Dangoron: Network Construction on Large-scale Time Series Data across Sliding Windows

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CCS CONCEPTS

• Information systems → Data management systems; Stream management;

KEYWORDS

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1 PROBLEM AND MOTIVATION

The monitoring and analysis of large-scale time series data has become a significant area of interest within the database community. Constructing dynamic correlation-based complex networks is a highly effective method for extracting insights from extensive time series data across a range of disciplines, such as neuroscience [2, 4, 11], climate science [3, 7], and finance [6, 12]. In a correlation-based network, nodes are defined by their respective time series, while edges represent the correlations between nodes within a specified time range. Typically, in most analyses, a series of correlation matrices are generated by calculating the pairwise correlation of all time series within sliding windows, given a query time range, a query window size, and a sliding step. Pearson's correlation serves as one of the most prevalent measures across various domains [1, 5, 8].

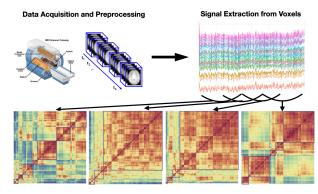
Motivation Example. Recently, dynamic analysis of blood oxygenation level-dependent functional magnetic resonance imaging (BOLD-fMRI) has provided valuable insights into brain network properties by quantifying functional connectivity metric changes over time [4]. This analysis relies on 4-D fMRI data, which contains temporal BOLD activity recordings [2]. Each 3-D fMRI dataset comprises approximately 100K-10M regions at each time point. Traditional 4-D fMRI data analysis involves brain parcellation on region-based connectivity matrices, which refers to distinct, discontinuous yet closely interacting brain partitions [11]. A superior alternative includes building a graph on voxel-level data and performing feature selection and graph embedding. However, constructing a network with raw voxel-level data is computationally

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Dynamic Functional Connectivity Computation

Figure 1: Network Construction on FMRI across Sliding Windows

infeasible due to the time-consuming pairwise correlation calculations required for voxel-based functional connectivity matrices within sliding windows. This paper introduces techniques to compute a sequence of correlation matrices on 3-D fMRI data for all brain regions

Problem Definition. We are given a collection of time series represented by matrix X of size $N \times L$. Here, we have N time series, and each row represents a time series of length L. Each element x_{ij} in X denotes the time-stamped value of a variable collected at location i at time j. We use X_i to represent the ith row, which corresponds to the *i*th time series. We assume all time series in Xare synchronized, meaning each time series has a value available at every periodic time interval or time resolution. This can be achieved through aggregation and interpolation on non-synchronized series. At query time, a user defines the query range r = (s, e), where s and e are the starting and ending points, respectively, the query window size *l*, the sliding step size η , and a threshold β . The problem requires computing a series of correlation matrices, $C = C^0, C^1, \dots, C^{\gamma}$, where each C^k is the correlation matrix of $Xk * \eta : k * \eta + l$ (the submatrix of X from the $k * \eta$ th column to the $k * \eta + l$ th column). In C^k , each element $cij^k (\geq \beta)$ denotes the Pearson correlation between X_i and X_j within the range of the kth sliding window. If $c_{ij}^k < \beta$, we replace it with 0.

The core task involves addressing the problem of large-scale, all-pair time-series correlation calculation across sliding windows. The key challenges include: 1) ensuring the efficiency of network construction and updates for large-scale data to achieve interactivity, 2) maintaining the robustness of the methods on datasets with varying distributions, and 3) optimizing the effectiveness of sketching techniques for subsequent network analysis.

1

2 BACKGROUND AND RELATED WORK

Correlation calculation across sliding windows has been explored through frequency-based transform [9, 10, 16, 17] and random projection [14, 15] approaches. Both aim to reduce time series dimensionality and identify highly-correlated pairs in low-dimensional spaces. Basic windows [17] were first proposed for time-series pairs with high correlation, later improved in parallel [9]. Parcorr [14] optimized incremental computation, achieving state-of-the-art efficiency. TSUBASA [13], the latest work, computes exact pairwise correlations on arbitrary time windows using a novel sketch framework, but lacks efficiency for sliding queries.

Existing techniques, except TSUBASA, face robustness issues due to data-dependency. Frequency-based transform methods struggle with dimensionality reduction for certain time series, only succeeding when energy concentrates in a few domains [15]. To date, no benchmark has been proposed to systematically test solution robustness.

3 APPROACH AND UNIQUENESS

In this work, we introduce Dangoron, a framework for efficiently computing dynamic correlation matrices with high accuracy, and Tomborg, a benchmark for generating time series datasets to test framework robustness.

The core concept of Dangoron is the relatively stable correlation when transitioning to the next sliding window. By computing future upper and lower bounds of correlation, we can optimize calculations. For instance, if the current correlation is below the threshold and the next upper bound is also below the threshold, we can skip the next time step computation. Estimating bounds for the next *k*th window allows us to determine the number of skippable steps and directly jump to the desired window.

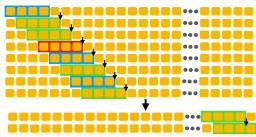


Figure 2: Jumping Structure of Dangoron

We employ the basic window framework by dividing a series into smaller basic windows, enabling data processing in smaller batches. Referring to the **Problem Definition**, let's consider a C_k from C and denote it as C. We select the ith and jth rows from X within the time range specified by C, and label them as $x = [\mathbf{x}_1, \dots, \mathbf{x}_m]$ and $y = [\mathbf{y}_1, \dots, \mathbf{y}_m]$. We define the sizes of basic windows as $\mathbf{B} = [B_1, B_2, \dots, B_m]$, where B_i represents the size of the i-th basic window. The exact Pearson's correlation between x and y is given by:

$$Corr(x,y) = \frac{\sum_{j=1}^{n_s} B_j(\sigma_{x_j}\sigma_{y_j}c_j + \delta_{x_j}\delta_{y_j})}{\sqrt{\sum_{i=1}^{n_s} B_i(\sigma_{x_i}^2 + \delta_{x_i}^2)} \sqrt{\sum_{i=1}^{n_s} B_i(\sigma_{y_i}^2 + \delta_{y_i}^2)}}$$

$$\delta_{x_i} = \overline{x_i} - \frac{\sum_{k=1}^{n_s} \overline{x_k}}{n_s}, \ \delta_{y_i} = \overline{y_i} - \frac{\sum_{k=1}^{n_s} \overline{y_k}}{n_s}$$
(1)

 σ_{x_i} (σ_{y_i}) represents the standard deviation of the basic window for σ_{x_i} (σ_{y_i}), σ_{z_i} is the correlation of basic windows σ_{z_i} and σ_{z_i} is the mean of the basic window σ_{z_i} (σ_{z_i}), and σ_{z_i} denotes the number of basic windows in a query window. Using Equation 1, we can precompute and store basic window statistics and calculate correlations for arbitrary query windows and sizes.

Figure 2 illustrates how Dangoron operates. Each yellow block represents a pair of basic windows. Initially, we compute the exact correlation using Equation 1; if it is lower than the threshold β , it is indicated by a blue block. We then determine k from the upper bound estimation, such as Equation 2, by solving for k such that $Corr_{i+k-1} < \beta$ and $Corr_{i+k} \ge \beta$ using binary search. In Figure 2, k=3, and we use a red block to signify an upper bound higher than β . After jumping k steps (skipping the green ones), we recompute the exact correlation value.

$$Corr_{1+k} \leq Corr_1 + \frac{1}{n_s} (k - \sum_{i=1}^{k} c_i) = Corr_{i+k} *$$
 (2)

We have proved Equation 2 under the assumption that each basic window comes from a sample distribution, as detailed in our technical report. For more complex cases, we have derived general bounds. Another feature proposed in Dangoron enables horizontal computation pruning. Given time-series x, y, and z, if we know the pairwise correlations c_{xz} and c_{yz} , we can determine the range of c_{xz} as $c_{xz}c_{yz} - \sqrt{(1-c_{xz}^2)(1-c_{yz}^2)} \le c_{xy} \le$ $c_{xz}c_{yz} + \sqrt{(1-c_{xz}^2)(1-c_{yz}^2)}$. The Tomborg framework involves: (1) generating C from a user-specified distribution, (2) generating § in frequency space, and (3) transforming them to X using inverse Fourier Transform. Step (2) is based on the fact that Discrete Fourier Transform (DFT) preserves the distance between coefficients and the original time series. We developed a real-value variant of the inverse-DFT, transitioning from a complex space to a real space (unlike the original inverse-DFT, which moves from a complex to complex space), and provided proof.

4 RESULTS AND CONTRIBUTIONS

We selected TSUBASA [13] as our baseline. On the *NCEA Data Set*¹, Dangoron is an order of magnitude faster than TSUBASA in terms of pure query time and achieves an accuracy above 90 percent, comparable to Parcorr. We plan to conduct more large-scale experiments upon completing the implementation of Tomborg. In this work, we make the following contributions: 1) We introduce Dangoron, a framework that solves the problem of correlation matrix computation across sliding windows, and is at least one order of magnitude faster than the baseline; 2) We propose Tomborg, the first benchmark for the problem of correlation matrix computation.

 $^{^{1}} https://www.ncei.noaa.gov/pub/data/uscrn/products/hourly02/2020/$

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