption, and it is that the observed sequence values are independent. To determine if the r_k values or the Δr_k values are independent or not, we use the sample correlation. We also create a histogram of the values to evaluate if it is approximately normal. If the random variables appear to be uncorrelated with an approximately normal distribution, then we will assume independence and can use those values for the classical sequential analysis method. The sparse baseline r values are shown in Fig. 19 - Fig. 21.
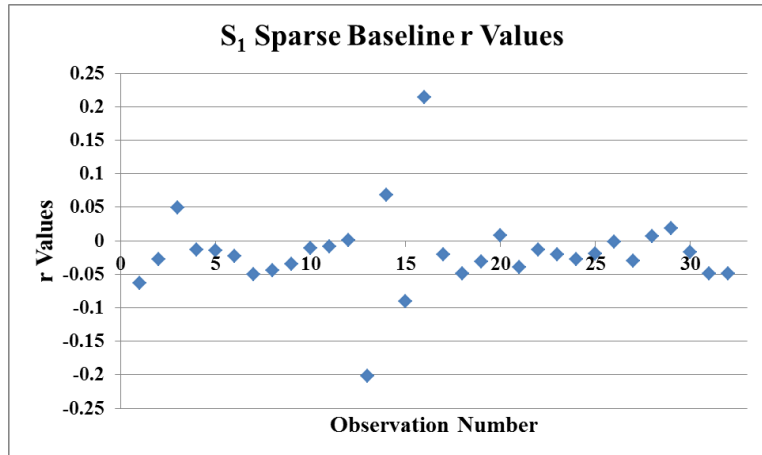
Fig. 19. Satellite S₁ Sparse r Baseline
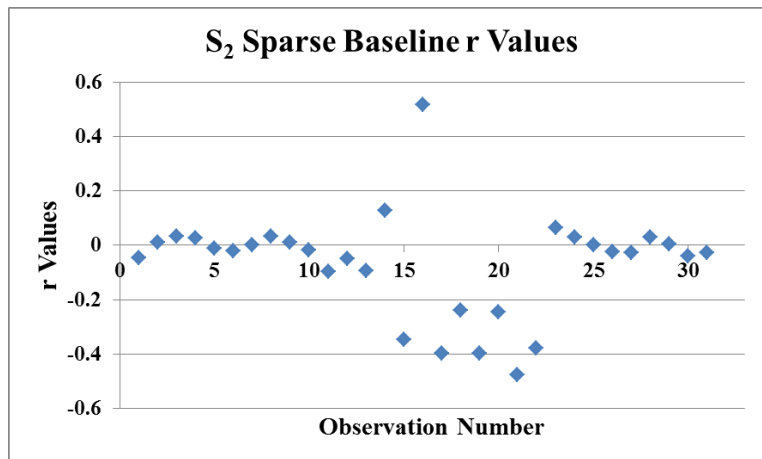
Fig. 20. Satellite S₂ Sparse r Baseline
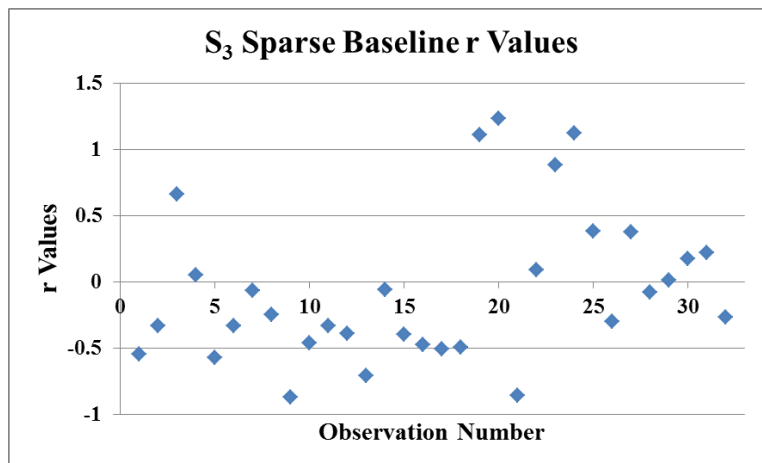
Fig. 21. Satellite S₃ Sparse r Baseline

To determine if the r_k and r_{k+1} values are correlated, we first calculated the correlation coefficient for each satellite for the sparse baseline values. Then, we used a t-test with $\alpha = 0.05$ on the null hypothesis that the correlation coefficient is equal to zero. The results for the r values are in Table 2, while the results for the Δr values are in Table

3. If the correlation coefficient is within the non-rejection region of the t-test determined by $\alpha = 0.05$, then we cannot reject the null hypothesis that the correlation coefficient is zero and therefore, that the values are uncorrelated.

Table 2. r Value Correlation Results

Satellite	Correlation Coefficient	Test statistic value	Non-rejection Region	Conclusion
S_1	-0.3521	-2.0259	(-2.045, 2.045)	uncorrelated
S_2	0.0007	0.0035	(-2.048, 2.048)	uncorrelated
S_3	0.3005	1.6969	(-2.045, 2.045)	uncorrelated

Table 3. Δr Value Correlation Results

Satellite	Correlation Coefficient	Test statistic value	Non-rejection Region	Conclusion
S_1	-0.7021	-5.2176	(-2.048, 2.048)	correlated
S_2	-0.6946	-5.0169	(-2.052, 2.052)	correlated
S_3	-0.1704	-0.9313	(-2.048, 2.048)	uncorrelated

Looking at Table 2, we see that by the t-test the baseline r values for all three satellites are uncorrelated. However, Table 3 shows us that the Δr values are only uncorrelated for S_3. Thus, we can use the classical sequential analysis on all three satellites for their r values, but we can only use it on the Δr values for S_3.

The data being uncorrelated is a necessary condition for the data to be independent, but to assure the data is independent, we must also satisfy a sufficient condition, such as the data is normally distributed. To determine if the sparse baseline r values are approximately normal, we plotted the histogram of the r values from Fig. 19 - Fig. 21. Fig. 22 shows the histogram of the baseline values for S_1, and the histogram supports normality. Fig. 23 displays the r value histogram for S_2, and it also supports normality. Fig. 24 illustrates the r value histogram for S_3. It does not appear normal. We will proceed with the assumptions that S_1 and S_2 are normal distributed.
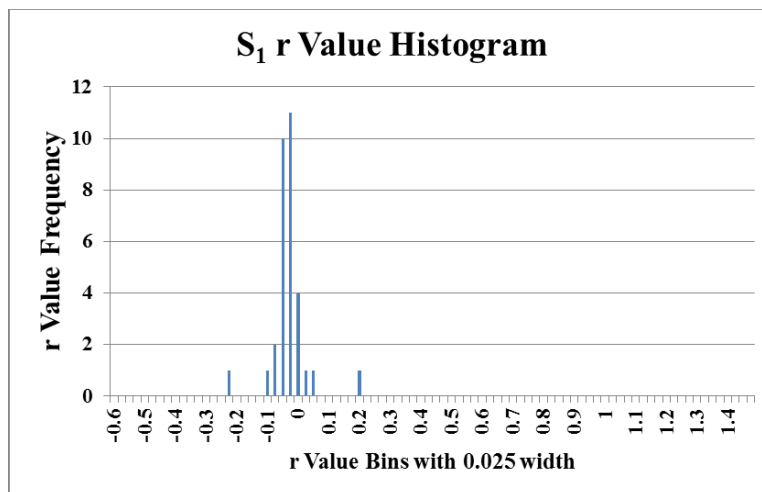
Fig. 22. Histogram of S_1 Baseline r Values
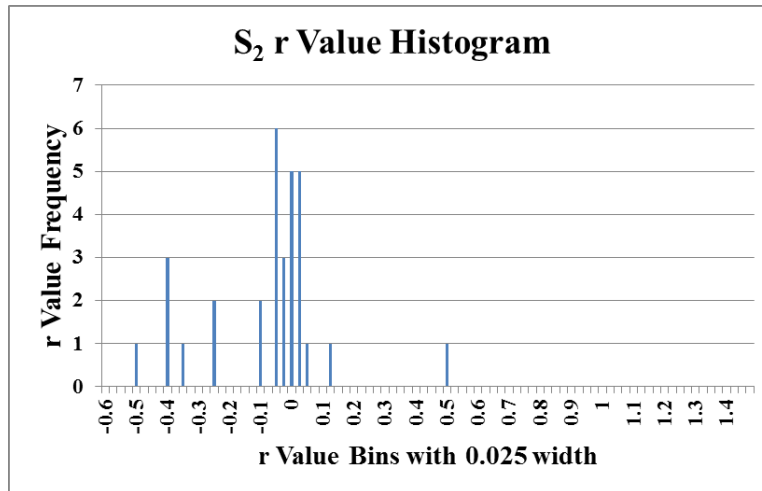
Fig. 23. Histogram of S₂ Baseline r Values
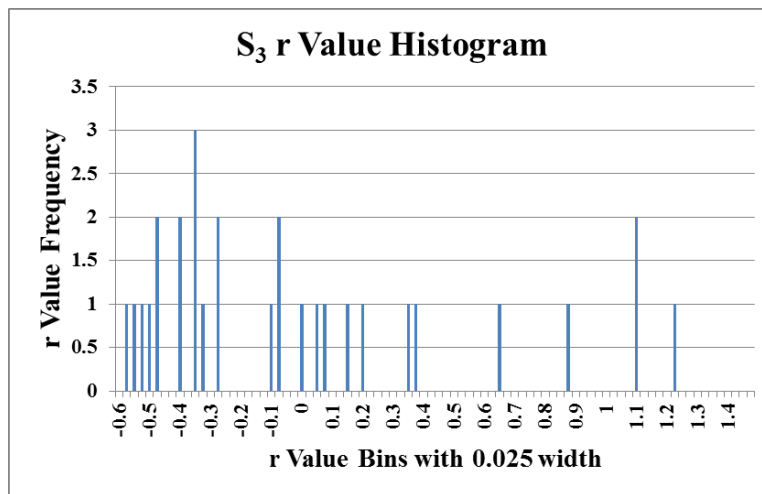
Fig. 24. Histogram of S₃ Baseline r Values

The full baseline for the Δr values is displayed in Fig. 25, and their histogram is shown in Fig. 26 to better demonstrate that the Δr values for S_3 are approximately normal. Therefore, we can assume the Δr values for S_3 are independent and use them for the classical sequential analysis method.
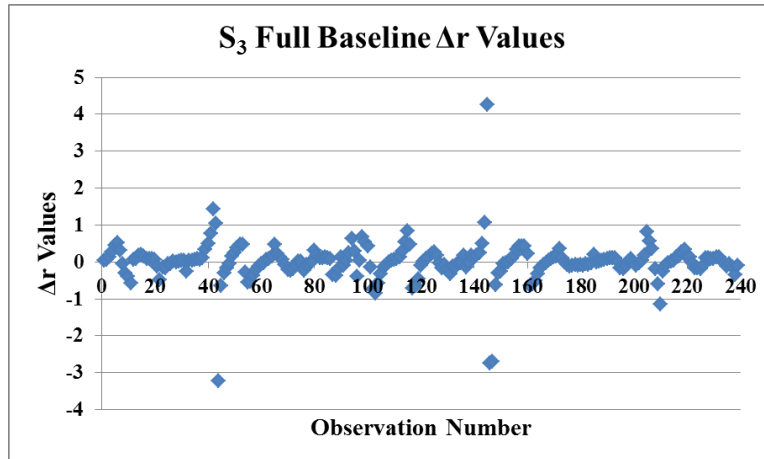
Fig. 25. Satellite S$_3$ Full Δr Baseline
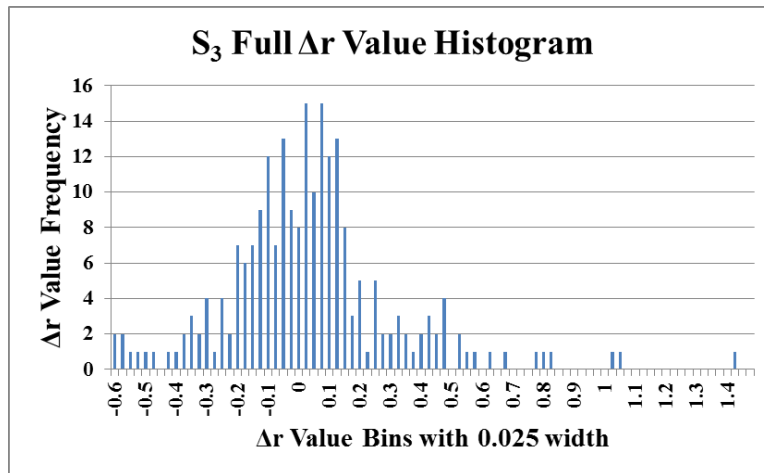
Fig. 26. Histogram of S$_3$ Full Baseline Δr Values

8.1.3   Brownian Motion Drift Analysis

The Brownian motion drift method requires the most assumptions. It requires the difference in values (between consecutive observation points) to be independent and normally distributed. Thus, if we are to use the r values for Brownian motion, then the Δr values must be independent and normally distributed. Unfortunately, for these examples the Δr values for S$_1$ and S$_2$ are not independent, since they are correlated, as demonstrated in Table 3. Therefore, we cannot use the Brownian motion method for S$_1$ and S$_2$. The Δr values for S$_3$ are independent and normally distributed as described in Section 8.1.2, so we can use the Brownian motion drift analysis for S$_3$.

8.2   Example 1

The examples consider that a regular but sparse collection of data is ongoing. Example 1 is the situation where all three satellites are still NOM. Therefore, there are no cross-tags present as seen in Fig. 27. The results are shown when 30 (i.e. k = 30) new observation data points have been collected. Note that the use of k = 30 is only meant for illustration. The same calculations are valid for any value of $k \geq 0$.

Example 1

Fig. 27. Example 1 Input Data

8.2.1 Z-test on r Values

Fig. 28 - Fig. 30 demonstrate the results of the Z-test for dependent data on r values for Example 1. Since the state of all three satellites remains NOM, we expect the Z-test for dependent data to determine that we should accept the null hypothesis, H_o. By looking at the three figures, we see that this is indeed the case for Satellite 1 and Satellite 2. However, Satellite 3 rejects the null hypothesis and concludes the satellite occurred a change at k=9 (or, for the cases when k < 9, this test would have determined Satellite 3 to be NOM). This conclusion can be further explained by referring to Fig. 15. In this plot, the new data's peaks align with the baseline's valleys, so the method is unable to detect NOM up to k = 30.
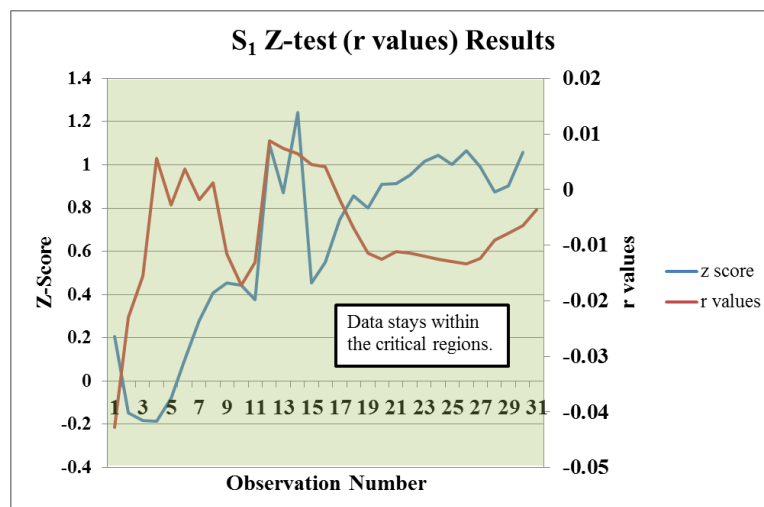
Fig. 28. Example 1 S_{1-1} Z-test on r values Results
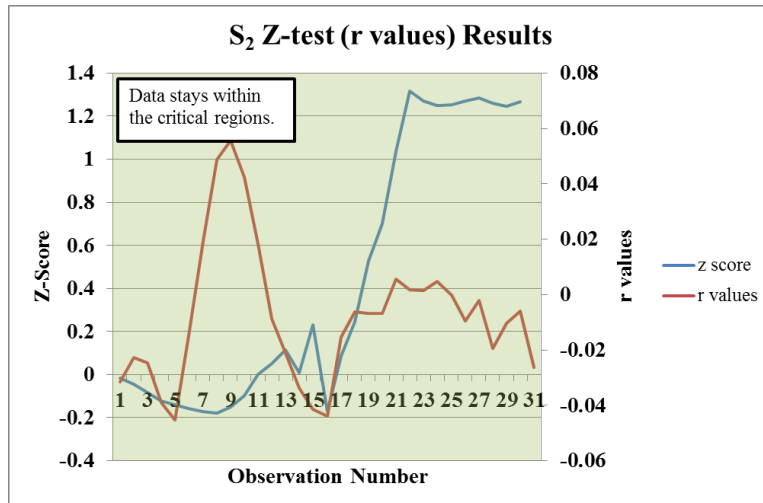
Fig. 29. Example 1 S_{2-2} Z-test on r values Results
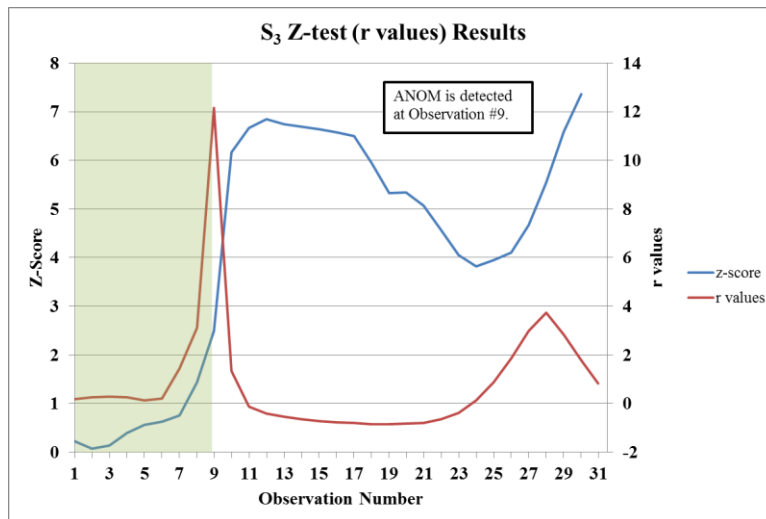
Fig. 30. Example 1 S_{3-3} Z-test on r values Results

8.2.2 Classical Sequential Analysis

Fig. 31 - Fig. 33 demonstrate the results of the classical sequential analysis method for Example 1. Since the state of all three satellites remains NOM, we expect the classical sequential analysis to determine we should accept the null hypothesis, H_o. By looking at the three figures, we see that this is the case for all the satellites. Thus, the classical sequential analysis provides us with the correct results for Example 1.
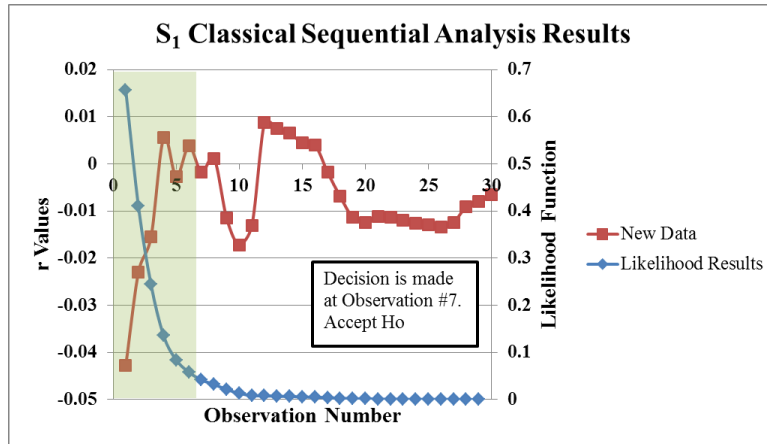
Fig. 31. Example 1 S_{1-1} Classical Sequential Analysis Results
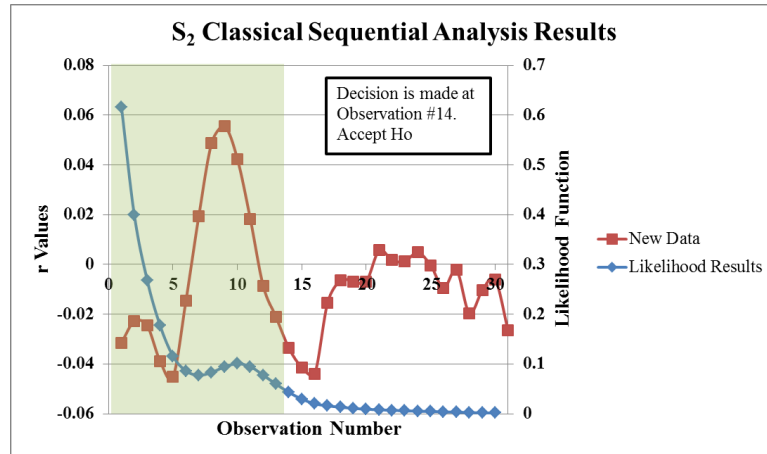
Fig. 32. Example 1 S_{2-2} Classical Sequential Analysis Results
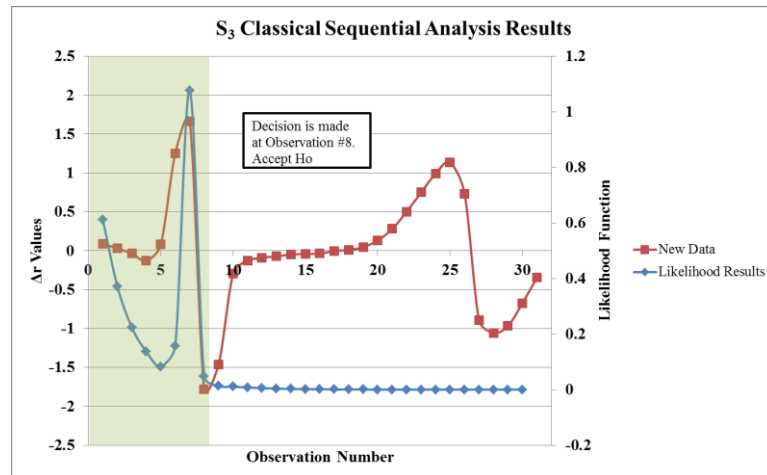
Fig. 33. Example 1 S_{3-3} Classical Sequential Analysis Results

8.2.3 **Brownian Motion Drift Analysis**

Fig. 34 shows the results of the Brownian motion drift analysis for Example 1 for S_3. Since all three satellites remain NOM, we expect the Brownian motion test to conclude that we should accept H_o and match the classical sequential analysis results. From Fig. 34, we see this is the case, and the Brownian motion test provides us with consistent results for Example 1.
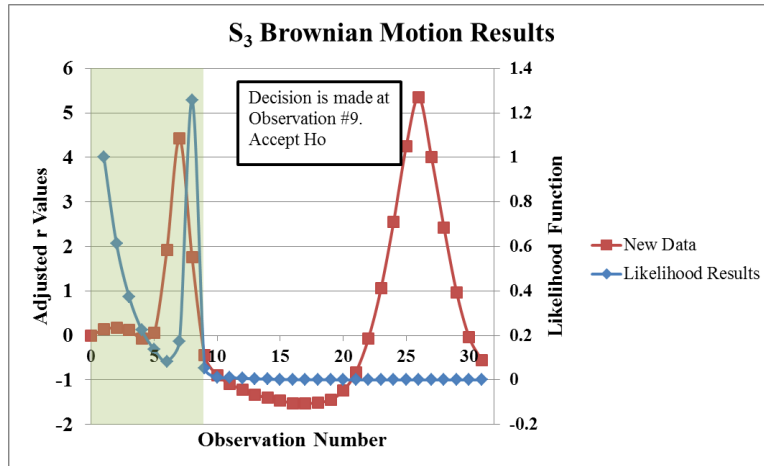
Fig. 34. Example 1 $S_{3\text{-}3}$ Brownian Motion Results

8.2.4 **Z-test on P(NOM|r) Values**

Fig. 35 - Fig. 37 demonstrate the results of the Z-test for dependent data method performed on the P(NOM|r) values for Example 1. Since the state of all three satellites remains NOM, we expect the Z-test for dependent data to determine that we should accept the null hypothesis, H_o. By looking at the three figures, we see that this is the case for all the satellites. Thus, the Z-test for dependent data on the P(NOM|r) values provides us with the correct results for Example 1.
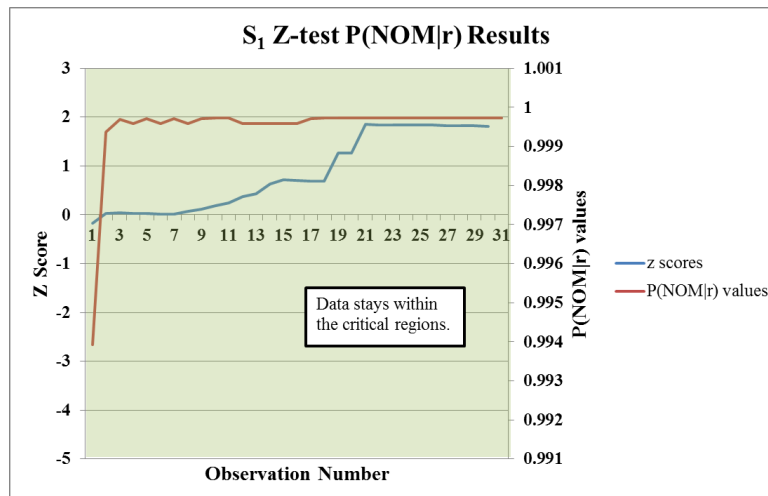
Fig. 35. Example 1 $S_{1\text{-}1}$ Z-test on P(NOM|r) Results
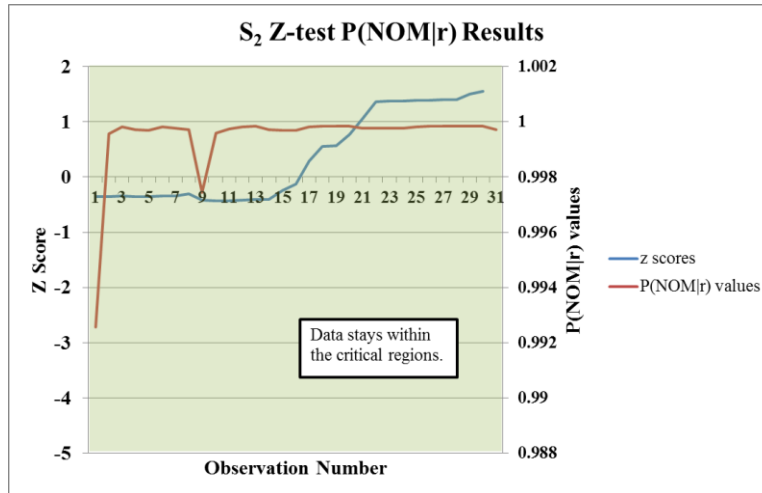
Fig. 36. Example 1 S_{2-2} Z-test on P(NOM|r) Results
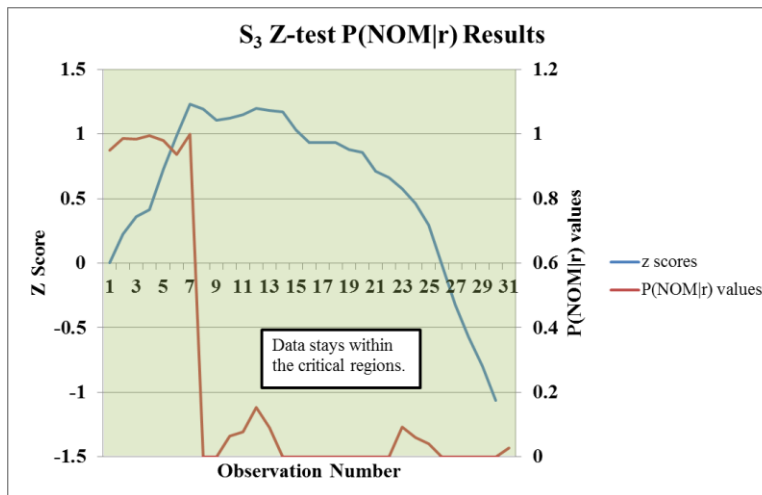
Fig. 37. Example 1 S_{3-3} Z-test on P(NOM|r) Results

8.2.5 Data Association

Table 4 shows the results for the three tests we are able to perform on all three satellites. For S_1, all three tests conclude it is still NOM, so we will accept that S_1 is NOM. All three tests also conclude S_2 is still NOM, so we will accept that it is also NOM. For S_3, the Z-test for dependent data on r values concluded it was ANOM. Since both of the other two satellites are NOM, we know that S_3 is not cross-tagged with another satellite in its cluster, but we do not know whether the satellite is truly NOM or if something else has happened, such as a panel offset change, to cause the satellite to now be ANOM. This is addressed in Section 7.

Table 4. Example 1 Results Chart

Satellite	r Value Z-test	Classical Sequential Analysis	P(NOM|r) Z-test
S_1	NOM	NOM	NOM
S_2	NOM	NOM	NOM
S_3	ANOM	NOM	NOM

8.3   Example 2

Example 2 is where the baseline data for S_1 is paired with the new data from S_2 (orange box), which we will denote as S_{1-2} and is shown in Fig. 39.The baseline data for S_2 is paired with the new data from S_1 (yellow box), denoted as S_{2-1} as shown in Fig. 40. This creates a cross-tag between S_1 and S_2. Fig. 38 depicts the new input data for Example 2. Fig. 39 and Fig. 40 show how the signature of the baseline satellite matches the signature of the satellite of the new observations. For S_{1-2} and S_{2-1}, the signatures do not have significant overlap, so we expect all four methods to produce accurate results because the r and P(NOM | r) values should be distinct. Lastly, the baseline of S_3 is paired correctly with the new data from S_3 (magenta box), so S_3 is still NOM.

Example 2

Fig. 38. Example 2 Input Data
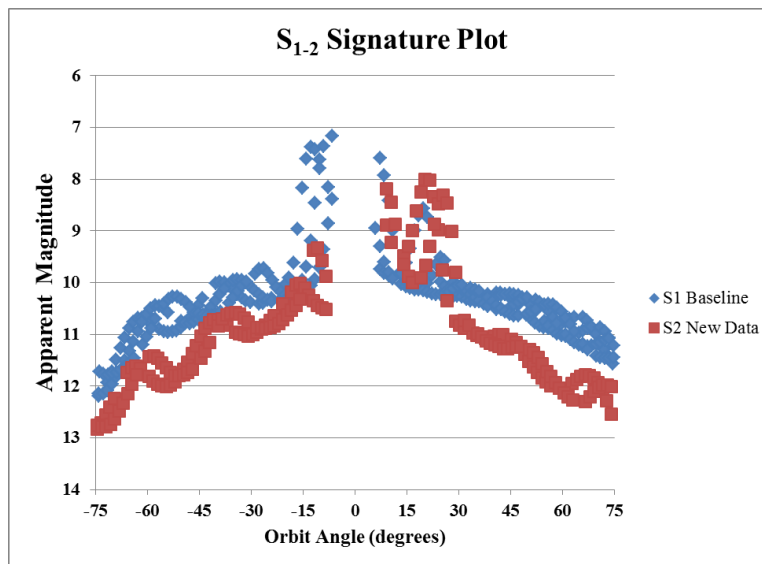
Fig. 39. S_{1-2} Signatures
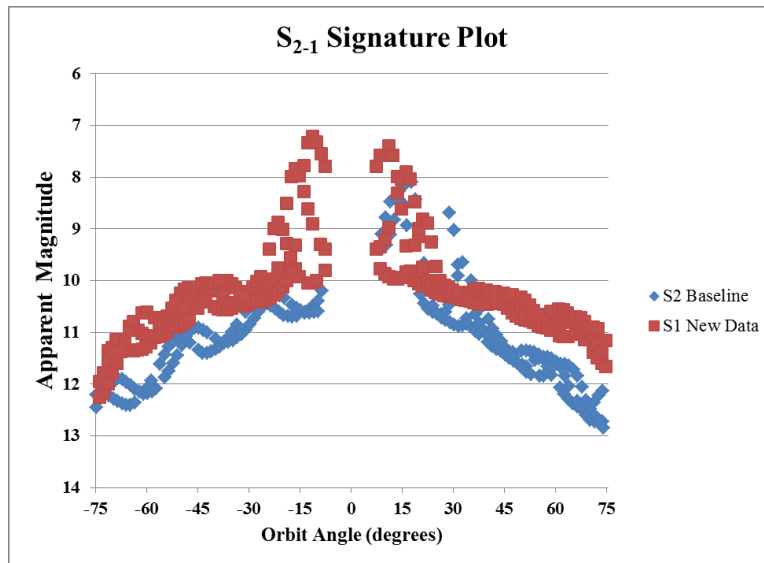
Fig. 40. S$_{2-1}$ Signatures

8.3.1 Z-test on r values

The Z-test for dependent data results using the r values for Example 2 are shown in Fig. 41 - Fig. 43. Since there is a cross-tag between S$_1$ and S$_2$, we expect to accept H$_a$ for S$_1$ and S$_2$ and accept H$_o$ for S$_3$.The Z-test does correctly conclude H$_a$ for S$_1$ and S$_2$; however, as in Example 1, S$_3$ is cross-tagged with itself, so the reason we accept H$_a$ is stated in Section 8.2.1.
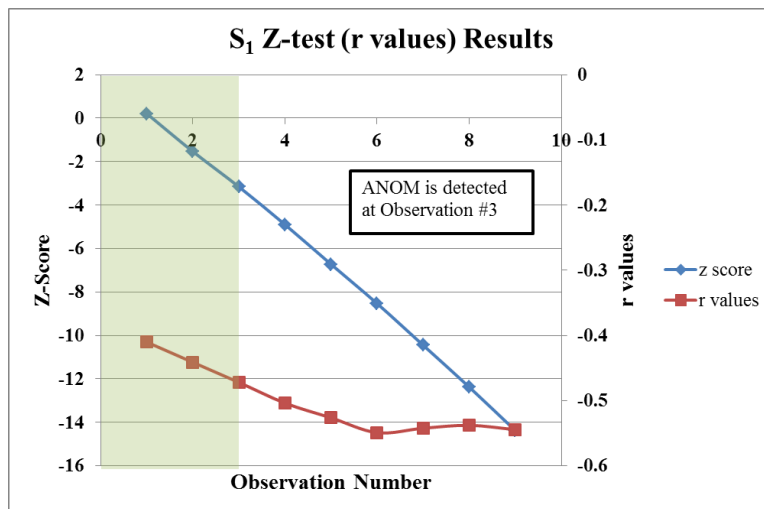
Fig. 41. Example 2 S$_{1-2}$ Z-test on r values Results
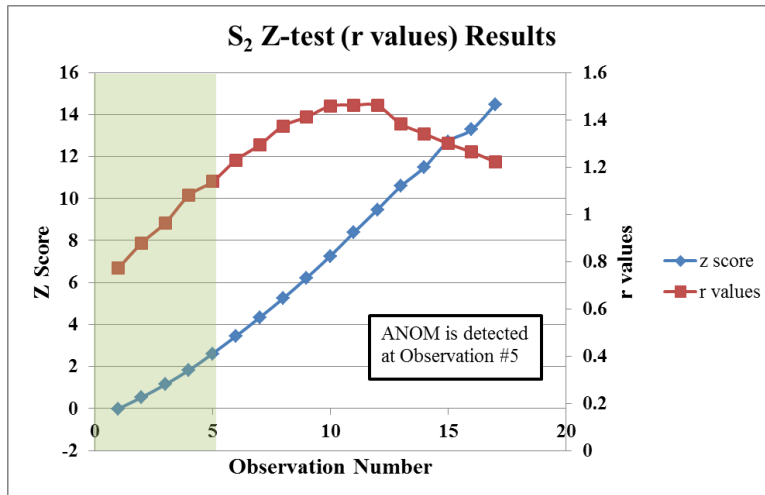
Fig. 42. Example 2 $S_{2\text{-}1}$ Z-test on r values Results
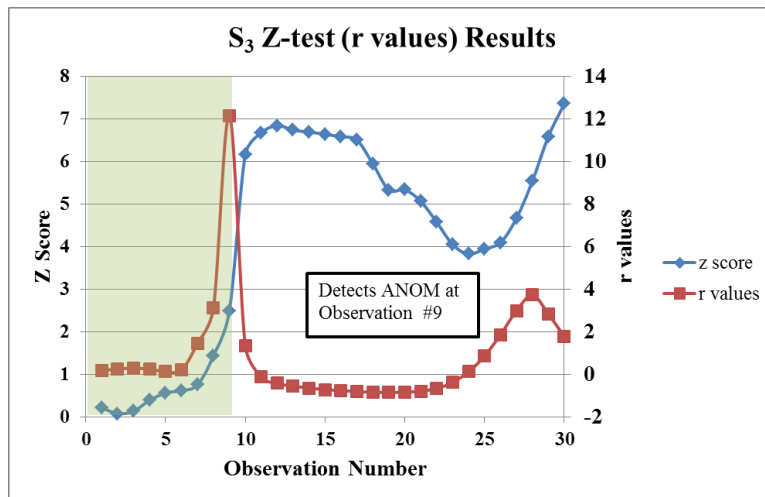
Fig. 43. Example 2 $S_{3\text{-}3}$ Z-test on r values Results

8.3.2 Classical Sequential Analysis

The classical sequential analysis results for Example 2 are shown in Fig. 44 - Fig. 46. Since there is a cross-tag between S_1 and S_2, we expect to accept H_a for S_1 and S_2 and accept H_o for S_3. By looking at the three figures, we see that this is the case. Thus, the classical sequential analysis provides us with the correct results for Example 2.
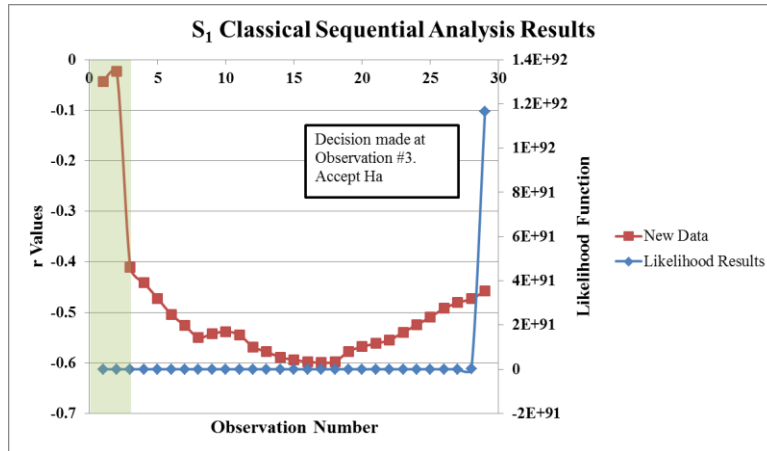
Fig. 44. Example 2 S_{1-2} Classical Sequential Analysis Results
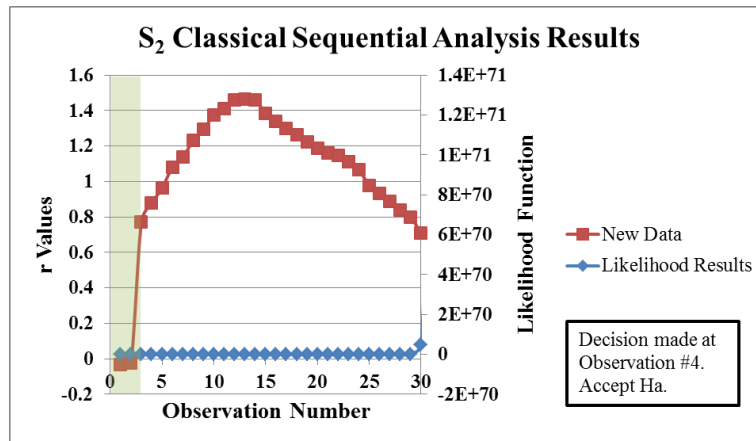
Fig. 45. Example 2 S_{2-1} Classical Sequential Analysis Results
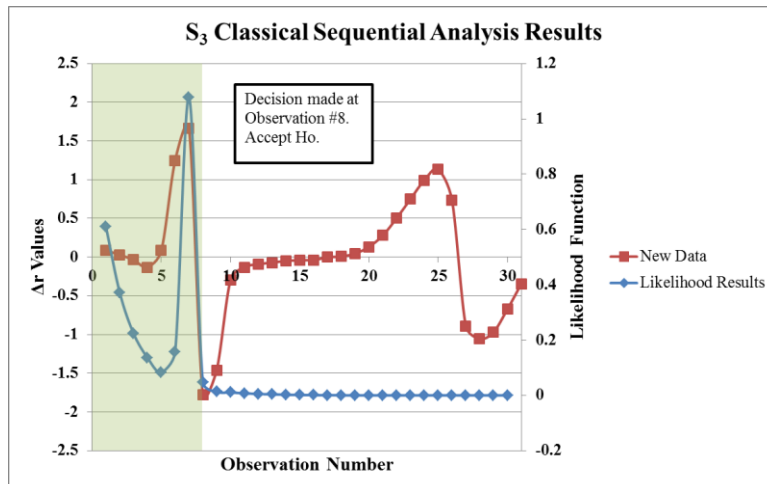
Fig. 46. Example 2 S_{3-3} Classical Sequential Analysis Results

8.3.3 Brownian Motion Drift Analysis

The Brownian motion drift analysis result for Example 2 is shown in Fig. 47. S_3 is paired with itself, so we expect to accept H_o. Fig. 47 indicates this is the case, so Brownian motion provides the correct result for S_3 by concluding that the drift is zero.
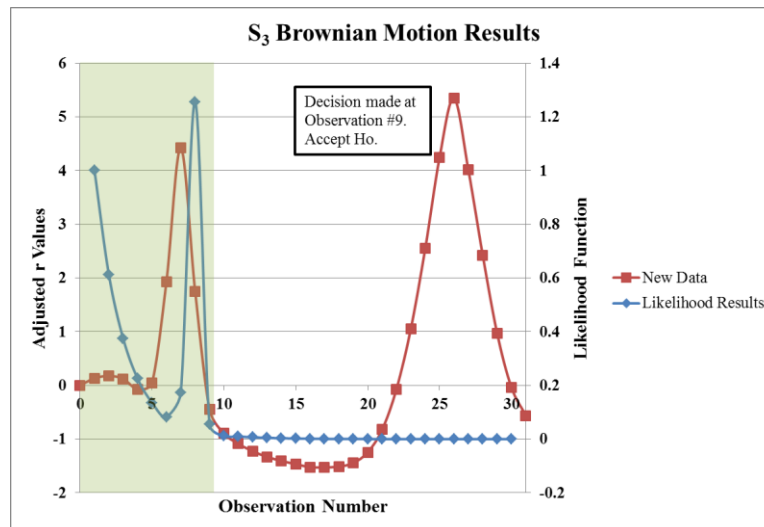
Fig. 47. Example 2 S_{3-3} Brownian Motion Results

8.3.4 Z-test on P(NOM|r) Values

The Z-test for dependent data results for Example 2 are shown in Fig. 48 - Fig. 50. Since there is a cross-tag between S_1 and S_2, we expect to accept H_a for S_1 and S_2 and accept H_o for S_3. By examining the three figures below, we see that the Z-test for dependent data performed on the P(NOM|r) values accepts H_a for S_1 and S_2 and accepts H_o for S_3. Thus, the Z-test for dependent data provides accurate results for Example 2.
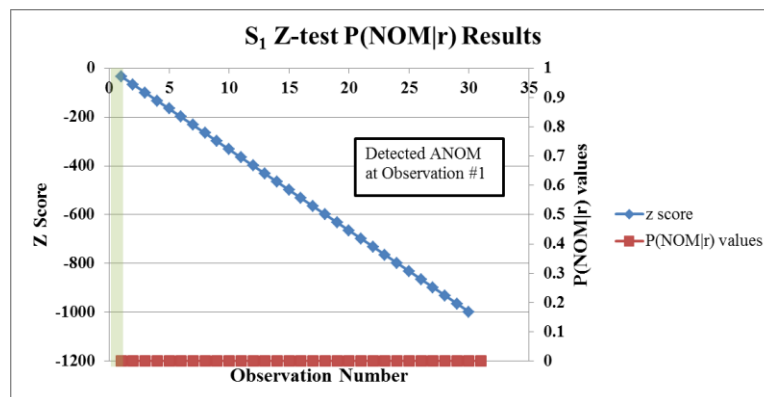
Fig. 48. Example 2 S_{1-2} Z-test on P(NOM|r) Results
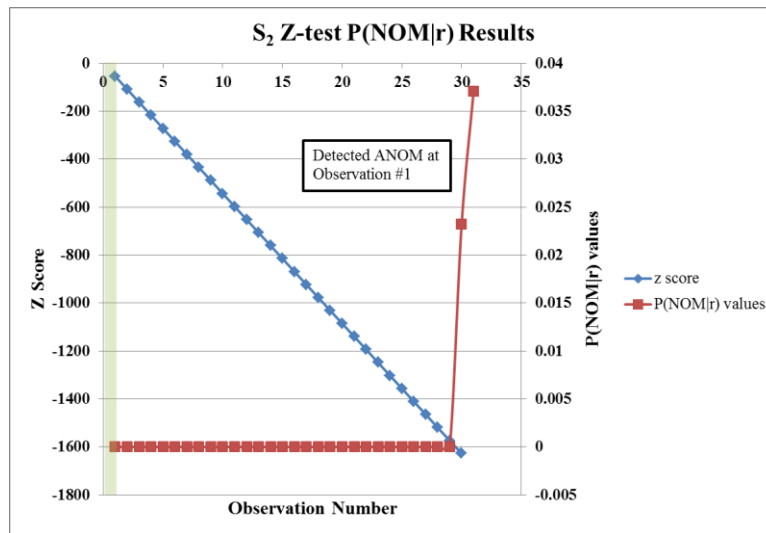
Fig. 49. Example 2 S$_{2\text{-}1}$ Z-test on P(NOM|r) Results
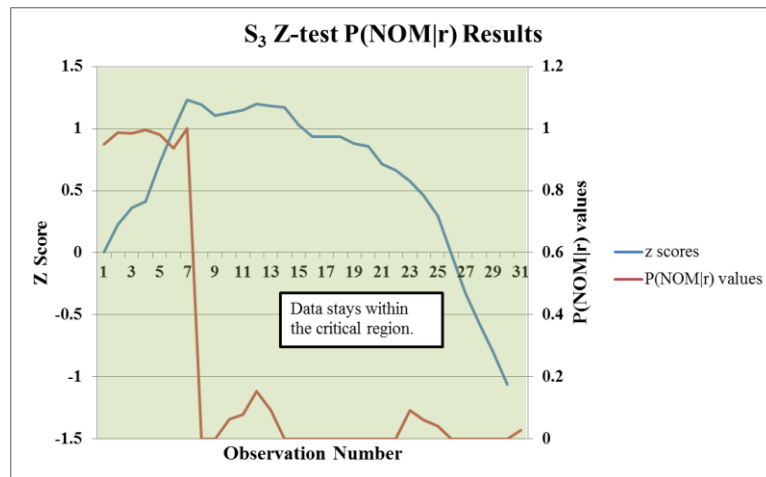
Fig. 50. Example 2 S$_{3\text{-}3}$ Z-test on P(NOM|r) Results

8.3.5 Data Association

Table 5 summarizes the results for the three main tests. For S$_1$ and S$_2$, all three tests conclude ANOM, so we accept that they are both ANOM. For S$_3$, two tests conclude NOM and one ANOM, so we cannot conclude whether S$_3$ is NOM or ANOM. To try to resolve the change in satellites S$_1$ and S$_2$, we swap their new data, so the new data we were using for S$_1$ (orange box) we will use for S$_2$ and the new data we were using for S$_2$ (yellow box) we will use for S$_1$. Thus, we result with the same situation as Example 1 as seen below in Fig. 51. Therefore, we can conclude that in the original data for Example 2 S$_1$ and S$_2$ were cross-tagged, but after resolving the cross-tag, S$_1$ and S$_2$ are NOM and we are unsure about S$_3$, although we know it is not cross-tagged.

Table 5. Example 2 Results Chart

Satellite	r Value Z-test	Classical Sequential Analysis	P(NOM|r) Z-test
S$_1$	ANOM	ANOM	ANOM
S$_2$	ANOM	ANOM	ANOM
S$_3$	ANOM	NOM	NOM

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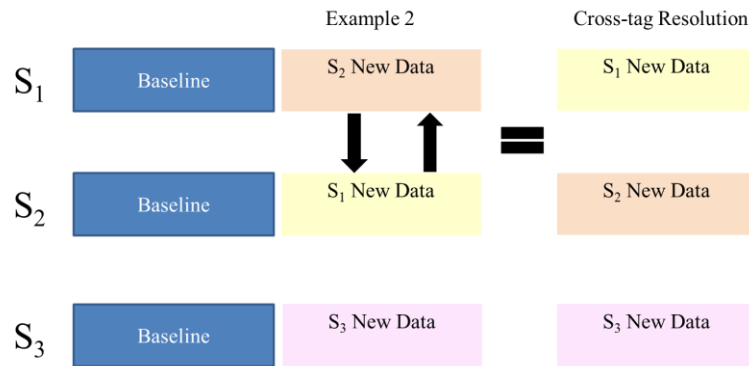
Fig. 51. Example 2 Cross-tag Resolution

8.4 Example 3

Example 3 contains a single cross-tag between S_1 and S_3, so the baseline data for S_1 is paired with the new data from S_3 (magenta box), S_{1-3} is shown in Fig. 53, and the baseline data for S_3 is paired with the new data from S_1 (yellow box); S_{3-1} is shown in Fig. 54. S_2, in this case, is still NOM. The input data for example 3 is illustrated in Fig. 52. Unlike the cross-tag between S_1 and S_2, where there was little overlap in the satellites' signatures, Fig. 53 and Fig. 54 show there is some overlap for the signatures of S_1 and S_3. Therefore, the methods in this section might have a harder time distinguishing between the two satellites.

Fig. 52. Example 3 Input Data
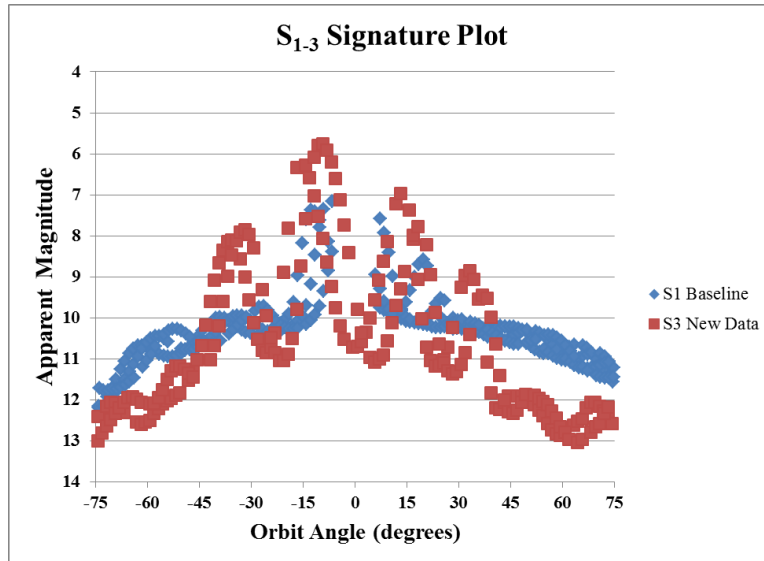
Fig. 53. S$_{1-3}$ Signatures
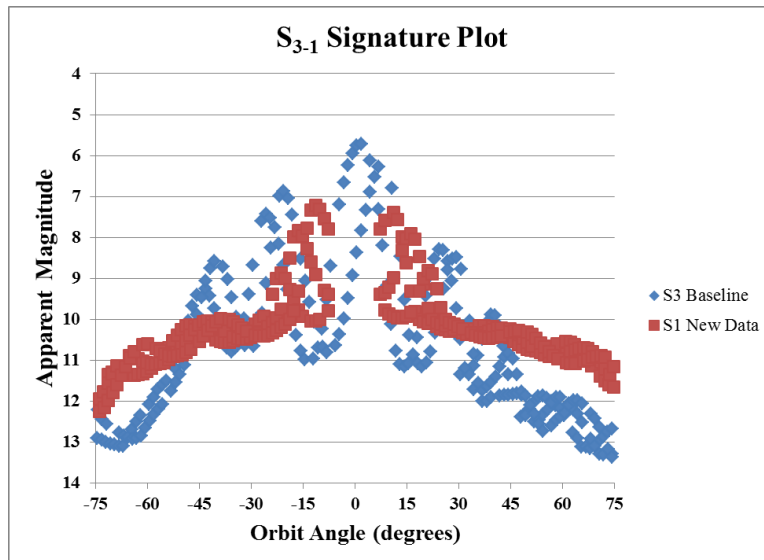
Fig. 54. S$_{3-1}$ Signatures

8.4.1 Z-test on r values

The Z-test for dependent data on r values results are provided in Fig. 55 - Fig. 57. Because S$_1$ and S$_3$ are cross-tagged, we anticipate this method to accept H$_a$ for S$_1$ and S$_3$ and accept H$_o$ for S$_2$. Thus, the Z-test for dependent data executed on r values provides accurate results for all three cases in Example 3.
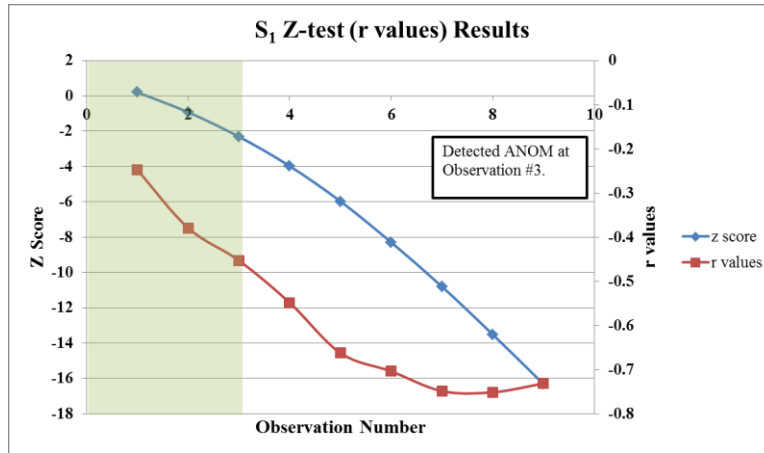
Fig. 55. Example 3 S_{1-3} Z-test on r values Results
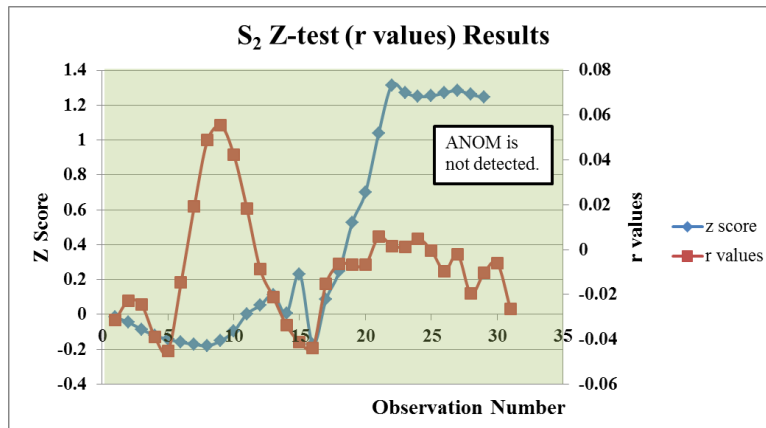
Fig. 56. Example 3 S_{2-2} Z-test on r values Results
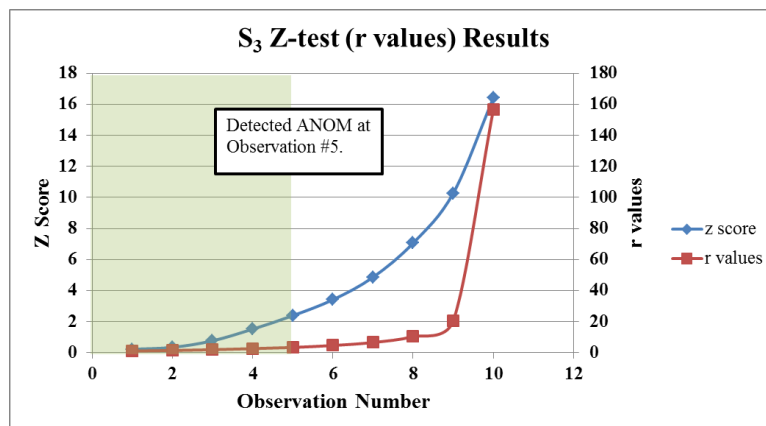
Fig. 57. Example 3 S_{3-1} Z-test on r values Results

8.4.2 Classical Sequential Analysis

Example 3 contains a cross-tag between S_1 and S_3, so we expect to accept H_a for S_1 and S_3 and accept H_o for S_2. The classical sequential analysis results for this example are shown in Fig. 58 - Fig. 60, and although it took longer to determine S_2 is NOM, we get the results we expect.
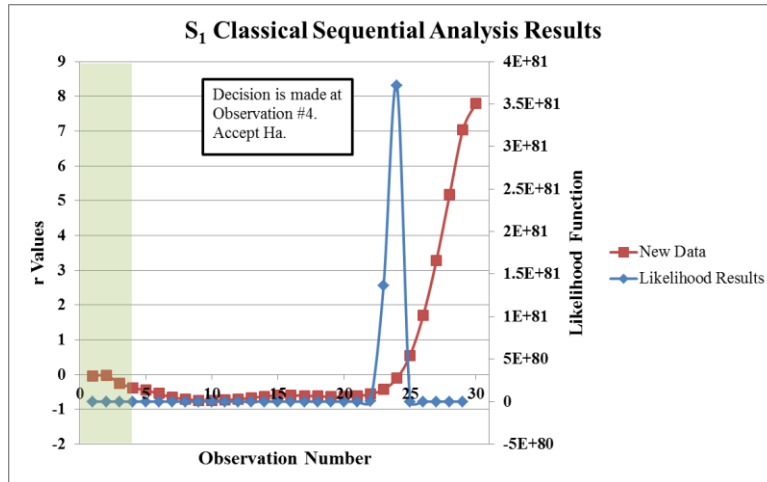
Fig. 58. Example 3 S$_{1-3}$ Classical Sequential Analysis Results
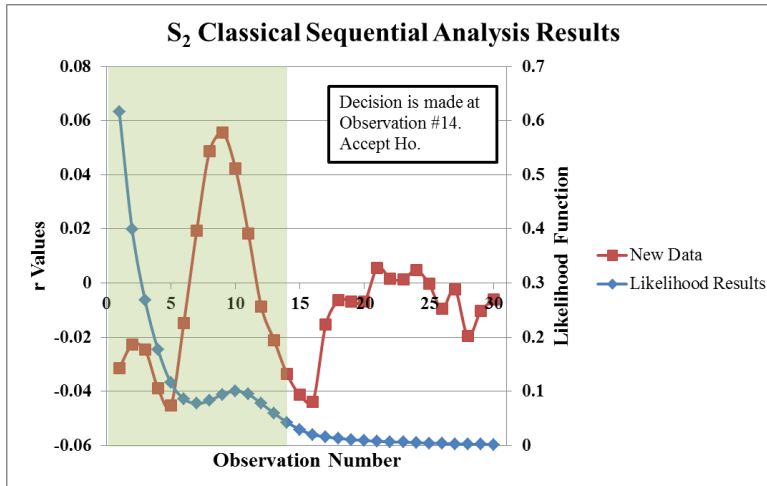
Fig. 59. Example 3 S$_{2-2}$ Classical Sequential Analysis Results
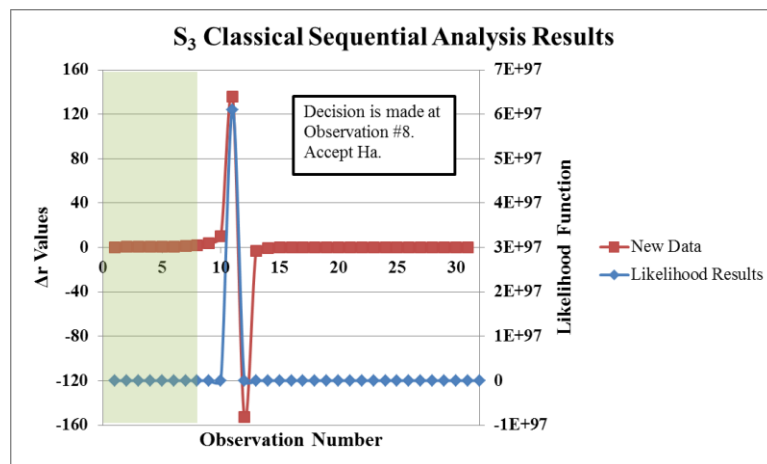
Fig. 60. Example 3 S$_{3-1}$ Classical Sequential Analysis Results

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8.4.3 Brownian Motion Drift Analysis

The result of the Brownian drift motion analysis for Example 3 is displayed in Fig. 61. The results for S_3 accurately conclude to accept H_a and confirm that there is a non-zero drift.
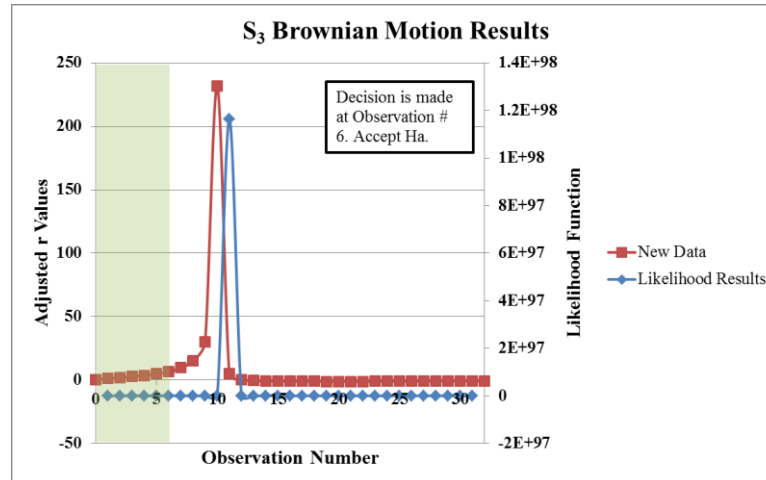
Fig. 61. Example 3 S_{3-1} Brownian Motion Results

8.4.4 Z-test on P(NOM|r) Values

The results for the Z-test for dependent data method performed on the P(NOM|r) values are shown in Fig. 62 - Fig. 64. In this example, S_1 and S_3 are cross-tagged, so we expect the test to accept H_a for S_1 and S_3. Conversely, S_2 receives new data from itself, so the test should accept the null hypothesis. Displayed below, the test correctly concludes to accept H_a for S_1 and accept H_o for S_2. The graph for S_3, on the other hand, accepts the null hypothesis, which does not correspond to what is expected.
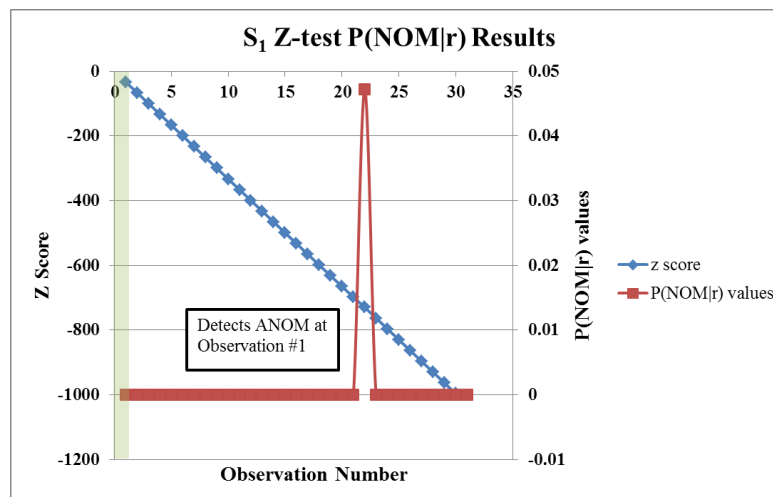
Fig. 62 Example 3 S_{1-3} Z-test on P(NOM|r) Results
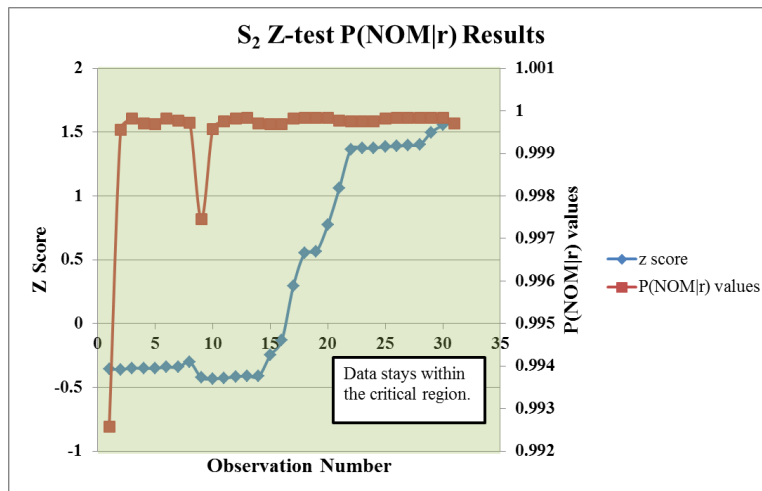
Fig. 63 Example 3 $S_{2\text{-}2}$ Z-test on P(NOM|r) Results
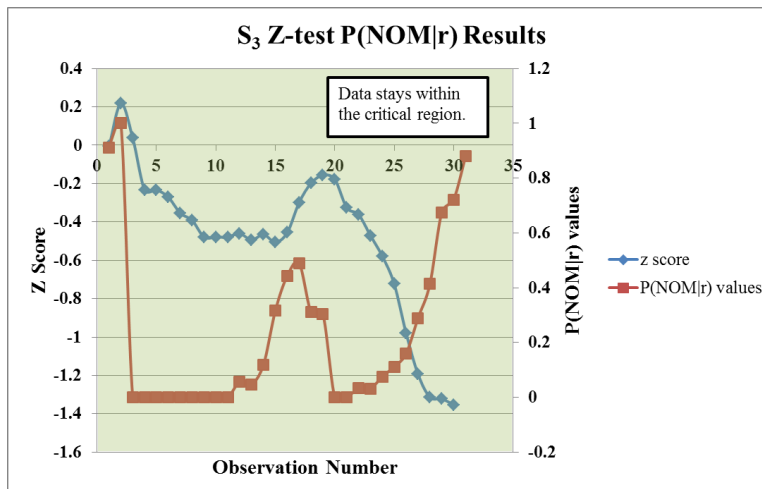
Fig. 64 Example 3 $S_{3\text{-}1}$ Z-test on P(NOM|r) Results

8.4.5 Data Association

Table 6 displays the overall results for Example 3. All three methods determine S_1 is ANOM and S_2 is NOM, so we will accept these conclusions. Only two methods conclude ANOM for S_3, so we are unsure of the state of S_3. To try to resolve why S_1 is ANOM we can swap its new data (magenta box) with the new data of S_3 (yellow box). Since Example 3 was created by swapping the new data of S_1 and S_3, this swap will correct the cross-tag, and we will have Example 1 again as seen in Fig. 65.

Table 6. Example 3 Results Chart

Satellite	r Value Z-test	Classical Sequential Analysis	P(NOM|r) Z-test
S_1	ANOM	ANOM	ANOM
S_2	NOM	NOM	NOM
S_3	ANOM	ANOM	NOM

Example 3   Cross-tag Resolution
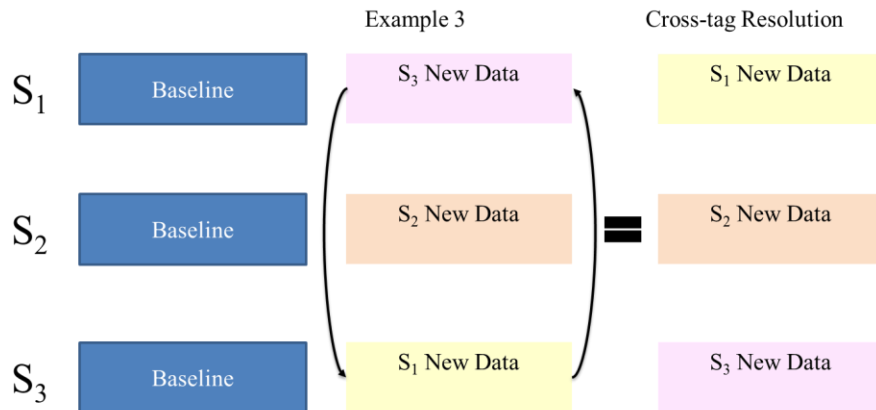
Fig. 65. Example 3 Cross-tag Resolution

8.5 Example 4

Example 4 is the last example with a single cross-tag. The cross-tag is between S_2 and S_3, so the baseline data for S_2 is paired with the new data from S_3 (magenta box), $S_{2\text{-}3}$ shown in Fig. 67, and the baseline data for S_3 is paired with the new data from S_2 (orange box), $S_{3\text{-}2}$ shown in Fig. 68. Thus, S_1 is NOM. The cross-tag between S_2 and S_3 has considerable overlap for the signatures of S_2 and S_3 as can be seen in Fig. 67 and Fig. 68. Therefore, the methods have a harder time distinguishing between the two satellites, and consequently, they might not be able to detect the cross-tag.
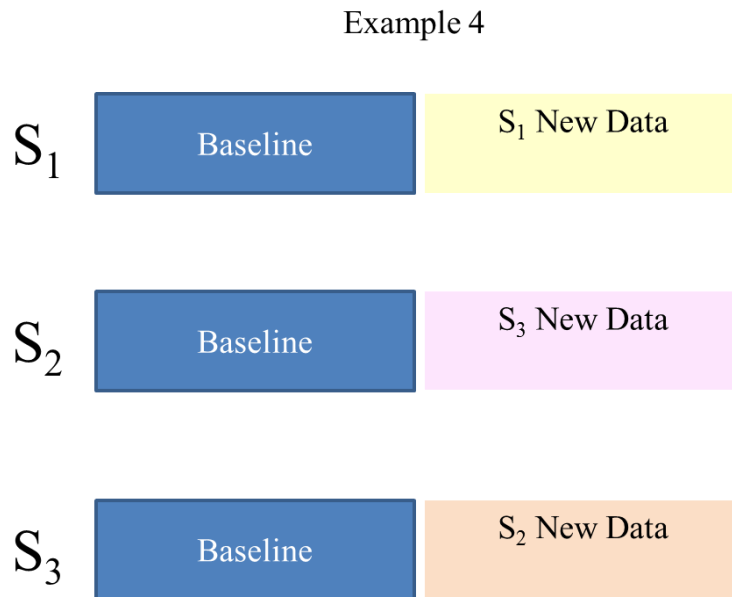
Example 4

Fig. 66. Example 4 Input Data
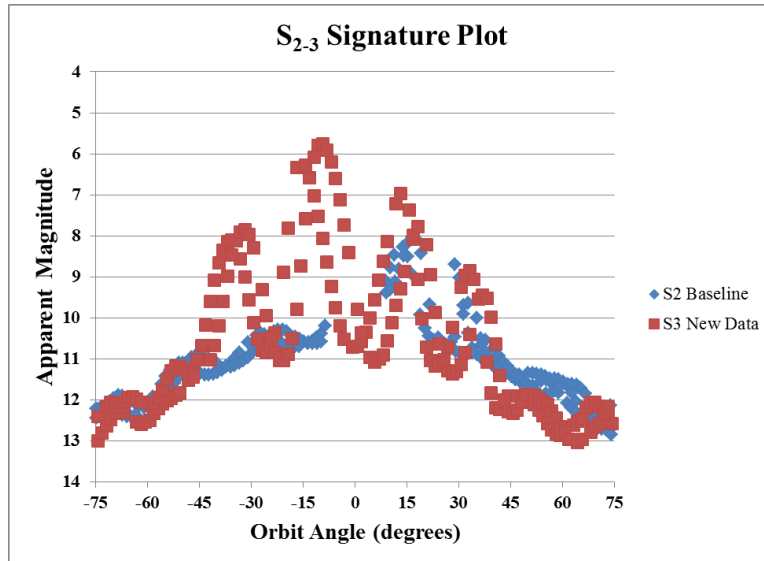
Fig. 67. S$_{2-3}$ Signatures
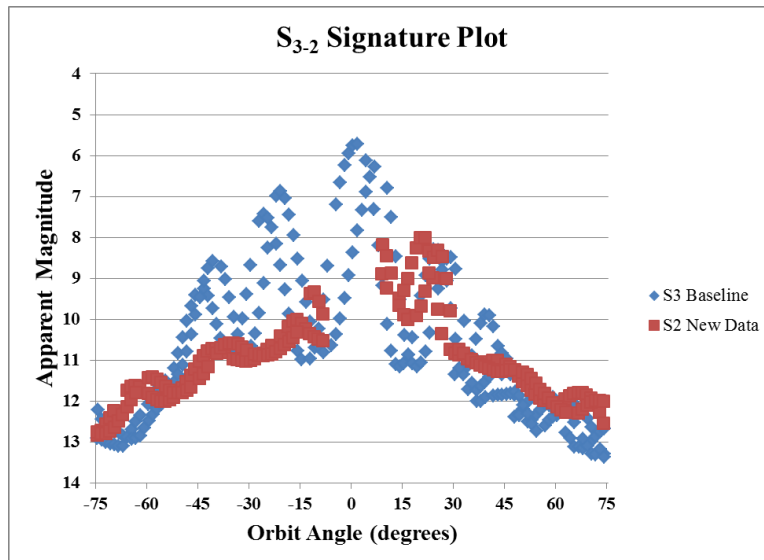
Fig. 68. S$_{3-2}$ Signatures

8.5.1 Z-test on r values

The results for the Z-test for dependent data on r values are shown in Fig. 69 - Fig. 71. Because S_2 and S_3 are cross-tagged in Example 4, our test is correct in concluding to accept H_a for S_2 and S_3 and to accept H_o for S_1. S_{2-3} does take more than the expected number of observations to reach a decision, but the reasoning for this is that the signatures are very similar to one another as seen in Fig. 67.
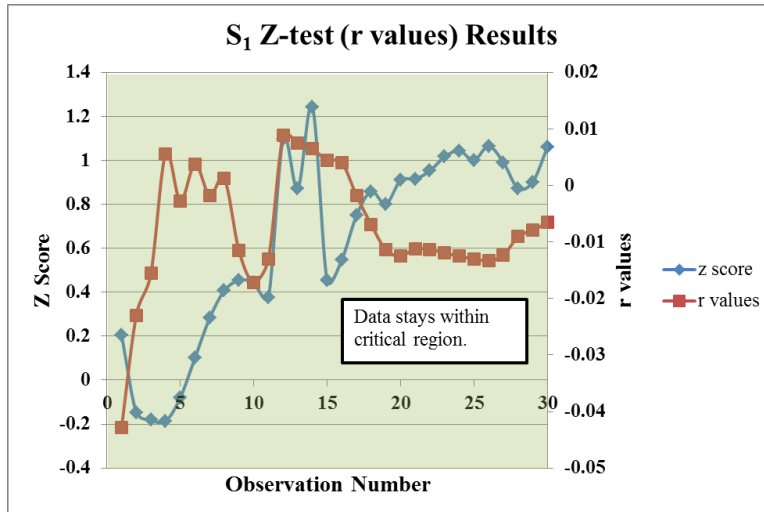
Fig. 69. Example 4 S_{1-1} Z-test on r values Results
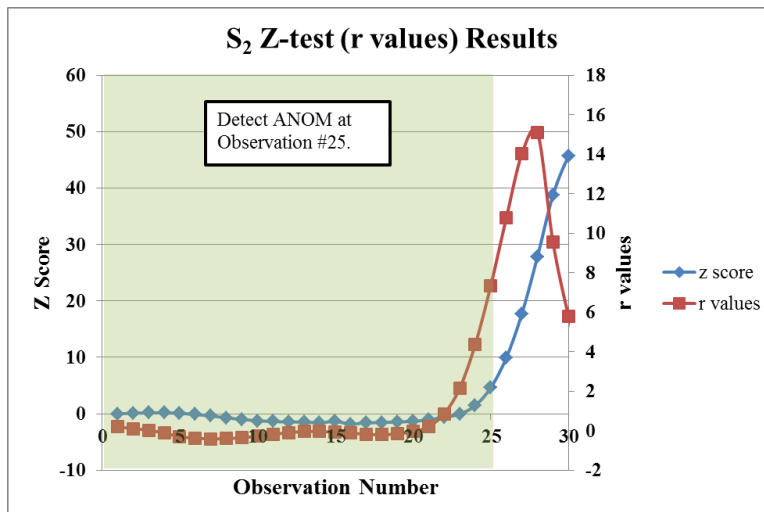
Fig. 70. Example 4 S_{2-3} Z-test on r values Results
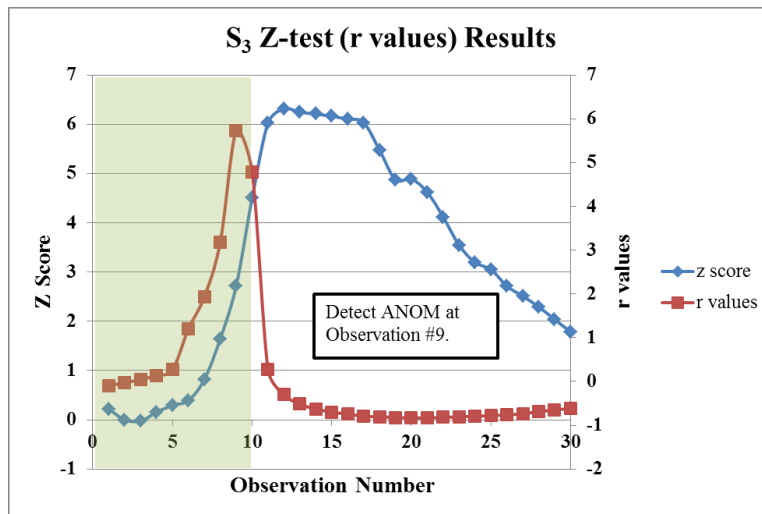
Fig. 71. Example 4 $S_{3\text{-}2}$ Z-test on r values Results

8.5.2 Classical Sequential Analysis

For Example 4, we expect to accept H_a for S_2 and S_3 and to accept H_o for S_1, because S_2 and S_3 are cross-tagged. Unfortunately, Fig. 72 - Fig. 74 show that the classical sequential analysis could not find the cross-tag for $S_{2\text{-}3}$ or $S_{3\text{-}2}$. However, for $S_{3\text{-}2}$, if we update the slider by moving it forward to halfway between the start of the new data and the initial conclusion to accept H_o and then restart the method over again, the second run of the classical sequential analysis accepts H_a at observation 10. Similarly, if we update the time slider for $S_{2\text{-}3}$, we would eventually obtain the conclusion to accept H_a at observation 24, but it takes several updates of the time slider. The classical sequential analysis has difficulty, especially for $S_{2\text{-}3}$, because of the orbit angle of the new observations. Observations 0 through 22 are in the orbit angle range -75 to -45, and Fig. 67 illustrates that the signatures of S_2 and S_3 at these orbit angles are very similar. This causes the r values that we are testing to be similar, so the test is unable to detect a change.
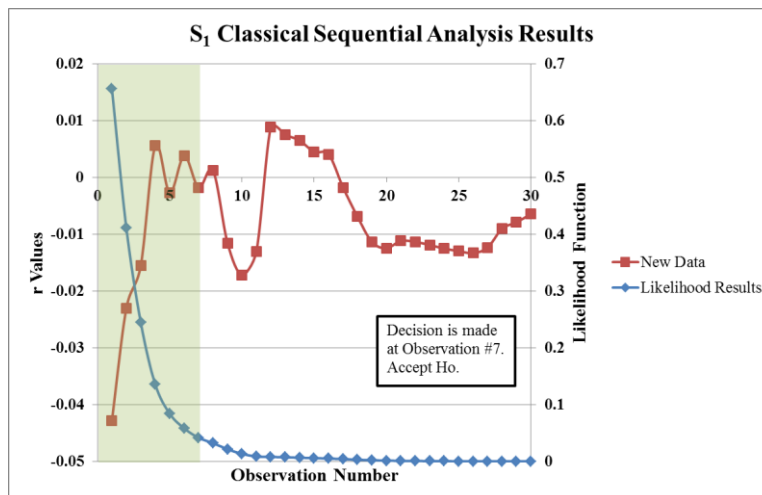

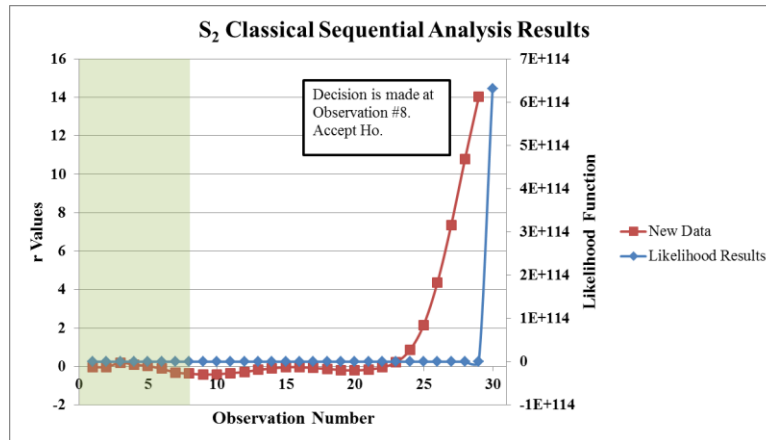**Fig. 72. Example 4 $S_{1\text{-}1}$ Classical Sequential Analysis Results**

Fig. 73. Example 4 S$_{2\text{-}3}$ Classical Sequential Analysis Results
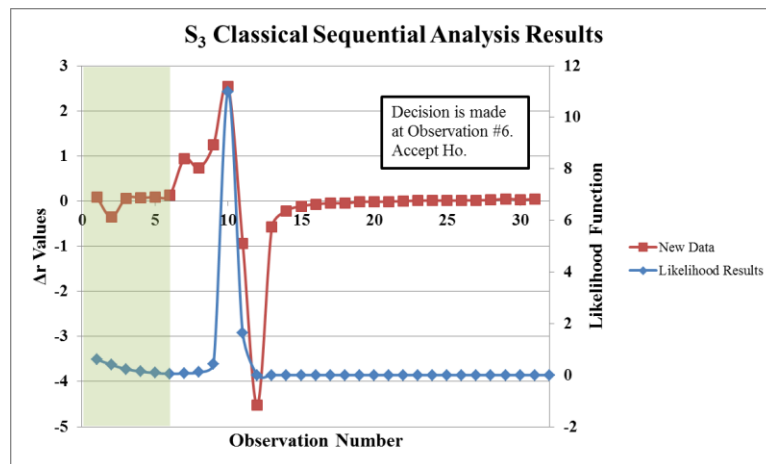

Fig. 74. Example 4 S$_{3\text{-}2}$ Classical Sequential Analysis Results

8.5.3 Brownian Motion Drift Analysis

The result for Example 4 for the Brownian motion drift analysis is better for S$_3$ than the classical sequential analysis results. Unlike the classical sequential analysis method, where we had to update the time slider, we can accept H$_a$ for S$_3$ the first time we run the test.
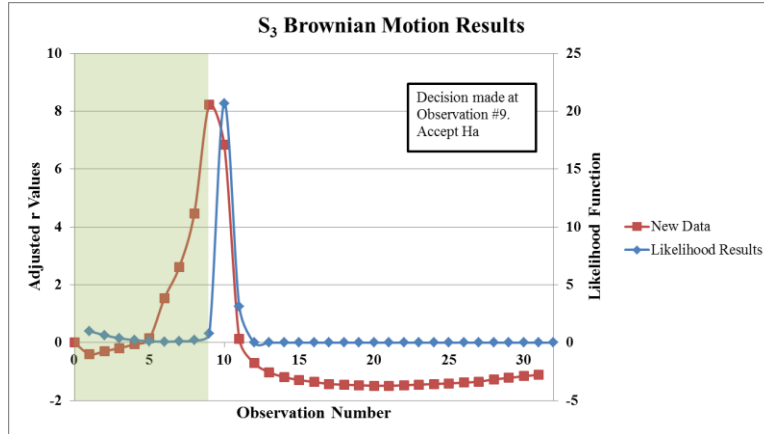
Fig. 75. Example 4 S_{3-2} Brownian Motion Results

8.5.4 Z-test on P(NOM|r) Values

In Example 4, S_2 and S_3 are cross-tagged, so the Z-test for dependent data on P(NOM|r) values results are expected to accept H_o for S_1 and accept H_a for S_2 and S_3. The results for this method are shown in Fig. 76 - Fig. 78. The test for this example correctly concludes H_o for S_1 and H_a for S_2 and S_3. Although it does take S_3 more observations than expected to come to a decision, we are attributing this to the similarities in their signatures in Fig. 68.
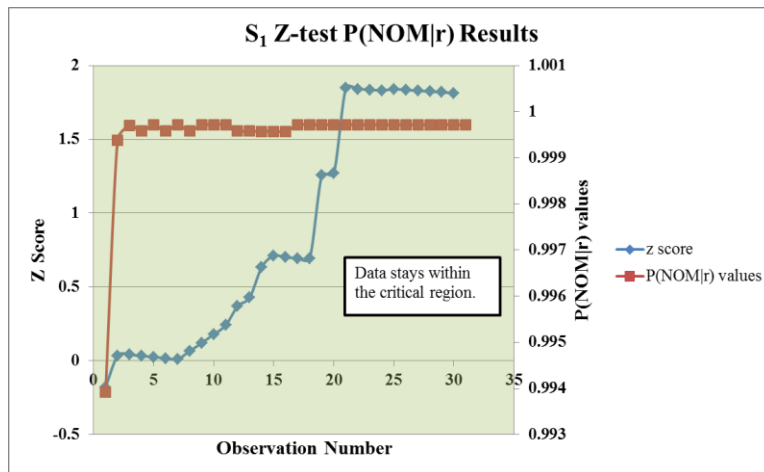
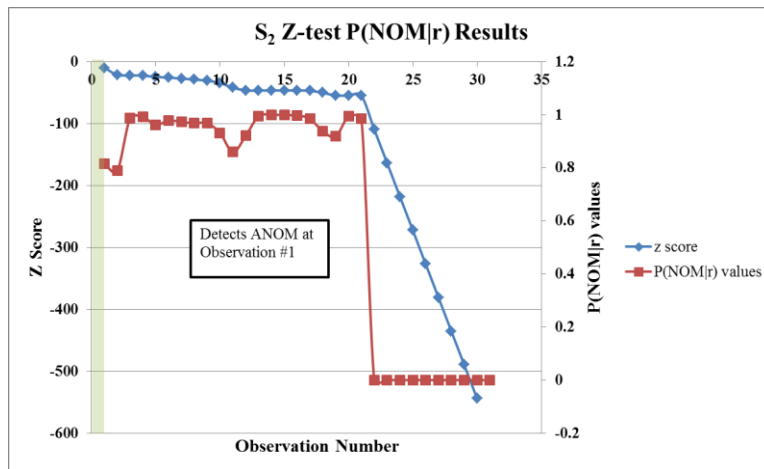

Fig. 76. Example 4 S_{1-1} Z-test on P(NOM|r) Results
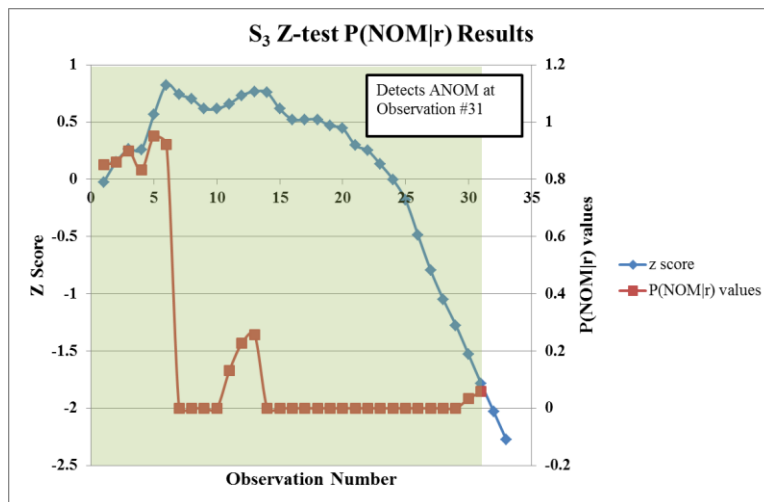
Fig. 77. Example 4 S₂₋₃ Z-test on P(NOM|r) Results

Fig. 78. Example 4 S₃₋₂ Z-test on P(NOM|r) Results

8.5.5 Data Association

Table 7 displays the results for Example 4. The only conclusion all three tests agree on is that S_1 is NOM. For both S_2 and S_3 the classical sequential analysis method determines NOM, while the other two methods determine ANOM. Thus, the only conclusion we can come to is that S_1 is NOM. If we want to try to resolve the potential change of S_2 and S_3, then we could try and swap their new data and run the tests again. Upon swapping the new data, we actually would reverse the cross-tag created for Example 4, and therefore, we would again end up with Example 1. The data swap is illustrated in Fig. 79.

Table 7. Example 4 Results Chart

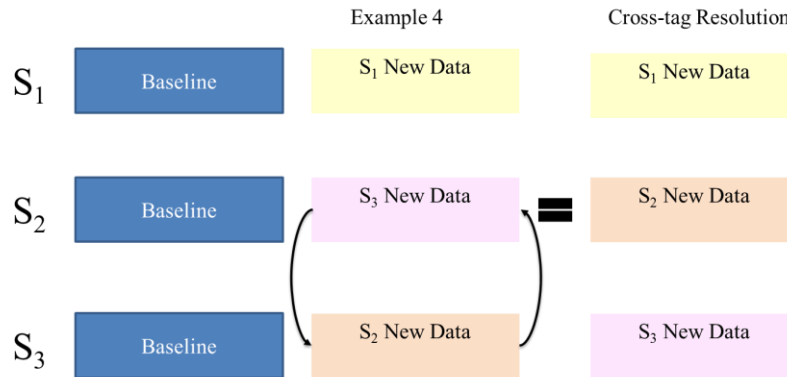| Satellite	r Value Z-test	Classical Sequential Analysis	P(NOM|r) Z-test
S_1	NOM	NOM	NOM
S_2	ANOM	NOM	ANOM
S_3	ANOM	NOM	ANOM

Fig. 79. Example 4 Cross-tag Resolution

8.6 Example 5

Example 5 contains a multi-satellite cross-tag. The baseline data for S_1 is paired with the new data from S_2 (orange box), denoted as S_{1-2}, the baseline data for S_2 is paired with the new data from S_3 (magenta box), denoted as S_{2-3}, and the baseline data for S_3 is paired with the new data from S_1 (yellow box), denoted as S_{3-1}. Therefore, there are no NOM satellites in this example.

Fig. 80. Example 5 Input Data

8.6.1 Z-test on r values

For the Z-test for dependent data on r values, the results are displayed in Fig. 81 - Fig. 83. This method has three different cross-tagged situations, and the test accurately accepts the alternative hypothesis for S_1, S_2, and S_3. Therefore, the Z-test for dependent data on r values is correct for all cases in Example 5.
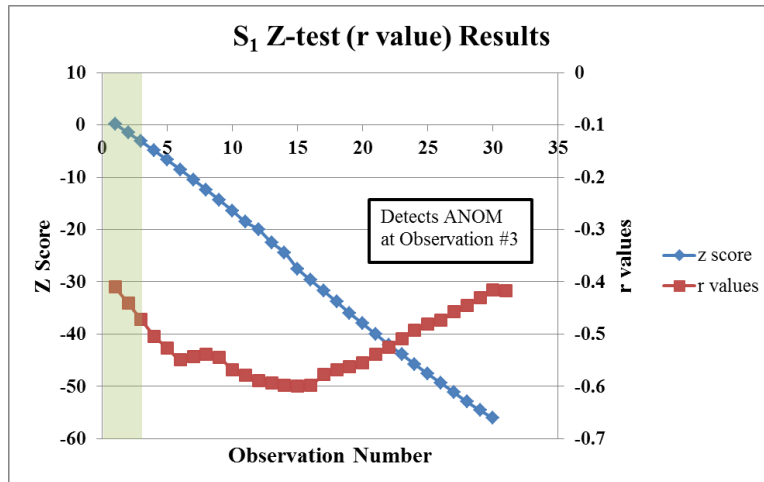
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Fig. 81. Example 5 S$_{1-2}$ Z-test on r values Results
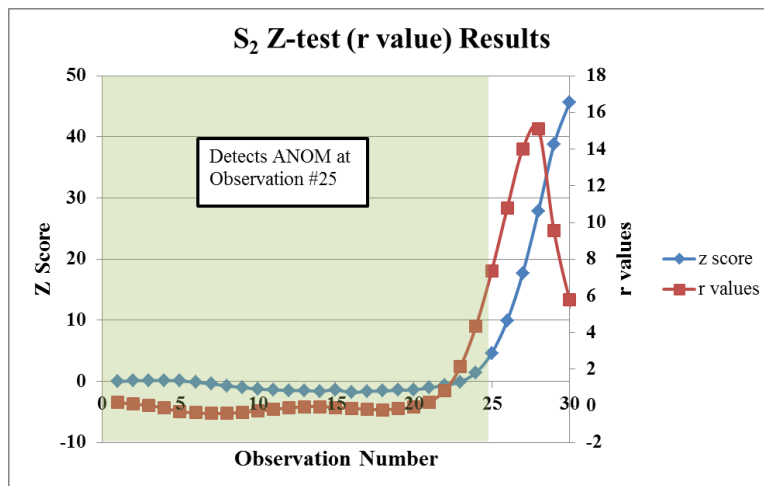
Fig. 82. Example 5 S$_{2-3}$ Z-test on r values Results
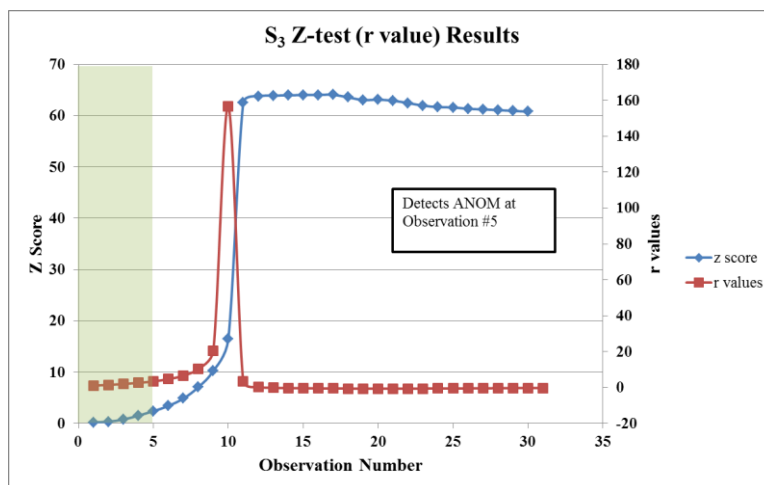
Fig. 83. Example 5 S$_{3-1}$ Z-test on r values Results

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8.6.2 Classical Sequential Analysis

The classical sequential analysis results for Example 5 are shown in Fig. 84 - Fig. 86. Although we expect to accept H_a for all three satellites, we only accept H_a for S_1 and S_3. The classical sequential analysis method is unable to determine the cross-tag for S_2. The reasons for this are discussed in Section 8.5.2.
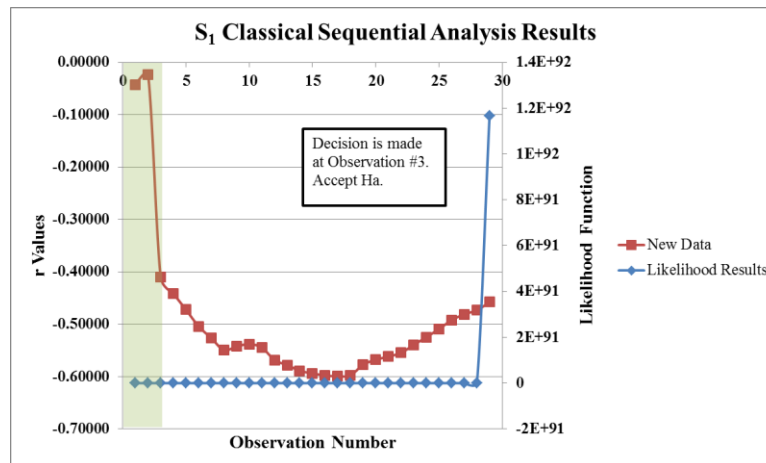

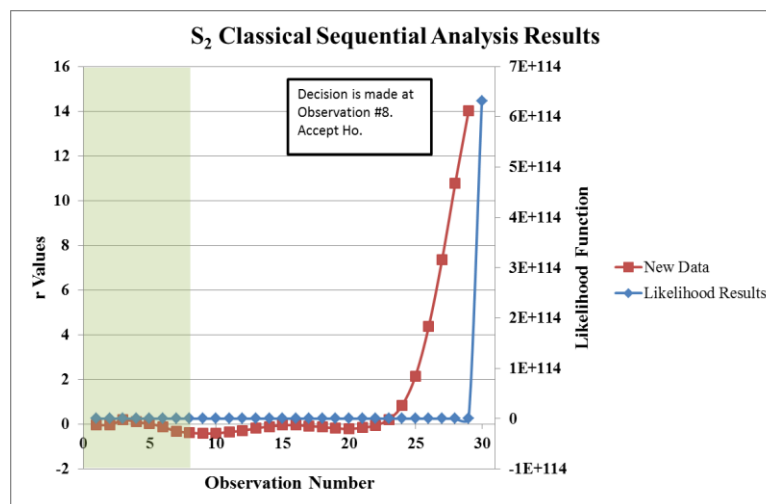**Fig. 84. Example 5 S_{1-2} Classical Sequential Analysis Results**

Fig. 85. Example 5 S_{2-3} Classical Sequential Analysis Results
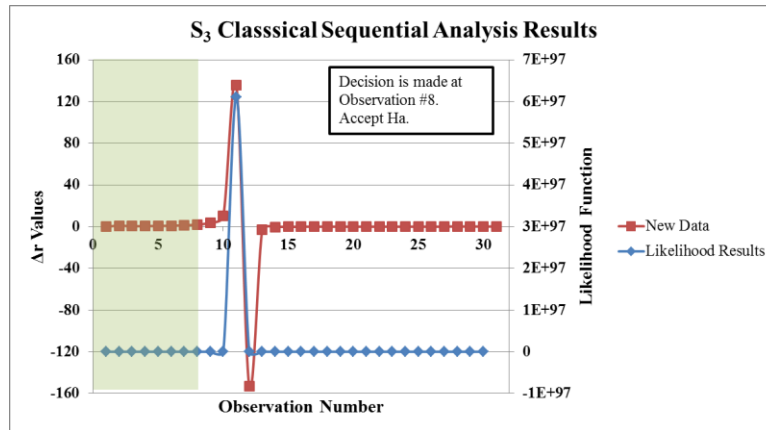
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Fig. 86. Example 5 S₃₋₁ Classical Sequential Analysis Results

8.6.3 Brownian Motion Drift Analysis

The result for Example 5 for Brownian motion drift analysis is seen in Fig. 87. The Brownian motion drift analysis correctly accepts H_a for S_3.
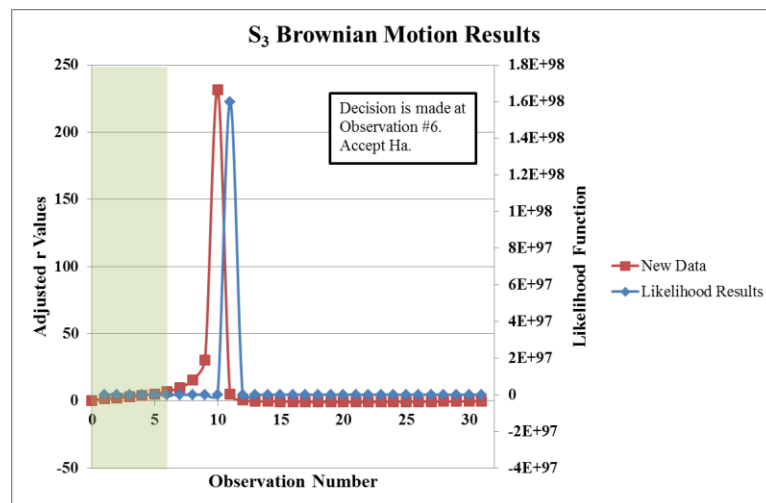

Fig. 87. Example 5 S₃₋₁ Brownian Motion Results

8.6.4 Z-test on P(NOM|r) Values

The results for the Z-test for dependent data on P(NOM|r) values are shown in Fig. 88 - Fig. 90. The test correctly identifies ANOM for S_1 and S_2. However, the Z-test for dependent data accepts H_o for S_3, which is not consistent with the results the test would expect.
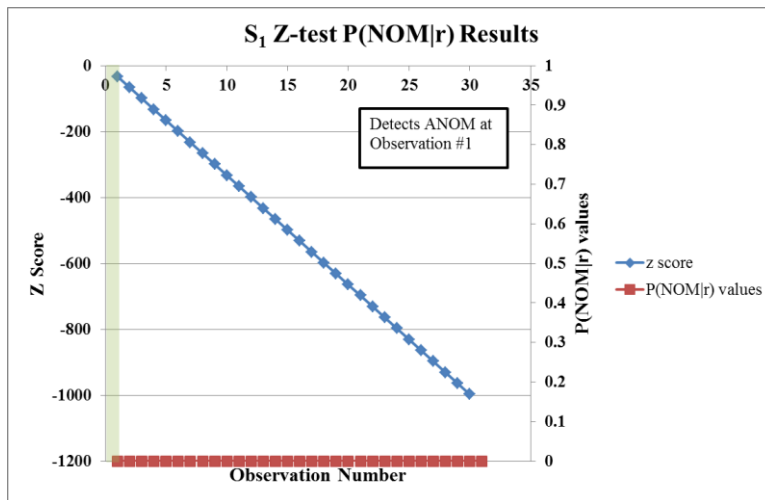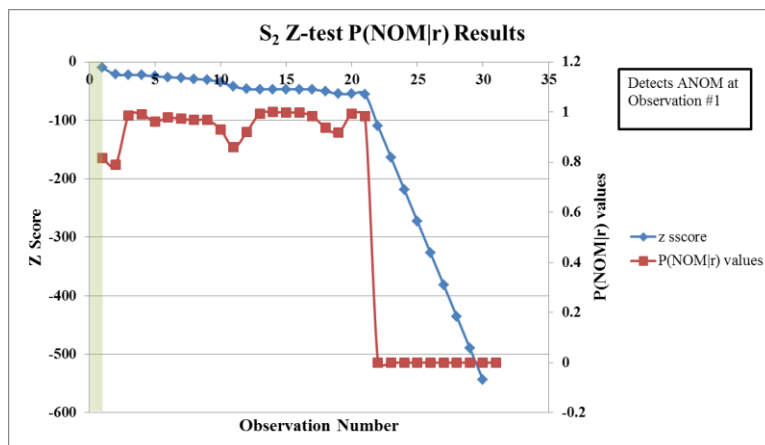
Fig. 88. Example 5 $S_{1\text{-}2}$ Z-test on P(NOM|r) Results

Fig. 89. Example 5 $S_{2\text{-}3}$ Z-test on P(NOM|r) Results
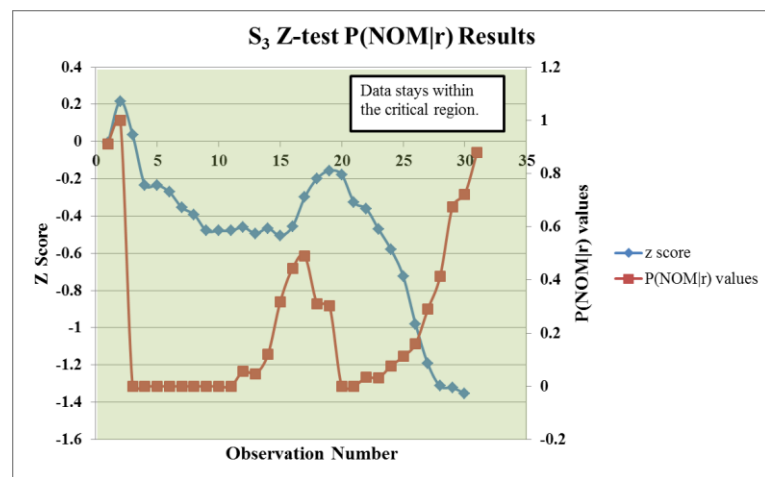
Fig. 90. Example 5 $S_{3\text{-}1}$ Z-test on P(NOM|r) Results

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8.6.5 Data Association

Table 8 summarizes the results for Example 5. All tests conclude S_1 is ANOM, but they do not all agree for S_2 and S_3. Therefore, we can only conclude S_1 is ANOM. To try and resolve that S_1 is ANOM, we can swap its new data (orange box) with one of the other two satellites. Unfortunately, both of the other satellites have two ANOM results and one NOM result, so there is no clue as which one to swap with S_1. Let us swap the new data of S_1 (orange box) with the new data of S_2 (magenta box). Since S_1 is cross-tagged with S_2, upon swapping the data and running the tests again, we would now conclude S_2 is NOM. Since the new data of S_2 was S_3, when we swap the data S_1 becomes cross-tagged with S_3 instead of S_2. S_3 is already cross-tagged with S_1, so we have Example 3 again. Section 8.4.5 describes how to resolve Example 3. Once the Example 3 cross-tag is resolved, Fig. 91 demonstrates the case of Example 1.

Table 8. Example 5 Results Chart

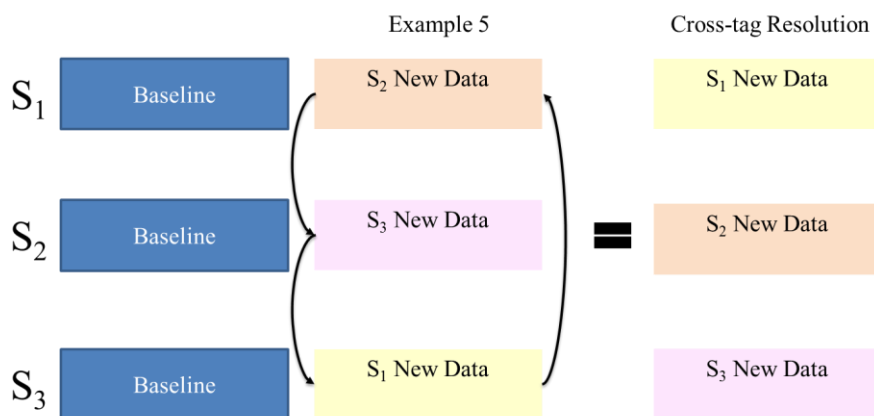| Satellite	r Value Z-test	Classical Sequential Analysis	P(NOM|r) Z-test
S_1	ANOM	ANOM	ANOM
S_2	ANOM	NOM	ANOM
S_3	ANOM	ANOM	NOM

Fig. 91. Example 5 Cross-tag Resolution

8.7 Example 6

Example 6 contains a multi-satellite cross-tag. The baseline data for S_1 is paired with the new data from S_3 (magenta box), denoted as $S_{1\text{-}3}$, the baseline data for S_2 is paired with the new data from S_1 (yellow box), denoted as $S_{2\text{-}1}$, and the baseline data for S_3 is paired with the new data from S_2 (orange box), denoted as $S_{3\text{-}2}$. Thus, there are no NOM satellites in this example. Fig. 92 illustrates the new input data for Example 6.

Example 6

S_1	Baseline	S_3 New Data
S_2	Baseline	S_1 New Data
S_3	Baseline	S_2 New Data

Fig. 92. Example 6 Input Data

8.7.1 Z-test on r values

Example 6 results for the Z-test for dependent data on r values are shown in Fig. 93 - Fig. 95. All three cases are expected to accept the alternative hypothesis. As seen below, S_1, S_2 and S_3 conclude to accept Ha. Thus, the Z-test for dependent data on r values is accurate for Example 6.
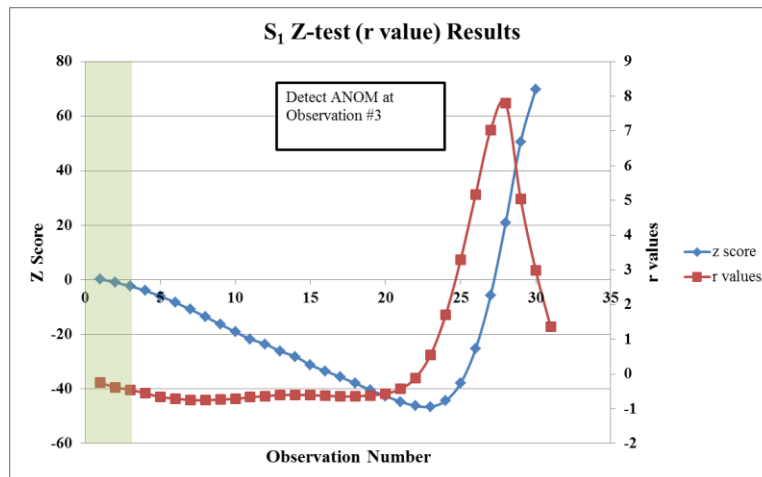

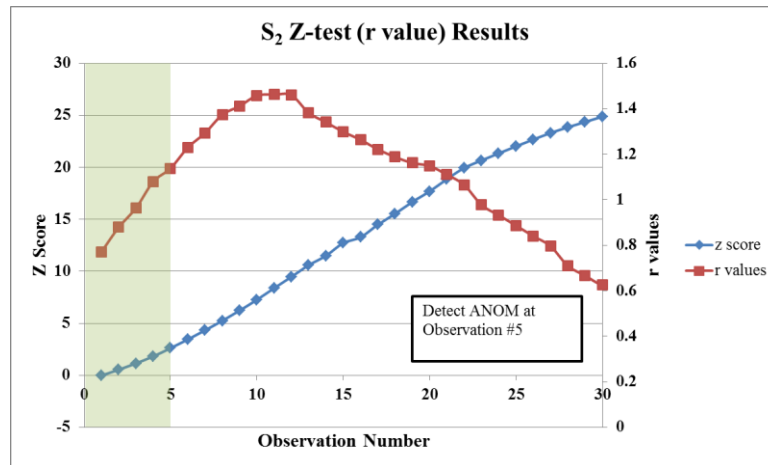**Fig. 93. Example 6 S_{1-3} Z-test on r values Results**

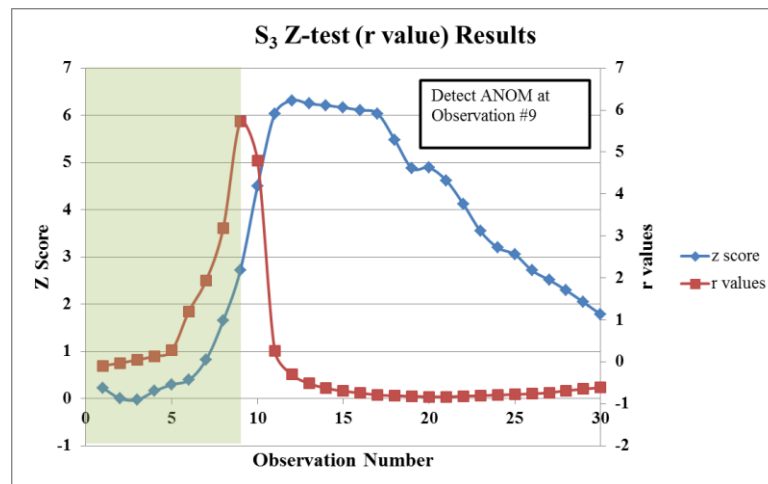**Fig. 94. Example 6 S$_{2-1}$ Z-test on r values Results**

Fig. 95. Example 6 S$_{3-2}$ Z-test on r values Results

8.7.2 Classical Sequential Analysis

The classical sequential analysis results for Example 6 are displayed in Fig. 96 - Fig. 98. Although we expect all three cases to conclude ANOM, the test for S$_3$ accepts H$_o$. The reasons for this are described in Section 8.5.2.
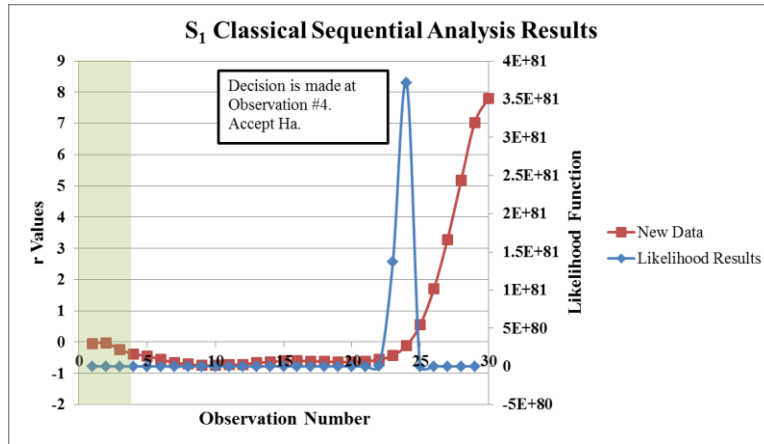
Fig. 96. Example 6 S_{1-3} Classical Sequential Analysis Results
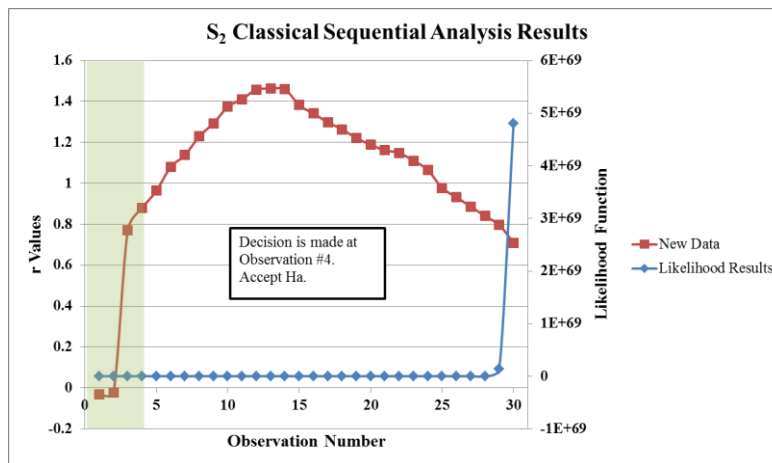

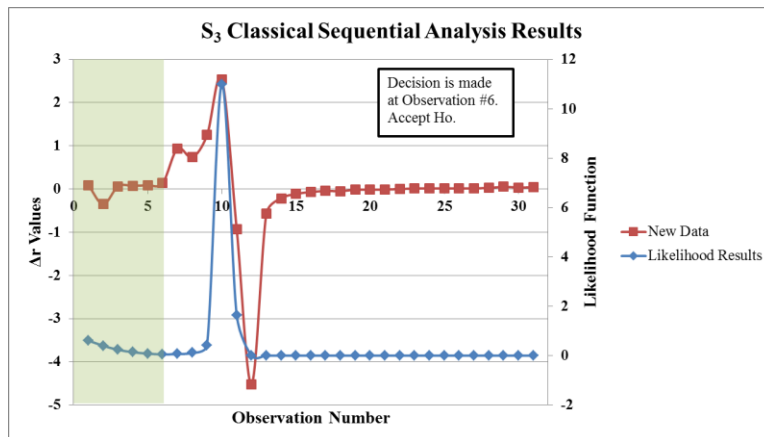Fig. 97. Example 6 S_{2-1} Classical Sequential Analysis Results

Fig. 98. Example 6 S_{3-2} Classical Sequential Analysis Results

8.7.3 Brownian Motion Drift Analysis

The Brownian motion drift analysis result for Example 6 is shown below in Fig. 99. Brownian motion correctly accepts H_a, so its results for S_3 are better than those of the classical sequential analysis.

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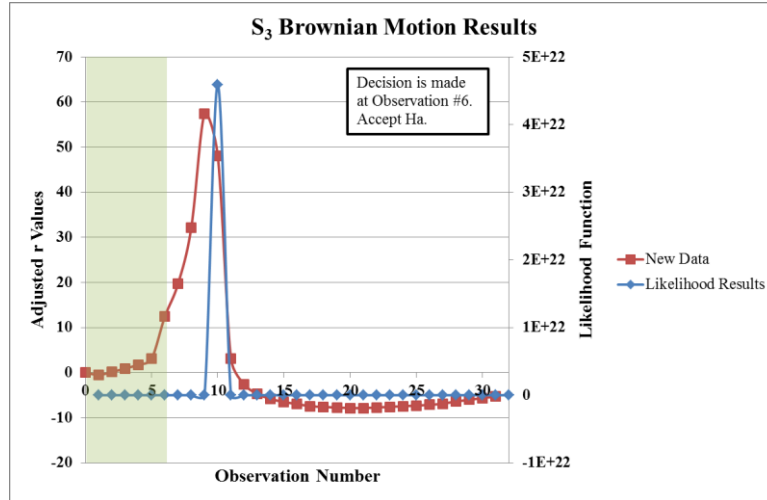
Fig. 99. Example 6 S$_{3-2}$ Brownian Motion Results

8.7.4 Z-test on P(NOM|r) Values

In this example, the Z-test for dependent data on P(NOM|r) values accepts the alternative hypothesis for S$_1$, S$_2$ and S$_3$. Because all three satellites have been cross-tagged with one another, this method provides accurate results for all three cases. The S$_{3-2}$ cross-tag situation does take significantly longer to detect ANOM compared to the other two cases. However, this is a result of the similar signatures graphs in Fig. 68. The results for the Z-test for dependent data on P(NOM|r) values are shown in Fig. 100 - Fig. 102.

Fig. 100. Example 6 S$_{1-3}$ Z-test on P(NOM|r) Results

Fig. 101. Example 6 S_{2-1} Z-test on P(NOM|r) Results
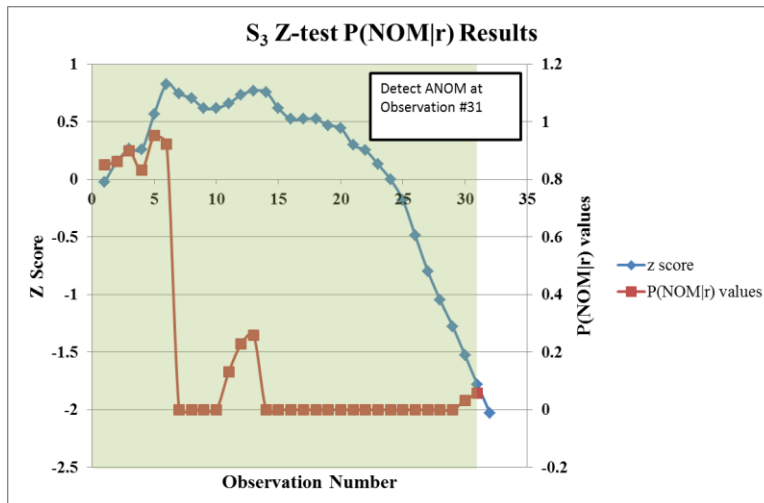
Fig. 102. Example 6 S_{3-2} Z-test on P(NOM|r) Results

8.7.5 Data Association

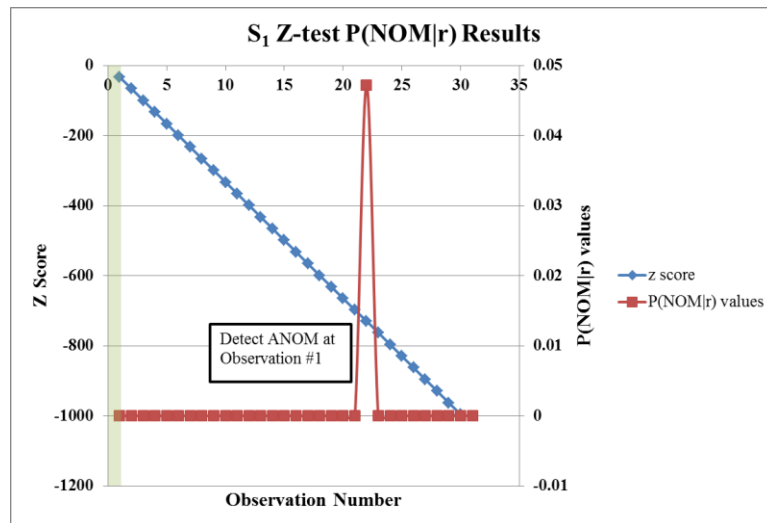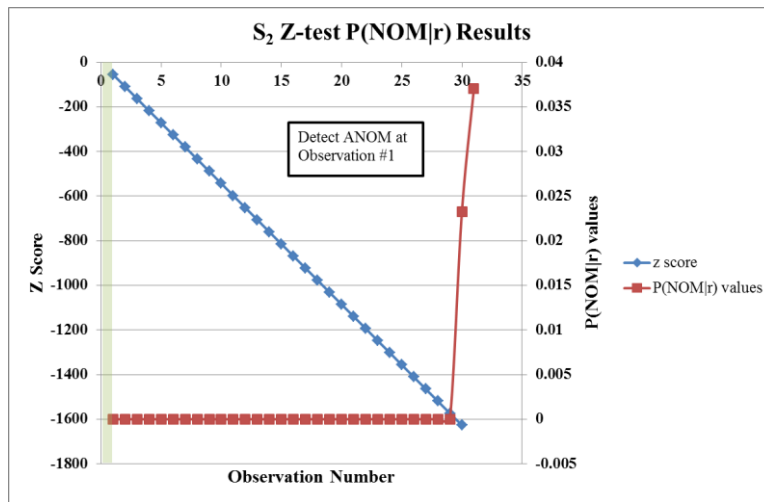The overall results for Example 6 are displayed in Table 9. All three tests find S_1 and S_2 to be ANOM, so we can conclude S_1 and S_2 are ANOM. Unfortunately, the classical sequential analysis method finds S_3 to be NOM, while the other two methods determine it to be ANOM. Therefore, we cannot make any conclusions about S_3. If we want to try to determine the cause for change in S_1 and S_2, then we can swap their new data. Since S_2 is cross-tagged with S_1 (yellow box), its new data is truly the new data from S_1. So when we swap their new data and run the tests again, S_1 becomes NOM. Then the new data of S_1 is S_3 (magenta box), so after swapping the data, S_2 becomes cross-tagged with S_3. Thus, this becomes equivalent to Example 4. The description of how to resolve Example 4 is in Section 8.5.5. A depiction of the cross-tag resolution for Example 6 is shown in Fig. 103.

Table 9. Example 6 Results Chart

Satellite	r Value Z-test	Classical Sequential	P(NOM|r) Z-test

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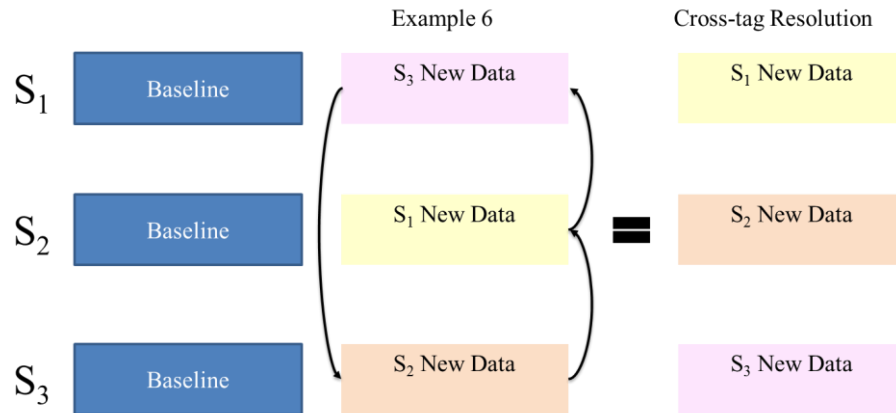|		Analysis	
S_1	ANOM	ANOM	ANOM
S_2	ANOM	ANOM	ANOM
S_3	ANOM	NOM	ANOM

Fig. 103. Example 6 Cross-tag Resolution

8.8   Summary of Cross-tag resolution

The six examples illustrate how the New Data for a cluster of three satellites may present itself with different combinations of cross-tags between satellites. The cross-tag resolution procedure comprised a successive and adaptive application of the Z-test and sequential analysis based on the preceding results of the composite hypothesis testing. The resolution of the situations in examples 2 through 4 required a two stage application of the composite hypothesis testing, while examples 5 and 6 required three stages. In each case, the cross-tag situations were reduced to the data analysis performed in Example 1. Therefore, although our original conclusions for an example might be that multiple satellites are ANOM, after resolving the cross-tags, we will conclude that S_1 and S_2 are NOM, and we cannot make a conclusion about S_3. Thus, the three methods used in the examples and results tables provided to be useful in all cases. The assessment is based on the use of P(type I error) = 0.05 and P(type II error) = 0.05. For the composite hypothesis test, the resultant P(type I error) = 3*0.05 or 15%.

Thus, there are several conditions when the results of the three tests do not agree with each other. The assessment of NOM or ANOM is performed only when all tests agree. To improve the test results (this is so that all tests agree with each other), we would first need to improve the Inversion Model and Prediction Model to obtain more accurate r and P(NOM|r) values to provide to the tests. To adjust the two models, we need more observations for each satellite, especially S_3. We also need new observations in order to detect the occurrence of ANOM on an ongoing basis. In the present work, the Inversion Model and Predictive Model use the same physics procedure based on the two facet model [1]. Thus, the improvement of the Inversion Model also results in the improvement of the Predictive Model. This is described in Section 9.0.

8.9   Update of Baseline Signature

Once a satellite is determined to be NOM by the composite hypothesis test, we can update the baseline for that particular satellite. Updating the baseline is essential to be able to account for seasonal changes. After the baseline has been updated, testing is restarted to keep a current status of the satellite. Fig. 104 shows a notional example of updating the baseline for S_1. Since S_3 was determined to be ANOM in Example 1, we cannot truly update the baseline for the satellites in the cluster. However, this section demonstrates how the baseline could be updated if the conditions were satisfied.

The dotted lines in Fig. 104 show the movement of the time slider. Because the classical sequential analysis method determined S_1 was NOM at observation 7 in Example 1, the time slider is forwarded 7 points. It is up to the user to

decide how far forward the time slider is moved. The slider can be moved forward to any point in the region from the start of the new data up to where the classical sequential analysis method determines the satellite is NOM.
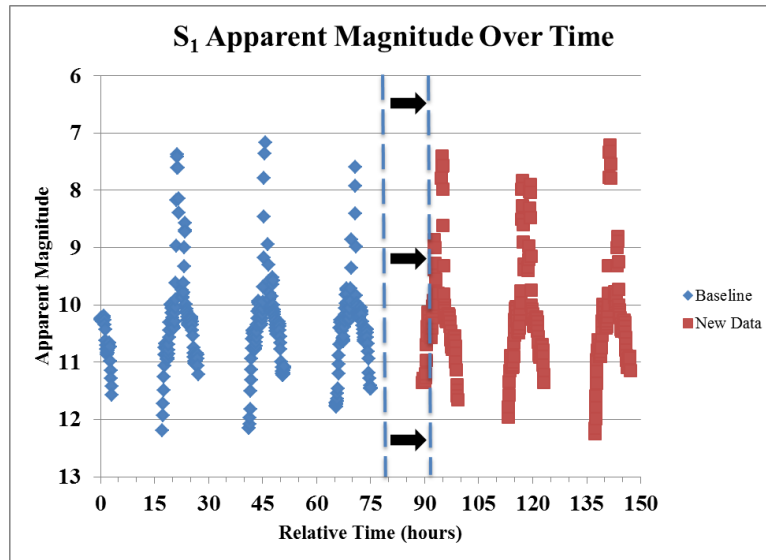

Fig. 104. S_1 Update of Baseline Signature

After move the time slider forward 7 observations, we can then use any of the methods described in Section 4.0 to begin reevaluating the new data. Fig. 105 shows the results of the classical sequential analysis method ran on S_1 using the updated baseline. The classical sequential analysis again determines S_1 is NOM. Thus, we could move the time slider forward once again and restart the process.
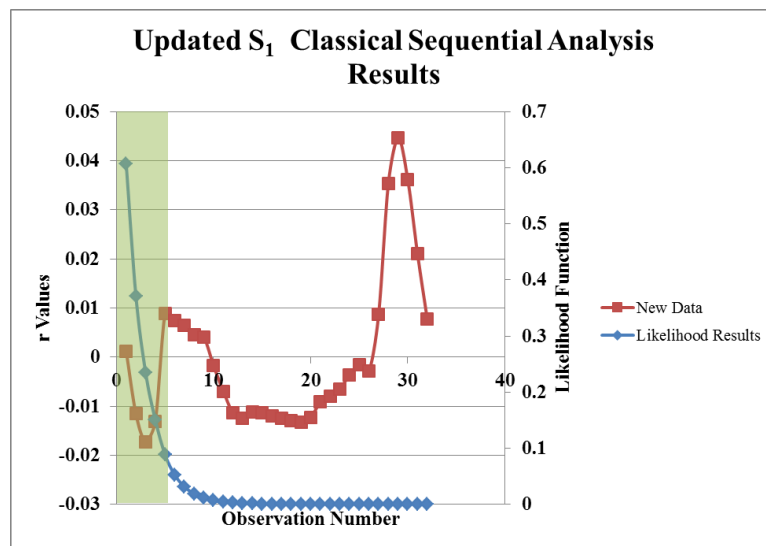
Fig. 105. S_1 Updated Classical Sequential Analysis Results

9.0   Sensor Tasking for Fine Feature Characterization

For the examples, our decision criterion did not lead the user to a definitive conclusion that S_3 was NOM or ANOM. This work considers that such a lack of conclusion can be due to two reasons. First, the fidelity of the Predictive Model may be too low. This results in the values of Brightness Ratio to exhibit significant scatter. Second, the

satellite may have changed, which results in a lower fidelity for the Predictive Model since it is derived from the inversion of baseline data. Or, the Predictive Model may have low fidelity and the satellite has changed. Accordingly, the goal of sensor tasking is to collect data so as to enable the dual goals of assessment of change and/or improvement of Predictive Model as efficiently as possible.

The motivation for the tasking method is from the maximum information entropy principle, which expresses the claim of maximum ignorance. The probability distribution function for a quantity of interest is chosen to be one that makes least claim to being informed beyond the baseline data [4]. The quantity of interest in sensor tasking is the definition of observation conditions; namely the direction of illumination and the view direction for the sensor. In this work, it is assumed that the effect of the illumination and observation conditions is captured by the value of a single entity, namely the orbit angle. The orbit angle is defined to be the projection of the sun-satellite-sensor angle in the orbital plane of the satellite. It is similar to the longitudinal phase angle, only difference being that the longitudinal phase angle is computed with respect to the equatorial plane. Or, for a satellite with a zero orbital inclination, the orbit angle is same as the longitudinal phase angle. This is a coarse yet practical approximation because a complete definition of the illumination and observation directions is a function of the geometry and orientation of the satellite solar panel and its body. At a minimum, it consists of four angles [5].

We consider that the change may occur such that it may not be observable from any value of the orbit angle. This is because the change may cause minimal net change in the projected geometry of the satellite with respect to the sun and the sensor. The orbit angle at which the change may be manifested in terms of difference in its brightness is function of the change itself and is unknown a priori. Thus, the sensor tasking for the purpose of change detection can make no assumption with respect to the choice of the orbit angle. Alternately, the choice of an orbit angle for the next observation needs to be chosen as per a uniform probability distribution function. This strategy is postulated to maximize the amount of new information per observation as per the principle of maximum information entropy.

We also note that the fidelity of the Predictive Model varies with the orbit angle. This is manifested in the random character of the Brightness Ratio versus orbit angle as shown in Fig. 2 - Fig. 4. The range of values for the Brightness Ratio is larger for S_3 as compared to S_1 and S_2. This is related to the reflection phenomenology as a function of the orbit angle. For example, at intermediate values of orbit angle, the satellite brightness is commonly governed by diffuse reflection. This is because the specular behavior of the solar panels is at smaller orbit angles (closer to 0°), and the specular behavior off the fine body features is typically at larger orbit angles (closer to 90°). It is generally easier to attain higher fidelity for the Predictive Model under diffuse reflection conditions at intermediate orbit angles rather than its values closer to 0° or 90°. This is particularly when there is no self-occlusion caused by any fine features on the body in the projected view of the satellite with respect to the sensor.

We also note that the fidelity of the Predictive Model varies with the orbit angle. This is manifested in the random character of the Brightness Ratio versus orbit angle as shown in Fig. 106 - Fig. 108. The range of values for the Brightness Ratio is larger for S_3 as compared to S_1 and S_2. This is related to the reflection phenomenology as a function of the orbit angle. For example, at intermediate values of orbit angle, the satellite brightness is commonly governed by diffuse reflection. This is because the specular behavior of the solar panels is at smaller orbit angles (closer to 0°), and the specular behavior off the fine body features is typically at larger orbit angles (closer to 90°). It is generally easier to attain higher fidelity for the Predictive Model under diffuse reflection conditions at intermediate orbit angles rather than its values closer to 0° or 90°. This is particularly when there is no self-occlusion caused by any fine features on the body in the projected view of the satellite with respect to the sensor.

Consider the situation when there was no change in the satellite. In such a case, the lack of conclusion in regards to NOM or ANOM for a satellite would depend on the fidelity of the Predictive Model. This is because the Predictive Model is utilized to predict the expected brightness of the satellite at point in the new data. If the fidelity of the Predictive Model is insufficient, the computed values of the Brightness Ratio at the new data points can be such that test statistic for the new data suggests a difference from the baseline data. This may be the case even though there is no statistically significant change.

The Predictive Model could be improved when additional data is collected. Any collection of additional data needs to be such that it maximizes new information. In this regard, the fidelity of the Predictive Model as a function of the orbit angle is postulated as being inversely related to the new information generated if the sensor tasking was defined to collect new data at that orbit angle. This postulation may be interpreted by considering two cases for the

orbit angle, one where the fidelity of Predictive Model is high and the second where it is low. This may be idealized further as intervals of orbit angle values where the Brightness Ratio equals zero and nonzero, respectively. When the Brightness Ratio is zero, the expected value of satellite brightness is equal to the predicted value, or there is no new information in regards to the improvement of the Predictive Model. When the Brightness Ratio is nonzero, there is new information that is useful in order to improve the Predictive Model. Thus, it is postulated that the sampling of orbit angle values during the collection of additional data be inversely proportional to the absolute value of the Brightness Ratio in order to maximize new information per observation.
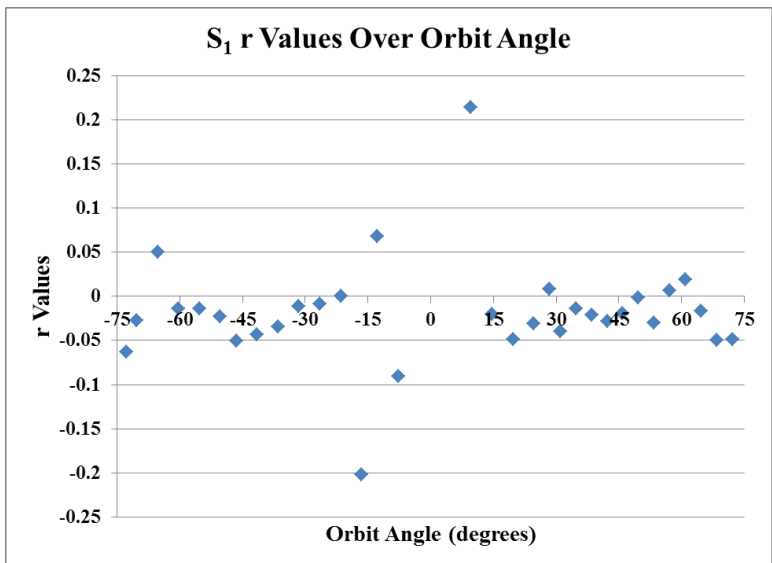

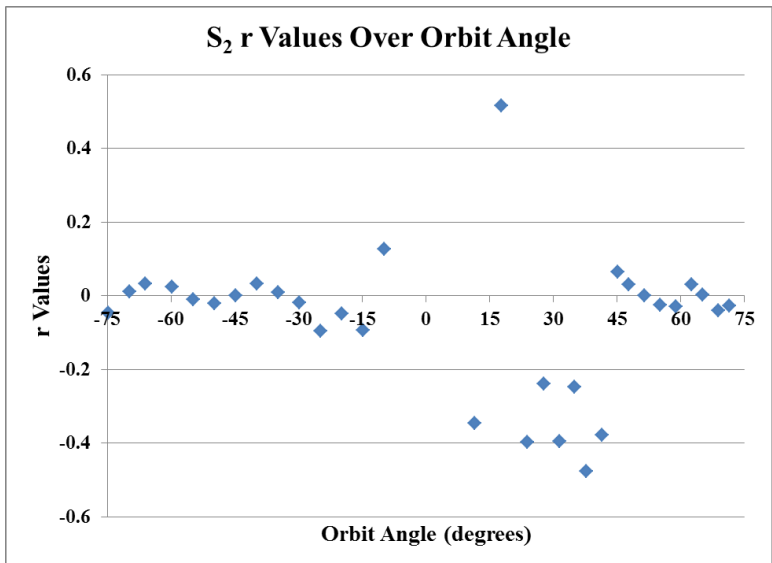Fig. 106. Satellite S_1 r Values Versus Orbit Angle
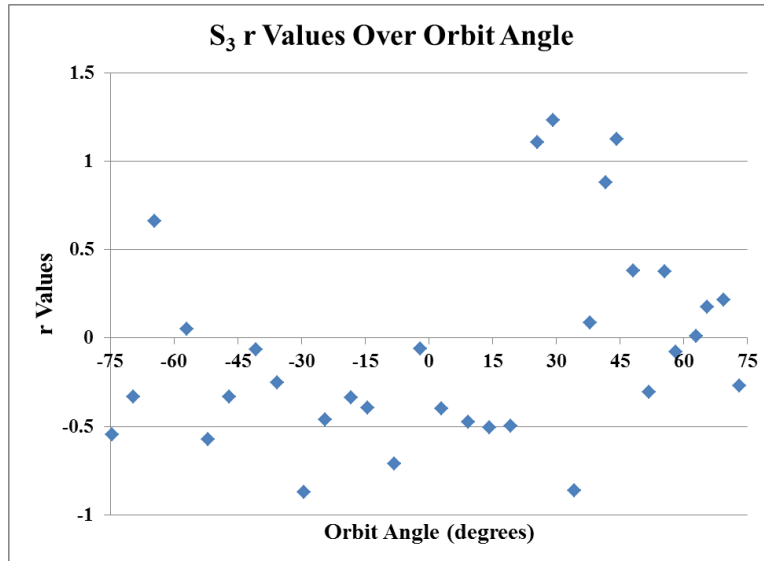

Fig. 107. Satellite S_2 r Values Versus Orbit Angle

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Fig. 108. Satellite S₃ r Values Versus Orbit Angle

Since S_3 is the satellite for which we require more data, we will focus on S_3 for the rest of this section. If the sensor was utilized in a staring mode (i.e. persistent observation), the sampling rate for the observation data would be uniform along the orbit angle axis. In such a case, the total new information would be proportional to the area under the curve of orbit angle versus the absolute value of the Brightness Ratio (i.e., r values). Accordingly, Fig. 109 shows a plot of new information versus orbit angle for S_3. The peaks of this graph are areas where the Predictive Model has lower fidelity, while the valleys are areas where the model has higher fidelity. Fig. 110 illustrates how the new information would accumulate if the sensor was to observe the satellite persistently. This graph is normalized to a maximum value of 1.0, which is meant to represent the totality of new information. We broke the total new information into 10% bins, which is meant to represent that persistent observations over each orbital angle bin would have the ability to provide 10% of the total new information. These bins are displayed in Fig. 111. Comparing Fig. 109 and Fig. 111, the smaller bins align with the areas with the most error.
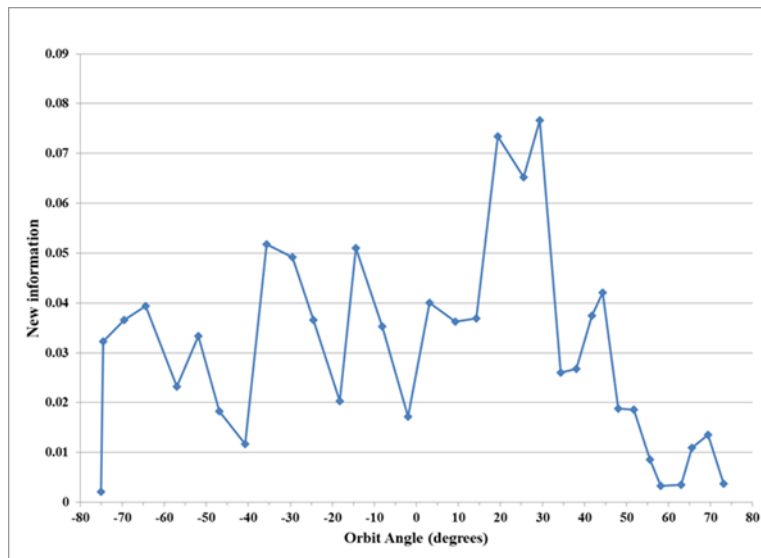
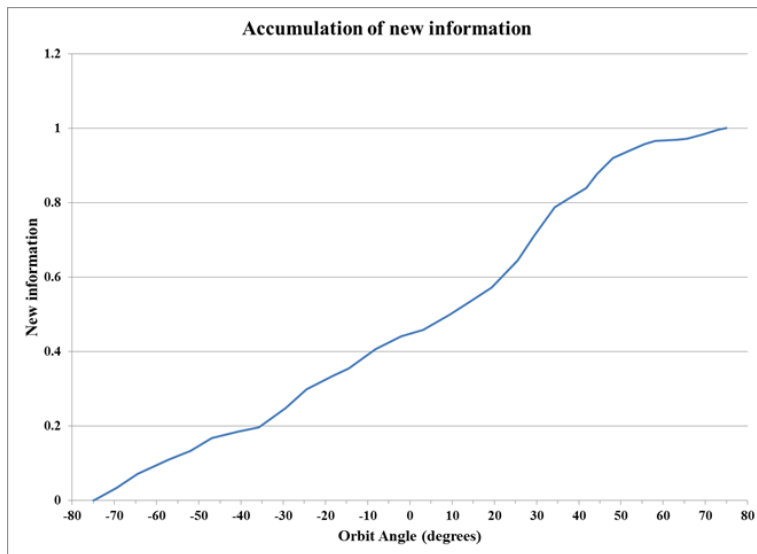**Fig. 109. New information as a function of orbit angle**

Fig. 110. Accumulation of new information as a function of orbit angle
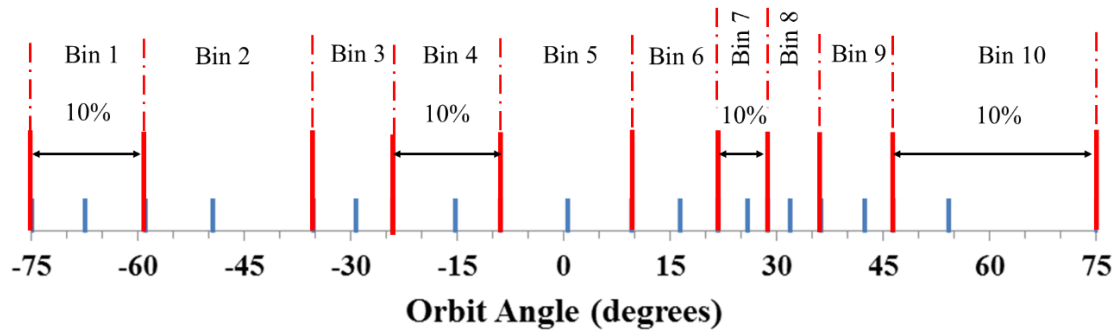
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Fig. 111. Orbit Angle Bins for New Data Collection

Consider a situation when the Predictive Model has limited fidelity and the satellite may have changed. For example, the lower fidelity of the Predictive Model could be caused by self-occlusion due to the fine features. Then the sensor tasking would have a joint goal of maximizing new information per observation for the purpose of improving the Predictive Model and/or detect change. The corresponding tasking strategy can be defined to combine the needs of the Predictive Model and change detection using a two-step approach as follows (Fig. 111):

- The probability of selection of an orbital bin is equal. This is to maximize new information with respect to change detection.
- The probability of selection of an observation condition within an orbital bin is uniformly distributed. This is to maximize new information with respect to the improvement of fidelity of the Predictive Model.

The characterization of fine features using such a two-step sensor tasking strategy is a part of our future work.

10.0 Ongoing work and closure

This paper provides a statistical assessment technique for the resolution of multi-satellite cross-tag by making an adaptive use of sequential analysis techniques. The method for cross-tag detection and resolution is useful irrespective of the different types of cross-tag scenarios feasible for a cluster and when the signatures of the satellites have significant overlap. Although the technique is demonstrated for a three satellite cluster, it can be extended to clusters containing a larger number of satellites.

The current work uses simplified composite hypothesis testing, which allows a decision to be made only when all tests agree. The next step is to enhance the composite test method by calculating the probabilities of all possible incorrect conclusions, so that the user can make more informed decisions about the status of the satellites. This will likely involve simulation due to the dependency of the hypothesis tests involved. .

The current analyses assume an idealized cross-tag situation where the cross-tag in the new data does not change unless it is rectified. The next step is to extend the statistical assessment to the case of a switching or time-dependent cross-tag. This is when a single set of new data for a satellite is cross-tagged with different satellites.

The current Inversion Model and Prediction Model use a 0th order two-facet model. The next step is to enhance the models to include the contribution of new data collected as per the principle of maximum information entropy in order to better account for the antennae, dishes and self-occlusions.

11.0 Acknowledgement

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12.0 References

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2. Wald, A., *Sequential Analysis*, John Wiley and Sons, ISBN: 978-0486615790
3. Siegmund, D., *Sequential Analysis: Tests and Confidence Intervals*, Springer-Verlag, ISBN: 0387961348
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5. https://en.wikipedia.org/wiki/Entropy_(information_theory)
6. Abbot, R.I., and Wallace, T.P., "Decision Support in Space Situational Awareness", Lincoln Laboratory Journal, Vol. 16, No.2, 2007

13.0 Appendix A: Notation

Text notation:

Brightness: Value of Brightness Data at a single data point

Brightness Data: Single point brightness data point collected by a ground or space-based sensor during the routine synoptic search operation. This data is collected along with the angles only metric data

Brightness Ratio: Ratio of observed Brightness to predicted Brightness

Body: Body of a GEO satellite

Change: Modification of state of a satellite from NOM to ANOM or vice versa.

Change Detection: To recognize that the state of satellite has undergone Change

Cluster Peer: A pair of satellite in a cluster can be cross-tagged

NOM: Nominal status of a satellite. This is when the correlation coefficient between the observed Brightness and the predicted Brightness exceeds a user-defined threshold limit.

ANOM: Anomalous status of a satellite. This is when the correlation coefficient between the observed Brightness and the predicted Brightness is below the user-defined threshold limit for NOM.

Panel: Panel term for a GEO satellite (it combines the effect of both solar panels into a single term)

PDF: Probability distribution function

CDF: Cumulative distribution function

Signature Data: A sequence of Brightness measurements collected by a dedicated sensor during a single pass for a target satellite. For GEO satellites, such data is collected at a frame rate such as one data point per minute, etc.

Mathematics notation:

r_k = ratio of observed Brightness of the satellite at pass k to predicted Brightness of the satellite at pass k. This ratio is defined only at the orbital location when Brightness data is collected

Δr_k is the difference between r_k and r_{k-1}

$\tilde{r}$ denotes the adjusted r value after it has subtracted μ and divided by σ

k = Index for an orbital pass number. The time slider origin is k = 0. Prior data is for k < 0. New data is for k $\geq$ 0.

I_{Ok} is the observed single point brightness

I_{Mk} is the expected single point brightness

$E(r_k)$ denotes the expected value

α = the level of significance of the test = P(Type I Error)

β = P(Type II Error)

δ is the number of standard deviations that mean drift mu is away from null hypothesis mean drift 0

$P(NOM|r_k)$ = Probability that satellite is NOM after pass k given the Brightness Ratio r_k

H_o denotes the null hypothesis

H_a denotes the alternative hypothesis

μ is the mean for the prior data

σ is the standard deviation for the prior data

Ln denotes the use of a likelihood function