Data Dimension Reduction and Network Sparsification based on Minimal Algorithmic Information Loss*

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Abstract

We introduce a family of unsupervised, domain-free, and (asymptotically) model-independent algorithms based on the principles of algorithmic information theory designed to minimize the loss of algorithmic information. The method coarse-grains data in an algorithmic fashion by collapsing regions that can be procedurally regenerated from the compressed version. We show that the method can preserve the salient properties of objects and structures in the process of data dimension reduction and denoising. Using suboptimal approximations of efficient (polynomial) estimations to algorithmic complexity by recent numerical methods of algorithmic probability we demonstrate how these algorithms can preserve structure properties, outperforming other algorithms in e.g. the area of network dimension reduction. As a case study, we report that the method preserves all the graph-theoretic indices measured on a well-known set of synthetic and real-world networks of very different nature, ranging from degree distribution and clustering coefficient to edge betweenness and degree and eigenvector centralities, achieving equal or significantly better results than other data reduction and some of the leading network sparsification methods.

Keywords: denoising; coarse-graining; algorithmic machine learning; renormalization; lossy compression; causal data reduction; feature selection; graph complexity; model-based image segmentation.

*Corresponding author: hector.zenil@ki.se Online implementation is freely available at http://www.complexitycalculator.com/MILS and source code in R (for strings) and in Wolfram Language (strings and arrays) is available at https://github.com/algorithmicnaturelab/MILS
1 Introduction and Motivation

The study of large and complex datasets, or big data, organised as networks, has emerged as one of the central challenges in most areas of science and technology, cellular and molecular networks in biology being one of the prime examples. Hence, a number of techniques for data dimensionality reduction, especially in the context of networks, have been developed.

Data reduction consists in the transformation of numerical or alphabetical digital information into a simplified smaller representation preserving certain properties of ‘interest’, which are usually defined as the most meaningful parts. The question germane to the area of data reduction concerns how low dimensional structures can be detected in high dimensional data. The main purpose of data dimensionality reduction involves two sides of the same coin. On the one hand there is the minimization of the loss of information, and on the other, the maximal preservation of the most ‘meaningful’ features characterizing an object (i.e. feature selection). Traditionally, such meaningful features of interest are defined in terms of a user-centric, subjective criterion. For example, linear algebraic (e.g. matrix analysis) and statistically-based dimensionality reduction techniques attempt to minimize statistical information loss under certain algebraic (interpreted as signal and noise) conditions, as a consequence maximizing the statistical mutual information between the desired information and the dimensionally-reduced output.

However, statistical approaches and classical information theory cannot preserve computable features without some statistical signature, no matter how important they may be in characterizing the object (thus making the choice of preserving statistical information arbitrary and fragile) [35, 39]. That is, such techniques (e.g. PCA [26]) will miss any non-linear and algorithmic regularity if it does not show a statistical property. Because the number of algorithmic features outgrows the number of statistical ones (the set of statistical features is a proper subset of the algorithmic), PCA, like all other computable measures for data reduction and clustering techniques, will miss fundamental properties of interest [35] by virtue of being only statistical and not algorithmic, it being already known that it would miss, for example, non-linear embeddings impossible to find with statistical and linear techniques. Improving on some of these limitations, topological data analysis can reduce data by minimizing its size or dimension into a non-linear surface of low algorithmic complexity, e.g. a torus, or an S-shaped function.

The success of both linear and non-linear techniques can thus be simplified by looking for the shortest specification they can achieve. For linear
algorithms this is usually approached by traditional statistical techniques, while for non-linear algorithms, some domain-specific subset of algorithms is considered (e.g. the set of all possible geometric shapes). Here, by not confining ourselves to a domain, we take a step forward towards more universal techniques, free of domains and particular implementations.

For example, if datapoints can be embedded in a low-dimensional subspace or topological submanifold (such as a torus), an algorithmic loss minimization process would approximate the shortest description of the generative mechanism of the torus.

Here we introduce a family of semi-computable algorithms that specifically target the preservation of computable properties (hence both statistical and algorithmic), and can thus be seen as a generalization of all dimension reduction procedures. The methods constitute an interesting approach to designing theoretically optimal lossy compression techniques based on principles and estimations to theoretical optimal lossless compression.

Graphs have been used as an efficient formal structure for representing data. Network science is now central to many areas, including molecular biology, serving as a framework for reconstructing and analyzing relations among biological units [3, 14, 25, 4].

The main aim of dimension reduction in a network is to approximate a network with a sparse network. There are several methods available in the literature for graph sparsification. Chew [9] used the shortest-path distance between every pair of vertices as a criterion for sparsifying a network. The concept of cut problems has been utilised for sparsification by Benczur and Karger [6]. In one of the latest methods, spectral similarity of graph Laplacians has been used for sparsification by [31].

For network dimensionality reduction one may choose as a criterion the preservation of graph-theoretic properties such as graph distance, clustering coefficient or degree distribution, or a finite (usually small) combination of these or other indices. But no finitely computable approach can find all possible features of interest in a dataset, for example, all those recursively enumerable features that the set of all Turing machines can characterize, all at the same time [35], which means that the observer is forced to make an arbitrary choice of features of interest (see e.g. [39]).

We will test our algorithms on non-trivial cases against state-of-the-art algorithms, including sophisticated non-linear (spectral) methods involving simple graphs where statistical regularities are even easier to conceal and thus may easily fool weaker, linear and computable measures [39].

This approach opens a path towards evaluating the success of all other reduction techniques and for achieving optimal reduction based on the min-
imization of algorithmic information loss (thus the non-linear generalization of all techniques), rather than only preserving statistical or domain-specific algebraic properties. While the algorithms introduced are independent of approximating method and can be implemented using Entropy or lossless compression, here we use a method based on [40]. Our results indicate that we either match the results of the best current algorithms or, most of the time, outperform them for both local and global graph properties.

2 Preliminaries and Background

2.1 Cellular automata

A cellular automaton is a computer program that applies in parallel a global rule composed of local rules on a tape of cells with symbols (e.g. binary). Broadly speaking, it consists of a set of states, a neighbourhood template and a local rule $f$. Here we will use space-time diagrams of cellular automata to illustrate the way in which the MILS algorithm operates.

Thoroughly studied in [43], Elementary Cellular Automata (or ECA) are defined as one-dimensional cellular automata that take into consideration in their local rules the cell next to the centre cell and the centre cell. In the case of 1-dimensional CA it is common to introduce the radius of the neighbourhood template, which can be written as $\langle -r, -r+1, \ldots, r-1, r \rangle$ and has length $2r + 1$ cells. Given a radius $r$, the local rule is a function $f : \mathbb{Z}_{|S|}^{2(2r+1)} \rightarrow \mathbb{Z}_{|S|}$ with $\mathbb{Z}_{|S|}^{2(2r+1)}$ rules.

Elementary Cellular Automata (ECA) have a radius $r = 1$ (closest neighbours), having the neighbourhood template $\langle -1, 0, 1 \rangle$, meaning that the neighbourhood comprises a central cell. From this it follows that the rule space for ECA contains $2^{23} = 256$ rules.

Enumeration of ECA rules: It is common to follow the lexicographic ordering scheme introduced by Wolfram [43]. According to this encoding, the 256 ECA rules can be encoded by 8-bits.

A space-time diagram captures the evolution of a cellular automaton for a given initial condition and is read from the top starting from time step $t = 0$ (the initial condition) and evolving towards the bottom of the diagram (see Fig. 2.1).
Figure 1: A: Reduction and coarse-graining of two simple cases for illustration purposes of the space-time evolution of Elementary Cellular Automata rules 22 and 158 by minimization of algorithmic information loss. Depicted are steps after application of MILS, starting from the original (A) and second step (B), highlighting the regions that are earmarked to be omitted (in grey) versus the features that are kept along the way, thereby optimally preserving the main properties of these objects, properties whose persistence enables a ranking of such features. Unlike statistical approaches, the algorithm can also approximate (and thus preserve/extract) features that are of an algorithmic nature and which are not statistically apparent as it was in this case (see [40, 39]) and next examples.
2.2 Graph definitions and notation

Graphs (or networks) are mathematical structures that allow a simple representation of systems consisting of a set of agents and a set of interactions between them. Formally, we may define a graph as follows.

**Definition 2.1.** A graph is an ordered pair $G = (V, E)$ comprising a set $V(G)$ of vertices and a set $E(G)$ of edges, which are 2-element subsets of $V(G)$. For simplicity, we will often let $V = V(G)$ and $E = E(G)$.

A graph $H$ is contained in $G$, and we write $H \subseteq G$, if $V(H) \subseteq V(G)$ and $E(H) \subseteq E(G)$. In this case, we say $H$ is a subgraph of $G$. If either $V(H) \neq V(G)$ or $E(H) \neq E(G)$, we say $H$ is a proper subgraph of $G$, and we normally use $H \subset G$ to denote this situation. If on the other hand $V(H) = V(G)$ and $E(H) = E(G)$, we say the graphs $H$ and $G$ are equal.

We say that two vertices $v, w \in V$ are adjacent if there is an edge $e = \{v, w\}$ in $E$ that connects them, and call $v$ and $w$ the endpoints of such edge. A simple graph is a graph without loops (edges with a single endpoint) and multiple edges (edges with the same endpoints). A directed graph is a graph where the edges have a direction associated with them. In a directed graph, we represent edges by ordered pairs $(v, w)$, such that $v$ is the source vertex and $w$ is the target vertex of the edge. In this paper, we will normally refer to simple undirected graphs as just graphs.

The adjacency matrix $A = (a_{ij})$ of $G$ is a matrix that encodes all the adjacency relationships of the graph. The entries of this matrix are $a_{vw} = 1$ if vertices $v$ and $w$ are adjacent and $a_{vw} = 0$ otherwise. Note that while the adjacency matrix of an undirected graph is always symmetric, this is not necessarily true for a directed graph where adjacency can be asymmetric. The list of eigenvalues of the graph’s adjacency matrix sorted from largest to smallest is known as the spectrum of the graph.

The degree $d(v)$ of $v$ is the number of vertices to which $v$ is connected, that is $d(v) = \sum_{w \in V} a_{vw}$. The degree matrix $D = (d_{ij})$ of $G$ is a diagonal matrix that contains information about the degree of each vertex, and is defined by $d_{ij} = d(i)$ if $i = j$ and $d_{ij} = 0$ otherwise. We are now in the position to introduce the notion of graph Laplacian, which will be of interest for us in forthcoming sections. Consider the following definition.

**Definition 2.2.** Let $G$ be a simple graph on $n$ vertices. The Laplacian matrix (of order $n$) of the graph $G$ is defined as $L = D - A$, where $D$ is the degree matrix and $A$ is the adjacency matrix of $G$.

Throughout the text, and trusting that it does not lead to confusion, we will use the terms nodes and vertices, and links and edges, interchangeably.
2.3 Classical Information Theory and Shannon Entropy

Central to information theory is the concept of Shannon’s information entropy, which quantifies the average number of bits needed to store or communicate the statistical description of an object. Shannon’s entropy determines that one cannot store an object with \( n \) different components in less than \( \log(n) \) bits, and also a lower limit below which no object can be further compressed, not even in principle. We define it as follows.

**Definition 2.3.** Let \( X = (R, p) \) be an ensemble, where \( R \) is the set of all possible outcomes (the random variable), \( n = |R| \) and \( p(x_i) \) is the probability of an outcome \( x_i \in R \). The Shannon entropy of \( X \) is given by

\[
H(X) = - \sum_{i=1}^{n} p(x_i) \log_2 p(x_i).
\]

(1)

It is clear from this definition that in order to calculate \( H(X) \) one has to know or assume the probability mass function of ensemble \( X \).

While entropy can be used as a measure of the information contained in a graph (or another object), we will restrict our analyses to the Block Decomposition Method, which we describe in Section 2.6.

2.4 Graph information content

The algorithmic information content \( C(G) \) of a graph \( G \) (also known as its complexity) is given by the so-called algorithmic coding theorem \([19, 12, 29]\), which establishes that:

\[
C(G) = - \log_2 AP(G),
\]

(2)

where \( AP(G) \) is the Algorithmic Probability of the adjacency matrix of \( G \) defined by the output frequency probability of being produced by a random 2-dimensional Turing machine (a typical deterministic Turing machine whose single head can move up and down as well as left and right) starting from an empty 2-dimensional grid (instead of the typical 1-dimensional tape Turing machine) as defined in \([33]\).

A Turing machine is a general abstraction of a computer program, similar to cellular automata but sequential, that given an input, produces an output and halts. The Turing machine is thus an algorithmic mechanistic causal explanation of the output and is at the centre of the algorithms introduced here. The idea is to find a short Turing machine that explains an object (e.g. a network) by explaining smaller overlapping segments of the object \([34, 37]\).
2.5 Element information value/contribution

All methods are based on the information difference among the elements of an object, or in other words, on the information contribution of the elements of a system to the whole, e.g. of nodes or links to a network. This is based on a concept of algorithmic/causal perturbation analysis as introduced in [33, 37, 38]. The procedure consists in the perturbation of all elements of a system by the removal of elements whose effects on its algorithmic information content are measured and ranked accordingly.

Formally, let $G$ be a graph with edges $e_1, \ldots, e_{|E(G)|}$, $G \setminus e_i$ denote the graph obtained by removing $e_i$ from $G$, and $I(G, e_i)$ denote the information difference or information value/contribution of $e_i$ to $G$ given by

$$I(G, e_i) = C(G) - C(G \setminus e_i),$$

where $C(G)$ is the algorithmic information content of graph $G$ as defined in [33] (see Methods). This difference can also be referred to the graph’s nodes, but here we will restrict our attention to the edges.

When taking the difference $C(G) - C(G \setminus e_i)$ by itself we will refer to it as the graph (dis)similarity between graph $G$ and $G \setminus e_i$. $I$ applied to graphs suggests a similarity distance between graphs based on algorithmic information content (in [36], we show that this similarity measure can classify networks by the family they belong to, differentiating variant synthetic and natural network topologies similar to graph motifs, as shown in [24]).

In the description of the algorithm that follows, replacing the underlying methods to approximate the (algorithmic) information content by, e.g., Shannon entropy or lossless compression algorithms represents special cases of the more general algorithm based on algorithmic complexity, and thus it covers all these less powerful cases. The idea of a dynamic study/calculus of the (possible) changes that can be wrought upon an object to evaluate the contribution of each of its components for different purposes was introduced in [38], and here we extend these ideas to the area of data/network dimension reduction.
2.6 Graph complexity

The concept of algorithmic probability (also known as Levin’s semi-measure) yields a method for approximating Kolmogorov complexity related to the frequency of patterns in the adjacency matrix of a network, including therefore the number of subgraphs in a network. The algorithmic probability \[30, 19, 8\] of a subgraph \(H \subseteq G\) is a measure that describes the probability that a random computer program \(p\) will produce \(H\) when run on a 2-dimensional tape universal (prefix-free\(^1\)) Turing machine \(U\). That is, 
\[
m(G) = \sum_{p:U(p)=H \subseteq G} 1/2^{|p|}.
\]

An example of a popular 2-dimensional tape Turing machine is Langton’s ant \[18\], commonly referred to as a Turmite.

The probability semi-measure \(m(G)\) is related to Kolmogorov complexity \(C(G)\) in that \(m(G) \geq 2^{-C(G)}\), given that the shortest program carries the greatest weight in the sum. The algorithmic Coding Theorem \[12\] further establishes the connection between \(m(G)\) and \(C(G)\) as \([19]\): 
\[
|−\log_2 m(G) − C(G)| < c
\]
(Eq. 2), where \(c\) is some fixed constant, independent of \(s\). The theorem implies that \[12\] one can estimate the Kolmogorov complexity of a graph from the frequency of production from running random programs by simply rewriting Eq. (2) as: 
\[
C(G) = −\log_2 m(G) + O(1).
\]

In \[13\] a technique was advanced for approximating \(m(G)\), and hence \(C(G)\), by means of a function that considers all Turing machines of increasing size (by number of states). Indeed, for small values of \(n\) states and \(k\) colours (usually 2 colours only), \(D(n, k)\) is computable for values of the Busy Beaver problem \[27\] that are known, providing a means to numerically approximate the Kolmogorov complexity of small graphs, such as network motifs. The Coding theorem then establishes that graphs produced with lower frequency by random computer programs have higher Kolmogorov complexity, and vice versa. Here we will use the Block Decomposition Method (BDM) as an estimator of algorithmic complexity, but the algorithm and methods introduced are independent of the particular method used to approximate algorithmic complexity.

The BDM consists in decomposing the adjacency matrix of a graph into subgraphs of sizes for which complexity values have been estimated, then reconstructing an approximation of the Kolmogorov complexity of the graph by adding the complexity of the individual pieces according to the rules of information theory, as follows:

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\(^1\) The group of valid programs forms a prefix-free set (no element is a prefix of any other, a property necessary to keep \(0 < m(G) < 1\)).
\[ C(G) = \sum_{(r_u, n_u) \in \text{Adj}(G)_{d \times d}} \log_2(n_u) + C(r_u) \] (3)

where \( \text{Adj}(G)_{d \times d} \) represents the set with elements \((r_u, n_u)\), obtained when decomposing the adjacency matrix of \( G \) into all subgraphs of size \( d \) contained in \( G \). In each \((r_u, n_u)\) pair, \( r_u \) is one such submatrix of the adjacency matrix and \( n_u \) its multiplicity (number of occurrences). As can be seen from the formula, repeated subgraphs only contribute to the complexity value with the subgraph BDM complexity value once plus a logarithmic term as a function of the number of occurrences. This is because the information content of subgraphs is only sub-additive, as one would expect from the growth of their description lengths. Applications of \( m(G) \) and \( C(G) \) have been explored in \([13, 29, 28, 34]\), and include applications to graph theory and complex networks \([33]\) and \([34]\), where the technique was first introduced.

The only parameters used in the application of BDM are the use of strings up to 12 bits for strings and 4 bits for arrays given the current best CTM approximations \([29]\) and the suggestions in \([40]\) based on an empirical distribution based on all Turing machines with up to 5 states, and with no string/array overlapping in the decomposition for maximum efficiency (as it runs in linear time), and for which the error (due to boundary conditions) has been shown to be bounded \([40]\).

2.7 Minimal Information Loss Sparsification (MILS)

MILS is an unsupervised and mostly parameter-free algorithm, i.e. asymptotically independent of model or domain, as it does not need to be instructed or designed to preserve any particular property, and maximizes the preservation of all computable elements that contribute to the algorithmic information content of the data.

Let \( G \) be a graph and \( k \) denote its number of edges. MILS seeks to reduce \( G \) to a graph on \( N < k \) edges so that the loss of information is minimized after each step of the algorithm. It does this by calculating the difference \( G \setminus S \) and then finding the subset \( F \subset E \) such that \( I(G, F) \leq I(G, S) \) for all non-empty proper subsets of edges \( S \subset E \), repeating this task with \( G = G \setminus F \) until the target size is reached (when \(|E(G)| = N\)). The algorithm’s time complexity is clearly in \( O(\exp) \) because of how MILS performs searches and deletions across all subsets of edges, but significant improvements to this bound are still possible.
A more efficient but suboptimal version of MILS iterates over single elements (nodes or edges) or singletons. Algorithm 1 performs sequential deletions of edges, and then removes the edge that contributes less to the information content of the graph before moving to the next step.

Algorithm 1 MILS with sequential perturbation by deletion on edges

1: function Perturb\((G)\)
2: \(\text{informationLoss} \leftarrow \emptyset\)
3: \(\text{for } e \in E(G) \text{ do}\)
4: \(\text{// store information contribution into informationLoss}\)
5: \(\text{informationLoss} \leftarrow \text{informationLoss} \cup \{I(G,e)\}\)
6: \(\text{// calculate minimal information loss across all edges}\)
7: \(\text{minLoss} \leftarrow \min(\text{informationLoss})\)
8: \(\text{for } e \in E(G) \text{ do}\)
9: \(\text{// if } e \text{ is a neutral edge}\)
10: \(\text{if } I(G,e) = \text{minLoss then}\)
11: \(\text{// remove } e\)
12: \(\text{return } G \setminus e\)

9: function Sparsify\((G, N), 1 \leq N \leq |E(G)|\)
10: \(\text{// until reaching target size}\)
11: \(\text{while } |E(G)| > N \text{ do}\)
12: \(\text{// perturb edges in } G\)
13: \(G \leftarrow \text{Perturb}(G)\)
14: \(\text{return } G\)

When \(e\) is such that \(I(G,e) = \text{minLoss}\), we call it a neutral information edge because it is the edge that contributes less to the information content of \(G\) (in particular, it minimizes information loss or the introduction of spurious information into the network according to the information difference when removed from the original network). The above pseudocode assumes that there is a unique such \(e\), which may not necessarily be the case. Algorithm 2 solves this problem by performing simultaneous perturbations on all edges with an information contribution of \(\text{minLoss}\), which can be done in time \(O(k^2)\) in the worst case for a graph on \(k\) edges. In the Results section we show that MILS is deterministic, and describe a criterion to select and remove the most neutral elements of an object. We use this more efficient version in all our experiments, and even in this limited form the procedure excels at preserving important characteristics of the networks under study.
Algorithm 2 Minimal Information Loss Sparsification (MILS)

1: function InfoRank($G$)
2:    $\text{informationLoss} \leftarrow \emptyset$
3:    // for each edge $e_i$
4:    for $e_i \in E(G)$ do
5:        // store information contribution into informationLoss
6:            $\text{informationLoss} \leftarrow \text{informationLoss} \cup \{I(G,e_i)\}$
7:    sort informationLoss in increasing order
8:    // return information rank
9:    return informationLoss

10: function MILS($G,N$), $1 \leq N \leq |E(G)|$
11: while $|E(G)| > N$ do
12:    // calculate minimal loss across all edges
13:        $\text{minLoss} \leftarrow \min(\text{InfoRank}(G))$
14:    // remove all candidate edges from $G$
15:        $G \leftarrow G \setminus \{e_i \in E(G) : I(G,e_i) = \text{minLoss}\}$
16: return $G$

In Algorithm 2 we describe a function called InfoRank, which produces a ranking of $e_1,\ldots,e_{|E(G)|}$ from least informative to most informative edge, i.e. a list of edges sorted in increasing order by their information contribution to $G$. This ranking facilitates the search for the most neutral elements of the system (see Section 3.1), which in turn helps MILS preserve the components that maximize the information content of the resulting object. Note that the same algorithm may be applied, mutatis mutandis, to nodes or to any data element of an object or dataset, e.g. a pixel of an image, or a row or column in a spreadsheet.

MILS is, by design, optimal and universal in the computability and algorithmic-information theoretic sense, and only dependent on the method for approximating algorithmic complexity in the preservation of any possible feature of interest that contributes to the (algorithmic) information content of a network such as, evidently, its degree distribution and other graph-theoretic, algebraic or topological features, even those not necessarily captured by any graph theoretic measure or classical information approach [39].
3 Results

Fig. 1 demonstrates the basic concept behind MILS using as examples two cellular automata. The examples illustrate the way in which regions with high or low algorithmic content can be ranked, selected or preserved for dimensional reduction purposes. The method performs an unsupervised lossy compression able to preserve the main features (not covered in grey) of both cellular automata, with no intervention and no parameter choice. MILS proceeds by deleting the regions with lowest algorithmic information content contribution and maximizing the preservation of the features that contribute the most to the algorithmic description of the objects.

Furthermore, Figs. 2, 3 and 4, and Figs. 5, 6 and 7 in the Appendix demonstrate how MILS preserves essential local and global properties of synthetic and natural networks of different types and topologies, performing at least as well as but usually better than leading algorithms in graph sparsification. We took a sample of well-known and previously thoroughly studied networks from [24]. These included genetic regulatory networks, protein, power grid and social networks. We applied MILS to each of these networks and compared with two powerful sparsification methods: Transitive reduction [1] and Spectral sparsification [31]. A transitive reduction of a directed graph is therefore a graph with as few edges as possible that has the same reachability relation as the given graph. A good introduction to spectral graph sparsification may be found in [5]. The method was designed to reduce the network dimension based upon spectral similarity of graph Laplacians which guarantees the preservation of important properties of the graph by way of its adjacency matrix Laplacian spectrum.

Fig. 2 shows how MILS preserves the degree distribution and the edge betweenness distribution of a typical synthetically (recursively) generated Erdős-Rényi (ER) random graph (in this example of low edge density it is very sparse) compared with random edge deletion and spectral sparsification. While MILS is not significantly better at preserving the clustering coefficient of random networks, Fig. 3 shows that MILS does significantly better at preserving the clustering coefficient of real-world (biological, social and electric grid) networks taken from [24], outperforming both Transitive and Spectral reduction/sparsification methods. Figs. 5(SI), 6(SI) and 7(SI) illustrate how MILS outperforms spectral sparsification at preserving edge betweenness, and degree and eigenvector centralities.
3.1 Uniqueness and time complexity

In previous sections, we restricted our attention to graphs in order to describe the MILS algorithm, but MILS can actually be applied to any general object. Let $U$ be an object and $I(U, u_i)$ be the information contribution (or difference) of an element $u_i \in U$ to $U$, defined by $I(U, u_i) = C(U) - C(U \setminus u_i)$. If $u_i$ is a neutral element then by definition it does not contribute to the algorithmic information content of $U$, and so $I(U, u_i) = \log |U|$, which means that $u_i$ is part of the dynamical causal path of $U$ and $U$ can regenerate $u_i$ by its normal dynamical course. In general, however, if there is no element $u_i$ such that $I(U, u_i) = \log |U|$, the most neutral element in $U$ to be removed in the application of MILS is $I(U, u_i) = \min\{|C(U) - C(U \setminus u_i)| \sim \log |U|\}$, that is, the element with an information contribution closest to $\log |U|$.

For MILS to be well-defined, we need to guarantee that the deletion of an element (e.g. node or edge in a graph) produces a unique object in a deterministic fashion. The problem is when there are elements $u_i, u_j \in U$ such that $I(U, u_i) = I(U, u_j)$ and the algorithm cannot uniquely decide whether to remove $u_i$ or $u_j$ first, which potentially (and likely) leads to the production of different objects. The following algorithm tweak avoids this problem and shows that the algorithm is robust.

**Theorem 3.1.** MILS is a deterministic algorithm.

**Proof sketch.** Let $u_i$ and $u_j$ be two elements of an object $U$ (whose size is to be reduced by the application of MILS) with $I(U, u_i) = I(U, u_j)$, then MILS will remove $u_i$ and $u_j$ from $U$ simultaneously. This element deletion condition helps MILS to always produce the same output for a given input, which makes it a deterministic algorithm.  

This also produces a speedup, with the MILS time complexity for graphs, for example, now ranging between the original $O(|U|(|U| - 1)/2) \sim O(|U|^2)$ and constant time when all elements have the same information value and thus are to be deleted at the same time. For example, any attempt to reduce the dimension of the complete graph (either by, e.g., single-node or single-edge deletion) will produce an empty graph. A minor, and perhaps useful variation of the algorithm is an heuristic allowing a random selection of elements when they have the same information value.
4 Discussion

Because approximations to algorithmic complexity are lower semi-computable (computable from below), the algorithms introduced here inherit the same limitations and advantages. One limitation is that exact values are not finitely attainable in general, but among the advantages is the universality and asymptotic robustness of the approximating methods [13, 29]. The method followed here, called the BDM (standing for Block Decomposition Method) has been designed to produce results in linear time for a non-computable task (by exchanging computation time for memory, running the algorithm and reusing the results), and its accuracy can always be increased by increasing the computational effort (only once), converging at the limit to the actual values of the algorithmic complexity of an object, independent of the chosen representation language or reference programming language (per the so-called invariance theorem [23]). The algorithms are designed to maximize the preservation of information while deleting the information that contributes the least to the algorithmic content, thus allowing an unbiased non-user centric approach to algorithmic dimension reduction, that is, the reduction of the model explaining the data to a model explaining most/or the main features of the data.

The algorithm and methods introduced here are independent of the method used to approximate algorithmic complexity. We used a state-of-the-art method based on Algorithmic Probability as introduced previously [34, 13, 29, 40]. Our rationale is that checksum procedures and embedded decompression instructions popular in lossless compression algorithms such as LZW are not sufficiently sensitive to detect such minor changes [42] required in the kind of resolution needed for MILS to work. Furthermore, Shannon entropy has even greater limitations, as it is only constrained to detect trivial statistical regularities when no other updating procedure is available to properly calculate the likelihood and prior of the underlying ensemble [40].

5 Conclusions

We have demonstrated that MILS outperforms general and leading dimensionality reduction algorithms for networks and, interestingly, that MILS can be generalized to any data, as we have shown on space-time diagrams of discrete dynamical systems (cellular automata) that can also be seen as images, thus making the algorithms introduced here applicable to challenges of im-
age segmentation, the chief advantage being that MILS is optimal whenever optimal methods are used to approximate algorithmic complexity.

To test the algorithm we used a number of well-known networks commonly used in the literature to test algorithms, on which we also applied algorithms that have been reported to outperform previous algorithms.

The results provide evidence that MILS seems to outperform these algorithms on all indices at preserving all features of possible interest, which we define as all possible features that are recursively enumerable and therefore possible to characterize using a universal Turing machine, unlike measures that are computable and cannot, even in principle, achieve such a goal.

Our results are, in this sense, what is to be expected from the theory of algorithmic information. Moreover, they importantly demonstrate that numerical approximations to uncomputable measures are sufficiently accurate to outperform other current heuristic—even if computable—techniques for dimensionality reduction.

Other potential applications for this method are also conceivable. For example, to safeguard weak elements identified by this method, preserving the information structure of the network that may be targeted in an accident or in an attack. Or, alternatively, to design network attacks based on this algorithmic information calculus to maximize information loss by targeting the elements that hold the greatest information content in a network [41].

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Supplementary Information

5.1 Spectral sparsification

Generally speaking, the goal of network sparsification is to approximate a given graph $G$ by a sparse graph $H$ on the same set of vertices. If $H$ is close to $G$ in some appropriate metric, then $H$ can be used as a signature preserving important properties of $G$ for faster computation after reducing the size of $G$ and without introducing too much error. Obvious trivial sparsification methods include edge deletion by some criterion, such as the outermost ones (called the $k$-shell method [7, 16], often used to identify the core and the periphery of the network), but most of these methods (such as this shell one) are rather arbitrary or ad-hoc, rather than general methods aimed at preserving important algebraic, topological or dynamical properties of the original graph, all of which constitute and contribute to the information content of the graph, that is, the information necessary to fully describe a network and reconstruct the network from that description.

A popular sparsification algorithm is the spanning tree [15] designed to preserve node distance but clearly destroy all other local node properties, such as the clustering coefficient. Not many non-trivial methods for network sparsification exist today. Some clearly destroy local properties, such as the spanning tree algorithm, which destroys the clustering coefficient. It is acknowledged [31, 32, 5], however, that spectral graph sparsification is among the most efficient, both at preserving important algebraic and dynamical properties of a network and in terms of fast calculation. In part the dearth of methods is due to a lack of assessment tools to decide whether one method is better than another in general terms, rather than being designed to preserve one or another specific graph theoretic property (e.g. the transitive edge deletion method destroys the clustering coefficient of the original graph [1]). The spectral method considered in this paper is a high-quality algorithm described in [5, 31].

Transitive reduction was introduced in [1]. A graph $G$ is said to be transitive if, for every pair of vertices $u$ and $v$, not necessarily distinct, $(u, v) \in G$ whenever there is a directed path in $G$ from $u$ to $v$. That is, if there is a path from a vertex $x$ to a vertex $y$ in graph $G$, there must also be a path from $x$ to $y$ in the transitive reduction of $G$, and vice versa. If a given graph is a finite directed acyclic graph, its transitive reduction is unique, and is a subgraph of the given graph.

Graph sparsification is the approximation of an arbitrary graph by a sparse graph. Here we compare MILS against random, simple (e.g. span-
ning tree) and two powerful graph sparsification and reduction methods (spectral and transitive). Spectral graph sparsification is based on the spectral similarity of graph Laplacians. A spectral sparsifier is a subgraph of the original whose Laplacian quadratic form is approximately the same as that of the original graph on all real vector inputs. Spectral graph sparsification is a stronger notion than cut sparsifiers [32] and is considered one of the most, if not the most, sophisticated sparsification or network reduction method, as it is believed to preserve some of the most important algebraic, topological and potentially dynamical properties of a network.

5.2 Graph-theoretic measures

The global clustering coefficient of $G$ is the fraction of paths of length 2 in $g$ that are closed over all paths of length two in $G$. The mean or average clustering coefficient is the mean over all local clustering coefficients of vertices of $G$.

The betweenness centrality for a vertex $i$ in a connected graph is given by $\sum_{s,t \in V \setminus \{i\}} \frac{n_{i,s,t}^i}{n_{s,t}}$, where $n_{s,t}$ is the number of shortest paths from $s$ to $t$ and $n_{s,t}^i$ is the number of shortest paths from $s$ to $t$ passing through $i$. The ratio $\frac{n_{i,s,t}^i}{n_{s,t}}$ is taken to be zero when there is no path from $s$ to $t$.

Degree centrality is a measure of the centrality of a node in a network and is defined as the number of edges (including self-loops) that lead into or out of the node. The degree centrality of $G$ is the list of nonnegative integers (“degree centralities”) lying between 0 and $n - 1$ inclusive, where $n$ is the number of vertices of $G$, and identifies nodes in the network by their influence on other nodes in their immediate neighbourhood.

Eigenvector centrality is a list of normalized nonnegative numbers (“eigenvector centralities”, also known as Gould indices) that are particular centrality measures of the vertices of a graph. Eigenvector centrality is a measure of the centrality of a node in a network based on the weighted sum of centralities of its neighbours. It therefore identifies nodes in the network that are connected to many other well-connected nodes. For undirected graphs, the vector of eigenvector centralities $c$ satisfies the equation $c = 1/\lambda_1 a.c$, where $\lambda_1$ is the largest eigenvalue of the graph’s adjacency matrix $a$. 

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5.3 Figures

Figure 2: MILS or *neutral edge* deletion (blue) outperforms random edge deletion (red) at preserving both edge degree distribution (top, showing removed edges) and edge betweenness distribution (bottom) on an Erdős-Rényi random graph of node size 100 and low edge density (∼ 4%) after up to 60 edges were removed (degree distribution comparison) and 150 edges were removed (edge betweenness) out of a total of 200 edges (notice also the scale differences on the x-axis).
Figure 3: MILS mean clustering coefficient preservation against two other sophisticated graph sparsification methods based on graph spectral and transitive reduction techniques on biological, electric and social networks taken from [24]. The transitive method does not allow selection of edges to be deleted, and in some cases it either fails to significantly reduce the network size if no cycles are present (such as, generally, in electric and genetic networks) and/or takes the clustering coefficient to 0 (e.g., for protein networks) if cycles are only local. Comparisons with other methods are unnecessary because they destroy local or global properties by design, such as clustering coefficients for the spanning tree algorithm.
Figure 4: Histograms showing preservation of degree distribution from 20% to 80% edge removal. Green highlights the overlapping and the preserved area of the distributions after random deletion (top), MILS and spectral removal (bottom pairs).
Figure 5: Stacked histograms showing edge betweenness preservation of MILS versus spectral sparsification across different families of networks. The similarity in height of each segment is an indication of the preservation of such properties. Blue bars (MILS) approximate yellow (original) bars better than spectral sparsification. On average MILS was 1.5 times the edge betweenness distribution of these representative graphs measured by the area similarity of the respective bars.
Figure 6: Stacked histograms showing the preservation of degree centrality after application of MILS versus spectral sparsification across different families of networks: bars with height closest to the original graph signify better preservation. Blue bars (MILS) approximate yellow (original) bars compared with spectral sparsification. MILS only slightly outperformed spectral sparsification in this test but never did worse.
Figure 7: Stacked histograms showing eigenvector centrality preservation of MILS versus spectral sparsification across the different families of networks: bars with height closest to the graph’s original bar signify better edge betweenness distribution preservation. Blue bars (MILS) approximate yellow (original) bars better than spectral sparsification both in distribution shape and individual bar height. On average MILS preserved the eigenvectorcentrality distribution of these representative networks 1.5 times better.