



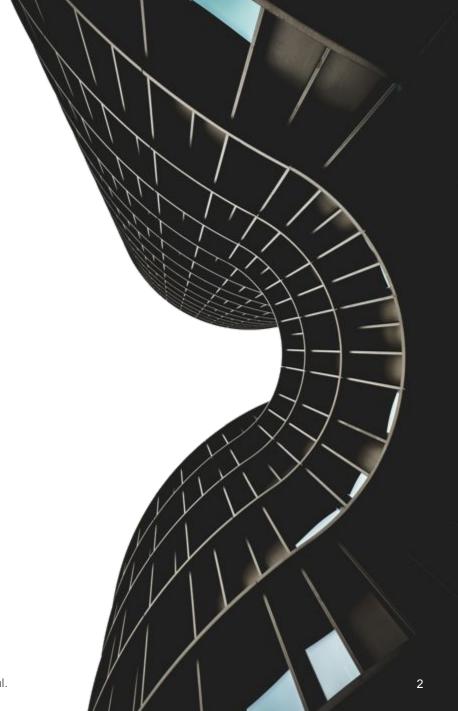
Lightweight Real-Time Feature Monitoring

Master Thesis Defense

July 24th, 2020



Context





Context

Feedzai working context

 Feedzai uses Machine Learning (ML) models to monitor streams of credit card transactions to detect fraud.

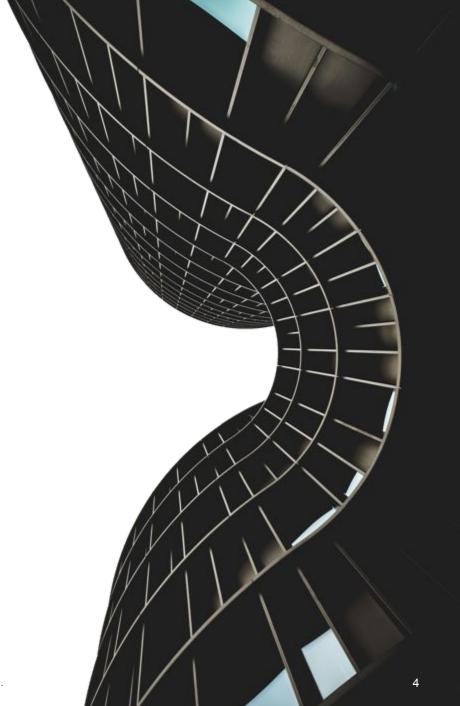
 In the field of ML, change in distributions of the data stream is known as concept drift [1,2].

 In the presence of concept drift, the performance of these models gradually deteriorates.

 Feedzai has model monitoring systems that alert for this performance decay, indicating the model needs retraining.



Challenge



Challenge

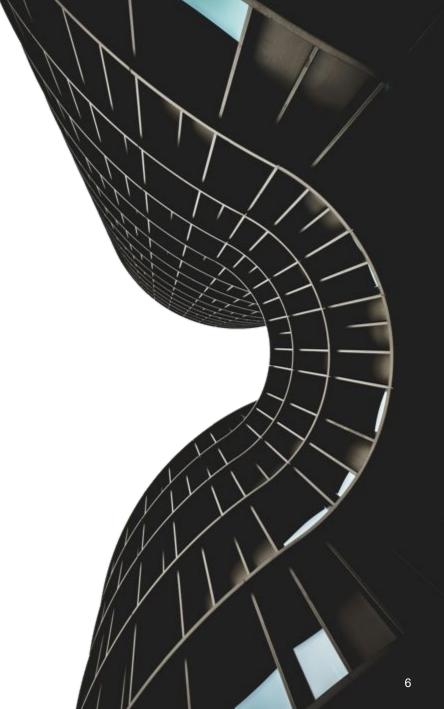
 Detect concept drift and alert system administrators so they can reconfigure their systems before its performance declines.

 Move from a "Train, Detect performance decay and Retrain" paradigm to a "Train, Detect concept drift and Retrain" paradigm.

 Devise a generic method that assists any system (not just ML models) that learn from past data and whose performance depends on the how well the assumptions made hold for future data.



Previous Work



Previous Work

• **SAMM** [3] is an unsupervised **concept drift detection** method for data streams. Identifies **short term abrupt changes**.

SAMM monitors the prediction scores of ML models.

Issue #1: does so based on model scores, so the changes already impacted the model (our system performance already suffered).



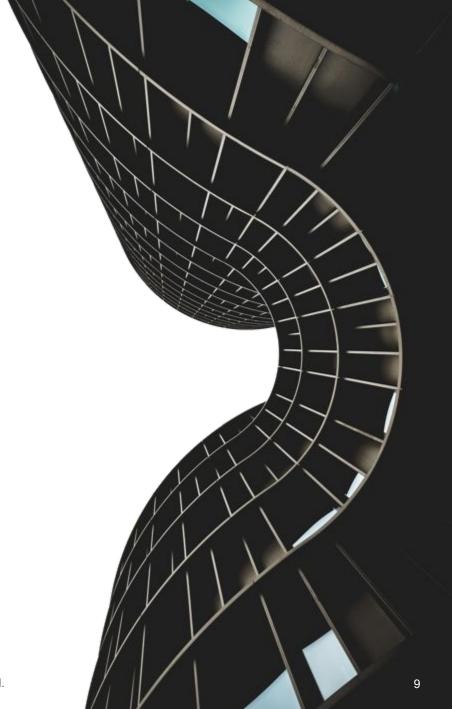
Previous Work

• SAMM works with a **two-windowed model**: a static one and a sliding one over the data stream.

Issue #2: it keeps both in memory (linear memory complexity), so it is used with small windows.



Objectives





Objectives

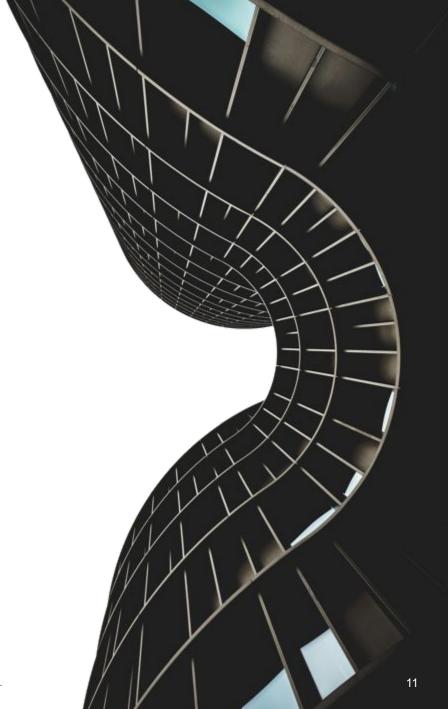
- Lightweight: memory complexity grows sublinearly with window size.
- Real-time: process data stream events in real-time.
- Feature Monitoring: monitor data patterns and alert for changes in the underlying distribution of individual features.

Detect data pattern shifts and alert admins of a third party mission-critical system that performs an analysis on the stream of data and depends on assumptions made over a fixed reference period before its performance decays.



Feature Monitoring

A two-phased method





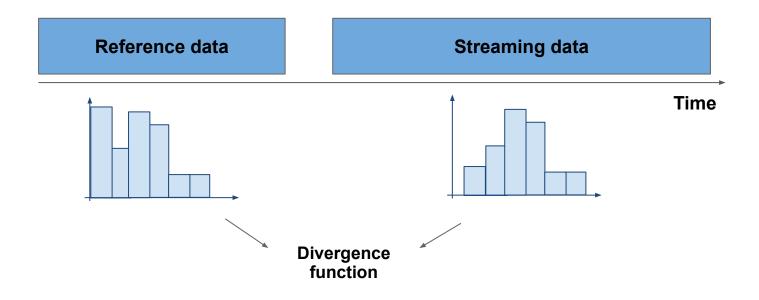
A two-phased method

- Our method has two phases:
 - 1. A batch analysis over the reference period.
 - 2. A stream analysis over the target period (online event-by-event processing).
- The reference window is static: it is the ground-truth of our system from which we make our assumptions (e.g., the data used for model training).
- The target window is a simulated sliding window of streaming data (e.g., transactions a model sees in production).
- Our method works for numerical (and encoded categoricals) features only.

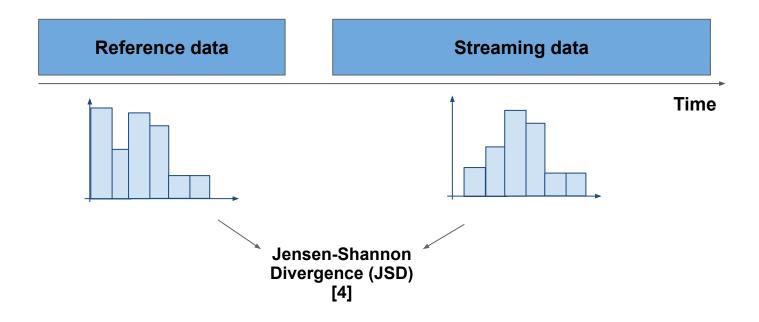


Reference data
Streaming data
Time

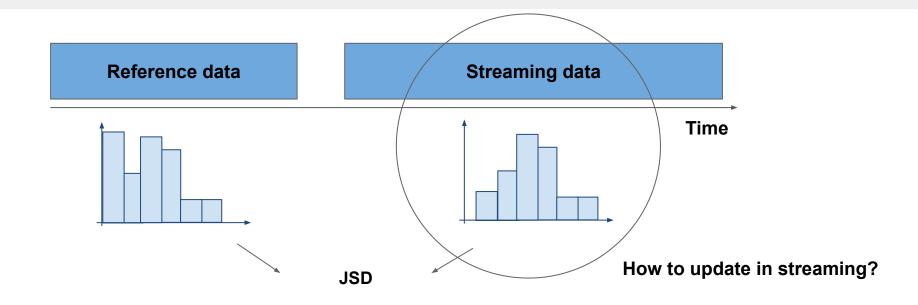












Streaming Histogram

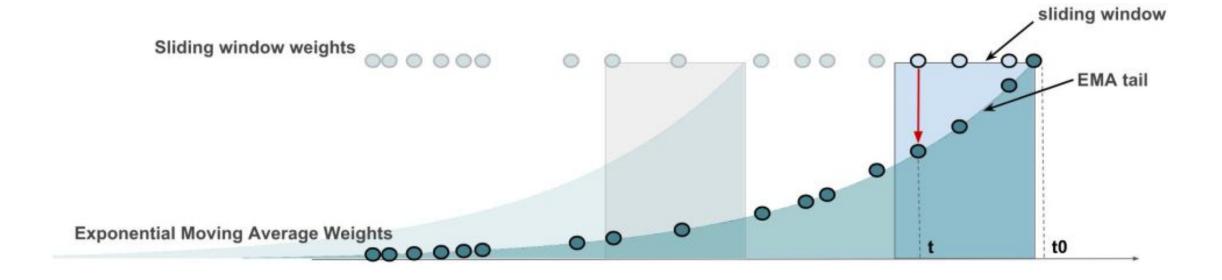
- The streaming histogram has to be updated.
- That implies inserting new events and expiring old ones.
- The "subtract-on-evict" method has linear memory complexity regarding the sliding window size, as we have to keep every value in memory to know when to remove the oldest.

 We propose an approximated histogram aggregation based on Exponential Moving Averages (EMAs).



Exponential Moving Averages

 An Exponential Moving Average (EMA) [5,6,7] is a type of moving average that places a greater weight and significance on the most recent data points.





Exponential Moving Averages

EMA-count based histogram

EMAs are recursive:

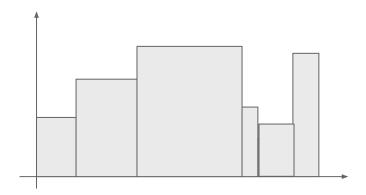
$$EMA_t = val_t + EMA_{t-1} * smoothing_factor$$

 The approximated histogram is made up of N bins and each bin holds an EMA-count.

- Constant memory complexity (number of bins does not grow).
- Updated in constant time (simple increment times suppression).

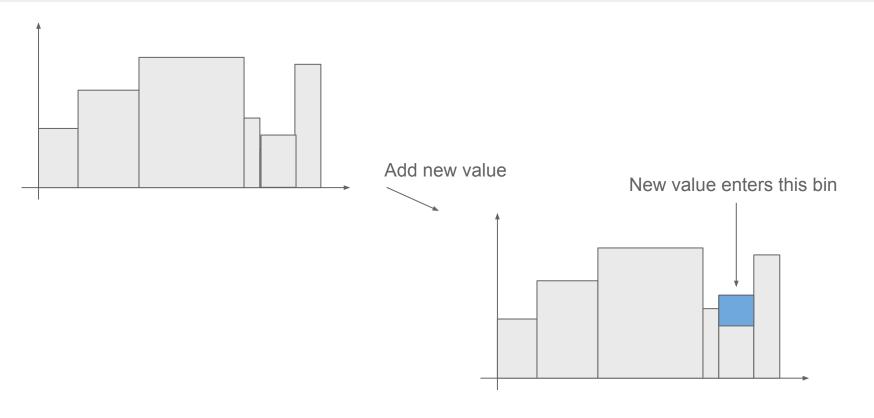


EMA-like histogram



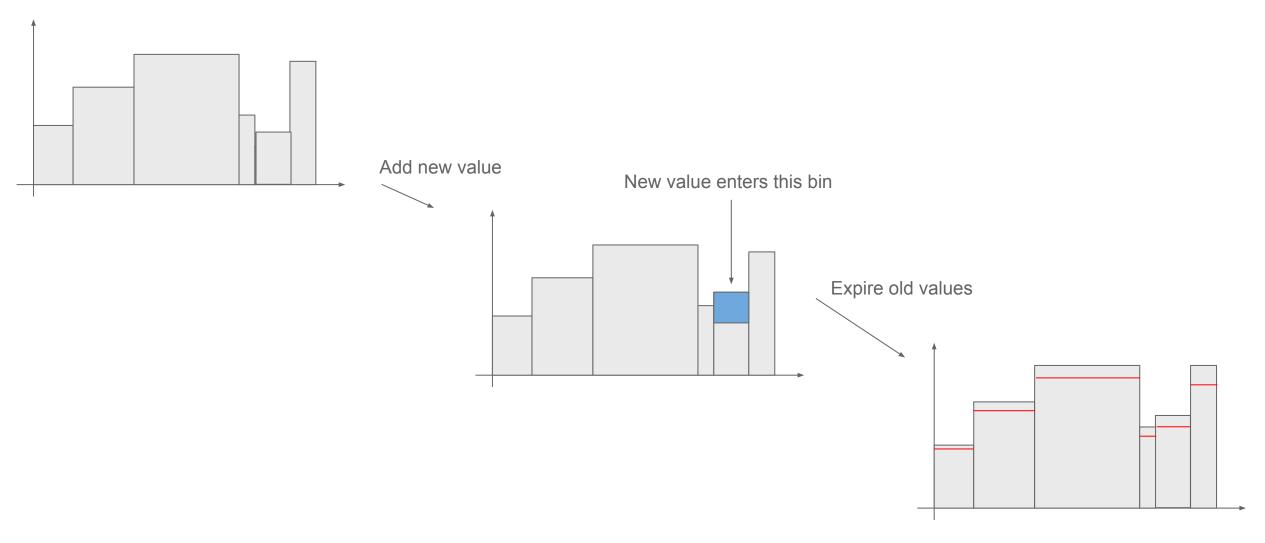


EMA-like histogram

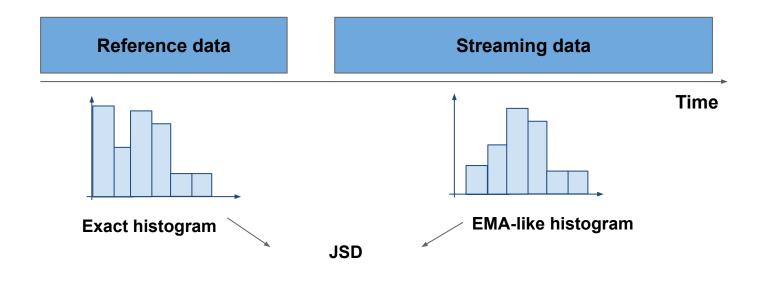




EMA-like histogram









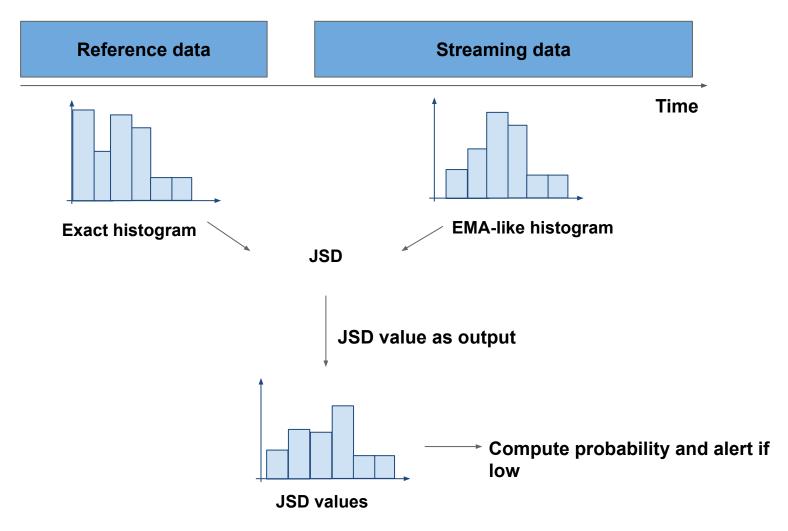
A two-phased method

But what JSD value should we expect?

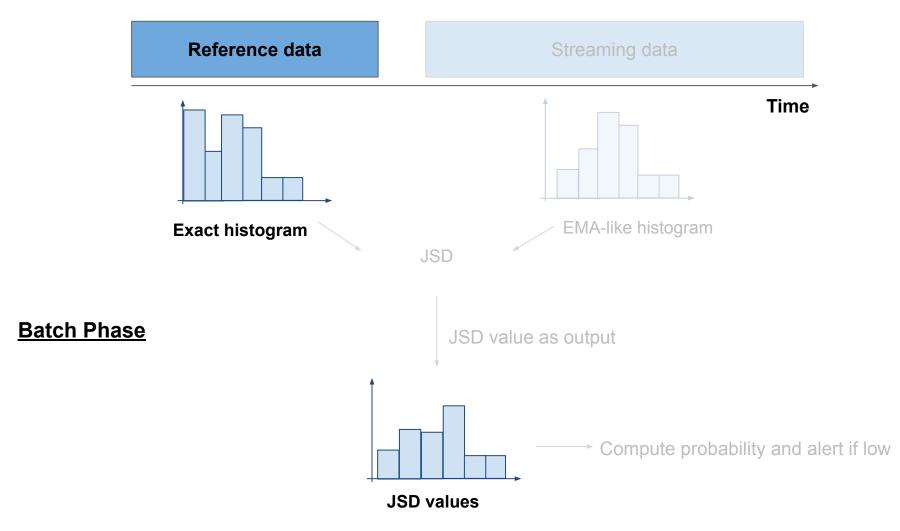
 Somehow we need to encode the probability of this JSD value to raise an alert if low.

 To achieve this we build a distribution of JSD values through a sampling process in batch.

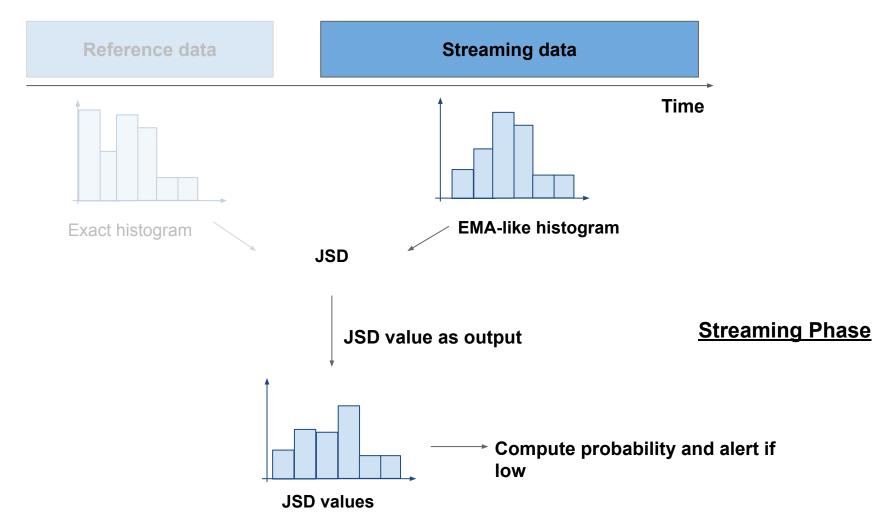








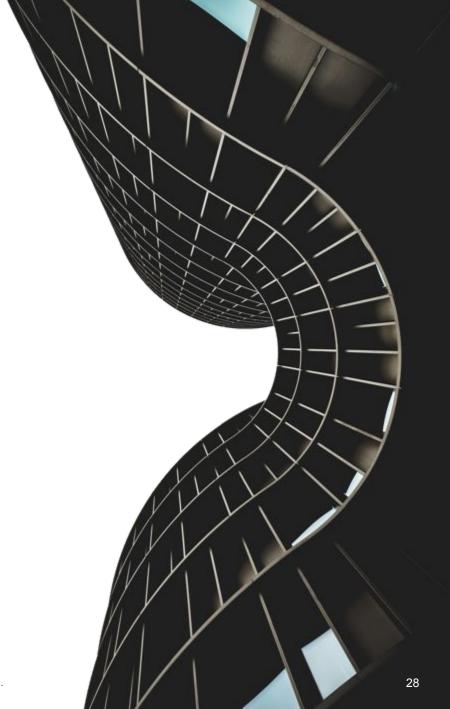






Batch Phase

A two-phased method

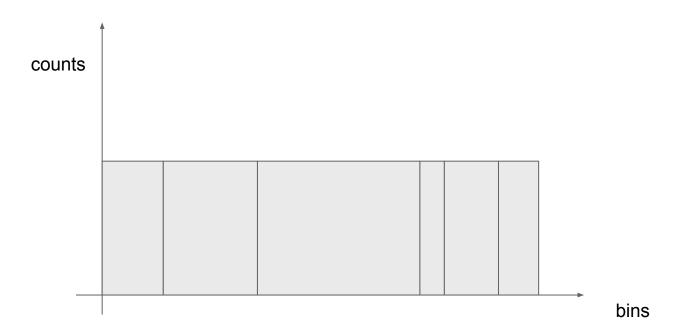




A two-phased method

For each feature:

1. Compute the reference histogram from the reference data set having equal counts per bin (implies different sized bins).

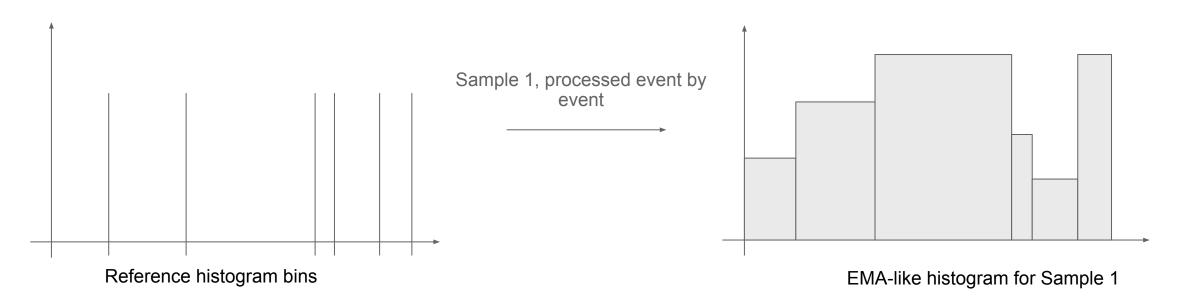




A two-phased method

2. Make **S** samples of transactions, each with K tuples.

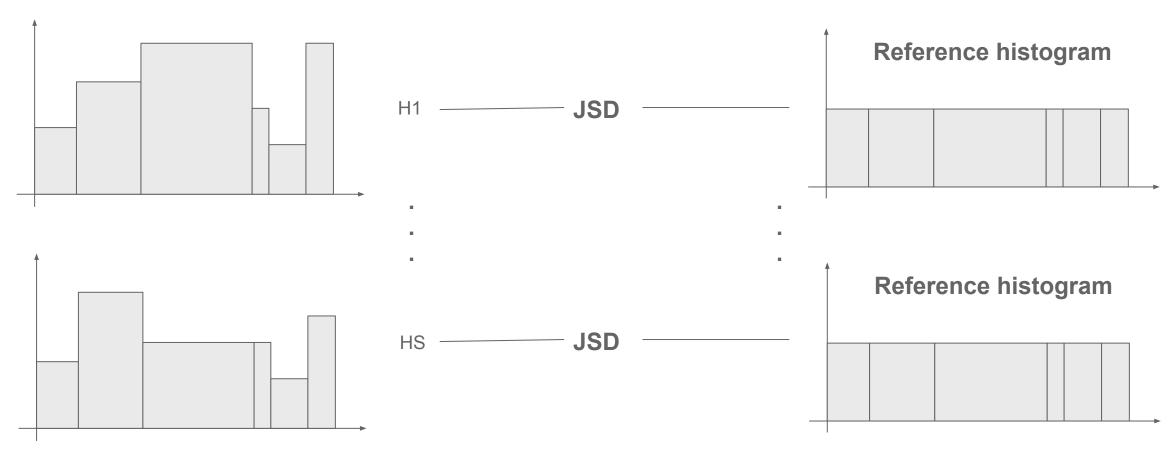
For each sample, compute an approximated **EMA histogram** using the **bins** from the **reference histogram**.





A two-phased method

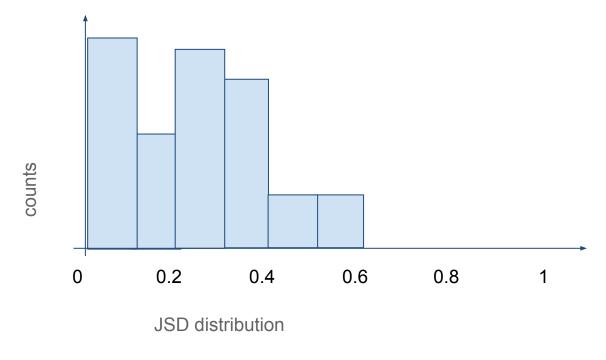
3. Compute S JSDs between the S histograms and the reference one.





A two-phased method

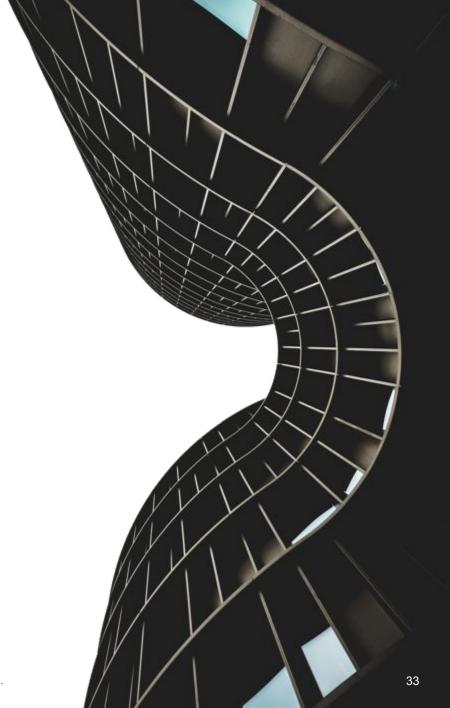
 Build the histogram below that encodes the distribution of JSD values using the S JSD values from the sampling process.





Streaming Phase

A two-phased method





Stream analysis

A two-phased method

For each feature:

• Initialize the **EMA histogram** as the last sample's histogram from batch analysis to simulate the burn-in period.

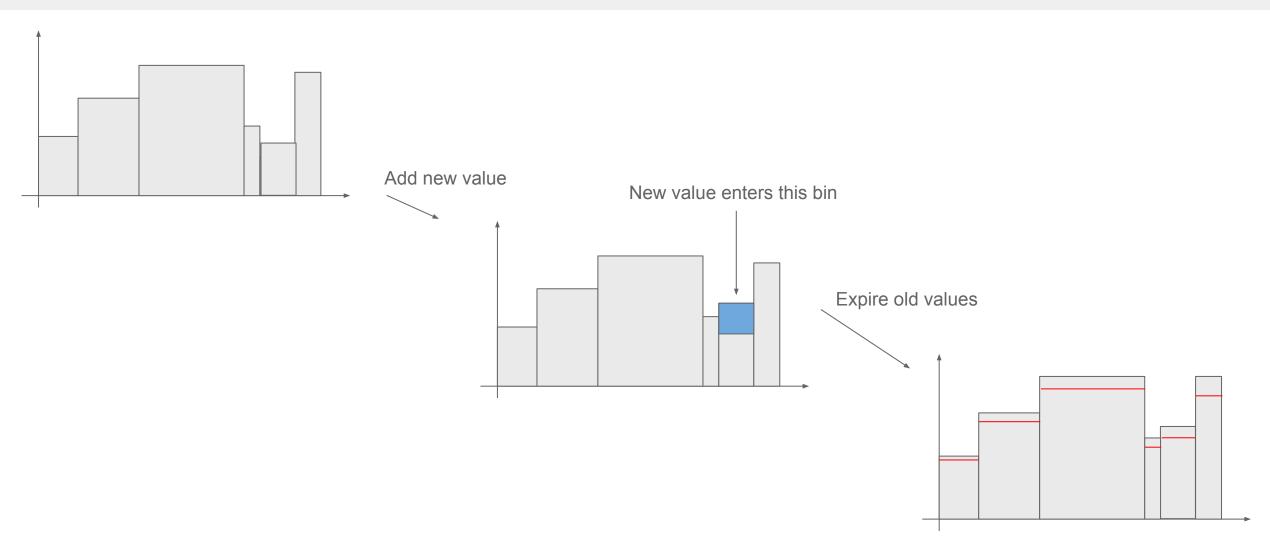
For each event and for each feature:

1. Update the **EMA histogram**.

Add the value to the correct bin and then apply the suppression factor to all bins.



Recall





Stream analysis

A two-phased method

Periodically apply the divergence test:

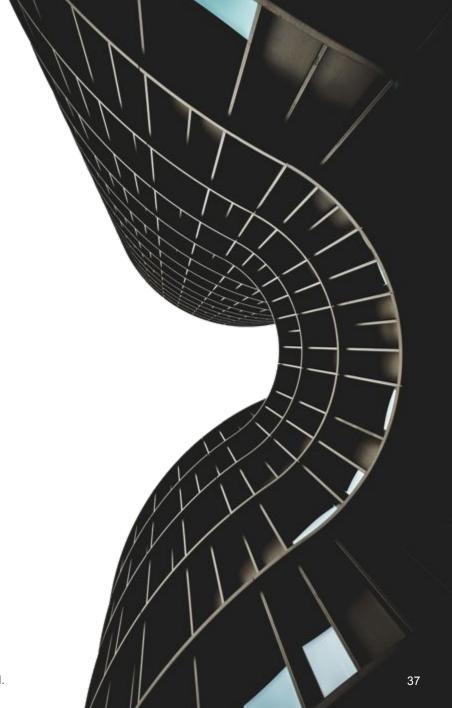
2. Compute JSD between the reference histogram and the streaming histogram.

3. Test in which percentile the **JSD value** is in the histogram of **JSDs of the batch analysis** and alert values with low probabilities (low p-values).



Divergence Test

The multiple comparison problem





Multiple Testing Correction

Online phase alerts

- For each feature we compute a JSD value.
- For each JSD value we compute its probability and check if it is lower than
 a user predefined threshold.
- When repeating this analysis for multiple features we encounter a multiple comparison problem [8,9,10,11].
- The more comparisons made, the larger the false positive rate: considering one hypothesis true when it is not.



The Holm-Bonferroni method

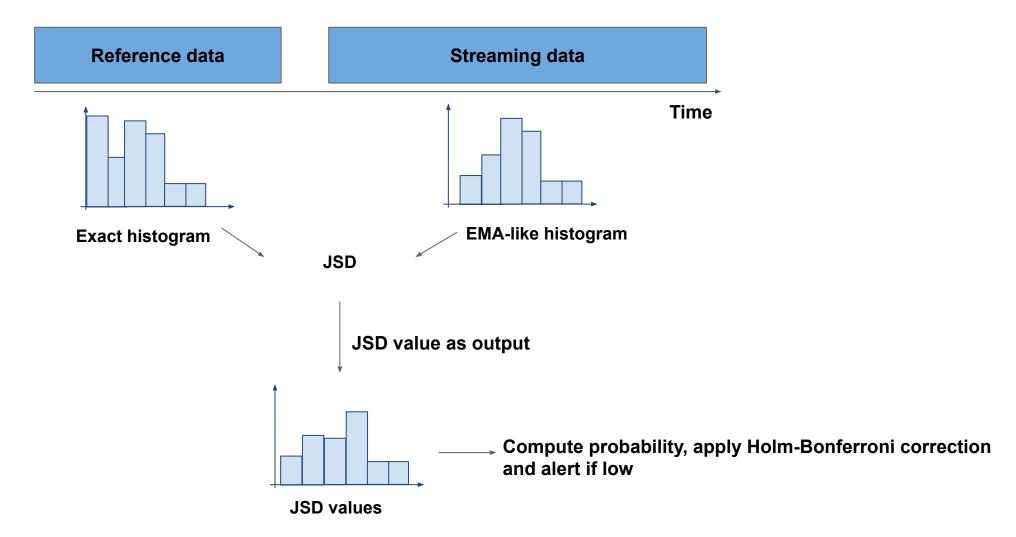
Multiple testing correction

To solve this, we apply the Holm-Bonferroni multiple test correction [12].

 The Holm—Bonferroni method controls the probability to have one or more false positives by adjusting the rejection criteria for each of the individual hypotheses.

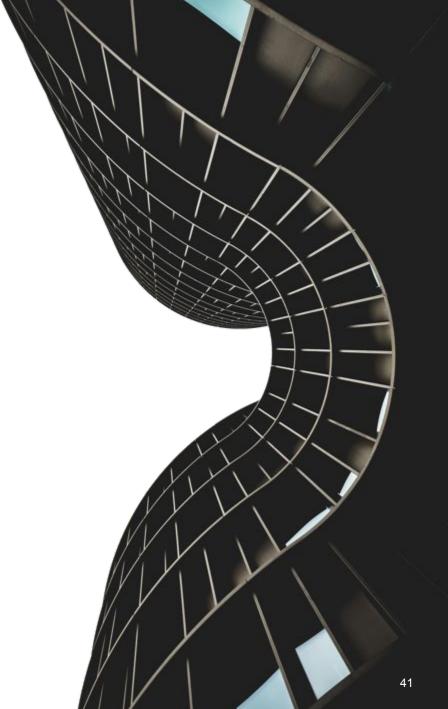


An overview





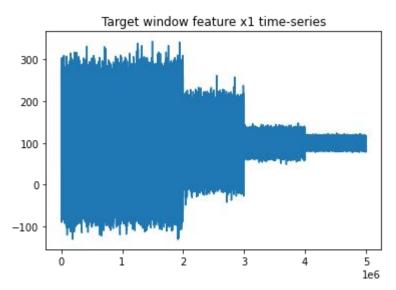
Sanity Checks





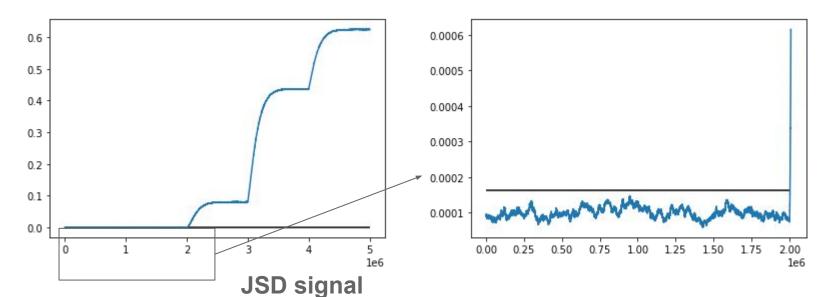
Sanity check

• For a single feature (x1) scenario on a synthetic dataset.



Target data, simulated stream, feature x1 values

x-axis: event number y-axis: event value



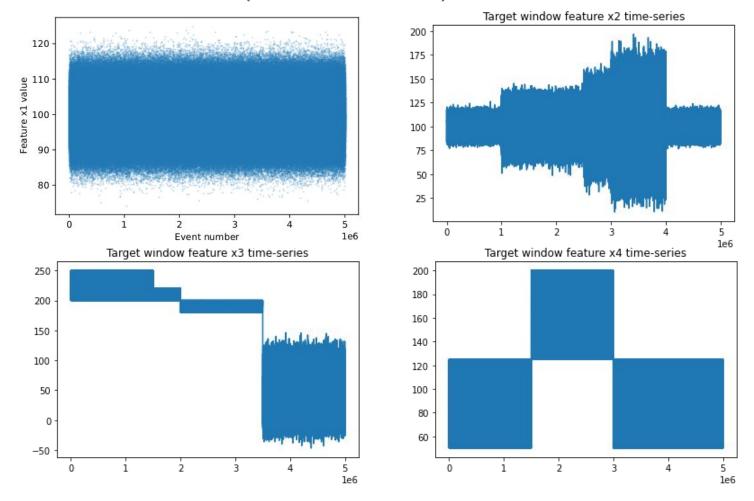
x-axis: event number

y-axis: jsd value between target histogram and reference histogram horizontal black line: tukey threshold



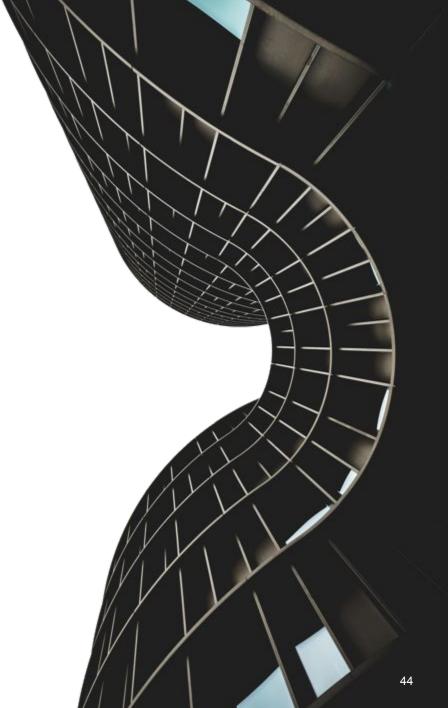
Sanity check

• For a multi-feature scenario (x1, x2, x3, x4).





Real world data





Merchant data

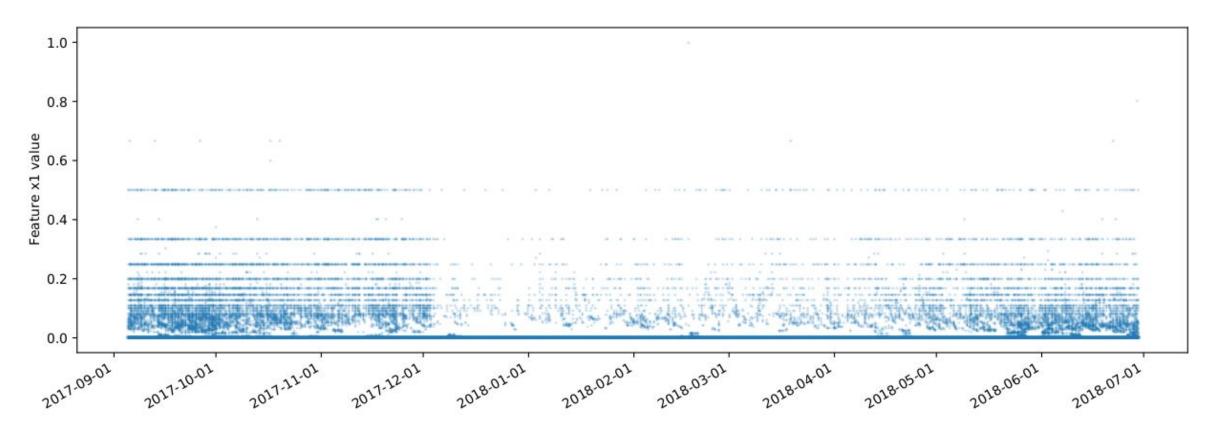
 The table below shows summary statistics for the used reference and target period datasets from a merchant that uses Feedzai's fraud detection system.

| Dataset | From | То | Transactions |
|-----------|----------------------------|-----------------------|--------------|
| Reference | Tuesday, September 5, 2017 | Friday, June 29, 2018 | 1,604,509 |
| Target | Friday, June 29, 2018 | Sunday, June 30, 2019 | 4,032,505 |



Merchant data

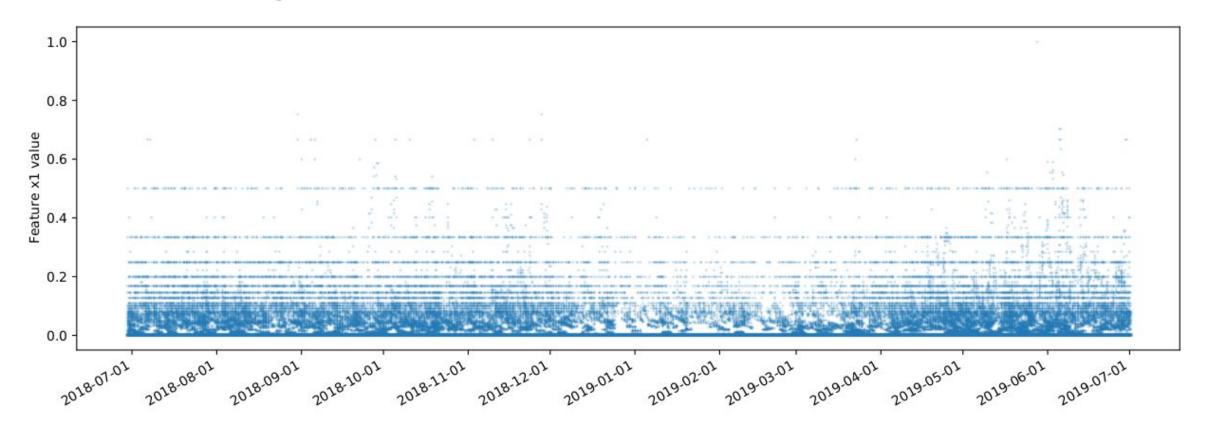
• Feature x1 reference time-series.





Merchant data

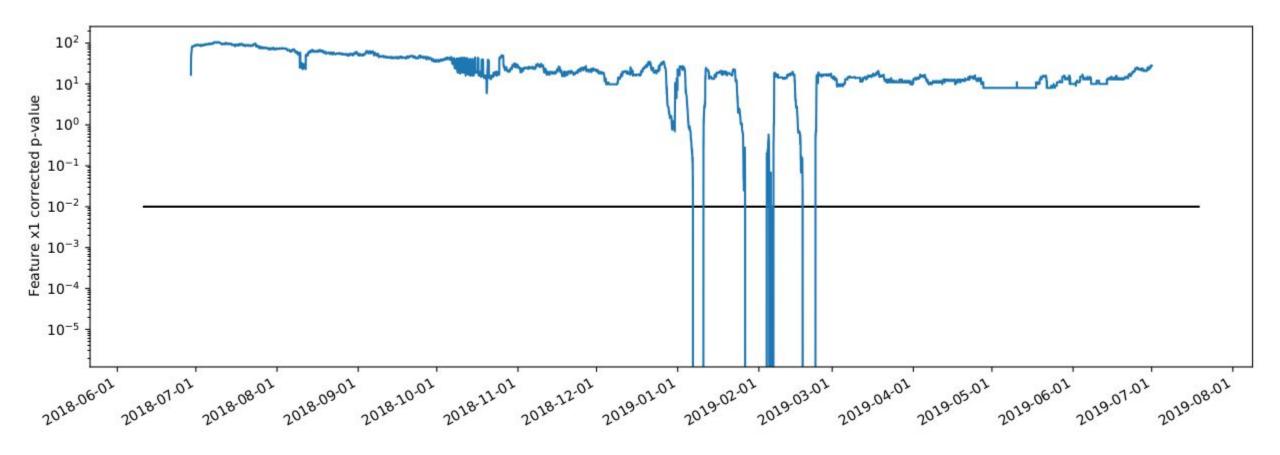
Feature x1 target time-series.





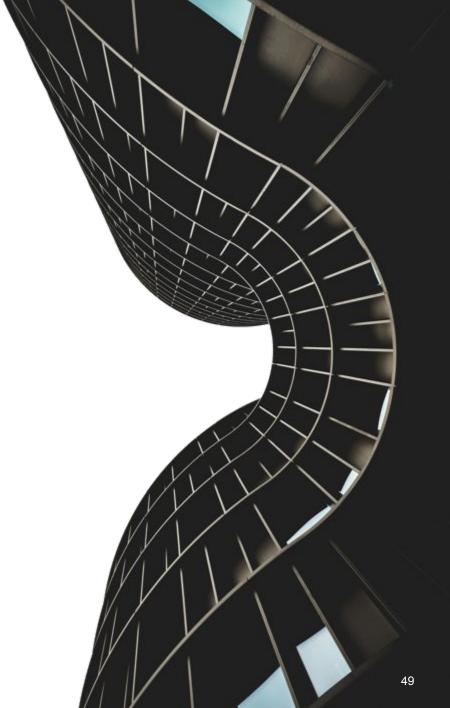
Merchant data

Feature x1 corrected p-value plot and alarm threshold.





Ablation Study





Building an Accurate Divergence Measure Distribution

Ablation study

 In this ablation study we use a custom built JSD distribution which is the best possible fit for the streaming JSD values.

 To do so we traverse the streaming period, collect all JSDs and build the distribution from that.

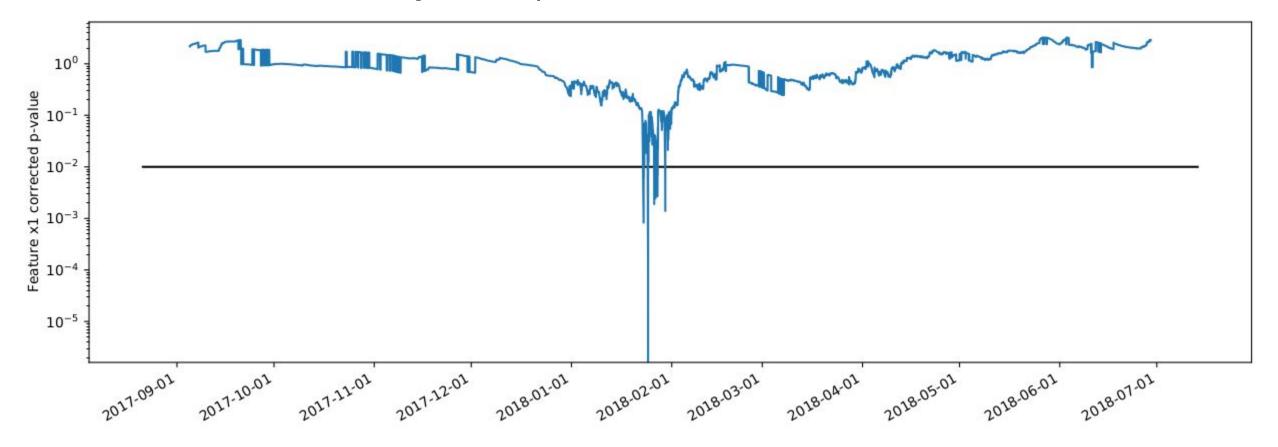
 We then run our streaming analysis once again using this accurate distribution.



Building an Accurate Divergence Measure Distribution

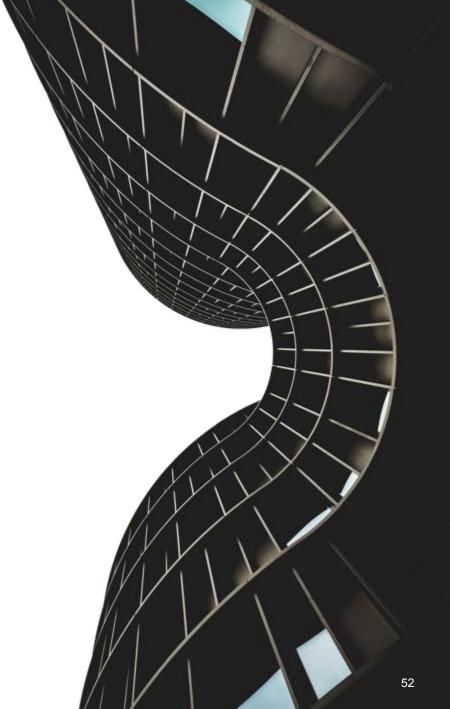
Ablation study

Feature x1 corrected p-value plot and alarm threshold.





Conclusions



Conclusions

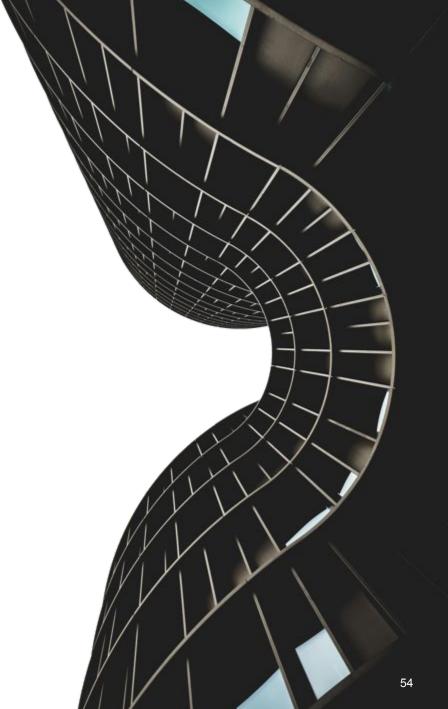
• Single and multi-feature synthetic data induced anomalies were all reported. We know this because we had the ground-truth (the one we created).

 On real data, we don't have a ground truth, but at least visually the results seem to make some sense.

In our ablation studies, where we remove the batch distribution and use a
perfect fit, we got very few and short lasting alerts (the 99th percentile JSD
values) as expected.



Contributions

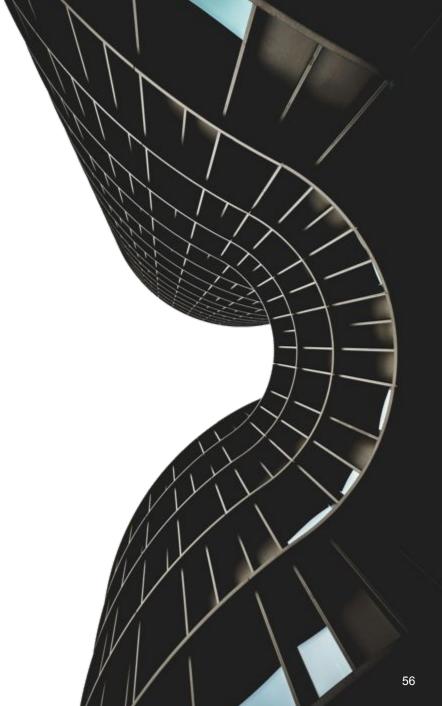


Contributions

- 1. A two-phased and two-windowed univariate subsequence outlier detection method (taxonomy of [13]) that is lightweight and works for real-time stream monitoring.
- 2. A histogram aggregation based on EMAs.
- 3. A set of synthetic datasets and experiments where the method in question accurately detected anomalies.
- 4. Experiments on real data where we provide insights and possible hypotheses to test for future work.



Future Work



Future Work

Experiment making more samples to build a more accurate JSD distribution.

2. Test with **other divergence measures**. We suggest trying the Wasserstein [14] distance.

3. Test with other multiple test correction methods.

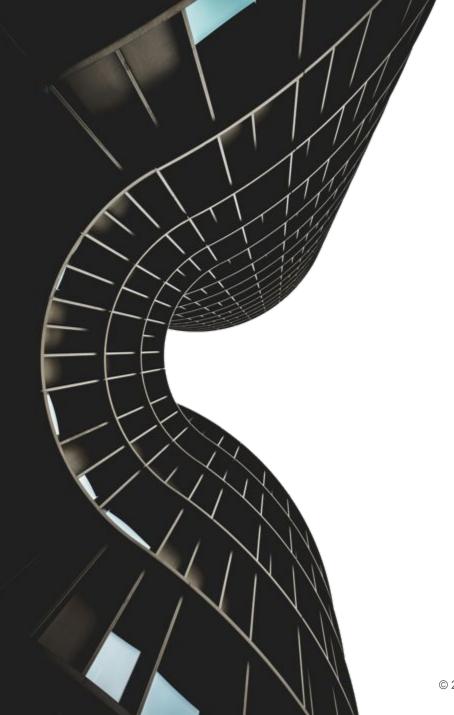


Thank you



References

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Auxiliary slides for committee questions



Batch analysis

A two-phased method

Why compute multiple sample histograms?

To encode the distributions of smaller time periods since there may be pattern changes within the large reference period.

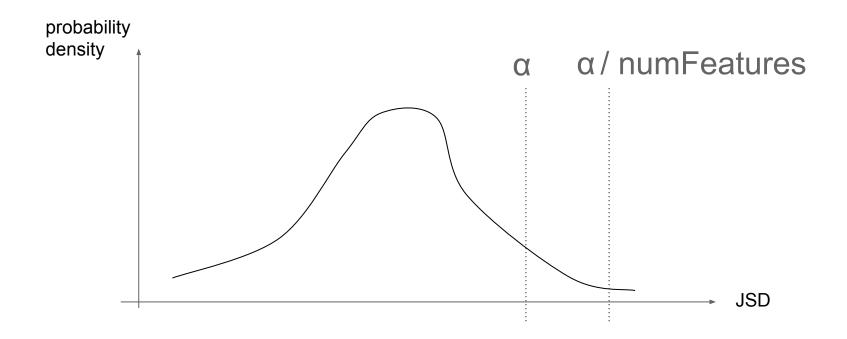
• Why an approximated histogram?

To mimic the streaming EMA histogram we will incrementally maintain in the streaming environment.



Minimum number of samples

 We need to estimate reliably the upper tail of the JSD distribution. With the Holm-Bonferroni correction the upper tail of the distribution is the region α/numFeatures





Minimum number of samples

• γ is the probability of having zero sample JSD points in the upper tail.

• According to the [3], the **minimum number of samples** to make is:

$$n_{samples} = \frac{\log \gamma}{\log \left(1 - \frac{\alpha}{n_{features}}\right)}$$



Minimum number of samples

$$n_{samples} = \frac{\log \gamma}{\log \left(1 - \frac{\alpha}{n_{features}}\right)}$$

• For 180 features, γ = 1% and α = 1%, we have around ~83k samples



Sample size

- We set a half-life value and then multiply it by a constant factor of 4 to get the size of the samples to make.
- Processing 4xhalf-life events means the oldest event's contribution is approximately 6%.

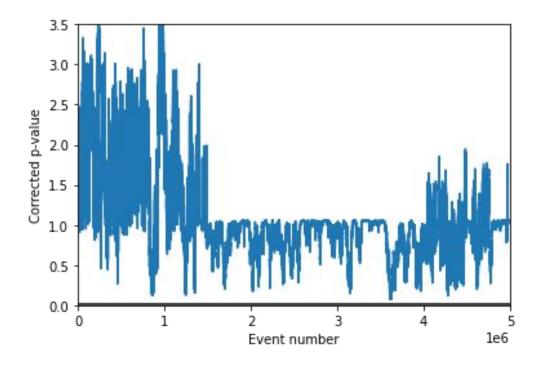
$$(2^{-\frac{1}{n_{1/2}}})^{4n_{1/2}} = 2^{-\frac{4n_{1/2}}{n_{1/2}}} = 2^{-4} \approx 0.06 = 6\%$$

We consider 6% low enough and don't process any more events.



Experimental Results

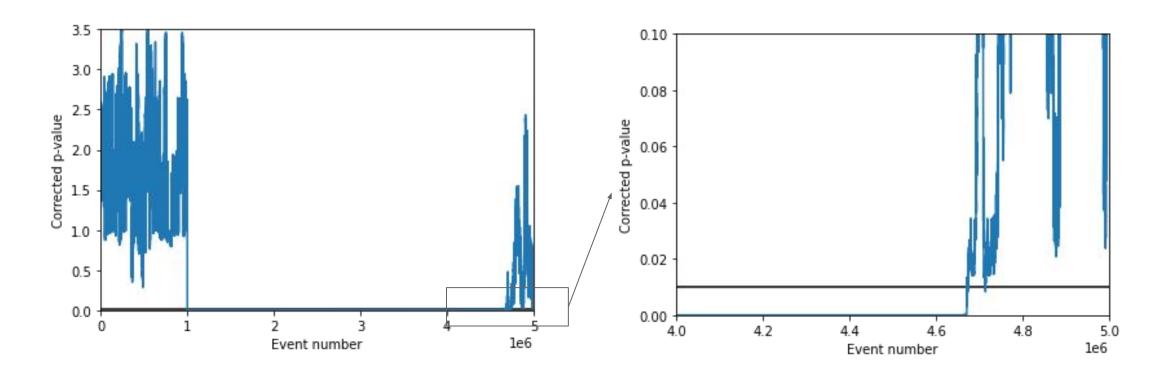
 x1 never diverged from its reference, so we expect to see the corrected Holm-Bonferroni p-values above the 1% probability threshold





Experimental Results

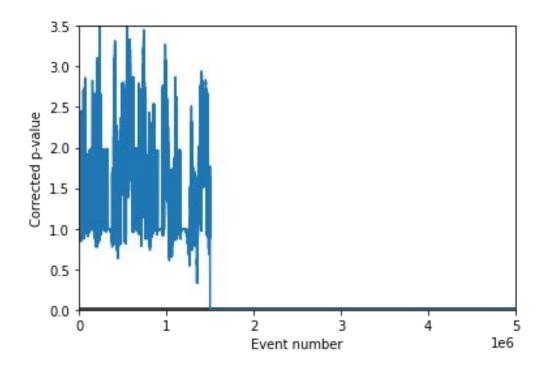
 x2 diverges quite a lot but eventually returns to its original distribution: as a result we see it drops below the threshold until it resumes the reference distribution





Experimental Results

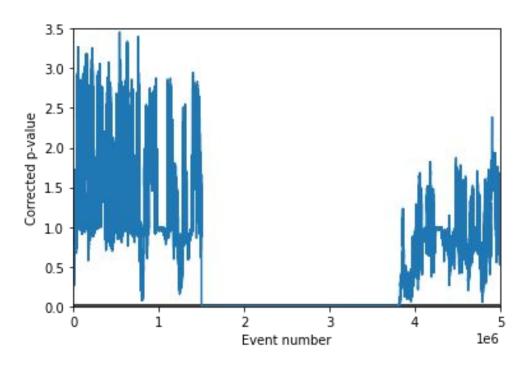
x3 diverges quite a lot as well and never resumes its reference distribution





Experimental Results

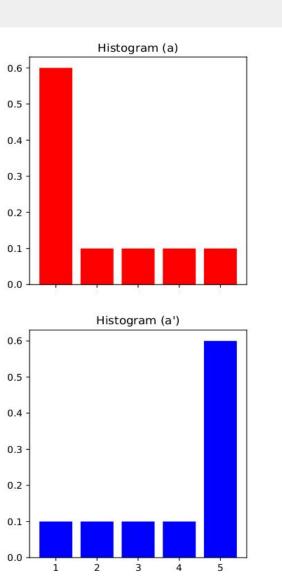
x4 diverges but returns to its original distribution

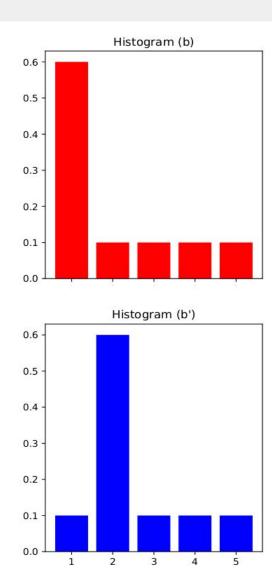




Future Work

Test with other divergence measures then JSD.
 We suggest trying the Wasserstein distance next.





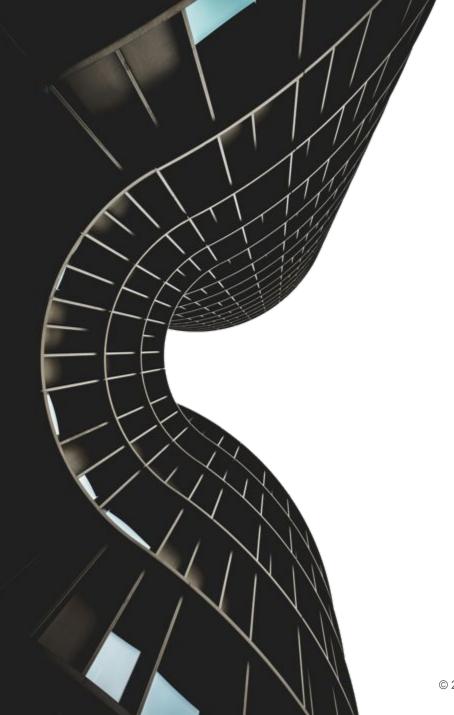


Future Work

• JSD value is the same for both distribution pairs while Wasserstein is not.

 Wasserstein takes into account the amount of probability mass that has to be transported.

| Distribution #1 | Distribution #2 | Wasserstein Output | Jensen-Shannon Output |
|-----------------|-----------------|--------------------|-----------------------|
| a | a' | 2.0 | 0.4451 |
| b | b' | 0.5 | 0.4451 |





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