An Alternative Metric for Detecting Anomalous Ship Behavior Using a Variation of the DBSCAN Clustering Algorithm

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Abstract

There is a growing need to quickly and accurately identify anomalous behavior in ships. This paper applies a variation of the Density Based Spatial Clustering Among Noise (DBSCAN) algorithm to identify such anomalous behavior given a ship’s Automatic Identification System (AIS) data. This variation of the DBSCAN algorithm has been previously introduced in the literature, and in this study, we elucidate and explore the mathematical details of this algorithm and introduce an alternative anomaly metric which is more statistically informative than the one previously suggested.

Keywords — clustering, anomaly detection, trajectory mining, maritime surveillance

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1 Introduction

In this paper we identify anomalous behavior in ships given their Automatic Identification System (AIS) data. AIS data is reported by all ships, and among other things, these data include a ship’s position (latitude & longitude), speed, and course (direction) over time. We use this data to identify spatial and behavioral patterns of ships. With these patterns identified from the training data, we can potentially spot anomalous behavior in other ships given their new/incoming AIS data. We do this by applying a variation to the DBSCAN (Density Based Spatial Clustering Among Noise) algorithm ([4]). The DBSCAN algorithm is typically used to create spatial clusters of data (see [3], [7], [9]). The variation to the DBSCAN algorithm we consider was introduced by Liu et al. ([5]). In this paper, we review and expand on the anomaly detection methods given in Liu ([5] & [6]), and we also offer an alternative (and in some cases more flexible and informative) way of identifying anomalous behavior.

This paper begins by showing the data and briefly discussing the problem at hand. This is done in Section 2. Simply stated, the problem is this: “How does one identify anomalous behavior among the ships that are reporting AIS data?” An easy way to answer such a question would be to create spatial clusters of AIS positional data using the DBSCAN algorithm. If a new ship then reported AIS positional data which was geographically far from any of these clusters, such data may be considered unusual, or anomalous. But what if one wished to detect anomalies with respect to other variables, such as speed or direction, in addition to the positional/spatial variables? For example, how would it be possible to identify if a ship were traveling in an unusual direction and/or at an unusual speed, yet was (geographically) very close to a cluster of the training data? Spatial clusters can not be used to answer such questions. In such cases, other types of clusters need to be made, and the DBSCAN algorithm is ill-fitted to make them. To create appropriate clusters for this problem, the DBSCAN algorithm needs to be modified. Section 2 of this paper discusses how Liu et al. ([5]) modify the DBSCAN algorithm to create appropriate clusters. It also states and clarifies some mathematical assumptions that were made in their methodology. Section 3 then explains how these clusters can be used to test for anomalous behavior. Section 4 specifically discusses how Liu ([6]) use these clusters to create gravity vectors and stationary sampling points. These vectors and points are summaries of the training data that are necessary in calculating an anomaly score of new/incoming trajectories. The statistical properties of Liu’s anomaly score, and those of an alternative anomaly score that we propose are also discussed in Section 4.

2 The Data

In this paper, we look at AIS data that was reported on January 1 of 2017 along the mid-Atlantic coast of the United States. This data is publicly available at MarineCadastre.gov. These data are shown in
Figure 1: The Training Data, $\mathcal{P}$.

Figure 1 and this is the data set we will use for training purposes. We will denote the training data as $\mathcal{P}$ and assume there are $n$ observations in this data set, making

$$\mathcal{P} = \{ \mathbf{z}_i^{\mathcal{P}} : i = 1, 2, \ldots, n \} ,$$

where

$$\mathbf{z}_i^{\mathcal{P}} = (y_i^{\mathcal{P}}, x_i^{\mathcal{P}}, s_i^{\mathcal{P}}, c_i^{\mathcal{P}}) ,$$

$y_i^{\mathcal{P}}$ is the latitudinal position of the $i^{th}$ observation, $x_i^{\mathcal{P}}$ is the longitudinal position of the $i^{th}$ observation, $s_i^{\mathcal{P}}$ is the “s”peed of the $i^{th}$ observation, and $c_i^{\mathcal{P}}$ is the “c”ourse of the $i^{th}$ observation. Figure 1 of course, only shows the latitude and longitude of the training data.

The goal of this paper is to identify patterns among this training data using as few assumptions as possible. Any other data which exhibits significant departures from these patterns will be considered an anomaly.

A way to identify spatial patterns in the data while making no distributional assumptions is to apply the DBSCAN algorithm. Although this is not the algorithm we ultimately use to create our clusters, we do use a close variation of it. Section 3 reviews the DBSCAN algorithm and then provides details on how Liu et al. ([6]) altered it to accommodate our needs. Recall that our needs involve clustering the data not just with respect to position, but with respect to position, speed, and course.

### 3 Clustering the Data

To cluster spatial data using the DBSCAN algorithm, two parameters need to be specified, $\epsilon$ and $N_{\text{min}}$. The parameter $\epsilon$ specifies the maximum distance each observation in a cluster is from another observation in that same cluster, and $N_{\text{min}}$ specifies the minimum number of objects in a cluster. The following definitions (borrowed directly from [4] yet applied to $\mathcal{P}$) will be used to define the DBSCAN algorithm with more mathematical clarity.

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1 We denote this training data set as $\mathcal{P}$ since it is from this data set that we will discover “P”atterns. We choose $\mathcal{P}$ rather than $\mathcal{T}$ (for “T”raining) since the superscript of the elements within the set is meant to indicate what set the element is a part of. Having a superscript of $\mathcal{T}$ may confuse the reader in thinking that a transpose is being taken.
**Definition 1** A point \( z^P_i \) is *directly density-reachable* from an object \( z^P_j \) with respect to \( \epsilon \) and \( N_{\text{min}} \) in the set of objects \( P \) if

1. \( z^P_i \in N_{\epsilon}(z^P_j) \), where \( N_{\epsilon}(z^P_j) \) is the subset of \( P \) contained in the \( \epsilon \) neighborhood of \( z^P_j \).
2. \(|N_{\epsilon}(z^P_j)| \geq N_{\text{min}} \), where \(|N_{\epsilon}(z^P_j)| \) is the cardinality of the set \( N_{\epsilon}(z^P_j) \).

To visualize the concept of two points being directly density-reachable, imagine the point \( z^P_j \) and all of the objects in the set \( P \) that are within \( \epsilon \) from \( z^P_j \). If there are at least \( N_{\text{min}} \) objects that are within \( \epsilon \) of \( z^P_j \), and \( z^P_i \) is one of those elements, then \( z^P_i \) is directly density-reachable from the object \( z^P_j \). Figure 2 illustrates objects that are directly density-reachable.

**Definition 2** An object \( z^P_i \) is *density-reachable* from an object \( z^P_j \) with respect to \( \epsilon \) and \( N_{\text{min}} \) in the set of objects \( P \) if there is a chain of points \( p_1, p_2, \ldots, p_n \), with \( p_1 = z^P_j \) and \( p_n = z^P_i \) such that \( p_i \in P \forall i \) and \( p_{i+1} \) is directly density-reachable from \( p_i \) with respect to \( \epsilon \) and \( N_{\text{min}} \).

Density-reachability is different from two points being directly density-reachable in the sense that it implies that there is a sequence of directly density-reachable points from \( z^P_j \), and \( z^P_i \) is directly density reachable from one of the points in that sequence. Figure 3 illustrates objects that are density-reachable from one-another.

**Definition 3** An object \( z^P_i \) is *density-connected* to an object \( z^P_j \) with respect to \( \epsilon \) and \( N_{\text{min}} \) in the set of objects \( P \) if there is a point \( z^P_o \in P \) such that both \( z^P_i \) and \( z^P_j \) are density-reachable from \( P \) with respect to \( \epsilon \) and \( N_{\text{min}} \) in \( P \).

Figure 4 illustrates the concept of two elements in \( P \) being density-connected.
Figure 4: $z_i^P$ and $z_j^P$ are Density-Connected with respect to $\epsilon$ and $N_{\text{min}} = 5$. Observe that both are Density-Reachable from $z_0^P$

In the DBSCAN algorithm, all elements in the same cluster are density-connected. Another (and perhaps more intuitive) way to communicate this is to say that for every element in a DBSCAN cluster, there is at least one other element in that same cluster which is $\epsilon$ units away. And it must be the case that for at least one of the elements that is $\epsilon$ units away, there are at least $N_{\text{min}}$ observations within $\epsilon$ of it.

Applying the DBSCAN algorithm to the training data shown in Figure 1 with $\epsilon = .02$, $N_{\text{min}} = 5$, and $\text{dist}(z_i^P, z_j^P)$ being $\text{dist}(z_i^P, z_j^P) = \| (y_i^P, x_i^P)^T - (y_j^P, x_j^P)^T \|$, we get the results shown in Figure 5. Note that the distance we calculate between two points is the Euclidian distance between the two points’ latitude and longitude coordinates. Our methodology thus assumes a flat earth. The more locally we apply our algorithm, the more valid this assumption.
The results in Figure 5 cluster points based on their location. We wish to cluster with respect to location, speed, and direction, however. Let us specifically assume that we wish to cluster such that points $z_i^p$ and $z_j^p$ are in the same cluster if $\text{dist}(z_i^p, z_j^p) < \epsilon_{\text{Dist}}$, $|c_i^p - c_j^p| < \epsilon_{\text{Crs}}$, and $|s_i^p - s_j^p| < \epsilon_{\text{Spd}}$. To do this, an edited version of the DBSCAN algorithm is necessary since DBSCAN is only engineered to consider one distance between two points. Liu et al. (5) edit the DBSCAN algorithm to accommodate these wishes. Their edited version of the DBSCAN algorithm is called DBSCANSD, where the “SD” stands for “S”peed and “D”irection.

The DBSCANSD algorithm applied to the training data set $P$ is given below and requires that the additional thresholds $\epsilon_{\text{Crs}}$ and $\epsilon_{\text{Spd}}$ be specified. Liu et al.’s (5) addition to the standard DBSCAN algorithm is shown in red.

We apply the DBSCANSD algorithm to the “moving” members of $P$, $P_{\text{mov}}$, and the DBSCAN algorithm to the stationary members of $P$, $P_{\text{stat}}$ to get the results shown in Figure 6. It should be noted that in this application, the speed threshold used was 2.5 knts and the direction threshold used was 90 degrees ($\epsilon_{\text{Spd}} = 2.5$ knts and $\epsilon_{\text{Crs}} = 90$ degrees)
Algorithm 1: DBSCANSND

Procedure: DBSCANSND
input: $\mathcal{P}$, $N_{\min}$, $\epsilon_{\text{Dist}}$, $\epsilon_{\text{Crs}}$, $\epsilon_{\text{Spd}}$
output: cltrList
cltrList $\leftarrow$ empty list
for each unclassified point $z_i^P \in \mathcal{P}$ do
Mark $z_i^P$ as classified
neighborPts $\leftarrow$ QueryNeighborPoints ($\mathcal{P}$, $z_i^P$, $N_{\min}$, $\epsilon_{\text{Dist}}$, $\epsilon_{\text{Crs}}$, $\epsilon_{\text{Spd}}$)
if neighborPts is not NULL then
cltrList.add (neighborPts)
for each cluster $C$ in cltrList do
for each cluster $C'$ in cltrList do
if $C$ and $C'$ are different clusters then
if MergeClusters ($C$, $C'$) is TRUE then
cltrList.remove ($C'$)

Procedure: QueryNeighborPoints
input: $\mathcal{P}$, $z_i^P$, $N_{\min}$, $\epsilon_{\text{Dist}}$, $\epsilon_{\text{Crs}}$, $\epsilon_{\text{Spd}}$
output: cluster
cluster $\leftarrow$ empty list
for each point $X_j^P$ in $\mathcal{P}$ do
if distance $\left((y_i^P, x_i^P)^T, (y_j^P, x_j^P)^T\right) < \epsilon_{\text{Dist}}$ then
if $|c_i^P - c_j^P| < \epsilon_{\text{Crs}}$ then
if $|s_i^P - s_j^P| < \epsilon_{\text{Spd}}$ then
cluster.add ($z_j^P$)
if cluster.size $\geq N_{\min}$ then
Mark $z_i^P$ as core point

Procedure: MergeClusters
input: $clusterA$, $clusterB$
output: merge
merge $\leftarrow$ FALSE
for each point $z_j^P$ in $clusterB$ do
if point $z_j^P$ is core point and $clusterA$ contains cluster $Q$ then
merge $\leftarrow$ TRUE
for each point $z_j^P$ in $clusterB$ do
clusterA.add ($z_j^P$)
From this point on, we will denote the set of points put in cluster $j$ as a result of the DBSCAN algorithm as $P_{mv, cl_j}$, and we will assume that the number of observations in this cluster is $n_{mv}^j$, making

$$P_{mv, cl_j} = \left\{ z_{mv, cl_j}^1, z_{mv, cl_j}^2, \ldots, z_{mv, cl_j}^{n_{mv}^j} \right\}.$$ 

The set of points put in cluster $l$ as a result of the DBSCAN algorithm will be denoted as $P_{st, cl_l}$, and we will assume that the number of observations in this cluster is $n_{st}^l$, making

$$P_{st, cl_l} = \left\{ z_{st, cl_l}^1, z_{st, cl_l}^2, \ldots, z_{st, cl_l}^{n_{st}^l} \right\}.$$ 

The next section discusses how we use these results to identify outliers or outlying/anomalous behavior in ships.

4 Identifying Anomalous Behavior

To identify anomalous behavior in a new ship’s trajectory, one first has to separate this new trajectory into a set of stationary points and a set of moving points. Just as Liu et. al ([6]) did, we identify the set of stationary points as that set such that the speed is less than 0.5 knots. The set of moving points is the complement of that. We will assume that there are a total of $m$ points in this new trajectory, and we will denote the set of points in this trajectory as $N$ (for “N”ew), where

$$N = \left\{ z_1^N, z_2^N, \ldots, z_m^N \right\}.$$ 

The set of points in $N$ that are moving is

$$N_{mv} = \left\{ z_i^N : s_i^N \geq 0.5 \text{ knts} \right\},$$
and the set of stationary points is
\[ N^{st} = \{ z_i^N : s_i^N < 0.5 \text{ knts} \}. \]

We will assume there are \( m^{mv} \) values in \( N^{mv} \) and \( m^{st} \) values in \( N^{st} \), making
\[ N^{mv} = \{ z_1^{mv}, z_2^{mv}, \ldots, z_{m^{mv}-1}^{mv}, z_{m^{mv}} \}, \]
and
\[ N^{st} = \{ z_1^{st}, z_2^{st}, \ldots, z_{m^{st}-1}^{st}, z_{m^{st}} \}. \]

We then see how the points in \( N^{st} \) depart from stationary points in the training data set, and how the points in \( N^{mv} \) depart from the moving points in the training data set. To do this, Liu et al. ([6]) first create two sets of points, one set which summarizes the stationary points in the training data, the other set which summarizes the moving points in the training data. These sets are respectively called the stationary sampling points and gravity vectors, and we denote these sets as \( S \) and \( G \). The set of new trajectory points, \( N \), are then compared to \( S \) and \( G \) (the set \( N^{st} \) is compared to \( S \), and the set \( N^{mv} \) is compared to \( G \)), and it is from this comparison that a trajectory is identified as being anomalous or not.

Subsection 4.1 describes how the gravity vectors and stationary sampled points are calculated. Subsection 4.2 describes how these set of points, \( S \) and \( G \), are compared to the new trajectory, \( N \). The subsection specifically reviews how Liu et al. ([6]) calculate and assign an anomalous score to a new trajectory and then discusses our alternative anomalous score.

### 4.1 Creating Gravity Vectors and Stationary Sampled Points

Generally speaking, a gravity vector is a point (or vector) that is meant to summarize and describe all of the moving points of the training set around it. We will let \( G^{cl} \) be the set of gravity vectors which summarize cluster \( j \), and we will assume there are \( n^{cl} \) gravity vectors associated with cluster \( j \), i.e.,
\[ G^{cl} = \{ g_1^{cl j}, g_2^{cl j}, \ldots, g_{n^{cl j}}^{cl j} \}. \]

To calculate all of the gravity vectors associated with cluster \( j \), one first has to calculate the average course (direction) of the entire cluster. We will call this average direction \( \overline{c}^{mv, cl j} \) and calculate it as
\[ \overline{c}^{mv, cl j} = \frac{1}{n^{mv j}} \sum_{k=1}^{n^{mv j}} c^{mv, cl j}. \]

After calculating \( \overline{c}^{mv, cl j} \), one must define a line along this direction and divide this into segments of length \( \delta \). Liu et al. ([6]) set \( \delta = \epsilon \), and we do the same to achieve our results. All of the observations that are then within a particular band (of width \( \delta \)) are considered and their average latitude, longitude, speed, direction, and median distance from the average position are calculated and reported in one gravity vector. This concept is illustrated in Figure 7, and in this paper we mathematically formalize the calculation of these vectors. This is done in the text box below.

![Figure 7: Calculating Gravity Vectors](image-url)
Calculating Components of $g_{cl}^{l,j}$

The line along the direction of $r_{mv}^{cl,j}$ is of length $L_{mv,cl,j}$, where

$$L_{mv,cl,j} = \left\{ \max_i \left[ y_i^{mv,cl,j} \right] \right\} \cos \left( r_{mv,cl,j} \right) - \min_i \left[ y_i^{mv,cl,j} \right] \cdot \cos \left( r_{mv,cl,j} \right) \right\}.$$ 

We are dividing this line into bands of width $\delta$, making the value of $n_{grv}^{cl,j}$

$$n_{grv}^{cl,j} = L_{mv,cl,j} / \delta.$$ 

The observations in cluster $j$ to be considered in the calculation of the $l^{th}$ gravity vector ($1 \leq l \leq n_{grv}^{cl,j}$) vector are then

$$T_{grv}^{cl,j} = \left\{ z_i^{mv,cl,j} : (l - 1) \cdot b \cdot \delta \leq y_i^{mv,cl,j} \leq (l - \delta) \cdot b \cdot \delta \right\},$$

where $b = \min_i \left( y_i^{mv,cl,j} / \cos \left( r_{mv,cl,j} \right) \right)$, making the $l^{th}$ gravity vector in cluster $j$

$$g_{cl}^{l,j} = \left( \frac{cl,j}{grv} \right)_{i}^{l} = \frac{cl,j}{grv} \left( \begin{array}{cccc} y_{cl,j}^{mv,grv} & x_{cl,j}^{mv,grv} & z_{cl,j}^{mv,grv} \end{array} \right)^{T},$$

where

$$\left( y_{cl,j}^{mv,grv}, x_{cl,j}^{mv,grv}, z_{cl,j}^{mv,grv} \right) = T_{grv}^{cl,j} \left\{ \sum_{x_i \in P_{grv}^{cl,j}} z_i^{P} \right\},$$

and

$$d_{grv}^{cl,j} = \text{median}_{x_i \in P_{grv}^{cl,j}} \left\{ \left\| z_i^{mv,cl,j} - x_i^{mv,cl,j} \right\| \right\}.$$

Stationary sampling points are meant to describe the stationary points in the training set. For each stationary cluster, the number of stationary sampled points meant to summarize it are $N/\epsilon$, and they are randomly selected according to the following algorithm:

Algorithm 2: Extracting Stationary Sampling Points from $P_{st, cl,j}$

```
input: $P_{st, cl,j}$, $N_{min}$, $\epsilon_{Dist}$
output: $S_{cl,j}$
$S_{cl,j} \leftarrow \emptyset$
Lat$_1$, Lat$_2$ \leftarrow minimum and maximum of all points’ latitude in $P_{st, cl,j}$
Lon$_1$, Lon$_2$ \leftarrow minimum and maximum of all points’ longitude in $P_{st, cl,j}$
Area \leftarrow |(Lat$_1$ - Lat$_2$) \cdot (Lon$_1$ - Lon$_2$)|
if Area = 0 then
    sample.size = 1
else
    sample.size = ceiling (Area / (\pi \cdot \epsilon_{Dist}))
count \leftarrow 0
while count < sample.size do
    Randomly select one point from cluster $P_{st, cl,j}$
    if Randomly selected point is far from all points in $S_{cl,j}$ then
        Add point to $S_{cl,j}$
        count \leftarrow count + 1
```

Assume there are $n_{asp}^{cl,j}$ stationary sampled points in stationary cluster $j$. We will call this set of points $S_{cl,j}^{cl,j}$, and

$$S_{cl,j}^{cl,j} = \left\{ s_{cl,j}^{1,j}, s_{cl,j}^{2,j}, \ldots, s_{cl,j}^{n_{asp}^{cl,j}} \right\},$$

where

$$s_{cl,j}^{1,j} = \left( y_{asp}^{cl,j}, x_{asp}^{cl,j}, z_{asp}^{cl,j} \right).$$

It is with the gravity vectors and stationary points that an anomaly score is calculated. The subsection below explains how Liu (3) calculates this anomaly. We add some mathematical and statistical detail.
to their calculations and also introduce an alternative and more flexible way to measure anomalous behavior.

### 4.2 Calculating Anomalous Behavior

To assign an anomaly score to \( \mathcal{N} \), Liu et al. ([6]) first split the new track into its stationary and moving parts, \( \mathcal{N}^{\text{ext}} \) and \( \mathcal{N}^{\text{mov}} \). For each point in \( \mathcal{N}^{\text{ext}} \), they calculate the smallest distance between it and the set of stationary sampled points. This distance is called the Absolute Distance Deviation (ADD), and for point \( i \) in \( \mathcal{N}^{\text{ext}} \), it is calculated as

\[
\text{ADD}_{i}^{\text{ext}} = \min_{j} \left( \left\| \left( y_{i}, x_{i} \right)^{T} - \left( y_{j}^{\text{st}}, x_{j}^{\text{st}} \right)^{T} \right\| \right).
\]

For each point in \( \mathcal{N}^{\text{mov}} \), they calculate two distance metrics, the Relative Distance Deviation (RDD) and the Cosine Division Distance (CDD). The RDD is similar to the ADD in that it calculates the smallest distance between a point and the set of gravity vectors, but this metric is different in that it accounts for the variation and geographical spread around the gravity vector. It does this by dividing the distance by the median of the associated gravity vector. For the \( i \)-th point in \( \mathcal{N}^{\text{mov}} \), RDD is calculated as

\[
\text{RDD}_{i}^{\text{mov}} = \min_{l,j} \left\{ \left\| \left( y_{i}^{\text{mov}}, x_{i}^{\text{mov}} \right)^{T} - \left( y_{l}^{\text{grv}} + \alpha x_{l}^{\text{grv}} \right)^{T} - \left( y_{j}^{\text{mov}}, x_{j}^{\text{mov}} \right)^{T} \right\| / d_{l,j}^{\text{grv}} \right\}.
\]

The CDD accounts for any difference in heading and/or speed a point in \( \mathcal{N}^{\text{mov}} \) may have from the closest gravity point. For point \( i \) in \( \mathcal{N}^{\text{mov}} \), it is calculated as

\[
\text{CDD}_{i}^{\text{mov}} = \cos(\alpha) \cdot \frac{\min \left( s_{i}^{\text{grv}} - s_{i}^{\text{mov}}, s_{i}^{\text{mov}} \right)}{\max(\alpha_{i}^{\text{grv}} + \alpha_{i}^{\text{mov}})}
\]

where \( \alpha = |c^* - c_{i}^{\text{mov}}| \), and \( c^* \) and \( s^* \) are the course and speed components of gravity vector \( g^* \), where

\[
g^* = \arg\min_{g \in g_{i,j}} \left\{ \left( y_{i}^{\text{mov}}, x_{i}^{\text{mov}} \right)^{T} - \left( y_{l}^{\text{grv}} + \alpha x_{l}^{\text{grv}} \right)^{T} \right\} / d_{l,j}^{\text{grv}} \right\}.
\]

In this case, the smaller the value of \( \text{CDD} \), the greater the anomaly.

It should be noted that our definition of CDD is different than how it is written in Liu et al. ([6]). They write CDD as

\[
\text{CDD}_{\text{Liu}}^{\text{mov}} = \max_{l,j} \left\{ \cos \left( |c_{l}^{\text{mov}} - c_{i}^{\text{mov}}| \right) \cdot \frac{\min \left( s_{i}^{\text{grv}} - s_{l}^{\text{mov}}, s_{l}^{\text{mov}} \right)}{\max(\alpha_{i}^{\text{grv}} + \alpha_{i}^{\text{mov}})} \right\}
\]

but this definition seems unclear. As they have written it, they are looking for a gravity vector with a speed and course which most closely matches the speed and course of point \( i \) in \( \mathcal{N}^{\text{mov}} \). The location of this gravity vector is not considered. Given their definition of CDD, it would be possible for the point \( i \) in \( \mathcal{N}^{\text{mov}} \) to be in the proximity of points going in an opposite direction and at a much different speed, yet still have a CDD value that went unnoticed. With this in mind, we modified/rewrote the definition of CDD. For each point \( i \) in \( \mathcal{N}^{\text{mov}} \), we evaluate CDD at the closest gravity vector. The closest gravity vector is that which minimizes RDD (\( g^* \) in Equation 1).

With these three metrics (ADD, RDD and CDD) calculated, Liu et al. ([6]) score each observation in \( \mathcal{N} \) depending on whether the calculated ADD, RDD, or CDD are beyond a certain threshold. For points in \( \mathcal{N}^{\text{ext}} \), the score is calculated as

\[
\text{Scr}_{\text{Liu}} \left( z_{i}^{\text{ext}} \right) = \begin{cases} 1 & \text{if } \text{ADD}_{i}^{\text{ext}} > \text{ADD}_{\text{Threshold}} \\ 0 & \text{otherwise} \end{cases}
\]

For points in \( \mathcal{N}^{\text{mov}} \), the score is calculated as

\[
\text{Scr}_{\text{Liu}} \left( z_{i}^{\text{mov}} \right) = \begin{cases} 1 & \text{if } \text{RDD}_{i}^{\text{mov}} > \text{RDD}_{\text{Threshold}} \text{ or } \text{CDD}_{i}^{\text{mov}} < \text{CDD}_{\text{Threshold}} \\ 0 & \text{otherwise} \end{cases}
\]
They then calculate the total anomaly score for the new trajectory, \( N' \), as

\[
\text{Anom}_{\text{Liu}} \left( N' \right) = m^{-1} \left( \sum_{j=1}^{m_{\text{st}}} \text{Scr}_{\text{Liu}} \left( z_{j}^{\text{st}} \right) + \sum_{j=1}^{m_{\text{mv}}} \text{Scr}_{\text{Liu}} \left( z_{j}^{\text{mv}} \right) \right)
\]

One way they obtain these three thresholds, \( ADD_{\text{Threshold}} \), \( RDD_{\text{Threshold}} \), and \( CDD_{\text{Threshold}} \) is by considering an entirely different data set, \( D \) (for “D”ifferent), calculating the distribution of \( ADD \), \( RDD \) and \( CDD \) values in this data set, and then letting \( ADD_{\text{Threshold}} \) and \( RDD_{\text{Threshold}} \) be the 95th percentile of the distribution in the \( ADD \) and \( RDD \) values, and \( CDD_{\text{Threshold}} \) be the 5th percentile of the distribution in the \( CDD \) values. This is mathematically formulated in the textbox below.

### Calculating Threshold Values

We assume \( D \) has \( r \) observations, \( r_{\text{st}} \) which are stationary and \( r_{\text{mv}} \) which are moving. From this data set, we calculate \( r_{\text{st}} \) values of \( ADD \), written as

\[
ADD^{D} = \left\{ ADD^{D}_{i} : 1 \leq i \leq r_{\text{st}} \right\},
\]

and \( r_{\text{mv}} \) values of \( RDD \) and \( CDD \), written as

\[
RDD^{D} = \left\{ RDD^{D}_{j} : 1 \leq j \leq r_{\text{mv}} \right\},
\]

and

\[
CDD^{D} = \left\{ CDD^{D}_{j} : 1 \leq j \leq r_{\text{mv}} \right\}.
\]

\( ADD_{\text{Threshold}} \) is the 95th percentile of \( ADD^{D} \), \( RDD_{\text{Threshold}} \) is the 95th percentile of \( RDD^{D} \), and \( CDD_{\text{Threshold}} \) is the 5th percentile of \( CDD^{D} \).

A setback to the method that Liu et al. use to measure anomalous behavior is that it fails to highlight the extremity of the anomaly. For example, if \( N' \) were a set of stationary points, all of which were just barely beneath \( ADD_{\text{Threshold}} \), its anomaly score would be 0. Its anomaly score would also be 0 if all these stationary points were significantly below \( ADD_{\text{Threshold}} \). Yet another setback to Liu et al.’s method is that the statistical significance of their anomaly is not immediately transparent. For instance, if \( \text{Anom}_{\text{Liu}} \left( N' \right) = 0.3 \), it is not obvious from this statistic what the probability is of observing an anomaly as or more extreme than the one observed.

Part of the novelty proposed in this paper is in how we calculate the anomaly of a new trajectory. We calculate the anomaly in such a way that the two extreme cases described above would have considerably different scores. The statistical significance of our anomaly score is also transparent (we ultimately report a \( z \)-score).

We begin by scoring each observation not with a 1 or a 0 (as Liu et al. did), but with the fraction of \( ADD^{D} \), \( RDD^{D} \), and \( CDD^{D} \) values that are more extreme than the one observed. These scores are written below in Equations 2 and 3.

\[
\text{Scr}_{\text{Botts}} \left( z_{i}^{\text{st}} \right) = \frac{1}{r_{\text{st}}} \sum_{j=1}^{r_{\text{st}}} \mathbb{1} \left( ADD^{D}_{j} \geq ADD_{i}^{\text{st}} \right), \quad \text{and}
\]

\[
\text{Scr}_{\text{Botts}} \left( z_{i}^{\text{mv}} \right) = \min \left\{ \frac{1}{r_{\text{mv}}} \sum_{j=1}^{r_{\text{mv}}} \mathbb{1} \left( RDD^{D}_{j} \geq RDD_{i}^{\text{mv}} \right), \quad \frac{1}{r_{\text{mv}}} \sum_{j=1}^{r_{\text{mv}}} \mathbb{1} \left( CDD^{D}_{j} \leq CDD_{i}^{\text{mv}} \right) \right\}.
\]

The quantity \( \text{Scr}_{\text{Botts}} \left( z_{i}^{\text{st}} \right) \) estimates the probability that any randomly selected \( ADD \) value will be more extreme than the one observed. The quantity \( \text{Scr}_{\text{Botts}} \left( z_{i}^{\text{mv}} \right) \) considers the probability of observing an \( RDD \) greater than the one observed and a \( CDD \) less than the one observed, and returns the smaller of the two. The distribution of \( \text{Scr}_{\text{Botts}} \left( z_{i}^{\text{st}} \right) \) can be approximated with that of a uniform random variable, \( U_{1} \), where \( \mathbb{E} \left( U_{1} \right) = 0.5 \) and \( \text{Var} \left( U_{1} \right) = 1/12 \). The distribution of \( \text{Scr}_{\text{Botts}} \left( z_{i}^{\text{mv}} \right) \) can be approximated
with that of the minimum of two uniform random variables, \( U_2 \) and \( U_3 \). If \( U_{\min} = \min(U_2, U_3) \), then 
\[
\mathbb{E}(U_{\min}) = \frac{1}{3} \quad \text{and} \quad \operatorname{Var}(U_{\min}) = \frac{1}{18}.
\]

With \( \text{Scr}_{Botts} \left( \mathbf{z}^{\text{rst}}_i \right) \) and \( \text{Scr}_{Botts} \left( \mathbf{z}^{\text{mv}}_j \right) \) approximated by these distributions that have known first and second moments, we can apply the central limit theorem and conclude that
\[
W^{\text{rst}} = \left\{ \left( m^{\text{rst}} \right)^{-1} \sum_{j=1}^{m^{\text{rst}}} \text{Scr}_{Botts} \left( \mathbf{z}^{\text{rst}}_j \right) - 0.5 \right\} \sqrt{\frac{1}{12m^{\text{rst}}}} \xrightarrow{d} N(0, 1) \quad \text{as} \quad m^{\text{rst}} \to \infty,
\]
and
\[
W^{\text{mv}} = \left\{ \left( m^{\text{mv}} \right)^{-1} \sum_{j=1}^{m^{\text{mv}}} \text{Scr}_{Botts} \left( \mathbf{z}^{\text{mv}}_j \right) - 1 \right\} \sqrt{\frac{1}{18m^{\text{mv}}}} \xrightarrow{d} N(0, 1) \quad \text{as} \quad m^{\text{mv}} \to \infty.
\]

Our final anomaly statistic, \( \text{Anom}_{Botts}(N) \), combines the two asymptotically normal random variables in Equations 4 and 5 as shown below in Equation 6.

\[
\text{Anom}_{Botts}(N) = \begin{cases} 
W^{\text{rst}} & \text{if} \ m^{\text{mv}} = 0 \\
W^{\text{mv}} & \text{if} \ m^{\text{st}} = 0 \\
(W^{\text{rst}} + W^{\text{mv}}) / \sqrt{2} & \text{if} \ m^{\text{st}} > 0 \land m^{\text{mv}} > 0
\end{cases}
\]

Assuming independence across observations in the track \( N \), and assuming independence of the variables \( ADD, RDD, \) and \( CDD \), the expected value and variance of \( \text{Anom}_{Liu}(N) \) are

\[
\mathbb{E}[\text{Anom}_{Liu}(N)] = 0.05 \cdot (m^{\text{mv}} / m) \cdot (0.05 - 0.05^2),
\]
and

\[
\operatorname{Var}[\text{Anom}_{Liu}(N)] = (m^{\text{st}} + m^{\text{mv}})^{-2} \left[ m^{\text{st}} \cdot 0.05 \cdot 0.95 + 2m^{\text{mv}} \cdot 0.05 \cdot 0.95 + m^{\text{mv}} \cdot 0.05^2 \cdot (1 - 0.05^2) \right],
\]
and the asymptotic distribution of \( \text{Anom}_{Botts}(N) \) is \( N(0, 1) \), making

\[
\mathbb{E}[\text{Anom}_{Botts}(N)] = 0 \quad \text{and} \quad \operatorname{Var}[\text{Anom}_{Botts}(N)] = 1.
\]

Theorem 1 in Section A of the Appendix calculates the expected value and variance of \( \text{Anom}_{Liu}(N) \). Theorem 2 in Section A of the Appendix justifies the asymptotic normality of \( \text{Anom}_{Botts}(N) \). In Section B of the Appendix, some simulation results are provided which illustrate this asymptotic normality.

We would expect normal/in-family trajectories to have \( \text{Anom}_{Liu}(N) \) and \( \text{Anom}_{Botts}(N) \) values close to these expected values. For anomalous trajectories, we would expect \( \text{Anom}_{Liu}(N) \) to be considerably larger than its expected value, and \( \text{Anom}_{Botts}(N) \) to be considerably less than its expected value. Remember that \( \text{Anom}_{Liu}(N) \) counts the fraction of points in \( N \) that are beyond a certain threshold. The larger the value of \( \text{Anom}_{Liu}(N) \), the more anomalous a trajectory is. \( \text{Anom}_{Botts}(N) \) considers the fraction of values in \( ADD^D, RDD^D, \) and \( CDD^D \) that are more extreme than those observed in \( N \) and turns this into a \( z \)-score. The smaller the value of \( \text{Anom}_{Botts}(N) \), the more anomalous a trajectory is. It is thus expected that \( \text{Anom}_{Liu}(N) \) and \( \text{Anom}_{Botts}(N) \) will jointly go in opposite directions of their respective expectations.

Figures 8 and 9 show normal trajectories with values of \( \text{Anom}_{Liu}(N) \) and \( \text{Anom}_{Botts}(N) \) that are close to their expected values. Figures 10 and 11 show abnormal trajectories. In these cases, \( \text{Anom}_{Liu}(N) \) is higher than expected, and \( \text{Anom}_{Botts}(N) \) is significantly lower than expected. Assuming the \( ADD, RDD, \) and \( CDD \) values in \( N \) come from the same distribution as those in the training set and \( D \), the probability of observing \( \text{Anom}_{Botts}(N) \) scores as or more extreme than the ones observed in Figures 10 and 11 is less than \( 10^{-6} \).

Figures 12 and 13 show other sets of \( N \) with surprising results of \( \text{Anom}_{Liu}(N) \) and \( \text{Anom}_{Botts}(N) \). In both cases, the values of \( \text{Anom}_{Liu}(N) \) do not suggest anomalous behavior, yet the values of \( \text{Anom}_{Botts}(N) \) do. They are less than expected for a normal trajectory. The probabilities of observing \( \text{Anom}_{Botts}(N) \) scores as low as those observed in Figures 12 and 13 are lower than \( 2 \times 10^{-15} \) and \( 2 \times 10^{-14} \), respectively. In both of these figures, the difference between the two metrics illustrates why \( \text{Anom}_{Botts}(N) \) may be a preferred metric to \( \text{Anom}_{Liu}(N) \).

In Figure 12 \( N \) is made up entirely of stationary points, and they are all (nearly) at the same location. Each point has an \( ADD \) that is approximately \( 0.017 \), which is beneath the \( ADD \) threshold of \( 0.034 \). Since they are all beneath the threshold, \( \text{Anom}_{Liu}(N) = 0 \). \( \text{Anom}_{Botts}(N) \), however, does capture how extreme these values of \( ADD \) are, since it does not depend on a threshold and merely counts the number of \( ADD^D \) values that are greater than it.

The same principle applies in Figure 13. In this case, very few \( RDD \) values in the moving part of \( N \) are below the \( CDD \) threshold of \( -0.746 \), and no \( RDD \) values are above the \( RDD \) threshold of \( 2.255 \), yet \( 62\% \) of \( N \)'s \( RDD \) values are within the 95th and 70th percentile of the \( RDD \) values in \( RDD^D \).
5 Conclusion

In this memo, we illustrate and clarify the DBSCANSD clustering algorithm presented in Liu et al. ([5] & [6]). The DBSCANSD algorithm allows us to cluster AIS data based on location, speed, and course. With these clustering results, we offer an alternative and more informative way of identifying anomalous behavior in ships.

Figure 8: The values of $N$ are in black, $m^s = 69$, and $m^{mv} = 176$. $E[\text{Anom}_{Liu}(N)] = 0.0841$, $\text{StDev}[\text{Anom}_{Liu}(N)] = 0.0184$, $E[\text{Anom}_{Botts}(N)] = 0$, and $\text{StDev}[\text{Anom}_{Botts}(N)] = 1$. $\text{Anom}_{Liu}(N) = 0.094$, and $\text{Anom}_{Botts}(N) = 0.767$. These numbers indicate no abnormality, and the picture illustrates a common ship path north of Long Island, NY.
Figure 9: The values of $\mathcal{N}$ are in black, $m^s = 31$, and $m^m = 172$. $\mathbb{E}[\text{Anom}_{\text{Liu}}(\mathcal{N})] = 0.0902$, $\text{StDev}[\text{Anom}_{\text{Liu}}(\mathcal{N})] = .0210$, $\mathbb{E}[\text{Anom}_{\text{Botts}}(\mathcal{N})] = 0$, and $\text{StDev}[\text{Anom}_{\text{Botts}}(\mathcal{N})] = 1$. $\text{Anom}_{\text{Liu}}(X^P) = 0.064$, and $\text{Anom}_{\text{Botts}}(\mathcal{N}) = -2.564$. These numbers indicate no severe abnormality, and the picture illustrates a common ship path in the Delaware River.

Figure 10: The values of $\mathcal{N}$ are in black, $m^s = 37$, and $m^m = 249$. $\mathbb{E}[\text{Anom}_{\text{Liu}}(\mathcal{N})] = 0.0914$, $\text{StDev}[\text{Anom}_{\text{Liu}}(\mathcal{N})] = .0178$, $\mathbb{E}[\text{Anom}_{\text{Botts}}(\mathcal{N})] = 0$, and $\text{StDev}[\text{Anom}_{\text{Botts}}(\mathcal{N})] = 1$. $\text{Anom}_{\text{Liu}}(X^P) = 0.706$, and $\text{Anom}_{\text{Botts}}(\mathcal{N}) = -17.616$. These numbers suggest abnormal behavior, and the picture illustrates abnormal behavior off the coast of New Jersey.
Figure 11: The values of $\mathcal{N}$ are in black, $m^\text{st} = 39$, and $m^\text{inv} = 379$. $E[\text{Anom}_{\text{Liu}}(\mathcal{N})] = 0.0931$, StDev $[\text{Anom}_{\text{Liu}}(\mathcal{N})] = 0.0149$, $E[\text{Anom}_{\text{Botts}}(\mathcal{N})] = 0$, and StDev $[\text{Anom}_{\text{Botts}}(\mathcal{N})] = 1$. $\text{Anom}_{\text{Liu}}(\mathcal{N}) = 0.770$, and $\text{Anom}_{\text{Botts}}(\mathcal{N}) = -23.776$. These numbers suggest abnormal behavior, and the picture illustrates abnormal behavior off the coast of New Jersey.
Figure 12: The values of $N$ are in black, $m^{st} = 34$, and $m^{mv} = 0$. $E[\text{Anom}_\text{Liu} (N)] = 0.05$, $\text{StDev}[\text{Anom}_\text{Liu} (N)] = 0.0374$, $E[\text{Anom}_\text{Botts} (N)] = 0$, and $\text{StDev}[\text{Anom}_\text{Botts} (N)] = 1$. $\text{Anom}_\text{Liu} (N) = 0.0$, and $\text{Anom}_\text{Botts} (N) = -8.191$. $\text{Anom}_\text{Liu}$ suggests no abnormal behavior, yet $\text{Anom}_\text{Botts}$ does. In this case, the stationary points in $N$ are just below the threshold used in calculating $\text{Anom}_\text{Liu}$. 
Figure 13: The values of $N$ are in black, $m^{rt} = 0$, and $m^{mv} = 160$. $E[\text{Anom}_{\text{Liu}}(N)] = 0.0975$, $\text{StDev}[\text{Anom}_{\text{Liu}}(N)] = 0.0247$, $E[\text{Anom}_{\text{Botts}}(N)] = 0$, and $\text{StDev}[\text{Anom}_{\text{Botts}}(N)] = 1$. $\text{Anom}_{\text{Liu}}(N) = 0.063$, and $\text{Anom}_{\text{Botts}}(N) = -3.640$. In this case, Anom$_{\text{Liu}}$ suggests no abnormal behavior, yet Anom$_{\text{Botts}}$ does. Nearly all of the moving points in $N$ have RDD values just below the threshold used in calculating Anom$_{\text{Liu}}$.

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In this theorem,

\[ \mathcal{V}^0 = \{ V_1^0, V_2^0, \ldots, V_{m}^0 \}, \quad \mathcal{V}^N = \{ V_1^N, V_2^N, \ldots, V_{m}^N, V_{m+1}^N \}, \]

\[ \mathcal{Y}^0 = \{ Y_1^0, Y_2^0, \ldots, Y_{r}^0 \}, \quad \mathcal{Y}^N = \{ Y_1^N, Y_2^N, \ldots, Y_{r}^N \}, \]

\[ \mathcal{Z}^D = \{ Z_1^D, Z_2^D, \ldots, Z_{r}^D, Z_{r+1}^D \}, \quad \mathcal{Z}^N = \{ Z_1^N, Z_2^N, \ldots, Z_{r}^N \}. \]

Assume these sets of random variables are independent of one another and also assume that the variables within each set are independent of another. We will also assume that all values in \( \mathcal{V}^0 \) and \( \mathcal{V}^N \) follow the common distribution \( f_V(v) \), all the values in \( \mathcal{Y}^0 \) and \( \mathcal{Y}^N \) follow the common distribution \( f_Y(y) \), and all the values in \( \mathcal{Z}^D \) and \( \mathcal{Z}^N \) follow the common distribution \( f_Z(z) \). With these definitions, consider the statistic \( T_1(\alpha) \), where:

\[
T_1(\alpha) = \frac{1}{m^\text{Tot}} \sum_{j=1}^{m^\text{Tot}} \left[ \mathbb{1}(V_j^N \geq \hat{Q}_{V_{r-st}}(1 - \alpha)) + \sum_{j=1}^{m^\text{mov}} \left[ \mathbb{1}(Y_j^N \geq \hat{Q}_{Y_{r-mov}}(1 - \alpha)) \text{ or } Z_j^N \leq \hat{Q}_{Z_{r-mov}}(\alpha) \right] \right]
\]

where \( m^\text{Tot} = m^\text{st} + m^\text{mov} \), and \( \hat{Q}_{V_{r-st}}(\gamma) \) is the \( \gamma \)th percentile of \( \mathcal{V}^D \). Then

\[
\mathbb{E}[T_1(\alpha)] \rightarrow \alpha + \frac{[m^\text{mov}/(m^\text{st} + m^\text{mov})] \cdot (\alpha - \alpha^2)}{\text{min}(r^\text{st}, r^\text{mov})} \text{ as } \min(r^\text{st}, r^\text{mov}) \rightarrow \infty, \quad \text{and}
\]

\[
\text{Var}[T_1(\alpha)] \rightarrow \left( m^\text{Tot}^{-1} \right)^2 \left[ m^\text{st} \alpha(1 - \alpha) + 2m^\text{mov} \alpha(1 - \alpha) + m^\text{mov} \alpha^2(1 - \alpha)^2 \right], \text{ as } \min(r^\text{st}, r^\text{mov}) \rightarrow \infty.
\]

Proof. First observe that \( \hat{Q}_{V_{r-st}}(\gamma) \overset{d}{\rightarrow} Q_V(\gamma) \) as \( r^\text{st} \rightarrow \infty \), where \( Q_V(\gamma) \) is the number such that \( P(V \leq Q_V(\gamma)) = \gamma \). (see Serfling [8]). This implies \( \left( V_j^N \geq \hat{Q}_{V_{r-st}}(\gamma) \right) \overset{d}{\rightarrow} \left( V_j^N \geq Q_V(\gamma) \right) \) as \( r^\text{st} \rightarrow \infty \). Since

\[
\sup_{r^\text{st} \geq 1} \left\{ \mathbb{E} \left[ \mathbb{1}(V_j^N \geq \hat{Q}_{V_{r-st}}(\gamma)) | l \right] \right\} < \infty \quad \text{for any } l,
\]

\( \mathbb{1}(V_j^N \geq Q_{V_{r-st}}(\gamma)) \) is uniformly integrable (see Athreya & Lahiri [11]). With uniform integrability, we...
can apply expectations to get

\[ \mathbb{E} [T_1(\alpha)] \to (m^{\text{Tot}})^{-1} \left\{ \sum_{j=1}^{m^{\text{st}}} \mathbb{E} [\mathbb{I} (V_j \geq Q_V(1-\alpha))] + \sum_{j=1}^{m^{\text{mov}}} \mathbb{E} [\mathbb{I} (Y_j \geq Q_V(1-\alpha) \text{ or } Z_j \leq Q_Z(\alpha))] \right\} \]

\[ = (m^{\text{Tot}})^{-1} \left\{ \sum_{j=1}^{m^{\text{st}}} \mathbb{P} [V_j \geq Q_V(1-\alpha)] + \sum_{j=1}^{m^{\text{mov}}} \mathbb{P} [(Y_j \geq Q_V(1-\alpha) \text{ or } (Z_j \leq Q_Z(\alpha))] \right\} \]

\[ = (m^{\text{Tot}})^{-1} \left\{ m^{\text{st}} \cdot \alpha + m^{\text{mov}} \cdot [\mathbb{P}(Y \geq Q_V(1-\alpha)) + \mathbb{P}(Z \leq Q_Z(\alpha))] \right\} - \mathbb{P}(Y \geq Q_V(1-\alpha) \text{ and } Z \leq Q_Z(\alpha))] \]

\[ = (m^{\text{Tot}})^{-1} \left\{ m^{\text{st}} \cdot \alpha + m^{\text{mov}} \cdot (\alpha + \alpha - \alpha^2) \right\} \]

\[ = \alpha + \left( \frac{m^{\text{mov}}}{m^{\text{Tot}}} \right) \cdot (\alpha - \alpha^2) \]

\[ \mathbb{V}ar [T_1(\alpha)] \to (m^{\text{Tot}})^{-2} \left\{ \sum_{j=1}^{m^{\text{st}}} \mathbb{V}ar [\mathbb{I} (V_j \geq Q_V(1-\alpha))] + \sum_{j=1}^{m^{\text{mov}}} \mathbb{V}ar [\mathbb{I} (Y_j \geq Q_V(1-\alpha) \text{ or } Z_j \leq Q_Z(\alpha))] \right\} \]

\[ = (m^{\text{Tot}})^{-2} \left\{ m^{\text{st}} \cdot \alpha(1-\alpha) + m^{\text{mov}} \mathbb{V}ar [\mathbb{I} (Y \geq Q_V(1-\alpha))] + m^{\text{mov}} \mathbb{V}ar [\mathbb{I} (Z \leq Q_Z(\alpha))] \right\} + m^{\text{mov}} \mathbb{V}ar [\mathbb{I} (Y \geq Q_V(1-\alpha) \text{ and } Z \leq Q_Z(\alpha))] \]

\[ = (m^{\text{Tot}})^{-2} \left\{ m^{\text{st}} \cdot \alpha(1-\alpha) + 2 \cdot m^{\text{mov}} \cdot \alpha \cdot (1-\alpha) + m^{\text{mov}} \alpha^2 \cdot (1-\alpha^2) \right\} \]

\[ \square \]

**Theorem 2.** With the same definitions of \( V^D, V^N \), etc. established in Theorem 1, consider the statistic \( T_2 \), where:

\[ T_2 = \left\{ \begin{array}{ll}
S_1 & m^{\text{mov}} = 0 \\
S_2 & m^{\text{st}} = 0 \\
S_1 + S_2 / \sqrt{2} & m^{\text{st}} > 0 \text{ and } m^{\text{mov}} > 0,
\end{array} \right. \]

\[ S_1 = \left\{ \left( (m^{\text{st}})^{-1} \sum_{j=1}^{m^{\text{st}}}(1 - \hat{F}_{V,j^{\text{st}}}(V^{N}_j)) - \frac{1}{2} \right) \right\} / \sqrt{\frac{1}{12m^{\text{st}}}}, \]

\[ S_2 = \left\{ \left[ (m^{\text{mov}})^{-1} \sum_{j=1}^{m^{\text{mov}}} \min \left( (1 - \hat{F}_{Y,j^{\text{mov}}}(Y^{N}_j)), \hat{F}_{Z,j^{\text{mov}}}(Z^{N}_j) \right) \right] - \frac{1}{3} \right\} / \sqrt{\frac{1}{18m^{\text{mov}}}}, \]

and \( \hat{F}_{V,j^{\text{st}}}(V^{N}_j) = (r^{\text{st}})^{-1} \sum_{i=1}^{r^{\text{st}}} \mathbb{I} (V^{D}_i \leq V^{N}_j) \). Then \( T_2 \xrightarrow{d} N(0,1) \) as \( \hat{m}^N \) & min \( (r^{\text{st}}, r^{\text{mov}}) \to \infty \).

where

\[ \hat{m}^N = \left\{ \begin{array}{ll}
m^{\text{st}} & m^{\text{mov}} = 0 \\
m^{\text{mov}} & m^{\text{st}} = 0 \\
\min \( m^{\text{st}}, m^{\text{mov}} \) & m^{\text{st}} > 0 \text{ and } m^{\text{mov}} > 0.
\end{array} \right. \]

**Proof.** For calculating the asymptotic distribution of \( T_2 \), we first have to remember that from the Dvoretzky-Kiefer-Wolfowitz inequality (2), we get

\[ \mathbb{P} \left\{ \sup_{v \in \mathbb{R}} \left| \hat{F}_{V,j^{\text{st}}}(v) - F_V(v) \right| \geq \epsilon \right\} \leq 2 \exp \left\{ -2r^{\text{st}}\epsilon^2 \right\} \]

\[ \implies \mathbb{P} \left\{ \left| \hat{F}_{V,j^{\text{st}}}(V^{N}_j) - F_V(V^{N}_j) \right| \geq \epsilon \right\} \leq 2 \exp \left\{ -2r^{\text{st}}\epsilon^2 \right\}. \quad (7) \]

From Equation 7, it follows that \( \hat{F}_{V,j^{\text{st}}}(V^{N}_j) \xrightarrow{p} F_V(V^{N}_j) \) as \( r^{\text{st}} \to \infty \). Since convergence in probability implies convergence in distribution, we get

\[ \hat{F}_{V,j^{\text{st}}}(V^{N}_j) \xrightarrow{d} F_V(V^{N}_j) \text{ as } r^{\text{st}} \to \infty. \]

\(^{3}\) In this theorem \( T_2 \) takes the form of Anom\textsubscript{Bottla} (\( N \)).
The quantities $S_1$ and $S_2$ thus, respectively, converge in distribution to the values $S_1^*$ and $S_2^*$ as $r^{st}, r^{mv} \to \infty$, where

$$
S_1^* = \left\{ \left( (m^{st})^{-1} \sum_{j=1}^{m^{st}} \left( 1 - F_v(Y_j^N) \right) \right) - \frac{1}{2} \right\} \sqrt{\frac{1}{12m^{st}}}, \quad \text{and}
$$

$$
S_2^* = \left\{ \left( (m^{mv})^{-1} \sum_{j=1}^{m^{mv}} \min \left( 1 - F_v(Y_j^N), F_z(Z_j^N) \right) \right) - \frac{1}{3} \right\} \sqrt{\frac{1}{18m^{mv}}}.
$$

For calculating the asymptotic distributions of $S_1^*$ and $S_2^*$ as $m^{st} \& m^{mv} \to \infty$, it is important to remember that $1 - F_v(Y_j^N) \sim \text{Unif}(0,1)$. Since the expected value and variance of a uniform random variable are $\frac{1}{2}$ and $\frac{1}{12}$, respectively, it follows (by the central limit theorem) that $S_1^* \overset{d}{\to} N(0,1)$ as $m^{st} \to \infty$.

The random variables $\left( 1 - F_v(Y_j^N) \right)$ and $F_z(Z_j^N)$ also follow uniform distributions, making $A_j = \min \left[ \left( 1 - F_v(Y_j^N) \right), F_z(Z_j^N) \right] \sim f_A(a)$, where

$$
f_A(a) = 2(1-a), \quad 0 \leq a \leq 1.
$$

The expected value and variance of $A$ are $\frac{1}{3}$ and $\frac{1}{18}$, respectively, implying (by the central limit theorem) that $S_2^* \overset{d}{\to} N(0,1)$ as $m^{mv} \to \infty$.

With $S_1 \overset{d}{\to} N(0,1)$ as $r^{st} \& m^{st} \to \infty$, $S_2 \overset{d}{\to} N(0,1)$ as $r^{mv} \& m^{mv} \to \infty$, it follows that $(S_1 + S_2)/\sqrt{2} \overset{d}{\to} N(0,1)$ as $\bar{m}^N \& \min(r^{st},r^{mv}) \to \infty$, making $T_2 \overset{d}{\to} N(0,1)$ as $\bar{m}^N \& \min(r^{st},r^{mv}) \to \infty$.

\section{Simulations}

In this section, we perform simulations which illustrate the asymptotic result proven in Theorem 2. The histogram and Q-Q plot of 5000 values $T_2$ are provided in Figures 14 - 17. The conditions of each simulation are provided in the caption.

![Histogram and Q-Q plot of 5000 values of $T_2$. In this case, $r^{st} = r^{mv} = 1000$, $f_Y(v)$ is an exponential distribution with $\lambda = 2$, $f_Y(y)$ is a gamma distribution with $\alpha = 2$ and $\beta = 4$, and $f_z(z)$ is a chi-squared distribution with 8 degrees of freedom. For this simulation, $m^{st} = 100$ and $m^{mv} = 200.$](image)

Figure 14: Histogram and Q-Q plot of 5000 values of $T_2$. In this case, $r^{st} = r^{mv} = 1000$, $f_Y(v)$ is an exponential distribution with $\lambda = 2$, $f_Y(y)$ is a gamma distribution with $\alpha = 2$ and $\beta = 4$, and $f_z(z)$ is a chi-squared distribution with 8 degrees of freedom. For this simulation, $m^{st} = 100$ and $m^{mv} = 200.$
Figure 15: Histogram and Q-Q plot of 5000 values of $T_2$. In this case, $r^{\text{st}} = r^{\text{mv}} = 1000$, $f_{v}(v)$ is a normal distribution with $\mu = 2$, and $\sigma = 4$, $f_{y}(y)$ is a cauchy distribution with $y_0 = 0$ and $\gamma = 1$, and $f_{z}(z)$ is an F distribution with $d_1 = 8$ and $d_2 = 18$. For this simulation, $m^{\text{st}} = 200$ and $m^{\text{mv}} = 100$.

Figure 16: Histogram and Q-Q plot of 5000 values of $T_2$. In this case, $r^{\text{st}} = 1000$, $r^{\text{mv}} = 1000$, and $f_{v}(v)$ is a t distribution with $\nu = 2$. For this simulation, $m^{\text{st}} = 300$, and $m^{\text{mv}} = 0$. 
Figure 17: Histogram and Q-Q plot of 5000 values of $T_2$. In this case, $r^{st} = 1000$, $r^{mv} = 1000$, $f_Y(y)$ is a
cauchy distribution with $y_0 = 4$ and $\gamma = 2$, and $f_Z(z)$ is an F distribution with $d_1 = 1$ and $d_2 = 20$. For this
simulation, $m^{mv} = 200$, and $m^{st} = 0$. 