Abstract

Both science and engineering rely on the use of high-level descriptions. These go under various names, including “macrostates,” “coarse-grainings,” and “effective theories”. The ideal gas is a high-level description of a large collection of point particles, just as a set of interacting firms is a high-level description of individuals participating in an economy and just as a cell a high-level description of a set of biochemical interactions. Typically, these descriptions are constructed in an \emph{ad hoc} manner, without an explicit understanding of their purpose. Here, we formalize and quantify that purpose as a combination of the need to accurately predict observables of interest, and to do so efficiently and with bounded computational resources. This State Space Compression framework makes it possible to solve for the optimal high-level description of a given dynamical system, rather than relying on human intuition alone.

In this preliminary report, we present our framework, show its application to a diverse set of examples in Computer Science, Biology, Physics and Networks, and develop some of technical machinery for evaluating accuracy and computation costs in a variety of systems.
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1 Introduction

Historically, scientists have defined the “level”, “scale”, or “macrostate” of a system in a purely informal manner, based on insight and intuition. For example, we usually construct descriptions of a biological system by neglecting the complexity of the subunits: in doing organismal biology, we describe a cell in terms of its organelles, or an organism in terms of its cells; in doing ecology we talk in terms of species, neglecting within-species diversity, or even in terms of trophic levels, ignoring the differences between predators, when we describe the biosphere as a whole. In economics we often define the macrostates of the world’s socioeconomic system in terms of its firms, its industrial sectors, or even nation-states, and neglect the internal structure of these highly complex entities. Similar examples arise in physics, where we define the macrostates of a fine-grained system by reference to thermodynamic variables, such as temperature or pressure, that characterize its most relevant features.

How do we know that these choices for the macrostates are the best ones? Might there be alternatives? Are there even alternatives that are superior to our choices? A superior choice might, for example, allow greater accuracy in our prediction of the evolution of the system, and/or reduce the computational cost of making such predictions. Given the possibility that superior choice might exist, can we solve for the optimal macroscopic state space with which to analyze a system?

This is the general problem of state space compression, and the problem is general indeed. Many of the observables of interest that are theoretically and experimentally analyzed in the sciences are considered interesting precisely because they make good macrostates: their use leads to lowered computation and measurement cost while balancing the need for accuracy in predicting a given observable of interest.

To address these issues, we consider the question of how to quantify the quality of a proposed map $x_t \rightarrow y_t$ that we wish to use to compress a dynamically evolving “fine-grained” variable $x_t$ into a dynamically evolving “coarse-grained” variable $y_t$. To decide what makes for a good compression of the dynamics of a system, we should not try to formalize the intuitive notion of a “macrostate” as scientists often do.

\[^{1}\text{Here we will use the term “coarse-graining” interchangeably with “compression”, and so will allow arbitrary coarse-graining maps. There is a large literature that instead interprets the term “coarse-graining” to refer to the special case where $x$ is the spatial position of a set of $N$ particles and we wish to map each $x$ to the spatial position of $m < N$ “effective particles”. See [71] for a review. There is also work that interprets the term “coarse-graining” to refer to the special case where $x$ is a network structure, and we wish to map each $x$ to a smaller network (see [41][16]). For discussion of the general problem of coarse-graining for computational, cognitive, and social systems see [25].}^{1}\]
have used that term in the past. We are, rather, utilitarian: state space compression has a practical benefit, and quantifying that benefit drives our analysis.

Given such a definition and a fine-grained variable \( x_t \), we can try to solve for the best map compressing \( x_t \) into a higher-scale macrostate \( y_t \). The dynamics of such an optimally chosen compression of a system can be viewed as defining its emergent properties. Indeed, we may be able to iterate this process, producing a hierarchy of scales and associated emergent properties, by compressing the macrostate \( y \) to a yet higher-scale macrostate \( y' \).

2 State space compression

2.1 The benefit of state space compression

Here we adopt the view that the benefit of a State Space Compression (SSC) \( X \rightarrow Y \) is to reduce the cost of computing the dynamics over \( X \). Our job as scientists is to find a compression map \( X \rightarrow Y \), dynamical laws for evolution over \( Y \), and a map from \( Y \) to the observable of interest. The idea is that there is a dynamical process over \( Y \) that is far easier to compute than the dynamics over \( X \) and/or that acquiring a measurement of the state of \( Y \) is cheaper than doing so for \( X \), and yet which provides accurate predictions of what we want to know concerning future values in \( X \). Stated prosaically, we wish to simulate the dynamics of \( x_t \), using a simulation that optimally trades off its computation and measurement cost with its accuracy in predicting some observable of interest concerning future values of \( x \).

Note that we will usually not be interested in predicting any given microstate \( x \) in toto. Rather, there are certain observables associated with \( x \) that we are interested in reconstructing. An illustration of this, based on Ex. 1 in Sec. 4, is where we are not interested in predicting where each individual bird in a flock is at some future time, but rather are just interested in where the center of mass of the birds is, along with the axes of an optimal ellipsoid fit to the distribution of the birds in the flock about that center of mass.

So for the purposes of this paper, a state-space compression \( X \rightarrow Y \) is beneficial if

1. Our choice of the dynamics over \( Y \) is far easier to calculate than the dynamics over \( X \). Often, but not always, this will imply that \( |Y| \) is significantly smaller than \( |X| \); and

2. The observables of \( x_t \) that we are interested in at a future time \( t \) can be accurately estimated from the corresponding values \( y_t \in Y \).

From the perspective of coding theory, we are compressing a system’s fine-grained state down to an element in a (usually) smaller space, evolving that compressed
state, and then using it to predict the observables of interest concerning the future fine-grained state.

In many cases, maps \( x \to y \) that are good compressions of a dynamical system in the sense just outlined often have the property that the dynamics of \( y_t \) is (first-order) Markovian. (Indeed, as mentioned below, obeying exactly Markovian dynamics is a core component of the definition of a “valid compression” considered in [77, 33, 32, 43].) Even if the best compression is not Markovian, so long as we are considering a good compression of \( x_t \) into \( y_t \), once we set the initial value of \( y \) we can well-approximate the future values of \( y_t \) with a Markovian process, with little further information needed from later \( x_t \) to correct that dynamics. (As discussed below, this is the desideratum defining “good compression” considered in [40, 39, 63].) For these reasons, we often restrict attention to compressed spaces whose associated dynamics are Markovian.

In many scenarios the issue is how closely the predicted observable of interest is to the correct value. In these cases it makes sense to use metric over the possible values of the observable to quantify the accuracy. There are other cases where it makes sense to use information theoretic concepts such as mutual information, conditional entropy, or Kullback-Leibler divergence—as happens, for example, when there is no clear metric over the space of observables.

We will be concerned with the prediction of the entire future evolution of a system, rather than just of its value at a single particular moment in the future. This reflects the fact that often we will not be interested in just one specific future moment that we know ahead of time. Typically we will be interested in future behavior, which is an inherently multi-timestep phenomenon. Finally, as a formal concern, it is by requiring that the compression / decompression accurately reconstructs the time-series as a whole that we ensure that it is capturing the dynamics of the system.

Compressing the state space of a system to reduce computation and measurement cost while maintaining predictive accuracy is not only a core concern in science and engineering. It is also a guiding principle in how the human nervous system operates. Computation is very costly for a biological brain, in terms of heat generated that needs to be dissipated, calories consumed, etc. Moreover, at an abstract level, the (fitness-function mediated) purpose of one’s senses and the resultant computation by the brain is for those senses to compress the state of the environment into a form that is then processed by the brain to produce accurate predictions of certain fitness-relevant observables concerning the future state of the environment [20, 48, 74]. So in “designing” the human brain, natural selection is faced with the precise problem of optimal state space compression as we have formulated it. This suggests that we may be able to construct powerful heuristics for optimal SSC by considering how the human nervous system processes information.
There are also human-constructed artifacts that reflect the tradeoffs considered in SSC, and for which SSC might be useful for future engineering endeavors. One such example occurs in CPU design and the problem of branch prediction. In modern CPUs, whenever a conditional “if-then-else” statement is encountered, the CPU first guesses—based on certain heuristics and its record of previous branches—which branch of the conditional to take, and starts speculatively computing as though that branch were taken; if it later discovers that it guessed wrong, it terminates the speculative computation and continues on the correct, having incurred a delay for guessing incorrectly and having to replace the speculative computation by the correct one.

We see here the tradeoff between accuracy and computation cost: it only makes sense to do branch prediction if there is a computationally efficient predictor that is correct most of the time. In any other case, branch prediction would end up wasting more CPU cycles than it saves. Branch prediction is enormously successful in practice, partially because, based on the prior distribution of how most people (or compilers) write and use conditional statements, relatively simple heuristics that are easy to compute give (almost shockingly) accurate results. Interestingly, some of the currently best branch predictors are in fact based on (very) simple models of neurons, as suggested in the discussion above (see, e.g., [44]).

### 2.2 Basic concepts and notation

Throughout this paper we adopt the convention that upper case variables indicate either a space or a random variable defined over that space, with the context making the meaning clear; lower case variables indicate elements of a space or values taken by a random variable, again with the context making the meaning clear. We also adopt the convention of letting the context make clear whether we are talking about a probability distribution or a probability density function, the associated meanings of conditional distributions, and other standard conventions from probability and statistics.

In addition, the measures of the integrals we will write will all be implicitly matched to the associated space. So when we use the integral symbol for a countable space, we are implicitly using the counting measure, turning that integral into a sum.

Formalizing the issues discussed in Sec. 2.1 leads to the following definitions. The first four are specified exogenously by the problem being studied:

1. The microstate \( x \in X \), which evolves in time according to a (usually) Markovian process \( P(x, \ldots) \), which in particular specifies a prior distribution over the value of \( x \) at a current time \( t_0 \);
2. A space of possible values of an **observable** $\Omega$, and an associated observation conditional distribution $O(\omega \in \Omega \mid x)$, which may be deterministic.\(^2\)

3. A (typically) real-valued **accuracy function** $C : \Omega \times \Omega \rightarrow \mathbb{R}$—typically a metric—that we use to quantify how good a predicted value is from the true observable;

4. A **weight function** $W(t)$ used to weight the relative importance of predictions for the observable at all moments in the future.

The remaining three objects are chosen by the scientist, possibly, as we suggest here, by SSC optimization:

5. A **macrospace** or **compressed space** $Y$, with elements $y$, called **macrostates**, that evolve according to a (usually) Markovian stochastic process $\phi_{t,0}(y_t \mid y_0)$;

6. A **compression** distribution, $\pi(y \mid x)$, which compresses $x$ to $y$ (and may be a deterministic function);

7. A **prediction** distribution $\rho(\omega \in \Omega \mid y)$ which gives the prediction for the observable based on ("produced by decompressing") the compressed state $y$.

Typically we will require that $\phi$ and $P$ be time-homogenous. We will sometimes refer to the compression distribution as an “encoding” distribution, and refer to the prediction distribution as a “decoding” distribution. We will typically apply the metric $C$ on the observable space to compare the distribution $\rho(\omega \mid y_i)$ with the distribution $O(\omega \mid x_t)$.

As an example of a microstate process, it could be a time-homogenous Markov chain with generator $p$ that is set by Nature. However its marginal distribution at time 0, $P(x_0)$, is set by the scientist (albeit implicitly): it is the *a priori* probability that she will want to predict the future of a system whose initial condition is $x_0$. In this case the full Markovian process is given by

$$P(x_0, x_1, \ldots) = P(x_0)\prod_{t=1}^{\infty}p(x_t \mid x_{t-1}) \tag{1}$$

In many situations we will be exogenously provided a space $\Omega \neq X$ and associated observation distribution $O$. However an important special case is where

\(^2\)In addition to allowing stochastic dynamics, whenever it was natural to use a function $f : A \rightarrow B$ between two spaces, we instead allow the more general setting of a conditional distribution $d_f(b \mid a)$. With the exception of the stochastic dynamics, whenever we allow this level of generality, little intuition is lost by instead considering a deterministic function $f$ between the two spaces, although the more general setting may be useful in particular applications.
we are not provided those, or for some other reason wish to take $\Omega = X$ and $\mathcal{O}$ to be the identity function (i.e., a delta function). In such cases, $\rho$ is a map from the simulation’s value at time $t$, $y_t$, to a prediction for $x_t$, the true value that $X$ has at time $t$.

Typically accuracy costs are non-negative, and equal zero whenever their arguments are identical. They are also often symmetric in their arguments. A very common example of an accuracy function $C(\omega, \omega')$, occurring when $\Omega \subseteq \mathbb{R}^n$ for some $n$, is quadratic loss or Euclidean distance, $|\omega - \omega'|^2$. If instead $\Omega$ is a countably space of abstract symbols, often accuracy cost will be the Kronecker delta function, $C(\omega, \omega') = \delta_{\omega, \omega'}$: 1 if $\omega = \omega'$ and 0 otherwise.

Three terms will contribute to our overall state compression objective function. The first is the average future value of the accuracy function, evaluated under $W(t)$. We call this the accuracy cost. The second term is the average future computation cost of iterating both $\phi$ and $\rho$.

The third term is the cost of evaluating $\pi$ once—or otherwise performing a measurement, e.g., of the physical world—to initialize $y$. Although for simplicity we include this in the computation cost, in general it is just a quantification of mapping an initial $x$ to an initial $y$. This may have nothing to do with “computation”, per se. For example, it may reflect a process of physically measuring an initial value $x$, with a noisy observation apparatus producing a value $z \in Z$ according to a distribution $P(z \mid x)$, where the observed initial value $z$ is then mapped to the starting value of our simulation via a distribution $P(y_0 \mid z)$ that we set. In this case $\pi(y \mid x) = \int dz \ P(y_0 \mid z)P(z \mid x)$, where $P(z \mid x)$ might be more accurately described as a “measurement cost”. Whenever we write “computation cost,” it should be understood in this more general manner.

Unless specified otherwise, we take the weight function $W(t)$ to be a probability distribution over $t$. A particularly important type of $W(t)$ is a simple future geometric discounting function, $W(t) \propto [1 - \gamma]^t$. In particular, this is often appropriate when there is a priori uncertainty on how far into the future the scientist will end up running the computation. As alternatives, we could consider the (undiscounted) average accuracy cost and average computation cost over some temporal window $t \in [0, T]$. Another alternative, for computations known to halt, is to consider the average of those two costs from $t = 0$ to the (dynamically determined) halting time. Formally, this means extending the definition of $W$ to be a function of both $t$ and $y_t$.

We, the scientists, are provided the original stochastic process $P(x_{t'} \mid x_t)$. The observable $\mathcal{O}$ and weight function $W(t)$ capture what aspects of the system we are

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3 Also see the literature on decision theory, where geometric discounting with a constant $\gamma$ is justified as necessary to maintain consistency across time in how a decision-maker makes a decision, and especially the literature on reinforcement learning and dynamic programming [86].
interested in. Our task (should we choose to accept it) is to choose the compression function $\pi$, associated space $Y$, compressed state dynamics $\phi$ and prediction map $\rho$ to the space of observables, such that the encoding $\pi$, stochastic dynamics $\phi$, and decoding $\rho$ are relatively simply to calculate, compared to calculating the dynamics of $x$, directly, while the resultant accuracy costs are minimal (e.g., while the resultant predictions for $\hat{y}(t')$ for $t' > t$ are minimal distortions of the true values). The best such tuple $\{\pi, Y, \phi, \rho\}$ is the one that best trades off the cost of implementing $\pi$ and the (average) cost of calculating the dynamics of $y$, on the one hand with the (average) quality of the reconstructed time series on the other. In essence, a good state compression is like a good encoding of a video movie, producing a compact file that is simple to decode, and from which we can recover the characteristics of the original movie that the human user is attuned to, with high accuracy.

2.3 Roadmap

In Sec. 3 we present high-level illustrations of our notation. Then in Sec. 4 we work through three examples of applying SSC in detail.

Having seen SSC in action, we then discuss (Sec. 5) how SSC relates to previous work in the literature. We begin that discussion with a focus on work that is relatively abstract and formal, being driven by information-theoretic considerations, but without specifically considering the overall goal of SSC, of reducing computation cost while preserving predictive accuracy.

We then discuss work, primarily from the applied sciences and engineering communities, that directly considers that goal. In contrast to the work we present here though, these particular work has been on a case-by-case basis, using highly problem-specific analyses, and without a concern for the broader goal of grounding much of science as a whole in SSC.

After comparing SSC to related work, we then return to its technical development, presenting the broadly applicable, fully formal SSC framework. To do this we must provide the full SSC objective function, the goal of SSC being to find compressions that minimize that objective function. We begin in Sec. 6 where we show how one can quantify accuracy cost (i.e., negative reconstruction accuracy), both for the case of an exogenously provided accuracy function and for the case when there is no such function, so that it makes sense to use an information-theoretic accuracy cost. Then in Sec. 7 we discuss various ways to formalize computation cost. After that, in Sec. 8 we illustrate one way to combine accuracy cost and computation/measurement cost into an overall objective function.

We expect that the particular costs we present below will be appropriate in a broad range of scenarios. However we emphasize that—in keeping with the underlying motivation of SSC as a formalization of real-world computational
problems—there is no right or “wrong” way to quantify these costs. The problem at hand should determine how they are quantified.

Next in Sec. 9 we show how SSC provides a natural way to quantify some notion of “complexity.” In that section we also show it provides a way to quantify information flow among different-scale representations of the same system. We emphasize that we do not try to claim that these measures based on SSC are in some sense the correct ways to quantify those quantities. Rather, we show how these measures have attributes that match up well with informal notions of complexity and information flow. Prior formalizations of those concepts have often been motivated purely by intuitive notions (see [53] for a summary of just a few of the prominent formalizations of complexity). By contrast, measures based on SSC are not formalizations of intuition, but rather are directly motivated by precisely defined concerns fundamental to the scientific enterprise. We conclude, briefly, in Sec. 10.

SSC is a framework, and its use requires that we make explicit choices for things such as the accuracy and the computation costs. Rather than provide discipline-independent prescriptions, we emphasize that the problem at hand should always determine the choices adopted for the various terms arising in the SSC framework. We view this as an advantage of using SSC to analyze any given scientific problem—by construction, the SSC analysis will be formulated in a way that is tightly coupled to that scientific problem.

3 Illustrations of our notation

In this section we present several high-level illustrations, to help clarify the meaning of our notation, and to give the beginnings of an idea of how SSC coupled be applied in various settings.

Example 1. Consider a flock of N labelled birds exhibiting coordinated flight [14, 2, 21]. The mass of each bird is fixed. The microstate of the flock, x, is the phase space position of the flock, i.e., the positions and velocities of all N birds; in particular, the space of microstates is then $X = (\mathbb{R}^3)^2N$. The stochastic dynamics $P(x_t \mid x_0)$ of the microstate is given by some bird-level rule governing how each bird’s acceleration is determined by its current position and velocity as well as the positions and velocities of the other birds in the flock. For the purposes of this example, we are assuming that higher-order derivatives of the positions of the birds—e.g., their accelerations—are not relevant if we know the positions and velocities of all the birds. Say we are interested in predicting the center of mass of the flock at all future times; thus our observable space $\Omega$ will be $\mathbb{R}^3$, corresponding to the center of mass, and the observation conditional distribution
\( \mathcal{O}(\omega \mid x) \) is a deterministic function \( \mathcal{O} : \mathbb{R}^{6N} \rightarrow \mathbb{R}^3 \) giving the center of mass. We take as our accuracy cost \( C : \Omega \times \Omega \rightarrow \mathbb{R} \) the Euclidean distance between two points in \( \Omega = \mathbb{R}^3 \).

One way to successfully predict the position of the center of mass is to evolve the stochastic dynamics of the microstate. This may be computationally challenging for \( N \) large, however, since \( X = \mathbb{R}^{6N} \). As an alternative, a successful state space compression of the microstate dynamics would be a map from the high-dimensional vector \( x \) to some other much smaller-dimensional vector of “sufficient statistics”, \( y \), such that we can easily and accurately compute the evolution of \( y \) into the future and at each future moment \( t \) recover the center of mass of the flock from \( y_t \). As an example, it may be that due to the details of the microstate dynamics, a macrostate \( y \) comprising the \( \mathbb{R}^3 \times \mathbb{R}^3 \times (\mathbb{R}^3)^3 = \mathbb{R}^{15} \) vector

\( \{ \text{Position of the center of mass of the flock; Momentum of the entire flock; Components of a Gaussian ellipsoid fit to the shape of the flock} \} \),

...can be easily and accurately evolved forward in time, without concern for any other information in \( x \) not reflected in those fifteen real numbers. Since one component of this particular \( y \) is precisely the quantity we are interested in (the position of the center of mass of the flock), the recovery of what we are interested in from \( y_t \)—i.e., the prediction map \( \rho : Y \rightarrow \Omega \)—is simply a projection. Since (by hypothesis) the evolution of \( y \) is accurate, this is a good state compression, with a small combined value of the computation cost of the dynamics of \( Y \) and the Euclidean error of the prediction of the center of mass.

**Example 2.** Consider an agent-based simulation of the behavior of \( N \) humans in a set of interacting firms in an economy evolving in real time, where each player has time-varying observational data concerning the history of the entire economy and a (time-varying) set of endowments. The microstate \( x \) at each moment is the set of associated observation vectors and endowment sets of each of the \( N \) players. Let the dynamics of the system be a set of stochastic rules for each of the players saying what move it makes at each moment as a function of its current observation vector and endowment set.

Say that what we are interested in is the total GDP of the economy specified in \( x \), and in particular with how that GDP depends on some exogenous parameter of the system that an external regulator can set. Then we take the space of observables \( \Omega \) to be \( \mathbb{R}_{\geq 0} \), representing the total GDP, and the observation map \( \mathcal{O}(x) \) to be the total GDP of the economy specified by \( x \). We take the accuracy function \( C : \Omega \times \Omega \rightarrow \mathbb{R} \) to be the absolute value of the difference between the simulated and actual GDP. Even if we posit a precise microscopic stochastic dynamics \( x_t \), and therefore how GDP depends on the exogenous parameter, it may be
very challenging to calculate the GDP for any particular value of the exogenous parameter.

On the other hand, depending on the details of the microscopic rules for how the agents behave, it may be that we can coarse-grain \( X \) into a compressed space \( Y \) that specifies only the current state of each of the firms—not any individuals within the firms, or non-firm individuals—and that we can both evolve \( y \in Y \) accurately and then infer the GDP at each time \( t \) very accurately knowing only \( y_t \). In this case the coarse-graining of the economy into characteristics of the firms in the economy is a good compression of the state space of the economy.

However it may be that this state compression does not work well, giving large expected error for the prediction of future GDP. It may be that some other state compression, e.g., that couples the states of players from multiple firms at once, results in better predictions. In this example, if we could find that better compression, it would provide major insight into what drives the evolution of the economy. Working with often highly restricted classes of \( \pi \)'s and \( \phi \)'s this is the aggregation problem of economics [19, 36].

**Example 3.** Consider a cylinder of fixed dimensions with a moveable partition separating it into two half-partitions, with an ideal gas on each side of the partition. Let \( z \) be the position of the partition. Our microspace \( X \) will thus be the space of configurations of the particles in each of the ideal gases, together with the position \( z \) of the partition. Assume that at some time \( t_0 \) the partition has a pre-fixed value of \( z \), and there is a pre-fixed temperature and pressure of the two ideal gases, with higher values of both in the ideal gas lying above the partition, at higher values of \( z \). Assume that at that time \( t_1 \) the partition starts sliding towards smaller values of \( z \) at a very slow (essentially adiabatic) constant and pre-fixed rate, stopping when the system reaches equilibrium. Suppose, however that we do not know \( t_1 \); it is instead distributed according to a Gaussian distribution centered about some particular time. Let the observable of interest be the temperatures and pressures of the two ideal gases; the observable space \( \Omega \) is thus \( \mathbb{R}^4 \geq 0 \) (with the temperatures in Kelvin). We take our accuracy function \( C: \mathbb{R}^4 \times \mathbb{R}^4 \rightarrow \mathbb{R} \) to be Euclidean distance, for simplicity.

Consider the compressed space \( Y \) which consists only of the position \( z \) of the partition. In this case, given the current value \( y_0 \), we can perfectly predict the future values \( y_{t'} \) with \( t' > t \), i.e., the future positions of the partition, since we know the rate of movement of the partition. In turn, because we know the dimensions of the cylinder and the initial temperatures and pressures of the two ideal gases, we can calculate the temperatures and pressures of the two gases from knowledge of the position of the partition. That is, the prediction map \( \rho: Y \rightarrow \Omega \) computes the pressures and temperatures of the two ideal gases based solely on the position of the partition. (The “knowledge” of the initial values of the temperatures and
pressures are built in to the map $\rho$, but $\rho$ itself is just a function of $z$, since that is all that is present in the compressed space $Y$.) So in this case, the compression map $\pi : x \rightarrow y = z$ is perfect, in that it allows perfect prediction of the future states of the observables that we are interested in.

4 Examples of SSC

We now work through several detailed applications of SSC.

The first example presents an abstract analysis of SSC, showing how to optimize both the compression map and associated dynamics over the compressed space, in the setting of arbitrary first-order Markovian dynamics over finite state spaces, formulated in terms of Markov chains and finite automata. In this work we impose several natural restrictions on the types of compression $\pi$, dynamics $P$, and dynamics $\phi$, and solve for the optimal choices of $\pi$ and $\phi$ that satisfy those restrictions.

The remaining examples also concern first-order Markovian dynamics over $X$. However they are concretely motivated, by scenarios from two different scientific disciplines. The focus is not on solving for the optimal compression and dynamics, but on illustrating how SSC provides insight into those scientific scenarios.

The second example address a core problem in the biological sciences: the origin of multicellularity. This worked-out example illustrates how SSC may be used to decide between a finite list of candidate compressions that might otherwise be based on hunches or scientific insights.

The third example analyses the principled coarse-graining of complex networks. While prior research on the renormalization of networks has described how the statistical properties of static networks vary under coarse-graining, SSC allows us to study the dynamical properties of a network, and provides a framework within which to address the utility of coarse-graining for prediction and control.

These three examples illustrate how the underlying concerns of SSC apply to many different scientific fields, and provide a clear roadmap for the use of these concepts to generate novel approaches to long-standing problems.

4.1 Example 1: finite state spaces, Markov chains, and automata

We take as our first detailed example systems in which the microspace $X$ is finite, and its dynamics are Markovian, i.e., $X$ is a finite Markov chain.

In this section, we only do the analysis for the deterministic case, but we believe our results provide some intuition for the general case, and that our analysis
can be extended to the general case of Markov chains, which we hope to do in a later version of this report. Because we are able to analyze it completely in closed form, we begin with the case of a deterministic Markov chain, in which all transition probabilities are either 0 or 1. Already from this case we will be able to see how the choice of prior distribution $P(x_0)$, the choice of weight function $W(t)$, and the choice of accuracy and computation cost can affect the optimal state space compression.

Although a deterministic Markov chain is the same thing as a deterministic finite automaton over a one-letter alphabet, here we are concerned with the dynamics of the automaton, rather than its ability to solve certain computational problems. As such, unlike the typical setup of finite automata, we will not care about any particular start state (beyond that specified by the prior distribution $P(x_0)$) nor about any accepting/rejecting/halting states. Nonetheless, it may be that taking a dynamical viewpoint on computational processes could yield insights lower bounds in computational complexity, which we hope to explore in future work. Although much is known about finite automata, a slight generalization of multi-letter Markov chains (i.e., probabilistic finite automata) yields quantum finite automata, about which there are many open questions.

Since here we aren’t applying this to any particular domain of inquiry, we pick some generic definitions for the space of compressions we consider, the accuracy cost, and the computation/measurement cost, and we consider essentially arbitrary observable functions. The choices we make are in no way inherent to SSC, but merely meant to illustrate the SSC framework in a particular setting.

### 4.1.1 Observables and accuracy cost

For simplicity, we only consider observable functions $\mathcal{O}: X \rightarrow \Omega$ (rather than conditional distributions $\mathcal{O}(\omega|x)$). We will allow $\Omega$ to be any finite space, and $\mathcal{O}$ to be any function $X \rightarrow \Omega$. We take our accuracy cost to be simply whether or not the observable is correct; equivalently, we take our cost function $C: \Omega \times \Omega \rightarrow \mathbb{R}$ to be the equality function $C(\omega, \omega) = 1$ and $C(\omega, \omega') = 0$ for all $\omega' \neq \omega$. (In a domain-specific application, one could imagine the observable function associates real values to states $x \in X$, and then consider Euclidean distance, but, again, in the absence of domain-specific information we stick with the equality function for simplicity.) Given these definitions, the observables we are considering are essentially just partitions of the states of $X$: the observable function simply identifies which part of the partition a given state is in.
4.1.2 Which compressions to consider

Even when the microspace $X$ is finite, there are in general infinitely many possible compressions one could consider—for example, deterministic dynamics that depends on many previous states, deterministic dynamics that depends on an unbounded number of previous states, or probabilistic variants of these. If we restrict attention to macrodynamics given by a Markov chain, there are still infinitely many possibilities, but they form a finite-dimensional topological space. However, even if we loosen the restriction a little, to Markovian but not necessarily of any fixed order—that is, the current state can depend on $k$ previous states, but $k$ may be any finite number—the space of possibilities becomes a countably-infinite-dimensional topological space. It is possible that one could perform optimization over such spaces, but for illustrative purposes we restrict ourselves here to much simpler spaces. We consider either (1) the macrodynamics is itself given by a deterministic first-order Markov chain, or (2) the macrodynamics is given by a first-order Markov chain (that need not be deterministic).

For both of these cases, as mentioned above we restrict attention to the case in which the compression map $\pi$ is unrestricted, and we separately consider the case in which $\pi$ is a so-called quotient map, a standard concept \[37\] defined as follows:

**Definition 1.** A map $\pi: X \to Y$ between two deterministic Markov chains with transition functions $f_X: X \to X$ and $f_Y: Y \to Y$, respectively, is a quotient map or homomorphism if $f_Y(\pi(x)) = \pi(f_X(x))$ for all $x \in X$.

That is, a quotient map between two deterministic Markov chains is one in which it doesn’t matter whether you first advance the state of the source chain and then apply the map, or first apply the map and then advance the state in the target chain.

For maps whose target and/or source are general Markov chains, there are several possibilities for the definition of a quotient map. We adopt one natural such possibility here.

**Definition 2.** A map $\pi: X \to Y$ between two Markov chains with transition matrices $p_X$ and $p_Y$, respectively, is a quotient map or homomorphism if $p_Y(y|y') = \frac{1}{\|x',\pi(x')=y'\|} \sum_{x: \pi(x)=y} \sum_{x': \pi(x')=y'} p_X(x|x')$.

That is, in a quotient, various subsets of $X$ are “clumped together,” with the probability between two “clumps” being proportional to the sum of the probabilities from each element of the source “clump” to each element of the target “clump.” Under this definition, a map $\pi$ is a quotient map whenever the prior $P_X(x')$ is uniform. However for other priors, this may not be the case. This distinguishes it from the issue of whether the Markov chain over $y$ is a “lumpable”
version of the one over $x$. [90]. (There are many other related approaches to analyzing compression of Markov chains. See [3, 80, 19, 36, 33, 32, 43, 28, 27] for just a small sample of these other approaches.)

Note that given a Markov chain on finite space $X$, and a finite set $Y$, any onto function $\pi: X \to Y$ can be made a quotient map by assigning transition probabilities to $Y$ as in the preceding definition. In SSC, we get to pick (or are optimizing over) the choice of $Y, \pi$, and the dynamics of $Y$; this says that although quotient maps are restricted, they still encompass a wide array of possible compressions. (In the case of deterministic quotient maps this is much less true: for example, the only deterministic quotients of a cycle of length $n$ are cycles whose lengths evenly divide $n$. In the deterministic setting quotient maps are analogous to group homomorphisms.)

4.1.3 Classifying deterministic Markov chains and their homomorphisms

Here we consider a system $X$ with finitely many states and with a deterministic transition function $x_{t+1} = f(x_t)$. As it will be useful in the following analysis, we begin by recalling a complete description of all such deterministic finite-state systems. Since $X$ is finite, the trajectory $x_t$, starting at any state, must eventually end in a cycle (where we count a fixed point as a cycle of length 1). We can then partition the states of $X$ according to which cycle they eventually end up in; we call each part of this partition a “connected component” of $X$. Each state thus follows an initial path into its corresponding cycle, and then gets stuck in the cycle. Consider two states that eventually end up in the same cycle; their paths may merge before reaching the cycle. Thus, in general, the transition diagram consists of a collection of disjoint cycles, and each cycle may have some directed trees feeding into it at various points.

Note that the only deterministic Markov chains that are reversible—in the sense that every state has a unique previous state—are those whose transition diagrams consist only of (disjoint unions of) cycles. In particular, any finite-state model of a time-reversible physics system must consist only of cycles.

(We note that all that changes if we allow $X$ to be infinite is that some of the “cycles” may become infinitely long—that is, an infinitely long directed path—and that the trees hanging off the cycles may also be infinite. If we define a generalized cycle to be either a finite cycle or an infinitely long path, then the description in terms of possibly infinite trees feeding into generalized cycles remains valid. Having infinite paths would also affect the analysis below, but we leave that for future work.)

As mentioned above, it is not hard to show that that the only quotient maps from a deterministic Markov chain whose transition diagram is a cycle of length $n$ are the cycles whose length evenly divides $n$. This says what a quotient map
must look like on the limit cycles of the deterministic Markov chain. For the trees that feed into the limit cycles, the quotient map can be much more complicated, e.g., by identifying together various branches of the tree. In thinking about this, note that the definition only requires equality to be preserved, but not necessarily inequality: for example, suppose $X = \{0, 1, 2\}$ with transition function $f(0) = f(1) = 2$ and $f(2) = 2$, so that 2 is a limit cycle (in this case, a fixed point). Any homomorphism $\pi$ from $X$ to any other deterministic Markov chain $Y$ must send 0 and 1 to two states of $Y$ such that $f_Y(\pi(0)) = f_Y(\pi(1))$. (And furthermore, $\pi(0)$ must be a fixed point of $Y$, by what we said above about cycles.) However, although $0 \neq 1$ are distinct states of $X$, $\pi$ may map them to the same state of $Y$. This gives some idea of how a homomorphism may map the trees feeding into a limit cycle.

Note that if the transition diagram of $X$ is disconnected, then two distinct limit cycles of $X$ may get mapped onto the same limit cycle of $Y$. However, when the transition diagram of $X$ is connected, if we only consider $\pi$ that are quotient maps, then without loss of generality we need only consider $Y$ whose transition diagrams are also connected.

4.1.4 Computation and measurement cost

Here we consider computation time as our primary measure of computation and measurement cost. For deterministic Markov chains, we argue that the computation time is proportional to some small power (e.g., 1 or 2) of the logarithm of the number of states, based on computation time in most standard models of computation such as Turing machines or random access machines. In contrast, for general Markov chains, the issue of how to measure computation time becomes thornier, as there is a question (at least) of how accurately we compute the probabilities involved.

Consider computing the transition function for a deterministic Markov chain. That is, given the current state $x$, compute the next state $f(x)$. In all cases, the states of the Markov chain are identified by, say, binary strings, which we may interpret as integers if we so desire. In the case that the transition diagram consists of just a single cycle, we may consider the $n$ states as labeled by the numbers $0, 1, \ldots, n-1$ in order (which state is labeled 0 may be chosen arbitrarily), and then the transition function is just $k \mapsto (k + 1) \mod n$.

One simple approach to quantifying computation cost is to assume that in each clock cycle of the computer exactly one bit in the binary string can be updated, and then count the total number of clock cycles. When computing the “add 1” function modulo $n$ in binary, although certain transitions involve very few bits—for example, if $k$ is even and $k < n-1$, then adding 1 modulo $n$ simply involves changing the low-order bit from a 0 to a 1—on average over all the transitions,
$\Omega(\log n)$ bits must be touched, giving an average-case lower bound of $\Omega(\log n)$. (If we wanted, we could compute the constant in front of the $\log_2 n$ exactly, or we could even consider one transition at a time rather than the average, but for the results we get here this would be a needless complication. In a real application such delicate calculations might be more warranted.) Moreover, adding $1$ modulo $n$ may be performed in $O(\log n)$ steps in any standard computational model. Thus, when the transition diagram is a single cycle, the computation time can be nailed down pretty exactly to $\Omega(\log n)$.

Even in a more complicated case, we can always compute the transition function by table lookup, since there are only finitely many states. Table lookup can easily be performed in $O(\log^2 n)$ steps (or $O(\log n)$ steps in a word RAM of word size $\Theta(\log n)$). In a real application, nailing this down more exactly might be worthwhile, but for our general illustrative purposes here, we simply take the computation cost of the dynamics of an $n$-state deterministic Markov chain to be $c \log_2 n$ for some constant $c$ that will depend on $\phi$ and leave it at that.

These general results can also be motivated by considerations of thermodynamic cost associated with any physical implementation of the computer. As above, assume that $Y$ is represented as a string of $\log n$ bits. Then in each timestep of the computation update each bit $b_i$ using $\log n$ physically isolated physical systems to do so. Assume that for each of the two possible new values of each bit $b_i$, there is a non-zero probability (formed by averaging over the entire computation) of both values for the preceding state of $b_i$. Therefore to guarantee that the bit is updated correctly, there is a Landauer entropic erasure cost of $kT \log 2 \log n$, where $T$ is the temperature of the system [50, 13]. (Note though the crucial nature that the computer be thermodynamically decomposable into $\log n$ subsystems — since the entire computation over all $Y$ is one-to-one, we can construct a physical device that will implement that computation with zero entropy being generated [9, 10].)

The computation and measurement cost should, in general, also take into account the cost of evaluating the compression map $\pi$. Here again we consider table look-up, as this is not far from the average-case optimum. If the macrospace has $m$ states and the microspace has $n$ states, then we get a cost of $O(\log n \log m)$.

We discuss the computation time for general Markov chains in Section 4.1.7.

### 4.1.5 The weight function

We consider two different weight functions. One is the time-discounted weight function $w(t) = (1 - \gamma)^t$ discussed in Section 2.2 above. The other—particular to the case of finite state systems—is the average error over all time. Because the system is eventually periodic, the average error over all time essentially amounts to the average error that occurs once the system has reached its limit cycle, which
is then a finite sum over one period of the limit cycle.

4.1.6 Deterministic Markov chains / one-letter finite automata

Here we give the complete analysis for deterministic Markov chains. We begin with the simplest interesting case and then gradually add back in complications. In particular, we start with the case in which the observable is just the microstate itself: $\Omega = X$ and $\Theta = \text{id}_X$.

**Average error over all time.** First we consider the average error over all time, or equivalently, a weight function $W(t) = 1$ for all $t$. More formally, we consider the limit $\lim_{T \to \infty} \frac{1}{T} \sum_{t=0}^{T} \text{accuracy cost at time } t$; this only works in this setting because all trajectories eventually end up in finite limit cycles, so the limit actually exists. Moreover, any transient behavior—before the system has reached a limit cycle—contributes 0 to this limit. Thus we are reduced to considering only the limit cycles, which simplifies the analysis considerably. Nonetheless, even this seemingly simple case exhibits a number of phenomena of the State Space Compression framework.

As discussed above, in the case of cycles, the computation cost of a $n$-cycle is some constant multiple of $\log_2 n$, which we abbreviate as $\log n$ (without specifying the base). Since the compression map $\pi$ is computed only once, the computation cost of $\pi$ also does not contribute anything to the limiting value of the time-averaged computation cost.

We begin our analysis with the case in which the microdynamics is connected, i.e., consists of a single $n$-cycle. Since only limit cycles contribute to the average over all time, we may assume without loss of generality that the macrodynamics also consists of a single $m$-cycle, for some $m \leq n$. Choose an arbitrary microstate and label it 0; the microstates will be labeled by 0, ..., $n - 1$ in the obvious manner, so that the microdynamics is given by adding 1 modulo $n$. Let 0 also denote the macrostate which is the unique image of the microstate 0 under $\pi$; the macrostates are labeled 0, ..., $m - 1$ and the macrodynamics is given by adding 1 modulo $m$. Every $\text{LCM}(n, m)$ time steps—where LCM denotes the Least Common Multiple—the pair (microstate, macrostate) evolves through all the values it will ever take. Since the dynamics are cyclical, given $n$ and $m$ it is easy to see that the optimal choice of compression map always maps the first $m$ states consecutively: 0 maps to 0, 1 maps to 1, ..., $m - 1$ maps to $m - 1$. It is clear that no $\rho$ can do better than to map the macrostate $k$ to the microstate $k$ as well. Although such maps need not be homomorphisms, since they can map the states $m, m + 1, \ldots, n - 1$ arbitrarily, how those latter states are mapped has no effect on any of the costs, so we may as well choose to map $m$ to 0, $m + 1$ to 1, and so on. When $m$ divides $n$, this is a homomorphism.

Thus, given $n$ and $m$, out of every $\text{LCM}(n, m)$-length cycle of the (microstate,
macrostate) pair, only \( m \) time steps are predicted correctly. Thus the accuracy cost is

\[
\frac{\text{LCM}(n, m) - m}{\text{LCM}(n, m)} = 1 - \frac{\text{GCD}(n, m)}{n},
\]

where GCD denotes the Greatest Common Divisor; recall that \( \text{LCM}(n, m) = \frac{nm}{\text{GCD}(n, m)} \). This cost is minimized when \( \text{GCD}(n, m) \) is maximized. Given that \( \text{GCD}(n, m) \leq m \leq n \), the GCD is maximized when \( \text{GCD}(n, m) = m \), i.e. when \( m \) divides \( n \), and when \( m \) is as large as possible. Thus, if we ignore computation cost, the maximum accuracy cost is achieved by not compressing at all, as expected. If we use the heuristic that we will only consider \( m \leq M \) for some threshold \( M \), then we find a more interesting behavior: the accuracy cost is maximized by choosing the largest \( m \leq M \) such that \( m \) divides \( n \).

Now consider what happens when we also take into account the computation cost. In this case, we are trying to minimize the SSC objective function (see Sec. 8 for the general formulation):

\[
\alpha \left( 1 - \frac{\text{GCD}(n, m)}{n} \right) + \kappa \log m,
\]

where \( \alpha \) and \( \kappa \) represent the relative weights we place on the accuracy and computation costs, respectively. Since rescaling the objective function does not change its minimizer, there is really only one relevant parameter here, namely the ratio between \( \alpha \) and \( \kappa \); however, giving two independent parameters allows for the possibility of either of them being zero, without having to worry about dividing by it.

**Lemma 1.** The objective function is always minimized by a homomorphism.

**Proof.** Write \( m = m_n m' \) where \( m_n = \text{GCD}(n, m) \). As a function of these two variables, the objective function is \( \alpha (1 - m_n/n) + \kappa (\log m_n + \log m') \). For any given \( m_n \), the objective function is clearly minimized by minimizing \( m' \), that is, by taking \( m' = 1 \), or equivalently by choosing \( m \) to divide \( n \). By the argument above, for any given \( m_n \), the objective function is thus minimized by a homomorphism. \( \square \)

Thus we may assume that \( m \) divides \( n \), and for such \( m \) the objective function is \( \alpha (1 - m/n) + \kappa \log m \). Taking the derivative with respect to \( m \), we get \(-\alpha/n + \kappa/m\); taking the derivative again we get \(-\kappa/m^2\). Thus whenever computation cost is considered—i.e., \( \kappa > 0 \)—the second derivative is negative and the minimum can only be achieved at the extreme values \( m = 1 \) or \( m = n \). Which of these values wins is a simple comparison of the objective function at the points. To summarize: when the microdynamics consists of a single cycle and the observable is the microstate:
• The accuracy cost alone is minimized by not compressing at all. If we force compression by requiring the microdynamics to have at most $M$ states, the accuracy cost is minimized by choosing the largest $m \leq M$ that divides $n$ evenly.

• When computation cost is sufficiently prioritized, namely when $\alpha/\kappa < \frac{n}{n-1} \log n$ (or maybe it would be better to say: when accuracy cost is not too prioritized), then compressing down to the trivial one-state (fixed) macrodynamics is optimal. Otherwise, again not compressing at all is optimal.

4.1.7 Towards general Markov chain compressions of deterministic Markov chains

In this section we begin to contemplate if there is anything to be gained by considering probabilistic compressions of deterministic Markov chains—that is, where the dynamics of the compressed space are governed by a (not necessarily deterministic) Markov chain. In order to do this in the SSC framework, we have to specify both the accuracy cost and computation cost in this probabilistic setting.

Considering these issues leads to an important distinction. When considering a finite Markov chain with transition probabilities $\phi(i \mid j)$ from state $j$ to state $i$, we have (at least) two choices. One choice is to consider the state space as the usual finite space, say $\{1, \ldots, n\}$, with probabilistic transitions. The other choice is to consider state space compression over the space of probability distributions over $\{1, \ldots, n\} \in \mathbb{R}^n$ with deterministic time evolution given by multiplying a probability distribution—represented as a vector—by the transition matrix. Since we integrate over possible trajectories in computing the accuracy cost (see Sec. [6] for the general formalization), these two representations of the same system should have the same accuracy costs. However, their computation costs may differ.

In a system with stochastic evolution over a finite state space, the computation cost is not much different than in the deterministic case. That is, even in the worst case, we can imagine a lookup table which now tells us all possible next states together with the probability distributions over the next state, given the current state. There are then several standard ways of “rolling a die” to decide which state to proceed to next. In actual computer implementations, these “dice rolls” are typically performed by pseudorandom generators, rather than using “true” randomness (such as that from thermal noise in the CPU), which could potentially increase the computation cost. The amount by which it is increased is presumably related to the largest denominator needed to accurately describe

\[\text{\footnotesize With the possible exception of information-theoretic costs, as in Sec. [7.3] where the use of true randomness can in fact lower the computation cost, as the computation is essentially taking heat from the environment in order to proceed randomly.}\]
the probabilities involved (here we assume the probabilities are rational numbers; irrational numbers introduce further complications into the evaluation of the computation cost, which we begin to discuss below). We thus take as our measure of computation cost $O(\log^2 n + \sum_{i,j} \log d_{ij})$ where $d_{ij}$ is the denominator of the transition probability $\phi(i \mid j)$. We alter the computation cost of the compression map $\pi$ similarly.

In contrast, consider $Y$ to be the space of probability distributions over a finite set $\{1, \ldots, n\}$ (note that here $Y$ is infinitely larger than the original space $X$, yet we can nonetheless reasonably consider $Y$ as a compression of $X$). In actuality, there are several possibilities to consider here, for example: (a) we could work with exact probability distributions whose probabilities are real numbers, and consider a model of computation with real arithmetic operations at unit cost (e.g., [17]), b) we could work with exact probability distributions over the rationals, in which case we may need to take into account the bit-length of the rational numbers involved, or c) we could work with approximate probability distributions over approximate reals (e.g., floating-point arithmetic), in which case we will have to take into account issues of numerical accuracy—which can affect the prediction accuracy—in addition to other considerations.

4.2 Example 2: a simple model of multi-cellular organisms

In this section, in addition to showing an illustrative example applying SSC to biology, we illustrate how SSC can be used to select between different proposed compressions.

Evolution occurs at many different scales. DNA is replicated within organelles like the nucleus and mitochondria, mitochondria reproduce within cells, cells can reproduce inside or outside of multicellular organisms, and multicellular organisms can reproduce as whole entities. These scales are typically referred to as “levels of selection” and indicate that evolutionary forces act within nested levels or hierarchies.

To determine how entities within such hierarchies evolve, evolutionary computations typically choose a scale based on heuristic or historical reasons. Often the scale is implied in the observable of interest itself. For example, if one wanted to understand the co-evolution of a predator and prey in a simple two species system, it may make more sense to work at the scale of species rather than say cells within an individual. However, as the complex dynamics of parasites within foodwebs makes clear, this may not always be the case. Here, we consider an example of a multicellular organism with a simple developmental program composed of three cell types (Fig 1).

We want to understand the dynamics of these cell types

\[\text{This is in fact a simple but nontrivial example of a branching process \cite{1, 47}; we defer}\]
over time. While, the observable of interest is the number of cells of each type, the state space compressions we consider will operate above the cellular level.

Figure 1: A model of a simple developmental program with germ/soma distinction in a multicellular organism. The microstate dynamics keep track of each individual group organism and the number of A, B, and C cells it contains.

4.2.1 The microstate dynamics: a developmental program

The microstate dynamics follow a population of multicellular organisms each adhering to a four stage developmental program (see Fig. 1). Each multicellular organism begins as a single A cell, the germ line. The first time A divides, it produces a B cell (a somatic cell). The next round of cell division results in two additional B cells. At this point, the organism prepares for reproduction of the multicellular organism. In the subsequent round of cell division, the A cell produces another A cell while all B cells produce C cells (also somatic cells). Finally, in the last stage of the life cycle the organism releases two A cell propagules and all B and C cells within the body die. The released A cells begin the life cycle again as new, independent multicellular organisms (which just happen to consist of single cells at this early point of development).

Although the order of the stages of the developmental program is fixed, there is some probability of when each stage is realized. To simplify the simulations we

discussion of this connection in future work.
impose a discretization of time. At each time step, there is a fixed probability $q$ that the organism transitions to the next stage of the life cycle. Alternatively with a probability $1 - q$ the organism may remain at the same life cycle stage. In addition, we also implement death in the model such that multicellular organisms (and all cells contained within) can die at any stage of the life cycle with probability $p$. Thus, if the organism proceeds directly through the life cycle without any pauses (probability $q^4$) then there is a probability of $(1 - p)^4$ that it doesn’t die before reproducing.

Simulating the microstate dynamics requires keeping track of the cells and the groups they belong to as well as what stage of the life cycle each group is in. Our observable of interest is the number of A, B, and C cells in the population at any given time.

We consider a few possible compressions and use the SSC objective function (as formalized in Sec. 8) to compare them. We expect this to be a common use case, as it will often be much easier to do this kind of analysis than fully optimizing the SSC objective function.

### 4.2.2 Compression via Life History Stages

One compression of this system that can be done is to focus on the four life history stages (see Fig 2). We can store the number of organisms in the population at each stage in the life cycle in a $4 \times 1$ vector $\mathbf{s}_t$, such that the first element of $\mathbf{s}_t$ is the number of groups in the population at the first stage of the life cycle at time $t$. We can then write a transition matrix $M$ for the mean population movement over one time step through these life history stages so that $\mathbf{s}_{t+1} = M \mathbf{s}_t$. In principle, this captures exactly the same data as the microstate itself. The difference is that in

\begin{figure}[h]
\centering
\includegraphics[width=0.5\textwidth]{figure2.png}
\caption{One possible state space compression tracks the number of entities at each stage of the life cycle.}
\end{figure}
this compression the space we consider is essentially the space of probability distributions over life stages (de-normalized to give raw population numbers instead of ratios), as compared to a list of all groups; see the discussion of deterministic evolution of probability distributions versus stochastic evolution of a microstate in Sec. 4.1.7.

\[
M = \begin{pmatrix}
(1 - q)(1 - p) & 0 & 0 & 2q(1 - p) \\
q(1 - p) & (1 - q)(1 - p) & 0 & 0 \\
0 & q(1 - p) & (1 - q)(1 - p) & 0 \\
0 & 0 & q(1 - p) & (1 - q)(1 - p)
\end{pmatrix}
\]

To recover the observable of interest, i.e., the number of A, B, and C cells at time \( t \) we simply multiply the vector \( s_t \) by a matrix \( K \) that converts the number of groups at life history stages into a vector of the number of A, B, and C cells at time \( t \) (call this vector \( \mathbf{k}_t \)). So to get the observable at time \( t + 1 \) given information from state \( t \) is simply: \( \mathbf{k}_{t+1} = KM\mathbf{s}_t \).

\[
K = \begin{pmatrix}
1 & 1 & 1 & 2 \\
0 & 1 & 3 & 3 \\
0 & 0 & 0 & 3
\end{pmatrix}
\]

### 4.2.3 Compression via Groups as Wholes

As an alternative to the first state compression we could go even further and ignore life history divisions but rather consider groups as identical entities with an average number of each cell type (see Fig 3).

![Figure 3: Another possible state space compression simply tracks the number of groups without regard to life history stages.](image)

In this case, we can fit a net growth parameter for the groups by taking the dominant eigenvalue of the matrix \( M \) from the life history compression; call it \( \lambda_M \). Although the matrix \( M \) is not stochastic—the sum of probabilities in its first row exceeds 1, reflecting the fact that the population can grow—the eigenvalues are easy to calculate symbolically as a function of \( p \) and \( q \), and there is nonetheless a unique largest real eigenvalue, namely \( \lambda_M = (1 + (2^{1/4} - 1)q)(1 - p) \).
The parameter $\lambda_M$ reports the average growth of the population of groups; note that if $q$ is sufficiently small (specifically, less than $\frac{p}{2^{1/4} - 1 + 1/p}$, see Figure 5), then $\lambda_M$ will be less than 1 and the population is expected to die out over time.

As there is a unique largest real eigenvalue with a one-dimensional eigenspace—in this case, the scalar multiples of the eigenvector $\vec{v} = (2^{3/4}, \sqrt{2}, 2^{1/4}, 1)^T$—in the long-time limit the populations of each life stage should become proportional to $\vec{v}$, from which we can then calculate the expected number of A, B, and C cells. For A cells, there is 1 cell in stage 1, 1 cell in stage 2, 1 cell in stage 3, and 2 cells in stage 4, so the expected number of A cells at time $t$ for large $t$ is then $A_0 \lambda_M^t \vec{v} \cdot (1, 1, 1, 2) \propto 6.285 \lambda_M^t$ (where $A_0$ is a scaling factor, including the initial population). Similarly, the expected number of B cells for large $t$ is $B_0 \lambda_M^t \vec{v} \cdot (0, 1, 3, 3) \propto 7.982 \lambda_M^t$ and the expected number of C cells is $C_0 \lambda_M^t \vec{v} \cdot (0, 0, 0, 3) \propto 3 \lambda_M^t$. If, as before, $\vec{k}_t$ is the vector of the predicted population of A, B, and C cells at time $t$, then $\vec{k}_t$ is proportional to $\lambda_M^t (6.285, 7.982, 3)$.

As an illustration, we consider what happens if instead of using the leading eigenvector, we simply consider the average number of A, B, and C cells within the groups across the life history stages (as though the leading eigenvector were $(1, 1, 1, 1)$). We refer to this as the naive group compression. This illustrates what happens with a prediction which we expect to be worse than the prediction above. The number of A cells averaged uniformly across life stages is $\frac{5}{4}$; similarly we get $\frac{7}{4}$ and $\frac{3}{4}$ for B and C cells, respectively. If as before $\vec{k}_t$ is the vector of the predicted population of A, B, and C cells at time $t$ then $\vec{k}_t = (\lambda_M^t)^{(\frac{5}{4}, \frac{7}{4}, \frac{3}{4})}$. In terms of the ratios, compare the $(5, 7, 3)$ ratio here to the $(6.285, 7.982, 3)$ ratio given by using the leading eigenvector. In the comparison below, we only consider the naive average as in this paragraph (and not the analysis based on the leading eigenvector).

### 4.2.4 Comparison of compressions

We compare the compressions over a range of $p$ and $q$ values, using 100 replicate simulations for each combination of $p$ and $q$. Each simulation of the microstate dynamics begins with 1000 groups randomly sampled (uniform distribution) from stages of the life cycle. We then develop the population over 30 time steps. At each time step we obtain an approximation from each compression and compare it to the microstate dynamics. We record the time it takes to generate each prediction as well as its Euclidean distance from the true numbers of A, B, and C cells. Figure 4 shows the log$_{10}$ ratio of computation costs (the computer clock time) for running the life history compression versus the group compression. The result is that the life history compression always takes longer to run in comparison with the group compression— as seen by the entire contour being nonnegative. The time
difference is largest for higher values of $q$ and low values of $p$, corresponding to the region of exponential growth (see Fig. 6).

Figure 4: The $\log_{10}$ ratio of computer clock time for the life history compression versus the group compression.

Similarly, we compare the $\log_{10}$ ratio of accuracy costs between the compressions over combinations of $p$ and $q$. Figure 5 shows the $\log_{10}$ ratio of summed Euclidean distances between approximated and true values of the observables for the life history compression versus the group compression. The result is that the life history compression does better than the group compression for most values of $p$ and $q$ (negative areas of the colormap, i.e. red to dark blues). Interestingly, one area that the group compression does better is intermediate $q$ values close to 0.2 (dark red area). In this area, the life history stages quickly mix so that the population is equally distributed across stages. This is the underlying assumption of the group compression and so it performs well. The life history compression, however, still computes a bias in the distribution of life history stages and so makes inaccurate approximations to the observable.

4.2.5 Conclusions

In this system, because there is a unique leading eigenvector, most predictions—suitably normalized—should in fact become more accurate at large time scales, as they approach a scalar multiple of the eigenvector. We expect this to be a general phenomenon that applies to any system with a unique, globally attractive
fixed point. (The only question is how quickly the fixed point is approached, as compared to which time values one is interested in, specified by the weight function $W(t)$.) In the comparisons done here, we only considered thirty time steps.

In this particular example, while the naive group compression always is faster than the life history compression, it often suffers in accuracy. By comparing Figs. 4 and 6 we see that the life history compression takes more time as one gets farther into the growth regime ($\lambda_M > 1$); in the entire non-growth regime ($\lambda_M < 1$) it appears that the life history compression takes about ten times as long as the group compression. Similarly, we see that the further into the growth regime, the more accurate the life history compression becomes compared to the naive growth compression.

The more “noise” there is in progressing between life history states, the better the group compression does in terms of accuracy (corresponding to $q$ values around .2). Higher values of $q$ make the life history stages progress with fewer fluctuations and potentially tilt the preferred compression in favor of a life history approach.
Figure 6: Parameter values in the shaded region are those for which the population grows on average (the largest real eigenvalue $\lambda_M$ is strictly greater than 1). For parameter values in the unshaded region ($p > \frac{(2^{1/4} - 1)q}{1 + (2^{1/4} - 1)q}$), the population shrinks exponentially on average. Compare these regions to those in Figs. 4 and 5.
4.3 Example 3: renormalization as state-space compression of dynamics on complex networks

A centerpiece of modern physics are “renormalization” arguments that allow us to understand how and when we may replace finer-grained theories with simpler, coarse-grained descriptions. In the physical sciences, renormalization explains why (for example) it is possible to build reliable accounts of the coarse-grained world of high-school physics while remaining agnostic about fundamental processes at finer-grained levels.

The use of physics to describe the structure and evolution of disordered networks, and the central role of such networks to the understanding of non-physics systems [61, 7, 26], ranging from the brain [62] and the genome [23, 34] up to large-scale human social systems [57, 42, 6] and ecosystems [67, 87], has spurred a great deal of attention to extending the practice of renormalization to these systems. State space compression provides a general framework within which to understand renormalization, and thus provides a path to connect core successes of 20th Century physics to contemporary mathematical problems in biology, cognition, and the social sciences.

A major stumbling point for these interdisciplinary applications has been the difficulty of knowing how to construct the coarse-grained compressed space. In the physics case, both intuition and basic assumptions of locality suggest that nearby points in spacetime should be “lumped” together by a process such as decimation or local averaging. These rely on there being no action at a distance, and on a fine-grained dynamics in which information not only cannot leap across long distances without passing through intermediate points, but tends to decay with distance from the source.

In the dynamics of non-physical systems however, action at a distance is not only possible but often mandatory: gene regulation occurs between distant locations on a chromosome, cabling in the brain makes connections between widely separated locations, and economic and social systems, particularly in the modern era, rely fundamentally on the long-range connections provided by electronic communication and modern transportation. “Distance” in these settings is thus better captured by a network of interactions than by physical distance. Because the geometry of these networks need not look like the standard geometry of physics, it is far from clear if the intuition of “lumping together” nearby points transfers from physics to these more exotic geometries, and if it does, how to implement it.

The networks that define these systems are generically described as “complex” and in this section we address the problem of dynamics on complex networks with arbitrary connectivity. By looking at the ways in which coarse-graining affects one’s ability to predict the future state of a system, SSC provides a new approach to the problem of renormalizing complex networks. Rather than lumping together
the topologically “nearby” features of the network [83, 30, 68], SSC relies on network dynamics to determine how well a candidate coarse-graining performs.

At the same time as it provides a new set of criteria for network renormalization, it also provides new insight into how underlying dynamical laws make compressed prediction easier or harder. In particular, below we argue that compression is most difficult—the best possible gain in the SSC objective function is small—in the intermediate regime between network order and disorder.

We consider a discrete-time complex network with nodes $\sigma_i$, with two indices—a “network location” index $i$, labeling the position in the network, and a time index $t$ labeling the time-step—where we remind the reader that these systems may live in spaces of far greater dimension, and far less homogeneity, than the Euclidean or metric spaces of the physical world.

We can then define a space-time action for a configuration $\sigma$,

$$S[\sigma] = \frac{\sum_{i,j,t} J_{ij} H_{tt'} \sigma_i \sigma_j}{Z(J,H)},$$

where $J_{ij}$ defines a (time-independent) connectivity, $H_{tt'}$ the influence between time-steps, and $Z(J,H)$ is the normalization constant; the probability of a particular microstate $\sigma$ is then

$$P[\sigma] = \exp S[\sigma].$$

We assume a standard statistical physics setting—the canonical ensemble—extended over all times as well as locations, so that the Boltzmann distribution gives the full matrix of (probabilities) across all states and times, $\sigma$. If we set $H_{tt'}$ equal to $\delta_{t+1,t}$, then the equilibrium distribution factors:

$$P(\sigma) = e^{S[\sigma]} \propto \exp \sum_{ij} J_{ij} \sigma_i \sigma_j \times \exp \sum_{ij} J_{ij} \sigma_i \sigma_j \times \ldots$$

$$\times \exp \sum_{ij} J_{ij} \sigma_i \sigma_j \times \ldots.$$  

Fig. [7] illustrates how for this $H_{t,t'}$ the connectivity of a complex network defined by the connectivity $J_{ij}$ “unrolls” into a space-time action that defines both a stationary distribution and the stochastic process we consider here. Expanding a single-moment projection of a configuration $\sigma$ as a list $\{\eta_1, \ldots, \eta_i, \ldots\}$ of the states $\eta_i$ of each node $i$, for our $H_{t,t'}$ we have a Markovian dynamical law,

$$P(\eta'|\eta) = \frac{\exp \sum_{ij} J_{ij} \eta_i \eta'_j}{Z(J)},$$

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For studying dynamics of networks—rather than on them—one can allow $J_{ij}$ as well as $\sigma$ to be dynamical features of the system.
Figure 7: From space to space-time. Top panel: a three node network with (in this case complete) connectivity, $J_{ij}$; bottom panel: the unrolled network that shows how influence propagates between nodes at time $t$ and $t+1$ in the space-time action of Eq. \[\text{Eq.} \]
where $Z(J)$ is the normalizing constant, and perfect knowledge of the system at time $t$—i.e., knowledge of which configuration, $\eta$, obtains at time $t$—provides optimal knowledge of the distribution over configurations at time $t + 1$.

Under many quantifications of computation cost, that cost rises exponentially with the number of nodes, since we must keep track of the probability distributions over all configurations. What happens if we have insufficient resources to track all nodes? A simple response to this problem is to track only a subset of the nodes, $i \in I$; in the physics jargon, we *trace over* the nodes in the complement, $\bar{I}$. In this case, we can talk about distributions over equivalence classes of the microscopic configurations $\eta$; two configurations $\eta$ and $\eta'$ are in the same equivalence class if and only if they agree for all nodes in $I$.

Assume the classes are time-independent, as is the case if they define the space $Y$ and associated map $\pi$ of SSC. Then we can label them as $\hat{\eta}$, and we can write the dynamical law in this compressed space as

$$P(\hat{\eta}'|\hat{\eta}) = \sum_{\eta' \in \hat{\eta}' \atop \eta \in \hat{\eta}} P(\eta'|\eta) \frac{P(\eta)}{\sum_{\eta'' \in \hat{\eta}} P(\eta'')} , \quad (6)$$

where $P(\eta)$ is the probability of finding the system in configuration $\eta$ of (4), independent of time—the prior.

We first consider the case where the observable space is identical to the compressed space. Even in this case, where we are interested in predicting only the coarse-grained configuration—i.e., $\hat{\eta}$—reliance on Eq. 6 leads to reduced predictive power. Since coarse-graining destroys information about which microstate obtains at time $t$, coarse-graining and then evolving forward in time is not equivalent to evolving forward in time and then coarse-graining.

Our goal here is to use an initial observation of $\hat{\eta}$ to produce an accurate emulation of the resultant stochastic dynamics over the coarse-grained states $\hat{\eta}$. By the discussion in Sec. [5.2.3] below, this suggests that it makes sense to use the appropriately averaged Kullback-Leibler divergence to quantify accuracy cost. Indeed, we can quantify the information loss for predicting $\hat{\eta}'$ (the future compressed state) from $\hat{\eta}$ (the current compressed state) rather than from $\eta$ (the current microstate) as the $\eta$-averaged Kullback-Leibler divergence from the prediction of the next value of the observable given total knowledge to the prediction given only knowledge.

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More precisely, because it seems we need to keep track of probability distributions over all configurations, it is intuitively plausible that the computation costs rise exponentially with the number of nodes. Formally, the desired conclusion follows from the widely-held belief in computational complexity theory that $P \neq \#P$; see, e.g., [31].
of the current coarse-grained state,

$$KL_1 = - \sum_{\eta} \left[ \sum_{\hat{\eta}} P(\hat{\eta}' | \eta) \log \frac{P(\hat{\eta}' | \hat{\eta})}{P(\hat{\eta}' | \eta)} \right] P(\eta),$$  \hspace{1cm} (7)

where $\hat{\eta}$ is the equivalence class containing $\eta$. In the language of Sec. 2.2, we take the coarse-grained macrostates to be our observables $\omega \in \Omega$ of interest (which makes our prediction distribution, $\rho$, the identity), and setting $\pi(\eta) = \hat{\eta}$. 

Kullback-Leibler (KL) divergence is the (unique) information-theoretic method for characterizing the failure of an approximation and is a natural choice for accuracy function in the absence of an exogenous utility function. It measures the minimum number of excess bits required to encode a sequence of $\hat{\eta}$ observations when the code is constructed from the approximation rather than the true distribution; equivalently, it measures the average excess surprisal of an observer who expects the approximating distribution but observes the true one. An important non-epistemic interpretation relates to dissipation out of equilibrium: KL divergence is proportional to the work available when a system maintained in the approximating distribution relaxes to a thermodynamic equilibrium described by the true distribution \[78\, 85\].

Depending on the nature of the underlying system, the information loss may be greater or less. Consider, for example, the classic example of the Ising model. Adjusting the strength of the connectivity $J_{ij}$ by multiplying it by a constant $\beta$, we may push the system from the disordered state ($\beta$ close to zero) to an ordered state ($\beta$ very large); in between these two regimes, we have a phase transition where the system goes through criticality. A related transition takes place in the case of a spin glass, where $J_{ij}$ drawn from some distribution that takes both positive and negative values, and when the variance of $J_{ij}$ becomes sufficiently large.

In the disordered state, little is gained from knowledge of the microstate, since system dynamics are only very loosely coupled from moment to moment. Therefore at small values of $\beta$ we expect information loss and accuracy penalties to be low upon coarse-graining. Similarly, in the ordered state, the system is strongly correlated; knowledge of only part of the system is sufficient to predict the future evolution, and again, accuracy penalties are low. It is in the critical state, in between these two regimes, where we expect the information cost from state-space compression to be high.

As an explicit example, we consider a very simple 5-node, fully connected network with discrete states; our coarse-grained states track only three nodes in the system\[8\] Fig. 8, which plots $KL_1(\beta)$, confirms our intuition of the previous para-

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\[8\] Given the symmetries of the problem, and our identification of $\Omega$ with $Y$, the choice of coarse-graining $\pi$ becomes simple. For more networks with fewer symmetries, or more complicated choices for $\Omega$, the choice of $\pi$ is non-trivial.
Figure 8: Information loss from state-space compression. In both the high-noise (disordered phase, low $\beta$) and “frozen” phase (high $\beta$), there is little accuracy cost to state-space compression. In the intermediate, critical regime, the penalty for prediction in the compressed space is higher. The solid line plots information loss when one attempts to predict observables directly from their dynamics (Eq. 7, solid line); the dashed line shows how the use of mesoscopic information leads to lower accuracy cost for the same prediction task (Eq. 8). In both cases, prediction becomes most difficult in the intermediate, critical regime.
Our greatest accuracy penalty comes in the intermediate regime, where we lose significant information about the observable when forced to rely on resource-limited computation.

If we care about time-steps further in the future (if our weight function $W$ is non-zero for $\Delta t > 1$), we can retain the probability distribution over states $\tilde{\eta}'$ at time $t + 1$ computed via Eq. (6). We can then make an approximate prediction for time $t + 2$ using $P(\tilde{\eta}'|\tilde{\eta})$, which amounts to assuming that the microstates retain their equilibrium distribution within any particular macrostate.

If we are allowed to observe $\tilde{\eta}$ in the future, however, this would lead to non-Markovian dynamics in $\phi$, the coarse-grained law, since the full dynamics on the macrostates are a Hidden Markov model. The use of prior observations to refine predictions would lead to higher accuracy, but also a higher computation cost. As a simple example of this, imagine that we have partial observations of an Ising model past the critical point, where we can observe only 90% of the spins. If we observe all of them to be up time $t$, and only 70% of them up at time $t + 1$, we will have very different beliefs about the remaining 10% than if we had observed all of them down at time $t$.

If we wish to keep the computation cost Markovian and time-homogenous—i.e., the computational cost at time $t$ for predicting the coarse-grained state $t + 1$ independent of $t$—we need to truncate the trace over possible paths. A natural way to do this is to make the assumption that the microstates are in equilibrium conditional upon our knowledge of the macrostate, which allows us to use Eq. (6) at all times. This will lead to accuracy costs: in the partial observation sequence described above, we will over-predict the possibility that the number of up spins will further decline.

So far, we have considered the compressed space to be identical to the observable space. But what if we have sufficient resources to track more than the nodes in the observable space? Taking the compressed space configurations to be $\tilde{\eta}$, our dynamical laws as the same as before, Eq. (6) but our degradation is less, since we can use the finer-grained information present in $\tilde{\eta}$ to predict $\tilde{\eta}$.

$$KL_1' = - \sum_\eta \left[ \sum_{\tilde{\eta}'} \sum_{\tilde{\eta}''} P(\tilde{\eta}'|\eta) \log \left( \frac{\sum_{\tilde{\eta}''} P(\tilde{\eta}'|\eta)}{\sum_{\tilde{\eta}''} P(\tilde{\eta}'|\eta)'} \right) \right] P(\eta).$$  \hspace{1cm} (8)

Fig. [9] provides a diagrammatic interpretation of the meaning of $KL_1$ and $KL_1'$. The quantity $KL_1$ is the information loss that occurs when making predictions via path (a) instead of path (b); while $KL_1'$ is the cost of predicting via path (c) instead of path (b). The computation cost—taken here to be proportional to the size of the

\footnote{Note that it is this assumption—that microstates thermalize—that is implicitly made in standard renormalization arguments associated with quantum field theories.}
Figure 9: A diagrammatic interpretation of accuracy costs, $\text{KL}_1$ and $\text{KL}'_1$, in terms of non-commuting paths. $\text{KL}_1$ is the information loss from predicting via path (a) instead of path (b); $\text{KL}'_1$ is the cost of predicting via path (c) instead of path (b). In both cases, losses peak when the underlying dynamics at the microstate level are near criticality.

probability space—is higher for path (c) than path (a), and the computation cost for the “ideal” prediction, path (b), is highest of all. In all cases, the differences between the paths depends upon the underlying dynamics, and it is precisely when one shifts between the ordered and disordered phases that the differences in paths becomes large.

In Fig. 8 we overplot $\text{KL}'_1$ for the same 5-node network considered above, with the same observable set, but where we have sufficient resources to track four nodes as opposed to only three. As expected, the information loss is smaller; having access to greater computational resources—literally, here, the ability to include an additional node state in one’s calculations—leads to better prediction. The overall shape of the accuracy cost is as for the original problem, with greatest loss in the intermediate regime.

In the study of spatially-organized critical phenomena, the dynamical properties of the system at the critical point correspond to an unstable fixed-point of the renormalization process: away from the critical point, repeated renormalization leads to a drastic simplification of the system as the dynamical laws “flow” towards either randomness (the $\beta$ equal to zero) or stability ($\beta$ goes to infinity) [45]. A similar phenomenon takes place here: repeatedly compressing a network of $n$
nodes down to a network of \( n' < n \) nodes shifts the underlying dynamics towards one of the two “highly compressible” regimes depending on the position of the original network on this continuum.

SSC provides a new window onto this fundamental result in the physical sciences, as well as a new set of criteria for evaluating a proposed coarse-graining for more complex biological, cognitive, and social networks. By reference to forward prediction and the cost of computation, SSC shows how the optimal way to coarse-grain a network depends upon the underlying dynamics.

5 Related work

5.1 Previous work on SSC using approaches different from ours

Earlier work has tried to define whether a map \( x_t \rightarrow y_t \) is a “valid” compression, without trying to rank such maps or find an optimal solution. For example, the work in [33, 32, 43, 28, 27] starts with the set of four variables \( x_0, y_0, x_t \) and \( y_t \), where \( t \) is some fixed value greater than 0, and \( y_0 \) is produced by applying a proposed compression map to \( x_0 \), while \( y_t \) is produced by applying that same map to \( x_t \). It then considers \( y_t \) to be a valid compression of \( x_t \) if the associated dynamics \( y_t \) is (first-order) Markovian.

The work in [40, 39, 63] is also concerned with these four variables, \( x_0, y_0, x_t \) and \( y_t \). Here the stochastic relationship of these four variables is used to assign a real-valued quality to the map \( x_t \rightarrow y_t \), rather than specify whether it is (not) a valid compression. This quality measure is based on the amount of extra information that is needed from \( x_0 \), in addition to the value \( y_0 \), for us to accurately predict \( y_t \). This previous work also does not take computation or measurement cost into account. However it is precisely those costs, and how they trade off with accuracy cost, that lie at the heart of our SSC framework.

In [93], optimal compression was implicitly defined in terms of how accurately a compressed description of a system could predict the fine-grained description. Related work in [94] implicitly defined optimal state compression in terms of how different probability distributions were at coarse-grained and fine-grained scales. As with the works discussed above, these works do not consider computation cost, at least not directly.

This previous work on state compression makes compelling points, and generally accords with intuition. However one striking feature of this previous work is that none of it considers what a state compression of a fine-grained dynamics \( x_t \) is for. The general approach is in some respects an exercise in the sociology of science, trying to formalize the vague notion of a “good state space compression” as scientists appear to mean the term.
As a result, much of this earlier work can be vulnerable to *reductio ad absurdum*. For example, if \(y_t\) is just a constant, not evolving in time, then the dynamics \(y_t\) is perfectly Markovian, of first-order. So this state space compression, \(x \rightarrow \text{constant}\), is a "valid" compression, according to some of this earlier work.

Similarly, say that extra information from the fine-grained value \(x_0\) cannot provide extra help in predicting the future value \(y_t\) beyond just knowing \(y_0\). This then implies that extra information about \(x_t\) cannot provide extra help in predicting the future value \(y_t\) beyond just knowing \(y_0\). It might seem that in this case \(x \rightarrow y\) should be deemed a "good" state compression. After all, if extra future information about future fine-grained states \(x_t\) cannot help us predict future compressed states, then dynamics in the compressed space is "autonomous", essentially independent of \(x_t\). This is the motivation for much of the analysis in [63], for example.

However this reasoning should be used with care. In particular, say we used this reasoning to argue along with [63] that we have a good state space compression \(\pi : x \rightarrow y\) if the conditional mutual information \(I(y_t; x_0 \mid y_0)\) is small, i.e., if knowing \(x_0\) does not help us predict \(y_t\) any more than knowing \(y_0\) does. With this criterion, we would say that the compression map that sends \(x\) to a uniformly noisy value of \(y\), which is statistically independent of \(x\), is a "good state space compression"; it results in \(I(y_t; x_0 \mid y_0) = 0\). We would argue that such a "compression" is of little practical interest, and therefore should be considered a poor compression.

There are also important features of our focus on the full compression / decompression loop that are absent from all of this earlier related work. That earlier work considers only the compression \(\pi\), with no associated "decompression" map \(\rho\) that maps \(Y\) to an observable of interest. Instead, we consider the case where one is interested in "decompressing" future values of \(y\), to make predictions concerning observable functions of future values \(x_t\). In addition, this earlier work assumes that future values \(y_t\) are given by iteratively applying \(\pi\) to future \(x_t\). Instead, we allow dynamics in \(y_t\) to evolve according to an arbitrary map \(\phi\) from an initial value \(y_0 = \pi(x_0)\). This means that rather than just assign value to a compression map \(\pi\), we assign value to a triple \((\pi, \phi, \rho)\).

Finally, the core issue of SSC is trading off the cost of replacing a computation over \(X\) with a computation over a compressed space \(Y\) against the associated loss of accuracy in predicting the observable of interest. This requires quantifying computation cost explicitly, which often is not done in the earlier related work. Moreover, the kind of computation cost considered here will be based on iteratively running a single-step-into-the-future operation. This contrasts with some

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\(^{10}\)A related point is that in this earlier work the Bayes net relating the four variables is \(P(y_t \mid x_t)P(y_0 \mid x_0)P(x_t \mid x_0)\). In contrast, the Bayes net relating those four variables that we analyze below is \(P(y_t \mid y_0)P(y_0 \mid x_0)P(x_t \mid x_0)\). This difference reflects the fact that this earlier work is ultimately concerned with different issues from those we consider.
other measures of computation cost that have been analyzed, and that are based on having the computer operate just once, producing in one fell swoop the entire semi-infinite sequence of all the following states that will arise starting from the current state. Some examples of this alternative measure are based on comparing the information in the semi-infinite string of all future states with that of the current state, or between that string of all future states and the semi-infinite string of all previous states \[15, 34, 77, 91\]. Such a measure does not involve sums over single-step-into-the-future costs—it reduces the entire future to a single sequence, rather than evaluating a sum over the components of such a sequence. So it is not concerned with the kinds of costs that concern real-world users of computers; any motivation for such a measure that concerns semi-infinite strings should involve some other property of dynamics through \(Y\) rather than computation cost.

5.2 Causal states and SSC

The coarse-graining suggested in \[77, 76\] for defining a “macrostate” of a dynamical system is based on information theory. It trades off a type of “computation cost” and a type of “accuracy cost”. The authors consider a ratio of costs, rather than a linear combination of them as we do here.

That work considers a bi-infinite time series of states in some set \(S, \{\ldots, s_{-1}, s_0, s_1, \ldots\} \in S^\infty\) governed by a stochastic process, usually taken to be time-homogenous. This process need not be (first order) Markovian. (So the variables \(s_t\) do not match the variables \(x_t\) considered in SSC.) A causal state at time 0 is a maximal set of “past” semi-infinite strings \(s^0_\leftarrow \equiv \{\ldots, s_{-1}, s_0\}\) such that the probability distribution of the “future” semi-infinite string, \(s^0_\rightarrow \equiv \{s_1, s_2, \ldots\}\) conditioned on any member of that set is the same. So all past semi-infinite strings that are in the same causal set result in the same distribution over possible future semi-infinite strings. We write such a causal set that contains \(s^t_\leftarrow\) as \(\epsilon(s^t_\leftarrow)\).

Note that every causal state, being a set of semi-infinite strings, has an associated (unconditioned) probability, given by the time-homogenous stochastic process. The statistical complexity of that process is defined as the entropy of this distribution over causal states. Statistical complexity plays a role in the objective function of \[77\] that is loosely analogous to the role played by accuracy cost in the SSC objective function.

The causal sets at times \(t \neq 0\) will in general differ from the one at time 0 (and from one another). So for a given time-series \(\{\ldots, s_{-1}, s_0, s_1, \ldots\}\), we have an associated time-series of causal sets \(\{\ldots, \epsilon(s^{-1}_\leftarrow), \epsilon(s^0_\leftarrow), \epsilon(s^1_\leftarrow), \ldots\}\). That time series of causal sets is governed by a Markov process, which is first-order Markov (even though the dynamics of \(s\) need not be).

In \[77\] this framework is adopted to analyze a type of “coarse-graining”. The sequence \(\{s_t\} \equiv \{\ldots, s_{-1}, s_0, s_1, \ldots\}\) is viewed a “fine-grained” process, and
coarse-graining is a single-valued function from such a sequence of observations \( \{ s_t \} \) into a coarse-grained state. The single-valued coarse-graining function adopted is the map taking such a time-series \( \{ s_t \} \) to the associated time-series of causal sets, \( \{ \ldots, \epsilon(s_{t-1}), \epsilon(s_0), \epsilon(s_1), \ldots \} \).

This formulation of coarse-graining is rather different from SSC’s concept of compressing a state space. As mentioned above, the values \( s_t \in S \) do not evolve according to a first-order Markov process, and so cannot be identified with the fine-grained values \( x_t \) of SSC. On the other hand, as mentioned above, evolution over the space of causal sets is first-order Markov.

This suggests that we identify the causal states with SSC’s fine-grained space, not its compressed space. Under such an identification, the statistical complexity at any moment in time is identified with the entropy over \( X \) at that moment, not the entropy over \( Y \). So it measures a “computation cost” of the microspace dynamics, not of the compressed space dynamics. From this perspective, one can cast SSC as picking up where the work on causal states leaves off: SSC addresses the problem of principled lossy compression of the microspace dynamics, which throws out distinctions between the microstates (i.e., between causal states) in favor of computational efficiency.

5.3 Previous work on SSC using approaches similar to ours

There has been some previous work on SSC that focuses on the practical benefit of compression, as we do, and that can be seen as special cases of our approach. Much of this work has arisen in the fields of numerical analysis and/or engineering. For example, the “finite state projection method” (FSP) \cite{60, 59} was developed to map a microstate of a chemical reaction network evolving according to a chemical master equation to a compressed version, to speed up simulation of the evolution of that network. Generalizing from these networks, the FSP is applicable whenever the set of possible microstates \( X \) is countable and the stochastic process generating \( x_t \) is a Poisson process. The idea behind the FSP is to select a large subset \( X' \subset X \) and group all the states in \( X' \) into one new, absorbing state. The stochastic process rate constants connecting the elements of \( X \setminus X' \) and governing the probability flow from \( X \setminus X' \) into \( X' \) are not changed. The goal is to choose \( X' \) to be large and at the same time to have the total probability flow rate from \( X \setminus X' \) into \( X' \) be small. While somewhat ad hoc, the FSP has been found to work well in the domain for which it was constructed.

There are also whole fields that are related to state compression. For example, in Reduced-Order Modeling \cite{72, 5} (ROM) one explicitly forms a low-dimensional model of the dynamics of an engineered system to help us construct a system with near optimal (control-theoretic) behavior. In many regards the low-dimensional model can be viewed as a “compression” of the system. (ROM is
particularly relevant when the spaces involved are real-valued.) A closely re-
lated example is control theory and variants like Dynamic Programming (DP).
The same kinds of issues are also considered under the term “aggregation”, par-
ticularly in analysis of ecosystems [3] and in work in economics stretching back
decades [80, 19, 36].

In addition to these other fields, uncertainty quantification methods like poly-
nomial chaos and Karhunen-Loeve expansions may prove helpful in state com-
pression. In those approaches one does not form a low-dimensional projection of
\( x \), but rather a low-dimensional projection of (the potentially infinite set of param-
eters specifying) the Markov process \( P(x_t \mid x_{t<}) \). The image of such a projection
can be viewed as a “macro-state” in the space of probability distributions (as dis-
cussed above in Sec. 4.1.7. Note though that in the limit where the dynamics of \( x_t \)
is deterministic, such projections are not so well motivated.

6 Accuracy costs for state space compression

In this section, we show how one can quantify accuracy cost (i. e., negative re-
construction accuracy), both for the case in which an accuracy function is exoge-
nously provided and for the case in which it isn’t, in which case it may make sense
to use an information-theoretic accuracy cost.

6.1 Non-information theoretic accuracy cost

Given our definitions in Sec. 2.2. when an accuracy function is provided, our
associated accuracy cost is

\[
\mathcal{E}(\pi, \phi, \rho; P) \equiv \int_{\Delta t > 0} d\Delta t \int dx_0 dx d\omega_0 dy dy d\omega' \\
W(\Delta t) P(x_0) \pi(y_0 \mid x_0) P_{\Delta t}(x \mid x_0) \mathcal{E}(\omega \mid x) \phi_{\Delta t}(y \mid y_0) \rho(\omega' \mid y) C(\omega, \omega')
\]  

(9)

Note that for this type of accuracy cost, in both the microstate and the macrostate
we can combine the evolution of the state with the observable function to present
the accuracy cost in a more modular manner. In particular, if we replace the
combination of the Markov process \( \phi \) and the prediction distribution \( \rho \) with the
following hidden Markov process,

\[
\phi^{\Omega} = \int dy \phi_{\Delta t}(y \mid y_0) \rho(\omega' \mid y)
\]  

(10)
and if we similarly replace the Markov process $P$ and the observable distribution $O$ with the following hidden Markov process,

$$P_{\Delta t}(\omega \mid x_0) \equiv \int dx \, O(\omega \mid x)P_{\Delta t}(x \mid x_0)$$

(11)

then the accuracy function becomes

$$\mathcal{E}(\pi, \phi^\Omega; P) \equiv \int_{\Delta t>0} d\Delta t \int dx_0 dy_0 d\omega d\omega' W(\Delta t)P(x_0)\pi(y_0 \mid x_0)\phi^\Omega_{\Delta t}(\omega' \mid y_0)P_{\Delta t}(\omega \mid x_0)C(\omega, \omega').$$

(12)

Reformulated this way, the accuracy cost only involves two quantities that we must specify, $\pi$ and $\phi^\Omega$, since $O$ and $P_{\Delta t}$ are given exogenously. The price we pay for this simplification is replacing a pair of Markovian processes with a pair of non-Markovian (more precisely, hidden Markovian) processes that govern the evolution of $\omega$ and $\omega'$, respectively.

### 6.2 Information-theoretic accuracy costs

If an accuracy metric $C$ is not supplied by the problem nor obvious to construct, it may be appropriate to use a more information-theoretic definition of accuracy cost, requiring a slightly different expression than in the previous section. There may also be situations where an information-theoretic accuracy cost is appropriate based on the system itself.

#### 6.2.1 Accuracy cost based on mutual information for two time-steps

To begin, focus on the special case where there are only two timesteps, $t_0$ and $\Delta t$. Assume that we know $\omega'_\Delta$, and from that value and want to treat that value as a prediction of $\omega_{\Delta t}$. Then if we do not have an exogenously provided accuracy function, it is natural to quantify the quality of the prediction with the mutual information between the predicted value of $\omega'_\Delta \in \Omega$ made after state compression and the actual future observable value $\omega_{\Delta t}$ generated by the Markov process $P$ over $X$ and the observable distribution $O$.

Formally, this is

$$\mathcal{E}_{\Delta t}(\pi, \phi, \rho; P) = -I_{\mathcal{P}_{\pi, \phi, \rho}}(\Omega'_{\Delta t}; \Omega_{\Delta t})$$

(13)

where the negative sign reflects the fact that large mutual information corresponds to low misfit $C$, and where the joint probability $\mathcal{P}_{\pi, \phi, \rho}(\omega'_{\Delta t}, \omega_{\Delta t})$ defining the mutual information at time $\Delta t$ is given by the marginalization.
\[ P_{\pi,\phi,\rho}(\omega'_M, \omega_M) \equiv \int dx_0 \ P(x_0) P_{\pi,\phi,\rho}(\omega'_M, \omega_M, x_0) \]  

where \( P_{\pi,\phi,\rho}(\omega'_M, \omega_M, x_0) \) is defined as

\[ \int dy_0 dy_M \pi(y_0 \mid x_0) \phi(y_M \mid y_0) \rho(\omega'_M \mid y_M) P(x_M \mid x_0) \delta(\omega_M \mid x_M). \]  

Intuitively, the distribution \( P_{\pi,\phi,\rho}(\omega'_M, \omega_M, x_0) \) couples \( \omega'_M \) and \( \omega_M \) by stochastically inferring \( y_M \) from \( \omega'_M \), then “backing up” from \( y_M \) to \( y_0 \) and then to \( x_0 \), and finally evolving forward stochastically from \( x_0 \) to get an \( x_M \), which in turn gives us \( \omega_M \).

This ability to use information theory to define accuracy cost can be extended to the case where we not only are missing an accuracy function, but also do not have an exogenously specified \( \Omega \) or \( \delta' \). In such cases we must work with \( y_M \) directly, and \( \rho \) is superfluous. The associated mutual information is

\[ E_{\Delta t}(\pi, \phi; P) = -I_{P_{\pi,\phi,\rho}}(y_M \mid x_M) \]  

where \( P_{\pi,\phi,\rho}(y_M, x_M, x_0) \) is defined as

\[ \int dy_0 \pi(y_0 \mid x_0) \phi(y_M \mid y_0) P(x_M \mid x_0). \]  

It is due to its ability to quantify the accuracy of predicting the microstate from the compressed state even without an exogenous accuracy function that mutual information is used in much other work related to state space compression [77, 76, 40, 39, 63]. However our information-theoretic accuracy cost should be distinguished from these other information-theoretic costs. To illustrate this, for simplicity consider the case where there is no exogenously specified observable, so that Eq. (16) applies. In [63] the analogous accuracy cost, defined for the values of a process at a pair of times \( t_0 \) and \( t_1 > t_0 \), is the conditional mutual information \( I(Y_{t_1}; X_{t_0} \mid Y_{t_0}) \). Although there are scenarios in which both this cost and the cost \( E_{\Delta t}(\pi, \phi; P) \) in Eq. (13) are minimal, there are also scenarios in which the cost \( I(Y_{t_1}; X_{t_0} \mid Y_{t_0}) \) achieves its minimal value even though the cost \( E_{\Delta t}(\pi, \phi; P) \) is maximal. For example, the latter occurs if \( \pi \) is pure noise, so that dynamics in \( y \) implies nothing whatsoever about dynamics of \( x \).

\[ ^{11} \text{For example, this occurs if all of the conditional distributions } \pi, \phi \text{ and } P(x_M \mid x_0) \text{ are deterministic, measure-preserving functions, so that the dynamics in } y \text{ uniquely specifies dynamics in } x. \]

\[ ^{12} \text{This distinction between these two measures reflects the fact that they are motivated by dif-}
6.2.2 Accuracy cost based on mutual information for more than two time-steps

The natural extension of (13) to multiple times is

\[
\mathcal{E}(\pi, \phi, \rho; P) = \int d\Delta t \ W(\Delta t) \mathcal{E}_\Delta(\pi, \phi, \rho; P)
\]

\[
= - \int d\Delta t \ W(\Delta t) I_{\mathcal{P}_\pi,\phi,\rho}(\Omega'_\Delta; \Omega_\Delta)
\]

(18)

with \( \mathcal{P}_\pi,\phi,\rho(\omega'_\Delta, \omega_\Delta) \) defined as in Eq. (14) for all values of \( \Delta t \). For natural choices of \( W \), the preceding expression has the feature that many aspects of it can be analyzed in closed form. However, the following example illustrates a subtle but important problem that arises in using mutual information for accuracy cost at multiple times.

**Example 4.** Consider the case in which the dynamics of \( X \) are deterministic—i.e., \( P(x_t | x) \) is a delta function for all \( t \)—the initial distribution \( P(x_0) \) is uniform, \( Y = X \), and both \( \phi \) and \( \pi \) are bijective maps (but otherwise arbitrary). In this case, the mutual information accuracy cost of Eq. (18) is zero: at any \( t \), any value of \( y_t \) specifies a unique value for \( x_t \). However, the map relating \( y_t \) and \( x_t \) changes arbitrarily from one \( t \) to the next.

As a simple but more concrete illustration of this problem, consider a discrete-time system with \( X = \{0, 1\} \) with stationary dynamics \( P(x_{t+1} | x_t) = \delta_{x_t=x_{t+1}} \), and let \( Y = X \) but with non-stationary dynamics that swaps the two values at every time step. Suppose \( \pi: \{0, 1\} \rightarrow \{0, 1\} \) is the identity map. Then at the initial time \( t_0 \), the map \( \rho_{\text{even}}: Y \rightarrow X \) defined by \( \rho_{\text{even}}(0) = 0 \) and \( \rho_{\text{even}}(1) = 1 \) is a perfect predictor of \( x_{t_0} \) from \( y_{t_0} \); indeed, this same predictor works perfectly at every time that is an even number of steps from \( t_0 \). At those times \( t \) that are an odd number of steps from \( t_0 \), \( x_t \) can still be perfectly predicted from \( y_t \), but now by a different map \( \rho_{\text{odd}}: Y \rightarrow X \), which swaps the two values \( (\rho_{\text{odd}}(0) = 1 \) and \( \rho_{\text{odd}}(1) = 0) \). In such a situation, mutual information is maximal at all moments in time. However, there is no single, time-invariant map \( \rho \) that allows us to interpret \( y_t \) as a perfect prediction for the associated \( x_t \).

(This simple example can be made even worse by taking \( X \) and \( Y \) to be much larger spaces, and defining the dynamics of \( Y \) using an arbitrary permutation of \( Y \).)
The underlying difficulty is inherent in the very notion of using mutual information to define accuracy cost, and is intrinsic to consideration of the relation between \( Y \) and \( X \) at more than two moments in time. (Note that many of the approaches of previous work—see Sec. 5.1—only consider that relation at two moments, and therefore do not need to address this subtlety.)

One way to resolve this problem with using mutual information as an accuracy cost is to modify that accuracy cost to force the prediction map from \( Y \) to \( \Omega \) to be time-invariant. To state this formally, return to the motivation for using information theory in the first place: by constructing a space of codewords and an associated (prefix-free) coding function that allow us to map any value in \( Y \) to a value in \( \Omega \), taking as our accuracy cost the minimal expected length of those codewords (over all codes). To make this precise, construct a space \( Z \) and a (time-invariant) function \( f \) such that for any \( y, \omega \), there is a \( z \in Z \) such that \( f(y, z) = \omega \). From one \( t \) to the next, given \( y_t \), we have to choose a \( z_t \) so that we can recover \( \omega_t = \mathcal{C}(x_t) \) by evaluating (the time-invariant) function \( f(y_t, z_t) \). We then want to choose a code for \( Z \) that minimizes the length of (codewords for) \( z \)'s that allow us to recover \( x \) from \( y \), averaged over time according to \( W \) and over pairs \((\omega'_t, \omega_t)\) according to \( P_{\pi, \phi, \rho} \).

So we are interested in the \( t \)-average of expectations of (lengths of codewords specifying) \( z \)'s where those expectations are evaluated under \( P_{\pi, \phi, \rho; \omega} (x'_t, x_t) \). This is just the expectation under the single distribution given by \( t \)-averaging the distributions \( P_{\pi, \phi, \rho; \omega} (x'_t, x_t) \). Write that single \( t \)-averaged distribution as

\[
\overline{P}_{\pi, \phi, \rho}(\omega', \omega) \equiv \int dt W(t) P_{\pi, \phi, \rho; \omega} (\omega'_t, \omega_t)
\]  

(19)

The associated minimum of expected codelengths of \( z \)'s is just the Shannon entropy \( H_{\overline{P}_{\pi, \phi, \rho}}(\Omega | \Omega') \).

To normalize this we can subtract it from the entropy of the marginal, \( H_{\overline{P}_{\pi, \phi, \rho}}(\Omega) \). (Note that this entropy of the marginal is fixed by \( P \), independent of \( \pi, \phi \) or \( \rho \).) This gives us the change in the expected length of codewords for specifying values \( \omega_t \) that arises due to our freedom to have those codewords be generated with a different code for each value of the prediction \( \omega'_t \). Since higher accuracy corresponds to lower accuracy cost, this motivates an information-theoretic accuracy cost given by

\[
\mathcal{C}(\pi, \phi, \rho; P) = -I_{\overline{P}_{\pi, \phi, \rho}}(\Omega'; \Omega)
\]  

(20)

This information-theoretic accuracy cost is the mutual information under the \( t \)-average of \( P_{\pi, \phi, \rho}(\omega'_t, \omega_t) \), rather than Eq. (13)’s \( t \)-average of the mutual information under the individual \( P_{\pi, \phi, \rho}(\omega'_t, \omega_t) \)’s.
6.2.3 Alternative information-theoretic accuracy costs

While it seems fairly clear that the distribution $P_{\pi,\phi,\rho}(x'_{\Delta t}, x_{\Delta t})$ is often a good one to consider, in some circumstances associated mutual information may not give the accuracy cost we are concerned with.

For example, in non-information theoretic accuracy cost, all we are concerned with is the average discrepancy between the prediction $\rho(y_t)$ and the truth $x_t$. We do not try to “normalize” that average discrepancy. If it just so happens that the distribution over $x_t$ is close to a delta function, and $\rho(x'_t)$ is the center of that delta function, we typically say that the accuracy of the prediction is high; we do not try to normalize for the fact that $x_t$ could be accurately predicted even without access to the value $x'_t$, due to the fact that it is generated by a distribution that is almost a delta function.

In the context of our accuracy cost based on expected code lengths, this suggests that we not try to normalize the conditional entropy, $H_{P_{\pi,\phi,\rho}}(\Omega | \Omega')$, by subtracting it from $H_{P_{\pi,\phi,\rho}}(\Omega)$. In other words, to most closely align with what the term “accuracy cost” means in the context of non-information theoretic accuracy costs that are based on accuracy functions, we may want to use that conditional entropy as our information-theoretic accuracy cost, rather than the related mutual information, $-I_{P_{\pi,\phi,\rho}}(\Omega; \Omega')$, i.e., we may want to use

$$C(\pi,\phi,\rho; P) = H_{P_{\pi,\phi,\rho}}(\Omega | \Omega')$$

(21)

This accuracy cost will be small if and only if for every prediction $\omega'_t$ that arises (with significant probability) there is always a unique associated $\omega_t$ that occurs (with high probability, and averaged over times $t$).

Another example of why we may not want to use Eq. (20) to quantify an accuracy cost is the well-known fact that mutual information in general has a substantial “artifact” arising via the prior distribution over either of its two random variable arguments. This is one of the reasons that people often replace mutual information with measures like channel capacity (which, like $H_{P_{\pi,\phi,\rho}}(\Omega | \Omega')$, only depends on the conditional distribution $P_{\pi,\phi,\rho}(\omega_t | \omega'_t)$).

As a final example of why we may not want to use Eq. (20), recall it was motivated by presuming that “... we know $\omega'_t$ and want to treat that value as a prediction of $\omega_{\Delta t}$”. However there are other uses of a compressed space computation that can be formulated using information-theoretic accuracy costs. In particular, when the microstate Markov process $P_{\Delta t}(x | x_0)$ (or the observable $O$, for that matter) is not deterministic, we may want to use $x_0$ to predict the future evolution.

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13 As an extreme example, if some random variable $z$ is almost a constant, then the mutual information $I(Y; Z)$ is very close to zero, even if the conditional distribution $P(y | z)$ is highly accurate.
of the entire distribution over $\omega_{\Delta t}$ given by $\mathcal{O}(\omega_{\Delta t} | x_{\Delta t})P(x_{\Delta t} | x_0)$, rather than predict the future values of $\omega_{\Delta t}$. For example, we may want to do this if we want to use Monte Carlo sampling of the distribution over $Y$ values, $\mathcal{P}_{\pi,\phi,\rho}(\omega'_{\Delta t}, x_0)$, as an approximation to Monte Carlo sampling of $\mathcal{O}(\omega_{\Delta t} | x_{\Delta t})P(x_{\Delta t} | x_0)$.

It is this approach that we use in Sec. 4.3, generalizing to arbitrary $W(\Delta t)$, the natural accuracy cost for this scenario is

$$C(\pi, \phi, \rho; \mathcal{P}) \equiv -\int_{\Delta t > 0} d\Delta t \int dx_0 P(x_0) \text{KL}[\mathcal{P}_{\pi,\phi,\rho}(\Omega'_{\Delta t} | x_0) \| \mathcal{P}_{\pi,\phi,\rho}(\Omega_{\Delta t} | x_0)]$$

(22)

where the notation “$\text{KL}[P(A | b) \| R(A)]$” means the Kullback–Leibler distance between the two distributions over values $a \in A$ given by $P(a | b)$ and $R(a)$ [22, 55].

In general, as with all aspects of SSC, the precise problem at hand should determine what kind of accuracy cost is used. Nonetheless, one would expect that quite often using several different accuracy costs would all provide physical insight into “what is truly driving” the dynamics across $X$.

7 Computation cost

The core concern of SSC is how to choose $\pi, \phi$ and $\rho$ in a way that minimizes computation cost without sacrificing too much accuracy cost. To quantify this goal we need to quantify the computation cost associated with any tuple $(\pi, \phi, \rho; \mathcal{P})$ (with the associated $X, Y$ and $\mathcal{O}$ being implied). This section discusses some possible such quantifications. We emphasize again that we are not advocating for any one particular quantification of computation or measurement cost, nor even that one be selected from among the list we consider here. As with most aspects of the SSC framework, the computation/measurement cost should be selected appropriately for the problem at hand.

We consider three sources of motivation for the computation costs we present: (1) theoretical computer science, (2) information theory, and (3) pragmatism. Although theoretical computer science, and the field of computational complexity in particular, has had a solid quantification of computational resources since the 1960s [35], the types of quantifications considered there are hard to apply optimization techniques to. Thus we also consider several costs motivated by information theory that we hope are more tractable to optimize over.

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Note that there is not the same issue here involving dynamic changes to how we match each element of $y$ with an element of $x$ that arose for the accuracy function based on mutual information. The reason is that both the distributions in the Kullback–Leibler distance are defined over the exact same space.
As a final comment, we note that even if we wish to use a mathematical expression for computation cost, often it makes sense to be purely pragmatic, and ignore many of the subtleties discussed above. This is discussed below, in Sec. 8.2.

7.1 Interpretation of \( X, Y, \pi, \phi \) and \( \gamma \) for defining computation cost

Say we were concerned with an arbitrary computation, independent of any consideration of state compression. In this case \( x \in X \) would be a specification of some initial data of that computation, \( Y \) would be the state of our computer, \( \pi \) would be a function that uses \( x \) (in combination with a specification of the computer program) to initialize the state of the computer, and \( \phi \) would be the dynamics of the computer. A halt state of the computer is a fixed point of \( \phi \).

In this scenario, it may be natural to use geometric time-discounting—that is, \( W(t) = (1 - \gamma)^t \) for some parameter \( \gamma \). For example, such discounting in some sense captures the fact that the user of the computer might decide to abort the computation if it goes on “too long”.

The combination of the computer architecture and the compiler determine both \( \pi \) and \( \phi \). So changing either one would change \( \pi \) and \( \phi \), even if they do not change the quantity ultimately computed, i.e., do not change the map from an initial data set \( x \) to an associated attractor in \( Y \). In general, all those choices of \( \pi \) and \( \phi \) that result in the same “quantity ultimately computed” will have different computation costs, as the term is used below. The same quantity can be computed using many different programs, all differing in the cost to run those programs.

7.2 Measures of computation cost based on theoretical computer science

There are many ways to quantify computation cost. Indeed, quantifying scaling relationships among some of the different kinds of computation cost is a core concern of the entire field of computational complexity [58, 38].

One of the kinds of computation cost considered in computational complexity is the running time of the computation. This is also often a primary concern of real-world SSC, where we are interested in expected “wall-clock” time of a simulation (e.g., as in the example of Secs. 4.1.7 and 4.2). If we restrict attention to von Neumann architectures, then for many purposes this cost can be lower bounded by the sum of the expected code length of messages that its CPU sends to its RAM, over all iterations of the computer as it evolves.

As a practical issue, this measure is often accessible via profiling of the program (\( P \) or \( \phi \) as the case might be) that is running on the computer (e.g., as in the
example of Sec. 4.2). This can then be used to guide the search for a \((\pi, \phi, \rho)\) that optimizes the trade-off between computation cost and accuracy cost (see Sec. 8).

Often, though, we want a more broadly applicable specification of computation cost, represented as a mathematical expression; at a minimum this is needed for any kind of mathematical analysis. One obvious way to do this is to use Algorithmic Information Content (AIC), i.e., to quantify computation cost as the minimal size of a Turing machine that performs the desired computation \([18]\). This has the major practical problem that how one measures the size of a Turing machine \(T\) (i.e., what universal Turing machine one chooses to use to emulate the running of \(T\)) is essentially arbitrary. Furthermore, AIC is formally uncomputable, so one has to settle for results concerning asymptotic behavior. To get around this issue, people sometimes “approximate” the AIC of a string, e.g., with its length after Lempel–Ziv compression. However this in essence reduces AIC to Bayesian maximum a posteriori coding, where the prior probability distribution is implicit in the Lempel–Ziv algorithm. (There are also further problems in using either Lempel–Ziv—see, e.g., \([75]\)—or AIC—see, e.g., \([49]\).)

There are several reasonable variants of AIC that might also be appropriate for some types of analysis of SSC. One set of such variants are the many versions of Rissanen’s (minimum) description length (MDL \([69, 8]\)). Another one, quite close to the measure of running time mentioned just above, is logical depth \([12]\). However logical depth is still subject to the practical difficulties associated with AIC.

### 7.3 Measures of computation cost based on information theory

There are several different possible measures of computation cost that are based on information theory. A natural choice, investigated for purposes similar to SSC, is the mutual information between the semi-infinite history of previous states of (an instantiation of) the process and the semi-infinite set of future states \([15]\). However the typical motivation offered for this measure does not seem appropriate to our needs. In particular, it does not directly concern “wall-clock time” (discussed in Sec. 7.1) of a computation, nor any other obvious measure of the resources required by a computation.

From the perspective of our SSC framework, there are several other kinds of information-theoretic costs (i.e., expected codelength) that we might want to interpret as costs of a computation. To present them, throughout we consider a general information channel \(P(b \mid a)\) from a random variable with a set \(A\) of possible values to a random variable with a set \(B\) of possible values, and an associated prior \(P(a)\).
7.3.1 Landauer thermodynamic cost

Suppose that $A$ and $B$ are instantiated in the same physical system. For example, they could be states of the same Turing machine tape. Then running the channel for an input $a$ erases $a$, overwriting it with some $b$. For this kind of $A$ and $B$, as the channel becomes less reversible, the Landauer thermodynamic cost of implementing the channel—the minimal entropy that is lost to an external heat bath in implementing the function—rises.

Suppose that $P(b | a)$ were a single-valued function, that includes some one-to-one maps and two-to-one maps, without any other maps. Let $B^*$ be the set of all states in $B$ that are images of a two-to-one map. Then the Landauer cost is $kT \ln(2)P(b \in B^*)$, where $k$ is Boltzmann’s constant and $T$ is the temperature of the system [50, 51, 52, 9, 10, 11, 13, 56, 64, 79, 70, 29].

When the function includes $n$-to-one maps with $n > 2$, or $P(b | a)$ has noise (i.e., is not a single-valued function), Landauer’s bound must be modified [92]. Consider first the case where $n > 2$ but the map is noise-free. Define $B^*(n)$ as the set of $b \in B$ that are images of an $n$-to-one map. Then using Shannon’s noiseless source coding theorem, the Landauer cost can be upper-bounded by

$$- kT \ln(2) \sum_n \sum_{b \in B^*(n)} P(b) \left( \sum_a \ln P(a | b) \right) - 1$$

(23)

(Intuitively, the reason for this bound is that for large $n$ it is possible to compress the set of “history bits” that must be stored to recover $a$ from the $b \in B(n)$ in a lossless manner, but we must do so using a prefix-free code if the transition from $a \rightarrow b$ is only one step in a multi-step computation.)

When the distribution is not a single-valued function but includes noise, then the cost is reduced, since the computer can now operate as an entropy sink for the external heat bath [54, 13]. In general, the precise upper bound on the total entropy lost (or gained) from the environment in going from $a \rightarrow b$ will depend on the details of how $P(b | a)$ is decomposed into a combination of a deterministic many-to-one map and an introduction of noise from the external heat bath. However, we can upper-bound the entropy loss / gain over all such decompositions. In particular, when the many-to-one map is known to consist purely of $n$-to-one maps with $n$ large, we can bound it as

$$kT \ln(2)(H(A) - H(B))$$

(24)

Intuitively, this means that the more noise we need to remove from our computation (e.g., via error-correcting codes, more exacting construction of hardware, etc.), the smaller $H(B)$ must be, and therefore the greater this type of computation cost.

\[ \text{15 Additional modifications to Eq. (24) are required if—as is often the case with real-world} \]
7.3.2 Computation cost based on conditional entropy

In practice, the cost associated with computation is not the entropy generated, but rather the amount of space and/or time resources it takes to perform the computation. Both of these costs depend on the essentially arbitrary choice of what computer architecture to use. (This is an example of the dependence discussed above of cost measures like AIC or logical depth on the choice of universal Turing machine one uses to define them.) However there are several information-theoretic quantities that capture aspects of these costs, which we now discuss.

Consider the special case of a computer $P(b \mid a)$ that at each timestep takes an input $a$ from one section of its memory, performs a calculation using it, and reaches a conclusion $b$. It then sends a message with $b$ to a separate portion of its memory, whose state is updated based on $b$. That new portion of memory then provides the input for the next timestep of the computation. A simple example is a GPU that maps the result of each step of its computation to some RAM outside of the GPU itself, some RAM that provides the input for the next timestep of the GPU’s computation.

The expected number of bits in that message encoding $b$ (in an optimal prefix code) is $H(B \mid A)$ if we are allowed to encode the messages $b$ using different codes, depending on the value $a$. In practice though, typically the same code will be used for $b$, regardless of $a$. In this case the expected codelength is instead $H(B)$.

Alternatively, say that we interpret $P(b \mid a)$ not as a computer, but as an observation apparatus, producing datum $b$ as its observation of an external reality $a$. (For example, $a$ might be a scene, and $b$ a pattern on a CCD forming an image of that scene.) By construction, we cannot have the decoding of the same $b$ vary with $a$, since the whole point of the encoding of $b$ is to specify $a$. In other words, we have to use the same code for all $b$, without varying the code based on $a$. So the expected number of bits in an optimal encoding of the observation is again $H(B)$, as above.

In both scenarios, so long as the input physical system (the GPU in the first scenario, or the system being observed in the second scenario) is distinct from the destination physical system (the RAM in the first scenario, or the system storing the observation in the second scenario), there is no Landauer erasure cost. In both scenarios, we arrived at $H(B)$ as a quantification of the resource cost.

As an aside, note that some problems requires us to use the output $b$ from a channel $P(b \mid a)$ to infer what the value $a$ was that entered the channel, and then send a message with that inference. If we use a fixed code to encode that message, a code that does not vary with $b$, then the expected number of bits needed in the.

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computers—the dynamics is not first-order Markov but rather higher-order Markov. Loosely speaking, when this is the case entropies get replaced by entropy rates [92]. However in this paper we focus primarily on first-order processes, so this is not a concern.
optimal code to specify \( a \) is \( H(A) \). If instead we dynamically choose the code for the message specifying \( a \), using whichever code is optimal for the given output \( b \), we reduce the expected number of bits to encode the message specifying \( a \) to \( H(A \mid B) \). Accordingly the improvement in the number of bits needed to encode \( a \) that we gain by using \( b \) is the mutual information, \( I(A; B) \). In other words, \( I(A; B) \) is the amount of information in the outputs \( b \), concerning the value \( a \). So if we encode in a message exactly that information in \( b \) that is useful for inferring \( a \), \( I(A; B) \) is the expected length of our messages, and so we use it to quantify the cost of \( P(b \mid a) \).

This is the encoding cost considered in \([88, 84]\). Note that it is the opposite of the thermodynamic cost mentioned above. More precisely, for fixed \( P(a) \), this cost \( I(A; B) \) shrinks as the thermodynamic cost \( H(A \mid B) \) rises. In addition, as discussed at the beginning of this subsection, it does not seem a tight fit to what we wish to quantify with computation cost.

In the real world, there are also costs with constructing any conditional distribution \( P(b \mid a) \) in the first place, i.e., costs in building our computer and observation device.

### 7.3.3 Discussion of information-theoretic computation cost

Given these considerations, whether \( \pi \) is viewed as an observation apparatus or not, based on the considerations discussed in Sec. 7.3.2 above, it seems reasonable to quantify the cost of implementing \( \pi \) as \( H(Y_0) \). Note that in general this cost shrinks as the size of \( Y \) shrinks (e.g., if \( Y \) is countable and we measure its size in terms of the number of elements of \( Y \)). So minimizing this cost “pushes” us to have a small macrospace \( Y \). This is of course exactly what we want —our premise for why one should compress the state space in the first place is that small \( Y \) makes the computation of \( \phi \) require less work than the computation of the microstate’s dynamics directly.

In this regard, note that if we view dynamics in \( Y \) as being carried out by a “general purpose” computer, then \( \pi(x_0) \) will have to encode the program to be run by that computer, as well as the initial state of its memory. The total length (in bits) of that combination of program and initial state will take up a certain fraction of \( Y \)—but not all of it. In this scenario, we have to choose \( Y \) to be large enough to accommodate any pair of a program and initial data in some broad class of such pairs (with the “class” defined by in part by the support of \( P(x_0) \)). In addition, the size of that pair (e.g., measured in number of bits it takes to encode them) is essentially a “description length” \([69, 8]\). This means that minimizing \( H_P(Y_0) \) can be viewed as implementing a kind of minimum description length principle.

The same kinds of considerations might lead us to also quantify the cost of \( \rho \) based on the considerations discussed in Sec. 7.3.2 above.
It is not so clear though that any of the items discussed above are clearly the best way of quantifying the cost of $\phi$—which very often is the dominant cost of computation. Although the quantification in Sec. 7.3.1 is widely applicable, purely practical considerations will often lead us to quantify computation cost differently from all of the above possibilities, as discussed in the next subsection.

8 The full SSC objective function

Formally speaking, once we have defined both an accuracy cost function and a computation cost function, we are faced with a multi-objective optimization problem, of how to (choose $\pi$, $\phi$ and $\rho$ in order to) minimize both. There are many ways to formalize this problem. For example, as is common in multi-objective optimization, we might only wish to find the set of triples $(\pi, \phi, \rho)$ that lie on the Pareto function of those two functions. Alternatively, we might face a constrained optimization problem. For example, we might have constraints on the maximal allowed value of the accuracy cost, with our goal being to minimize computation cost subject to such a bound. Or conversely we might have constraints on the maximum allowed computation cost (say, in terms of minutes or dollars), with our goal being to minimize accuracy cost subject to such a bound.

In this paper, for simplicity we will concentrate on ways to reduce the multi-objective optimization problem into a single-objective optimization problem. To do this requires that we quantify the trade-off between computation and accuracy costs. In terms of an overall SSC objective function that we want to minimize. Such an objective function maps any tuple $(\pi, \phi, \rho; P)$ (with the associated $X$, $Y$ and $O$ being implied) into the reals. The associated goal of SSC is to solve for the $\pi, \phi$ and $\rho$ that minimize that function, for any given $P, X$ and $O$.

8.1 The trade-off between accuracy cost and computation cost

Perhaps the most natural overall SSC objective function is simply a linear combination of the computation cost and accuracy cost:

$$K(\pi, \phi, \rho; P) \equiv \kappa C(\pi, \phi, \rho; P) + \alpha E(\pi, \phi, \rho; P)$$

(25)

Linear combinations of these two costs can be particularly amenable to analysis when both types of cost are defined using information-theoretic formulations such as those discussed in Sec. 7.3. In that case, depending on the precise accuracy and computation costs adopted, it may be possible to reformulate this objective function as the expected length of a single type of codeword.

As mentioned throughout the paper, the computation/measurement cost $C$ can (in many situations, should) include the cost of mapping the original state to the
compressed state. In this case, the computation cost $C$ might include a term of the form, e.g., $H_{x,p}(Y_0)$ (Sec. 7.3.3). When all these costs are defined information-theoretically, this quantity has a nice interpretation as the minimum of the expected number of bits that must be transmitted to “complete the compression-decompression circuit”, i.e., the average number of bits needed to map

$$x_0 \rightarrow y_0 \rightarrow y_t \rightarrow \omega'_t.$$  

(26)

There are some interesting parallels between these objective functions and various “complexity measures” that have been proposed in the literature to map a (bit string representation of) infinite time-series $x_t$ to a real number, in particular those that are based on Turing machines. The cost of computing $\pi$ can be viewed as (analogous to) the length of a Turing machine that takes in $x_0$ and produces $y_0$. The remainder of the computation cost can be viewed as analogous to the time it takes to run a Turing machine for the dynamics of $y_0$. Finally, the accuracy cost term can be viewed as analogous to the amount of extra information that must be added to the result of running that Turing machine to generate (an approximation to) the full observable time-series of interest, $\omega'_t$.

So if we were to just minimize the computation cost of $\pi$, the resultant value is analogous to the algorithmic information content of (an infinite string representation of) the time series of all values $x_t$. Minimizing the combined computation cost of $\pi$, $\phi$, and $\rho$ is instead analogous to the logical depth of $\omega'_t$. On the other hand, the sum of the cost of $\pi$ and the cost of $\rho$ is analogous to the “description length” of the time series $\omega'_t$ [69, 8]. So minimizing the sum of those two terms is analogous to using one the MDL algorithms. The SSC objective function Eq. (25) combines the concerns of all three of these complexity measures. (This relation of SSC and complexity measures is returned to in Sec. 9 below.)

### 8.2 Heuristics for minimizing the SSC objective function

Because truly optimizing the SSC objective function—or doing some variant of the original multi-objective optimization—will often be quite difficult (if not formally uncomputable), there are several heuristics one might employ that could still yield advantages over the ad hoc nature of intuitive state space compressions.

We already started on this path when we decided to focus in this paper on the situation where $\phi$ is first-order Markovian (that being a “simpler” dynamics to calculate than higher-order stochastic processes, of the type that are typically used in time-series reconstruction using delay embeddings). An obvious next step—common in real-world instances of SSC, like those discussed in Sec. 5.3—is to fix $Y$ ahead of time to some space substantially smaller than $X$, rather than try to optimize it. (In the case of Euclidean $X$, $Y$ will also be a Euclidean space of much
smaller dimension; for finite $X$, $Y$ is also finite, but far smaller.) We may still optimize over $\pi$, $\phi$, and $\rho$, but in this heuristic the choice of $Y$ is fixed, decreasing the size of the search space dramatically.

Another heuristic that will often also make sense to restrict the set of compression maps $\pi$ that are considered, for example, to some parametrized class of maps. In particular, when $Y$ is Euclidean, we can restrict $\pi$ so that it cannot encode an arbitrary dimensional space $x \in X$ in an arbitrarily small dimensional $y \in Y$ with perfect accuracy, for example by restricting $\pi$ to a class of maps that are all continuously differentiable of a certain order, or Lipschitz. Without such restrictions, there will often be “valid” $\pi$ that depend sensitively on all infinitely many digits of $x$, such as the position along a space-filling curve; as a practical matter, such $\pi$ are impossible to compute. Even if we wish to consider $\pi$ that are distributions instead of functions, a parametrized family of distributions (e.g., a parametrized class of Gaussian processes) might prove fruitful. Optimizing the SSC objective function then amounts to optimizing of the parameter space of the chosen class of maps.

Another heuristic is to simply use the dimension of $Y$ (or its size, if finite) as a surrogate for the cost of implementing $\pi$, $\phi$, and $\rho$.

Note that to evaluate the minimum computation cost for a given map from $x_0$ to values $y_i$ would be equivalent to solving for the optimal compilation of a given computer program down to machine code. In real computers, design of optimizing compilers is still a very active area of research; calculating the cost of such an optimized compilation will not be possible in general.\footnote{Indeed, even we allowed an infinitely expandable RAM, such a cost would be uncomputable, in general.} Even calculating such costs for the abstracted version of real-world computers will likely prove intractable. However it should be possible to put bounds on such costs. Moreover, purely pragmatically, one can run a search algorithm over the space of $\phi$’s, finding a good (if not optimal) compilation, and evaluate its associated cost.

Examples of heuristic ways to approach SSC are already present in related work, as discussed in Sec. 5.3.

9 Applications of SSC to other topics in science

Although our SSC framework is most directly concerned with simplifying computation of the future of a dynamical system, it may have benefits for general theoretical understanding as well. In this section we present several potential such applications. We intend to investigate them in more depth in the near future.
9.1 A form of complexity motivated by SSC

In particular, say we find a particularly helpful compression, which substantially reduces the value of the objective function $K$ compared to its value “null compression” which leaves the original space $X$ unchanged. Formally, using id to indicate an identity map (with the spaces it operates varying and implicit), such a choice of $Y, \pi, \phi$ and $\rho$ results in a small value of

$$\frac{K(\pi, \phi, \rho; P) - K(id, id, id; P)}{K(id, id, id; P)},$$

(27)

close to $-1$ (assuming the objective function is guaranteed non-negative).

When this value is small (i.e., close to $-1$), we have found an emulation of the dynamical system that is both easy to evolve computationally and that accurately predicts the future of that dynamical system. When it is large however (i.e., only barely below zero), either the emulation is not very compressed (i.e., or computationally difficult to evolve) or it is a poor predictor of the future of the underlying system, or both. Accordingly, we define compression complexity as

$$\min_{\pi, \phi, \rho} \frac{K(\pi, \phi, \rho; P)}{K(id, id, id; P)},$$

(28)

ranging from 0 for highly compressible (non-complex) systems to 1 for highly incompressible (complex) systems. Note that, unlike algorithmic information content—which is high both for random strings and for “complex” strings—the SSC compression complexity is just as low for completely random systems as it is for “simple” systems (see below).

When compression complexity is low, the compressed system $\{Y, \pi, \phi, \rho\}$ may provide substantial physical insight into the dynamics $P$ of the microstate $X$, since the compressed system intuitively tell us “what’s important about $X$’s time-evolution”. As an example, similarly to Ex. 2 in Sec. 4, one can define a never-ending (multi-stage) noncooperative game among many players that models a set of employees of many firms interacting with one another, and posit a particular learning rule whereby the players determine their behavior. The dynamics of such a game is a stochastic process in a very high-dimensional space. The optimal state compression of that dynamics would provide a relatively small set of variables whose dynamics captures the salient aspects of the full underlying game. Potentially those coarse-grained variables equal certain characteristics of the firms that are being modeled. Intriguingly though, it may well be that those macrostates instead are characteristics of the relation among multiple firms, or between individuals and one or more firms. This would suggest that the proper way to model the economy of those firms is not on a firm-by-firm basis, but rather in terms of
the macrostate variables that involve the states of multiple firms and individuals simultaneously.

Analogously, this is precisely what happens in quantum mechanics: a description of a multi-particle system cannot merely describe the individual states of the particles, but must also include correlations between the particles, i.e., their entanglement.

As defined above, compression complexity is normalized, by the value $K(id, id, id; P)$. This is not always appropriate, e.g., if there is some concrete physical meaning associated with the value of the objective function. In such cases, we could modify the definition in several ways. For example, as discussed at the end of Sec.[8] compression complexity measure simultaneously incorporates quantities much like MDL-style description length, logical depth, and AIC. These values could often be normalized, e.g., by an original length of an input string to a Universal Turing machine. This is typically not done though. Accordingly, we could make the connection of compression complexity with these alternative measures even tighter by redefining compression complexity as $\min_{\pi, \phi, \rho} K(\pi, \phi, \rho; P)$. As always with SSC, the precise scenario being analyzed should motivate the precise definitions that are used.

Unlike many other complexity measures, compression complexity is tailored to measuring the complexity of *dynamic* systems. Indeed, in its simplest form, it does not apply to static objects like images. There are various modifications of compression complexity that can apply to static objects though. For example, if we have a generative process that creates images, we could measure the compression complexity of the generative process that produces that image. So we could always use the complexity measure defined here to quantify the complexity of every generative process that creates a given image, and then define the complexity of that image as the minimum over all such generative processes that live in some pre-specified class of their associated complexities. (*Mutatis mutandis* if we are interested in the complexity of a distribution over images rather than a single one.)

Most importantly, unlike many other complexity measures (including those that the first author has introduced), compression complexity is not grounded in informal notions that in practice often reduce to “I’ll know it when I see it”. Rather it arises as a side-effect of trying to do something completely different. One builds a concrete framework to address a very practical, almost engineering-like goal. Then, in a completely unanticipated way, that framework reveals an important characteristic of broad categories of systems — a characteristic that can be viewed as a measure of complexity.

This aspect of how this measure is motivated may mean that it has something to say about physical systems that we didn’t already know. Indeed, for the special case of an information-theoretic accuracy cost and an information-theoretic computation cost, all components of compression complexity are based on informa-
tion theory. Nothing is exogenously specified in this case except the fine-grained Markov process. This suggests that the associated analysis might lead to broadly applicable insights.

However we emphasize again that despite its name, compression complexity is not being pushed as “the” way to measure complexity. Rather we are simply highlighting that it has many aspects which match well to characteristics of complexity that have been proposed in the past, and that it may lead to novel insight into physical phenomena.

To illustrate compression complexity, consider the case where accuracy cost is the $-I_{\pi,\phi,\rho}(X' ; X)$, as in Eq. (20), while $\Omega = X$, and $\mathcal{O}$ is the identify map. Then if we have a fine-grained dynamics that is complete noise—$p(x_{t+1} | x_t) = p(x_{t+1})$ with a high entropy $H(X_t)$ — we cannot improve the value of the compression objective function by any choice of $\pi, \phi$ or $\rho$ beyond its value when no compression is used. The accuracy cost is bad regardless, and no “compression” is possible.

However consider compressing $X$ to a $Y$ that only contains a single element. We lose nothing in accuracy cost. But computation cost is now zero. So the value of the objective function has been greatly reduced. This illustrates that random bit strings are assigned an extremely small compression complexity.

The example of Sec. 4.3 shows how this notion of complexity relates to long-standing intuitions that critical points—boundaries in parameter space that separate highly ordered and highly disordered states—have high complexity. Near phase transitions, due to long-range coupling, predicting the entire system’s state at some future time $t$ based on partial knowledge of the current state is difficult; conversely, far from the phase transition, information from one part of the system flows slowly to other parts. Well chosen coarse-grainings should allow one to leverage this decoupling to allow for higher-accuracy predictions.

9.2 Using SSC to define information flow among scales of a system

Note that many measures of “information flow” in a stochastic dynamical system like causal information flow [4], transfer entropy [73, 65, 66], and Granger causality [46] are motivated by considering the flow between physically distinct subsystems of an overall dynamic system. This makes them inherently ill-suited to quantifying information flow among the scales of a single system, in which one would expect there to be a priori “biases” reflecting the fact that behavior at different scales of a single system cannot be completely independent. In fact, the complete opposite is frequently the case: the dynamics of the more detailed scale often completely determines the dynamics of the less detailed scale. As an example of the difficulties such biases cause for those measures, the most straight-
forward application of transfer entropy would quantify the information flow from $Y_t$ to $X_{t+1}$ as $I_{\pi,\phi,P}(X_{t+1}; Y_t \mid X_t)$. However this is identically zero, regardless of $\pi, \phi$ and $P$. (Note that this is not exactly the case for the calculations of transfer entropy between scales made in [89], since they do not adopt this simplest use of transfer entropy, in which, to use Schreiber’s notation, $k = l = 1$).

From a certain perspective, these biases mean that the very notion of information flowing from a high scale to a small scale of a single system is specious. After all, specification of the fine-scale state of a system typically completely specifies the high-scale state. Nonetheless, going back at least to the seminal work of Maynard-Smith and others, researchers have presumed that information does flow from the high (coarse-grained) scale down to the low (fine-grained) scale of a biological system organisms [82, 81, 89, 24]. Indeed, Maynard-Smith then made strong arguments that such high-to-low scale information flow has increased in each major transition in biological evolution. However without a well-motivated formal definition of such flow among scales, it is not possible to ground those arguments in a rigorous manner.

A similar phenomenon is seen in descriptions of algorithms or Turing machines. For example, consider an algorithm that determines whether its input is a prime number or not. On the one hand, the behavior of this algorithm is completely specified by its code: how it moves bits around in memory and combines them. On the other hand, the low-level bit-wise behavior of this algorithm may be described as being “determined” by its search for primality. When at some point it takes one branch of a conditional “if” statement rather than another, do we say that it took that branch because the memory was just in a certain position, or because the number 6 is not prime?

The SSC framework provides alternative ways to formalize the information flowing from a high scale down to a low scale of a single system, which are more directly grounded in the relation between the behaviors at different scales of a single system. The overall idea starts by using SSC to solve for the scale(s) at which to analyze the system, rather than rely on the scale(s) being pre-specified in an ad hoc manner. We then define the associated information flow from the coarse scale to the fine scale by treating ($\phi$ and) $\rho$ as an information channel. We refer to any such quantification based on SSC as **inter-scale causality**, in analogy with “Granger causality”.

As an example of inter-scale causality, we might argue that the amount of information needed to construct an observable of $X_t$, given any particular $y_t$, is the entropy of $X_t$ under the probability distribution conditioned on $y_t$ at the previous time step (for illustrative simplicity here we consider discrete time steps). Aver-
aging that over $y_t$ and then over $t$ gives us

$$- \int d\Delta t \ W(\Delta t) \ H_{\mathcal{P}_{\pi,\varphi,\rho}}(\Omega_{\Delta t} \mid \Omega'_{\Delta t-1})$$

(29)

A slight variant of this measure arises if we wish to normalize each of the conditional entropies $H_{\mathcal{P}_{\pi,\varphi,\rho}}(\Omega_{\Delta t} \mid \Omega'_{\Delta t-1})$ by subtracting it from $H_{\mathcal{P}_{\pi,\varphi,\rho}}(\Omega_{\Delta t})$. This difference tells us how much extra information about the value of $\omega_t$ is provided by $\omega'_{t-1}$, beyond the prior information concerning $\omega_t$. With this normalization our measure of information flow becomes

$$- \int d\Delta t \ W(\Delta t) \ I_{\mathcal{P}_{\pi,\varphi,\rho}}(\Omega'_{\Delta t} \mid \Omega_{\Delta t})$$

(30)

This is just the time-averaged mutual information presented in Eq. (18). After that original presentation, it was criticized, which led our replacing it with the mutual information of the time average, in Eq. (20), or even with the conditional entropy of the time average, $H_{\mathcal{P}_{\pi,\varphi,\rho}}(\Omega \mid \Omega')$. Note though that here we are interested in quantifying information flow from the time series over $\Omega'$ (predicted from the time series over $Y$) to the time series over $\Omega$ (the observable applied to the time series over $X$). We are not interested in formalizing how accurately we can predict $\omega_t$ from $\omega'_t$ (or $y_t$), which was our goal when discussing Eq. (18) and Eq. (20).

Note the essential difference between this way of formalizing the information flow from a coarse scale to a fine scale and formalizing it as the transfer entropy [73] from the coarse scale to the fine scale. A core concern in the definition of transfer entropy is that it only depend on how much the time series $y_t$ tells us about $x_t$ that does not arise through direct dependence of $x_t$ on $x_{t-1}$. For example, if $x_t \rightarrow y_t$ is a single-valued invertible mapping, then $y_{t+1}$ will have high mutual information with $x_{t+1}$, even though there is no novel information that flows from $y_{t+1}$ to $x_{t+1}$, only different echoes of $x_t$. Transfer entropy is explicitly designed to remove such effects arising from the direct dependence of $x_t$ on $x_{t-1}$.

However this “direct dependence” that transfer entropy is designed to ignore is precisely what we want to capture when considering information flow among scales. In particular, it is precisely what the measures suggested in Eq. (29) and Eq. (30) are designed to capture.

Simply put, information flow between scales of a single system is fundamentally different from information flow between physically separate systems, and therefore should be quantified differently.

### 9.3 Other potential applications of SSC

Several other potential applications of SSC to other topics in science suggest themselves:
• How complexity changes over time. Note that as we go from $t$ to $t + 1$ to $t + 2$, etc., we can evaluate the SSC compression complexity taking each of those times as the “initial time”. This would then give us a dynamics of the complexity of a system. In particular, this gives a formal framework in which to evaluate the degree to which statement such as “the complexity of biological systems grows in time” are true.

• Quantifying some aspects of the philosophy of scientific theories. Scientific theories have many aspects of value: pragmatic, economic, aesthetic, and others. From the pragmatic viewpoint of predictability, however, one aspect that is often not considered is that of the computational cost of calculating a prediction within a given scientific theory. Indeed, a scientific theory that makes predictions in theory, but for which in practice even simple predictions cannot be calculated in the lifetime of the universe is completely useless from the viewpoint of prediction. In contrast, the computational cost of prediction is a core concern of our SSC framework. Could this be used to evaluate candidate string theories? However beautiful it might be, if some candidate string theory is completely useless for predictions (even setting aside the issues of whether we’ll ever be able to build a device to carry out an experiment), then perhaps we might be better off considering a variant of the theory with more feasible predictive power.

• Comparing systems, from fields near and far. SSC provides a generic method of comparing systems: if two systems (say, of the same type—e. g. two networks, or two economies) have the same optimal SSC compression, this tells us something about the commonalities between the systems. More intriguingly, this statement holds even for completely different types of systems: if an economy has some good state-space compression that is the same as a state-space compression of some multi-cellular organism, that again highlights some commonality between the two.

10 Conclusions

This preliminary report has presented a new framework for understanding how we construct higher-level descriptions of complex systems. We have introduced the problem through a series of illustrations, defined the key quantities, and provided three explicit examples of how this framework can be applied to basic problems in computer science, biology, and the physics of networks. Having built an intuition for the method, we then compared this framework to a number of influential suggestions in the literature.
Our framework makes explicit two core questions for both the scientist and engineer: how accurate a theory is, and how difficult it is to work with. We have presented new theoretical results for how to quantify the answers to these questions, and how to combine them into a single objective function.

By formalizing the goals of a scientist engaged in providing a coarse-grained description of a system, state space compression allows us to compare and contrast a wide variety of systems. It provides novel ways to address long-standing problems that arise both within fields and between disciplines, where the question of “how much to ignore” becomes critical.

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References

[1] K. B. Athreya and P. E. Ney, Branching processes, Springer–Verlag, New York, 1972.

[2] Alessandro Attanasi, Andrea Cavagna, Lorenzo Del Castello, Irene Giardina, Tomas S Grigera, Asja Jelić, Stefania Melillo, Leonardo Parisi, Oliver Pohl, Edward Shen, et al., Information transfer and behavioural inertia in starling flocks, Nature Physics 10 (2014), no. 9, 691–696.

[3] Pierre Auger, R Bravo de La Parra, Jean-Christophe Poggiale, E Sánchez, and L Sanz, Aggregation methods in dynamical systems and applications in population and community dynamics, Physics of Life Reviews 5 (2008), no. 2, 79–105.

[4] Nihat Ay and Daniel Polani, Information flows in causal networks, Advances in Complex Systems 11 (2008), no. 01, 17–41.
[5] Zhaojun Bai, *Krylov subspace techniques for reduced-order modeling of large-scale dynamical systems*, Applied Numerical Mathematics 43 (2002), no. 1, 9–44.

[6] Abhijit V. Banerjee, Arun Chandrasekhar, Esther Duflo, and Matthew O. Jackson, *Gossip: Identifying central individuals in a social network*, MIT Department of Economics Working Paper, 2014.

[7] Alain Barrat, Marc Barthelemy, and Alessandro Vespignani, *Dynamical processes on complex networks*, Cambridge University Press, Cambridge, UK, 2008.

[8] Andrew Barron, Jorma Rissanen, and Bin Yu, *The minimum description length principle in coding and modeling*, Information Theory, IEEE Transactions on 44 (1998), no. 6, 2743–2760.

[9] Charles H Bennett, *Logical reversibility of computation*, IBM journal of Research and Development 17 (1973), no. 6, 525–532.

[10] ______, *The thermodynamics of computation—a review*, International Journal of Theoretical Physics 21 (1982), no. 12, 905–940.

[11] ______, *Time/space trade-offs for reversible computation*, SIAM Journal on Computing 18 (1989), no. 4, 766–776.

[12] ______, *Logical depth and physical complexity*, The Universal Turing Machine A Half-Century Survey, Springer, 1995, pp. 207–235.

[13] ______, *Notes on landauer’s principle, reversible computation, and maxwell’s demon*, Studies In History and Philosophy of Science Part B: Studies In History and Philosophy of Modern Physics 34 (2003), no. 3, 501–510.

[14] William Bialek, Andrea Cavagna, Irene Giardina, Thierry Mora, Edmondo Silvestri, Massimiliano Viale, and Aleksandra M Walczak, *Statistical mechanics for natural flocks of birds*, Proceedings of the National Academy of Sciences 109 (2012), no. 13, 4786–4791.

[15] William Bialek, Ilya Nemenman, and Naftali Tishby, *Predictability, complexity, and learning*, Neural Computation 13 (2001), no. 11, 2409–2463.

[16] Neli Blagus, Lovro Šubelj, and Marko Bajec, *Self-similar scaling of density in complex real-world networks*, Physica A: Statistical Mechanics and its Applications 391 (2012), no. 8, 2794–2802.
[17] Lenore Blum, Felipe Cucker, Michael Shub, and Steve Smale, *Complexity and real computation*, Springer-Verlag New York, Inc., Secaucus, NJ, USA, 1998.

[18] Gregory J Chaitin, *Algorithmic information theory*, vol. 1, Cambridge University Press, 2004.

[19] Pierre Andrè Chiappori and Ivar Ekeland, *New developments in aggregation economics*, Annu. Rev. Econ. 3 (2011), no. 1, 631–668.

[20] Andy Clark, *Whatever next? predictive brains, situated agents, and the future of cognitive science*, Behavioral and Brain Sciences 36 (2013), no. 03, 181–204.

[21] Iain D Couzin, *Collective cognition in animal groups*, Trends in cognitive sciences 13 (2009), no. 1, 36–43.

[22] T. Cover and J. Thomas, *Elements of information theory*, Wiley-Interscience, New York, 1991.

[23] Eric Davidson and Michael Levin, *Gene regulatory networks*, Proceedings of the National Academy of Sciences of the United States of America 102 (2005), no. 14, 4935–4935.

[24] PCW Davies, *The epigenome and top-down causation*, Interface Focus 2 (2012), no. 1, 42–48.

[25] Simon DeDeo, *Group minds and the case of Wikipedia*, Human Computation 1 (2014), In press. [arXiv:1407.2210](https://arxiv.org/abs/1407.2210)

[26] Simon DeDeo and David C. Krakauer, *Dynamics and processing in finite self-similar networks*, Journal of The Royal Society Interface 9 (2012), no. 74, 2131–2144.

[27] Salem Derisavi, *A symbolic algorithm for optimal markov chain lumping*, Tools and Algorithms for the Construction and Analysis of Systems, Springer, 2007, pp. 139–154.

[28] Salem Derisavi, Holger Hermanns, and William H Sanders, *Optimal state-space lumping in markov chains*, Information Processing Letters 87 (2003), no. 6, 309–315.

[29] Raoul Dillenschneider and Eric Lutz, *Comment on “minimal energy cost for thermodynamic information processing: Measurement and information erasure”*, Physical Review Letters 104 (2010), no. 19, 198903.
[30] K.-I. Goh, G. Salvi, B. Kahng, and D. Kim, *Skeleton and fractal scaling in complex networks*, Phys. Rev. Lett. 96 (2006), 018701.

[31] Leslie Ann Goldberg, Martin Grohe, Mark Jerrum, and Marc Thurley, *A complexity dichotomy for partition functions with mixed signs*, arXiv:0804.1932 [cs.CC], 2009.

[32] Olof Görnerup and Martin Nilsson Jacobi, *A method for inferring hierarchical dynamics in stochastic processes*, Advances in Complex Systems 11 (2008), no. 01, 1–16.

[33] _____, *A method for finding aggregated representations of linear dynamical systems*, Advances in Complex Systems 13 (2010), no. 02, 199–215.

[34] Nicholas J Guido, Xiao Wang, David Adalsteinsson, David McMillen, Jeff Hasty, Charles R Cantor, Timothy C Elston, and JJ Collins, *A bottom-up approach to gene regulation*, Nature 439 (2006), no. 7078, 856–860.

[35] J. Hartmanis and R. E. Stearns, *On the computational complexity of algorithms*, Trans. Amer. Math. Soc. 117 (1965), 285–306. MR 0170805 (30 #1040)

[36] Werner Hildenbrand, *Aggregation theory*, Entry for The New Palgrave of Economics 2 (2007).

[37] Mike Holcombe and WML Holcombe, *Algebraic automata theory*, vol. 1, Cambridge University Press, 2004.

[38] John E Hopcroft, Rajeev Motwani, and Ullman Rotwani, *Jd: Introduction to automata theory, languages and computability*, 2000.

[39] N. Israeli and N. Goldenfeld, *Computational irreducibility and the predictability of complex physical systems*, Physical Review Letters 92 (2004), 074105.

[40] Navot Israeli and Nigel Goldenfeld, *Coarse-graining of cellular automata, emergence, and the predictability of complex systems*, Physical Review E 73 (2006), no. 2, 026203.

[41] Shalev Itzkovitz, Reuven Levitt, Nadav Kashtan, Ron Milo, Michael Itzkovitz, and Uri Alon, *Coarse-graining and self-dissimilarity of complex networks*, Physical Review E 71 (2005), no. 1, 016127.
[42] Matthew O. Jackson, Tomas Rodríguez-Barraquer, and Xu Tan, Social capital and social quilts: Network patterns of favor exchange, American Economic Review 102 (2012), no. 5, 1857–97.

[43] Martin Nilsson Jacobi and Olof Goernerup, A dual eigenvector condition for strong lumpability of Markov chains, arXiv preprint arXiv:0710.1986, 2007.

[44] Daniel A. Jiménez, Improved latency and accuracy for neural branch prediction, ACM Trans. Comput. Syst. 23 (2005), no. 2, 197–218.

[45] Leo P Kadanoff, Wolfgang Götze, David Hamblen, Robert Hecht, EAS Lewis, VV Palciauskas, Martin Rayl, J Swift, David Aspnes, and Joseph Kane, Static phenomena near critical points: theory and experiment, Reviews of Modern Physics 39 (1967), no. 2, 395.

[46] Maciej Kamiński, Mingzhou Ding, Wilson A Truccolo, and Steven L Bressler, Evaluating causal relations in neural systems: Granger causality, directed transfer function and statistical assessment of significance, Biological cybernetics 85 (2001), no. 2, 145–157.

[47] Marek Kimmel and David E. Axelrod, Branching processes in biology, Springer-Verlag New York, Inc., New York, 2002.

[48] David C Krakauer, Darwinian demons, evolutionary complexity, and information maximization, Chaos: An Interdisciplinary Journal of Nonlinear Science 21 (2011), no. 3, 037110.

[49] James Ladyman, James Lambert, and Karoline Wiesner, What is a complex system?, European Journal for Philosophy of Science 3 (2013), no. 1, 33–67.

[50] Rolf Landauer, Irreversibility and heat generation in the computing process, IBM journal of research and development 5 (1961), no. 3, 183–191.

[51] ______, Minimal energy requirements in communication, Science 272 (1996), no. 5270, 1914–1918.

[52] ______, The physical nature of information, Physics letters A 217 (1996), no. 4, 188–193.

[53] S. Lloyd, Physical measures of complexity, 1989 Lectures in Complex Systems (E. Jen, ed.), Addison Wesley, 1990.

[54] Seth Lloyd, Use of mutual information to decrease entropy: Implications for the second law of thermodynamics, Physical Review A 39 (1989), no. 10, 5378.
[55] D.J.C. Mackay, *Information theory, inference, and learning algorithms*, Cambridge University Press, 2003.

[56] OJE Maroney, *Generalizing landauer’s principle*, Physical Review E 79 (2009), no. 3, 031105.

[57] Andrea Montanari and Amin Saberi, *The spread of innovations in social networks*, Proceedings of the National Academy of Sciences 107 (2010), no. 47, 20196–20201.

[58] Cristopher Moore and Stephan Mertens, *The nature of computation*, Oxford University Press, 2011.

[59] Brian Munsky and Mustafa Khammash, *The finite state projection algorithm for the solution of the chemical master equation*, The Journal of chemical physics 124 (2006), 044104.

[60] ________, *The finite state projection approach for the analysis of stochastic noise in gene networks*, Automatic Control, IEEE Transactions on 53 (2008), no. Special Issue, 201–214.

[61] Mark EJ Newman, *The structure and function of complex networks*, SIAM review 45 (2003), no. 2, 167–256.

[62] David Papo, Massimiliano Zanin, Jos Angel Pineda-Pardo, Stefano Boccaletti, and Javier M. Buld, *Functional brain networks: great expectations, hard times and the big leap forward*, Philosophical Transactions of the Royal Society B: Biological Sciences 369 (2014), no. 1653, 20130525.

[63] Oliver Pfante, Nils Bertschinger, Eckehard Olbrich, Nihat Ay, and Jürgen Jost, *Comparison between different methods of level identification*, Tech. Report 11-035, Santa Fe Institute, 2013.

[64] Martin B Plenio and Vincenzo Vitelli, *The physics of forgetting: Landauer’s erasure principle and information theory*, Contemporary Physics 42 (2001), no. 1, 25–60.

[65] Mikhail Prokopenko and Joseph T Lizier, *Transfer entropy and transient limits of computation*, Scientific reports 4 (2014), 5394.

[66] Mikhail Prokopenko, Joseph T Lizier, and Don C Price, *On thermodynamic interpretation of transfer entropy*, Entropy 15 (2013), no. 2, 524–543.
[67] Stephen R Proulx, Daniel EL Promislow, and Patrick C Phillips, *Network thinking in ecology and evolution*, Trends in Ecology & Evolution 20 (2005), no. 6, 345 – 353.

[68] Filippo Radicchi, José J. Ramasco, Alain Barrat, and Santo Fortunato, *Complex networks renormalization: Flows and fixed points*, Phys. Rev. Lett. 101 (2008), 148701.

[69] Jorma Rissanen, *A universal prior for integers and estimation by minimum description length*, The Annals of statistics (1983), 416–431.

[70] Takahiro Sagawa and Masahito Ueda, *Minimal energy cost for thermodynamic information processing: measurement and information erasure*, Physical Review Letters 102 (2009), no. 25, 250602.

[71] Marissa G Saunders and Gregory A Voth, *Coarse-graining methods for computational biology*, Annual review of biophysics 42 (2013), 73–93.

[72] Wilhelmus HA Schilders, Henk A Van der Vorst, and Joost Rommes, *Model order reduction: theory, research aspects and applications*, vol. 13, Springer, 2008.

[73] Thomas Schreiber, *Measuring information transfer*, Physical Review Letters 85 (2000), no. 2, 461–464.

[74] Reza Shadmehr, Maurice A Smith, and John W Krakauer, *Error correction, sensory prediction, and adaptation in motor control*, Annual review of neuroscience 33 (2010), 89–108.

[75] Cosma Shalizi, *Complexity, entropy and the physics of gzip*, 2003, [http://vserver1.cscs.lsa.umich.edu/~crshalizi/notebooks/cep-gzip.html](http://vserver1.cscs.lsa.umich.edu/~crshalizi/notebooks/cep-gzip.html).

[76] Cosma Rohilla Shalizi, *Causal architecture, complexity and self-organization in the time series and cellular automata*, Ph.D. thesis, University of Wisconsin–Madison, 2001.

[77] Cosma Rohilla Shalizi and Cristopher Moore, *What is a macrostate? subjective observations and objective dynamics*, arXiv preprint cond-mat/0303625, 2003.

[78] Robert Shaw, *The dripping faucet as a model chaotic system*, Aerial Press, Santa Cruz, CA, 1984, Science Frontier Express Series. ISBN 0-942344-05-7.
[79] Kousuke Shizume, *Heat generation required by information erasure*, Physical Review E 52 (1995), no. 4, 3495.

[80] Herbert A Simon and Albert Ando, *Aggregation of variables in dynamic systems*, Econometrica: journal of the Econometric Society (1961), 111–138.

[81] J. Maynard Smith, *Time in the evolutionary process*, Studium Generale 23 (1970), 266–272.

[82] J Maynard Smith, *The concept of information in biology*, Philosophy of Science 67 (2000), no. 2, 177–194.

[83] Chaoming Song, Shlomo Havlin, and Hernan A. Makse, *Self-similarity of complex networks*, Nature 433 (2005), no. 7024, 392–395.

[84] Susanne Still, *Information bottleneck approach to predictive inference*, Entropy 16 (2014), no. 2, 968–989.

[85] Susanne Still, David A. Sivak, Anthony J. Bell, and Gavin E. Crooks, *Thermodynamics of prediction*, Phys. Rev. Lett. 109 (2012), 120604.

[86] R. S. Sutton and A. G. Barto, *Reinforcement learning: An introduction*, MIT Press, Cambridge, MA, 1998.

[87] Ross M. Thompson, Ulrich Brose, Jennifer A. Dunne, Robert O. Hall Jr., Sally Hladyz, Roger L. Kitching, Neo D. Martinez, Heidi Rantala, Tamara N. Romanuk, Daniel B. Stouffer, and Jason M. Tylianakis, *Food webs: reconciling the structure and function of biodiversity*, Trends in Ecology & Evolution 27 (2012), no. 12, 689 – 697.

[88] Naftali Tishby, Fernando C Pereira, and William Bialek, *The information bottleneck method*, 2000.

[89] Sara Imari Walker, Luis Cisneros, and Paul CW Davies, *Evolutionary transitions and top-down causation*, arXiv preprint arXiv:1207.4808, 2012.

[90] Langford B White, Robert Mahony, and Gary D Brushe, *Lumpable hidden markov models-model reduction and reduced complexity filtering*, Automatic Control, IEEE Transactions on 45 (2000), no. 12, 2297–2306.

[91] Karoline Wiesner, Mile Gu, Elisabeth Rieper, and Vlatko Vedral, *Information-theoretic lower bound on energy cost of stochastic computation*, Proceedings of the Royal Society A: Mathematical, Physical and Engineering Science 468 (2012), no. 2148, 4058–4066.
[92] D. H. Wolpert, *The minimal entropy generated during an irreversible computation*, In preparation, 2014.

[93] D. H. Wolpert and W. Macready, *Self-dissimilarity: An empirically observable complexity measure*, Unifying Themes in Complex Systems, New England Complex Systems Institute, 2000, pp. 626–643.

[94] ______, *Using self-dissimilarity to quantify complexity*, Complexity 12 (2007), 77–85.