Regulatory Functions from Cells to Society

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Abstract

Regulatory functions are essential in both socioeconomic and biological systems, from corporate managers to regulatory genes in genomes. Regulatory functions come with substantial costs, but are often taken for granted. Here, we empirically examine regulatory costs across diverse systems—biological organisms (bacteria and eukaryotic genomes), human organizations (companies, federal agencies, universities), and decentralized entities (Wikipedia, cities)—using scaling analysis. We guide the empirical analysis with a conceptual model, which anticipates the scaling of regulatory costs to shift with the system's internal interaction structure—well-mixed or modular. We find diverse systems exhibit consistent scaling patterns—well-mixed systems exhibit superlinear scaling, while modular ones show sublinear or linear scaling. Further, we find that the socioeconomic systems containing more diverse occupational functions tend to have more regulatory costs than expected from their size, confirming the type of interactions also plays a role in regulatory costs. While many socioeconomic systems exhibit efficiencies of scale, regulatory costs in many social systems have grown disproportionally over time. Our finding suggests that the increasing complexity of functions may contribute to this trend. This cross-system comparison offers a framework for understanding regulatory costs and could guide future efforts to identify and mitigate regulatory inefficiencies.

1 Introduction

Regulatory functions and mechanisms are necessary and ubiquitous features across all biological and social complex adaptive systems, spanning scales from the cellular to societal level. Regardless of scale, organizational structure, or composition, these systems rely on dedicated components to regulate internal processes and mediate interactions among their constituent parts. For instance, in cells, some genes may be beneficial when expressed in isolation, but their expressed proteins can often interact adversely. Regulatory genes control the timing of gene expression, preventing these harmful interactions by ensuring that conflicting genes are not expressed simultaneously. Similarly, in companies, managers coordinate employee activities to prevent duplicated efforts and mitigate adverse interpersonal interactions. In broader societal contexts, legal professionals mediate interactions among citizens through legal processes, ensuring orderly conduct.

While necessary and ubiquitous, regulatory functions consume a significant amount of energy and resources. For example, regulatory genes in bacteria account for about 10% of the costs.

In the US, 15% of workforce compensation is paid to managers [\[1\]](#page-11-0). In US universities, administrative spending is on par with instructional spending, reaching \$122.3 billion in the 2014–15 school year, and has been cited as a key factor in the skyrocketing tuition of US universities [\[2,](#page-11-1) [3\]](#page-11-2). In fact, the burden of administrative costs is a significant concern in many aspects of society, including higher education [\[4\]](#page-11-3), health care [\[5\]](#page-11-4), manufacturing [\[6\]](#page-11-5), and the transition to renewable technologies [\[7\]](#page-11-6), As a result, regulatory costs have emerged as one of the major societal challenges of the 21st century. What aspects of regulatory function are set by fundamental requirements and which are malleable through changes in structure, culture, or procedure? The answers to these larger questions require more understanding of the mechanisms underlying regulatory functions across a wide range of systems.

Regulatory costs have been studied separately at the levels of organizations, societies, and biological organisms. In socioeconomic systems, the primary focus has been on best practices for management and regulations concerning profits and efficiencies [\[8\]](#page-11-7), while in biology, the emphasis has been on understanding the genetic and metabolic mechanisms of regulation such as complex feedback loops and signaling pathways that maintain cellular homeostasis and respond to environmental changes. These functions and expenses seem to correspond to the expenses related to governance, law enforcement, and social coordination to regulate and coordinate activities, monitor performance, and enforce rules within the organization [\[9\]](#page-11-8). As such, studies have identified several key determinants of regulatory costs, including size, measured by the number of employees [\[10\]](#page-11-9), internal structure, measured by the level of hierarchies and size of the sub-units [\[11\]](#page-11-10), and functional complexity [\[12\]](#page-11-11), often measured by the number of different tasks performed by individuals within the organization. Despite these valuable insights, a comprehensive and systematic understanding of the determinants of regulatory costs remains elusive.

In the study of biological organisms, we have a much clearer understanding of the fundamental and baseline requirements for regulatory function. A key assumption in the biological context is that the overall evolutionary process, involving vast species and timescales, leads to optimized regulatory costs. Thus, biological examples provide a case study for understanding essential or optimal regulatory functions. Furthermore, similar key determinants of size, internal structure, and complexity emerge from the biological literature. For instance, major transitions in biological architecture—–such as the evolution from bacteria, which lack internal compartments and allow any gene to interact with any other gene, to eukaryotes, which have compartmentalized cells, and from single-cell to multicellular organisms—each introduce new and distinct forms of regulation [\[13\]](#page-11-12). At a more detailed level, all cellular functions, including regulatory genes, are known to scale with organism size [\[14\]](#page-11-13), [\[15–](#page-11-14)[17\]](#page-12-0).

The identification of common key determinants—size, structure, and functional complexity—across both social and biological systems suggests the potential for a unifying and comparative perspective. Previous studies have successfully achieved this goal by using scaling analysis as a foundation for empirical analysis. By combining this with mechanistic models that explain scaling relationships, researchers have uncovered common mechanisms across a diverse range of systems, including those in physics, biology, ecology, as well as firms and cities [\[17](#page-12-0)[–21\]](#page-12-1). These studies reveal key connections between size, function, and architecture, illustrating how fundamental principles can be applied across different types of systems.

Here, we first conceptualize what gives rise to regulatory costs across complex systems based on managing adverse interactions by integrating the interaction of size, structure, and various kinds of costs. We compare and unify diverse systems across the dimensions of well-mixed to highly modular. At one end of the spectrum, well-mixed systems tend to be the simplest self-organized and agglomerate ones. At the other end, those with modular structures tend to be centrally planned or have gone through several transitions in architecture. For example, bacteria are defined by a cellular environment where most expressed

proteins in the liquid cytoplasm can diffuse and interact with any other expressed protein, posing unique regulatory challenges for governing protein co-expression. The growth in genome size for bacteria is a result of an emergent process of evolution. In contrast, companies are typically defined by hierarchical and modular structures that regulate interactions amongst individuals and are highly planned as companies grow in size. This pattern also applies to more complex organisms that have experienced multiple major evolutionary transitions in structure [\[13\]](#page-11-12). We then compile data on regulatory costs in biological and social systems, including regulatory genes in bacteria and eukaryote cells, managers in companies, governmental agencies, universities, administrators on Wikipedia, and lawyers in cities. Using scaling analysis, we quantify shifts in regulatory costs with entity size by the scaling exponents to reveal shared governing processes and principles across different systems.

2 Results

We define regulatory functions as entities whose primary role is to moderate, adjust, or coordinate the interactions among other entities. These include regulatory genes in cells, managers in companies, legal functions in cities, and administrators on Wikipedia. Examples of functions that do not fall in this category include primarily functional components, for example, functional genes in cells, factory workers in a manufacturing plant, and primarily maintenance and repair functions, such as janitors of a university.

2.1 Conceptualizing the mechanisms for baseline regulatory costs across systems

Figure 1: Conceptual illustration depicting three strategies complex systems could employ to manage adverse interactions among components. Each strategy incurs a cost, and the optimization of the total costs forms the basis of our model.

In this section, we present a simple mathematical framework to illustrate how baseline requirements for regulation may be derived from the interactions of a few key mechanisms. The central premise is that regulation arises as a response to potential adverse interactions among system components [\[22\]](#page-12-2). A complex system brings together a large number of individual components—such as genes in cells or employees in companies—to achieve certain benefits, like metabolic energy for cells or revenue for companies. We denote the amount of these benefits as B. However, adverse interactions among these components can diminish these benefits. In cells, such interactions may occur when expressed proteins interact in ways that are futile or detrimental to cellular metabolism. In organizations, adverse interactions can manifest as duplicated efforts or interpersonal conflicts between individuals. When two components of a system have an adverse interaction, we identify three responses the system can employ, as illustrated in Fig. [1.](#page-2-0) First, the system can do nothing and tolerate the adverse interaction. Second, it can use a regulator to manage these interactions. In cells, it takes the form of carrying a regulatory gene, which makes sure the genes encoding two negatively interacting proteins are not expressed at the same time. In organizations, it can take the form of assigning a manager to coordinate tasks and prevent duplicated work between individuals or mediate interpersonal conflict between two employees. Third, the system can separate the two components by creating compartments. In cells, this involves developing internal architecture, such as mitochondria, to ensure that certain genes are only expressed in specific sub-portions of the cell. In organizations, this approach could involve structuring individuals into separate teams, units or departments, thereby modularizing their efforts.

Each of these three strategies carries a cost. esebreak three categories as: the cost of adverse interactions, I , the cost associated with regulators in the system, R , and the cost associated with compartments C. Regulators and compartments each reduce adverse interactions, but come with their own costs such as the pay required to employ a manager or the energy dedicated to maintaining and expressing a regulatory gene. Compartments differ from regulators in that they use structural separation, such as organizational divisions or subcellular membranes, to isolate unnecessary interactions. It's important to note that the cost associated with regulators and compartments may interact. For instance, in companies, the establishment of a new compartment, like a new division, is typically accompanied by the appointment of a regulator, such as the division head.

We are interested in how these benefits and costs change with the system size, N , such as the number of employees in an organization or the number of genes in a genome. In particular, we specify the number of functional individuals, f , regulators, r , and the number of compartments, c, to arrive at the generic utility function

$$
\mathcal{L} = B(f, r, c) - I(f, r, c) - R(f, r, c) - C(f, r, c).
$$
\n(1)

The explicit expression of each term will depend on the system of interest. For example, in cells, the cost of compartments is related to the physical maintenance of these structures and, thus, is influenced by their surface area. In organizations, these costs may be linked to the implementation of codified processes and the coordination required between departments.

Equation [1](#page-3-0) enables the optimization of the utility function, given functional forms for the four terms over the number of regulators, r, and number of compartments, c. While the precise quantitative forms of these four terms still remain uncertain for specific systems, it is useful to define the simplest version of each term to understand the baseline optimization of $\mathcal L$ and how r and c scale with system size.

In a well-mixed environment, the addition of a new functional individual—whether an employee or gene—comes with a probability μ of having a negative interaction with all existing functional members of the system. Denoting the number of functional individuals as f , edge counting gives the total number of negative interactions as ρf (f − 1), with $\rho \equiv \mu/2$. Each of these negative interactions comes with a cost γ_1 , and we can remove negative interactions either by adding regulators or placing individuals in compartments. We assume that individuals contained within compartments are removed from pairwise negative interactions with the rest of the system. If we place η individuals into a compartment, and the system contains c compartments, then the total number of negative interactions becomes $\rho (f - \eta c) (f - \eta c - 1)$. For a fixed compartment size, negative interactions within a compartment simply become a fixed cost, which we will combine with compartment costs later. Additionally, if each regulator can reduce θ negative interactions, then the total number of negative interactions becomes $\rho (f - \eta c) (f - \eta c - 1) - \theta r$ leading to the final utility function,

$$
\mathcal{L} = bf - \gamma_1 \left[\rho \left(f - \eta c \right) \left(f - \eta c - 1 \right) - \theta r \right] - \gamma_2 r - \gamma_3 c. \tag{2}
$$

where γ_2 is the unit cost of a regulator and γ_3 is the unit cost of a compartment (including the cost of negative interactions and regulators within a compartment). Here we assume that there is a proportional cost of r and c and a linear increase in benefit associated with f such that $R = \gamma_2 r$, $C = \gamma_3 c$, and $B = bf$. All terms are measured in dollars or energy depending on the system of interest. It is also useful to note that the total size of the system, N , which is often what is measured, is the sum of functional and regulatory components, $N = f + r$.

Managing Costs with Only Regulators We now optimize \mathcal{L} as a function of r and c. Later we will show that compartments are not beneficial below a certain size, and so we begin by considering $\mathcal L$ with $c = 0$. From Equation [2,](#page-3-1) we see that regulators are only beneficial if $\gamma_1 > \gamma_2/\theta$. That is, the cost of regulating a negative interaction is less than the cost of the negative interaction itself.

The utility function is optimized when regulators mediate all adverse interactions, meaning $I(f, r) = 0$. This gives the optimal number of regulators,

$$
r_{opt} = \frac{f(f-1)\rho}{\theta} \sim \frac{f^2 \rho}{\theta} \tag{3}
$$

illustrating that r grows like f^2 adjusted by the ratio of the probability of negative interactions, ρ to the number of interactions that one regulator can mitigate θ . Given that $r \sim f^2$ we can also write the total size in terms of r alone where $N = f + r = \sqrt{\theta/\rho} r^{1/2} + r$. It is useful to note that we have two regimes here: $N \propto r^{1/2}$ for small f (which is also small r given the relationships above) and $N \propto r$ in the large f limit.

The first case compares well to bacteria where every expressed gene can interact with every other gene. Here the observed scaling is $r \sim N^{1.86}$ [\[17\]](#page-12-0), in rough agreement with this simple optimization where $r \propto N^2$.

For the second case, where $N \propto r$, there is a critical size at which regulators overwhelm the system causing $\mathcal{L} = 0$. For the optimal number of regulators, where $I = 0$, the utility function is

$$
\mathcal{L} = bf - \frac{\gamma_2 \rho f \left(f - 1 \right)}{\theta}.
$$
\n⁽⁴⁾

which equals zero at

$$
f_r = 1 + \frac{b\theta}{\gamma_2 \rho}.\tag{5}
$$

Here f_r is the maximum number of functional elements for a system with only regulators. This upper bound depends on the ratio of the benefit per functional element to an effective cost, the unit cost of a regulator times the likelihood of a negative interaction. The ratio of b θ to γ_2 could be quite large given that the probability of negative interactions could be small and the cost of an average individual, including regulators, γ_2 , should be small relative to the productive output, b, of an average individual. In addition, a regulator may be able to handle many interactions and θ should be much larger than 1. For example, if $\rho = 0.10$, $\gamma_2 = b/2$, and $\theta = 10$, then $f \approx 200$, implying that an organization that handles negative interactions with only regulators could reach significant size.

Including Compartments As we mentioned earlier, f_r defines the size at which regulators become the entire system and this implies the need for compartments. Optimizing the complete cost function of Equation [2](#page-3-1) with respect to c by setting $\partial \mathcal{L}/\partial c = 0$ yields the optimal number of compartments,

$$
c_{opt} = \frac{1}{2\eta} \left(2f - 1 - \frac{\gamma_3}{\gamma_1 \rho \eta} \right) \tag{6}
$$

This result shows that compartments are only advantageous for cells with a large enough number of functional genes since $c_{opt} > 0$ requires

$$
f_c > \frac{1}{2} \left(1 + \frac{\gamma_3}{\gamma_1 \rho \eta} \right). \tag{7}
$$

The critical value is set by the ratio of the unit cost of a compartment to the probability of negative interactions multiplied by the unit cost of a negative interaction and how many elements are put in a compartment. In this case, the unit cost of a compartment, denoted as γ_3 , should exceed the unit cost of negative interaction. This is because each compartment may entail the cost of physical space, regulators who maintain it, and coordination costs among compartments. The scale at which regulators become the entire system, f_r , will agree with the minimum size that compartments are feasible, f_c . The criterion for a smooth transition to compartments is thus given by $f_r = f_c$, which sets the following condition for the unit costs

$$
\gamma_3 = \gamma_1 \eta \left(\rho + \frac{2b\theta}{\gamma_2} \right). \tag{8}
$$

To give a sense of the size of the unit compartment costs, $\gamma_3 = 40\gamma_1\eta$ leads to the same transition point of $f_c \approx 200$ for the values of b and ρ used above.

Above the critical value f_c , the number of compartments scales like $c \sim f$, which also affects the scaling of the number of regulators. Given the optimal number of compartments, we can maximize the utility function by considering the point at which $\mathcal{L} = bf$, which occurs at

$$
r_{opt} = \frac{c\gamma_3 + \gamma_1 \rho (f - \eta c)(f - \eta c - 1)}{\gamma_1 \theta - \gamma_2} \tag{9}
$$

which given the solution for c_{opt} becomes

$$
r_{opt} = \frac{4\gamma_3 f - \gamma_1 \eta \rho - 2\gamma_3 - \gamma_3^2 / (\gamma_1 \eta \rho)}{4\eta (\gamma_1 \theta - \gamma_2)}
$$
(10)

which for large f is approximated by

$$
r_{opt} \approx \frac{\gamma_3}{\eta \left(\gamma_1 \theta - \gamma_2\right)} f. \tag{11}
$$

With compartments, these results show that $r \sim f$ and $c \sim f$. Because of this linear scaling, the total $N = f + r$ is also linear $r \propto N$ and $c \propto N$. In this regime, quadratic requirements of negative pairwise interactions are proportionally handled by compartments and regulatory genes. However, this only occurs after the transition where compartments become inexpensive enough to be viable.

This result is supported by the observation that in unicellular eukaryotes, the number of regulatory genes grows as $G^{1.26}$ [\[17\]](#page-12-0), which is much closer to one than the scaling observed in bacteria. Unlike bacteria, unicellular eukaryotes have various internal spatial partitions, including the partitioning of genes between the nucleus and mitochondria. The transition from prokaryotes to eukaryotes illustrates how the internal structure of organisms, hierarchy, and partitioning can alter the requirements for regulation.

Also, it should be noted that the scaling of r_{opt} in Equation [10](#page-5-0) can not continue indefinitely because eventually $I = 0$. This limit is given by

$$
r_{\text{max}} = \frac{1}{4\theta} \left(\frac{\gamma_3^2}{\gamma_1^2 \eta^2 \rho} - \rho \right). \tag{12}
$$

The number of regulators, r , saturates to a constant and thus should have effectively sublinear scaling over much of the range of size. Similarly, in the transition between only regulators and compartments, we expect r to scale slower than quadratically with f , especially if $f_r \neq f_c$, which occurs for a wide variety of parameter combinations. In addition, it is important to note that the unit costs, γ_i , could vary with attributes of the system. For example, the unit costs of compartments in cells depend on the surface area of these compartments. Similarly, the rate and cost of the negative interaction, ρ and γ 1 respectively, may change with system size. In Equation [10](#page-5-0) such cost scaling would cause r_{opt} to scale faster or slower than f. Taking all of these considerations into account, we should expect real-world systems in the most general sense to follow

$$
r \sim r_0 N^{\beta},\tag{13}
$$

where r_0 is the minimum cost for the smallest size $(N = 1)$, and β is the scaling exponent. The above framework gives us the common expectation of $\beta = 2$ for a compartment-free system, and $\beta = 1$ for a system with both regulators and compartments. We can interpret observed exponents that are closer to 2 as being well-mixed and compartment-free. Close to 1 indicates a system optimized on compartments with a mixed strategy. An exponent significantly larger than 1 and significantly smaller than 2 indicates the transition from regulators only to some compartmentalization. Exponents significantly less than 1 indicate the regime where compartments are expanding and regulators are becoming cumbersome and saturating, or where there are certain economies of scaling in the unit costs.

2.2 Empirical results

Figure 2: Examples of scaling of regulatory functions in bacteria, cities, and Norwegian companies (a) The number of transcription regulatory genes vs. the number of genes in the genome of bacteria [\[17\]](#page-12-0). (b) The number of lawyers vs. working population in US Metropolitan Statistical Areas. (c) The number of managers in companies in Norway.

We collect data on regulatory components and system size in both biological and socioeconomic systems to examine how regulatory costs scale with size. In biological systems, we focus on bacterial and unicellular eukaryote cells, specifically collecting data on the number of regulatory genes in their genomes. Regulatory genes are those that determine the timing and environmental conditions for gene expression by producing proteins that bind to other genes. We use data reported by [\[17\]](#page-12-0) for these biological systems. For socioeconomic systems, we gathered data on the number of lawyers in cities and the number of managers in Norwegian and Korean companies, US federal government agencies, and various types of US universities. We also synthesize results from another study measuring the number of administrators for Wikipedia pages [\[9\]](#page-11-8). For human systems, system size is measured by the population of the entity, such as the number of employees for companies and universities, and the number of editors for Wikipedia pages. The scaling exponents of these systems are estimated using Eq. [13,](#page-6-0) with β representing the scaling exponent. For detailed information on data sources and statistical methods used for estimation, see Data and Methods.

Based on the mathematical model, we expect the scaling of regulatory functions to vary according to the system's structure. Bacteria, representing the most well-mixed end of the spectrum, operate like a "soup," where any gene can interact with any other gene. Cities, while still relatively well-mixed, exhibit a lesser degree of mixing due to the bottom-up emergence of social network clustering. We anticipate that these systems will have higher, superlinear exponents. On the modular end of the spectrum are human organizations such as companies and universities, which predominantly feature strong departmental structures. We expect these entities to have scaling exponents close to linear.

In the data we gathered, regulatory costs scale with system size across diverse systems. Three examples are shown in Fig. [2:](#page-6-1) regulatory genes in bacteria, lawyers in cities, and managers in Norwegian companies. As predicted, the scaling exponents vary across system types, with regulatory genes in bacteria having the highest exponent at 1.84. The number of lawyers scales superlinearly with the urban population, with an exponent of 1.28 (Fig. [2B](#page-6-1)). This is similar to prokaryotic regulatory genes but does not reach quadratic scaling due to constraints on individuals' social interaction capacity and the overall network structure of cities. Theories of urban scaling based on these constraints have successfully predicted similar exponents for many socioeconomic outputs driven by interactions [\[23,](#page-12-3) [24\]](#page-12-4). Contrary to cities, human organizations—-such as government agencies, companies, and universities— typically exhibit a high degree of hierarchical structure, leading us to expect different scaling behaviors. In these organizations, managers play a crucial role in coordinating efforts and mitigating conflicts among subordinates. The scaling exponent for managers in Norwegian companies is 0.91 (Fig. [2C](#page-6-1)).

The scaling exponents for all data we have gathered, including the number of managers in all sectors of US universities, Norwegian and Korean companies, and US federal government agencies, as well as those in biological systems, are summarized in Fig [2.2.](#page-8-0) In all the modular systems, the number of managers scales sublinearly with small variations—from 0.94 for Federal agencies (highest exponent) to 0.72 for Korean companies (lowest exponent). The sublinear scaling shown in the data suggests the span of control, the number of subordinates per manager, increases with organization size. This finding aligns with previous studies of companies and public agencies in management science [\[10\]](#page-11-9), while is contrary to the popular belief that larger organizations are less efficient in coordination costs [\[25\]](#page-12-5). Even in Wikipedia, a supposedly decentralized system, the interaction network among editors has been shown to be highly modularized [\[9\]](#page-11-8). Interactions tend to cluster around specific topics of interest, allowing a smaller number of administrators to effectively manage issues that arise. As such, despite the decentralized nature of the system, administrators naturally oversee specific modules and thus sublinearly scale with the total contributors.

2.3 Function diversity associated with scaling deviations

We have formulated a conceptual framework to understand how size and structure influence the regulatory costs of systems and collected data to compare with this theory. The differences across the spectrum from well-mixed to modular systems indicate regulation may arise from the number and type of interactions across individuals. We further investigate this idea by looking at how the number of regulators is related to the function diversity of a system.

Functional diversity reflects the range of tasks performed by the components of a system. As society advances, its technology becomes more complex, and individual roles and functions become more specialized and diversified. A classic and prominent example is car assembly, which now requires specialized metal compounds for catalytic converters, computer chips, and software to manage many aspects of automobile operation. None of these components existed a half-century ago. Such an increasingly complex manufacturing operation necessitates the coordination of a broader range of components, leading to a higher potential for adverse interactions that the system needs to manage.

Motivated by our theory, we predict that greater functional diversity is associated with higher regulatory costs. To test this prediction, we will quantify functional diversity across a range of systems and demonstrate that it is positively associated with the scaling residuals. In other words, systems with higher functional diversity exceed the expected number of

Figure 3: The scaling exponents (β) and 95% confidence intervals for regulatory functions in various systems. With more well-mixed internal structures, such as bacteria cells and cities, regulatory functions tend to be superlinear. With more modular internal structures, such as companies and universities, the scaling exponents are linear to sublinear.

regulators according to the scaling curve, while those with lower functional diversity fall short.

We quantify functional diversity in an organization by analyzing the distribution of occupations within it. For this analysis, we utilize individual-level occupation information for US federal government agencies. To ensure robustness, we also test our predictions on companies. Although occupation information is not available at the company level, we study companies aggregated into industries, for which we have detailed accounts of the distribution of occupations. We measure functions using the finest occupational categories available in these datasets. For more details on data sources and occupation definitions, see Data and Methods.

We measure functional diversity using normalized Shannon entropy (H) , an informationtheoretic measure that quantifies the predictability of a function given all functions in the system. This measure has been successfully utilized to quantify diversity in socioeconomic systems [\[26\]](#page-12-6). Mathematically, it is defined as:

$$
H = -\sum_{i=1}^{D} p_i \frac{\log p_i}{\log D} \tag{14}
$$

where p_i is the relative frequency of function (occupation) i, $p_i = f_i / \sum f_i$, and f_i is the frequency of function i. The variable D is the number of distinct functions in the system. H is maximized when the abundance of functions follows a uniform distribution. The normalization by $log D$ allows comparison across systems with different total numbers of functions.

We also compute the scaling residual [\[27\]](#page-12-7) for each system, which quantifies the extent to which a system over- or under-performs relative to the scaling curve. The scaling residual for system *i*, ξ_i , is defined as, $\xi_i = \log r_i - \log r(N_i)$, where r_i is the number of regulators for system i in the data, and $r(N_i)$ is the regulators expected of its size according to Eq. [13.](#page-6-0)

Figure 4: Industry and Federal agencies colored by occupations' normalized entropy, a metric for the diversity of functions in the system. Higher values denote more diversity. The inset shows the correlation between the normalized entropy and scaling deviation. Systems that are more diverse have more managers than would be expected of their size. The Pearson correlation is 0.59 for industries and 0.20 for federal agencies.

Figure [4](#page-9-0) illustrates the relationship between managers and employees, with each entity colored according to its normalized entropy, where higher values indicate greater function diversity [\[28\]](#page-12-8). For both federal agencies and industries, entities with higher function diversity tend to have more managers than expected for their size. The insets of Fig. [4](#page-9-0) display the correlation between scaling residuals and normalized entropy. The correlation is 0.59 for industries ($p < 0.001$), and .20 for federal agencies ($p = 0.030$). These results support our initial hypothesis that greater function diversity is associated with greater regulatory costs due to greater coordination requirements.

3 Discussion

We have proposed a conceptual framework for unifying the prediction of regulatory costs across biological and socioeconomic systems by examining the interactions of fundamental features, size and internal structure. We also conducted an empirical analysis of regulatory costs across these systems. Our findings indicate that the variation of regulatory functions with system size depends significantly on the system's structure. The exponents range from nearly 2 for regulatory genes in bacteria, which have a well-mixed internal structure, to sublinear scaling for managers in hierarchically organized human organizations, such as federal agencies and universities. By characterizing regulatory functions based on their underlying mechanisms rather than the system type, our work represents a first step toward a unified understanding of maintenance functions across diverse systems.

Our conceptual model is based on the simplest assumptions about cost factors, intended to lay the groundwork for more advanced theories in the future, These future models should incorporate more accurate cost estimates tailored to different system types through empirical measurements. For example, in hierarchical human organizations, the cost of regulators within compartments should also be factored into future models. In biological systems, more precise cost calculations should consider the frequency of gene expression, which plays a critical role in determining the energetic cost in the cell.

The greater scaling exponents of biological systems do not necessarily imply biological systems are less efficient than socioeconomic ones. Creating compartmentalization and structure in biology is expensive—intricate physical structures need to be developed to separate the cell nuclei from the rest. Extending this idea, complex physical infrastructure also needs to be developed to enable organs in animals, where genes only get expressed in a certain tissue. While bacteria need to carry a rapidly increasing number of regulatory genes with increasing size, they save on the energetic cost of creating compartmentalization within the cell. In comparison, developing structure in social systems does not necessarily incur a physical cost. For example, a company's CEO can decide to create a new division in the company without employing new physical separations between divisions, and the re-organization can be accomplished in a matter of weeks. Humans are also naturally creatures of groups with limited social capacity, making modularity a common characteristic in many social systems, even decentralized ones such as cities. Indeed, the social interactions scale with $N^{1.2}$ accord-ing to phone network data [\[29\]](#page-12-9), which is far from the N^2 null prediction for a completely well-mixed group.

Furthermore, superlinear exponents, such as the nearly 2 scaling exponent observed in bacteria, impose a fundamental constraint on system size. With superlinear exponents, there is a maximum size beyond which all components would be regulatory. For bacteria to grow larger, they must fundamentally transform their organizational structure to one that leads to a lower scaling exponent. While the ≈ 2 exponent is inefficient for scaling up, it also has significant benefits. New genes can be easily added to the bacterial genome along with new regulation in a plug-and-play manner that provides remarkable flexibility to adapt to novel and changing environments. This insight may be transferred to small human organizations, such as start-up companies and local communities. These small organizations are similar to bacteria in the sense that new functions can be easily added with the caveat that everyone interacts directly with everyone else, leading both to a high degree of flexibility and unexpected conflicts. Our theory predicts this form of organization is limited by a predictable critical size. While this study did not collect data on start-up companies, it would be valuable for future research to analyze the regulatory costs and structure of start-up companies on a large scale and examine their transition to a more modular configuration.

Social systems, aided by the lower cost of compartmentalization, appear to gain an economy of scale with regulatory costs. However, many have the experience that larger organizations are more bureaucratic. These two observations do not necessarily contradict each other. The personal experience of regulation may reflect the experience of a non-regulatory employee complying with the structure and processes put in place by an organization. Future research should consider the cost of regulatory compliance in organizations and ask how this is traded off against regulators and compartments. It has also been noted that many regulatory costs have increased over time in many forms of organizations, such as universities [\[4\]](#page-11-3). Temporal and cross-sectional scaling behavior differ in many socioeconomic systems, the difference can be due to changes in the output in the whole system regardless of size [\[30\]](#page-12-10). Future research should extend our cross-sectional data gathering and theoretical analysis to a temporal one, to address why regulatory costs have grown in many sectors over time.

While our study makes predictions based on structure and focuses on measuring regulatory costs across system types, we have not formally quantified the degree of modularity in the systems' architecture. Our work uses qualitative accounts of these systems. It is an area of important future work to perform a careful quantitative assessment of modularity across a wide range of system types. This would also involve gathering detailed interaction network data and quantifying the modularity of these networks.

Our work makes several contributions to the literature. While most management studies treat regulation as an independent variable, examining its effects on other factors, our research offers a distinct perspective by exploring what determines the level of regulation itself. We conduct a comprehensive empirical comparison across socioeconomic and biological systems, analyzing these systems based on their underlying mechanisms. For the first time, we compare regulatory costs across both biological and socioeconomic systems, identifying their commonalities and differences. Additionally, we introduce a conceptual framework that, despite lacking system-specific details, provides a foundation for understanding baseline regulatory requirements through an optimization process. We hope our work paves the way for a unified science of regulatory costs.

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Data and methods

Data

Bacteria and Unicellular eukaryotes. Data on genome length and the number of regulatory genes are from van Nimwegen, E. Scaling laws in the functional content of genomes. In Power Laws, Scale-Free Networks and Genome Biology, 236–253 (Springer, 2006)

Cities. Data for occupations in cities were obtained from the Bureau of Labor Statistics in 2017. Data were downloaded from <https://www.bls.gov/oes/tables.htm> in May 2019. Lawyers are defined according to the 2010 Standard Occupational Classification (SOC) system. The boundaries of urban areas in this dataset use the Metropolitan Statistical Area established by the US Office of Management and Budget (OMB).

Federal agencies. Data on US Federal agencies were obtained from FedScope in 2018. Downloaded from https://www.fedscope.opm.gov/employment_access.asp in Oct 2019. The data provides individual-level information on all US federal government employees, including the federal agency employed under, and the occupation classification. The dataset contains 125 cabinet-level departments and independent agencies. The smallest agencies in this dataset contain two employees, which are Commission for the Preservation of America's Heritage Abroad and the Northern Border Regional Commission. The largest agencies contain hundreds of thousands of employees—the largest two being the Department of Veterans Affairs, with 391,187 employees, and the Department of the Army, with 249,074 employees. The FedScope data is compiled through human resource software used by the US federal government. Note that not all federal agencies are reported in this data set; however, all agencies available through FedScope are used in our analysis. Supervisors are defined as individuals coded to have supervisor status in the FedScope dataset. The occupation classification in this dataset is according to the OPM's Handbook of Occupational Groups and Families, available at [https://www.opm.gov/policy-data-oversight/](https://www.opm.gov/policy-data-oversight/classification-qualifications/classifying-general-schedule-positions/occupationalhandbook.pdf) [classification-qualifications/classifying-general-schedule-positions/occupat](https://www.opm.gov/policy-data-oversight/classification-qualifications/classifying-general-schedule-positions/occupationalhandbook.pdf)ionalhandbook. [pdf](https://www.opm.gov/policy-data-oversight/classification-qualifications/classifying-general-schedule-positions/occupationalhandbook.pdf). The occupation categories used in our analysis is on the 4-digit level, the finest level in the dataset.

Norwegian Companies The data on Norwegian companies were purchased from Statistics Norway in May 2022. The data are from the year 2019. For confidentiality, the company-level data was aggregated by Statistics Norway according to the following procedure. The companies are first sorted by the number of employees from large to small. For every five companies, both the number of employees and the number of distinct functions are aggregated by taking the mean of the log-transformed variables, i.e., $E[log y_i]$ where y_i is a variable for company i in that size bin. This data only includes companies with five or more employees for confidentiality reasons. Managers are classified according to the International Standard Classification of Occupations (ISCO-08), which is detailed at <https://www.ssb.no/en/klass/klassifikasjoner/7/versjon/33>. Note that this dataset only includes resident employees in Norway, and it does not include subsidiary companies in countries other than Norway. We filter for a minimum of 50 employees in company size.

Universities. The data on US universities are obtained from the Integrated Postsecondary Education Data System (IPEDS). The data was accessed from [https://nces.ed.gov/](https://nces.ed.gov/ipeds/use-the-data) [ipeds/use-the-data](https://nces.ed.gov/ipeds/use-the-data). The data used in our analysis are from the year 2016. The type of universities are classified based on the Carnegie 15 classification system, also available in this dataset. Bachelor-level and above institutions include universities classified as "Baccalaureate," "Master," or "Doctoral" universities in the Carnegie 15 classification system. Liberal Arts universities are coded as "Baccalaureate Colleges–Liberal Arts," Associate Colleges are coded as "Associates Colleges," Doctoral universities are coded as " Doctoral/Research Universities–Extensive" and "Doctoral/Research Universities–Intensive" in Carnegie 15. In our analysis, we filter for universities with a minimum of 50 employees.

Industries The data on US industries are obtained from the Bureau of Labor Statistics in 2018, downloaded from <https://www.bls.gov/oes/tables.htm>. Managers and other occupations are defined according to the 2010 Standard Occupational Classification (SOC) system.

Estimation of scaling exponents

The scaling exponents are derived from doing a linear fit after taking the log of both axes. For two variables x and y, the exponent β and its confidence interval are obtained by regression: $\log y = \beta \log x + \log c$.