

# Locating Data Flow Anomaly With Statistical Distance

Ruoyu Wang

**Abstract**—[abstract]

## I. INTRODUCTION

Big data industry has been blooming within this decade, reshaping the form of life and work across the globe. According to [17], 1.2ZB data had been produced from 2012 to 2014. And the amount doubles every two years. Currently, there are totally 2.7ZB data in the digital universe [1]. Big data analysis has been widely adopted in scientific experiments [20], electric business [2, 29, 9], healthcare [11], governments [16] and many other fields.

However, it will be harder in the future to harness the exploding volumes of data since problems have already appeared in data management and engineering, threatening trustworthiness and reliability of data flows inside working systems. Data error rate in enterprises is approximately 1% to 5%, and for some, even above 30% [23].

Those data anomalies may arise due to both internal and external reasons with respect to a certain system. From one hand, components inside the system may generate problematic source data. For example, in a sensor network, some sensors may generate erroneous data when it experiences power failure or other extreme conditions [22]. Data packages will be lost if sensor nodes fail to connect to network or some sensor hub goes down [12]. Also, human operators act as a heavily vulnerable part to bugs and mistakes. Some even deliberately modify system configurations for malicious compromises [24]. A study [31] found that 65% of organizations state that human errors are the main cause of data problems.

On the other hand, data manipulation [14] from outside hackers composes another potential threat of data quality and reliability. Taken Apache Hadoop as an example. It's security issues has long been discussed within communities and industry [26, 30, 15, 27]. As is shown in Figure 1, the two basic vulnerabilities: *lack of access control* and the *absence of encryption* expose the entire cluster to dangerous threats. Data flows can be intercepted and modified; services can also be altered and blocked [13]. Although there are several frameworks(e.g. Kerberos, Sentry, Knox etc.) and algorithms providing basic protection [39, 28, 33, 37, 10], clever attackers can always bypass the barriers and sneak into the core of data pipelines. Several approaches are developed as sentinels to detect probable infiltrations. However, these approaches are not able to locate corrupted data under carefully planned manipulations. Nor can they figure out the exact reasons and recover the original records. To locate and diagnose anomalies

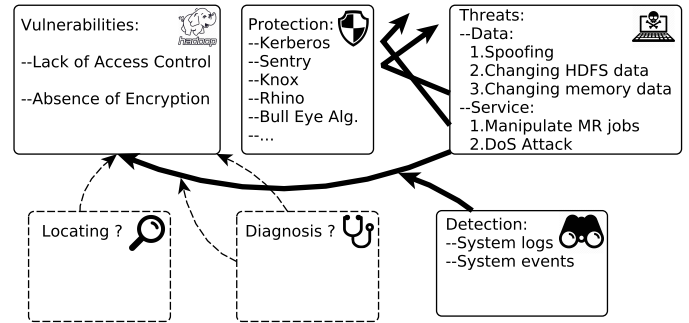


Fig. 1. Security Issues of Hadoop Clusters

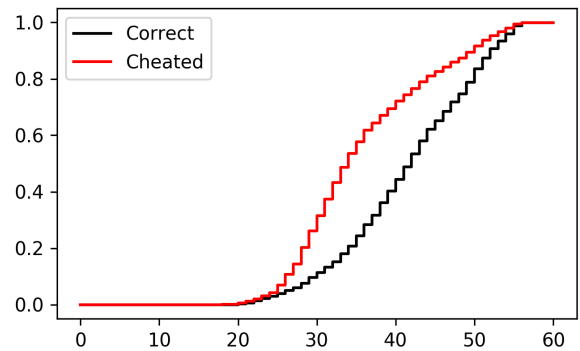


Fig. 2. Example Cumulative Distribution Function of Original And Modified Data

in data pipelines under carefully planned and disguised data manipulations are still on demand by industry and academia.

According to our observation, typical data manipulations on numerical data will lead to the drift of its distribution. For example, a Taobao online seller's transaction records can be "click farmed" to increase the volume of sales. Fig. 2 shows the sales distribution within one day. The curve for cheated data is emulated according to a popular method for click farming. It can be observed that there exists clearly a gap between these two distributions. These anomalies inside data pipelines will severely affect mining and learning algorithms and further change the final decision given by the entire system.

In order to address issues resulted from data manipulation and pipeline errors, we propose a novel mechanism to detect and locate corrupted data within a data pipeline via statistical

distance. As far as we know, this algorithm is the first attempt against data anomaly via statistical distance. Evaluations are performed on synthetic and real-world data sets, demonstrating the correctness and effectiveness of the mechanism.

The rest of the paper is organised as follow: Section II introduces preliminaries and recent works on data anomaly detection and statistical distance. Algorithm details are proposed in section III. Section IV presents evaluation results and further findings of the algorithm. And all contents are concluded in section V.

## II. PRELIMINARIES AND RELATED WORK

### A. Data Anomaly Detection

Anomaly detection, also known as outlier detection, has been studied for a long time and discussed in diverse research domains, such as fraud detection, intrusion detection, system monitoring, fault detection and event detection in sensor networks. According to a systematic classification in [8], anomaly detection algorithms deal with input data in the form of points(or records), sequences, graphs and spatial relationships, where point data is the simplest and well studied, others are attracting more attention in new studies.

Prevalent anomalies can be classified into *Point Anomalies*, *Contextual(or Conditional) Anomalies* and *Collective Anomalies*. Point anomalies refers to an individual data instance that is considered anomalous with respect to others. But if it is anomalous only in certain circumstances or a specific context, the instance is regarded as contextual anomaly. If a group of related data(e.g. a segment of sequence) instances is anomalous with respect to other groups in the data set(e.g. the entire sequence), it is called a collective anomaly.

Detection approaches can be categorized into three types according to whether data is labeled: *Supervised*, *Semi-Supervised* and *Unsupervised* anomaly detection. As the name suggests, supervised detection methods train models on completely labeled data while unsupervised detection leverages data without any labeling. Semi-supervised detection approaches train model on data that has labeled instances for only the normal class. Supervised detection is commonly applied when both normal and anomalous data can be obtained. When it comes to the circumstances that anomalous data is hard to obtain or there exist too many diverse types of anomalies to enumerate, semi-supervised or unsupervised approaches are usually taken into consideration.

To make the final decision, detection algorithms mostly yield a score from each input instance, denoting how likely it is anomalous. The algorithm then selects top few as anomalies or compare the score with a threshold. Or, detection algorithms output a label on each instance, then decide whether each label belongs to the normal class.

Currently, distance based [5, 4] and feature evolving algorithms [19, 18, 25] algorithms seize most attention. Others adopted tree isolation [38], model based [35] and statistical methods [40] in certain applications.

To detect collective anomalies, [6] adopted the *ART(Adaptive Resonance Theory)* neural networks to detect time-series anomalies. *Box Modeling* is proposed in

[7]. And *Longest Common Subsequence* was leveraged in [3] as similarity metric for symbolic sequence. Markovian modeling techniques are also popular in this domain[34, 32, 21]. [36] depicted groups in social media as combinations of different “roles” and compare groups according to the proportion of each role within each group.

### B. Click Farming Detection

### C. Statistical Divergence

Statistical divergence, also called statistical distance, is a function which describes the “distance” of one probability distribution to the other on a statistical manifold. Suppose  $S$  is a space of probability distributions, then a divergence is a function from  $S$  to non-negative real numbers:

$$D(\cdot||\cdot) : S \times S \rightarrow \mathbb{R}^+ \quad (1)$$

Divergence between two distributions  $P$  and  $Q$ , written as  $D(P||Q)$ , satisfies:

- 1)  $D(P||Q) \geq 0, \forall P, Q \in S$
- 2)  $D(P||Q) = 0$ , if and only if  $P = Q$

There are many ways to calculate divergence, such as f-divergences, M-divergences and S-divergences. Some of them provides better properties which brings conveniences to the design and implementation of our approach.

1) *Kullback-Leibler Divergence*:  $P, Q$  are discrete probability distributions,  $Q(i) = 0$  implies  $P(i) = 0$  for  $\forall i$ , the *Kullback-Leibler Divergence* from  $Q$  to  $P$  is defined to be:

$$KLD(P||Q) = \sum_{Q(i) \neq 0} P(i) \log\left(\frac{P(i)}{Q(i)}\right) \quad (2)$$

2) *Jensen-Shannon Divergence*:  $P, Q$  are discrete probability distributions, *Jensen-Shannon Divergence* between  $P$  and  $Q$  is defined to be:

$$JSD(P||Q) = \frac{1}{2}KLD(P||M) + \frac{1}{2}KLD(Q||M) \quad (3)$$

where  $M = \frac{1}{2}(P + Q)$ .

A more generalized form is defined to be:

$$JSD_{\pi_1, \dots, \pi_n}(P_1, \dots, P_n) = \sum_{i=1}^n \frac{1}{\pi_i} KLD(P_i||M) \quad (4)$$

where  $M = \sum_{i=1}^n \frac{1}{\pi_i} P_i$  and  $\sum_{i=1}^n \frac{1}{\pi_i} = 1$ .

Jensen-Shannon divergence has some fine properties:

- 1)  $JSD(P||Q) = JSD(Q||P), \forall P, Q \in S$ .
- 2)  $0 \leq JSD_{\pi_1, \dots, \pi_n}(P_1, \dots, P_n) \leq \log_k(n)$ . If a  $k$  based algorithm is adopted.
- 3) To calculate  $JSD(P||Q)$ , it need not necessarily to be true that  $Q(i) = 0$  implies  $P(i) = 0$ .

**[If P, Q are continuous distribution?]**

### III. ALGORITHM DETAILS

Diverse data sets in the real world show certain structures which may be resulted from hidden patterns or relationships among records in a collection of data. For example, the volume of vehicles in the highway and the business transaction records, they may show a relatively stable distribution in the daily scale. Manipulation on those data(e.g. Fig 2) results in a drift or distortion of the distribution, which can be captured to trigger the alarm. Although the population parameters(e.g. mean, variance, etc.) are unknown and usually impossible to obtain, it can be sampled and estimated according to the central limitation theorem.

#### A. Technical Points

[Can be divided and settled inside later two subsections]

- 1) Which classifier should be chosen?
- 2) How to determine the classifier threshold?[fixed value,  $3\sigma$ ]
- 3) How to locate the compromised component?
- 4) How to deal with slightly drifting distribution?
- 5) .[to be continued ...]

#### B. Divergence-Based Collective Anomaly Detection

Suppose data chunks in the given data set  $S$  are groups of instances sampled from a population driven by a static distribution. And we are given in advance an evidence set  $E$  which contains  $n(n \geq 2)$  collections of correct sample data. Then each data collection in  $S$  can be checked by the following algorithm.

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##### Algorithm 1 Basic Classification

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**Input:** Evidence set  $E = \{D_1, \dots, D_n\}$ ; New data collection  $D'$

**Output:** Whether  $D'$  is anomalous

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1: for  $i \leftarrow 1$  to  $n$  do
2:    $P_i \leftarrow$  the distribution of  $D_i$ 
3: end for
4:  $M \leftarrow \frac{1}{n} \sum_{i=1}^n P_i$ 
5: for  $i \leftarrow 1$  to  $n$  do
6:    $J_i \leftarrow JSD(P_i || M)$ 
7: end for
8:  $N \leftarrow$  normal distribution estimated from  $J_1, \dots, J_n$ 
9:  $P' \leftarrow$  distribution of  $D'$ 
10:  $J' \leftarrow JSD(P' || M)$ 
11:  $p \leftarrow$  probability density of  $J'$  in  $N$ 
12: if  $p < \text{threshold } T$  then
13:   Return True
14: else
15:   Return False
16: end if

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As shown in Algorithm 1,  $n$  evidence collections are used to estimate the ground truth population distribution  $M$ . Then  $n$  evidence divergences are calculated, composing a gaussian classifier to classify the new distribution sample. Although it is convenient to compute  $JSD(P_1, \dots, P_n, P')$  instead

of  $JSD(P_1 || M), \dots, JSD(P_n || M), JSD(P' || M)$ . It is not suitable for classification. Jensen-Shannon divergence of  $n+1$  distributions will dilute the affection of the abnormal one, in which case the difference between  $P'$  being normal and anomalous will become subtle when  $n$  goes larger.

Similar to the fact that sampling values around a certain parameter will yield a gaussian distribution, sampling divergences around a certain population distribution yields a gaussian distribution  $N(\mu, \sigma)$  where  $\mu$  is a value slightly larger than zero.  $\mu$  can not be zero according to line 4.  $M$  takes into consideration all existing values in every distribution sample and averages corresponding probabilities. Thus  $M$  may consist entries that does not exist in  $P_i$  and probability in certain entries in  $M$  may vary from that in  $P_i$ . For example, suppose  $P_1(1) = 0.5, P_1(2) = 0.3, P_1(3) = 0.2; P_2(1) = 0.3, P_2(2) = 0.4, P_2(3) = 0.3; P_3(1) = 0.3, P_3(3) = 0.5, P_3(4) = 0.2$ , then  $M(1) = \frac{11}{3}, M(2) = \frac{7}{3}, M(3) = \frac{10}{3}, M(4) = \frac{2}{3}$ . None of  $P_1, P_2, P_3$  is the same with  $M$ . Although the distance cannot be negative values, normal distribution is the closest to the distribution of all JSD values.

#### C. Distribution Histogram

Not all data collections can be assumed subject to known distribution models. Parameter approximation will probably lead to errors above our expectation. For example, the distribution of vehicle volume in the highway may not correspond to any of the prevalent distribution model. Few assumption of parameters can be made in advance on such data. For the sake of generality, non-parametric estimation should be applied.

Surely, the kernel density estimation approaches will give a smooth, continuous distribution curve under on any sampled data. The computational cost will be much higher than applying a coarse histogram approximation. Moreover, even if we applied a distribution model upon a collection of sampled data, yielding more accurate results, the computation of divergence will be much more complex on continuous functions than discrete distributions.

Histogram methods can not only be applied to non-parametric distributions, but also to miscellaneous data types. From a general point of view, as long as there exists a function mapping the input data instance into a subset of real numbers, this data collection can be counted into a histogram. For example, date, time and single characters.

In order to generate a accurate approximation, step size is the most important parameter the algorithm should determine. If the size is too small then the resulting histogram will be over fitting; but if the size is too large then the estimation will be too coarse to depict the original shape. According to statistics theory, when dealing with a sample size of  $k$ , a step size of  $l = c\sigma k^{-0.2}$  will give a best partition, where  $c$  is a constant relative to the shape of distribution(e.g. for normal distribution,  $c = 1.05$ ).

#### D. Threshold

One important factor in the algorithm is the value of threshold. A higher threshold rejects more instances, improving the sensitivity of anomalous data while increasing the number of

false alarms. A lower threshold provide higher true negative rates yet neglecting more possible threats.

A naive but prevalent approach is to set a fixed value as threshold. This approach is easy to implement and may give satisfying results in specific cases. However, a fixed threshold requires analysis of the specific problem, manual observation and tuning of parameters, which involves lots of human labor. The rule of “ $3\sigma$ ” can be used to automatically determine a threshold. But in some cases that the anomalous data intersecting at the boundary with normal instances, the threshold may fail more often to discover those manipulated ones.

However, applying divergence as the distance metric among data collection distributions provides a fine property. That is, divergences of normal data collections assemble together, forming a quasi-normal distribution. And those of anomalous data collections lies in the right-hand-side interval on the real number axis. As a result of further observation, the divergence of anomalous data collections also assemble to be a quasi-normal distribution, since statistical distance has been restricted by a strict upper bound.

**[Better give a point drawing for each JSD value]**

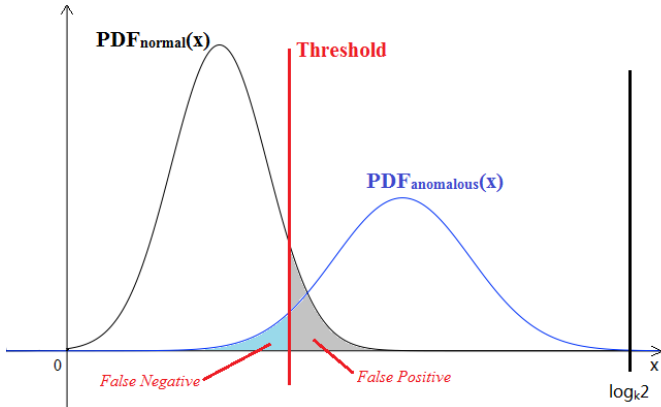


Fig. 3. Threshold Example

As shown in Fig 3, the black curve( $PDF_{normal}(x)$ ) displays the probability density function(PDF) fitting those JSDs calculated from normal data collections; the blue curve( $PDF_{anomalous}(x)$ ) displays the PDF derived from anomalous data collections. Threshold is to minimize total error(False Negative and False Positive).

Suppose:

$$PDF_{normal}(x) \approx N(\mu_n, \sigma_n) \quad (5)$$

$$PDF_{anomalous}(x) \approx N(\mu_a, \sigma_a) \quad (6)$$

Then the optimal threshold  $T$  is:

$$\begin{aligned} T &= \arg \min_T \int_0^T PDF_{anomalous}(x) dx + \int_T^{\log_k 2} PDF_{normal}(x) dx \\ &\approx \arg \min_T \int_{-\infty}^T \frac{e^{-\frac{(x-\mu_a)^2}{2\sigma_a^2}}}{\sqrt{2\pi}\sigma_a} dx + \int_T^{+\infty} \frac{e^{-\frac{(x-\mu_n)^2}{2\sigma_n^2}}}{\sqrt{2\pi}\sigma_n} dx \\ &= \frac{\mu_n\sigma_a + \mu_a\sigma_n}{\sigma_a + \sigma_n} \end{aligned} \quad (7)$$

According to equation(7), threshold value can be automatically determined. The optimal threshold will minimize total errors, yielding an optimal outcome. The only requirement for this technique is another evidence set containing data point derived from anomalous data collections.

However, this is not accurate enough, since equation(7) implicate an assumption that the chances are the same for a new data collection to be either anomalous or not. If we can determine the probability for a new data collection to be anomalous in any segment of data sequence, the equation should be modified as:

$$\begin{aligned} T &= \arg \min_T \alpha \int_0^T PDF_{anomalous}(x) dx + (1 - \alpha) \int_T^{\log_k 2} PDF_{normal}(x) dx \\ &\approx \arg \min_T \alpha \int_{-\infty}^T \frac{e^{-\frac{(x-\mu_a)^2}{2\sigma_a^2}}}{\sqrt{2\pi}\sigma_a} dx + (1 - \alpha) \int_T^{+\infty} \frac{e^{-\frac{(x-\mu_n)^2}{2\sigma_n^2}}}{\sqrt{2\pi}\sigma_n} dx \end{aligned} \quad (8)$$

Where  $\alpha$  is the anomaly probability. Equation(8) is much more complicated than (7). It can be reduced to a quadratic equation. But may not have real roots in all cases.

From another point of view, equation (7) can be regarded as a weighted averaging between two mean value:  $\mu_n$  and  $\mu_a$ . From this aspect, we can derive some similar approximations:

$$T = \frac{\mu_n\sqrt{\sigma_a} + \mu_a\sqrt{\sigma_n}}{\sqrt{\sigma_a} + \sqrt{\sigma_n}} \quad (9)$$

$$T = \frac{\mu_n\sigma_a\sqrt{-\ln(1-\alpha)} + \mu_a\sigma_n\sqrt{-\ln\alpha}}{\sigma_a\sqrt{-\ln(1-\alpha)} + \sigma_n\sqrt{-\ln\alpha}} \quad (10)$$

$$T = \frac{\mu_n\sqrt{|\ln[\sigma_a(1-\alpha)]|} + \mu_a\sqrt{|\ln(\sigma_n\alpha)|}}{\sqrt{|\ln[\sigma_a(1-\alpha)]|} + \sqrt{|\ln(\sigma_n\alpha)|}} \quad (11)$$

Due to the restriction sample capacity, the replacement of JSD distributions by gaussian distribution may lose too much accuracy. Compared with equation (9), (10) and (11), (8) may not give a best result.

#### E. Dynamic DCAD

Another important factor that should be seriously considered is the assumption in Algorithm 1. In most cases, real world data is always in the process of evolution and fluctuation. Therefore, the algorithms should automatically adapt to the trend at any time. To meet the need, a sliding window technique has been applied to the basic algorithm frame work. Considering discussion in section III-C and III-D, a dynamic version is proposed as follow:

**Algorithm 2** Dynamic DAD

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**Input:** Normal evidence set  $E_N = \{D_{N_1}, \dots, D_{N_n}\}$  by given order; Anomalous evidence set  $E_A = \{D_{A_1}, \dots, D_{A_m}\}$  by given order; New data collection  $D'$ ; Estimated anomalous probability  $\alpha$

**Output:** Whether  $D'$  is anomalous

```

1: for  $i \leftarrow 1$  to  $n$  do
2:    $P_{N_i} \leftarrow$  histogram of  $D_{N_i}$ 
3: end for
4: for  $i \leftarrow 1$  to  $m$  do
5:    $P_{A_i} \leftarrow$  histogram of  $D_{A_i}$ 
6: end for
7:  $P' \leftarrow$  histogram of  $D'$ 
8:  $M \leftarrow \frac{1}{n} \sum_{i=1}^n P_{N_i}$ 
9: for  $i \leftarrow 1$  to  $n$  do
10:   $J_{N_i} \leftarrow JSD(P_{N_i} || M)$ 
11: end for
12: for  $i \leftarrow 1$  to  $m$  do
13:   $J_{A_i} \leftarrow JSD(P_{A_i} || M)$ 
14: end for
15:  $J' = JSD(P' || M)$ 
16:  $(\mu_N, \sigma_N) \leftarrow$  estimated from  $\{J_{N_1}, \dots, J_{N_n}\}$ 
17:  $(\mu_A, \sigma_A) \leftarrow$  estimated from  $\{J_{A_1}, \dots, J_{A_m}\}$ 
18:  $T \leftarrow$  proper threshold derived from  $(\mu_N, \sigma_N), (\mu_A, \sigma_A)$  and  $\alpha$ 
19: if  $J' < T$  then
20:    $E_N \leftarrow E_N \setminus \{D_{N_0}\} \cup \{D'\}$ 
21:   Return False
22: else
23:    $E_A \leftarrow E_A \setminus \{D_{A_0}\} \cup \{D'\}$ 
24:   Return True
25: end if

```

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Algorithm 2 uses  $E_N$  and  $E_A$  as two sliding windows, keeping up with latest trend of both normal and anomalous features. Thus, the two window sizes  $n$  and  $m$  cannot be too large. Otherwise the evolving features will be flattened and aligned to the older ones. For the sake of estimation accuracy, they cannot be too small either. The size should refer to ratio of both data updates and feature evolution.

Line 20 and 23 update the evidence sets, replacing the most outdated one, moving the sliding window forward one step ahead. Moreover,  $\alpha$  can also be updated according to a history sequence of return values, if necessary.

## IV. EVALUATION

## A. Experiment Environment

The algorithm was implemented and interpreted in Python 3.6. All experiments was tested on Ubuntu 17.04.

## B. Methodology

**Raise and answer some research questions. Present test background and methods.**

## C. Experiment on Synthetic Data

**Test basic properties of statistical distance and algorithm**

## D. Experiment on Real World Data

**Test performance of algorithm**

## V. CONCLUSION

## ACKNOWLEDGEMENT

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