

ONLINE CLUSTERING OF PROCESSES

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PROBLEM

Setup: We have a growing body of sequences of data. Each sequence is generated by on of k unknown discrete-time stochastic process. The number k of distributions is known.

Data are observed in an online fashion:

→ New samples arrive at every time-step;
they either are continuations of previously
received sequences or a new sequences.

Class Labels	(never visible to the learne	er)	
	$X_1^1, X_2^1, \dots, X_{n_2}^1$	$_{1}(t)$	$X_{n_1(t)+1}^1, \dots, X_{n_1(t+1)}^1$
	$X_1^2, X_2^2, \dots, X_{n_2(t)}^2$)	$X_{n_2(t)+1}^2, \dots, X_{n_2(t+1)}^2$
2	$X_1^3, X_2^3, \dots, X_{n_3(t)}^3$		$X_{n_3(t)+1}^3, \dots, X_{n_3(t+1)}^3$
3	$X_1^4, \dots, X_{n_4(t)}^4$		
	$\dots, X_{n_5(t+1)}^5$		
$(2) X_1^6,.$	$\ldots, X_{n_6(t+1)}^6$		

Goal: Cluster the sequences at every time-step.

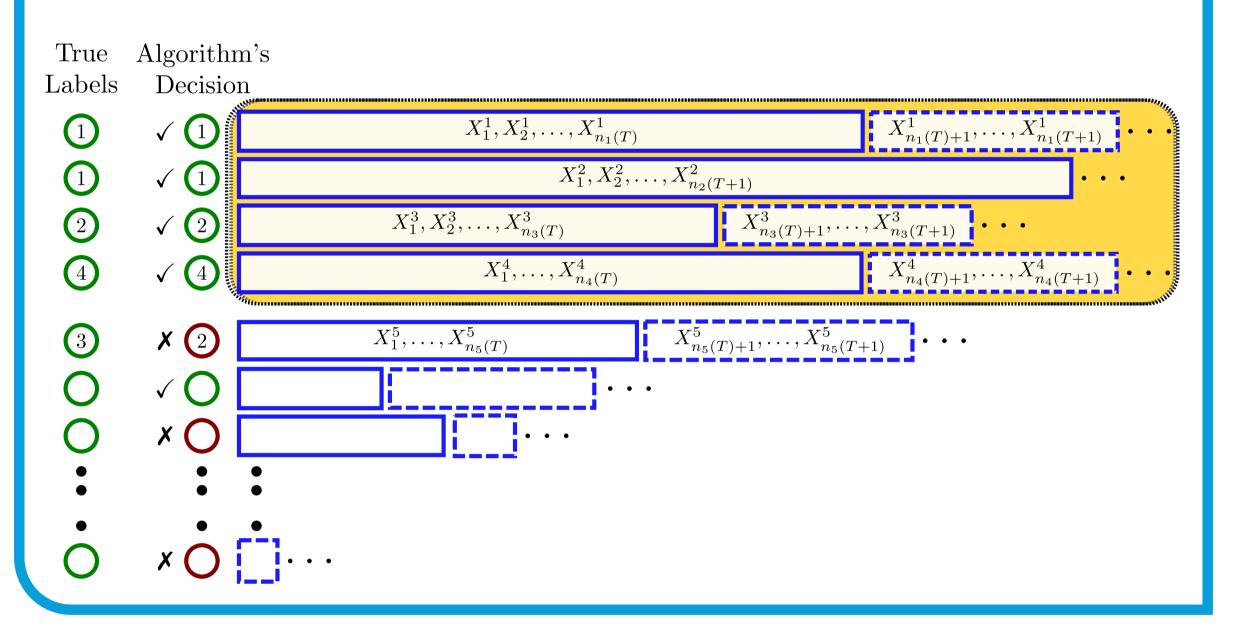
CONSISTENCY

In general it is hard to give a precise definition for "correct clustering".

But, a natural notion for correct clustering exists in the considered setting:

Sequences generated by the same process distribution should be grouped together.

Asymptotic Consistency: A clustering algorithm is (asymptotically) consistent if, with probability 1, for each $N \in \mathbb{N}$ from some time on, it clusters the first N observed sequences are clustered correctly.



ASSUMPTIONS ON DATA

- Data revealed in an arbitrary fashion.
- Our only assumption is that the distributions generating the data are stationary-ergodic.
- → The samples are allowed to be **dependent** and the dependence can be **arbitrary**, or even **adversarial**. No such assumptions as iid, Markov etc. **Remark:** In time-series literature, it is typically assumed that the distributions generating the data have a **known form**, ex. **Gaussian**, **HMMs** etc., and the samples are independent.

DISTANCE MEASURE

We measure the distance between two sequences $\mathbf{x}_1 \in \mathbb{R}^{n_1}$ and $\mathbf{x}_2 \in \mathbb{R}^{n_2}$ as

$$\hat{d}(\mathbf{x}_1, \mathbf{x}_2) := \sum_{m,l=1}^{\infty} 2^{-(m+l)} \sum_{B \in B^{m,l}} |\nu(\mathbf{x}_1, B) - \nu(\mathbf{x}_2, B)|$$

where $B^{m,l}$ $m,l \in \mathbb{N}$ is the set of all hypercubes of dimension m and edge-length 2^{-l} and $\nu(\mathbf{x},B)$ is the frequency with which \mathbf{x} crosses B.

Theorem: $(\hat{d}(\cdot, \cdot))$ is consistent) [1]

If \mathbf{x}_1 and \mathbf{x}_2 are generated by **stationary-ergodic** processes ρ_1 and ρ_2 , then $\hat{d}(\mathbf{x}_1, \mathbf{x}_2)$ converges to the so-called **distributional-distance**:

$$d(\rho_1, \rho_2) := \sum_{m,l=1}^{\infty} 2^{-(m+l)} \sum_{B \in B^{m,l}} |\rho_1(B) - \rho_2(B)|$$

REFERENCES

- [1] D. Ryabko. Clustering processes. ICML 2010.
- [2] CMU graphics lab motion capture database.
- [3] Lei Li and B. Aditya Prakash. Time series clustering: Complex is simpler! ICML 2011.
- [4] T. Jebara, Y. Song, and K. Thadani. Spectral clustering and embedding with HMMs. ECML 2007.

MAIN THEORETICAL RESULT

Theorem: There exists an online clustering algorithm that is asymptotically consistent provided that the distributions generating the data are stationary and ergodic.

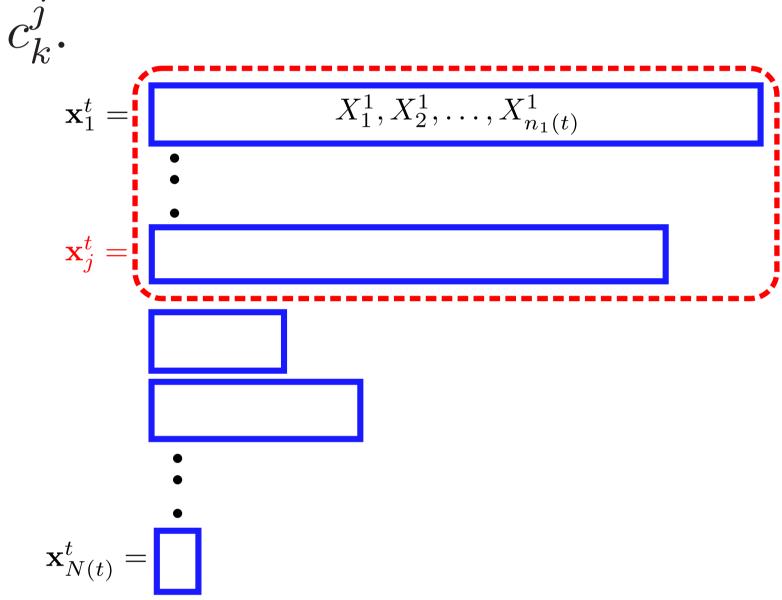
PROPOSED ALGORITHM

Key Idea:

Combine Batch Clusterings with Weights!

Algorithm

1. For j = k..N(t), use a (consistent) batch algorithm on $\mathbf{x}_1^t, \ldots, \mathbf{x}_j^t$ to obtain k cluster centers:



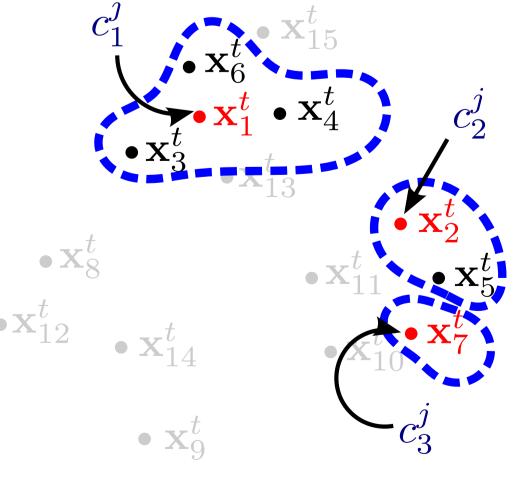
- 2. Calculate two sets of weights:
 - i. $\gamma_j = \min_{i \neq i' \in 1...k} \hat{d}(c_i^j, c_{i'}^j)$ ii. $w_j = j^{-2}$ the the min intercluster distance. chronological weight.
- **3.** Assign points to clusters: For every sequence \mathbf{x} , choose the index $i \in 1..k$, s.t. i minimizes,

$$\frac{1}{\eta} \sum_{i=1}^{N(t)} w_j \gamma_j \hat{d}(\mathbf{x}, c_i^j)$$

where, $\eta := \sum_{j=1}^{N(t)} w_j \gamma_j$ is the normalization factor.

IDEA OF THE PROOF

- 1. The distance $\hat{d}(\cdot, \cdot)$ is consistent:
- The performance weight γ_j converges to 0, when the cluster-centers are obtained from sequences generated by less than k processes.



- 2. The batch algorithm is consistent [1]:
- \rightarrow Once samples from all k clusters are observed, from some time on, the cluster-centers c_1^j, \ldots, c_k^j are consistently chosen to each, uniquely represent one of the k distributions.
- 3. Algorithm is not confused by "bad" points: Sets of sequences $\mathbf{x}_1^t, \dots, \mathbf{x}_j^t$ for larger j contain **potential** "bad" points: newly formed sequences, with inaccurate distance estimates. Decisions based on earlier sequences are more reliable.
- \rightarrow The chronological weight w_j gives precedence to cluster-centers c_1^j, \ldots, c_k^j produced earlier, i.e. smaller j.

EXPERIMENTAL RESULTS

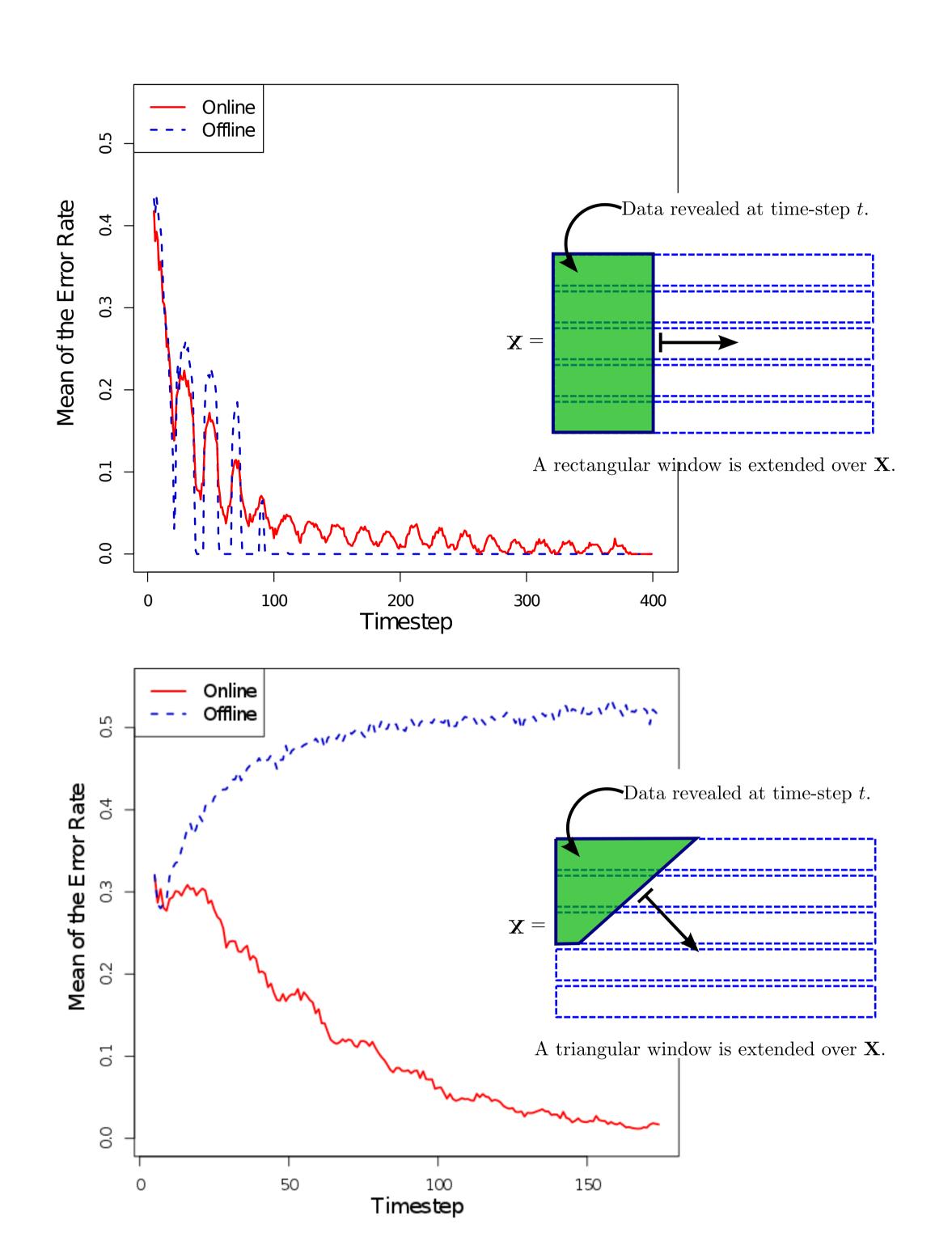
1. Synthetic Data

Setup: We generated a data matrix **X**, where each row a sequence generated by one of the five processes, k = 5.

Batch Simulation: Data revealed via a rectangular window extended over **X**.

Online Simulation: Data revealed via a triangular window extended over **X**.

Remark: We use processes that, while being stationary-ergodic do not belong to any "simpler" class. They cannot be modeled as a hidden Markov process with a countable set of states.



Top: error-rate vs. sequence-length in batch setting (both algorithms are consistent). Bottom: error-rate vs. # of samples in online setting (the offline algorithm is constantly confused by the new sequences).

2. Real Data:

(Clustering Motion Capture Sequences)

Setup: We used time-series data from [2] representing human locomotion; sequences are marker positions tracked spatially through time.



Objective: Cluster the video sequences based on the activity they represent, ex. Walking, Running, etc.

 $f(\cdot, \cdot)$

We compare against [3] and [4].

Dataset

Walk vs. Run (#35)	0.1015	0
Walk vs.Run (#16)	0.3786	0.2109
Dataset	[4]	$f(\cdot, \cdot)$
Ergodic Motions		
Run vs. Run/Jog	100%	100%
Walk vs. Run/Jog	95%	100%
NT 1º N/ (°		

Non-ergodic Motions

Jump vs. Jump fwd. 87% 100%

Jump vs. Jump fwd. 66% 60%

Top: Comparison against [3]; (performance measure: entropy of the true labeling with respect to the prediction) Bottom: Comparison against [4]; (performance measure: the percentage of correct classification). The numerical of [3, 4] results are taken directly from their corresponding articles.; the same sets of sequences, and means of evaluation are used.