Fundamental trade-offs in the robustness of biological systems with feedback regulation

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Abstract

Natural biological systems use a complex network of feedback regulation to effectively respond to their changing environment. Even though in engineered systems we understand how accurate feedback can be depending on the electronic or mechanical parts that it is implemented with, we largely lack a similar theoretical framework to study biological feedback. Specifically, it is not fully understood or quantified how accurate or robust the implementation of biological feedback actually is. In this paper, we study the sensitivity of biological feedback to variations in biochemical parameters using five example circuits: positive autoregulation, negative autoregulation, double-positive feedback, positive-negative feedback and double-negative feedback (the toggle switch). We find that of these examples of biological feedback are subjected to fundamental trade-offs, and we propose multi-objective optimisation as a framework to study them. The impact of this work is to improve robust circuit design for synthetic biology and to improve our understanding of systems biology.

Abbreviations

MOO

Keywords

synthetic biology, systems biology, biological feedback, sensitivity analysis, multi-objective optimization

1 INTRODUCTION

In biological systems, feedback can regulates and maintains the stability of the internal environments of organisms and cells, ensuring homeostasis despite changes in their external environments (*1–3*). Additionally, feedback in biological systems can generate dynamic responses such as oscillations, signal amplification, and facilitate rapid switching between multiple states (*4–8*). These roles of biological feedback are crucial for processes such as gene expression, metabolic regulation, and adaptation to environmental changes. Despite the prevalence of feedback in natural biological systems, its properties are not fully understood and moreover, its similarities and differences with engineered feedback remain understudied (*9*, *10*). In this work, we study the robustness of biological feedback to variations in its biochemical implementation and its system design properties.

In mechanical and electrical systems, feedback can be used to improve a system's robustness against disturbances (*11*). For example, negative feedback in electronic circuits can improve robustness for a specific input range though it can also reduce overall gain and introduce fragility elsewhere. Indeed, it is well-known in engineering that feedback cannot provide complete robustness against all disturbances and that the use of feedback can introducefundamental limitations on the system's performance (*12*, *13*). The use of feedback in engineering can create performance trade-offs in terms of speed, stability, and accuracy that

must be carefully balanced during system design.

In contrast, it remains mostly unknown whether feedback introduces similar trade-offs in biological systems (*14*). Previous research on this topic has experimentally validated a trade-off between efficiency and robustness in the glycolysis pathway of *Saccharomyces cerevisiae* (*15*). Other trade-offs were uncovered through modelling and mathematical analysis (*16–20*). However, we are still missing a general framework to study biological feedback and its trade-offs.

A second key difference between feedback in engineered versus biological systems is that inside cells, feedback is implemented with biochemical reaction rates that can vary across many orders of magnitude and that can change due to mutations, and internal and external stimuli (*21*). Even in synthetically engineered biological circuits, the biochemistry of a feedback loop can be altered by its genetic, cellular, and extracellular contexts (*22*, *23*). Largely, it remains unclear how robust biological feedback is to variations in the biochemical reaction rates that implement it (*10*, *24*).

In this paper, we quantify the robustness of five well-known models of biological motifs to variations in their biochemical parameters using sensitivity analysis. First, we consider the mathematical models of positive and negative autoregulation, the toggle switch, the double-positive feedback motif, and the positive-negative feedback motif. We construct sensitivity functions that capture how each motif's output changes with variations in its biochemical parameters. Subsequently, we pose and solve the multiobjective optimization problems of simultaneously minimizing pairs of sensitivity functions to determine the Pareto-optimal implementations of each motif.

We find that three of these biological examples are robust to variations in their biochemical parameters, while the negative autoregulation motif and the positive-negative feedback motif are constrained by robustness trade-offs. These results offer insight into how to optimally design robust, reliable synthetic circuits that can function robustly in changing environments.

The impact of our research is in providing a framework to studys how robustness is allocated feedback in biological systems and what trade-offs are created by the use of biological feedback. Additionally, our research enhances our knowledge of systems biology and informs the system design of synthetic biological circuits.

2 RESULTS AND DISCUSSION

2.1 Sensitivity Analysis

Intracellular feedback loops depend on physical parameters, such as the cooperativity and the binding affinity of biomolecules. Understanding how changes in these physical parameters change the concentrations of biochemical species in a system will give insight into the properties of feedback loops. Sensitivity analysis quantifies this relationship, revealing which parameters have the greatest impact on the behaviour of a biological system (*2*, *25*).

Throughout this paper, we will use sensitivity analysis to assess the robustness of biological systems with feedback to changes in their biochemical parameters such as binding and unbinding rates, cooperativities, and degradation rates. Here, we introduce the sensitivity function that we will use throughout the paper to determine how sensitive feedback loops are to variations in these parameters.

We assume that the biological systems we consider can be modelled using a system of nonlinear ordinary differential equations. The model is of the form:

$$\frac{dx}{dt} = f(x, \theta), \tag{1}$$

where $x = (x^1, \ldots, x^n)$ is a vector of n biochemical species, $\theta = (\theta^1, \ldots, \theta^k)$ is a vector of k biochemical parameters, and f is a nonlinear, continuous function representing the dynamics of x. Assuming that a steady-state exists, we must have that

$$0 = f(x_{ss}, \theta), \tag{2}$$

where x_{ss} is the vector of biochemical species x evaluated at steady-state. The steady-state condition creates an implicit equation with variables x_{ss} and θ.

A simple measure of the sensitivity of biological systems to their biochemical parameters is given by the sensitivity function at steady-state. For a biochemical species x^i_{ss} at steady-state, its sensitivity with respect to the parameter θ_j is given by

$$S_{\theta_j}(x^i_{ss}) = \frac{\partial x^i_{ss}}{\partial \theta_j} \frac{\theta_j}{x^i_{ss}}. \tag{3}$$

Here, $1 \leq i \leq n$ and $1 \leq j \leq k$. The sensitivity function can be thought of as a ratio between the fractional change in the biochemical species x^i_{ss}, given by $\partial x^i_{ss}/x^i_{ss}$, to the fractional change in its dependent parameter θ_j. If x^i_{ss} represents a biochemical species dependent on a parameter θ_j, then $S_{\theta_j}(x^i_{ss})$ represents the ratio of the fractional change in the species to the fraction that we have perturbed the biochemical parameter from its original value by.

To extend this idea further, the sensitivity function of a set of biochemical species at steady-state, $x_{ss}(\theta) = (x^1_{ss}(\theta), \ldots, x^n_{ss}(\theta))$ with respect to θ is simply

$$S_\theta(x_{ss}) = \left(S_\theta(x^1_{ss}), \ldots, S_\theta(x^n_{ss})\right) \ . \tag{4}$$

We briefly note that there are other methods to quantify the sensitivity of a system to variations in its parameters (*12*, *25*), but that we choose this local derivative-based sensitivity function for its simplicity and ease of application to nonlinear biological systems.

2.2 Pareto-Optimality

Throughout this paper, we will use the multi-objective optimization (MOO) theoretical framework to simultaneously minimize multiple sensitivity functions. This will ensure ro-

bustness in our biological systems to variations in multiple of their biochemical parameters.

Multi-objective optimization (MOO) is a type of optimization problem in which more than one objective function is optimized at the same time. In MOO problems, the objectives can conflict with each other, meaning that improving one objective may lead to a deterioration in another. The goal of MOO problems is not to find a single "best" solution but rather a set of optimal solutions, known as Pareto-optimal, where no single objective can be improved without worsening at least one other objective. This set of optimal solutions is called the Pareto front.

We formulate the multi-objective optimization problem for our examples as follows:

$$
\begin{aligned}
&\text{Minimize } \mid S_{\theta_i}(x_{ss}) \mid, \mid S_{\theta_j}(x_{ss}) \mid \\
&\text{Subject to } f(x_{ss}, \theta) = 0, \\
&x_{ss} \geq 0, \\
&\theta_i, \theta_j \geq 0.
\end{aligned}
$$

We assume that x_{ss} is the set of biochemical species at steady-state and that θ_i and θ_j are two of the biochemical parameters in the model in Equations (1) and (2).With this formulation, we aim to find the Pareto-optimal parameter set that simultaneously minimises a pair of sensitivity functions.

We note that MOO problems have previously been solved for the system design of synthetic circuits (*26*) and to understand other biological systems in (*27–29*).

2.3 Biological Systems and their Robustness Trade-offs

2.3.1 Positive autoregulation is unconstrained by trade-offs

Positive autoregulation occurs when a gene or protein enhances its own production by stimulating its own expression (*1*). In this type of regulatory feedback loop, the product of the gene, such as a protein or RNA, increases the rate of its own synthesis, leading to an

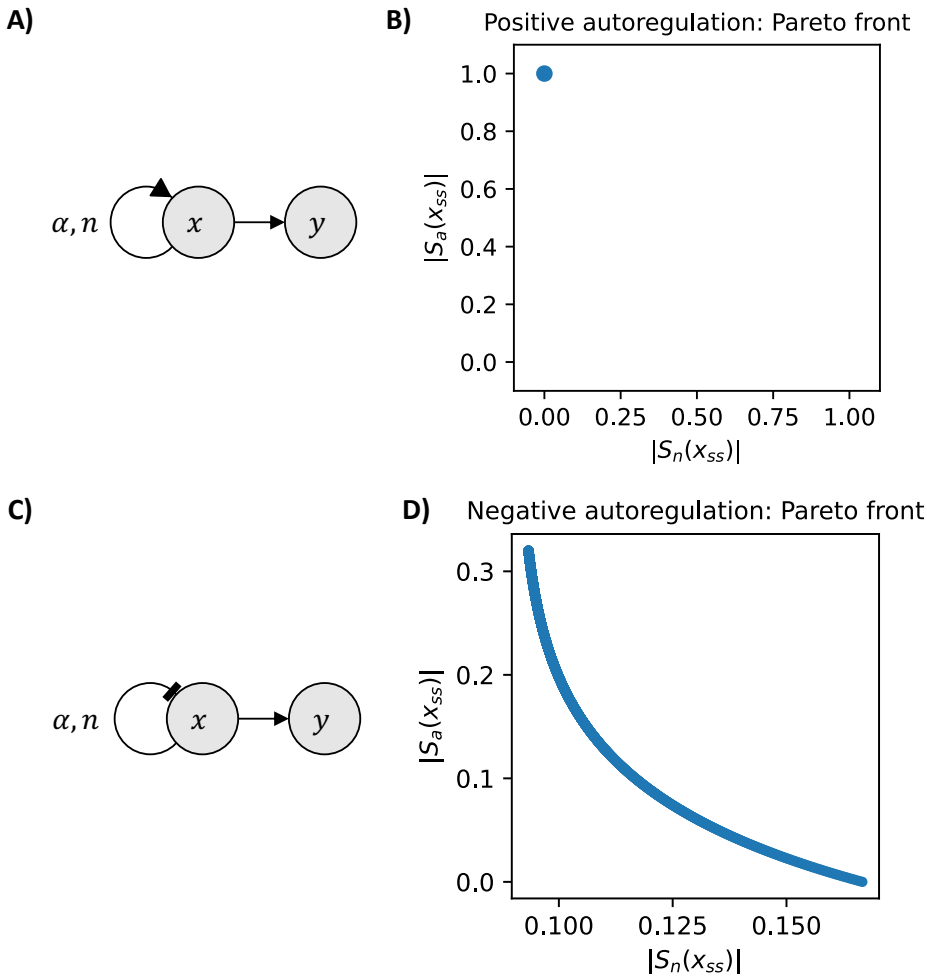

Figure 1: **Pareto fronts of the sensitivity functions for the positive and negative autoregulation systems. Panels A) and C)** show biological diagrams of the positive (A) and the negative (C) autoregulation of a biochemical species x. In **panel A)**, the pointed arrow represents positive feedback, where x enhances its own production, while in **panel C)**, the blunt arrow depicts negative feedback, where x represses its own production. We assume that species x also undergoes degradation and dilution within the cell, as indicated by the arrows pointed to the empty set symbol. The arrows indicate the parameter dependencies: n represents the binding cooperativity, while α represents the ratio of the production rate to the degradation rate per unit of dissociation constant concentration. We refer to α throughout the paper as the "feedback strength". **Panels B) and D)** illustrate the Pareto fronts corresponding to the simultaneous minimization of the absolute values of the sensitivities with respect to the feedback strength, α, and to the cooperativity, n. In **panel B)**, the Pareto front for the positive autoregulation system is the single point in blue. Solving the MOO problem shows that there is no trade-off between its two sensitivities. In **panel D)**, the Pareto front for the negative autoregulation system is the blue curve. Solving the MOO problem shows that there is a trade-off between the sensitivities of the negative autoregulation circuit.

amplification of its expression. This mechanism helps sustain high levels of gene or protein expression, which is crucial for processes like cell differentiation, developmental pathways, and signal amplification in biological systems.

The non-dimensionalised model of positive autoregulation from (*1*) is given by the following ordinary differential equation in species x:

$$\frac{dx}{dt} = \alpha \frac{x^n}{1 + x^n} - x \ . \tag{5}$$

In this model, n represents the cooperativity constant of species x. Cooperativity is a molecular phenomenon where the binding of a molecule such as a ligand to a protein or enzyme influences the binding of additional molecules, either by enhancing or reducing more binding. Parameter α represents the ratio of the production rate to the degradation rate per unit of dissociation constant concentration. Throughout the paper, we refer to α as the "feedback strength". Both parameters α and n are unitless quantities. We illustrate this biological circuit's diagram in Figure 1A).

The steady-states of Equation (5) occur when

$$0 = \alpha \frac{x_{ss}^n}{1 + x_{ss}^n} - x_{ss}. \tag{6}$$

We note that $x_{ss} = 0$ is always a solution to Equation (6). However, the sensitivity function $S_\theta(x_{ss})$ is ill-defined when $x_{ss} = 0$ due to division by zero. Hence the zero solution must be removed for our analysis. Thus, Equation (6) reduces to

$$0 = \alpha \frac{x_{ss}^{n-1}}{1 + x_{ss}^n} - 1. \tag{7}$$

Equation (7) can have up to two solutions, depending on the choice of parameters. When one solution exists, it is always stable. When two solutions exist, one is stable and the other is unstable. We are always interested in the stable solution, as this is the one that can be

observed and measured.

In the Supplementary Materials, we provide the derivations of the relative sensitivities with respect to biochemical parameters α and n. The resulting sensitivity functions are

$$S_\alpha(x_{ss}) = \frac{1}{1 - \frac{n}{1+x_{ss}^n}}, \quad S_n(x_{ss}) = \frac{n \ln(x_{ss})}{-n + 1 + x_{ss}^n}. \tag{8}$$

We note that sensitivity $S_\alpha(x_{ss}) \geq 1$ from Equation (8). We solve the MOO problem of simultaneously minimizing the absolute values of these sensitivities and illustrate the result in Figure 1B). We observe that there is no trade-off between the two sensitivities for the positive autoregulation circuit. Intuitively, it makes sense that positive feedback is not sensitive to the parameters in its implementation due to its ability to amplify signals to steady-state. This amplification may be insensitive to the biochemical parameter values. With these properties, positive autoregulation can make clear and decisive responses that are particularly useful in biological processes that require an all-or-nothing decision.

2.3.2 Negative autoregulation is constrained by a fundamental trade-off

Negative autoregulation is a regulatory mechanism in biological systems where a gene or protein inhibits its own expression (*1*). In this process, the product of a gene represses its own transcription, effectively reducing the level of its production. The role of negative autoregulation in biological systems is to quickly respond to changes in environmental conditions or cellular needs.

Previous research on the robustness of negative intracellular feedback has found that it is robust to variation in the cooperativity of the biochemical species, but sensitive to its production and degradation rates at specific values of these rates (*24*). We extend this result to reveal that a trade-off constrains negative autoregulation. We find that negative feedback cannot be robust to both variations in both cooperativity and feedback strength.

We start by considering a system of one biochemical species undergoing negative autoreg-

ulation. We assume the species is produced via Hill kinetics with cooperativity constant n and that its feedback strength is α (*1*). This system is illustrated in Figure 1C) and modelled by the following non-dimensionalized differential equation model:

$$\frac{dx}{dt} = \alpha \frac{1}{1 + x^n} - x \ . \tag{9}$$

The steady state of this system occurs when

$$x_{ss} = \alpha \frac{1}{1 + x_{ss}^n} \tag{10}$$

We note that Equation (10) has a unique steady-state solution. We want to assess the sensitivity of this steady state to changes in each of its two dependent parameters: α and n. We will therefore inspect the following sensitivity functions:

$$S_\alpha(x_{ss}) = -\frac{\alpha n \log(x) x^n}{x + \alpha n x^n + 2x^{1+n} + x^{1+2n}} \tag{11}$$

$$S_n(x_{ss}) = \frac{\alpha\,(1 + x^n)}{x + \alpha n x^n + 2x^{1+n} + x^{1+2n}} \tag{12}$$

In Figure 1D), we note that there is a trade-off between the sensitivity to cooperativity and the sensitivity to feedback strength. This implies that the negative autoregulation system must have either some sensitivity to changes in feedback strength or to changes in cooperativity. Therefore, for a negative autoregulation system with cooperativity n, a higher value of the feedback strength will provide robustness to small changes in the feedback strength, and vice versa. To build a negative autoregulation circuit that is highly robust to changes in parameters, our modelling suggests that the feedback strength α should be greater than value two and the cooperativity n should be as high as possible. Clearly, finding the trade-off between the sensitivities provides valuable information about the system design of a robust negative autoregulation synthetic circuit.

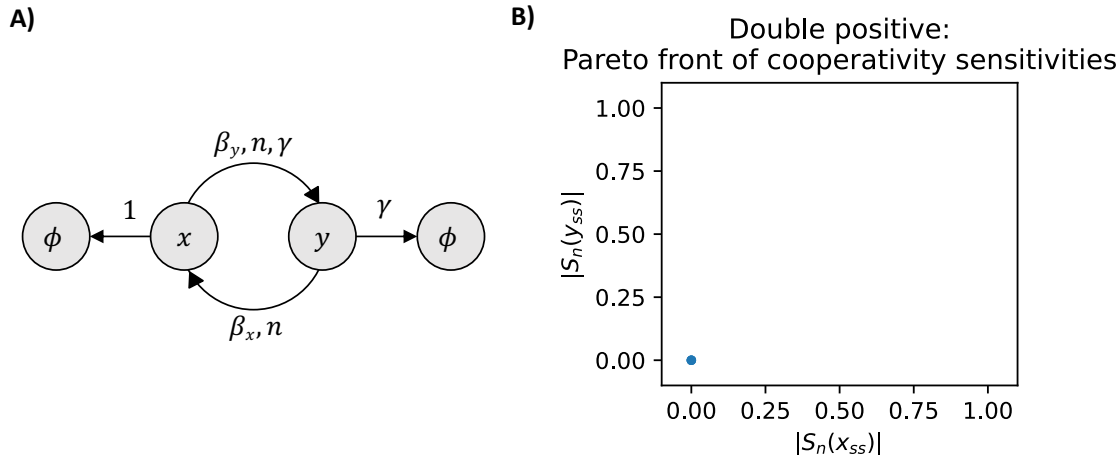

Figure 2: **The diagram of the positive-positive feedback system and the Pareto front of a representative pair of sensitivity functions. Panel A)** shows the diagram of the biological system with two positive feedbacks. The pointed arrows between species x and y represent positive feedback, where x enhances the production of y and vice versa. We assume that species x and y also undergo degradation and dilution within the cell, as indicated by the arrows pointed to the empty set symbol. The ratio of the rates of degradation and dilution is captured by the unitless parameter γ. After non-dimensionalization, the species x is degraded at a rate of 1, β_x is the rate of production of species x and $\beta_y\gamma$ is the rate of production of species y. Here, n represents the cooperativity of both species. **Panel B)** illustrates the Pareto front corresponding to the simultaneous minimisation of the absolute values of the sensitivities of species x and y with respect to the cooperativity n. The Pareto front for the positive-positive feedback system is the single point in blue. Solving the MOO problem shows that there is no trade-off between this pair of sensitivities. This result holds for all pairs of sensitivity functions.

2.3.3 Double-positive feedback is unconstrained by trade-offs

A biological system with two positive feedback loops, such as those found in T-cell differentiation, can reinforce a precursor cell's commitment to a specific lineage (*30*). These two feedback loops ensure a robust and irreversible decision, maintaining the differentiated state even after initial signals fade, and preventing partial differentiation. This design can be used in synthetic biology for stable state transitions or decision-making processes in cells (*31*).

The double-positive feedback loop, illustrated in Figure 2A, consists of two mutually promoting species, x and y, that each undergo degradation. The non-dimensionalized model of the double-feedback system can be described by the two ODEs in Equation (13).

$$\begin{cases} \dfrac{dx}{dt} = \left(\beta_x \dfrac{y^n}{1+y^n} - x\right) \\ \dfrac{dy}{dt} = \left(\beta_y \dfrac{x^n}{1+x^n} - y\right)\gamma \end{cases} \tag{13}$$

In this model, β_x and β_y are the ratios of the production rates to the degradation rates per unit of dissociation constants for species x and y, respectively. The constant γ is the ratio of the degradation rate of species x divided by the degradation rate of y. The constant n represents the cooperativity of the two species and we assume it to be the same for simplicity. We note that β_x, β_y, γ, and n are unitless and we refer to β_x and β_y as the strengths of the two positive feedbacks.

The steady states for this system, (x_{ss}, y_{ss}), occur when:

$$\begin{cases} x_{ss} = \beta_x \dfrac{y_{ss}^n}{1+y_{ss}^n} \\ y_{ss} = \beta_y \dfrac{x_{ss}^n}{1+x_{ss}^n} \end{cases} \tag{14}$$

We note that the ratio of the degradation rates, γ, is not present in the steady-state equations. Plotting the nullclines in the parameter ranges that we consider biologically relevant reveals a single non-zero steady-state solution that is stable. It is the only solution we consider for this analysis.

The sensitivities functions of each steady-state coordinate to parameters β_x, β_y and n are given in Table 2. We note that due to symmetry, it must be that $S_{\beta_x}(x_{ss}) = S_{\beta_y}(y_{ss})$. In Figure 2B), we illustrate a representative result of the problem of simultaneously minimising the absolute values of a pair of sensitivity functions. The Pareto front is comprised of a single point. This result holds across all pairs of sensitivity functions for combinations of both species (Supplementary Materials). Therefore, the double-positive feedback system is robust to changes in its biochemical parameters. This may be caused by the amplification created by the two positive feedbacks, mirroring the result of a single feedback system.

2.3.4 Positive-negative feedback loop is constrained by four trade-offs

The combination of positive and negative feedback is found in several biological processes such as the cell cycle. During the G2/M transition, positive feedback through cyclin-CDK complexes promotes rapid entry into mitosis, while negative feedback through checkpoint proteins such as p53 prevents progression if the DNA is damaged (*32*). The combination of positive and negative feedback is also believed to be responsible for robust oscillations found in natural systems. Synthetic circuits with these feedbacks were built in (*7*, *33*).

In the positive-negative feedback system, one species x promotes the expression of another species y, which in turn inhibits the production of x. We propose a simple mathematical model to capture these interactions. If we use similar biochemical assumptions to those in the derivation of the model for the double-positive feedback system, the dynamics of the positive-negative feedback system can be described by Equation (15) and are illustrated in Figure 3A).

$$\begin{cases} \dfrac{dx}{dt} = \left(\beta_x \dfrac{1}{1+y^n} - x\right) \\ \dfrac{dy}{dt} = \left(\beta_y \dfrac{x^n}{1+x^n} - y\right)\gamma \end{cases} \tag{15}$$

The steady states for this system, (x_{ss}, y_{ss}), occur when:

$$\begin{cases} x_{ss} = \beta_x \dfrac{1}{1+y_{ss}^n} \\ y_{ss} = \beta_y \dfrac{x_{ss}^n}{1+x_{ss}^n} \end{cases} \tag{16}$$

In this model, the nullclines intersect at a single steady-state solution, which is always non-zero unless $\beta_x = 0$. Thus, within our parameter ranges of interest, a single stable nonzero steady-state is found. We suspect that the model would require additional complexity to produce the oscillations observed in the literature.

For the single steady-state of the positive-negative system, we compute the sensitivity functions to variations in biochemical parameters and list them in Table 2. We note that

due to symmetry, it must be that $S_{\beta_x}(x_{ss}) = S_{\beta_y}(y_{ss})$. In Figure 3, we can observe trade-offs between the sensitivity function $S_{\beta_x}(x_{ss}) = S_{\beta_y}(y_{ss})$ and all the other sensitivity functions: $S_n(x_{ss}), S_{\beta_y}(x_{ss}), S_n(y_{ss})$, and $S_{\beta_x}(y_{ss})$. There are no trade-offs for other pairs of sensitivities.

The simultaneous minimization of $S_{\beta_x}(x_{ss})$ and $S_{\beta_y}(x_{ss})$, as well as $S_{\beta_x}(x_{ss})$ and $S_n(x_{ss})$ yields Pareto fronts at very high cooperativity values for n. Thus, to design a robust positive-negative feedback circuit, increasing the binding cooperativity as much as possible is the best design choice.

2.3.5 The double-negative feedback loop (the toggle switch) is unconstrained by trade-offs

The toggle switch is a classic synthetic circuit in which two species mutually inhibit one another while individually undergoing degradation (*34*). The toggle switch is a "winner takes all" system, where one species ends up depleted and the other plateaus to a higher steady-state concentration. The toggle switch, illustrated in Figure 4, can be described by the model in Equation (17). This is a gene-interaction level model obtained from (*35*).

$$\begin{cases} \dfrac{dx}{dt} = \left(\dfrac{\beta_x}{1+y^n} - x\right) \\ \dfrac{dy}{dt} = \left(\dfrac{\beta_y}{1+x^n} - y\right)\gamma \end{cases} \tag{17}$$

The steady-states for this system, (x_{ss}, y_{ss}), occur when:

$$\begin{cases} x_{ss} = \beta_x \dfrac{1}{1+y_{ss}^n} \\ y_{ss} = \beta_y \dfrac{1}{1+x_{ss}^n} \end{cases} \tag{18}$$

It is well-known that these two nullclines can intersect at up to three steady-state solutions. When three solutions are present, two are stable, and one is unstable. However, as the parameters change, the system undergoes a bifurcation where a stable and an unstable solution collide and disappear, leaving only a single stable solution. When only one stable

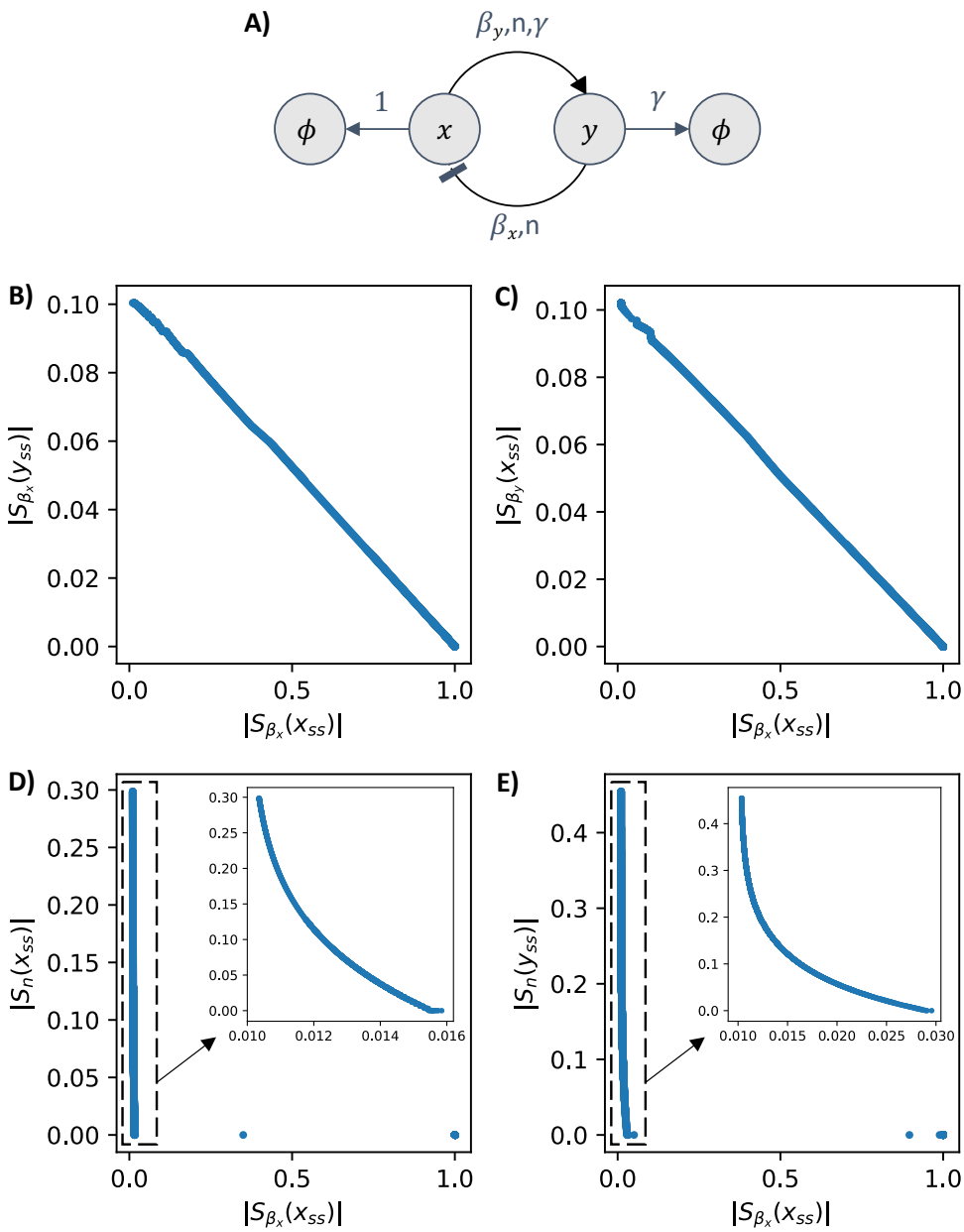

Figure 3: **The diagram of the positive-negative feedback system and the Pareto fronts of four pairs of sensitivity functions. Panel A)** shows the diagram of a biological system with positive feedback (pointed arrow) from species x to species y, and negative feedback (blunt arrow) from species y to species x. Both species undergo degradation. After non-dimensionalization, x is degraded at a rate of 1, y is degraded at a rate of γ, and production rates are β_x for x and $\beta_y\gamma$ for y. The binding cooperativity is n. **Panels B), C), D), and E)** display the Pareto fronts obtained from the simultaneous minimizations of the absolute sensitivity of species x to its production rate β_x against four other sensitivities. The four Pareto fronts, shown as blue lines, highlight trade-offs between these four pairs of sensitivities. The arrows in panels D) and E) point to a zoomed-in view of the Pareto fronts. Solving the multi-objective optimization problems reveals four distinct trade-offs in the positive-negative feedback system.

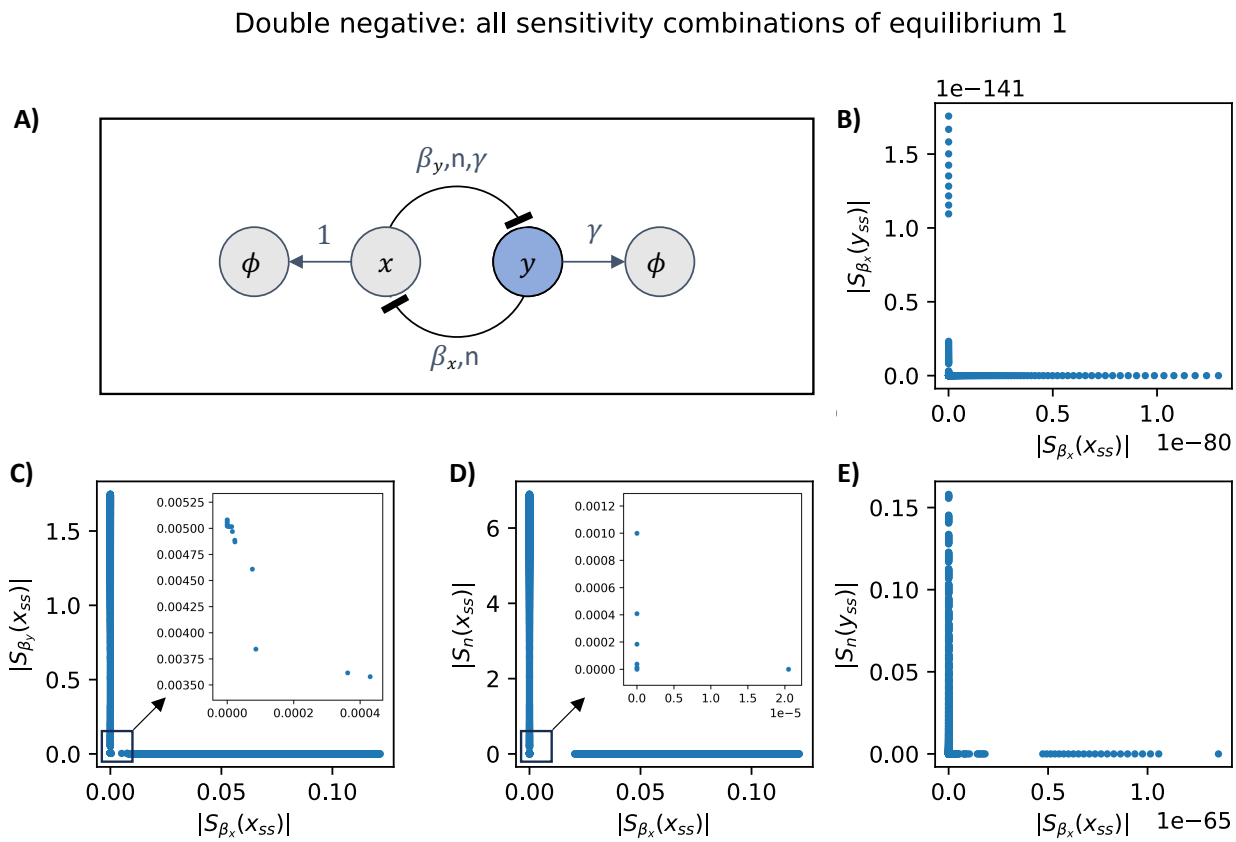

Figure 4: **The diagram of the toggle switch and four of its Pareto fronts. Panel A)** shows the diagram of two biochemical species x and y that mutually inhibit each other. The inhibitions are illustrated by blunt arrows. Both species x and y are subject to degradation, as indicated by arrows pointing to the empty set symbol. The reaction rates are listed above each arrow. **Panels B)- E)** show the Pareto fronts obtained by simultaneous minimisation of four sensitivity function pairs. In panels C) and D), we include the zoomed in version of the same figure. All four sensitivity function pairs are simultaneously minimised close to zero. Thus, no trade-offs are present in the model of the toggle switch.

steady-state exists, we compute its sensitivity function and later use it to supplement the two sensitivity functions that arise when two stable steady-states appear after the bifurcation.

The sensitivity functions associated with the stable steady-states of the toggle are given in Table 3. We note that due to symmetry, it must be that $S_{\beta_x}(x_{ss}) = S_{\beta_y}(y_{ss})$. In Figure 4, we illustrate representative results of the problem of simultaneously minimising the absolute values of a pair of sensitivity functions. We direct the reader to the Supplementary Materials for the all the results of simultaneously minimising pairs of sensitivity functions. All of these MOO problems are solved to find Pareto fronts close to value zero. Thus, the toggle circuit is free of trade-offs and robust to variations in its biochemical parameters.

3 CONCLUSION

In this paper, we introduced a general computational framework to analyse how robust biological systems that use feedback regulation are to variations in their biochemical parameters and we revealed the trade-offs in robustness that are present for these systems. Our computational framework uses multi-objective optimization to simultaneously minimize the sensitivities of these biological systems to variations in pairs of biochemical parameters. The results of the multi-objective optimization problems reveal whether trade-offs between the robustness to variations in pairs of parameters are present.

To illustrate this computational framework, we considered five examples of biological systems with feedback and analysed their sensitivity to variations in biochemical parameters. In single-species feedback, a trade-off between feedback the sensitivity to feedback strength and to cooperativity is found for negative autoregulation but is absent for positive autoregulation. Indeed, we find that in negative autoregulation, increasing the robustness to variations in cooperativity is only possible at a loss of robustness in feedback strength, and vice versa.

In dual-species feedback, we found several trade-offs between the strengths of feedback

and the cooperativity of biomolecules. In double-positive feedback and the toggle switch, no trade-offs arise, similar to positive autoregulation. However, positive-negative feedback is constrained by trade-offs, requiring that the system design carefully balances robustness to feedback strength and cooperativity.

Our work contributes to understanding trade-offs in the robustness of biological systems with feedback regulation. While it is well-known that engineered feedback is constrained by robustness trade-offs, as it cannot fully counteract all disturbances, similar insights for biological feedback systems remain underexplored. This paper helps bridge that gap by providing evidence of analogous trade-offs in biological contexts.

Future directions of this research include optimizing the sampling algorithm to efficiently solve multiple-objective optimization problems for parameter spaces in higher than three dimensions. We discuss the limitations of the grid-sampler and potential other algorithms in Section 4.4 of the Methods. Further research could replace the sensitivity functions evaluated at steady-state with the sensitivity functions for transient dynamics developed by Wu *et al.* (*36*) and assess the robustness of biological systems such as oscillators (*7*, *37*). Lastly, further research could use this computational framework to research other examples of biological feedback systems and to develop theoretical arguments for why some examples of feedback introduce robustness trade-offs, while others do not.

Our current research contributes to advancing the understanding of biological feedback in natural systems and to improving system design for synthetic biological circuits. Ultimately, we aim for our work to facilitate future research aimed at unraveling the complexities of feedback in biological systems and at enhancing the reliability of engineered biological applications.

4 METHODS

4.1 Non-dimensionalization of the mathematical models

Nondimensionalising biochemical kinetics involves defining the relationships between physical quantities with units and their unitless analogues, and performing a change of variables of the original equations. Table 1 lists the model pairs for each feedback mechanism, and the associated changes of variables.

Table 1: Mathematical models before and after non-dimensionalization for each of the biological systems studied in the paper. Tildes denote the unitless analogue of their original physical quantity. For simplicity, we use the variables without tildes in the unitless models.

	Original model	Change of variables	Unitless model
Positive autoregulation	$\frac{dx}{dt} = \alpha \frac{x^n}{k^n + x^n} - \gamma x$	$\tilde{x} = x/k$ $\tilde{t} = \gamma t$ $\tilde{\alpha} = \alpha/(k\gamma)$	$\frac{dx}{dt} = \alpha \frac{x^n}{1 + x^n} - x$
Negative autoregulation	$\frac{dx}{dt} = \alpha \frac{1}{k^n + x^n} - \gamma x$		$\frac{dx}{dt} = \alpha \frac{1}{1 + x^n} - x$
Double-positive	$\begin{cases} \frac{dx}{dt} = \beta_x \frac{y^n}{k^n + y^n} - \gamma_x x \\ \frac{dy}{dt} = \beta_y \frac{x^n}{k^n + x^n} - \gamma_y y \end{cases}$	$\tilde{x} = x/k_x$ $\tilde{y} = y/k_y$ $\tilde{t} = \gamma_x t$ $\tilde{\beta}_x = \beta_x/(k_x\gamma_x)$ $\tilde{\beta}_y = \beta_y/(k_y\gamma_y)$ $\gamma = \gamma_y/\gamma_x$	$\begin{cases} \frac{dx}{dt} = \left(\frac{\beta_x y^n}{1 + y^n} - x\right) \\ \frac{dy}{dt} = \left(\frac{\beta_y x^n}{1 + x^n} - y\right) \gamma \end{cases}$
Positive-negative	$\begin{cases} \frac{dx}{dt} = \beta_x \frac{1}{k^n + y^n} - \gamma_x x \\ \frac{dy}{dt} = \beta_y \frac{x^n}{k^n + x^n} - \gamma_y y \end{cases}$		$\begin{cases} \frac{dx}{dt} = \left(\frac{\beta_x}{1 + y^n} - x\right) \\ \frac{dy}{dt} = \left(\frac{\beta_y x^n}{1 + x^n} - y\right) \gamma \end{cases}$
Double-negative	$\begin{cases} \frac{dx}{dt} = \beta_x \frac{1}{k^n + y^n} - \gamma_x x \\ \frac{dy}{dt} = \beta_y \frac{1}{k^n + x^n} - \gamma_y y \end{cases}$		$\begin{cases} \frac{dx}{dt} = \left(\frac{\beta_x}{1 + y^n} - x\right) \\ \frac{dy}{dt} = \left(\frac{\beta_y}{1 + x^n} - y\right) \gamma \end{cases}$

4.2 Parameter ranges for the models of the biological systems

In this work, we assume that the synthesis rates $\alpha, \beta \in [0.02, 0.1]$ nM min^{-1} according to values from (*38*), that dissociation constants $k \in [0.01, 10]$ nM (*38*, *39*), and that the degradation and dilution rates $\gamma \in [0.01, 0.24]$ min^{-1}, as follows from the typical doubling times of bacterial and yeast cells (*40*, *41*).

From Table 1, unitless feedback strengths $(\tilde{\alpha}, \tilde{\beta})$ are defined as the ratio between the maximal production rate (α, β) and the product of dissociation constant (k) with degradation rate (γ). The range of values for the unitless feedback strengths is therefore $\tilde{\alpha}, \tilde{\beta} \in [1/120, 1000]$. For practicality, we sample the range $[0.01, 50]$.

Cooperative binding falls into four classes: binding that does not change the system dynamics $(n = 0)$, binding that impedes further binding $(0 < n < 1)$, binding that has no effect on subsequent binding $(n = 1)$ and binding that promotes further binding $(n > 1)$. At $n = 0$, the feedback disappears. Therefore, we consider $n > 0$. We set a lower bound of $n = 0.01$ for our numerical simulations. The upper bound was set to $n = 10$ to cover the single digit cooperativities that are common to biological systems (*42*).

4.3 Numerical methods

The equations for steady-states in Table 1 cannot typically be solved analytically to find their solutions x_{ss} and y_{ss}. Instead, we employ scipy.optimize.fsolve from Python to solve these equations numerically. The parameter set we use was obtained by evenly grid-sampling the parameter ranges of α, β and n. Additionally, since we are only interested in the stable steady-states of our biological systems, we filtered out the unstable steady-states by imposing the condition that the real part of their eigenvalues evaluated at the solutions is less than zero. The resulting solutions and their respective parameter values were then used to evaluate the corresponding sensitivity functions via the analytically derived formulas. We refer the reader to the linked Mathematica files for the analytical derivations of the sensitivity functions.

In the MOO problems, the Pareto front was found using the Python package paretoset, based on the method proposed by (*43*).

4.4 Limitations of the sampling algorithm

The correct identification of the Pareto front is dependent on sufficiently sampling the two- or three-dimensional biochemical parameter space. The grid-search sampler we use is a compu-

tationally expensive method. For example, to find the Pareto fronts for the MOO problems in the positive-negative feedback system, we use 10^9 samples for the three-dimensional grid.

The development of computationally efficient algorithms for solving multi-objective optimization problems remains an active area of research. More efficient methods such as Multi-Objective Simulated Annealing (*44*) could be used in future work to reduce the number of samples required to find the Pareto fronts.

4.5 Sensitivity functions

In this section, we include the analytical form of the sensitivity functions for all two-species examples in Tables 2 and 3.

5 Author Contributions

A.-A.B. conceptualized the project. N.H.N.T., A.N., and T.W.R. carried out the computational simulations. N.H.N.T. and A.-A.B. analyzed the results and wrote the manuscript.

The authors declare no competing interests.

Table 2: The sensitivity functions of the positive-positive feedback and the positive-negative feedback example systems.

Positive-Positive Feedback	$S_{\beta_x}(x) = \dfrac{\beta_x \beta_y}{n^2 x\left(-y+\beta_y\right)+\beta_x\left(n^2 y-\left(-1+n^2\right)\beta_y\right)}$
	$S_{\beta_y}(x) = \dfrac{n\beta_y}{n^2 y+\left(1-n^2+\frac{x}{-x+\beta_x}\right)\beta_y}$
	$S_n(x) = \dfrac{n\left(-ny\log[x]+(n\log[x]+\log[y])\beta_y\right)}{n^2 y+\left(1-n^2+\frac{x}{-x+\beta_x}\right)\beta_y}$
	$S_{\beta_x}(y) = \dfrac{n\beta_x}{n^2 x+\beta_x\left(1-n^2+\frac{y}{-y+\beta_y}\right)}$
	$S_{\beta_y}(y) = \dfrac{\beta_x \beta_y}{n^2 x\left(-y+\beta_y\right)+\beta_x\left(n^2 y-\left(-1+n^2\right)\beta_y\right)}$
	$S_n(y) = \dfrac{n\left(-nx\log[y]+(\log[x]+n\log[y])\beta_x\right)}{n^2 x+\beta_x\left(1-n^2+\frac{y}{-y+\beta_y}\right)}$
Positive-Negative Feedback	$S_{\beta_x}(x) = \dfrac{\beta_x \beta_y}{n^2(\beta_x-x)(\beta_y-y)+\beta_x\beta_y}$
	$S_{\beta_y}(x) = -\dfrac{n\beta_y(\beta_x-x)}{n^2(\beta_x-x)(\beta_y-y)+\beta_x\beta_y}$
	$S_n(x) = -\dfrac{n(n\ln(x)x+\ln(y)\beta_y)(\beta_x-x)}{n^2(\beta_x-x)(\beta_y-y)+\beta_x\beta_y}$
	$S_{\beta_x}(y) = \dfrac{n\beta_x(\beta_y-y)}{n^2(\beta_x-x)(\beta_y-y)+\beta_x\beta_y}$
	$S_{\beta_y}(y) = \dfrac{\beta_x \beta_y}{n^2(\beta_x-x)(\beta_y-y)+\beta_x\beta_y}$
	$S_n(y) = \dfrac{n(\ln(x)\beta_x-n\ln(y)(\beta_x-x))(\beta_y-y)}{n^2(\beta_x-x)(\beta_y-y)+\beta_x\beta_y}$

Table 3: The sensitivity functions of the toggle switch.

Negative-Negative Feedback	$S_{\beta_x}(x) = \dfrac{\beta_x \beta_y}{-n^2 (x-\beta_x)(y-\beta_y) + \beta_x \beta_y}$
	$S_{\beta_y}(x) = \dfrac{n (x-\beta_x) \beta_y}{n^2 x (-y+\beta_y) + \beta_x (n^2 y - (-1+n^2) \beta_y)}$
	$S_n(x) = -\dfrac{n (x-\beta_x) (ny \log[x] + (-n \log[x] + \log[y]) \beta_y)}{-n^2 y \beta_x + n^2 x (y-\beta_y) + (-1+n^2) \beta_x \beta_y}$
	$S_{\beta_x}(y) = \dfrac{n \beta_x (y-\beta_y)}{n^2 x (-y+\beta_y) + \beta_x (n^2 y - (-1+n^2) \beta_y)}$
	$S_{\beta_y}(y) = \dfrac{\beta_x \beta_y}{-n^2 (x-\beta_x)(y-\beta_y) + \beta_x \beta_y}$
	$S_n(y) = -\dfrac{n (nx \log[y] + (\log[x] - n \log[y]) \beta_x) (y-\beta_y)}{-n^2 y \beta_x + n^2 x (y-\beta_y) + (-1+n^2) \beta_x \beta_y}$

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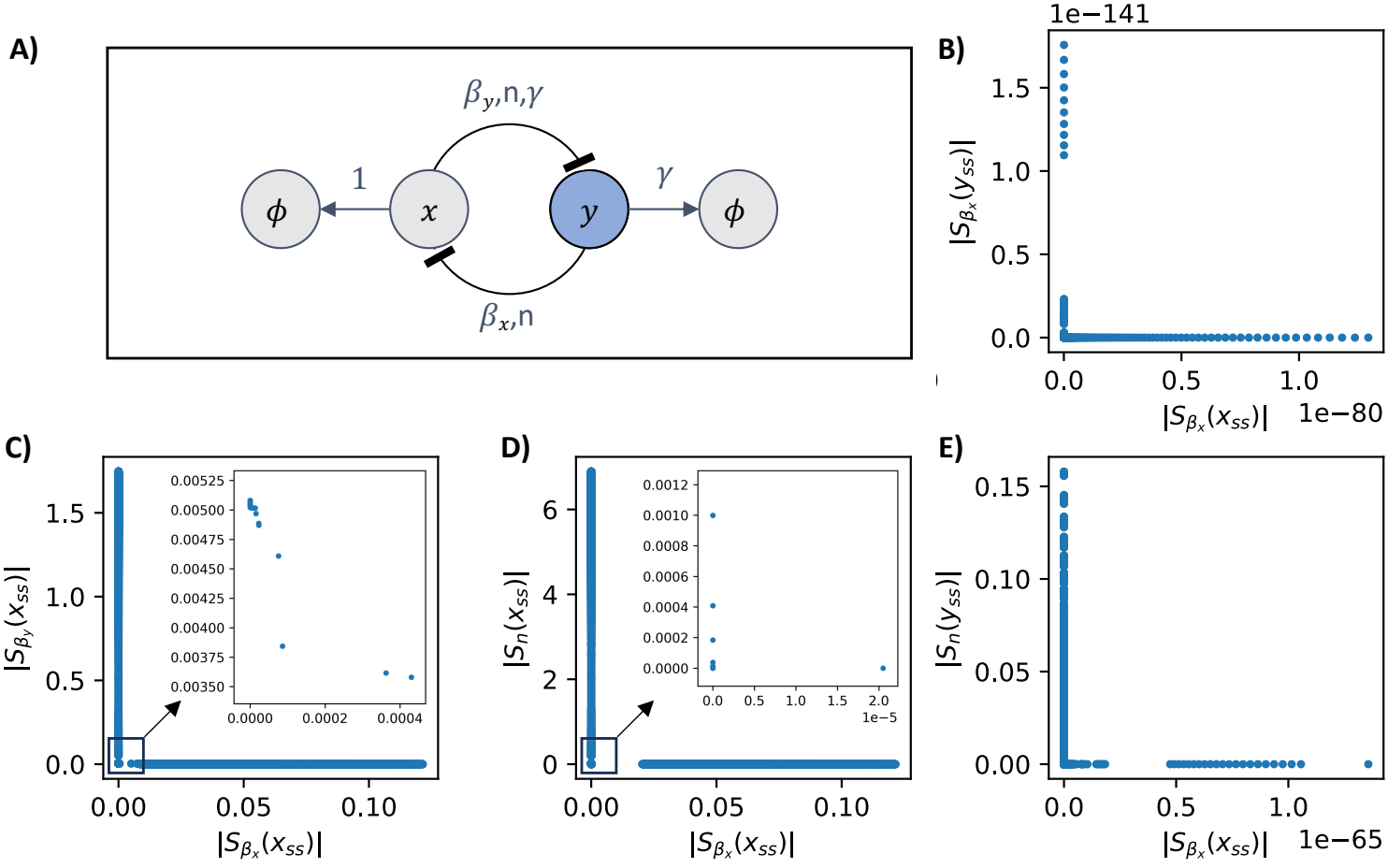
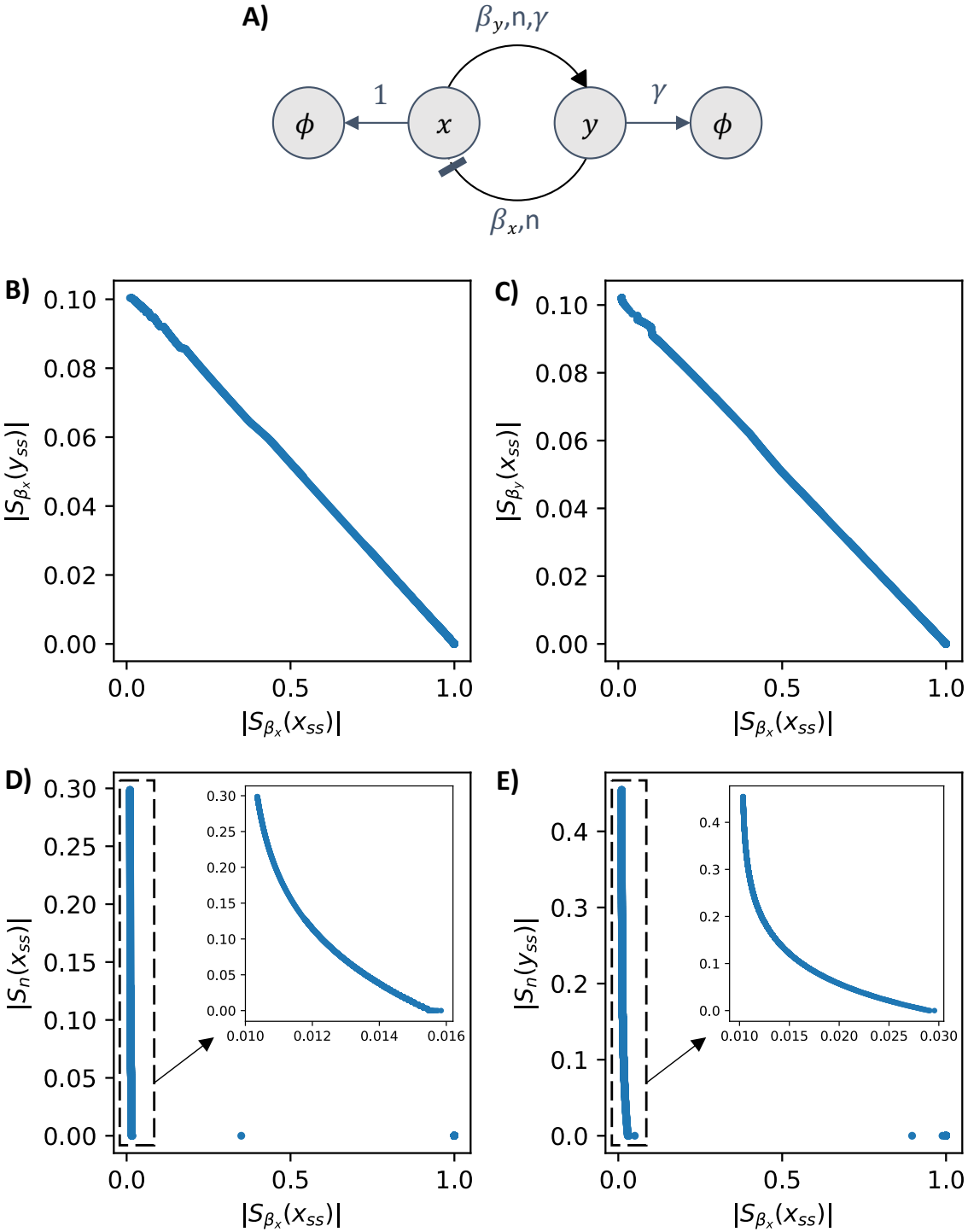
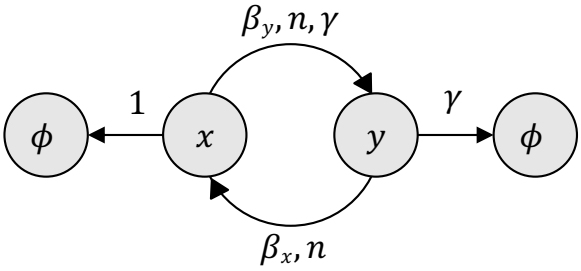
Double negative: all sensitivity combinations of equilibrium 1

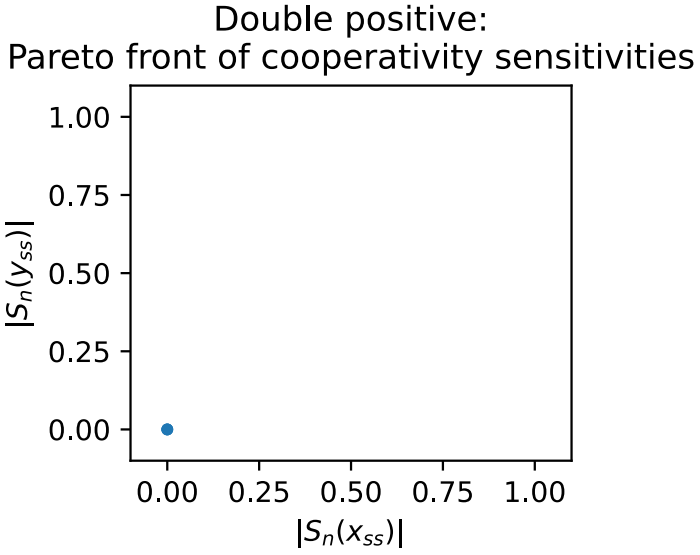


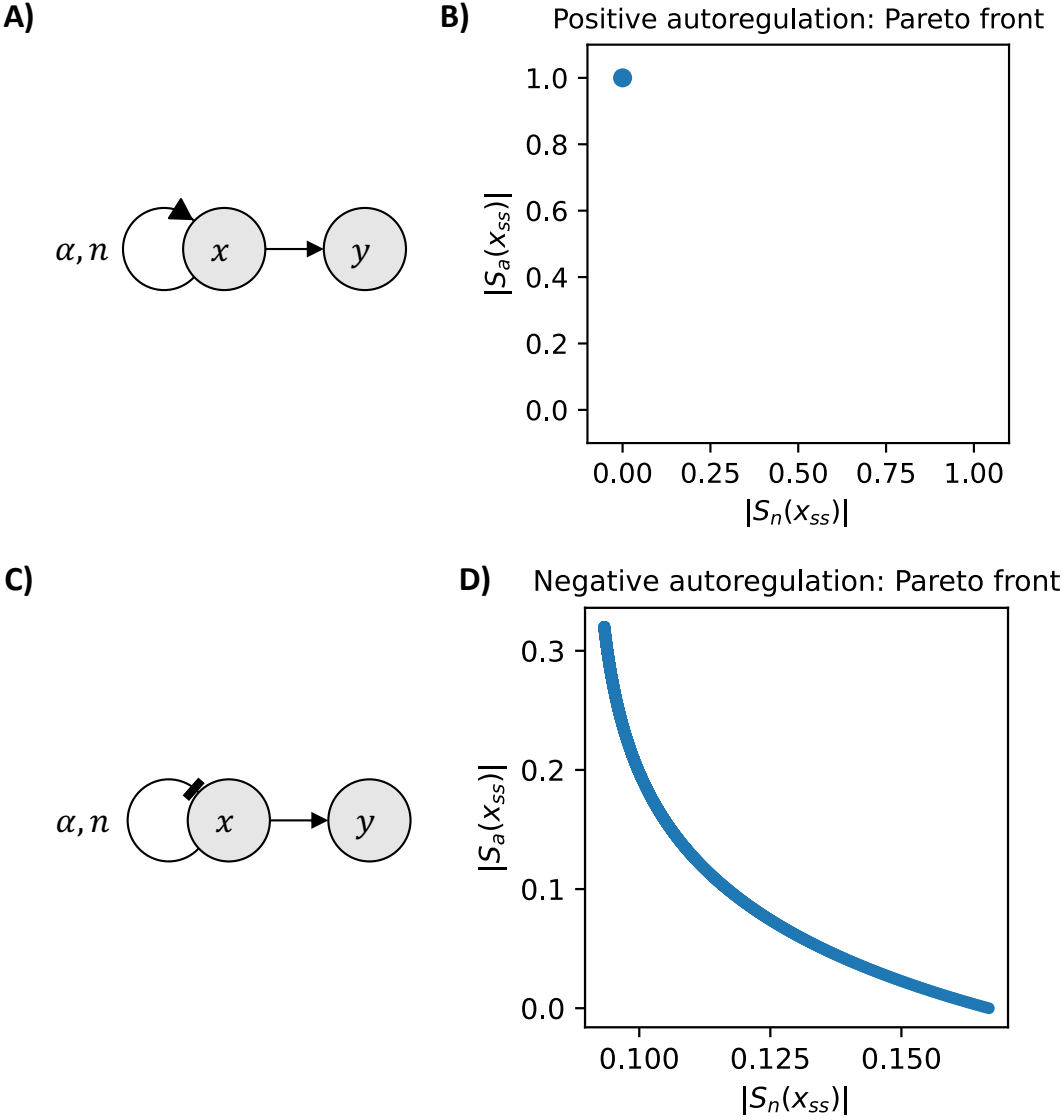

A)
β_y,n,γ
1
γ
ϕ
x
y
ϕ
β_x,n
B)
$|S_{\beta_x}(y_{ss})|$
$|S_{\beta_x}(x_{ss})|$
C)
$|S_{\beta_y}(x_{ss})|$
$|S_{\beta_x}(x_{ss})|$
D)
$|S_n(x_{ss})|$
$|S_{\beta_x}(x_{ss})|$
E)
$|S_n(y_{ss})|$
$|S_{\beta_x}(x_{ss})|$

A)


β_y, n, γ
1
γ
ϕ
x
y
ϕ
β_x, n

B)


Double positive:
Pareto front of cooperativity sensitivities
1.00
0.75
0.50
0.25
0.00
$|S_n(y_{ss})|$
0.00
0.25
0.50
0.75
1.00
$|S_n(x_{ss})|$


A)
α, n
x
y
B)
Positive autoregulation: Pareto front
1.0
0.8
0.6
0.4
0.2
0.0
$|S_a(x_{ss})|$
0.00
0.25
0.50
0.75
1.00
$|S_n(x_{ss})|$
C)
α, n
x
y
D)
Negative autoregulation: Pareto front
0.3
0.2
0.1
0.0
$|S_a(x_{ss})|$
0.100
0.125
0.150
$|S_n(x_{ss})|$