

Hypothesis and analysis on the relationship between bivariate data correlation and Mapper graph structure

Phillip Korolev

January 2026

1 Introduction

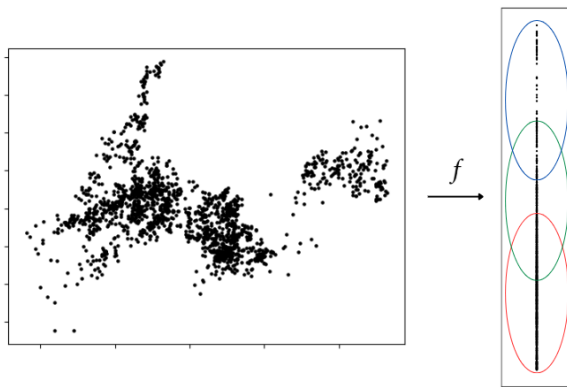
When tasked with analyzing data, we are often looking to draw intuitive, visual patterns. With bivariate time series data, our task is much simpler and typically narrows our available options for data analysis techniques. In this case, the goal is to draw some sort of pattern between our two observed values $X(t)$, $Y(t)$ over a portion or the entirety of our data set's time span T . Although a 2-dimensional scatter plot is often our first step to visualize some sort of correlation between the values, it can be difficult to tell just how populated clusters of points are, or to draw conclusions given unintuitive plot shapes.⁷

With methods in topological data analysis, we are granted techniques that let us explore the structure and correlation of our data past the initial scatter plot. In this informal analysis, we will introduce the Mapper algorithm, which transforms arbitrary dimensional data into a flat discrete graph with nodes, edges, and coloring, helping us identify things like cluster density and potential cycles in our time series data. In particular, we will analyze the structure of graphs generated from highly correlated and uncorrelated bivariate time series data sets.

2 Mapper Algorithm

Many more detailed versions of the algorithm and motivations can be found in outside resources. The general summary of the algorithm will be presented, as well as a more formal process.

Simply, the Mapper algorithm uses filtration processes (of our choice) to project data $X \subset \mathbb{R}^d$ onto \mathbb{R}^m with $m < d$. The filtration function is often called the lens, and typically we choose a function that projects our data onto \mathbb{R}^2 or \mathbb{R} . Based on given parameters, we look to construct overlapping covers of the lens space $f(X)$ to split and group the projected image points into their respective regime.



The colored portions of our lens space $f(X)$ above represent a different cover (interval) of the space and help us classify our original points $f^{-1}(X)$. After classifying the original points and applying some clustering algorithm, we are able to construct a graph where each node represents some cluster, and an edge is only present if there are overlapping points between two clusters. Also note that the size of a particular node depends on the respective cluster's density (population).

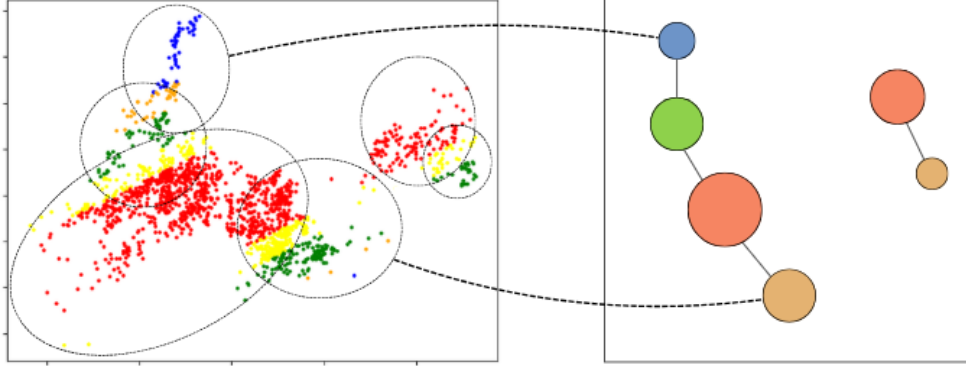


Figure 1: Clustering classified data points and generating graph

Generally, the process aims to accomplish the following:

1. Normalize our data set $X \subset \mathbb{R}^d$ using a normalization function of choice $\text{Norm} : X \rightarrow \tilde{X}$
2. Choose a filtration (lens) function $f : \mathbb{R}^d \rightarrow \mathbb{R}^m$, typically with $m \in \{1, 2\}$, and build the image set $f(\tilde{X}) = \{f(x) : x \in \tilde{X}\}$
3. In the image space, construct a cover $\mathcal{U}_f = \{U_a\}_{a \in A}$, with A an arbitrary index set, such that:
 - (i) their union covers all of the image space: $f(\tilde{X}) \subseteq \bigcup U_a$
 - (ii) for $a, b \in A$: U_a, U_b adjacent $\iff U_a \cap U_b \neq \emptyset$
4. Classify points $x \in \tilde{X}$ with class c if $f(x) \in U_c$
5. Apply clustering to our data \tilde{X}
6. Construct the graph $G = (V, E)$ with vertices v_i representing clusters C_i and edges e_i connecting two vertices v_i, v_j if and only if there exists a point $x \in \tilde{X}$ such that $x \in C_i \cap C_j$

In the case of the experiments of this paper, the algorithm can be slightly more defined. To start, we are interested in bivariate data. That is, our data set X is 2-dimensional of the form $X = \{(x_i, y_i)\}$, so the normalization we use is the process $\text{Norm}_Z : X \rightarrow \tilde{X}$, defined by:

$$\text{Norm}_Z(x, y) = \left(\frac{x - \mu_x}{\sigma_x}, \frac{y - \mu_y}{\sigma_y} \right),$$

with μ_x and σ_x the mean and standard deviation with respect to the x argument in X . Likewise for μ_y, σ_y .

With X as described above, we are restricted to using filtration functions in $\mathcal{F} = \{f \mid f : \mathbb{R}^2 \rightarrow \mathbb{R}^2 \cup f : \mathbb{R}^2 \rightarrow \mathbb{R}\}$. In the experiments seen in further sections, we use the filtration function $f : \mathbb{R}^2 \rightarrow \mathbb{R}$ defined by

$$f(x, y) = |x - y|,$$

to stay on the theme of correlation. Given that \tilde{X} is the normalized data set, the function f above gives us a good idea of how far apart the values \tilde{x}_i and \tilde{y}_i are. For some intuition, a perfectly correlated normalized dataset \tilde{X} would lie on the line $y = x$ in \mathbb{R}^2 . In our case, the image space $f(\tilde{X})$ lies on the real number line, so our collection of overlapping covers is just a collection of overlapping intervals I_1, I_2, \dots, I_N satisfying:

$$\bigcup_{i=1}^N I_i = [\min f(\tilde{X}), \max f(\tilde{X})].$$

To achieve some overlap, we set an overlap parameter $\alpha \in (0, 1)$ that tells the interval construction algorithm the amount of overlap that should occur between each consecutive interval. Note that for any two consecutive intervals I_k, I_{k+1} we have that $I_k \cap I_{k+1} = [\min I_{k+1}, \max I_k]$ and with guaranteed overlap, this intersection is never empty.

Example. Interval Construction

Take the interval $\mathcal{I} = [0, 10]$, we build $N = 3$ equally wide intervals with overlap $\alpha = 0.5$ such that I_1, I_2, I_3 cover all of \mathcal{I} . We want to do so "efficiently", so our first interval I_1 should begin at $\min \mathcal{I} = 0$, and $I_N = I_3$ should have maximum $\max \mathcal{I} = 10$. This algorithm is described below, but for the sake of the example, our covers would be the following:

$$I_1 = [0, 5]; I_2 = [2.5, 7.5]; I_3 = [5, 10],$$

with intersections $I_1 \cap I_2 = [2.5, 5] = [\min I_2, \max I_1]$ and $I_2 \cap I_3 = [5, 7.5] = [\min I_3, \max I_2]$.

The following is the algorithm used to generate graphs and results seen in this paper. As described above, it is tuned for exploring correlation structures in bivariate data.

Algorithm 1: Mapper Construction with Absolute-Difference Filtration

Input: Data set $X \subset \mathbb{R}^2$, number of intervals N , cover overlap parameter α

Output: Nerve graph G

1. $\tilde{X} \leftarrow \text{Norm}_z(X)$
 2. Define function $f(x, y) = |x - y|$
 3. $Y \leftarrow f(\tilde{X})$
 4. $\mathcal{I} \leftarrow [\min f(\tilde{X}), \max f(\tilde{X})]$
 5. $\mathcal{U} \leftarrow \text{getCovers}(\mathcal{I}, N, \alpha)$
 6. **foreach** $I_i \in \mathcal{U}$ **do**
 - Classify points $c_i \leftarrow \{f(x) \in Y : f(x) \in I_i\}$
 - Pull back $V_i \leftarrow f^{-1}(I_i)$
 - Compute clusters $\mathcal{C}_i \leftarrow \mathcal{C}(V_i)$
 7. Construct graph G :
 - (i) add node N_i representing cluster \mathcal{C}_i
 - (ii) add edge (N_i, N_j) if and only if $\mathcal{C}_i \cap \mathcal{C}_j \neq \emptyset$ for $i \neq j$
- return** G
-

For the cover construction process described previously, and seen in Algorithm 1 (**getCovers**), we use the following. Note that the algorithm constructs intervals as we assume that all filtration functions used throughout the experiments in the paper are of the form $f : \mathbb{R}^2 \rightarrow \mathbb{R}$.

Algorithm 2: Interval Construction in \mathbb{R}

Input: Interval $\mathcal{I} \subset \mathbb{R}$, number of intervals N , overlap parameter α

Output: List of intervals I_1, \dots, I_N covering \mathcal{I}

```

1. Initialize list  $L$ 
2.  $w \leftarrow (\max \mathcal{I} - \min \mathcal{I}) / (N - (N - 1)\alpha)$ 
3.  $s \leftarrow w(1 - \alpha)$ 
4. for  $i \in \{0, 1, \dots, N - 1\}$  do
     $l \leftarrow \min \mathcal{I} + i \cdot s$ 
     $u \leftarrow l + w$ 
     $L \leftarrow I_i = [l, u]$ 
return  $L$ 

```

3 Hypothesis

We wish to gain an intuition on Mapper graph structures based on the bivariate data set X which it is built from. Conversely, we also want to identify if our original data set X is highly correlated based on the generated Mapper graph. *For the rest of the section, we will assume that X has already been normalized, and in later experiments, we use Norm_Z described previously to normalize synthetic data.*

Given a normalized and well-connected bivariate data set $X = \{x_i, y_i\}_{i=1}^N$ with $x = (x_1, x_2, \dots, x_n)$, $y = (y_1, y_2, \dots, y_n)$, the lens function $f : \mathbb{R}^2 \rightarrow \mathbb{R}$ defined by $f(x, y) = |x - y|$, fixed interval construction parameters (N, α) , and some fixed clustering algorithm, we expect the resulting Mapper graph to contain the following properties:

1. As $|\rho(x, y)| \rightarrow 1$, the likeliness of resulting graph G being fully connected $\mathbb{P}[\beta_0(G) = 1]$ increases, and the expected number of independent cycles $\mathbb{E}[\beta_1(G)]$ tends to 0.
2. As $|\rho(x, y)| \rightarrow 0$, the expected number of cycles $\mathbb{E}[\beta_1(G)]$ increases.

Note that the Betti numbers β_0, β_1 track connectedness and cycles (loops) of a graph respectively. In the case that $\beta_0 = 1$, the graph is fully connected, i.e.: there always exists a path from node v_i to node v_j . On the other hand, $\beta_0 > 0$ signals that the graph has multiple disconnected components. In the same manner, $\beta_1 = 0$ tells us that there are no cycles in our graph, while $\beta_1 > 0$ signals the existence of one or more cycles.

To understand the intuition behind the statement in the first expected result, we assume that the series x, y of data set X are highly correlated. From a regression standpoint, the regression line plotted against the plot of X fits our data almost perfectly ($R^2 \approx 1$). With appropriate normalization, the points in X lie almost exactly on the line $y = x$, so we can write each point $(x, y) \in X$ as $(x, x + \varepsilon)$ for some small value $\varepsilon \in \mathbb{R}$. The lens function given above captures the distance of any point in X from the 1-dimensional diagonal manifold $y = x$. With each point $(x, y) = (x, x + \varepsilon)$, the image space $f(X)$ is contained in the interval $[0, \varepsilon] \subset \mathbb{R}$. Since points $f(x, y) \in f(X)$ are so closely connected, any interval cover \mathcal{I}_a of $f(X)$ will satisfy $I_k \cap I_{k+1} \neq \emptyset$ since we guarantee some overlap α , which causes a chain of overlaps and consequently, each pullback $f^{-1}(I_k)$ is connected. Thus, for a highly correlated (by series) bivariate data set X , we expect a Mapper graph with one globally connected component:

$$\rho(x, y) \rightarrow 1 \implies \mathbb{E}[\beta_0(G)] \rightarrow 1$$

Staying on the first expected result, we explore the second half of the statement similarly. To obtain a value $\beta_1 > 0$, we must have some cycle in our cluster chain:

$$C_k \longleftrightarrow C_{k+1} \longleftrightarrow C_{k+2} \longleftrightarrow C_k.$$

Again, we have the image space $f(X) \subset [0, \varepsilon]$ with each pullback $f^{-1}(I_K)$ a diagonal band of thickness proportional to $|I_K|$. With the data tube thickness ε much smaller than the band width, each band intersects the data in a single connected strip. Moreover, that strip only overlaps with strips from adjacent intervals, thus we obtain the cluster chain below, which is a tree and thus $\beta_1 = 0$.

$$C_1 \longleftrightarrow C_2 \longleftrightarrow C_3 \longleftrightarrow \dots$$