

# Inferring bifurcations between phenotypes

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A dissertation submitted in fulfillment  
of the requirements for the degree of

**Doctor of Philosophy**

at

**King's College London**

Randall Division of Cell & Molecular Biophysics



funded by **Microsoft Research Cambridge**



October 29, 2021

# Abstract

The gene-expression history of an organism and its environment determine the organism's phenotype. The phenotype is an inherently qualitative state, deduced by relative biochemical concentration measurements collected by methods such as flow cytometry or fluorescence microscopy. The biochemical threshold concentrations that distinguish different phenotypes can be modelled by applying bifurcation analysis to differential equation models and the search for these boundaries in experimental data can be done using dimensionality reduction and clustering techniques. This establishes a relationship between bifurcations, phenotypes and machine learning techniques that are the subject of this thesis.

The first chapter presents an interactive tool for exploring phenotypes in flow cytometry data. In particular we explore a multi-tissue, high-dimensional, immune cell dataset. The tool bridges machine learning methods and the popular FlowJo, used to annotate cells with gating strategies. An assortment of dimensionality reduction techniques are applied to create two dimensional embeddings and confusion matrices are used to quantify annotation agreement between immunologists. By leveraging the geospatial mapping library OpenLayers to render, annotate and analyze cells, immunologists can now efficiently navigate the phenotype space of Human Cell Atlas datasets.

The next chapter focuses on a model-driven approach for exploring and designing phenotypes, where we demonstrate how model-guided design of synthetic E. Coli can elucidate pattern formation mechanisms in multicellu-

lar development. We infer the parameters of a biochemically motivated system of differential equations against time course fluorescence data acquired from plate reader experiments. Our design goals however were not in the temporal domain, rather we wanted to control the shape and size of a cusp bifurcation in the space of experimentally controlled input concentrations.

To address these limitations, I define a differentiable semi-supervised cost function that uses bifurcation locations as targets. Bifurcations are encouraged by an unsupervised term that extremises the curvature of the determinant of the Jacobian. By exploring the cost landscape for minimal models that span the space of saddle-nodes and pitchforks, I show that the parameter space basins define regions of qualitatively equivalent differential equations. The differentiability of the cost function enables efficient optimisation using libraries such as Flux.jl that leverage automatic differentiation. The impact of this work would enable experimentalists to efficiently navigate design spaces of differential equation models.

# Acknowledgements

Acknowledgements to people I love

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## Chapter 1

# Introduction & Motivation



*one thing that won't change with time is the memories of younger years*

---

Minuet of Forest — Ocarina of Time

The advent of the modern digital computer, as formalised by Alan Turing,[1] ignited the field of computational physics, aided by pre-existing theoretical formulations of algorithms. Starting from the first experiments with Monte Carlo (MC) simulations in the 1930s by Fermi and the formulation of the Markov-Chain Monte Carlo (MCMC) technique by Ulam in the 1940s, von Neumann programmed the 18,000 vacuum-tube Electronic Numerical Integrator and Computer (ENIAC) computer to investigate neutron diffusion in fissionable materials.[2] This success paved the way for the integration of Newton's equations of motion to compute the time evolution of a many-body system.

Consider being Marian Adam Rejewski, a Polish mathematician and cryptologist in 1932, almost seven years before the beginning of World War II. It was known at the time that the Germans were using a machine called *Enigma I* to send secret messages, but no one knew what the machine looked like nor how it worked. Based on a handful of intercepted encrypted mes-

sages and pictures of the operating instructions obtained by Polish intelligence, he derived a set of permutation equations that allowed him the reverse-engineer the machine [3]. The cryptologic achievements of Rejewski and colleagues Jerzy Różycki and Henryk Zygalski are considered the some of the greatest feats in reverse-engineering of the 20th century.



**Figure 1.1:** *Enigma I* reverse engineered by Marian Adam Rejewski

Today we are getting ever closer to reverse-engineering the cell. The fields of synthetic and systems biology are beginning resemble engineering disciplines; genetic engineering is becoming more precise, high-throughput in vitro experiments are performed by robots and measurements of many desired observables can be obtained with high spatio-temporal resolution. Advances in micro-fabrication [4] and in-vitro reconstitutive methods [5] have allowed biologists isolate pathways and mechanisms to a level of mathematical and computational tractability [6]. This section outlines the scientific paradigms in these fields, their methods and limitations, and finally what this thesis will attempt to contribute.

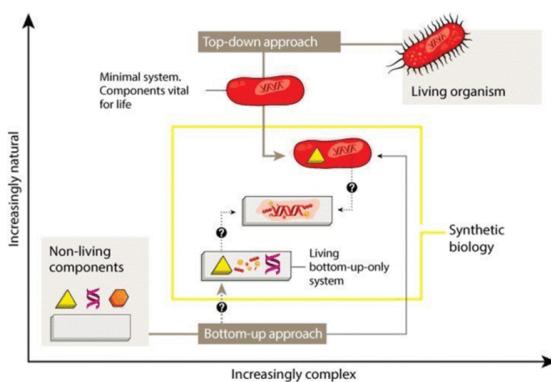
## 1.1 Bottom-up and Top-down Biology

Fortunately for biologists copies of the target of their reverse-engineering attempts are available all around us. Less fortunate is the fact that most attempts at deconstructing the cell end in loss of function and destruction of the individual components. This restriction motivates system biologists to manipulate environmental signals *in vivo* and build mechanistic models from correlations between signals and responses [7]. Models focus on

relationships between macroscopic variables where the underlying mechanisms are not known.

*In vitro* reconstitutive methods aim to isolate minimal mechanisms from the complexity of the whole organism in order to unpick the relative importance of microscopic details [5]. In situations where purified proteins and crystal structures are available these methods can quite accurately characterise the kinetics of proteins. Relating these parameters to the *in vivo* context however may not be relevant, as too much of the complexity may have been stripped away.

From a theoretical modelling perspective, it is important to choose a time-scale and space-scale that is relevant to the problem. If one is interested in tissue dynamics, attempting to model DNA conformations within each cell will render the problem intractable. As George Booth aptly put “*most models are wrong but some are useful*” so the role of theoretical descriptions in these settings is not necessarily to describe the way reality *is* but serve as tools to bridge the non-intuitive gap between bottom-up and top-down approaches. Where intuition fails is where the *in silico* hypothesis testing playground becomes most valuable [6].

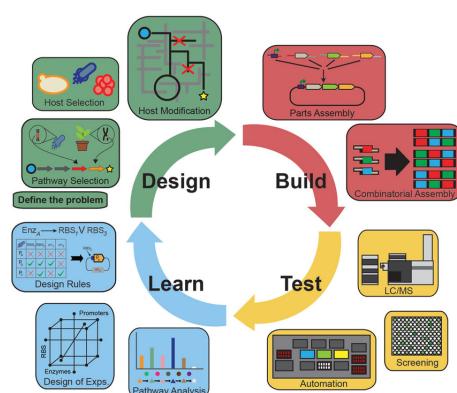


**Figure 1.2:** Top-down and bottom-up modelling methods

## 1.2 Design, Build, Test, Learn

Systems and synthetic biology have historically made progress through a process of brute force trial and error. This usually involves the interaction of many custom-made parts that are iteratively optimised by human intervention. A trend first observed in the 1980s known as *Eroom's law* reveals that discoveries in biotechnology are becoming slower and more expensive over time, despite improvements in technology [8]. This problem is compounded by the ongoing reproduciblility crisis [9]. In the effort to transform methods used in academia and industry to become more systematic and predictable, a standard for the Design–Build–Test–Learn cycle has emerged – showin in figure 1.3.

This workflow has now been established as a paradigm with some aspects that have been automated by liquid handling robots, bioreactor environments and image processing pipelines. However, humans in the loop and custom moving parts still persist. The challenge in automating these processes lies in defining a programming language that has a sufficiently high level of abstraction for transparent implementation while allowing for low-level customisation [10].



**Figure 1.3:** Design-Build-Test-Learn cycle from synthetic biology

This thesis will focus on modelling and inference using systems of differential and partial differential equations, which fits into the Design–Learn

part of the cycle. Differential equations occupy a small subset of possible modelling tools, however they are amongst the most popular due to their ease of use formulation and simulation. This ease of access creates a zoo of models in literature making it difficult to identify the key ingredients that distinguish different models. Furthermore the relationship between multiple plausible *and* in-plausible hypotheses is rarely investigated. This motivates desire for an automated Design–Learn pipeline – outlined in Section 1.4 – which can generate and catalogue models in a transparent manner while producing insights for the Build stage. This pipeline is applied in an experiment-theory collaboration described in Chapter 3.

## 1.3 State of the Art

### 1.3.1 Inference of Differential Equations

Following the initial literature on smooth and match estimators [11] – which overcome the bottleneck having to integrate a proposed hypothesis for every parameter update – a plethora of methods for the inference of differential equations became available [12, 13]. The essence of these methods is to estimate the derivatives of the data rather than integrate the model and simultaneously estimate the qualitative and quantitative behaviours. In most biological experiments batch-to-batch variations decrease the certainty with which it is possible to quantify a behaviour. Whether or not a parameter is identifiable, redundant or sloppy have become key questions in biology [14, 15, 16].

### 1.3.2 Model Reduction and Classification

Sloppiness and sensitivity analysis have been extensively used in the search for reduced models. Linear mappings between models that preserve stoichiometry and reactant structure were investigated [17, 18] and computational tools based on partition-refinement were released [19]. Structural similarity between reaction networks can be revealed by such mappings, elucidating the functional aspects of complex networks in terms of simpler

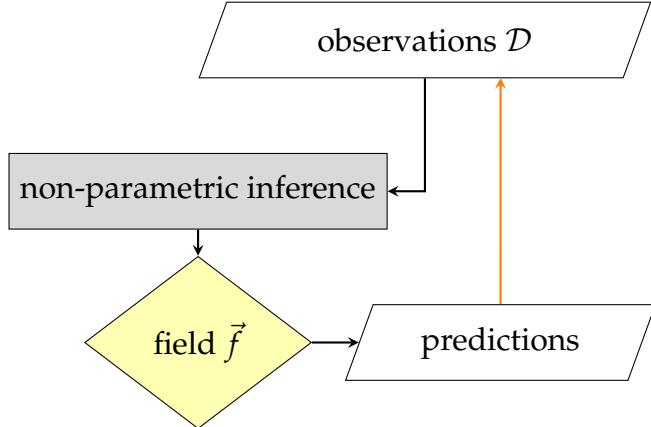
networks. The aim of the Design–Learn pipeline is to extend this framework to nonlinear mappings with an emphasis on geometry rather than kinetics. Most inference techniques attempt to match geometry and kinetics simultaneously in an attempt to obtain a quantitative model. This thesis emphasises that geometry alone should be prioritised in order to obtain qualitatively equivalent models. Furthermore recent results in pattern formation theory [20] do not depend on kinetics at all, only geometry.

## 1.4 Design–Learn Pipeline

This section outlines the proposal for a design–learn pipeline for the purposes of model reduction and system design. Suppose experimental collaborators have provided us with time-course gene expression data  $\mathcal{D}$ , which could be taken via time-lapse microscopy of cells growing on microfluidic plates, optical density measurements from microtiter plate assays or temporal snapshots of flow cytometry measurements. On the other hand one may want to specify a behaviour  $\mathcal{H}$  which may have not yet been observed. This would be specified with top-down constraints, i.e. there exist oscillations of a fixed frequency or a region of bistability.

### 1.4.1 Experimental Design Loop

The experimentalists may want to know whether the data collected could result in a model of predictive power without mechanistic knowledge of the underlying biochemistry. Moreover it would be desirable gain insights in parameter regimes in the vicinity of observations, without having to wait for the theorists to produce a refined model. Such real-time insights would guide data collection protocols, optimising the amount of information gained while keeping the number of experiments performed to a minimum. Often data is noisy and at worst case contradictory; these issues must also be exposed.



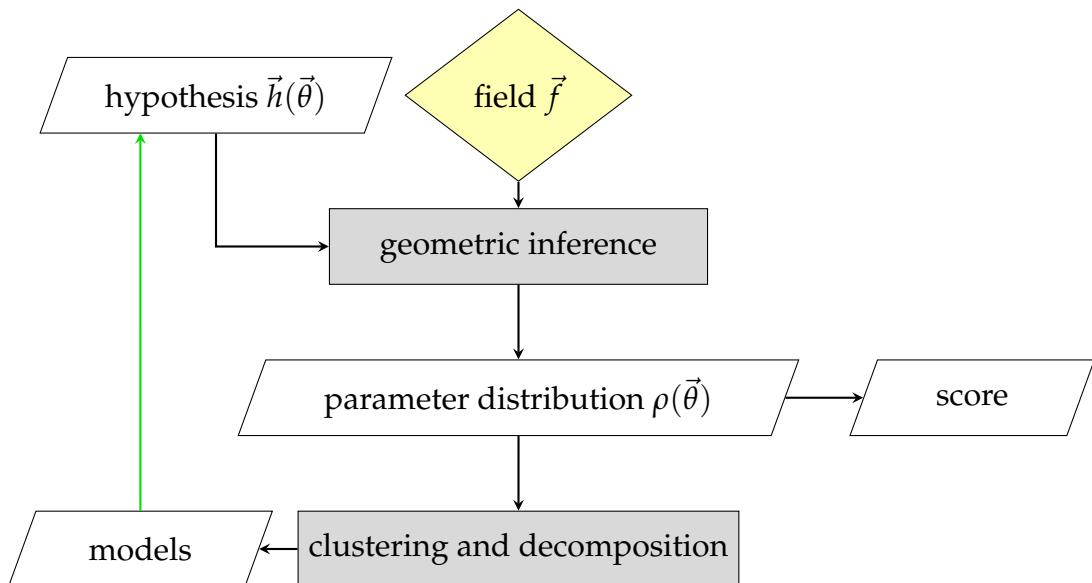
**Figure 1.4:** Workflow loop for optimal experimental design, without mechanistic model

Figure 1.4 outlines the workflow for optimal experimental design. The term *non-parametric* defines the procedures that have prioritised functional generality and flexibility over mechanistic insights gained from the values of the parameters and shapes of the mathematical forms. Neural networks and Gaussian process regressors are examples of non-parametric estimation procedures, which produce an estimate of the field  $\vec{f}$  that predicts gene expression rates at given expression levels. Based on these predictions, the experimentalist may proceed to collect data in the most informative parameter regions, which would in turn more accurately estimate  $\vec{f}$ .

### 1.4.2 Hypothesis Scoring and Model Refinement Loop

Often predictions from field  $\vec{f}$  are not enough. Models constructed with feasible biophysical assumptions  $\vec{h}(\vec{\theta})$  have the potential to extrapolate predictions and give concrete biophysical meanings to each parameter  $\vec{\theta}$ . This way the experimentalist knows exactly which modification to the system they must make in order to achieve a desired behaviour. More often than not it is also unclear whether the model and its assumptions are reasonable, which brings us to the desire to score our hypotheses. For increased accuracy and efficiency [21] the mechanistic model  $\vec{h}(\vec{\theta})$  is inferred against non-parametric estimate  $\vec{f}$  rather than the data  $\mathcal{D}$  directly. Furthermore as discussed in Section 1.3 the aim is to optimise geometry rather than kinetics.

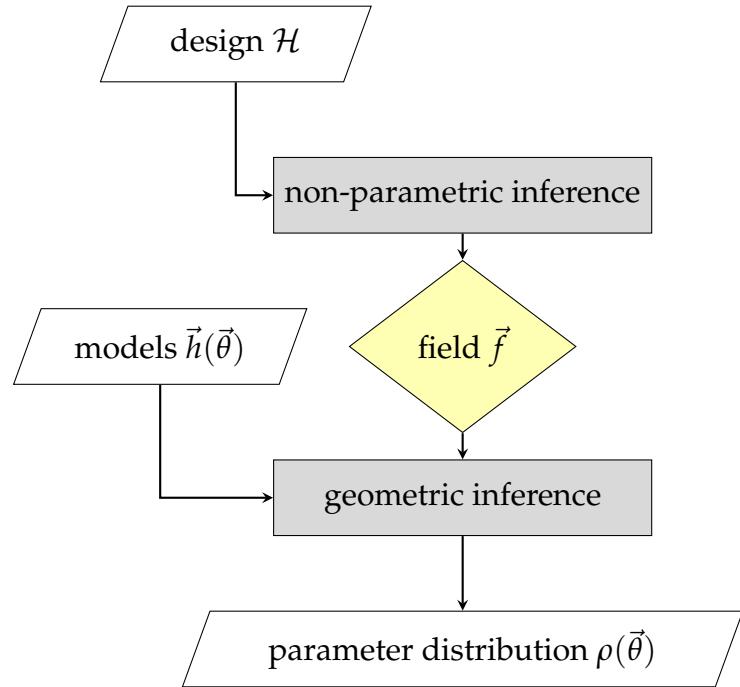
Alternatively one may construct  $\vec{h}(\vec{\theta})$  to cover a whole class of models, such as those that satisfy mass-action. The expectation is that most of the parameters would be zero but some would be informative. One can obtain a distribution of optimal parameters  $\rho(\vec{\theta})$  by running multiple optimisations. From this distribution one may construct alternative hypotheses and update  $\vec{h}(\vec{\theta})$ . By iterating this procedure one would identify the minimal model within the model class that explains the data. This process is known as model refinement or reduction.



**Figure 1.5:** Overview of hypothesis scoring pipeline and model refinement loop

### 1.4.3 System Design

Suppose now that refined mechanistic models of the form  $\vec{h}(\vec{\theta})$  have been obtained using the model refinement loop. These could be a library of known parts that have been individually characterised, but never combined to form a larger system. The experimentalists would like to create a system with a specified behaviour  $\mathcal{H}$  and would like to know which parts to combine and which modifications to make. The model refinement loop can be used with the design as an input.



**Figure 1.6:** Overview of system design pipeline

## Chapter 2

# Theoretical Background

*melody that will draw you into infinite darkness*

---

Ocarina of Time

Convolutional neural networks trained on large databases [22, 23] have shaped machine learning research over the past couple of decades. Today they serve as canonical learning material in courses and are often used as initial *vanilla* approaches for data exploration and classification tasks and before creating more bespoke machine learning pipelines. The widespread success of much models created an expectation in the research community that with sufficient data and computational power provided by one of the reigning consumer internet businesses, a data-driven black-box model can be created for any application ranging from quantum mechanics to economics. Convolutional architectures together with language models eventually inspired recurrent architectures and attention models where are the key ingredients in the creation of *Alpha Fold* [24] that takes a substantial step towards solving the protein-folding problem. Biotechnology researchers are eager to apply these methods but face the following obstacles

- **Insufficient data** due to strategic experimental designs
- **Low extrapolation accuracy** for black box-models

In this section we will set the scene for chemical reaction systems and

their methods of analysis of steady state and network perspectives. Dynamical methods makes use of field flow, linear stability and bifurcation analysis.

## 2.1 Describing Phenotypes with Bifurcations

$$\frac{\partial u}{\partial t} = F(u, t) \quad (2.1)$$

Consider  $N$  particles of  $S$  species in a finite volume  $\Omega$ . These particles can undergo  $R$  possible reactions when they meet within the volume. Suppose the timescales of equilibration with respect to volume and temperature are much faster than that of species number equilibration. This means that non-reactive collisions occur more frequently than collisions that trigger any of the  $R$  reactions. This is the essence of the *well-mixed* approximation [25].

This suggests that at any time  $t$  we may ignore spatial inhomogeneities and pin down the state of the system by a vector of species populations  $s(t) \in \mathbb{N}^S$ . All possible reactions in the mixture are encoded into a stoichiometric matrix  $\Gamma \in \mathbb{Z}^{S \times R}$  whose columns  $\Gamma[r] \in \mathbb{Z}^S$  represent the population change vector for a given reaction  $r$ . Each reaction has a propensity  $\omega(r|s) \in [0, \infty)$  defined though transition probabilities for an infinitesimal time interval given population  $s$ ;

$$\omega(r|s)dt := \mathbb{P}(s + \Gamma[r], t + dt | s, t) \quad (2.2)$$

Suppose  $\sigma[r]dt$  gives the probability that the reaction  $r$  will occur within the time interval  $dt$  independent of population  $s$ . The constant  $\sigma[r]$  could be in principle calculated from the microscopic physics of the reaction. In quantum mechanics this would involve calculating the wavefunction overlap or transition rates between initial and final configurations.

The propensity is proportional this rate, up to combinatoric multiplicity taking into account the species population  $s$ . A reaction  $r$  chooses  $g[i, r]$  particles for each reactant species  $i$  from the *well – mixed* solution containing

$s[i]$  particles. Thus the multiplicity is simply given by a binomial coefficient per species. This results in a propensity that is polynomial in the components  $s[i]$ , where the highest power term gives us the *order* of the reaction.

$$\omega(r|s) = \sigma[r] \prod_{i=1}^S \binom{s[i]}{g[i,r]} \quad (2.3)$$

For reactions involving distinguishable particle species, all components  $g[i,r] \in \{0,1\}$  and simplifies the combinatoric term to a product of all reactant populations.

$$g[i,r] \in \{0,1\} \quad \forall i,r \quad \implies \quad \omega(r|s) = \sigma[r] \prod_{i=1}^S s[i]^{g[i,r]} \quad (2.4)$$

### 2.1.1 Chemical Master Equation

By applying the laws of probability and taking the  $dt \rightarrow 0$  one can derive a time-evolution equation  $\mathbb{P}(s,t)$  involving the definition (2.2) which has become known as the Chemical Master Equation [25, 26]. Note here the complexity lies within the non-linear state dependence in the propensity  $\omega(r|s)$ . Were it not for this, we could solve this equation using spectral methods.

$$\partial_t \mathbb{P}(s,t) = \sum_{r=1}^R \omega(r|s - \Gamma[r]) \mathbb{P}(s - \Gamma[r],t) - \omega(r|s) \mathbb{P}(s,t) \quad (2.5)$$

Multiplying the Chemical Master Equation (2.5) by  $s$  and summing over all  $s$  obtains a system of differential equations for the first moment  $\langle s \rangle$  in terms of vectorised propensity  $\omega(s|\Gamma) \in [0, \infty)^R$  which couples to higher order moments, unfolding an infinite hierarchy.

$$\partial_t \langle s \rangle = \Gamma \langle \omega(s|\Gamma) \rangle \quad (2.6)$$

## 2.1.2 Reaction Equation

The mean field approximation factorises higher order moments, implying  $\langle f(s) \rangle = f(\langle s \rangle)$  for any nonlinear function  $f$ . This is equivalent to neglecting fluctuations in the  $N, \Omega \rightarrow \infty$  thermodynamic limit, and it is here where the mass-action assumption becomes manifest [26].

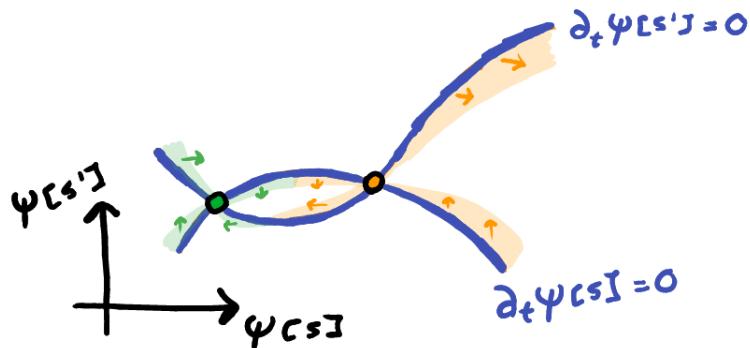
This closes the infinite hierarchy (2.6) yielding a nonlinear set of coupled ordinary differential equations for a continuous vector field  $\psi(t) \in [0, \infty)^S$ . These have come to be known as the Reaction Rate Equations, and are typical for modelling processes in systems biology.

$$\partial_t \psi = \Gamma \omega(\psi | \Gamma) \quad (2.7)$$

## 2.1.3 Bifurcation Analysis

In the mean field approximation (2.7) we may investigate the steady state  $\partial_t \psi = 0$ . This gives rise to a set of  $S$  polynomial equations in the components  $\psi[s] \in [0, \infty)$  of steady state  $\psi^*$ . These define  $S - 1$  dimensional nullcline hypersurfaces embedded in  $S$  dimensional state space.

$$\sum_{r=1}^R \Gamma[s', r] \sigma[r] \prod_{s=1}^S \left( \frac{\psi[s]}{g[s, r]} \right) \Big|_{\psi=\psi^*} = 0 \quad \forall s' = 1, 2, \dots, S \quad (2.8)$$



**Figure 2.1:** Schematic of two nullclines with their orthogonal local field flows intersecting at **stable** and **unstable** fixed points  $\psi^*$

Nullclines determine local direction of evolution of the system. On a given nullcline  $\partial_t \psi[s] = 0$  the flow of the field must be orthogonal to the direction of  $\psi[s]$ . At intersections between two nullclines, the flow must be orthogonal to the plane defined by two axes. At the interactions between all nullclines we may find the fixed points  $\psi^*$  as shown in Figure 2.1.

Classification of fixed points  $\psi^*$  is done by linearising the equation of motion (2.7) with respect to field perturbation  $\varepsilon(t)$  in their vicinity and determining the eigenvalues of the resultant  $S \times S$  Jacobian  $\mathbf{J}(\psi)$  evaluated at each fixed point  $\psi^*$ .

$$\varepsilon(t) \sim \mathbf{J}(\psi)|_{\psi=\psi^*} t \quad (2.9)$$

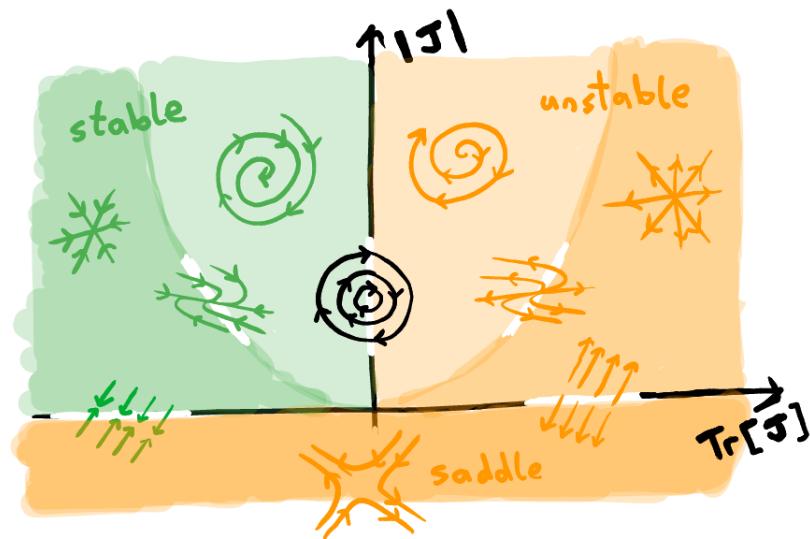
$$\text{where } \mathbf{J}[i,j] = \sum_{r=1}^R \sigma[r] \left( H(\psi[i]) - H(\psi[i] - g[i,r]) \right) \Gamma[j,r] \prod_{s=1}^S \binom{\psi[s]}{g[s,r]} \quad (2.10)$$

$$H(x) = \int_0^1 \frac{1-t^x}{1-t} dt \quad \text{are generalised Harmonic Numbers} \quad (2.11)$$

For reactions involving one or two distinguishable particles as in (2.4) the nullclines become hyperplanes and the Jacobian simplifies. We can see that both the reaction topology given by stoichiometric coefficients  $\Gamma[i,j]$  and the reaction rates  $\sigma[r]$  contribute to rotating and shifting the hyperplanes and determining the location and stability of their intersections.

$$\mathbf{J}[i,j] = \sum_{r=1}^R \sigma[r] |\Gamma[i,r]| \Gamma[j,r] \prod_{s \neq i} \psi[s]^{g[i,r]} \quad g[i,r] \in \{0,1\} \quad \forall i,r \quad (2.12)$$

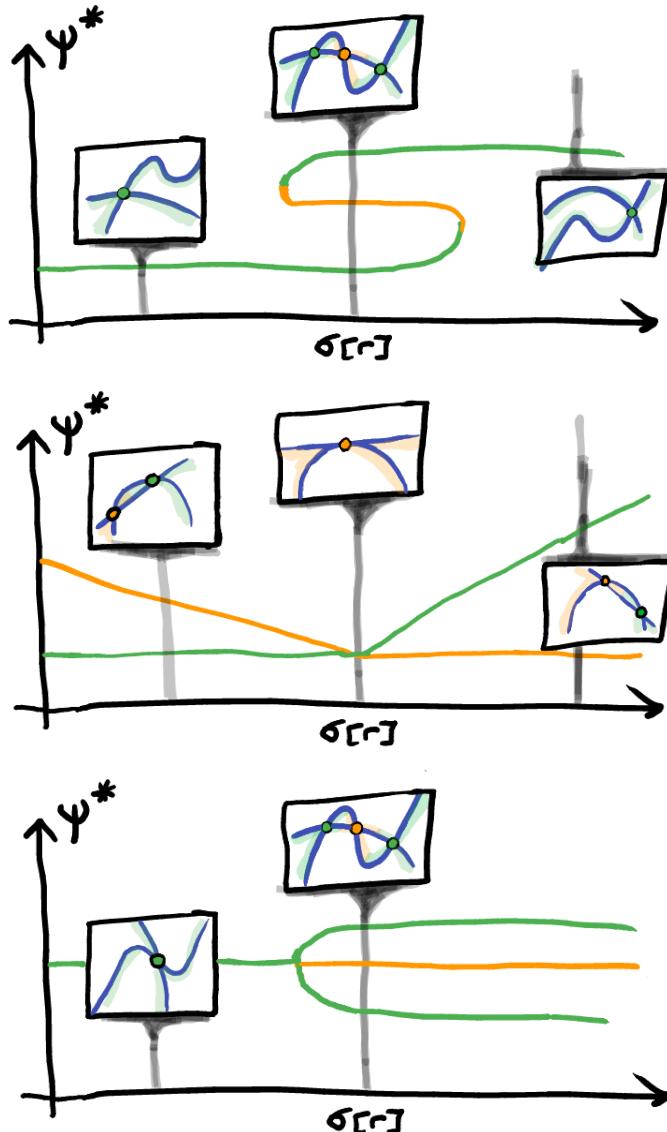
The sign of eigenvalues  $\lambda$  of Jacobian  $\mathbf{J}$  determine whether a fixed point is stable  $\lambda < 0$  or unstable  $\lambda > 0$ . As an illustrative example we can characterise fixed points given an arbitrary two dimensional Jacobian. Figure 2.2 reveals the regions of stability and phase space flows.



**Figure 2.2:** Classification of **stable** and **unstable** fixed points for a general two dimensional Jacobian in terms of trace  $\text{Tr}[J]$  and determinant  $|J|$

Varying the continuous parameters  $\sigma[r]$  moves the nullclines and may result in the creation or annihilation of fixed points of different classes. While an individual fixed point may change location and local phase space flow, it cannot change class without involving another fixed point.

These are called bifurcations and also fall into various categories. Figure 2.3 illustrates some of the possible one parameter supercritical bifurcations; subcritical cases are obtained by permuting stabilities of fixed points. Note the hysteresis loop in the saddle-node bifurcation.

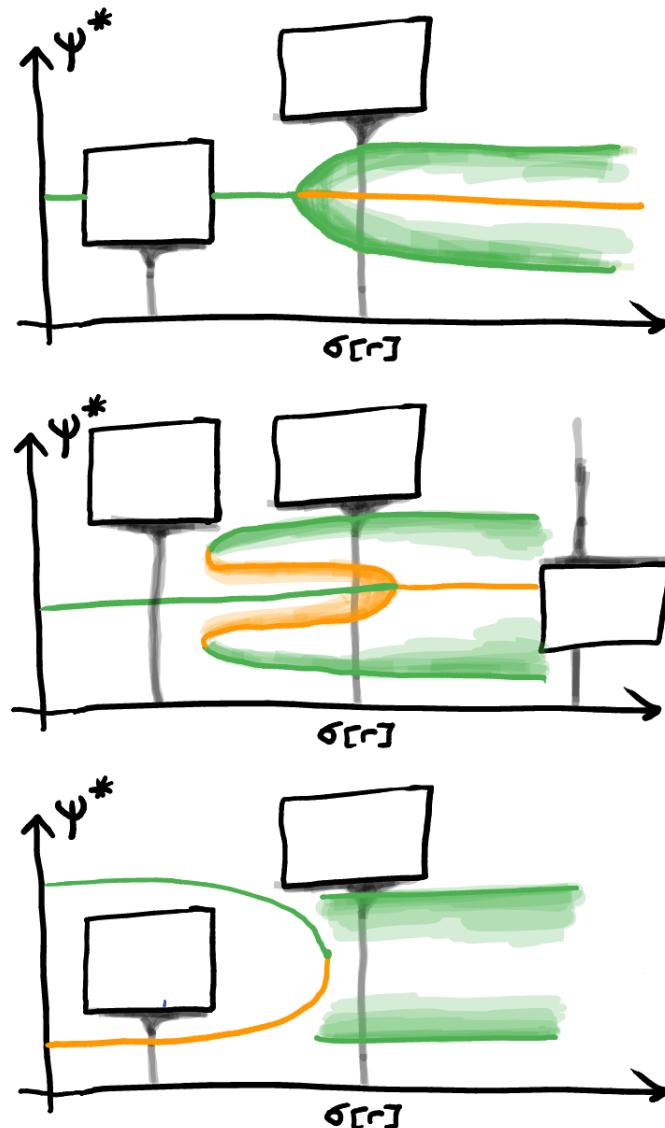


**Figure 2.3:** Saddle-node, Transcritical and Pitchfork bifurcation diagram showing **stable** and **unstable** fixed points  $\psi^*$  as a function of parameter  $\sigma[r]$ . Insets show nullcline intersections.

Another category of bifurcations involves limit cycles, which emerge from fixed points where the linearised Jacobian eigenvalues have no real part. Limit cycles have circulating field flow as shown in Figure 2.2 along the  $\text{Tr}[J] = 0, |J| > 0$  axis.

Note how oscillations emerge at small amplitudes in the Hopf bifurcation, whereas the large amplitude oscillations may instantly emerge in an infinite-period or cyclic-fold bifurcation. In Figure 2.4 the shaded regions

represent the peaks and troughs of the oscillations.



**Figure 2.4:** Hopf, Cyclic-fold and Infinite-Period bifurcation diagram showing stable and unstable fixed points and limit cycles as a function of parameter  $\sigma[r]$ . Insets show nullclines [tbc]

#### 2.1.4 Attractor Geometry and Universality

In this section we would explore the geometrisation of phase space, lyapunov exponents and universality. Perhaps a discussion on phase transitions and the relation to Landau-Ginzberg approaches is required. Maybe also periodic orbit theory? Depends how useful it is.

### 2.1.5 Reaction-Diffusion

Here we first introduce diffusion macroscopically by simply adding the laplacian to mean field equation (2.7). We introduce the turning bifurcation and show how linear stability analysis is insufficient to capture pattern formation and rich inhomogeneous steady states. A promising approach may be geometrisation of the moving local equilibria [20].

## 2.2 Phenotype Inference with Machine Learning

- Preface on SciML community and gray-box modelling

### 2.2.1 Classification and Regression

- Logistic regression
- Nearest neighbour methods
- Mixture Models

### 2.2.2 Dimensionality Reduction Methods

- UMAP and Tsne
- Sloppy parameters and identify-ability

### 2.2.3 Clustering Methods

## Chapter 3

# Interpretation of morphogen gradients by a bistable circuit

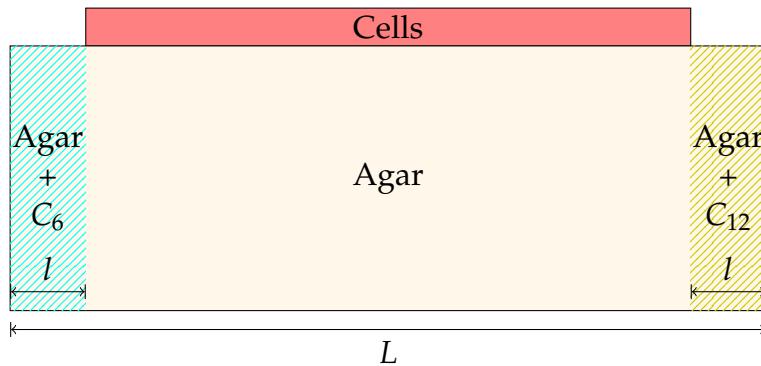
*memory of younger days*

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Ocarina of Time

### 3.1 Preface

1. Keep focus on developmental biology
2. Revised supplement as this chapter



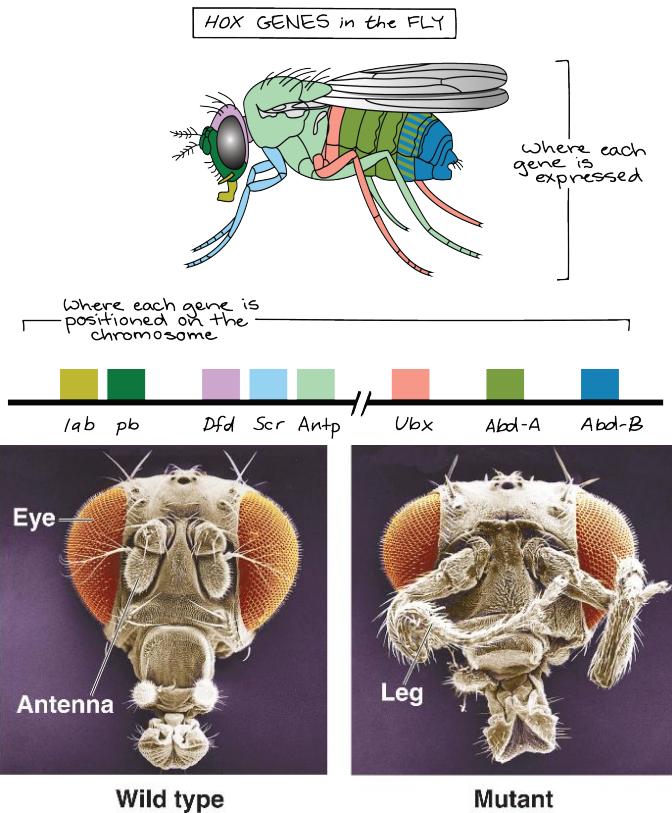
**Figure 3.1:** Geometry of opposing gradients experiment

This section outlines how the Design—Learn pipeline may help achieve a specific aim in a typical collaboration between theory, computation and experiment. The aim of this project is to reconstitute and control minimal

self-organisation mechanisms which are believed play crucial roles in developmental biology. To this end *E. Coli* has been genetically engineered to produce orthogonal responses to two different input signals — henceforth this organism will be referred to as the *double exclusive reporter* circuit [27]. The colony of reporters serve as a reduced model for a multi-cellular organism during embryonic stages of development. While patterns with sharp boundaries have successfully been realised, producing Turing instabilities remains challenging as the system needs to be such that patterns develop before the colony reaches stationary phase. The role of theory and computation in this project is to help identify the parameter regimes that produce controllable and self-organised patterns.

### 3.1.1 Developmental Context

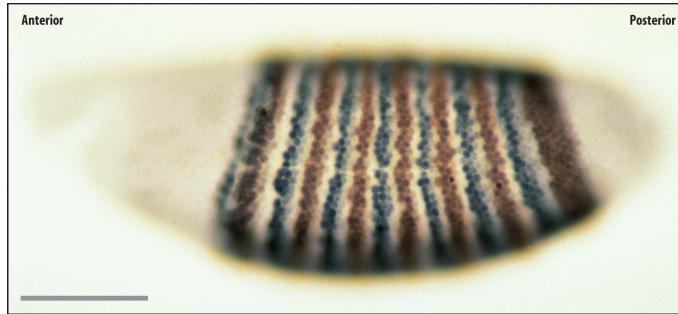
During the development of any organism a hierarchy of self-organisation takes place that leads to the breaking of symmetry from a spherical cluster of undifferentiated cells to the formation of organ segments and limbs. This process is known as morphogenesis. figure 3.2 shows an example in which *Hox* gene expression patterns in the body segments of *Drosophila* can drastically affect its development.



**Figure 3.2:** Top: *Hox* gene expression patterns in body segments of drosophila.  
Bottom: Mutation where legs grow in-place of antenna

### 3.1.2 Morphogen-driven Patterns

One of the central questions in developmental biology is how positional information is sensed by a population of cells and how sharp gene expression boundaries between populations are maintained for robust organ and body segment development. The French Flag model [28] proposes that cells have a threshold response to external signalling molecules – henceforth referred to as morphogens – which pre-pattern the organism from anterior to posterior and laterally. Some examples of morphogens include Wingless, Decapentaplegic and Sonic Hedgehog. figure 3.3 show the *Gap* expression patterns that partition the Drosophila embryo into segments which are later differentiated by *Hox* genes.



**Figure 3.3:** Expression patterns of pair-rule *Gap* genes in *Drosophila* embryo []

### 3.1.3 Self-organised Patterns

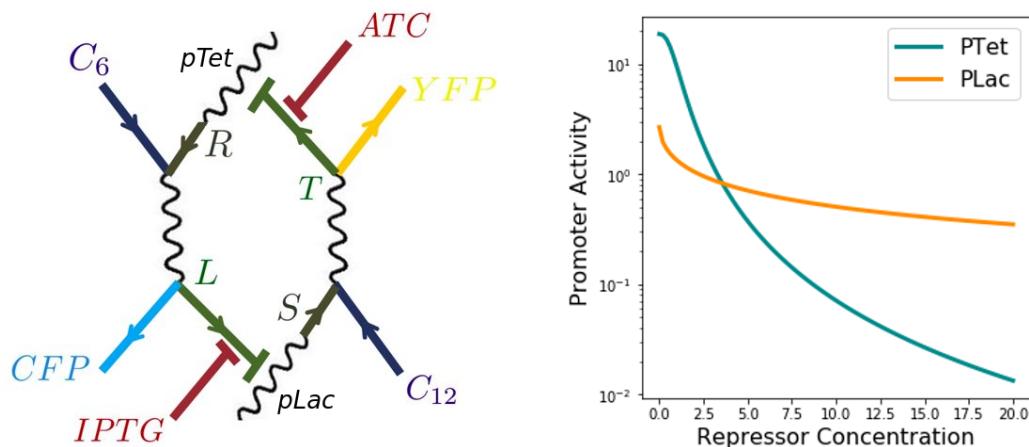
How are morphogen gradients set up and maintained? How can they be robust against changes in size and geometry? A canonical example of self-organisation in bacteria is the quorum sensing system [29]. Each cell secretes a signalling molecule resulting in the total concentration being proportional to the population density. This signal induces adaptive responses in metabolic and mobility in the whole colony. A long standing mathematical hypothesis that Turing patterns underlie self-organisation in cell populations. Recent literature suggests both morphogen-driven and Turing patterning mechanisms play a role in development [30]



**Figure 3.4:** Pigment patterns hypothesised to be generated by Turing mechanism

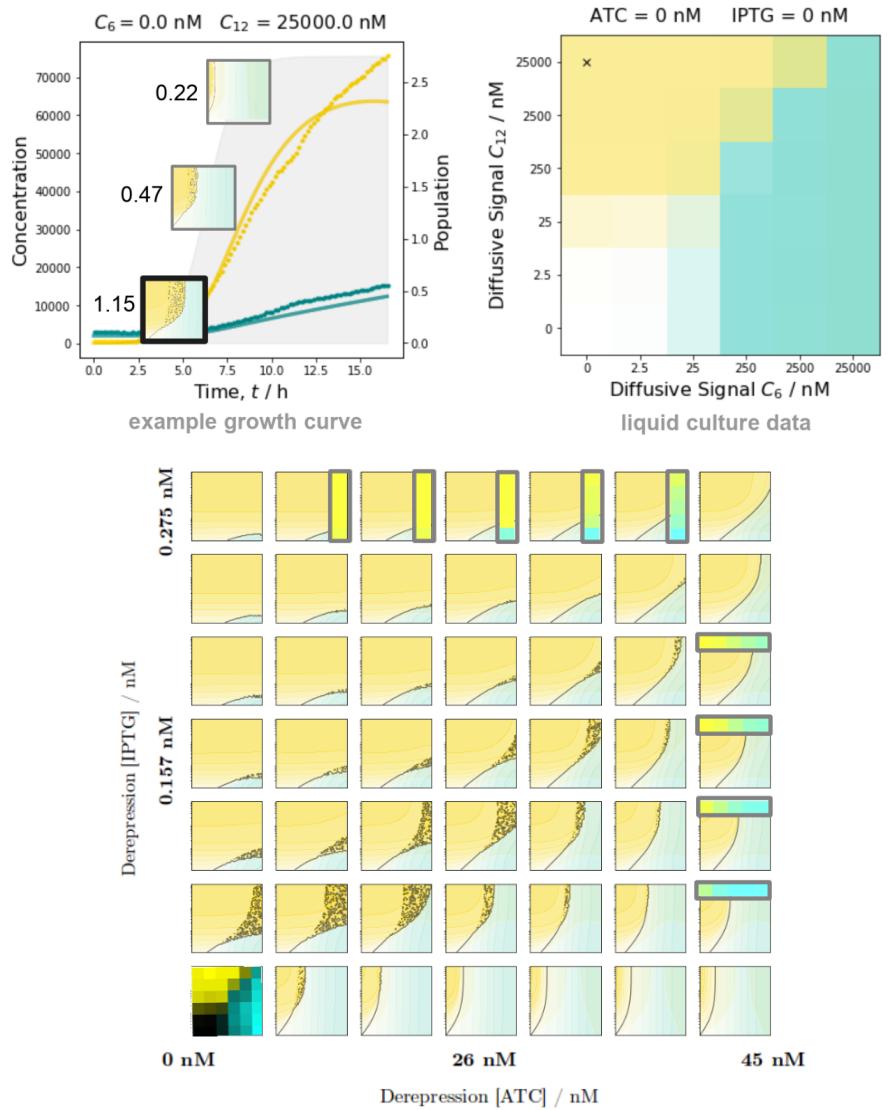
### 3.1.4 Learnings & Limitations

This section outlines the results on determining the bi-stability landscape for the *double-exclusive reporter*, and how its geometry helps determine the conditions for moving and stationary sharp boundary formation. The design of the device is summarised in figure 3.5. Each wiggly line represents a promoter. Incoming solid lines to a vertex represents the formation of a complex, which lead to the induction of a promoter. Outgoing solid lines represent the transcription-translation of genes downstream of a promoter. Arrows that end in t-junctions represent the repression of a pathway.



**Figure 3.5:** Left: Diagram of double exclusive reporter showing wiring between promoters and complexes Right: Repression of  $p_{Tet}$  and  $p_{Lac}$  promoters via  $TetR$  and  $LacI$  respectively

The observable chemicals, labelled *YFP* and *CFP*, are proportional to their upstream promoter activities. The experimentally controllable chemicals are quorum sensing molecules  $C_6$ ,  $C_{12}$  and de-repressors *ATC*,*IPTG*. All other chemicals cannot be directly observed. The double-negative feedback loop leads to bi-stability in the observable signals, which is key to producing sharp gene expression boundaries.



**Figure 3.6:** Top Left: Optical density measurements obtained for one well. Top Right: Final fluorescence values at 16h across different  $C_6$ ,  $C_{12}$  concentrations. Bottom: Steady state predictions between data regions.

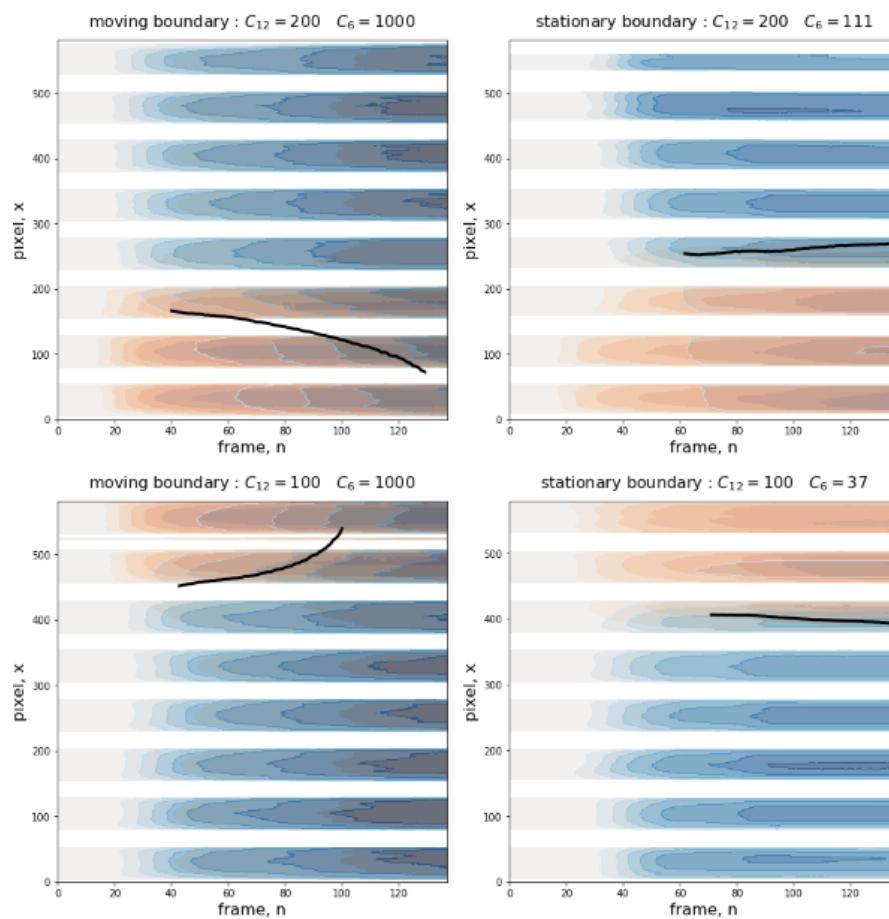
### 3.1.5 Microtiter Plate Data

The synthetic bacterial cultures are grown in suspended media and plated on 96 well microtiter plates in different concentrations of signalling molecules  $C_6$ ,  $C_{12}$  and de-repressors  $ATC, IPTG$ . Then optical density measurements in  $YFP$  and  $CFP$  are taken from each well every 20min for 16 hours. Cells begin to grow in exponential phase where the circuit is assumed to function optimally, until the population eventually reaches sta-

tionary phase. figure 3.6 across several different conditions overlayed on top of a model what predicts the steady state behaviour between collected data regions.

### 3.1.6 Spatial Experiments

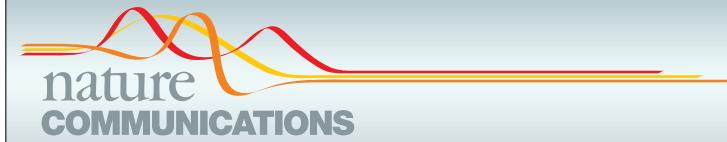
Simulations of the model revealed that if the final homogenous concentrations of  $C_6$  and  $C_{12}$  lie within the bistable region, then the prepatterned signals will form a sharp boundary at their interface. Spatial experiments shown in figure 3.7 confirm this prediction.



**Figure 3.7:** Merge channel yfp/cfp kymographs showing stationary (right) and moving boundaries (left)

### 3.1.7 Contributions

Contributions for this work are as follows



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<https://doi.org/10.1038/s41467-020-19098-w>

OPEN

# Interpretation of morphogen gradients by a synthetic bistable circuit

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During development, cells gain positional information through the interpretation of dynamic morphogen gradients. A proposed mechanism for interpreting opposing morphogen gradients is mutual inhibition of downstream transcription factors, but isolating the role of this specific motif within a natural network remains a challenge. Here, we engineer a synthetic morphogen-induced mutual inhibition circuit in *E. coli* populations and show that mutual inhibition alone is sufficient to produce stable domains of gene expression in response to dynamic morphogen gradients, provided the spatial average of the morphogens falls within the region of bistability at the single cell level. When we add sender devices, the resulting patterning circuit produces theoretically predicted self-organised gene expression domains in response to a single gradient. We develop computational models of our synthetic circuits parameterised to timecourse fluorescence data, providing both a theoretical and experimental framework for engineering morphogen-induced spatial patterning in cell populations.

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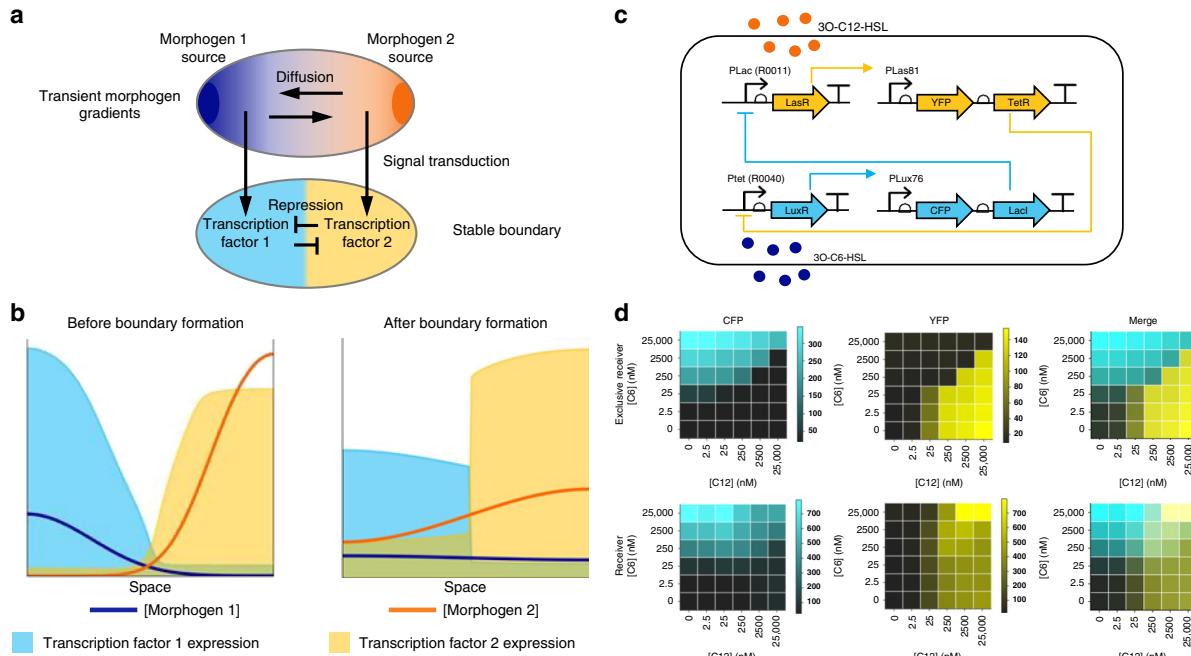
The positional information solution to the French flag problem, in which cells compute their spatial position by responding to the concentration of a morphogen in a gradient<sup>1</sup>, provides crucial insight into how patterns of gene expression form in a developing organism. The simplest formulation of this model – concentration thresholds leading directly to gene expression states – requires a static morphogen gradient to produce a stable pattern of gene expression<sup>2,3</sup>. However, quantitative measurements in developing embryos reveal that morphogen gradients are both dynamic and transient<sup>4,5</sup>, and genetic perturbations reveal that pattern formation is robust to changes in morphogen concentration<sup>6–8</sup>. A gene regulatory network topology of mutual inhibition downstream of antiparallel morphogen gradients<sup>9–12</sup> (Fig. 1a) has been proposed to robustly interpret dynamic gradients (Fig. 1b). However, while certain features of this topology are common to a number of developmental contexts such as the early *Drosophila* embryo and the vertebrate neural tube (reviewed in<sup>3</sup>), demonstrating how this network functions and whether it is indeed sufficient remains a challenge, due to the complexities of the different biological contexts in which it operates. Recent work in synthetic biology has proven the utility of building multicellular patterning circuits both for understanding development and for learning engineering principles<sup>13–18</sup>.

Here we show that the mutual inhibition motif<sup>19</sup> is sufficient to produce stable domains of gene expression in response to dynamic and transient morphogen gradients. By taking a synthetic biology approach<sup>20–23</sup> we have built a morphogen-induced

mutual inhibition circuit from scratch that acts in isolation in *E. coli* and used it to investigate the conditions under which patterning occurs. We have also added morphogen production to the core circuit to create a reaction-diffusion patterning system that responds to a single gradient by producing two domains of gene expression with a self-organized boundary. The experimental control and precise measurement afforded by a synthetic biology framework allowed us to understand the behaviour of these patterning mechanisms at a quantitative level in the context of a mathematical model parameterized against data, and to uncover general design principles for engineering multicellular systems.

## Results

**Engineering mutual exclusivity.** To investigate whether a simple mutual inhibition network topology can interpret dynamic gradients, we built a synthetic Exclusive Receiver circuit (Fig. 1c), based on a previous Receiver circuit design (pR33S175<sup>24</sup>) that responds to two homoserine lactone (HSL) input signals, 3O-C6-HSL (C6) and 3O-C12-HSL (C12) with fluorescent protein outputs. We engineered mutual inhibition by introducing genes encoding TetR, expressed bicistronically with eYFP, and LacI, expressed bicistronically with eCFP. In addition, the C12-binding receiver protein LasR was expressed under the control of a LacI-repressible promoter, while the C6-binding receiver protein LuxR was expressed under the control of a TetR-repressible promoter. The Exclusive Receiver therefore consists of two signalling pathways that mutually repress each other, such that LasR, eYFP and TetR are expressed in the



**Fig. 1 A synthetic gene circuit for morphogen interpretation.** **a** Schematic representation of a developing embryo. Mutual inhibition of transcription factors (cyan and yellow) downstream of antiparallel morphogen gradients (dark blue and orange) has been hypothesized to produce mutually exclusive domains of gene expression. **b** Morphogen gradients can be dynamic and transient, yet sharp, stable boundaries are observed between domains of gene expression. **c** A diagram of the Exclusive Receiver circuit. When 3O-C12-HSL (C12) levels are high, C12 binds to LasR, activating the expression of YFP and TetR, which represses the expression of LuxR, preventing expression of CFP and LacI. When 3O-C6-HSL (C6) levels are high, C6 binds to LuxR activating expression of CFP and LacI, which represses the expression of LasR, preventing expression of YFP and TetR. **d** Fluorescence output, measured in microplate fluorometer assays, of the Exclusive Receiver (top) and the Receiver (bottom) circuits represented as a ratio of CFP- (left) or YFP- (right) fluorescence to RFP fluorescence during exponential phase<sup>38</sup>, cultured in the presence of the concentrations of C6 and C12 indicated. Data are representative of  $n=3$  biological replicate experiments conducted on different days. See Supplementary Figs. 11 and 12 for replicates. Source data are provided as a Source Data file.

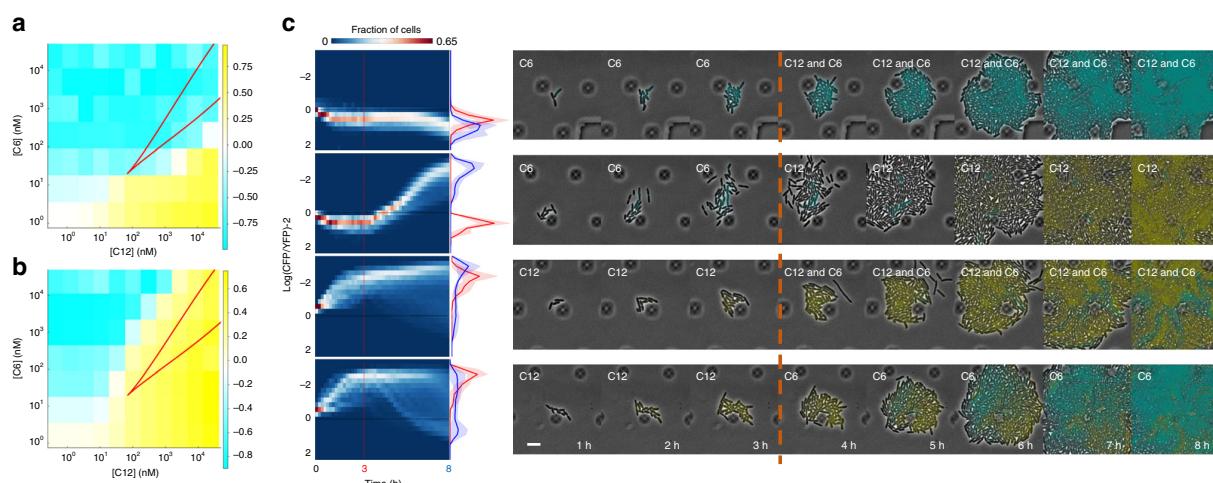
presence of the signal C12, while LuxR, eCFP and LacI are expressed in the presence of the signal C6. Unlike the Receiver circuit, which responds to the presence of both signals by producing both fluorescent proteins, the Exclusive Receiver was designed to respond exclusively to the two signals, by producing either eCFP or eYFP. Mutually exclusive reception will only occur when the repressors (TetR and LacI) are expressed such that the level of repression produced by high concentrations of one HSL is sufficient to repress detectable quantities of the other and low concentrations of HSL produce little repression. We used this mutually exclusive response as a design goal for the Exclusive Receiver circuit. We constructed a range of designs and chose a variant that exhibited a strong difference between CFP- and YFP-expressing states while maintaining a roughly equal sensitivity to the two HSLs (Supplementary Fig. 1).

To characterise the response of the Exclusive Receiver circuit to varying concentrations of C6 and C12, we performed timecourse plate fluorometry assays and calculated the promoter activity from the CFP and YFP channels using a ratiometric method<sup>25</sup>. The circuit responded to high concentrations of C6 and C12 by producing CFP and YFP, respectively. As intended by the mutual inhibition design, mixtures of both signals resulted in only one fluorescent protein being produced, depending on the relative concentrations of the two signals (Fig. 1d; Supplementary Fig. 2). We confirmed these gene expression states at the single cell level using flow cytometry (Supplementary Fig. 3). In contrast, a Receiver circuit lacking mutual inhibition produced both fluorescent proteins simultaneously when both signals were present (Fig. 1d; Supplementary Figs. 2 and 3). Similar results were obtained when chemical inducers were used to suppress the repressors in the Exclusive Receiver circuit (Supplementary Fig. 4).

**Mutual inhibition results in bistability.** Central to the ability of mutual repression to produce a robust signal response is the

property of bistability, in which two stable steady states of gene expression are possible<sup>20</sup>. We first explored this property mathematically by developing a dynamic (ordinary differential equation) model of the Exclusive Receiver circuit. The model is based on one derived for the Receiver circuit<sup>24</sup>, but incorporates the repressor proteins, TetR and LacI, and their regulation of LuxR/LasR expression (see Supplementary Methods for a complete derivation). We identified parameter values that enabled the model to reproduce timecourse fluorescence data using a previously established inference methodology in which a sequence of parameter inference tasks are applied to models and data for circuits of increasing complexity<sup>26</sup> (Supplementary Methods). This enabled us to simplify the identification of parameter values of the Exclusive Receiver model by reusing values of the subset of parameters that also appear in the Receiver model. We then applied numerical continuation methods to our data-constrained model to locate saddle-node bifurcations (see Supplementary Methods), and thus the concentrations of C12 and C6 for which bistability was predicted (Fig. 2a,b, red lines).

To test whether the Exclusive Receiver circuit exhibited hysteresis, a hallmark of bistability, at the concentrations predicted by the model, we first conditioned cells in either C6 or C12 and then exposed them to varied concentrations of both signals. At concentrations that produce bistability, we expected C6-conditioned and C12-conditioned cells to remain in the CFP-expressing and YFP-expressing states, respectively. In contrast, at concentrations that produce monostability, gene expression states would be determined solely by the final concentrations. We measured CFP and YFP expression by flow cytometry (Supplementary Fig. 5). The C6-conditioned cells expressed CFP at a wider range of concentrations, while C12-conditioned cells expressed YFP at a wider range of concentrations (Fig. 1b, Fig. 2a, b). We interpret this history-dependent difference in gene expression to be due to hysteresis. Thus, the region in concentration space in which we observe this difference is the



**Fig. 2 Mutual inhibition produces bistability.** Cells transformed with the Exclusive Receiver circuit were conditioned in either 500 nM C6 (a), or 500 nM C12 (b), and then exposed to the combinations of concentrations of C6 and C12 indicated. Cells were measured using flow cytometry and their normalized CFP minus YFP expressions were plotted. The region of bistability predicted by the parameterized model is the area within the red lines. See Supplementary Fig. 3 for gating strategy for all flow cytometry and Supplementary Fig. 13 for replicates. Source data are provided as a Source Data file. c Microfluidics cultures of cells transformed with Exclusive Receiver circuit in changing combinations of signals. Cells were grown for 3 h in the presence of either 37 nM C6 (rows 1 and 2) or 100 nM C12 (rows 3 and 4). Then media was changed to 100 nM C12 + 37 nM C6 (rows 1 and 3) or 100 nM C12 (row 2) or 37 nM C6 (row 4). Cells were imaged with a frame rate of (1 frame/10 min). Left panels are kymographs of the log-ratio of CFP expression per-cell to YFP expression per-cell, and fraction of cells as a heat map. Histograms represent the populations at 3 h (red) and 8 h (blue). Lines and shaded region represent the mean and standard deviation, respectively, over  $n = 4$  biological replicates performed on 4 different days. Right panels are sample montages of cells switching state (rows 2 and 4) or exhibiting bistability (rows 1 and 3); phase contrast and fluorescence channel ranges chosen for display. Scalebar = 6  $\mu$ m.

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region of bistability. This region was slightly larger than that predicted by the model but was qualitatively similar, which suggested that our model captured the essential features of our circuit.

To determine whether individual cells were switching or retaining their gene expression states in response to signal combinations, as suggested by our flow cytometry data, we used microfluidic devices to observe the dynamics of single cells over time. We cultured cells with 37 nM C6 or 100 nM C12, concentrations expected to produce bistability in combination, and then switched to the opposite signal. We found that cells with high fluorescence expression could, indeed, switch to the alternative state (Fig. 2c rows 2 and 4, Supplementary Fig. 6), even when we used the much higher concentration of 1  $\mu$ M C6 (both to initially condition cells and to switch their state Supplementary Figs. 7 and 8). When cells conditioned with either C6 or C12 were exposed to both signals, the cells exhibited bistable behaviour, mostly maintaining their initial fluorescence states (Fig. 2c rows 1 and 3, Supplementary Figs. 6–8) although a comparatively small population of C12-conditioned cells do begin expressing CFP in response to mixed signals (Fig. 2c, row 3) indicating some heterogeneity in the population with respect to bistability. We hypothesize that cell to cell differences in gene expression result in differences in the HSL concentration regimes in which the cells exhibit bistability resulting in heterogeneity in switching behaviour. Together, these data indicate that, when signal concentrations gave rise to bistability, the final gene expression state was determined by the history of exposure to signals.

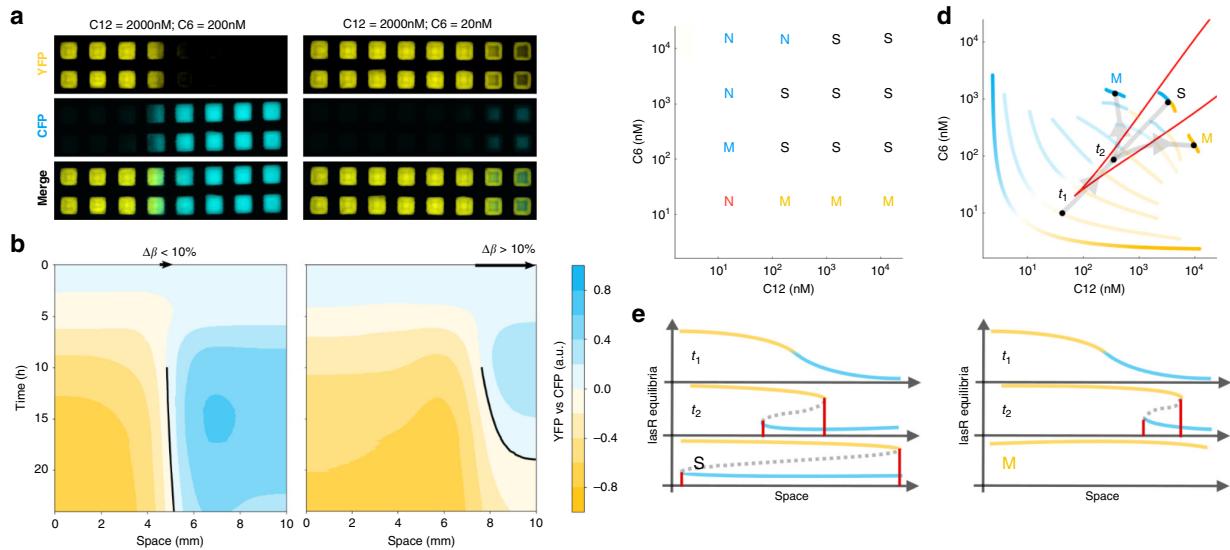
**Hysteresis produces stable boundaries.** To test how the Exclusive Receiver circuit interpreted dynamic morphogen gradients, we grew cells on filter paper printed with hydrophobic ink, such that growing colonies remained within the square in which they were inoculated but signals could diffuse through the agar beneath the filter<sup>24,27</sup>. We performed these experiments in agar containing 10  $\mu$ M IPTG (1% of the standard induction concentration of 1 mM) to create a regime in which both CFP-dominating and YFP-dominating regions were observed. The addition of IPTG was required to compensate for differences in culture conditions between solid and liquid cultures (see Supplementary Fig. 34 for experiments without IPTG). While the precise mechanism is unknown, differences in culture conditions when switching to solid culture appeared to shift the bistability region such that even very low concentrations of C6 enabled bistability, preventing the appearance of a YFP-dominant regime. This was redressed through addition of IPTG, which partially derepresses LacI, shifting the region to coincide with the region in liquid culture. We cast either C6 or C12 into the agar at each end of the filter paper at varying concentrations and performed timelapse imaging of the fluorescence output of the circuit in response to the dynamic gradients produced by diffusion. When C6 and C12 were provided at concentrations that, if allowed to diffuse to homogeneity would result in 200 nM C6 and 2000 nM C12, (i.e., a 200 nM and 2000 nM spatial average, respectively), a sharp boundary was produced between mutually exclusive domains of CFP and YFP (Fig. 3a). Plotting the point in space at which CFP and YFP expression were equal (see Supplementary Methods) against time revealed that the boundary between domains did not move over time (Fig. 3b). In contrast, when spatial average concentrations of 20 nM C6 and 2000 nM C12 were used, there was an initial production of CFP near the source but it was quickly overwhelmed by YFP production and the point of equal expression moved toward the C6 source (Fig. 3a). These images measured bulk (rather than per-cell) fluorescent protein

expression so highly stable fluorescent proteins would remain detectable even after they stopped being expressed. It was therefore unsurprising that CFP remained detectable in cells close to the C6 source due to protein perdurance. Importantly, however, the CFP intensity did not increase, whereas the level of YFP did increase, indicating that the circuit had switched from CFP expression to YFP expression in these cells. At varying combinations of signal concentrations we classified boundaries (see Supplementary Methods) as static (S), moving (M), or not present (N) (Fig. 3c, Supplementary Fig. 9, Supplementary Movie 1) and observed that static boundaries occurred at signal concentrations similar to those that produced hysteresis (Fig. 2a and b).

To understand this behaviour we performed simulations and analysis of our mathematical model. We plotted the concentration of C6 and C12 experienced by physically separated cells and visualized the changes in concentration that they experienced due to diffusion (Fig. 3d, Supplementary Movie 2). We observed that cells at different points in space all converge to the spatial average concentration, but they do so by taking different paths, resulting in differences in CFP and YFP expression. Points closest to the C6 source begin in the monostable CFP region, whereas those closest to the C12 source begin in the monostable YFP region. This means that the cells are traversing the bistable region along different paths and will therefore exhibit hysteresis as they converge to the spatial average. If the spatial average concentrations lie within the bistable region, which is defined in concentration space, all cells will eventually experience concentrations within this region as the morphogens diffuse. Thus, over time, the region of cells in physical space that exhibit bistability expands to encompass the entire domain (Fig. 3e, S; Supplementary Movie 3). The result is that a cell's state will be determined by its history and cells with different histories that originated on different sides of the boundary will end up in different stable states. The cells close to the C6 source will behave like cells conditioned in C6 and express CFP while the cells close to the C12 source will behave like cells conditioned in C12 and express YFP (as in Fig. 2) and will maintain their states even after the two morphogens mix via diffusion. The result is the formation of two mutually exclusive domains of gene expression with a sharp boundary that is stable and stationary, even though the morphogen gradients that produced those domains were only present transiently. If, on the other hand, the spatial average concentrations lie outside the bistable region, a transient boundary will form and cells will switch fates as they leave the bistable region, taking on the fate determined by the morphogen of greater concentration (Fig. 3e, M; Supplementary Movies 4 and 5).

**A secondary gradient creates self-organized domains.** Given the ability of the mutual inhibition topology to produce stable domains of gene expression in response to antiparallel morphogen gradients, we hypothesized that it could function similarly in response to a single morphogen gradient with the addition of a secondary gradient produced by the cells themselves, which functions as a lateral inhibitor<sup>28</sup>. This circuit mimics the sequential induction of organizing centres found in *C. elegans* vulval development<sup>29</sup>, the rhombomeres of the vertebrate hindbrain<sup>30,31</sup>, and the *Drosophila* wing disc<sup>32</sup>.

To explore this mechanism we added previously characterized Relay circuits<sup>24</sup>, which produce one signal in response to the other, to the Exclusive Receiver circuit. This created an Exclusive Relay circuit that both produces and interprets morphogen gradients (Fig. 4a and Supplementary Methods). We created a transient gradient of C6 by replacing a cylinder of agar in the centre of a plate with agar containing 40  $\mu$ M C6, and plated cells



**Fig. 3 Formation of stable boundaries.** **a** Endpoint fluorescence microscopy of Exclusive Receiver cells grown in transient gradients of signals (C12 diffusing from the left, C6 diffusing from the right) at the spatial average concentrations indicated and in the context of 10  $\mu$ M IPTG throughout. Representative examples ( $n=3$  biological replicates performed on 3 different days) of a static boundary (left) and a moving boundary (right). **b**, Corresponding kymographs of CFP and YFP fluorescence (intensity) over time (y-axes, hours) at different spatial positions (x-axes, mm). If the location of the boundary (location of equal normalized CFP and YFP fluorescences, black lines) at the end of the timelapse minus its location when it became detectable ( $\Delta\beta$ , arrows) was less than 10% of the domain size we considered the boundary stable. **c** Boundaries were evaluated as above at the signal concentrations indicated by letters. S indicates equilibrium concentrations at which static boundaries were observed. M indicates a moving boundary. "N" indicates no boundary. The colour of the letter indicates which FP was dominant and red indicates neither FP dominant. See supplementary Figs. 31-33 for replicates. **d** Schematic representation of the concentrations of C6 and C12 experienced by cells at different points in physical space (cyan and yellow curves) as gradients diffuse to homogeneity. Paler curves represent different timepoints. If the spatial average concentrations lie within the region of bistability, the boundary will be static (S), otherwise the boundary will move (M) and will eventually be abolished as cells adopt either CFP or YFP expression.  $t_1$  and  $t_2$  indicate timepoints considered in **e**. **e** Corresponding schematic representing LasR expression, coloured according to resultant fluorescent protein expression. Dashed line indicates the location of an unstable local equilibrium. Red lines indicate the spatial location in which cells are exhibiting bistability. In the case of a stationary boundary (S), the region of space containing cells exhibiting bistability expands to encompass all cells and their gene expression state is determined by their history. In the case of a moving boundary (M), the region exhibiting bistability moves rightward and disappears and the domain becomes dominated by a single monostable state.

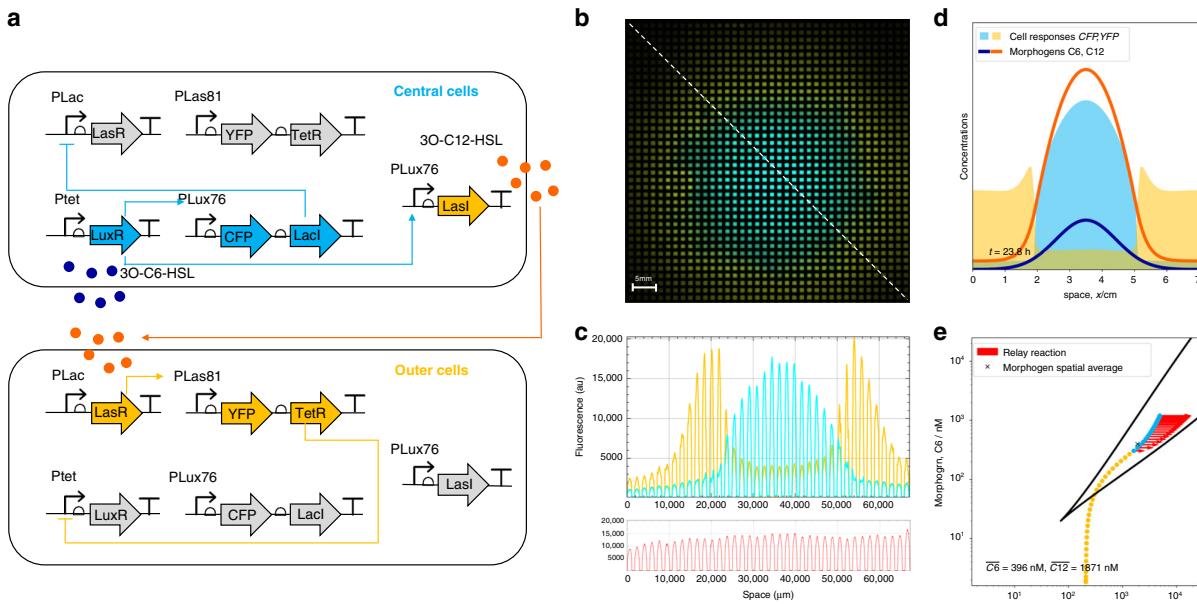
transformed with the Exclusive Relay circuit onto gridded filters. The primary C6 gradient resulted in cells in the centre expressing CFP, LacI, and LasI (Fig. 4b and c). These cells produced C12 but were unable to sense it because they did not express LasR due to its repression by LacI. The gradients of C6 and C12 overlapped but the C12 gradient could extend further due to C12 being actively produced by a large region of cells (Fig. 4d). At a certain distance from the source of C6, the ratio of C12 to C6 favoured the C12 state such that the bistable switch 'flipped' and cells expressed YFP and TetR, repressing LuxR and the ability to sense C6. The result was two domains of mutually exclusive gene expression from a single primary morphogen gradient. As in the case of antiparallel gradients, the stability of the boundary between these domains of gene expression can be understood using the same framework: The spatial average concentration of the primary morphogen remained constant as the total density that was added at the beginning of the experiment was unchanging. The secondary morphogen, in contrast, was being produced by cells so the total density increased over time. The spatial average of both morphogens therefore moved along the axis of the secondary morphogen as cells that were sensing the primary morphogen produced the secondary (Fig. 4e, red arrows). The result is that a metastable boundary is produced that is present as long as the system remains within the region of bistability but will eventually be abolished as the secondary morphogen accumulates. Transforming the Exclusive Receiver

with a P81-LuxI Relay and creating a C12 primary gradient resulted in equivalent patterning with the physical location of the states reversed (Supplementary Fig. 10).

## Discussion

By building a synthetic gene circuit composed of mutual inhibition downstream of diffusible morphogens, we have shown that this network topology in isolation is sufficient to recapitulate the behaviour, seen in multicellular developmental systems, of mutually exclusive domains of gene expression separated by a boundary that is sharp and stable despite transient and dynamic morphogen gradients. This topology also proves to be robust to differences in morphogen concentration, as variations in concentration spanning orders of magnitude result in only small changes in boundary location (Supplementary Fig. 9, Supplementary Movie 1). In addition, we have built a patterning circuit that creates a self-organised boundary between two gene expression domains in response to a primary morphogen by creating a secondary morphogen that functions as a lateral inhibitor. This circuit shares features of both a positional information model<sup>1</sup>, in that it interprets a preexisting morphogen gradient to produce domains of gene expression, and a reaction-diffusion model<sup>33,34</sup>, in that morphogen production is coincident with interpretation. These two models have previously been presented in opposition to each other, but it is likely that both mechanisms are at work in development<sup>35</sup>. Our Exclusive Relay

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**Fig. 4 Addition of a relay circuit creates self-organized domains of gene expression.** **a** Circuit diagram of Exclusive Receiver cells co-transformed with a Relay circuit (P76-LasI) that responds to C6 by producing C12. **b** Isogenic cells transformed with the circuit shown in **a** and grown for 24 h in the presence of a gradient of C6 diffusing from the centre. Cells that experience high levels of C6 (central cells) will express CFP, LacI, and LasI, causing them to produce C12 but be unable to sense it. Neighbouring cells (outer cells) that do not experience C6 will sense C12 and express YFP and TetR, resulting in mutually exclusive domains of gene expression. Cells also constitutively express mRFP1 via a genomic transgene. Image is representative of 3 biological replicates performed on 3 different days. **c** Quantitation of fluorescence along the dotted line in **b**. Cyan, yellow, and red indicate CFP, YFP, and RFP expression, respectively. **d** Final timepoint of simulation shows a secondary gradient of C12 (orange) produced in response to the primary C6 gradient (dark blue). Cyan and yellow indicate simulated CFP and YFP expression, respectively. **e** Final time point of simulation in C6-C12 space labelling points in physical space by their CFP and YFP expression (cyan and yellow points), and showing the production of C12 as vectors (red arrows) that move the spatial average (x) toward increasing C12 (see supplementary video 6).

circuit forms patterns by using two in-phase morphogen gradients to produce a primary response whose spread is limited by the gradient of the secondary morphogen, due to its larger magnitude and diffusive radius. The result is concentration-dependent domains of gene expression produced in response to a morphogen gradient, just as in the French flag model. However, due to the hysteresis of the bistable core of the circuit, these domains of gene expression are metastable even though the primary morphogen gradient diffuses to homogeneity. It is worth noting that the boundary between the eYFP-expressing domain and the domain that expresses neither fluorescent protein is determined simply by the threshold of response to C12 and is therefore not a stable boundary. This boundary could be stabilised by recapitulating the mechanism we have described via the addition of a third morphogen (and mutual inhibition with C12) either diffusing from the opposite direction to the primary gradient (as in Fig. 3) or as a second relay mechanism (as in Fig. 4). The fact that genetic circuits optimized in different contexts can be directly composed to produce more complex patterns suggests that the synthesis of reaction-diffusion and positional information mechanisms may be readily obtainable through evolution, and therefore common in development. This also provides a blueprint for designing synthetic gene circuits that produce spatiotemporal patterns in cell populations, which could lay the groundwork for rationally designing self-organizing, self-repairing materials and tissues.

**Methods**

**Plasmid construction.** The exclusive receiver circuit and variants described in Supplementary Fig. 1 were cloned using Gibson Assembly<sup>36</sup> using pRS3S175<sup>24</sup> as a

starting point. Primers used for Gibson assembly can be found in Supplementary Table 1.

**Plate fluorometer assays.** The exclusive reporter construct was transformed into EC10G *E. coli* cells with a chromosomally integrated mRFP1 construct<sup>24</sup>. Overnight cultures were grown from glycerol stocks in M9 media supplemented with 0.4% glucose, 0.2% casamino acids, and 50 µg/ml kanamycin (supplemented M9) then diluted back 1:100, allowed to grow to an OD of 0.3 then diluted 1:1000. Cultures were aliquoted into black-walled, clear-bottom 96-well plates (Greiner µClear) in a volume of 200 µl per well and measurements taken every 10 min for ~1000 min in a BMG FLUOstar Omega plate fluorometer using BMG FluoStar Omega Reader Control Software 5.10R2. 3-oxohexanoyl-homoserine lactone, C6, (Cayman Chemicals) and 3-oxododecanoyl-homoserine lactone C12, Cayman Chemicals were dissolved to a concentration of 200 nM in DMSO then C6 was diluted in supplemented M9 to the concentrations described, while C12, due to its limited solubility in aqueous media, was first diluted 1:50 in ethanol then diluted in supplemented M9 medium to the concentrations described.

**Flow-cytometric analysis of hysteresis.** EC10G cells transformed with the exclusive receiver construct were grown overnight from glycerol stocks as described for plate fluorometer assays. Overnight culture was diluted 1:100 and incubated until OD 0.2. Cells were then resuspended 1:100 in supplemented M9 supplemented with either C6 or C12 at 500 nM each and conditioned for 2 h. Following conditioning, cells were washed three times in supplemented M9 by centrifugation at 3200 × g for 4 min. and seeded at 1:1000 into wells of a 96-well plate containing combinations of varying concentrations of C6 and C12 as indicated in Supplementary Fig. 5. The plate was incubated for 5 h with continuous OD monitoring. OD measurements at 5 h were consistently within the exponential growth range (0.3–0.8). Following 5 h incubation, cells were diluted 1:6 in PBS and analysed by flow cytometry on a BD FACSCelesta (BD Biosciences, San Jose, CA, USA) equipped with HTS and a standard optical setup. Data was collected using FACSDiva 8.01. CFP was excited with violet laser 405 nm and detected with 525/50 BP filter - 505 LP mirror combination. YFP was excited with blue laser 488 nm and detected with 530/30 BP filter - 505 LP mirror combination. RFP was excited with yellow-green laser 561 nm and detected with 610/20 BP filter - 600 LP mirror combination. Instrument quality control was performed prior to each experiment

using BD CS&T beads. Fluorescence compensation parameters were determined using induced and untreated exclusive reporter cells and 30,000 events were counted within RFP gate for each sample. Data analysis was performed with FCS Express v.7 software (DeNovo Software, Glendale, CA, USA). The gating strategy for all flow cytometry was the same and is shown in Supplementary Figs. 3c and 5c.

**Microfluidics.** Glycerol stocks of EC10G transformed with the Exclusive Receiver were streaked on LB agar plates. Colonies were picked into M9 and grown at 37 °C overnight, then diluted 1:1000 into M9 and grown for 4 h 45 min at 37 °C into exponential phase. The culture was typically diluted 1:100 in M9 before being loaded into the CellASIC ONIX B04A-03 microfluidic device using the manufacturer's protocol (EMD Millipore Corporation). Cells were supplied with media using a pressure of 5 psi in the device. The entire device, along with most of the microscope, was incubated at 37 °C during movie acquisition. Cell segmentation was done on the RFP channel using the published Schnitzcells software (release 1.1, 2005)<sup>37</sup>. The mean YFP and CFP fluorescence normalized to cell area was then calculated by averaging the corresponding pixels in the respective channels. Movies with no cells or non-growing cells were excluded by keeping only those movies with greater than 20 and 50 cells at 3 and 6 h, respectively. Non-cell segmentation artefacts were excluded by area (<200 pixels) and Euler number (<1) computed with the regionprops function of MATLAB 2014a.

**Microfluidics microscopy.** Microfluidics devices were imaged using a widefield microscope with epifluorescence and phase contrast imaging modes (Nikon Ti-eclipse, Nikon, UK) equipped with the Nikon Perfect Focus (PFS) Unit. Illumination for the epifluorescence was provided by a white light LED source (SOLA SE Light Engine or Spectra X Light Engine, Lumencor, USA), transmitted by a liquid light guide (Lumencor, USA), through a fluorescence filter cube (YFP Channel: 49003; ET/Sputtered series ET-EYFP, exciter: ET500/20x, dichroic: T515LP, emitter: ET535/30m; CFP Channel: 49001; ET/Sputtered series ET-CFP, exciter: ET436/20x, dichroic: T455LP, emitter: ET480/40m; RFP Channel: 41027-Calculm Crimson, excitation: HQ580/20x, dichroic: Q595LP, emitter: HQ630 /60m, Chroma, USA), and a CFI Plan Apochromat 100x oil immersion objective (NA 1.45, Nikon). Phase contrast illumination was provided by a 100 W lamp via a condenser unit (Nikon). Images were acquired on CoolSNAP HQ2 camera (Photometrics, USA). The sample was held in motorized stages (Nikon). The sample was incubated along with much of the microscope body using a temperature controlled, heated chamber (Solent Scientific, UK). The microscope was controlled with MetaMorph software (version 7.8.10.0, Molecular Devices, USA). Fluorescent beads (TetraSpeck microspheres, 0.5 μm, Molecular Probes, USA) were imaged as a calibration standard.

**Solid culture assays.** Exponential phase cultures were grown to an OD of 0.3 and plated onto Iso-Grid membranes (Neogen) on supplemented M9 with 1.5% agar at a volume of 0.5 μl per square. Gradients were created by cutting holes in supplemented M9-agar (1.5%) plates (cast in OmniTray [Nunc]) containing 10 μM IPTG. Holes were cut on both ends of a domain to be inoculated at a size of 25% of the domain, each. Holes were then filled with liquid M9-agar to which either 3O-C6- or 3O-C12-HSL had been added at 4X concentration. After hardening, excess agar was cut away leaving each domain isolated. For relay circuit assays, circular holes were punched in the centre of plates using the back of a pipette tip and the holes were filled with ~200 μl of liquid agar containing 40 μM of the appropriate HSL. Plates were sealed with parafilm and imaged using a motorized Leica M205 FA fluorescence stereo microscope controlled using Leica LAS X software. Plates were incubated at 37 °C using a DigiTherm microscope temperature control air bath (Tritech Research). Illumination was an LED white light source (Lumencor) with excitation filters of 426–446 nm, 490–510 nm, and 555–589 nm, and emission filters of 460–500 nm, 520–550 nm, and 608–682 nm. Tiled images were taken every 10 min and were stitched using Leica LAS X software.

**Reporting summary.** Further information on research design is available in the Nature Research Reporting Summary linked to this article.

## Data availability

Source data are provided with this paper. Plate fluorometer and flow cytometry datasets can be found in supplementary file sourcedata.zip. Raw microscopy images (Figures 2c, 3a, 4b) are available on request to the authors. The exclusiver receiver plasmid is available from Addgene (Addgene ID 160376). All other relevant data are available from the authors upon reasonable request. Source data are provided with this paper.

## Code availability

Code is available at GitHub repository <https://github.com/gszep/double-exclusive-reporter>. Source data are provided with this paper.

Received: 15 July 2020; Accepted: 23 September 2020;

Published online: 02 November 2020

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**Acknowledgements**

We would like to thank Jeremy Green for helpful comments on the manuscript.

**Author contributions**

P.K.G., N.D., J.H., and A.P. conceived and designed the study. P.K.G. designed and built the genetic circuits. P.K.G., O.P., and V.C. performed the experiments. G.S., J.H., and N.D. conceived and implemented theory and modelling and wrote the supplementary information. All authors analysed and interpreted the data. P.K.G. and A.P. wrote the main text. All authors provided input into the manuscript.

**Competing interests**

The authors declare no competing interests.

**Additional information**

Supplementary information is available for this paper at <https://doi.org/10.1038/s41467-020-19098-w>.

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**Peer review information** *Nature Communications* thanks the anonymous reviewer(s) for their contribution to the peer review of this work. Peer reviewer reports are available.

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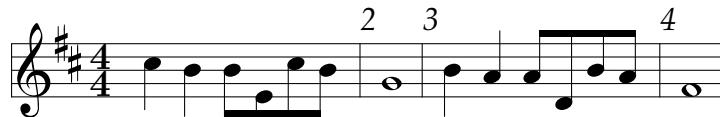


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## Chapter 4

# Parameter Inference with Bifurcation Diagrams



*the melody that will draw you into the infinite darkness*

---

Nocturne of Shadow — Ocarina of Time

### 4.1 Preface

The novel inference method presented in this chapter addresses the specific limitations encountered during the interdisciplinary collaboration in synthetic developmental biology presented in Chapter 3 and lays the foundations for machine learning methods that leverage bifurcation theory. These methods would be relevant in fields where modelling and designing qualitative changes in behaviour is important, observations are scarce and have experiments with highly variable outcomes.

In Chapter 3 the genetic engineers wanted to design synthetic *E. Coli* with a bistable cusp bifurcation with respect to two input signals as shown in Figure 3.9. The qualitative design goal was bistability in a region where both signals are present beyond some threshold concentration and monostable otherwise. The next step would have been to engineer an oscilla-

tory region in the input signals — a Hopf bifurcation. Combining these two designs could have lead to a candidate genetic circuit for forming self-organised patterns across the bacterial colony.

The hierarchical monte-carlo approach — details of which can be found in Appendix A.2.1 — enabled the incorporation of knowledge from subsystems and variants of the synthetic *E. Coli* under one model, in an effort to guide genetic engineers through a high dimensional design space towards their design goals. Model parameters were estimated using time-course fluorescence microplate measurements that included information about dynamical transients and colony growth in liquid culture as shown in Figure 3.6. The biological design goals, however, were in state-space rather than the time-domain and are observed in flow cytometry measurements of colonies in exponential phase as shown in Supplementary Figure A.3. The disconnect between the domain that the data lives in and the domain of the design goals poses the risk of over-fitting the model on undesired information that exists in the data domain.

In this early days of this thesis, we investigated whether it was possible to transform the time-domain data into the same domain that the design goals lived in: the state-space. This approach, and related works, are discussed in Section 4.1.1 and can in principle be used with the microfluidic fluorescence microscopy data shown in Figure 3.9c for parameter inference. However, the accuracy of the cell trajectories was limited by cell segmentation and tracking algorithms. Initial investigations into this approach also suggested that trajectories need to be of sufficient temporal resolution and sampled from a wide variety of initial conditions. Such data is not widely available and ultimately we decided to focus on a method that could be used with a well-known workhorse in biomedical research: flow cytometry.

Section 4.1.2 describes an experimental design for flow cytometry for the purposes of extracting bifurcation information from cells. The experiments were designed and performed by **Paul Grant** and **Valerie Coppard**.

Circling back to the original design goals, Section 4.1.3 illustrates how the *bifurcation measure*, introduced in the incorporated publication in Sections 4.2 — 4.7, can be extended for Hof bifurcations. **Grisha Szep** prepared the manuscript, designed the cost function, derived mathematical results, wrote and released the Julia package under the supervision of **Neil Dalchau** and **Attila Czicasz-Nagy**.

### 4.1.1 State Field Geometry in Trajectory Data

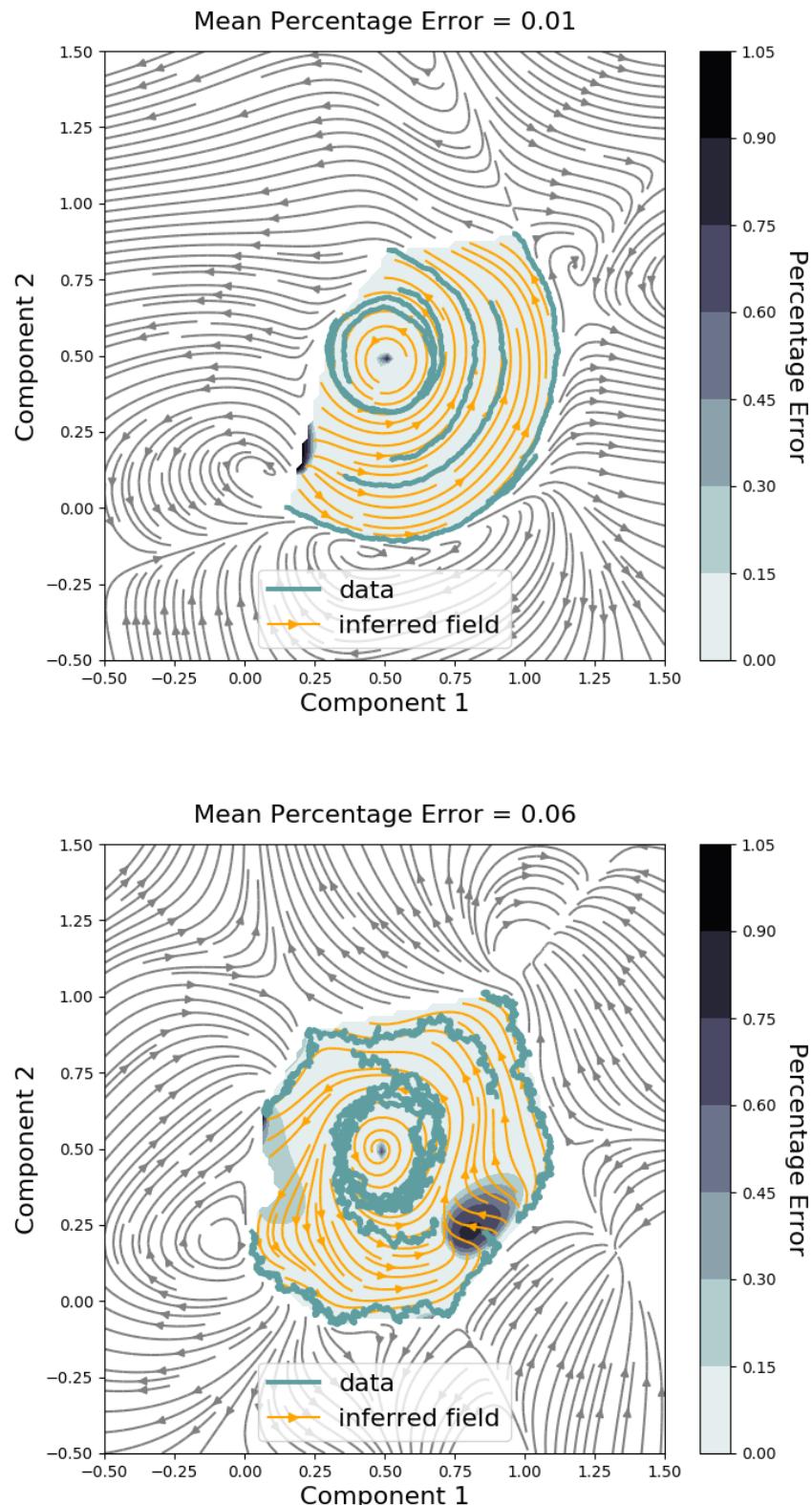
Consider we are given  $K$  cell trajectories  $\mathcal{D}_1, \mathcal{D}_2 \dots \mathcal{D}_K$ , each containing  $N$  noisy observations of the state of the cell. Let the cell state be represented by state vector  $u(t) \in \mathbb{R}^N$  which is hypothesized to obey a set of ordinary differential equations of the form (2.1). Instead of integrating the equations (2.1) we would find an estimate for the derivative of the trajectories  $\hat{f}$ .

This is known as the *smoothing* step [11] should be done using unsupervised methods, for example with Gaussian Process Regressors [31] as shown in in Figure 4.1. This requires the inversion of an  $K' \times K'$  data matrix where  $K' := \sum_k |\mathcal{D}_k|$  is the total number of trajectory data points. This has a computational complexity  $K'^3$  which is only tractable with sparse datasets.

Let the region  $\partial\mathcal{D}$  be a boundary defined by the Delaunay tessellation of the input data. Let us define the estimate  $\hat{f}$  only within the region  $\partial\mathcal{D}$  so that there are no extrapolation artefacts. For the Gaussian Process approach the estimate would be

$$\hat{f}(u) \sim \mathcal{N}(\mu(u), \Sigma(u)) \quad \text{for } u \in \partial\mathcal{D} \quad (4.1)$$

where at any given state  $u$  the field estimate  $\hat{f}$  is generated by Gaussian distributions of mean vector  $\mu$  and covariance matrix  $\Sigma$ . Solving for these requires a choice of matrix-valued kernel function  $\mathbf{K}(u, v)$  which encodes our knowledge about the local structure of the field. Sophisticated kernels for learning vector fields exist [32] for decomposing fields in conservative and solenoidal components, which aid in localising fixed points and cycles.



**Figure 4.1:** Gaussian process regressors estimating derivative of the trajectories  $\hat{f}$  from example trajectory datasets  $\mathcal{D}_1 \dots \mathcal{D}_K$  with varying signal to noise ratios. Interpolation error  $E$  is shown as a heatmap; extrapolation fails

The simplest choice of kernel assumes the components are independent and have a finite correlation length  $\gamma$ , such as Gaussian radial basis functions. Here  $\mathbf{I}$  is the identity matrix and the hyperparameter  $\gamma$  has to be optimised.

$$\mathbf{K}(\vec{u}, \vec{v}) = \mathbf{I}^{-\gamma|\vec{u}-\vec{v}|^2} \quad (4.2)$$

The second step is called *matching* where the estimated field  $\hat{f}$  is used as an optimisation target against some parametrised function  $F_\theta$  with unknown parameters  $\theta$ .

In our setting we would like to match the geometry of the field but not its magnitude; in this sense we are focusing on the qualitative aspects of the dynamics of a set of differential equations, rather than the quantitative dynamics or kinetics. This could be achieved with the following objective function

$$\mathcal{L}(\theta | \mathcal{D}) := e^{-\frac{\hat{f} \cdot F_\theta}{|\hat{f}| |F_\theta|}} \quad (4.3)$$

where the cost is minimal when the data derivative  $\hat{f}$  and the parametrised model  $F_\theta$  point in the same direction and maximal when they point in opposing directions.

Although we are getting close to focusing on qualitative features of a model, this objective function is still sensitive to the locations and shapes of fixed point and limit cycles. What if we cared about even higher-level features such as the number of fixed points? Or perhaps whether a system oscillates or not? This is where the language of bifurcation theory described in Chapter 2 is optimally suited for this task, but first we need to discuss how to set up experiments to detect bifurcations from flow cytometry data.

### 4.1.2 Bifurcations in Flow Cytometry Data

### 4.1.3 Extending the Bifurcation Measure for Limit Cycles

# Parameter Inference with Bifurcation Diagrams

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## Abstract

Estimation of parameters in differential equation models can be achieved by applying learning algorithms to quantitative time-series data. However, sometimes it is only possible to measure qualitative changes of a system in response to a controlled condition. In dynamical systems theory, such change points are known as *bifurcations* and lie on a function of the controlled condition called the *bifurcation diagram*. In this work, we propose a gradient-based semi-supervised approach for inferring the parameters of differential equations that produce a user-specified bifurcation diagram. The cost function contains a supervised error term that is minimal when the model bifurcations match the specified targets and an unsupervised bifurcation measure which has gradients that push optimisers towards bifurcating parameter regimes. The gradients can be computed without the need to differentiate through the operations of the solver that was used to compute the diagram. We demonstrate parameter inference with minimal models which explore the space of saddle-node and pitchfork diagrams and the genetic toggle switch from synthetic biology. Furthermore, the cost landscape allows us to organise models in terms of topological and geometric equivalence.

## 1 Introduction

Inverse problems [1] arise in biology and engineering in settings when the model is not fully known and the desire is to match model behaviour to a given set of observations. This helps systematically guide both model and experimental design. While we would like to understand the quantitative details of a system, often only qualitative changes in response to varying experimental conditions can be robustly measured across independent studies [2, 3]. For example, several studies are likely to agree that the human immune system activates above a threshold concentration of a pathogen and deactivates at a lower threshold concentration, but may disagree on the exact quantities of the thresholds or the magnitudes of the immune response. Bifurcation theory provides us a framework for studying these transitions in a manner that is independent of quantitative details [4]. The emerging picture suggests that identification of the qualitative behaviour – the bifurcation diagram – should precede any attempt at inferring other properties of a system [5].

Inferring the parameters of a model directly from a bifurcation diagram is difficult because it is not obvious how multiple parameters in concert control the existence and position of a bifurcation. It could even be impossible for the model to bifurcate in the manner desired. Several approaches exist

to place bifurcations to desired locations once a manifold is present [6–8] yet typically resort to sampling techniques to search for them in the first place [9, 10]. Progress has been made in cases where model structure and stability conditions are used to refine the search space [11, 12] yet the resulting objectives are still not explicit in the bifurcation targets and also not differentiable. In the emerging field of scientific machine learning [13–15], parameters of structured mechanistic models are favoured over flexible models in larger parameter spaces. A scalable method for navigating the space of bifurcation diagrams would enable design of differential equations with high-level qualitative constraints. Furthermore one could begin organising models according to qualitatively distinct behaviours.

Back-propagation through differential equation solvers has been a breakthrough over the past couple of years [16, 17] that enabled scalable parameter inference for differential equations from trajectory data. Although one could use trajectory data to create the aforementioned qualitative constraints [18, 19] this would entail over-constraining information originating from the kinetics and dynamical transients of the model. Furthermore, such data usually does not contain sufficient information about dynamical transients in order to identify kinetic parameters. Techniques for back-propagating through implicit equation solvers have also been developed [20, 21] although to the best of the authors’ knowledge have not been applied to bifurcation diagrams at the time of writing this paper.

The problem of inferring differential equation parameters against a user-specified bifurcation diagram decomposes into two parts: searching for bifurcating regimes and matching the locations of bifurcation points to desired values. Matching bifurcation locations is a supervised problem where the data are expressed as bifurcations points [7, 10]. Searching for bifurcations is an unsupervised problem because when bifurcations are not present, there is no distance defined between data and prediction [9]. Therefore only properties of the model can be used to start the search. We propose a semi-supervised approach for performing both tasks in an end-to-end fashion. The bifurcation diagram encodes high-level qualitative information defined by state space structures, rather than kinetics. We apply the strategy of implicit layers [20, 21] to calculate gradients. To compute the diagram we use a predictor-corrector method called deflated continuation [22, 23] developed for partial differential equations.

We find that the cost function landscape contains basins that not only allow us to synthesise models with a desired bifurcation diagram but also allow us to organise models in terms of topological and geometric equivalence. We discuss the relevance of this in model selection. In summary, our paper has the following main contributions:

- An end-to-end differentiable method for locating bifurcations in parameter space and then matching their dependency on a control condition to user-specified locations
- Implementation of the method as a Julia package  
[github.com/gszep/BifurcationInference.jl](https://github.com/gszep/BifurcationInference.jl)
- Leveraging the cost landscape for a novel way of organising differential equation models in terms of geometric and topological equivalence

## 1.1 Preliminaries

Suppose we collected observations along a scalar control condition  $p \in \mathbb{R}$  and conclude that there are specific values of  $p$  for which there are qualitative changes in system behaviour. Let  $\mathcal{D}$  be the set of those values and let us hypothesise that these transitions occur due to bifurcations in the dynamics that drive the underlying mechanism. Let us model the mechanism with a parameterised set of differential equations for states  $u \in \mathbb{R}^N$  with a vector function  $F_\theta$  in a parameter space  $\theta \in \mathbb{R}^M$ .

For the purposes of introducing this work, we will consider the simplest class of bifurcations known as *co-dimension one* bifurcations not including limit cycles. Therefore  $\mathcal{D}$  should contain conditions for which we hypothesise changes in multi-stable behaviour. Let the equations be

$$\frac{\partial u}{\partial t} = F_\theta(u, p) \quad \text{where} \quad F_\theta : \mathbb{R}^{N+1} \rightarrow \mathbb{R}^N \quad (1)$$

In the context of the differential equations, and not considering limit cycles for now, a co-dimension one bifurcation can be defined by a set of conditions on the determinant of the Jacobian  $|\frac{\partial F_\theta}{\partial u}|$ . The determinant of the Jacobian quantifies the rate at which trajectories in a local patch of state-space  $u \in \mathbb{R}^N$  converge or diverge. Let  $s \in \mathbb{R}$  parametrise the curves that trace out the bifurcation

diagram. Any location on the curve  $u(s)$  and  $p(s)$  must satisfy the steady-state of equations (1). The determinant approaching zero along the diagram means that the dynamics of the system are slowing down, which is an important indicator for the onset of a transition between qualitative behaviours. Furthermore, the slowing down must necessarily be followed by a breakdown of stability; for this to be true it is sufficient *but not necessary* to require that the determinant cross zero with a finite slope, meaning that its directional derivative along the diagram  $\frac{d}{ds} \left| \frac{\partial F_\theta}{\partial u} \right|$  is not zero. The set of predicted values for the control condition  $\mathcal{P}(\theta) \subset \mathbb{R}$  at which bifurcations occur are defined as

$$\mathcal{P}(\theta) := \left\{ p \in \mathbb{R} : \exists u : F_\theta(u, p) = 0, \left| \frac{\partial F_\theta}{\partial u} \right| = 0, \frac{d}{ds} \left| \frac{\partial F_\theta}{\partial u} \right| \neq 0 \right\} \quad (2)$$

A proof of how the conditions (2) are sufficient but not necessary for local bifurcations is detailed in Appendix B. The most common bifurcations between steady states, not including limit cycles, are saddle-nodes and pitchforks [24]. Saddle-node bifurcations, which often appear in pairs (Figure 1A) are defined by stable and unstable fixed points meeting and disappearing. Pitchfork bifurcations are special cases of the saddle-node where a single steady state splits into two stable and one unstable steady state (Figure 1B). To illustrate these bifurcations, we define minimal models (Figure 1) that span the space of saddle-node and pitchforks, where indeed zero crossings in the determinant with a finite slope define the set of prediction  $\mathcal{P}(\theta)$ . The location of these crossings in general may not match the targets  $\mathcal{D}$ .

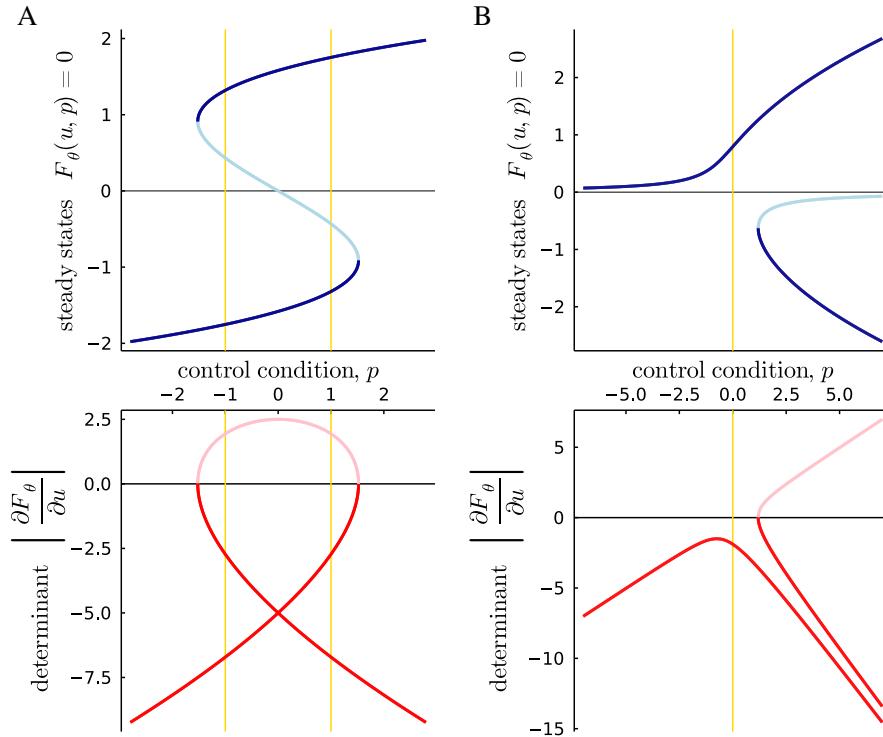


Figure 1: Illustration of bifurcation diagrams for minimal models of bifurcations. A. Saddle-node bifurcations arise for  $F_\theta(u, p) = p + \theta_1 u + \theta_2 u^3$  when  $\theta = (\frac{5}{2}, -1)$ . B. Pitchfork bifurcations arise for  $F_\theta(u, p) = \theta_1 + pu + \theta_2 u^3$  when  $\theta = (\frac{1}{2}, -1)$ . Targets are illustrated by light yellow vertical lines. Bifurcation curves are shown as solid blue and red lines, with lighter shades indicating the determinant crossing zero at locations  $\mathcal{P}(\theta)$  giving rise to unstable solutions.

For a given set of parameters  $\theta$  one could compute the set of predicted bifurcations  $\mathcal{P}(\theta)$  using parameter continuation methods [23, 22]. Our goal is to find optimal parameters  $\theta^*$  that match predictions  $\mathcal{P}(\theta^*)$  to specified targets  $\mathcal{D}$ . We must design a suitable cost function  $L$  so that

$$\theta^* := \operatorname{argmin}_\theta L(\theta | \mathcal{D}) \quad (3)$$

The optimal  $\theta^*$  is not expected to always be unique, but is in general a manifold representing the space of qualitatively equivalent models. Ideally, the cost function  $L$  should reward  $\theta$  for which the number of predicted bifurcations is equal to the number of targets,  $|\mathcal{P}(\theta)| = |\mathcal{D}|$ . This is especially important in the case where there are no predictions  $|\mathcal{P}(\theta)| = 0$ .

## 2 Proposed Method

### 2.1 Semi-supervised Cost Function

To identify parameter sets that give rise to bifurcation diagrams with specified bifurcation points, we propose a semi-supervised cost function that comprises two terms. The role of the supervised term is simply to reward predicted bifurcations to coincide with the specified target locations. This of course relies on such bifurcations existing. The role of the unsupervised term is to encourage an optimiser to move towards parameter regimes that do exhibit bifurcations.

#### 2.1.1 Supervised term: matching bifurcations to target locations

In order for predicted bifurcations  $p(\theta) \in \mathcal{P}(\theta)$  to match targets  $p' \in \mathcal{D}$  we need to evaluate an error term  $|p(\theta) - p'|$ . A naive approach might take an average over the norms for all prediction-target pairs. However this gives rise to unwanted cross-terms and the possibility of multiple predictions matching the same target without any penalty for unmatched targets. Therefore, we choose a geometric mean over the predictions and an arithmetic mean over targets:

$$E(\theta, \mathcal{D}) = \frac{1}{|\mathcal{D}|} \sum_{p' \in \mathcal{D}} \prod_{p(\theta) \in \mathcal{P}(\theta)} |p(\theta) - p'|^{\frac{1}{|\mathcal{P}|}} \quad (4)$$

The supervised term is only zero when each target is matched by at least one prediction and allows for cases where the number of predictions is greater than or equal to the number of targets  $|\mathcal{P}| \geq |\mathcal{D}|$ . An alternative approach, which undesirably introduces more hyper-parameters, would be to let each prediction  $\mathcal{P}(\theta)$  represent the centroid of a mixture distribution and use expectation-maximisation to match the centroids to targets  $\mathcal{D}$ .

#### 2.1.2 Unsupervised term: encouraging bifurcations

We can see from Figure 1 and definition (2) that predictions  $p(\theta)$  can be identified by looking for points along the curve where the determinant crosses zero  $|\frac{\partial F_\theta}{\partial u}| = 0$  with a finite slope  $\frac{d}{ds} |\frac{\partial F_\theta}{\partial u}| \neq 0$ . Using these quantities we can define a positive semi-definite measure  $\varphi_\theta(s)$  of zero crossings in the determinant along a curve parameterised by  $s$  which we define as

$$\varphi_\theta(s) := \left( 1 + \left| \frac{\frac{d}{ds} |\frac{\partial F_\theta}{\partial u}|}{\frac{d}{ds} |\frac{\partial F_\theta}{\partial u}|} \right| \right)^{-1} \quad (5)$$

The bifurcation measure  $\varphi_\theta(s)$  is maximal at bifurcations and has finite gradients in non-bifurcating regimes (Figure 2). More specifically, the measure  $\varphi_\theta(s)$  is one at bifurcation points and goes to zero an odd number of times between bifurcations. This is because  $|\frac{\partial F_\theta}{\partial u}|$  must eventually turn around in order to return back to zero, resulting in the directional derivative  $\frac{d}{ds} |\frac{\partial F_\theta}{\partial u}|$  going to zero. Hence the measure  $\varphi_\theta(s)$  goes to zero for each turning point (see Figure 2).

On the other hand, as the determinant  $|\frac{\partial F_\theta}{\partial u}|$  diverges, we approach regimes far away from any bifurcations and hence  $\varphi_\theta(s) \rightarrow 0$ . Since we would still like to have non-zero gradients with respect to  $\theta$  in these regimes we designed the measure to go to zero sufficiently slowly.

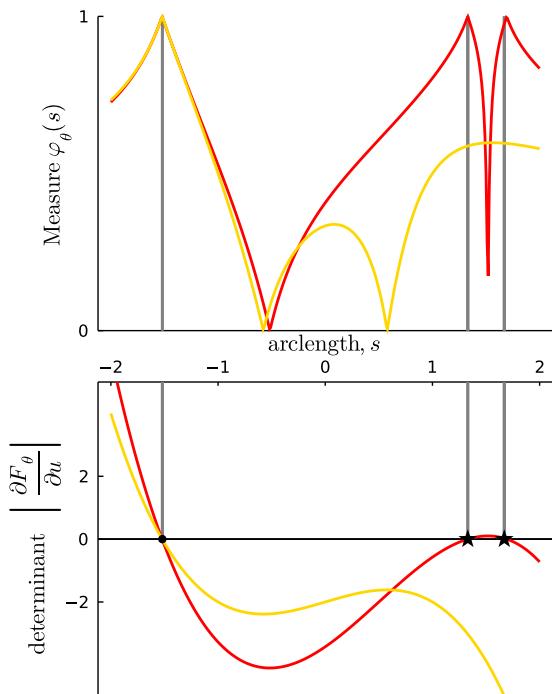


Figure 2: Bifurcation measure  $\varphi_\theta(s)$  and determinant  $|\frac{\partial F_\theta}{\partial u}|$  along the arclength  $s$  of two different bifurcation curves demonstrating how maximising the measure along the curve maintains the existing bifurcation marked by a circle, while encouraging new bifurcations marked by stars.

While the calculation of the determinant is straightforward, its directional derivative requires a tangent vector to the bifurcation curve. Fortunately the tangent vector  $T_\theta(s)$  at the solution  $u(s), p(s)$  anywhere along the curve  $s$  can be calculated as the nullspace of the rectangular  $N \times (N + 1)$  Jacobian

$$\frac{\partial F_\theta}{\partial(u, p)} \Big|_{F_\theta(u(s), p(s))=0} \cdot T_\theta(s) = 0 \quad (6)$$

This equation guarantees that the tangent vector  $T_\theta(s)$  is orthogonal to all hyper-planes defined by the components of  $F_\theta$ . In this setting the dimension of the nullspace is always known, and therefore can reliably be calculated using QR factorisation methods [25].

Equipped with a measure that quantifies the appearance of bifurcations along a bifurcation arc we can define the total measure for a bifurcation diagram as

$$\Psi(\theta) := \frac{\int_{F_\theta(u, p)=0} \varphi_\theta(s) ds}{\int_{F_\theta(u, p)=0} ds}. \quad (7)$$

Here we denote  $\int_{F_\theta(u, p)=0} ds$  as the sum of the line integrals in  $(u, p) \in \mathbb{R}^{N+1}$  defined by the level set  $F_\theta(u, p) = 0$  with  $s$  being an arbitrary parametrisation of the curves. The total measure  $\Psi(\theta)$  is normalised such that  $\Psi(\theta) \rightarrow 1$  in the regimes where the controlled condition region  $p$  is densely packed with bifurcations. The total measure  $\Psi(\theta)$  is added to the supervised term as if it were a likelihood. This defines the semi-supervised cost function as

$$L(\theta|\mathcal{D}) := (|\mathcal{P}| - |\mathcal{D}|) \log \Psi(\theta) + E(\theta, \mathcal{D}), \quad (8)$$

The pre-factor  $|\mathcal{D}| - |\mathcal{P}|$  in the unsupervised term ensures that the gradients are always pushing optimisers towards a state where  $|\mathcal{D}| = |\mathcal{P}|$ . This can be seen as a step-wise annealing of the unsupervised term until the desired state is reached.

## 2.2 Differentiating the semi-supervised cost function

To make use of gradient-based optimisers to locate desired bifurcation diagrams, we show here how to differentiate the cost function. First, we note that while individual bifurcations  $p(\theta)$  depend smoothly on  $\theta$ , the total number of predictions  $|\mathcal{P}|$  does not have gradient contributions with respect to  $\theta$ . Therefore, we can safely drop the dependency in the prediction counter and now proceed in taking gradients with respect to  $\theta$  knowing that the only dependencies we need to track are for individual bifurcations  $p(\theta)$  within the definition the supervised term (4) and the total measure (7). Therefore,

$$\frac{\partial L}{\partial \theta} = (|\mathcal{P}| - |\mathcal{D}|) \lambda \frac{\partial \Psi}{\partial \theta} \Psi(\theta)^{-1} + \frac{1}{|\mathcal{D}||\mathcal{P}|} \sum_{p'} \prod_{p(\theta)} |p(\theta) - p'|^{\frac{1}{|\mathcal{P}|}} \sum_{p(\theta)} \frac{\partial p}{\partial \theta} (p(\theta) - p')^{-1} \quad (9)$$

In a similar vein to back-propagation through neural differential equations [16] we would like to be able to calculate the gradient  $\frac{\partial L}{\partial \theta}$  without having to differentiate through the operations of the solver that finds the bifurcation diagram  $F_\theta(u, p) = 0$  and the bifurcation locations  $p(\theta)$ . To calculate the gradient of the measure  $\frac{\partial \Psi}{\partial \theta}$  we need to differentiate line integrals that depend on  $\theta$ . Fortunately this can be done by the application of the generalised Leibniz integral rule, details of which can be found in Appendix C.

The gradient of the bifurcation points  $\frac{\partial p}{\partial \theta}$  is found by application of the implicit function theorem to a vector function  $G_\theta : \mathbb{R}^{N+1} \rightarrow \mathbb{R}^{N+1}$  whose components represent the two constraints  $F_\theta(u, p) = 0$  and  $\left| \frac{\partial F_\theta}{\partial u} \right| = 0$ . By following a similar strategy to that used by implicit layers [20] we yield an  $(N + 1) \times M$  Jacobian representing a deformation field [26] for each  $\theta$  direction. The gradient we are looking for becomes

$$\frac{\partial p}{\partial \theta} = -\hat{p} \cdot \frac{\partial G_\theta}{\partial(u, p)}^{-1} \frac{\partial G_\theta}{\partial \theta} \Big|_{G_\theta(u, p)=0} \quad \text{where} \quad G_\theta(u, p) := \begin{bmatrix} F_\theta(u, p) \\ \left| \frac{\partial F_\theta}{\partial u} \right| \end{bmatrix} \quad (10)$$

Here  $\hat{p}$  is a unit vector in  $(u, p) \in \mathbb{R}^{N+1}$  that picks out the deformations along the  $p$ -direction. If we wanted to place the bifurcation at target steady state  $u'$  as well as target control condition  $p'$  we would use the full  $(N + 1) \times M$  deformation matrix. Calculation of this matrix involves inverting an

$(N+1) \times (N+1)$  Jacobian  $\frac{\partial G_\theta}{\partial(u,p)}$ . Instead of explicitly inverting the Jacobian the corresponding system of linear equations is solved. The determinant of this Jacobian goes to zero in the degenerate case where  $\frac{d}{ds} \left| \frac{\partial F_\theta}{\partial u} \right| = 0$ , further justifying our choice of measure  $\Psi(\theta)$  which discourages the degenerate case.

The cost function is piece-wise smooth and differentiable with undefined gradients only in parameter contours where the number of predictions  $|\mathcal{P}|$  changes; this is when  $\Psi(\theta)$  is undefined and the inverse of  $\frac{\partial G_\theta}{\partial(u,p)}$  does not exist. Given a set of solutions to  $F_\theta(u, p) = 0$  and locations  $p(\theta)$  the gradient  $\frac{\partial L}{\partial \theta}$  can be evaluated using automatic differentiation methods [27–29] without needing to back-propagate through the solver that obtained the level set  $F_\theta(u, p) = 0$  in the forward pass.

### 3 Experiments & Results

In this section, we apply the method first to minimal examples that can produce saddle-node and pitchfork bifurcations, and then a more complex model that has multiple parametric regimes that produce saddle-node bifurcations.

#### 3.1 Minimal Models

Optimisations of two parameters  $(\theta_1, \theta_2)$  using simple gradient descent from Flux.jl with learning rate  $\eta = 0.01$  for the minimal saddle-node and pitchfork models yield trajectories approaching lines of global minima in the cost function (Figures 3) which represent a set of geometrically equivalent models. Two bifurcation diagrams are geometrically equivalent if the number, type and locations of bifurcations match the specified targets  $\mathcal{D}$ .

We can see that the geometrically equivalent lines are contained within larger basins where the correct number and type of bifurcations are present but do not match the locations of targets  $\mathcal{D}$ . All models within this basin are in some sense topologically equivalent. This hierarchical classification allows us to identify the set of models that satisfy observed qualitative behaviour [5] before any attempt at inferring kinetic parameters, which is done by choosing a model along the line of geometrically equivalent models.

Optimisation trajectories for the two minimal models appear mostly circumferential. This is because the models were set up such that the radial direction from the origin in  $\theta$  space mostly scale kinetics whereas the circumferential direction changes the bifurcation topology. This suggests that the gradients of our cost function seek to change model geometry over kinetics.

#### 3.2 Genetic Toggle Switch

In this section we optimise a model where the states share a Hill function relationship with co-operatively  $n = 2$ ; these models often emerge from mass action kinetics with quasi-steady state approximations and are used to model species concentrations. After re-scaling the equations governing the dynamics of concentrations, the simplified equations for state  $u_1$  and  $u_2$  become

$$\partial_t u_1 = \frac{a_1 + (pu_2)^2}{1 + (pu_2)^2} - \mu_1 u_1 \quad \partial_t u_2 = \frac{a_2 + (ku_1)^2}{1 + (ku_1)^2} - \mu_2 u_2 \quad (11)$$

where  $a_k$  is the baseline production rate for species  $k$  in the absence of the other species. Each species has a finite degradation rate  $\mu_k$ . Finally we have two sensitivity constants  $p$  and  $k$ , one of which is chosen as our control condition. A baseline production rate  $a_k > 1$  recovers an inhibitor type hill function for species  $k$  and is an activator otherwise. The sensitivities are proportional to the slope of the hill productions. Solving for the steady states, substituting the equation for  $u_1$  into  $u_2$  and rearranging gives rise to the relationship

$$\frac{k}{\mu_1} = \frac{(1 + (\frac{p}{\mu_2} u')^2) \sqrt{a_2 - u'}}{(a_1 + (\frac{p}{\mu_2} u')^2) \sqrt{u' - 1}} \quad \text{where } u' := u_2 \mu_2 \quad (12)$$

which reveals that only  $a_1, a_2$  and the ratio between the sensitivity and degradation parameters,  $\frac{k}{\mu_1}$ , affect the solutions to this equation, and hence the locations of the bifurcations (Figure 4A). In 98% of 800 runs, optimisation using the ADAM optimiser [30] from Flux.jl with learning rate  $\eta = 0.1$

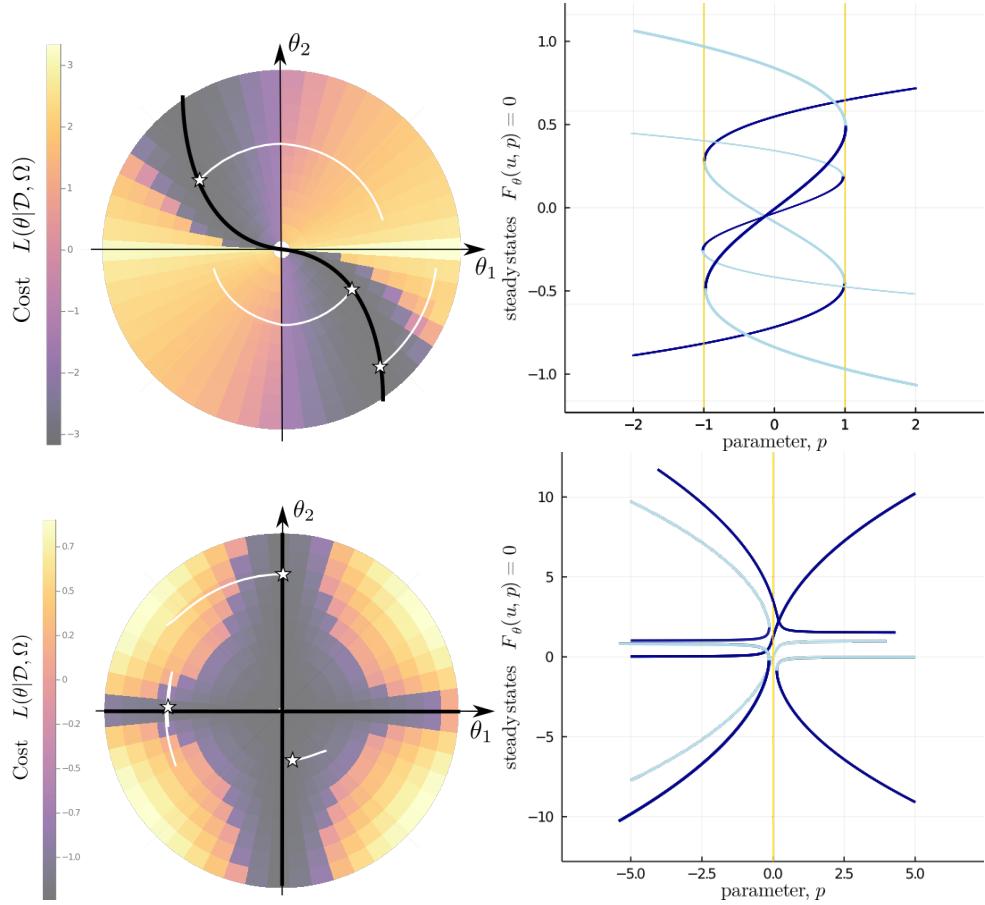


Figure 3: Saddle-node  $F_\theta(u, p) = p + \theta_1 u + \theta_2 u^3$  and pitchfork  $F_\theta(u, p) = \theta_1 + up + \theta_2 u^3$  optimised with respect to  $\theta$  so that predicted bifurcations  $\mathcal{P}(\theta)$  match targets  $\mathcal{D}$  in control condition  $p$ . The right panel shows bifurcation diagrams for the three optimal  $\theta^*$  marked by stars on the left panel. The optimisation trajectories in white follow the gradient of the cost, approaching the black lines of global minima in the left panel

converged to one of two clusters: mutual activation ( $a_1 < 1, a_2 < 1$ ; cluster 1) and mutual inhibition ( $a_1 > 1, a_2 > 1$ ; cluster 2) regimes. Example bifurcation diagrams illustrate how the bifurcation curves of each species are positively correlated in mutual activation and negatively correlated for mutual inhibition (Figure 4B).

In order to maintain biological interpretability, optimisation was restricted to the positive parameter regime by transforming the parameters to log-space  $\theta \rightarrow 10^\theta$ . At the beginning of each optimisation run an initial  $\theta$  was chosen in the log-space by sampling from a multivariate normal distribution with mean zero and standard deviation one.

### 3.3 Complexity

Performing one iteration of the optimisation requires the computation of the gradient of the cost (9), requiring a computation of the bifurcation diagram with parameter continuation methods, which includes the evaluation of matrix inversions (10). Instead of evaluating the inversions directly, we solve a system of linear equations, applying the same strategy as implicit layers [20, 21]. This leaves us with the computational bottleneck of calculating the determinant of the state space Jacobian, required in both the bifurcation measure (5) and gradient (10). This calculation scales like  $N^2$  where  $N$  is the number of state space variables (Figure 5).

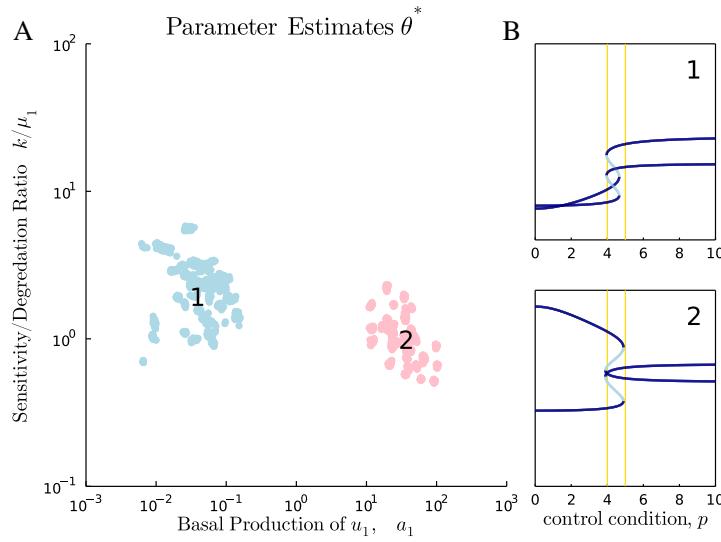


Figure 4: Bifurcation inference for the two-state model (11). A. Optimal parameter estimates  $\theta^*$  for the targets  $\mathcal{D} = \{4, 5\}$  reveal two clusters of qualitatively different regimes: mutual activation ( $a_1 < 1$ ; cluster 1) and mutual inhibition ( $a_1 > 1$ ; cluster 2). B. Example bifurcation diagrams indicate positively and negatively correlated dependencies between the two model states, as a function of the control condition.

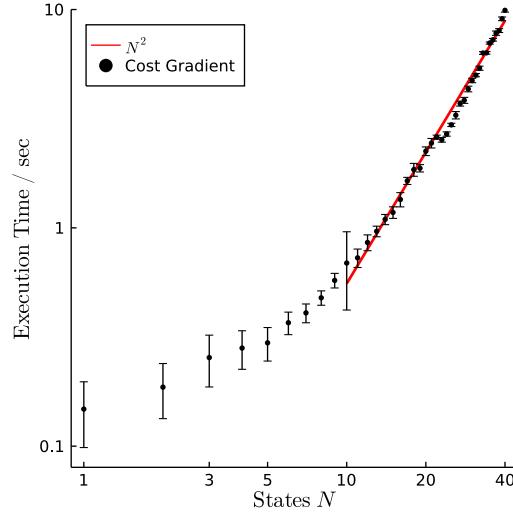


Figure 5: Complexity scaling of calculating the gradient of the cost function. Calculations were performed on an Intel Core i7-6700HQ CPU @ 2.60GHz x 8 without GPU acceleration

For this calculation a model (13) was chosen that so that it is extensible both in the number of parameters  $M$  and the number of states  $N$ .

$$\begin{cases} \partial_t u_1 = \sin^2 p - (\theta_1 \sin^2 p + 1)u_1 \\ \partial_t u_n = u_{n-1} - (\mu_n^2 + 1)u_n \end{cases} \quad 2 \leq n \leq N \quad (13)$$

In this model only the first state  $u_1$  defines the shape of the bifurcation diagram, while the remaining states are merely linearly proportional to the first. The parameters  $\mu_n$  contain sums of  $\theta_m$  allowing us a flexible choice on the number of parameters while maintaining stable solutions for the bifurcation diagram.

While still tractable on laptop computers for states  $N < 100$  our implementation currently does not scale well for partial differential equations where a large the number of states  $N$  arises from discretisation of the spatial variables. The only reason we need this determinant is because it

is an indicator of bifurcations. We can address the computational bottleneck by finding a more computationally efficient way of calculating this indicator. One approach would be to take the product of a finite subset of eigenvalues of the system. Note that any more efficient calculation must still permit back-propagation through it.

## 4 Conclusion & Broader Impact

We proposed a gradient-based semi-supervised approach for inferring the parameters of differential equations that produce a user-specified bifurcation diagram. By applying implicit layers [20, 21] and the generalised Leibniz rule [31] to the geometry of the implicitly defined steady states [32] it is possible to use automatic differentiation methods to efficiently calculate gradients. We defined a bifurcation measure that uses the determinant of the state-space Jacobian as an indicator for bifurcating parameter regimes in the unsupervised term of the cost function. The gradients of the cost can be efficiently computed using automatic differentiation methods. The computational bottleneck is the evaluation of the state-space Jacobian determinant which limits the implementation to ordinary differential equations.

We demonstrated our approach on models with one bifurcation parameter that can give rise to pitchforks and saddle-nodes. The estimated parameters form distinct clusters, allowing us to organise models in terms of topological and geometric equivalence. In the case of the genetic toggle switch we recovered mutual activation and inhibition regimes.

Although we did not consider limit cycles, our approach can be modified using the conditions for Poincaré-Andronov-Hopf bifurcations instead of the conditions on the Jacobian determinant. Our approach generalises naturally to bifurcation manifolds such as limit point curves or surfaces. This is because the normal components of implicit derivatives can still be calculated for under-determined systems of equations [26, 33, 34]. In the case of manifolds it would be more appropriate to use isosurface extraction algorithms rather than continuation to obtain the steady-state manifold. Our approach does not depend on the details of the steady-state solver and therefore can still be applied.

In dynamical systems theory the geometry of state-space determines all of the qualitative behaviours of a system. Our work makes progress towards designing models directly in state-space, rather than the spatial or temporal domain. This is valuable to experimentalists who only have qualitative observations available to them and wish to navigate the space of qualitative behaviours of their system. Our work lies within a trend of progress in the scientific machine learning community, where structured domain-informed models are favoured over flexible models that live in large parameter spaces.

## 5 Acknowledgements

We would like to acknowledge Kieran Cooney for the fruitful conversations that helped guide the derivations and computational approach. A special thanks go to Romain Veltz and the Julia community for helpful pointers on package development and discussions over Slack.

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## Chapter 5

# Exploring bifurcations between phenotypes

*Who knows what might happen to those who are consumed by greed*

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Ocarina of Time

## 5.1 Flow Cytometry

### 5.1.1 FlowJo

### 5.1.2 Immunophenotyping

### 5.1.3 Human Cell Atlas

## 5.2 Data Exploration

### 5.2.1 Dimensionality Reduction

### 5.2.2 Dataset Integration

### 5.2.3 Interactivity

## 5.3 FlowAtlas.jl

### 5.3.1 Julia & SciML

### 5.3.2 OpenLayers & Data-driven Documents

## **Chapter 6**

# **Conclusions**

*A childish mind will turn  
to noble ambition*

---

Ocarina of Time

### **6.1 Limitations**

### **6.2 Future work**

1. How can thesis results be applied to biological computing [33]

## **Appendix A**

# **Interpretation of morphogen gradients by a bistable circuit**

## Supplementary Information

### *Interpretation of morphogen gradients by a synthetic bistable circuit*

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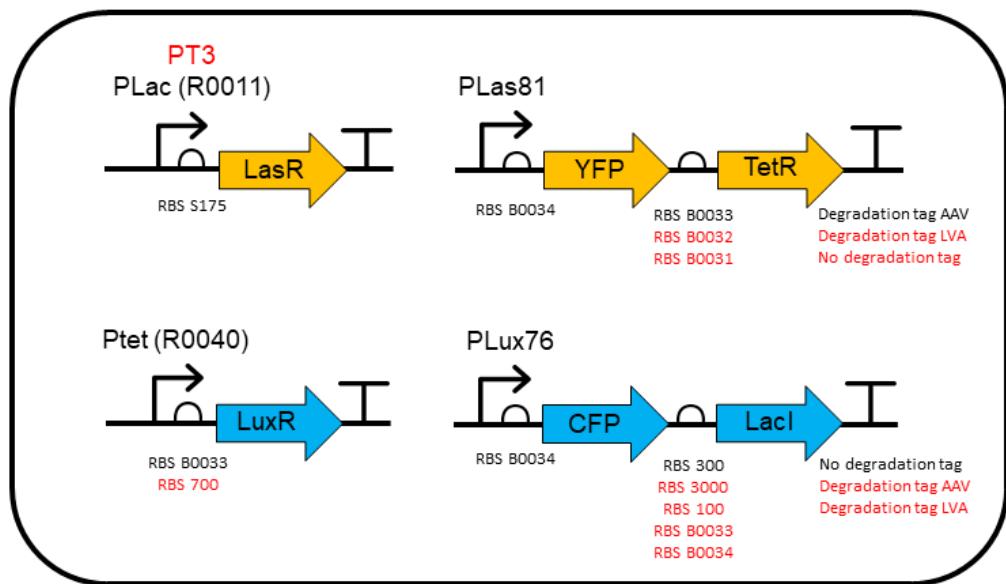
<sup>8</sup>Present address: Department of Genetics, Harvard Medical School, Boston, MA 02115, USA

<sup>9</sup>These authors contributed equally: Gregory Szep, Om Patange

## Contents

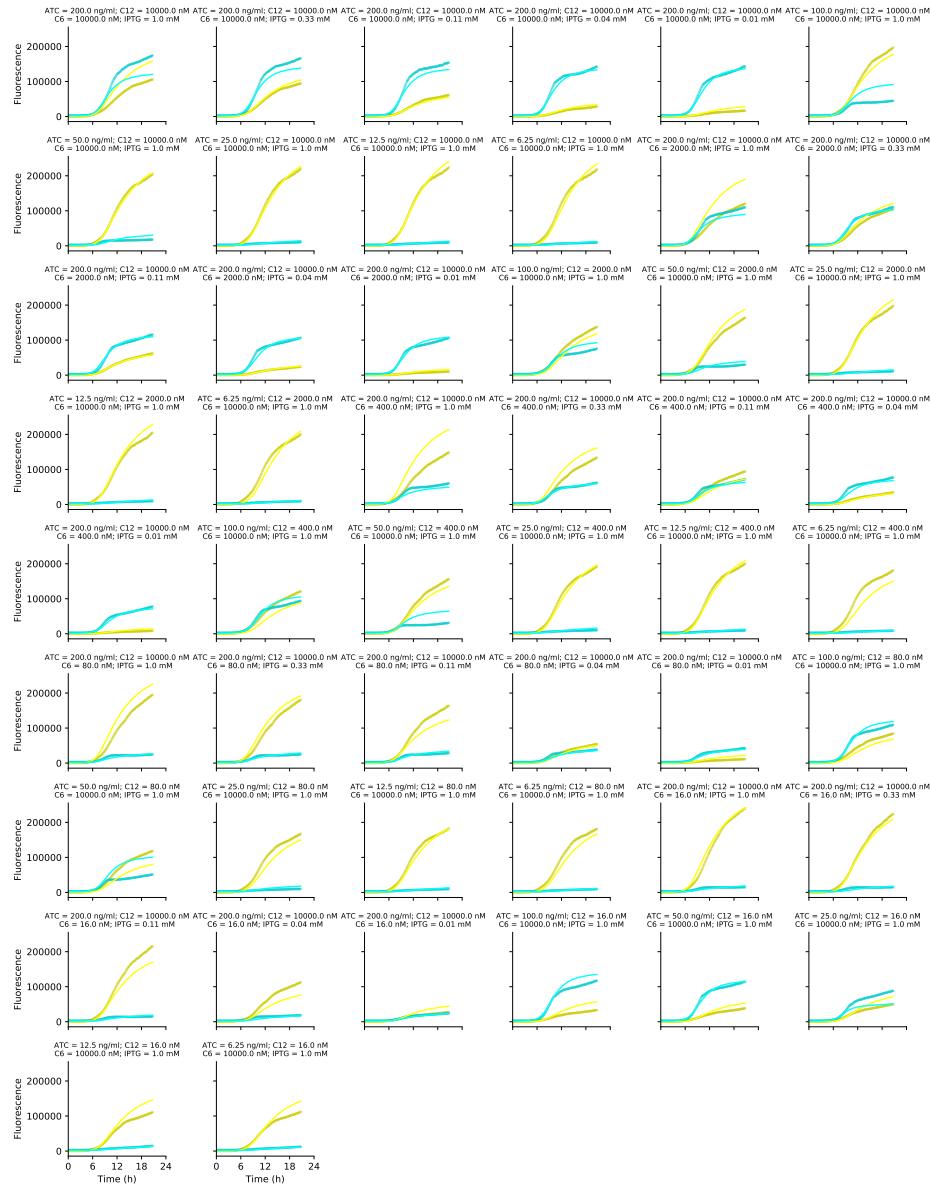
<b>1 Supplementary Figures</b>	<b>2</b>
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2.2 Bistability Analysis . . . . .	40
2.3 Boundary Experiments . . . . .	42
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## 1 Supplementary Figures

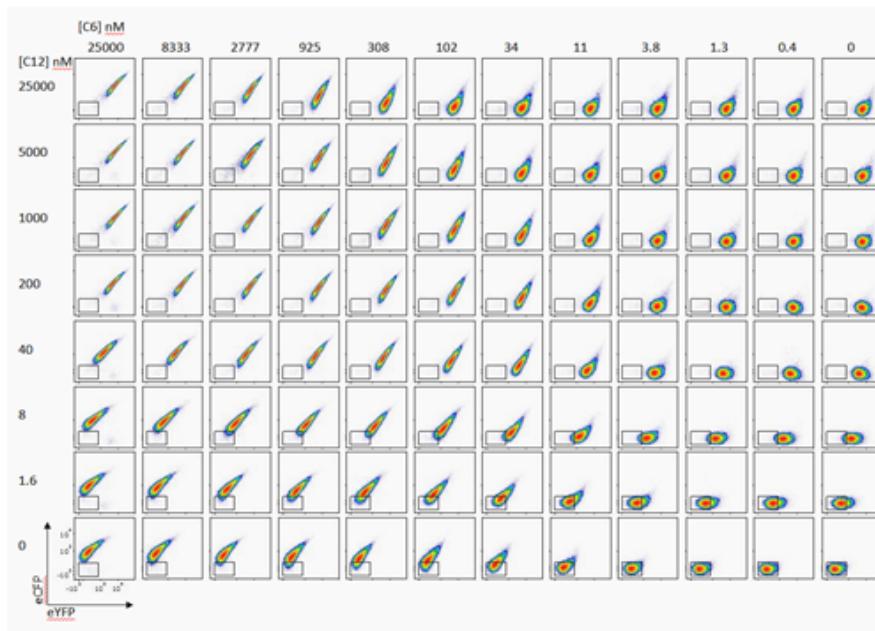
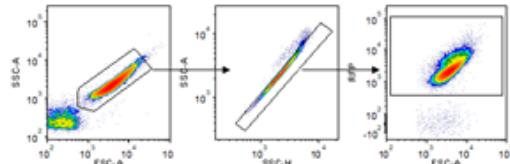


**Supplementary Figure 1: Circuit variants.** A circuit diagram of the exclusive receiver circuit with genetic parts labelled in black that were included in the final circuit and in red that were evaluated but discarded. Not all combinations of parts were tested.

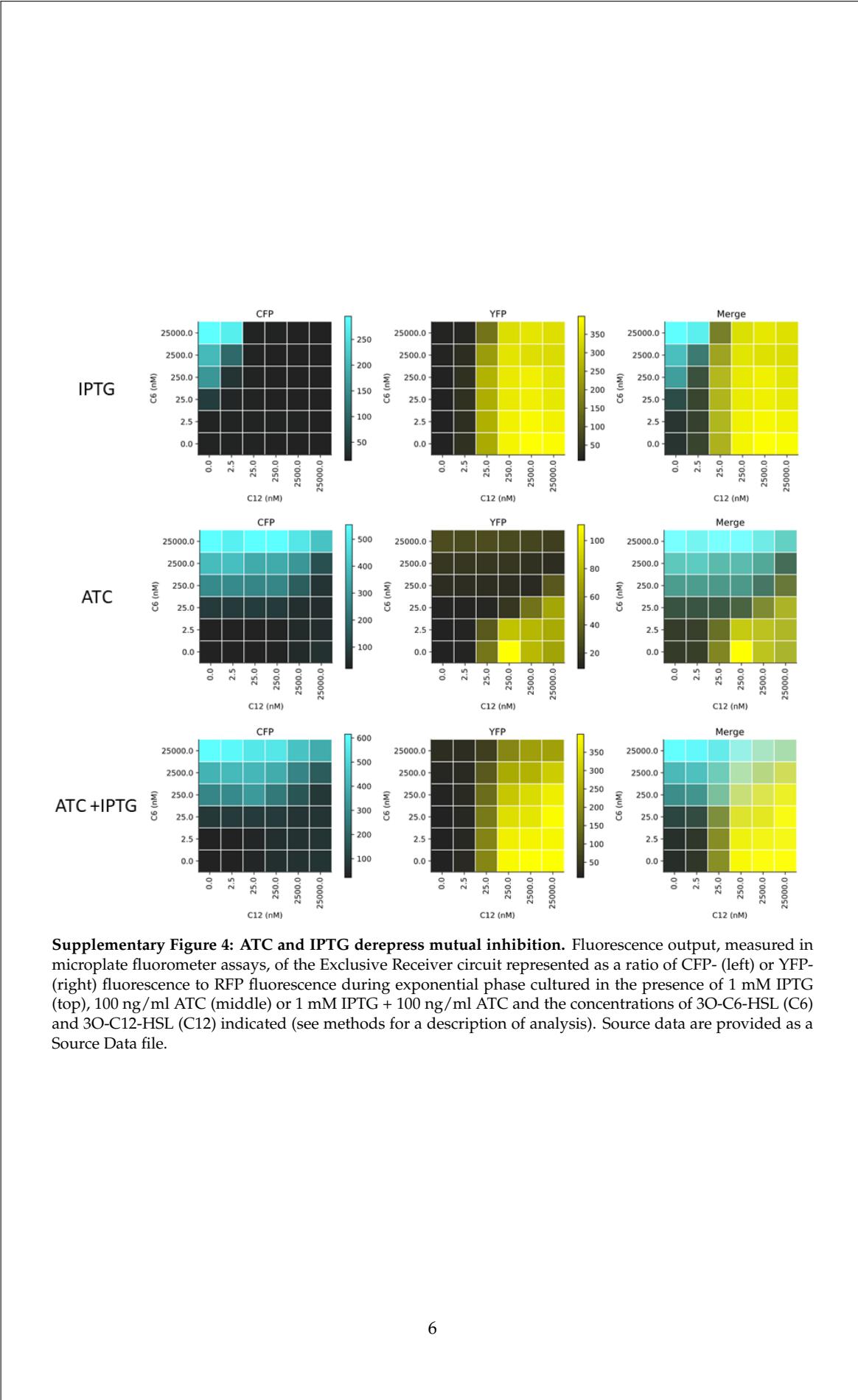


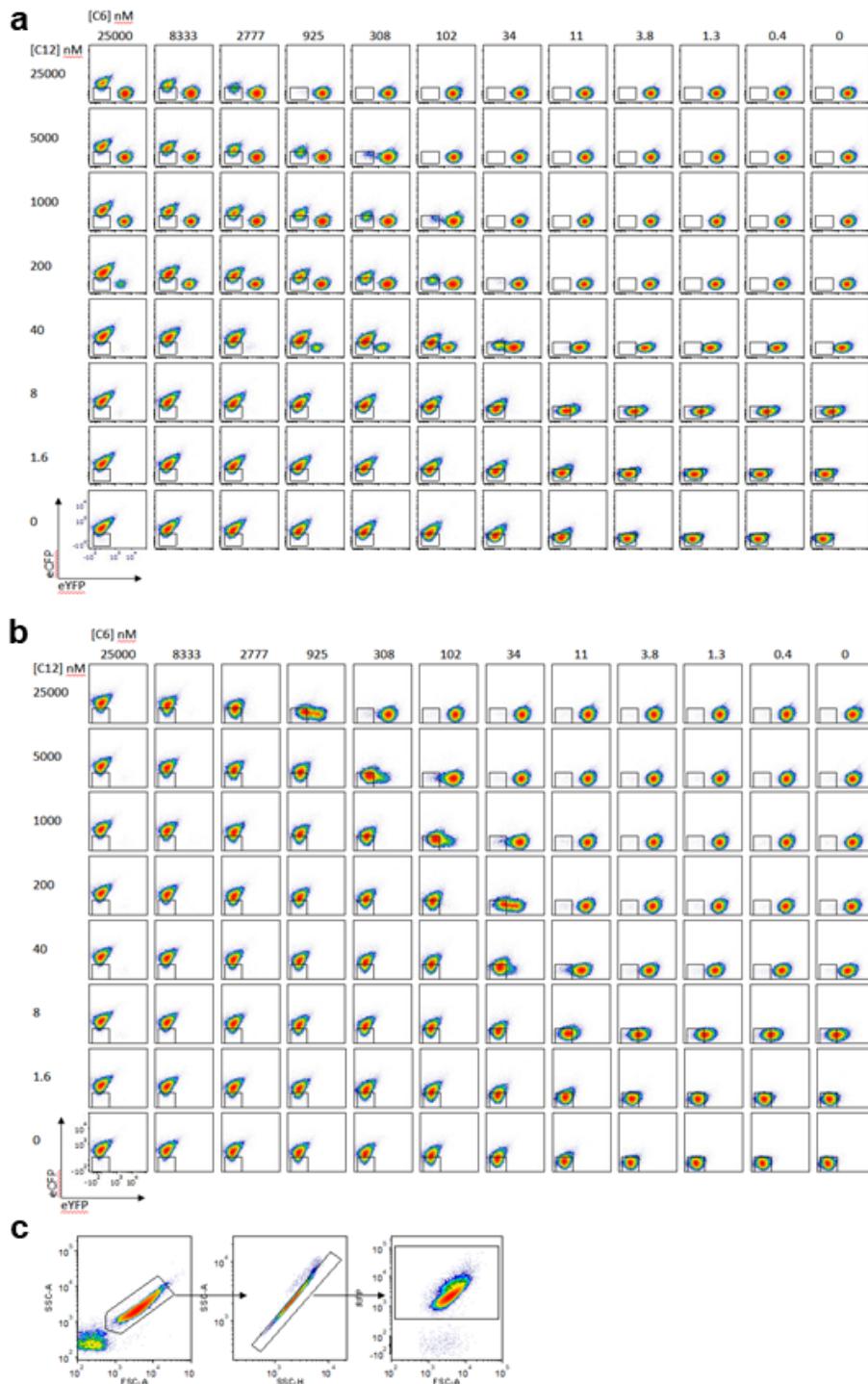


**Supplementary Figure 2: Raw timecourse fluorescence traces.** Fluorescence output, measured in microplate fluorometer assays, of the Exclusive Receiver circuit, plotted as CFP (dark cyan) and YFP (dark yellow) fluorescence against time, at the concentrations of C6, ATC, and IPTG indicated. Model simulations (cyan and yellow) of the maximum likelihood parameters are overlaid. Source data are provided as a Source Data file.

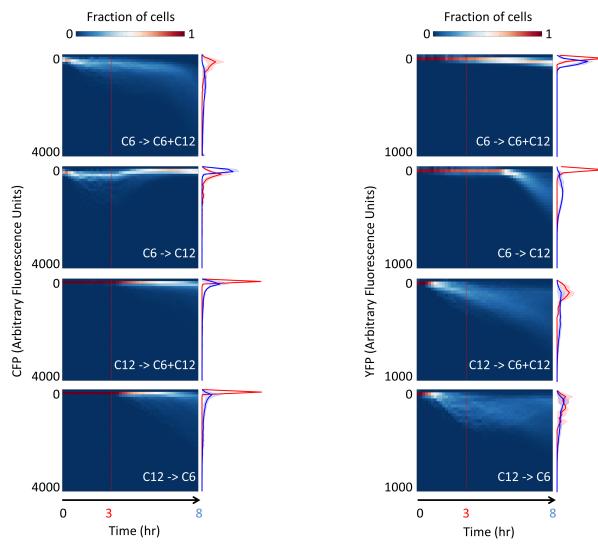
**a****b****c**

**Supplementary Figure 3: Flow cytometry measurements of naive cells** a, Exclusive Receiver cells cultured in the indicated concentrations of C6 and C12. YFP fluorescence is plotted on the X-axis while CFP fluorescence is plotted on the Y-axis. b, Receiver cells cultured in the indicated concentrations of C6 and C12. Square indicates the position of untreated cells. c, Gating strategy. Cells also constitutively express mRFP1 via a genomic transgene. Only RFP<sup>+</sup> cells were used for analysis and electronic noise, cell debris and cell clusters were excluded sequentially. Source data are provided as a Source Data file.

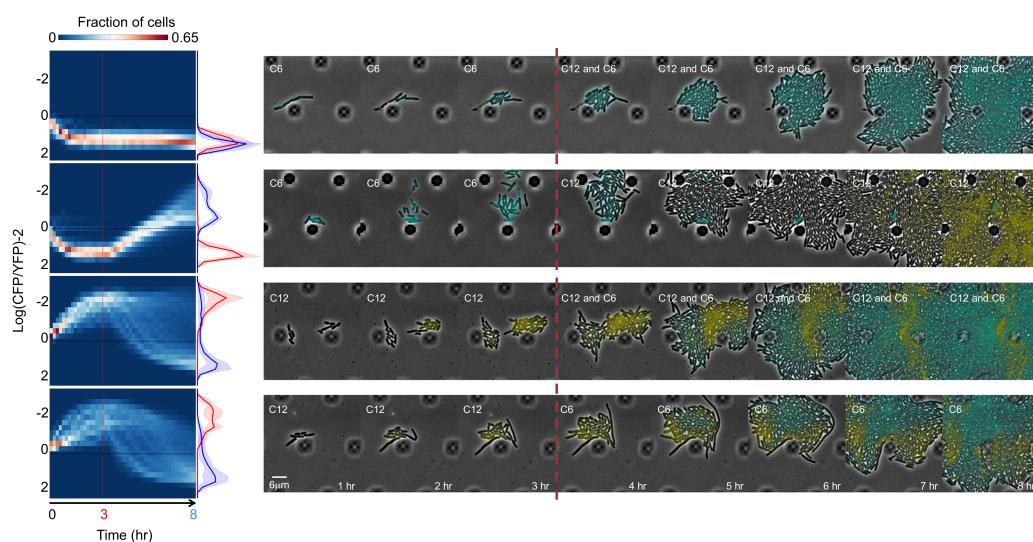




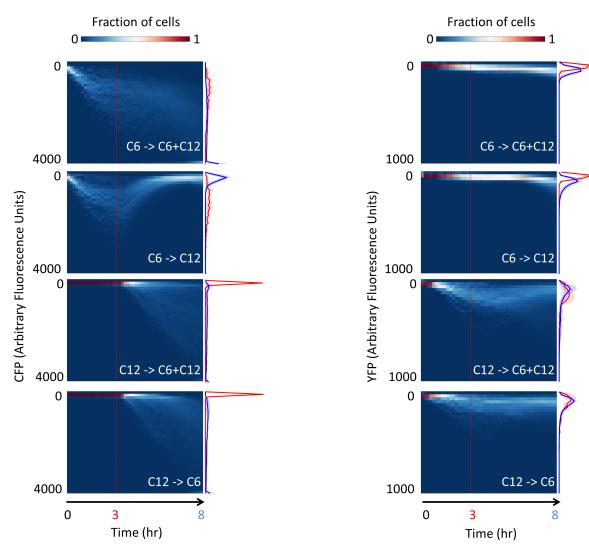
**Supplementary Figure 5: Flow cytometry measurements of conditioned cells** a, Cells conditioned in 500 nM C12 then exposed to the indicated concentrations of C6 and C12. YFP fluorescence is plotted on the X-axis while CFP fluorescence is plotted on the Y-axis. b, Cells conditioned in 500 nM C6 then exposed to the indicated concentrations of C6 and C12. Square indicates the position of untreated cells. c, Gating strategy. Cells also constitutively express mRFP1 via a genomic transgene. Only RFP<sup>+</sup> cells were used for analysis and electronic noise, cell debris and cell clusters were excluded sequentially. Source data are provided as a Source Data file.



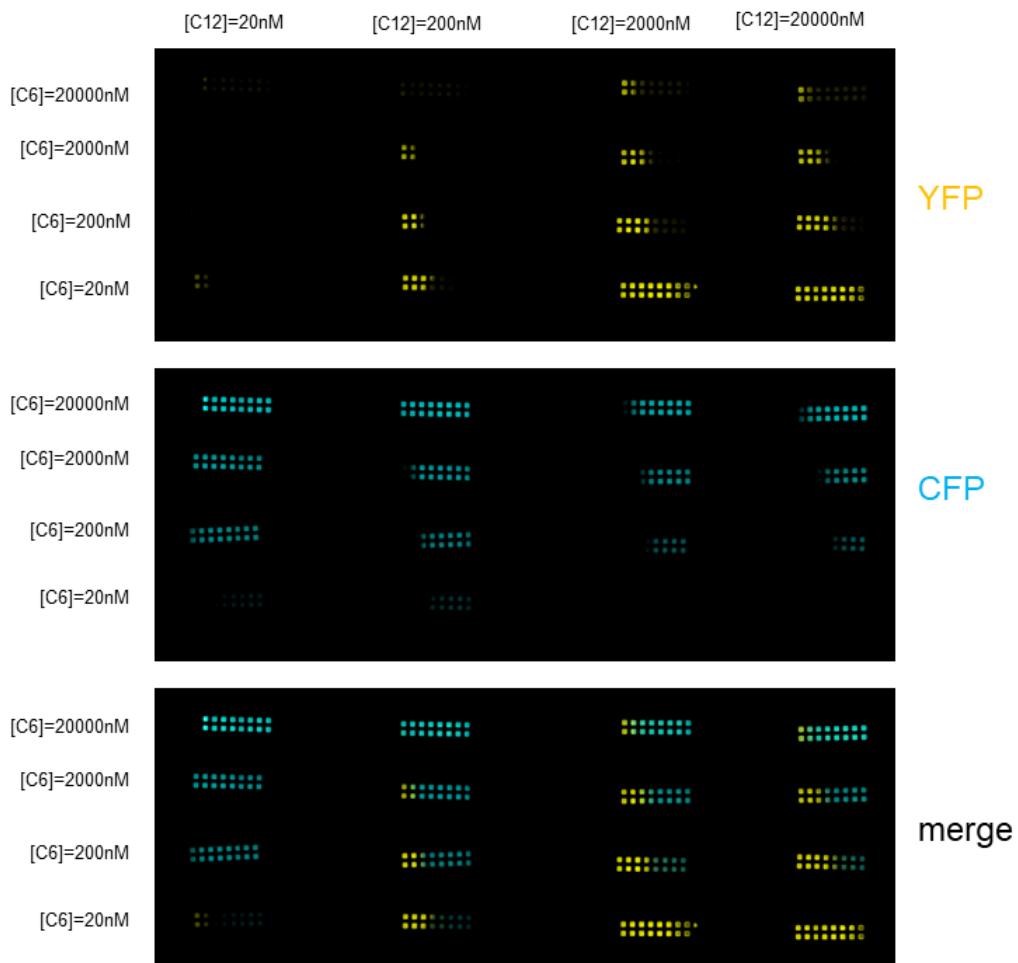
**Supplementary Figure 6: Microfluidics measurements of bistability.** Single-cell data used to compute ratios in Figure 2c. Cells were grown in microfluidic chips for 3 hours in the presence of either 37 nM C6 (rows 1 and 2) or 100 nM C12 (rows 3 and 4). Then media was changed to 100 nM C12 + 37 nM C6 (rows 1 and 3) or 100 nM C12 (row 2) or 37 nM C6 (row 4). Cells were imaged with a frame rate of (1 frame/10 minutes). Left panels in each column are kymographs of the CFP (left column) or YFP (right column) expression per-cell, and fraction of cells as a heat map. Histograms represent the populations at 3 hours (red) and 8 hours (blue). Lines and shaded region represent the mean and standard deviation, respectively, over  $n = 4$  biological replicates performed over 4 different days.



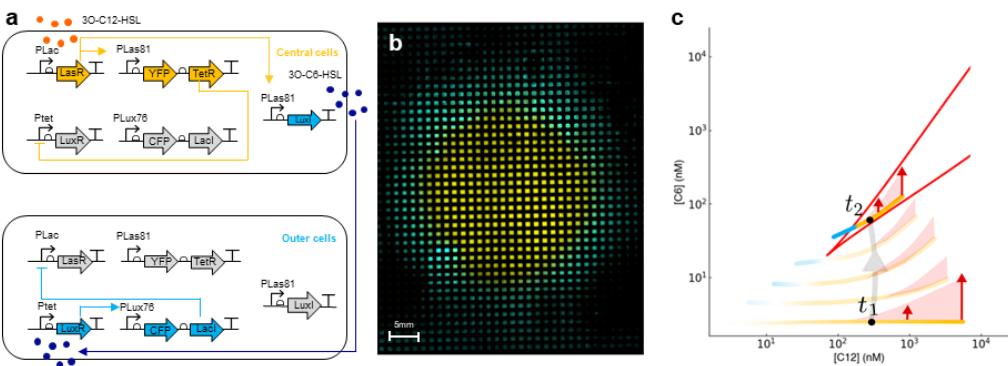
**Supplementary Figure 7: Bistability and switching of single cells is robust to high C6 signal concentration.** Cells were grown in microfluidic chips for 3 hours in the presence of either 1  $\mu\text{M}$  C6 (rows 1 and 2) or 100 nM C12 (rows 3 and 4). Then media was changed to 100 nM C12 + 1  $\mu\text{M}$  C6 (rows 1 and 3) or 100 nM C12 (row 2) or 1  $\mu\text{M}$  C6 (row 4). Cells were imaged with a frame rate of (1 frame/10 minutes). Left panels are kymographs of the log-ratio of CFP expression per-cell to YFP expression per-cell, and fraction of cells as a heat map. Histograms represent the populations at 3 hours (red) and 8 hours (blue). Lines and shaded region represent the mean and standard deviation, respectively,  $n = 4$  biological replicates performed over 4 different days. Right panels are sample montages of cells switching state (rows 3 and 4) or exhibiting bistability (rows 1 and 2); phase contrast and fluorescence channel ranges chosen for display.



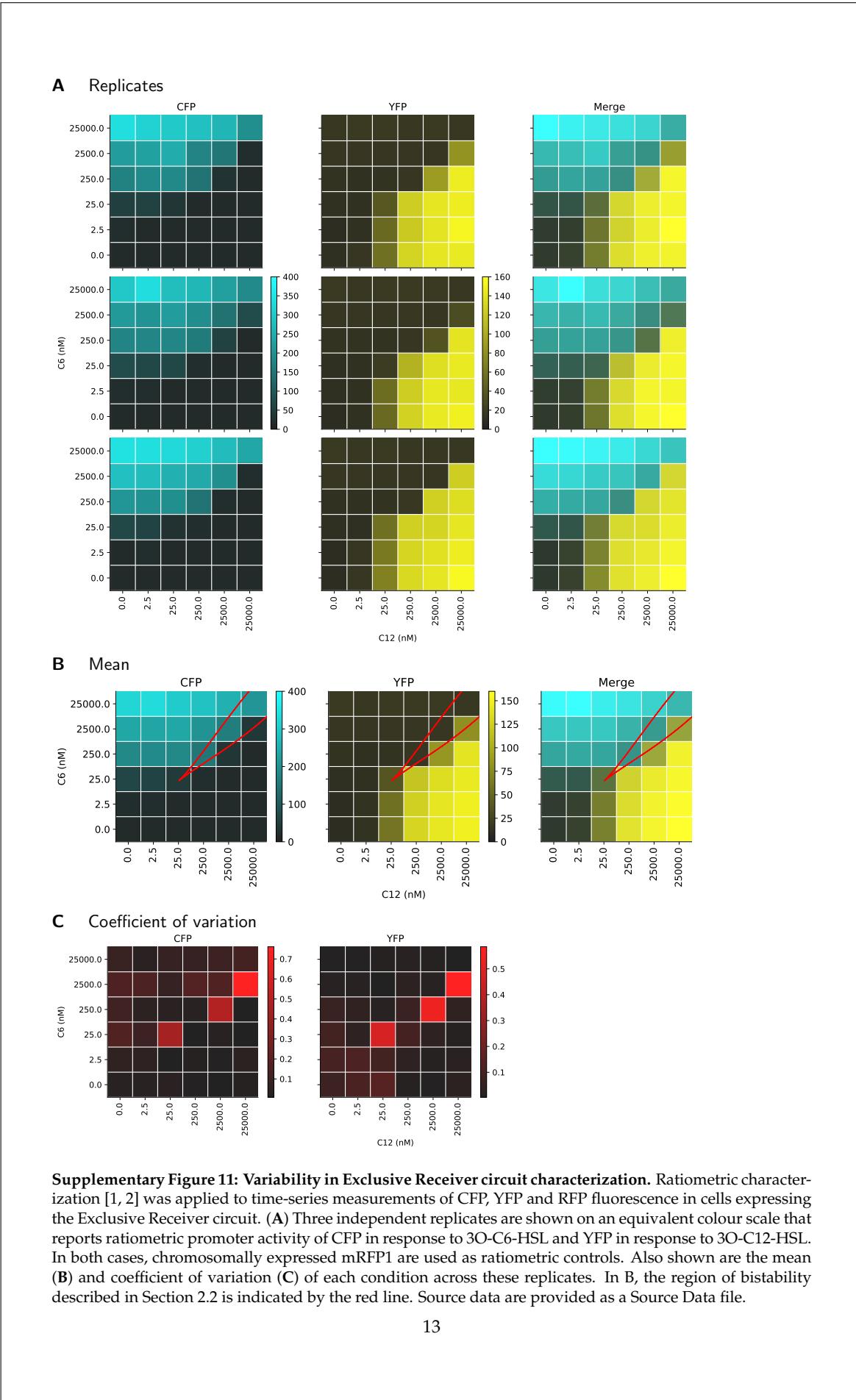
**Supplementary Figure 8: Microfluidics measurements of bistability with high C6 signal concentration.** Single-cell data used to compute ratios in 7. Cells were grown in microfluidic chips for 3 hours in the presence of either 1  $\mu$ M C6 (rows 1 and 2) or 100 nM C12 (rows 3 and 4). Then media was changed to 100 nM C12 + 1  $\mu$ M C6 (rows 1 and 3) or 100 nM C12 (row 2) or 1  $\mu$ M C6 (row 4). Cells were imaged with a frame rate of (1 frame/10 minutes). Left panels in each column are kymographs of the CFP (left column) or YFP (right column) expression per-cell, and fraction of cells as a heat map. Histograms represent the populations at 3 hours (red) and 8 hours (blue). Lines and shaded region represent the mean and standard deviation, respectively, over  $n = 4$  biological replicates performed over 4 different days.

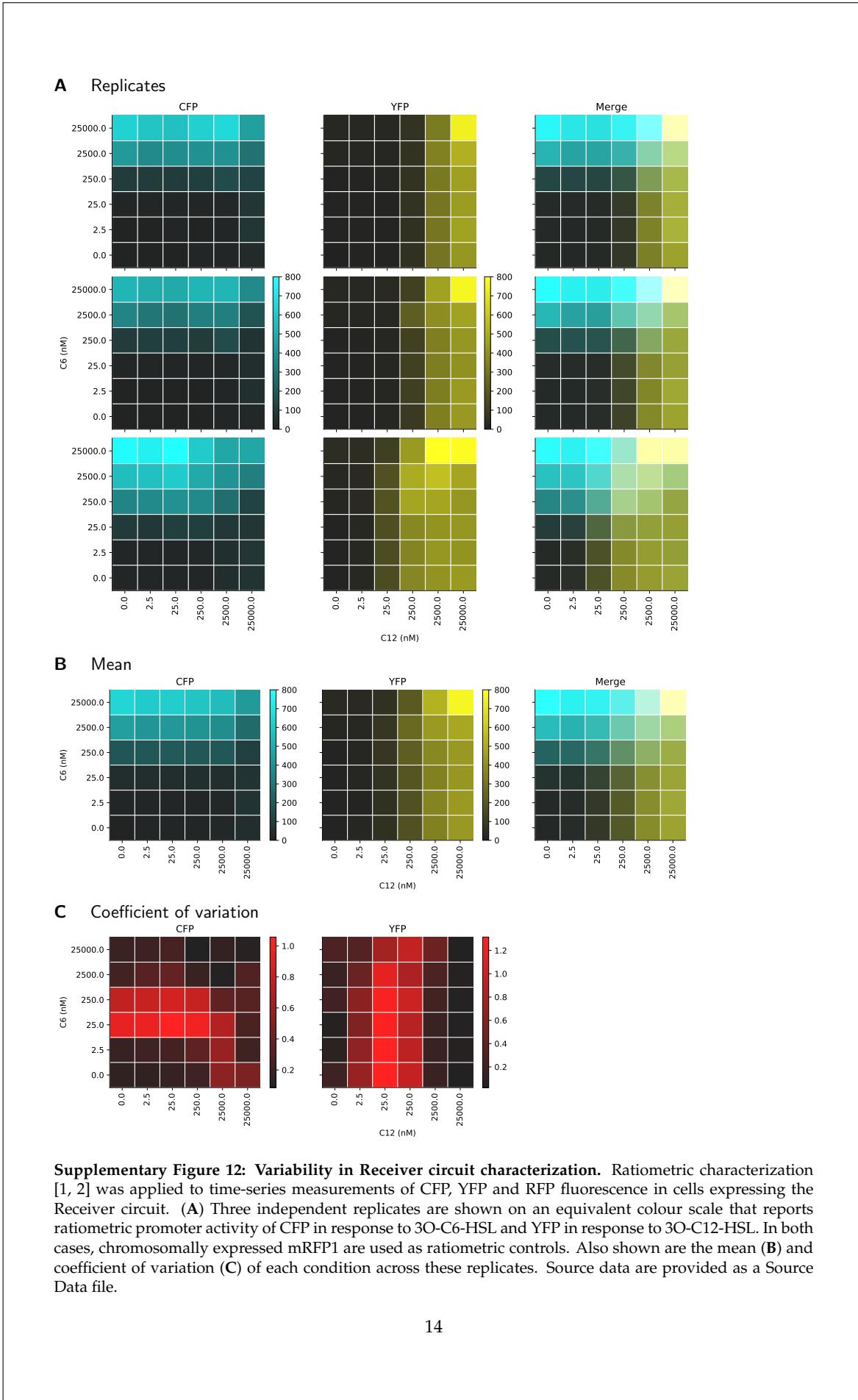


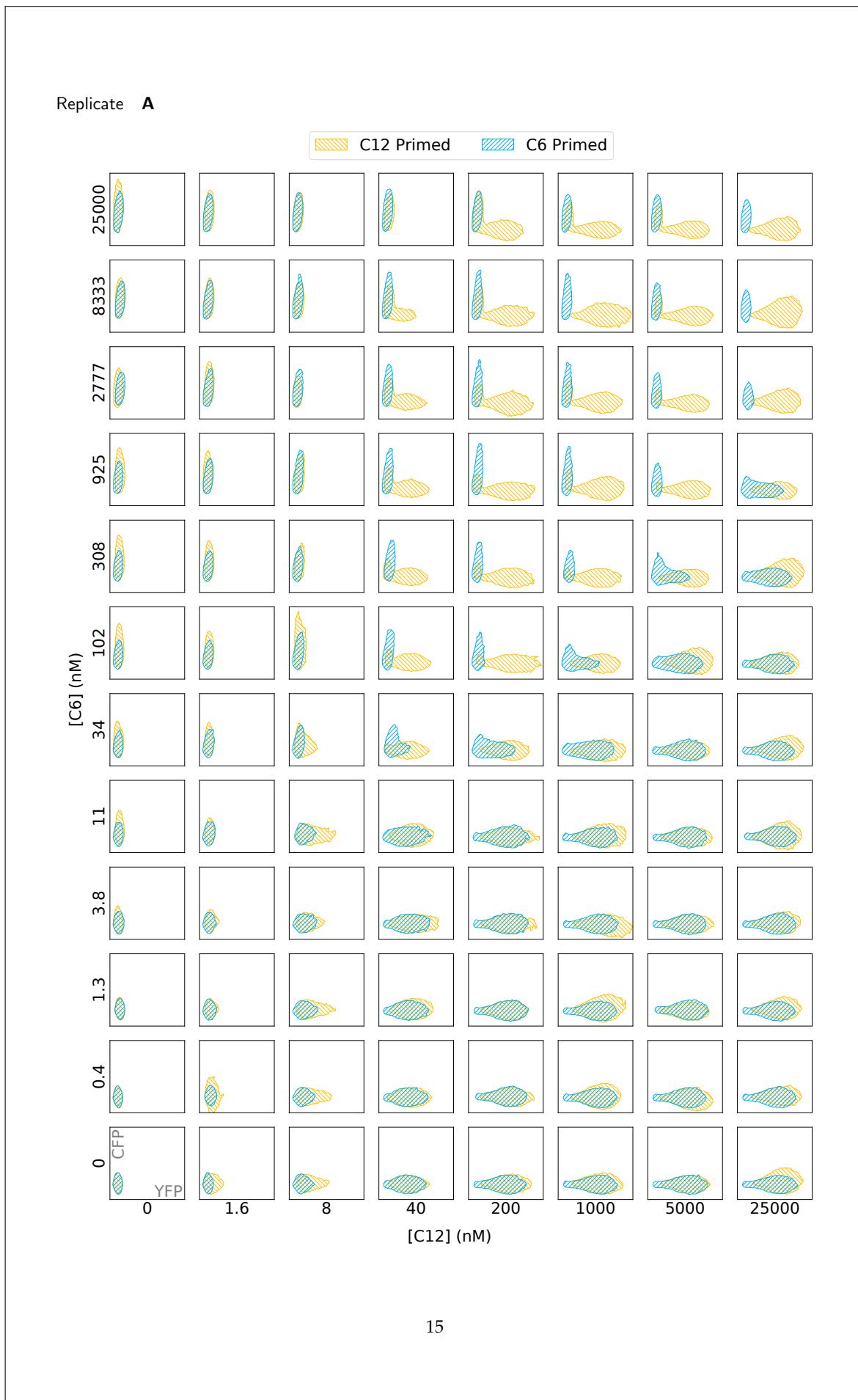
**Supplementary Figure 9: Boundaries summarized in Figure 3c** Endpoint fluorescence microscopy of Exclusive Receiver cells grown in transient gradients of signals (C12 diffusing from the left, C6 diffusing from the right) at the spatial average concentrations indicated and in the context of 10  $\mu$ M IPTG throughout.

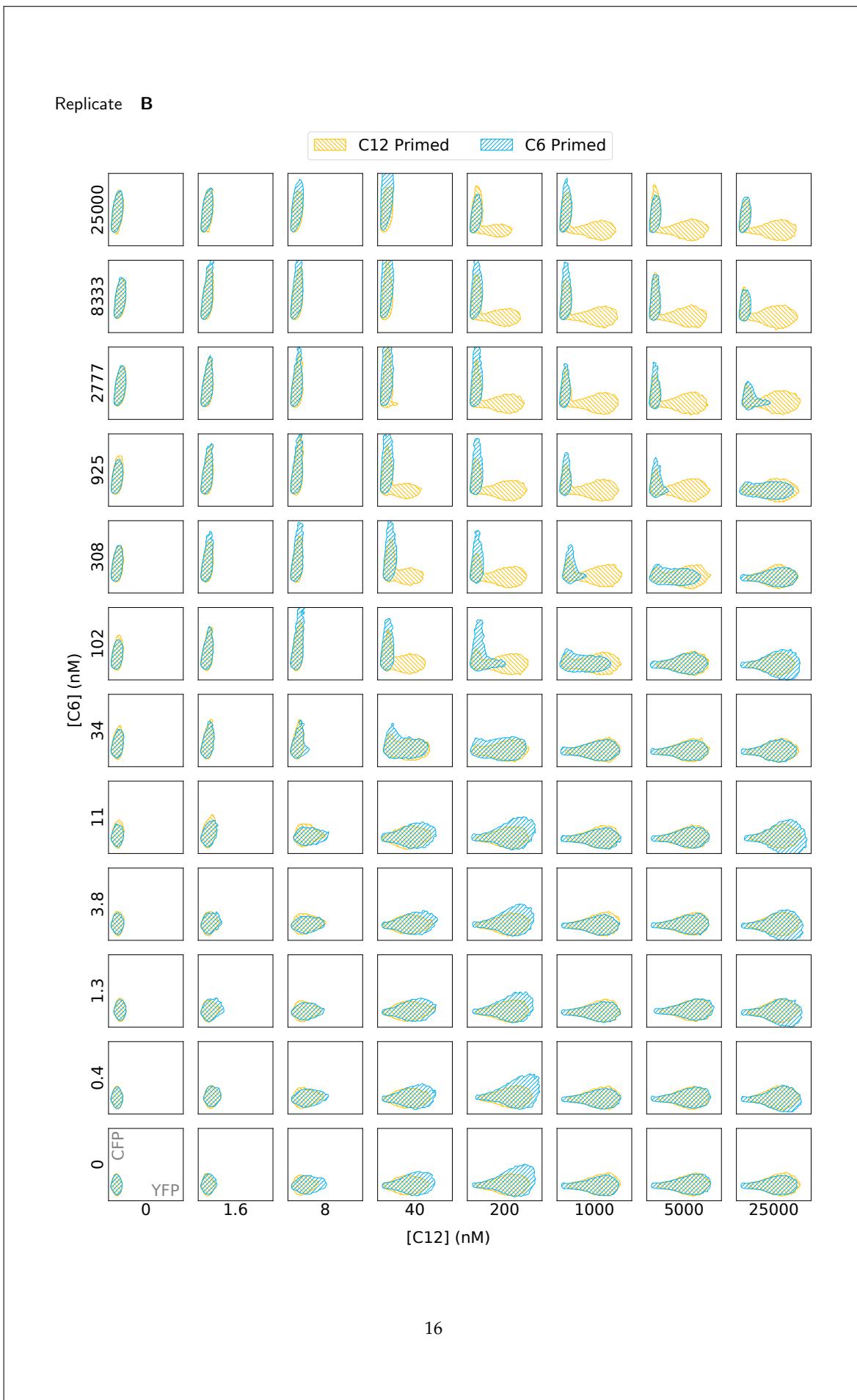


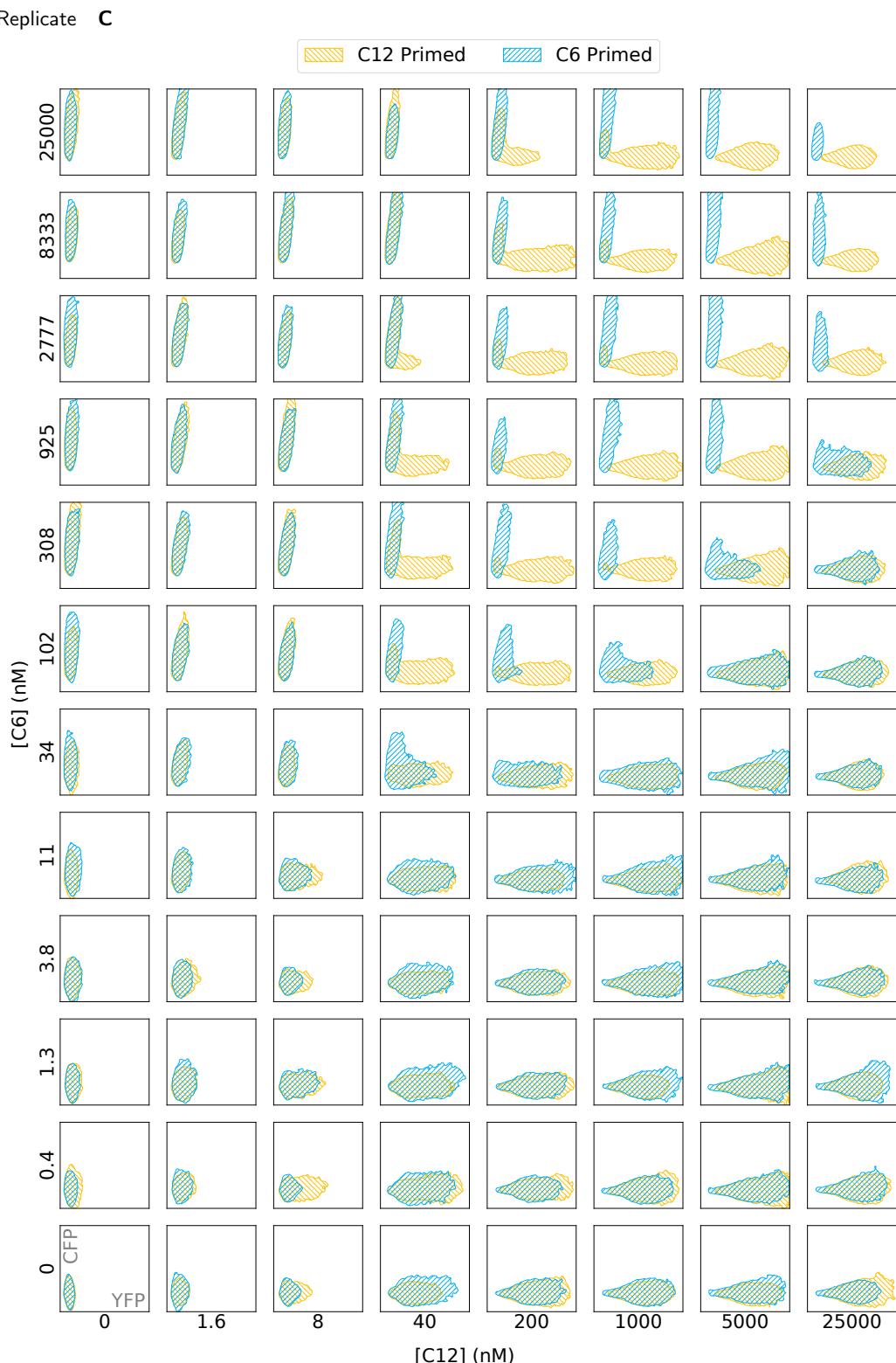
**Supplementary Figure 10: Swapping primary and secondary morphogens also produces patterning.** **a**, A circuit diagram of exclusive reporter cells co-transformed with the P81-LuxI relay device that responds to C12 by producing C6. Cells that experience high levels of C12 (central cells) will express YFP, TetR, and LuxI, causing them to produce C6 but be unable to sense it. Neighbouring cells (outer cells) that do not experience C12 will sense C6 and express CFP and LacI. **b**, Isogenic cells transformed with the circuit shown in (a) grown for 24 hours in the presence of a gradient of C12 diffusing from the centre express CFP and YFP in mutually exclusive domains of gene expression. **c**, A simulation in C6-C12 space over time ( $t_1$ - $t_2$ ) labelling points in physical space by their CFP and YFP expression (cyan and yellow points), and showing the production of C6 as vectors (red arrows) that move the spatial average (black point) toward increasing C6. The bistable region is outlined in red.











**Supplementary Figure 13: Hysteresis flow cytometry experiments.** Each replicate (A-C) is the overlay of two independent experiments with cells initialised in either 500 nM 3O-C6-HSL or 500 nM 3O-C12-HSL and transferred into varying concentrations of morphogens as indicated on the major axes. Regions of concentrations where the final population state depends on its initial state are visible along the diagonal. CFP and YFP fluorescence on the minor axes are normalised by RFP and centred such that auto-fluorescence of the 0 nM dilution is fixed in the bottom left. Source data are provided as a Source Data file.

## 2 Supplementary Methods

**Supplementary Table 1:** Primers used for Gibson assembly of the exclusive receiver circuit

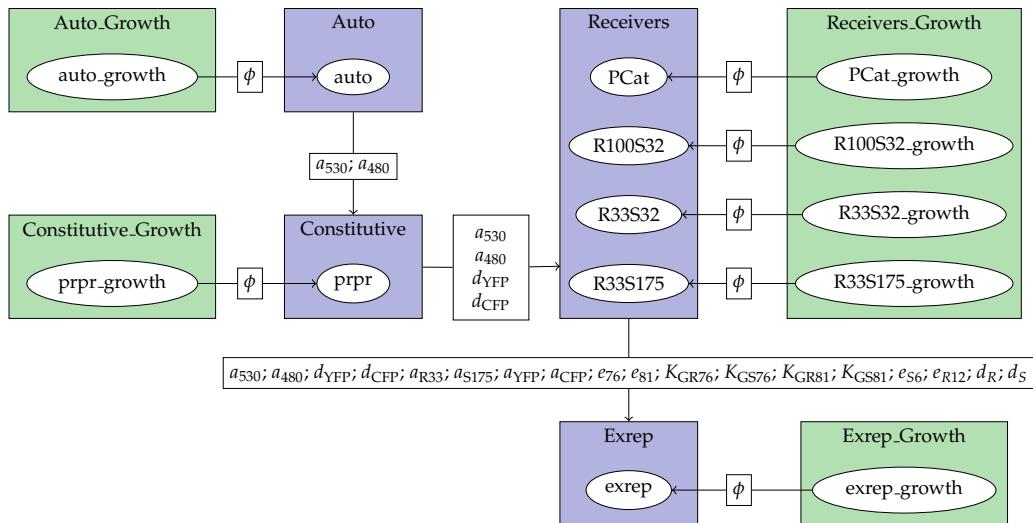
Primer name	Sequence
PGMSR014 LacIND F	TTTATTTGATGCCTGGCTTATTACTGCCCGCTTCCAGTCGG
PGMSR015 LacIND R	GCGGGCAGTAATAAAGCCAGGCATCAAATAAAACGAAAGG
PGMSR038 LacI300 F	TTTAGGACTGGACGGCGAAGGCCTGATGGAGTTCTAGTAT-
	TATTACTGTACAGCTCGTCCATGCC
PGMSR039 LacI300 R	AGAACTCCCATCAGGCCCTCGCCGTCCAGTCCTAAAATGGT-
	GAATGTGAAACCAGTAACGTTAT
PG081 Kan F	GGAATCGAACATGCAACCGGGC
PG082 Kan R	TGATGCGCTGGCAGTGTTC
PG342 Tet33 F	TCACACAGGACTACTAGATGTCCAGATTAGATAAAAG-
	TAAAGTGATTAACAGCGC
PG343 Tet33 R	ATCTAACATGGACATCTAGTAGTCCTGTGTGATTATTACTG-
	TACAGCTCGTCCATGCCG
PG373 TetAAV F	CGAAAAACTACGCTGCTGCTGTTAATAACCAGGCAT-
	CAAATAAAACGAAAGGC
PG374 TetAAV R	TGGTTATTAAACAGCAGCAGCGTAGTTTCGTCGTTGCTGCG-
	GACCCAC
JS3F Ori	GAGTGTATACTGGCTACTATGTTGGCACTG
JS3R Ori	CAGTGCCAACATAGTAAGCCAGTACACTC

## 2.1 Differential Equation Models and Parameter Inference

In this section, we derive ordinary differential equation (ODE) models for the reaction kinetics underlying the Exclusive Receiver circuit. These derivations broadly follow the derivations of the Receiver circuit in [3] and [4]. Importantly, we introduce differences in that original derivation that lead to changes in the location of bifurcations in (C12,C6) space, when those derivations are extended to incorporate dynamics of the repressor proteins LacI and TetR, and their chemical inhibitors IPTG and ATC.

### Dynamic characterization with inference graphs

In order to infer the parameters of the Exclusive Receiver circuit, we adopt the strategy described in [4], evaluating parameters of sub-circuits first, and propagating their inferred values to larger circuits that embed those same parameters. This results in an inference graph, where we infer parameters over a sequence of models and corresponding datasets.



**Supplementary Figure 14: Inference graph for characterizing the Exclusive Receiver circuit.** Blue rectangular nodes are inference problems for collections of synthetic gene circuit models, compared with CFP and YFP measurements, while green rectangular nodes are inference problems for the growth models of the circuits in the downstream blue nodes, compared with OD<sub>600</sub> measurements. Internal to the coloured nodes are white elliptical nodes, which correspond to individual synthetic gene circuits and one or more associated dataset(s). White rectangular nodes are the sets of inferred parameters that are propagated between nodes. To simplify the notation,  $\phi$  has been used to denote the set of growth model parameters, which are culture-specific (local) values for  $r$ ,  $K$  and  $t_{lag}$ , and are propagated as maximum likelihood estimates. All other parameters are global (non-culture-specific) values and propagated as marginal posterior estimates.

The simplest possible cell line to characterize is one in which there is no synthetic gene circuit at all. Applying dynamic characterization in this context enables us to quantify autofluorescence, and so we name this circuit *auto*. Therefore, we measured cells under a range of conditions to explore how gene expression capacity influenced time-series measurements at fluorescence wavelengths corresponding to CFP and YFP. Subsequently, we characterize a circuit (*prpr*) in which CFP and YFP are driven by constitutive promoters (PR), enabling us to characterize the rates of degradation of the fluorescent proteins. Next, we use four variants of simple HSL receiver (PCat, R100S32, R33S32 and R33S175) to characterize the genetic parts associated with LuxR and LasR receiver proteins and their interactions with HSL molecules 3OC6HSL (C6) and 3OC12HSL (C12). Finally, having obtained parameter estimates for parts associated with CFP, YFP, LuxR and LasR, we characterize the Exclusive Receiver circuit (*exrep*) itself, establishing quantitative estimates for the parts associated with TetR and LacI repressor proteins.

In the following, we introduce the models for each of the circuits just mentioned, define their parameters and present results of the inference.

### Autofluorescence model

The model we used for autofluorescence assumes that the rate of autofluorescence is constant, and that the fluorescent material dilutes with cell growth. As such, the equations for intracellular autofluorescence corresponding to CFP and YFP are

$$\frac{d\rho}{dt} = \gamma(\rho) \cdot \rho \quad (1a)$$

$$\frac{dc_{480}}{dt} = a_{480} - \gamma(\rho) \cdot c_{480} \quad (1b)$$

$$\frac{dc_{530}}{dt} = a_{530} - \gamma(\rho) \cdot c_{530} \quad (1c)$$

where  $\gamma(\rho) = r(1 - \frac{\rho}{K})$  is the specific growth rate of the cell culture with density  $\rho$ .

To compare with experimental measurements, we consider the bulk fluorescence given by

$$B_{480} = \rho \cdot c_{480} + b_{480} \quad (2a)$$

$$B_{530} = \rho \cdot c_{530} + b_{530} \quad (2b)$$

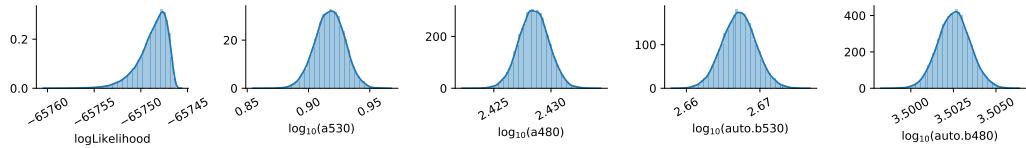
where  $c_{480}$  and  $c_{530}$  are modelled as in (1). Here, the quantities  $b_{480}$  and  $b_{530}$  represent background fluorescence at 480 nm and 530 nm, corresponding to CFP and YFP respectively.

**Inference.** We use the data in [4] to infer the parameters of the auto circuit. Cells were treated with EtOH to perturb cell growth, enabling us to determine how autofluorescence changes with different cellular growth rates. The priors used are detailed in the following table.

**Supplementary Table 2:** Priors for the auto circuit characterization. In the unit column, Fl denotes fluorescence units. The scaling column refers to the proposal distribution used to generate new parameters during MCMC.

Parameter	Description	Unit	Distribution	Scaling
$a_{480}$	Autofluorescence (CFP)	Fl.cell <sup>-1</sup> .h <sup>-1</sup>	$U(10^{-3}, 10^3)$	Log
$a_{530}$	Autofluorescence (YFP)	Fl.cell <sup>-1</sup> .h <sup>-1</sup>	$U(10^{-3}, 10^3)$	Log
$b_{480}$	Background fluor. (CFP)	Fl	$U(0, 10^4)$	Real
$b_{530}$	Background fluor. (YFP)	Fl	$U(0, 5 \times 10^3)$	Real

The marginal posterior estimates are shown in Figure 15. Simulation of the maximum likelihood estimate is shown in Figure 16.



**Supplementary Figure 15: Marginal parameter posterior estimates of the auto model parameters.** The marginal distributions are computed from 20 independent MCMC chains.



**Supplementary Figure 16: Comparison of auto model with fluorescence measurements.** Simulations are for  $B_{480}$  (cyan lines) and  $B_{530}$  (yellow lines), evaluated with the maximum likelihood parameter set. Measurements of bulk culture fluorescence are shown for the emission wavelengths corresponding to CFP (cyan circles) and YFP (yellow circles). EtOH treatment concentrations are indicated atop each panel.

### Constitutive (prpr) model

The prpr circuit described above uses the constitutive PR promoter to drive CFP and YFP expression, in two separate operons. Following the derivation in [4], we arrive at a system of equations that describe the time-evolution of the intracellular concentrations of CFP and YFP as

$$\frac{dc}{dt} = \gamma(\rho).c \quad (3a)$$

$$\frac{dc_{\text{CFP}}}{dt} = a_{\text{CFP}} - (d_{\text{CFP}} + \gamma(\rho))c_{\text{CFP}} \quad (3b)$$

$$\frac{dc_{\text{YFP}}}{dt} = a_{\text{YFP}} - (d_{\text{YFP}} + \gamma(\rho))c_{\text{YFP}} \quad (3c)$$

where  $a_{\text{CFP}}$  and  $a_{\text{YFP}}$  are aggregated parameters that incorporate the rate of transcription and translation of CFP and YFP respectively. To compare with bulk culture fluorescence data, we use the observer model

$$B_{480} = \rho.(c_{\text{CFP}} + c_{480}) + b_{480} \quad (4a)$$

$$B_{530} = \rho.(c_{\text{YFP}} + c_{530}) + b_{530} \quad (4b)$$

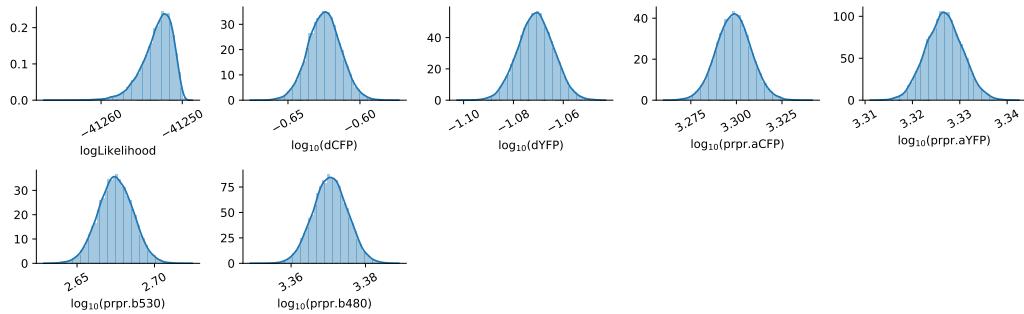
where the dynamics of  $c_{480}$  and  $c_{530}$  are governed by equations (1) above.

**Inference.** We use the data in [4] to infer the parameters of the prpr circuit. Cells were treated with chloramphenicol to perturb cell growth, enabling us to establish how constitutively expressed proteins are altered with different cellular growth rates. While the model above does not explicitly describe any explicit functional response to chloramphenicol, our general strategy of allowing the cell growth parameters to vary across different measurements enables the effect of chloramphenicol on growth rates to be implicitly captured. The quantification of autofluorescence was reused from the auto circuit (upstream in the inference graph), but the background fluorescence parameters were re-inferred. The priors used are detailed in Table 3. The marginal posterior estimates are shown in Figure 17.

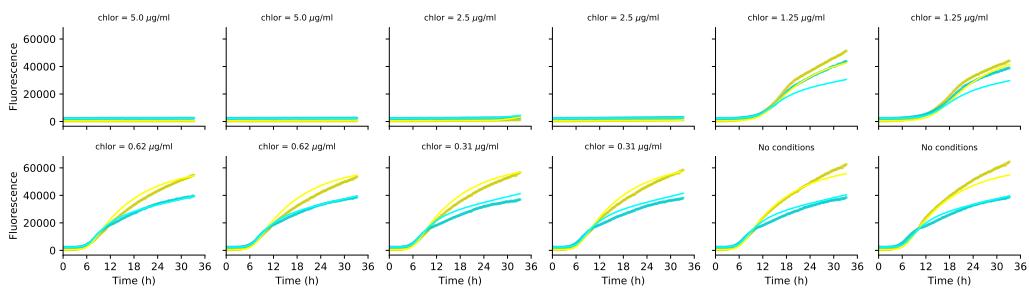
**Supplementary Table 3:** Priors for the prpr circuit characterization. In the unit column, Fl denotes fluorescence units. The scaling column refers to the proposal distribution used to generate new parameters during MCMC.

Parameter	Description	Unit	Distribution	Scaling
$d_{\text{CFP}}$	CFP degradation	$\text{h}^{-1}$	$U(10^{-3}, 10^0)$	Log
$d_{\text{YFP}}$	YFP degradation	$\text{h}^{-1}$	$U(10^{-3}, 10^0)$	Log
$a_{\text{CFP}}$	CFP synthesis	$\text{Fl.cell}^{-1}.\text{h}^{-1}$	$U(10^0, 10^5)$	Log
$a_{\text{YFP}}$	YFP synthesis	$\text{Fl.cell}^{-1}.\text{h}^{-1}$	$U(10^0, 10^5)$	Log
$b_{480}$	Background fluor. (CFP)	Fl	$U(0, 10^4)$	Real
$b_{530}$	Background fluor. (YFP)	Fl	$U(0, 5 \times 10^3)$	Real

Simulation of the maximum likelihood estimate is shown in Figure 18. The simulated CFP and YFP largely agree with the measured fluorescence at the culture level. As the effect of chloramphenicol is not explicitly modelled here, this comparison indicates that the majority of the effect of chloramphenicol can be described via its effect on cell growth. Any additional direct effect on CFP and YFP expression directly, is relatively minor.



**Supplementary Figure 17: Marginal parameter posterior estimates of the prpr model parameters.** The marginal distributions are computed from 20 independent MCMC chains.



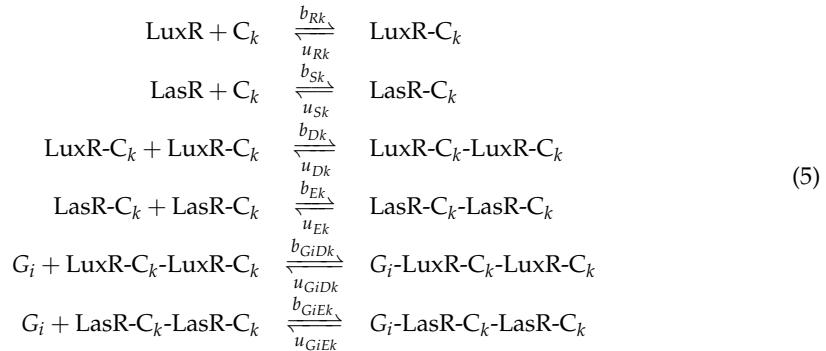
**Supplementary Figure 18: Comparison of prpr model with fluorescence measurements.** Simulations are of bulk CFP (cyan lines) and YFP (yellow lines) fluorescence, evaluated with the maximum likelihood parameter set. Measurements of bulk culture fluorescence are shown in for CFP (cyan circles) and YFP (yellow circles). Chloramphenicol treatment concentrations are indicated atop each panel.

### Receiver model

We consider the dynamic characterization of the HSL Receiver circuit introduced in [3] and modelled dynamically in [4, 5]. In this circuit, which we refer to in the main text as the Receiver, two variations of the wild-type PLux promoter, PLux76 and PLas81, were engineered to bind preferentially to activated LuxR and LasR complexes respectively. As LuxR favours binding of C6 and LasR favours binding of C12, optimized expression of LuxR and LasR can lead to near-orthogonal intracellular detection of C6 and C12. The Receiver device was originally measured with PLux76 upstream of the coding sequence for CFP, and PLas81 upstream of the coding sequence for YFP.

**Version 1 - Uniform degradation.** The first version of the model we introduce is derived in [4]. It is based on the assumption that all degradation processes are of the same order, e.g. LuxR monomers are degraded at a similar rate as LuxR Dimers bound to HSLs. Subsequently, we will introduce an alternative derivation where we assume that complexes are protected from degradation, i.e. that degradation mainly occurs on the monomer level. We start by repeating some of the derivation from [4].

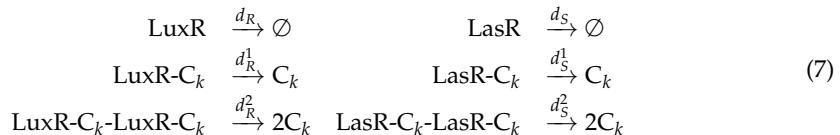
We denote by  $C_k$  the HSL molecule with length  $k$  carbon chain, and by  $G_i$  the PLux76 and PLas81 promoters. Then similar to the derivation in [3], we can specify all of the reactions between the HSLs, LuxR and LasR, and eventual binding of transcriptional regulators to PLux76/PLas81.



Constitutive expression of LuxR and LasR is described by

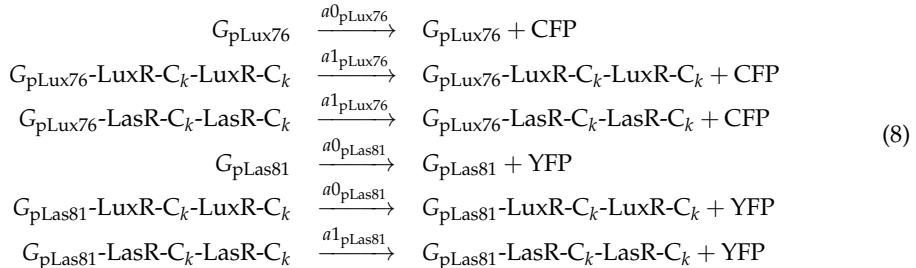


Degradation of LuxR and LasR is described by



where  $d_R^1$  and  $d_R^2$  are distinguishable from  $d_R$  to describe the effect of HSL molecules protecting receiver proteins from degradation.

Inducible expression of CFP and YFP by  $P_{OLux}$  and  $P_{OLas}$  respectively is described by



To produce a simplified ODE model amenable to parameter inference, we start with the equations describing LuxR and LasR protein, their complexes involving C<sub>6</sub> and C<sub>12</sub>, and the bound/unbound promoters. Crucially, in this first derivation, we make a *rapid equilibrium* assumption for the binding reactions (5), and obtain the following relationships

$$[G_i\text{-LuxR-C}_k\text{-LuxR-C}_k]^* = K_{GDk}[G_i][\text{LuxR-C}_k\text{-LuxR-C}_k] \quad (9a)$$

$$[\text{LuxR-C}_k\text{-LuxR-C}_k]^* = K_{Dk}[\text{LuxR-C}_k]^2 \quad (9b)$$

$$[\text{LuxR-C}_k]^* = K_{Rk}[c_R][C_k] \quad (9c)$$

where  $K_{Rk} = \frac{b_{Rk}}{\gamma + u_{Rk}}$ ,  $K_{Dk} = \frac{b_{Dk}}{u_{Dk}}$  and  $K_{GiDk} = \frac{b_{GiDk}}{u_{GiDk}}$ . Therefore (also symmetry of LuxR and LasR),

$$[G_i\text{-LuxR-C}_k\text{-LuxR-C}_k]^* = K_{GiDk}K_{Dk}(K_{Rk}[C_k][c_R])^2 \quad (10a)$$

$$[G_i\text{-LasR-C}_k\text{-LasR-C}_k]^* = K_{GiEk}K_{Ek}(K_{Sk}[C_k][c_S])^2 \quad (10b)$$

where the new K's are defined as above.

To reduce the system to fewer variables, we consider the evolution of total LuxR, and seek to co-ordinate this with the rapid equilibrium relationships above. By denoting the total concentration of LuxR as c<sub>R</sub>, we can write down its time-evolution as

$$\frac{d[R]_T}{dt} = \frac{d[c_R]}{dt} + \sum_k \left( \frac{d[\text{LuxR-C}_k]}{dt} + 2 \frac{d[\text{LuxR-C}_k\text{-LuxR-C}_k]}{dt} + 2 \sum_i \frac{d[G_i\text{-LuxR-C}_k\text{-LuxR-C}_k]}{dt} \right) \quad (11a)$$

$$= a_R - \gamma[c_R] - d_R[c_R] \dots \\ - \sum_k \left( (\gamma + d_R^1)[\text{LuxR-C}_k] + (\gamma + d_R^2)[\text{LuxR-C}_k\text{-LuxR-C}_k] + \gamma \sum_i [G_i\text{-LuxR-C}_k\text{-LuxR-C}_k] \right) \quad (11b)$$

If there are differences between d<sub>R</sub>, d<sub>R</sub><sup>1</sup> and d<sub>R</sub><sup>2</sup>, then further reduction is complicated. However, by assuming that HSL is not protective of receiver protein (d<sub>R</sub><sup>1</sup> = d<sub>R</sub><sup>2</sup> = d<sub>R</sub>), we obtain the simplification

$$\frac{dc_R}{dt} = a_R - (\gamma + d_R)c_R \quad (12)$$

Now using a conservation relationship for LuxR, we can obtain

$$c_R = [\text{LuxR}] + \sum_k \left( [\text{LuxR-C}_k] + 2[\text{LuxR-C}_k\text{-LuxR-C}_k] + 2 \sum_i [G_i\text{-LuxR-C}_k\text{-LuxR-C}_k] \right) \\ = [\text{LuxR}] + \sum_k \left( K_{Rk}[\text{LuxR}][C_k] + 2K_{Dk}K_{Rk}^2[\text{LuxR}]^2[C_k]^2 + \sum_i 2K_{GiDk}[G_i]K_{Dk}K_{Rk}^2[\text{LuxR}]^2[C_k]^2 \right)$$

When C<sub>k</sub> is low, total LuxR is closely approximated by free LuxR, c<sub>R</sub> ≈ [LuxR]. But when C<sub>k</sub> is high, c<sub>R</sub> should be partitioned between the [LuxR-C<sub>k</sub>-LuxR-C<sub>k</sub>] and [G<sub>i</sub>-LuxR-C<sub>k</sub>-LuxR-C<sub>k</sub>] species. Therefore, to simplify the analysis, we propose modelling this by using the assumption

$$c_R \approx [\text{LuxR}] + \sum_k [\text{LuxR-C}_k] = [\text{LuxR}] \left( 1 + \sum_k K_{Rk}[C_k] \right) \quad (13)$$

which still captures the saturation of LuxR by  $C_k$ , using the approximations

$$[\text{LuxR}] \approx c_R \cdot \frac{1}{1 + \sum_k K_{Rk}[C_k]} \quad (14\text{a})$$

$$[\text{LuxR-C}_k] \approx c_R \cdot \frac{K_{Rk}[C_k]}{1 + \sum_k K_{Rk}[C_k]} \quad (14\text{b})$$

$$[\text{LuxR-C}_k\text{-LuxR-C}_k] \approx K_{Dk}c_R^2 \left( \frac{K_{Rk}[C_k]}{1 + \sum_k K_{Rk}[C_k]} \right)^2 \quad (14\text{c})$$

$$[G_i\text{-LuxR-C}_k\text{-LuxR-C}_k] \approx K_{GR}^{(i)}[G_i]c_R^2 \left( \frac{K_{Rk}[C_k]}{1 + \sum_k K_{Rk}[C_k]} \right)^2 \quad (14\text{d})$$

where  $K_{GR}^{(i)} = K_{GiDk}K_{Dk}$  is assumed to be independent of which signal is bound ( $k$ ), equivalent to the derivation in [3]. By symmetry, we immediately obtain equivalent expressions for interactions between LasR, HSL and PLux promoters. We denote the total concentration of LasR as  $c_S$ .

In addition to the saturation of LuxR and LasR, our reduced model also allows for saturation of  $G_i$ . By taking advantage of the conservation law

$$\begin{aligned} N_i &= [G_i] + [G_i\text{-LuxR-C}_6\text{-LuxR-C}_6] + [G_i\text{-LuxR-C}_{12}\text{-LuxR-C}_{12}] + \dots \\ &\quad [G_i\text{-LasR-C}_6\text{-LasR-C}_6] + [G_i\text{-LasR-C}_{12}\text{-LasR-C}_{12}], \end{aligned}$$

we can derive the rate of production of mRNA as a function of  $c_R$ ,  $c_S$  [ $C_6$ ] and [ $C_{12}$ ]. For notational convenience we write  $c_6 := [C_6]$  and  $c_{12} := [C_{12}]$ . Then,

$$P_i(c_6, c_{12}, c_R, c_S) = \frac{\epsilon^{(i)} + K_{GR}^{(i)}B_R + K_{GS}^{(i)}B_S}{1 + K_{GR}^{(i)}B_R + K_{GS}^{(i)}B_S} \quad (15)$$

where the fractions of bound LuxR and LasR are defined by

$$B_R := c_R^2 \left( \frac{K_{Rk}c_k}{1 + \sum_k K_{Rk}c_k} \right)^{n_R}, \quad B_S := c_S^2 \left( \frac{K_{Sk}c_k}{1 + \sum_k K_{Sk}c_k} \right)^{n_S} \quad (16)$$

Here, we have introduce alternative exponents  $n_R$  and  $n_S$ , analogous to the usage of  $n$  in [3]. Accordingly, we obtain the following system of equations

$$\frac{d\rho}{dt} = \gamma(\rho) \cdot \rho \quad (17\text{a})$$

$$\frac{dc_R}{dt} = a_R - (d_R + \gamma(\rho)) \cdot c_R \quad (17\text{b})$$

$$\frac{dc_S}{dt} = a_S - (d_S + \gamma(\rho)) \cdot c_S \quad (17\text{c})$$

$$\frac{dc_{\text{CFP}}}{dt} = a_{\text{CFP}} \cdot P_{76}(c_6, c_{12}, c_R, c_S) - (d_{\text{CFP}} + \gamma(\rho)) \cdot c_{\text{CFP}} \quad (17\text{d})$$

$$\frac{dc_{\text{YFP}}}{dt} = a_{\text{YFP}} \cdot P_{81}(c_6, c_{12}, c_R, c_S) - (d_{\text{YFP}} + \gamma(\rho)) \cdot c_{\text{YFP}} \quad (17\text{e})$$

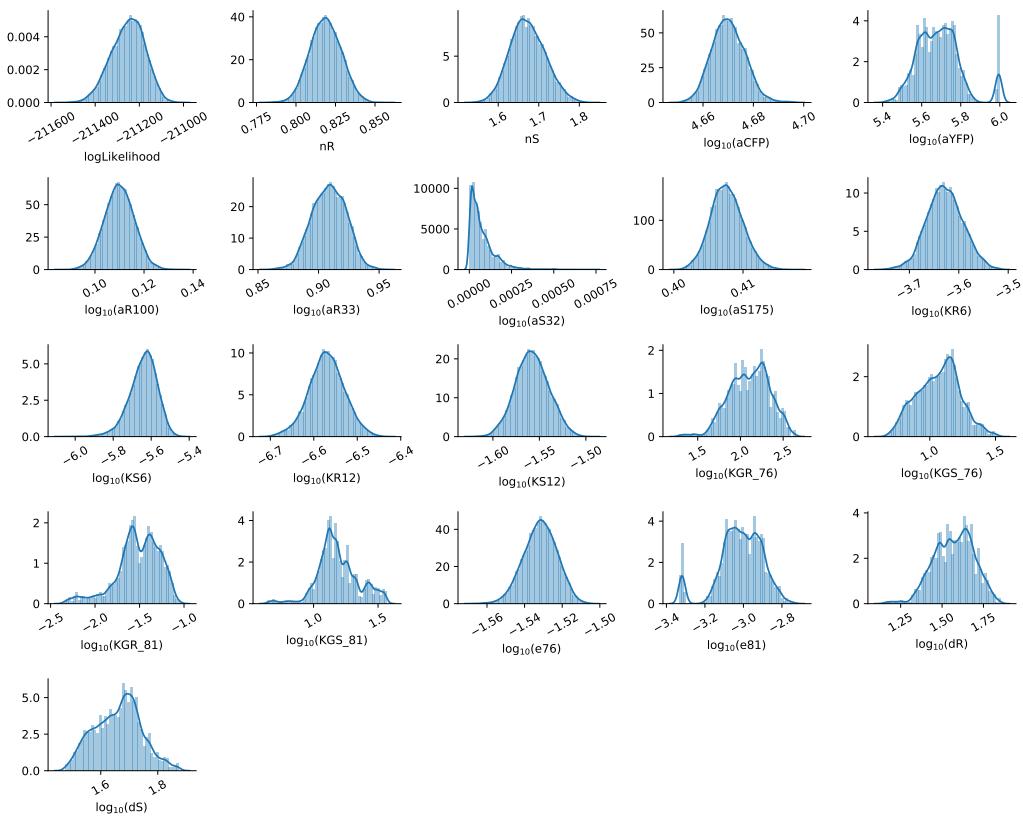
**Inference for version 1 (uniform degradation).** To characterize the LuxR and LasR signalling components, we used measurements of the response of four Receiver circuits from [3] to treatment with C6 and C12 over 3-fold dilutions. The maximum LuxR and LasR production rates were normalized to the values corresponding to the Pcat promoters, as done previously [3], thus setting the scale for unobserved concentrations of LuxR and LasR.

We used (uninformative) uniform priors on the previously uncharacterized parameters, and (informative) truncated Gaussian priors on  $f_{480}$ ,  $f_{530}$ ,  $d_{\text{CFP}}$  and  $d_{\text{YFP}}$  with mean and standard deviation taken from the marginal posteriors of the prpr circuit characterization. We did not propagate the marginal posteriors of  $a_{\text{CFP}}$  and  $a_{\text{YFP}}$  as the promoter involved differed between the prpr circuit and Receiver circuits. The priors used are detailed in the following table.

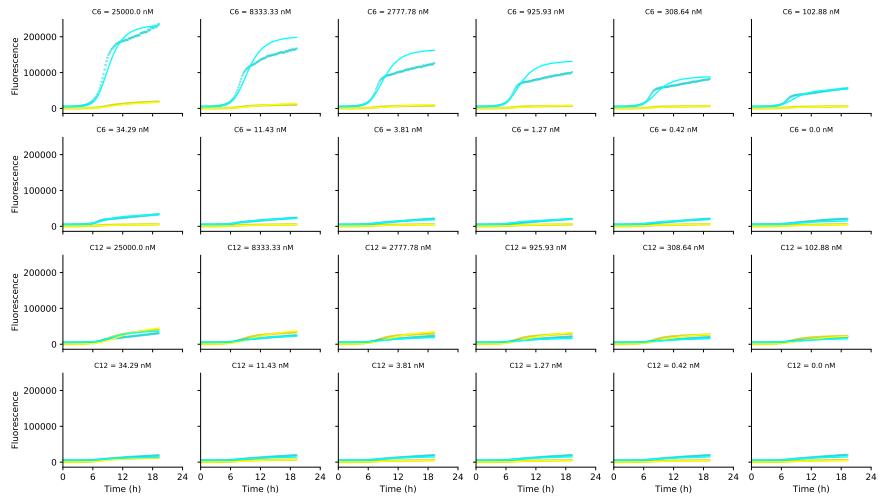
The marginal posterior estimates are shown in Figure 19. Simulation of the maximum likelihood estimate is shown in Figure 20.

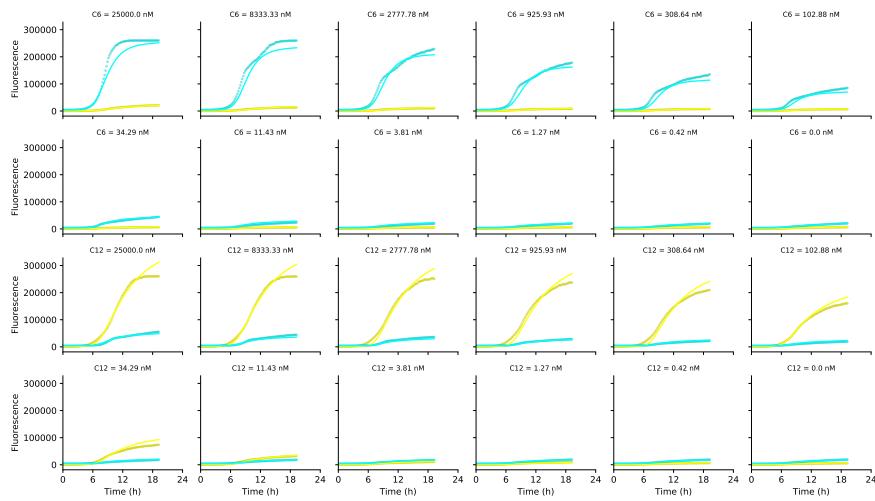
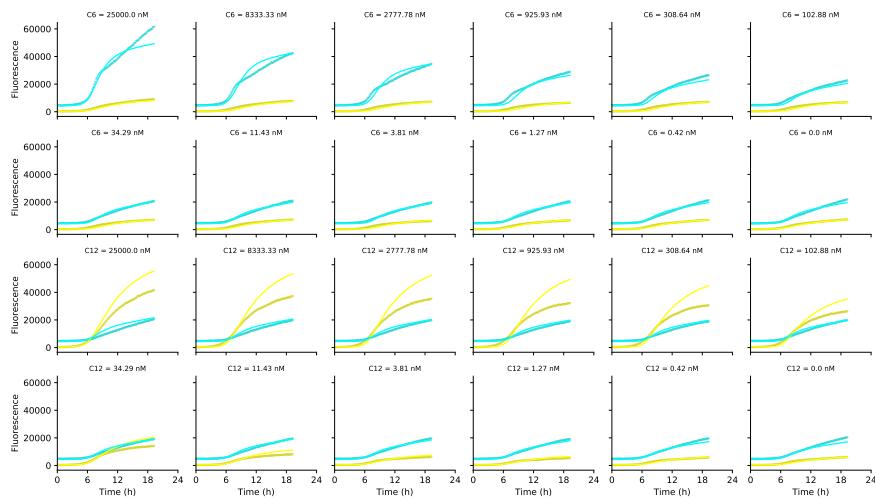
**Supplementary Table 4:** Priors for version 1 of the Receiver circuit characterization. In the unit column,  $M_R$  and  $M_S$  denote the normalised mass units for LuxR and LasR, and Fl denotes fluorescence units. The scaling column refers to the proposal distribution used to generate new parameters during MCMC.

Parameter	Description	Unit	Distribution	Scaling
$a_{R100}$	LuxR synthesis	$M_R \cdot h^{-1}$	$U(1, 10^2)$	Log
$a_{R33}$	LuxR synthesis	$M_R \cdot h^{-1}$	$U(1, 10^2)$	Log
$a_{S32}$	LasR synthesis	$M_S \cdot h^{-1}$	$U(1, 10^2)$	Log
$a_{S175}$	LasR synthesis	$M_S \cdot h^{-1}$	$U(1, 10^2)$	Log
$d_R$	LuxR degradation	$h^{-1}$	$U(10^{-2}, 10^2)$	Log
$d_S$	LasR degradation	$h^{-1}$	$U(10^{-2}, 10^2)$	Log
$K_{R6}$	Dissociation (LuxR-C6)	$nM^{-1}$	$U(10^{-8}, 1)$	Log
$K_{S6}$	Dissociation (LasR-C6)	$nM^{-1}$	$U(10^{-8}, 1)$	Log
$K_{R12}$	Dissociation (LuxR-C12)	$nM^{-1}$	$U(10^{-8}, 1)$	Log
$K_{S12}$	Dissociation (LasR-C12)	$nM^{-1}$	$U(10^{-8}, 1)$	Log
$K_{GR}^{(76)}$	Dissociation (P76-LuxR)	$M_R^{-2}$	$U(10^{-4}, 10^3)$	Log
$K_{GS}^{(76)}$	Dissociation (P76-LasR)	$M_S^{-2}$	$U(10^{-8}, 10^3)$	Log
$K_{GR}^{(81)}$	Dissociation (P81-LuxR)	$M_R^{-2}$	$U(10^{-8}, 10^3)$	Log
$K_{GS}^{(81)}$	Dissociation (P81-LasR)	$M_S^{-2}$	$U(10^{-4}, 10^3)$	Log
$n_R$	Hill constant (LuxR-HSL)	-	$U(0.5, 2)$	Real
$n_S$	Hill constant (LasR-HSL)	-	$U(0.5, 2)$	Real
$e^{(76)}$	Leak production (P76)	-	$U(10^{-4}, 1)$	Log
$e^{(81)}$	Leak production (P81)	-	$U(10^{-4}, 1)$	Log
$a_{CFP}$	CFP synthesis	$Fl \cdot cell^{-1} \cdot h^{-1}$	$U(10^2, 10^6)$	Log
$a_{YFP}$	YFP synthesis	$Fl \cdot cell^{-1} \cdot h^{-1}$	$U(10^2, 10^6)$	Log
$b_{480}$	Background fluor. (CFP)	Fl	$U(0, 10^4)$	Real
$b_{530}$	Background fluor. (YFP)	Fl	$U(0, 5 \times 10^3)$	Real



**Supplementary Figure 19: Marginal parameter posterior estimates of the Receiver model (version 1) parameters.** The marginal distributions are computed from 20 independent MCMC chains.

**A Pcat circuit****B R100S32 circuit**

**C R33S32 circuit****D R33S175 circuit**

**Supplementary Figure 20: Comparison of Receiver models with fluorescence measurements.** Simulations are of bulk CFP (cyan lines) and YFP (yellow lines) fluorescence, evaluated with the maximum likelihood parameter set. Measurements of bulk culture fluorescence are shown in for CFP (cyan circles) and YFP (yellow circles). C6 and C12 treatment concentrations are indicated atop each panel.

**Version 2 - Protected degradation.** Here we provide an alternative derivation for the model reduction based on the assumption that HSL complexes and dimers are protected from degradation, i.e. that degradation predominantly occurs on the level of LuxR/LasR monomers. This is supported by in vitro analysis of purified LuxR suggesting that LuxR protein is unstable in the absence of 3OC6-HSL [6]. Furthermore, we assume that all dilution effects occur on a slow time scale as compared to the kinetic. With this derivation, we obtain the same functional structure of the promoter activities of PLux76 and PLas81 from equation (15), but with the definitions of the bound fraction of LuxR and LasR given instead by

$$B_R := c_R^2 (c_6^{n_R} + (e_{R12} c_{12})^{n_R}), \quad B_S := c_S^2 ((e_{S6} c_6)^{n_S} + c_{12}^{n_S}) \quad (18)$$

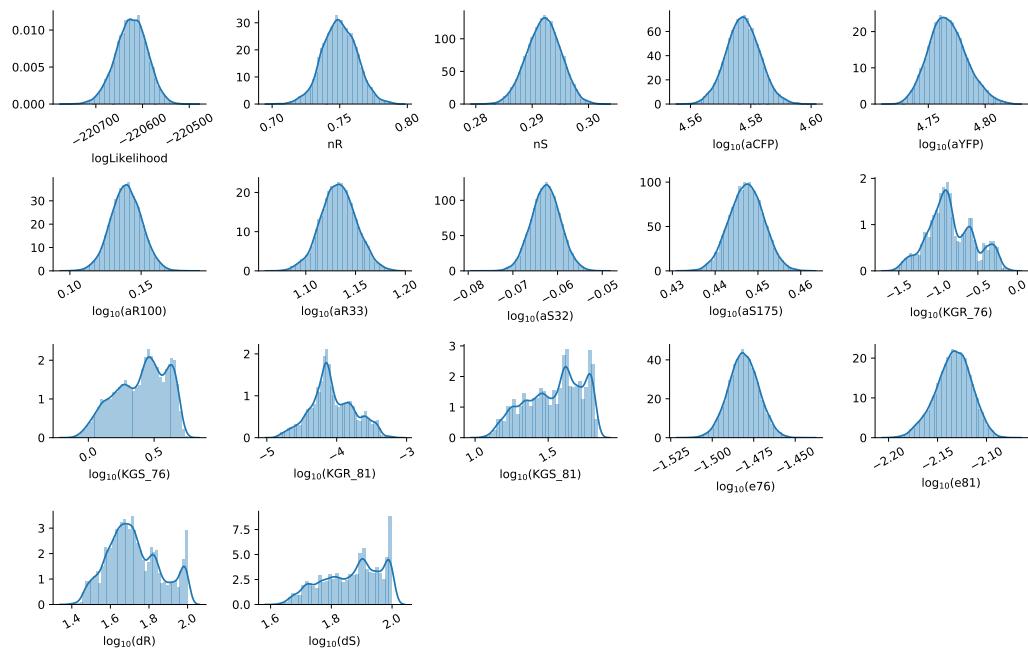
where  $e_{R12} = \frac{K_{R12}}{K_{R6}}$  and  $e_{S6} = \frac{K_{S6}}{K_{S12}}$  result from dividing by  $K_{R6}$  and  $K_{S12}$ . Consequently, the parameters  $K_{GR}^{(i)}$  and  $K_{GS}^{(i)}$  in equation (15) are rescaled by  $K_{R6}$  and  $K_{S12}$  respectively.

**Inference for version 2 (Protected degradation).** We carried out parameter inference for version 2 of the model directly equivalent to that done for version 1. The complete list of prior distributions for the parameters is as follows.

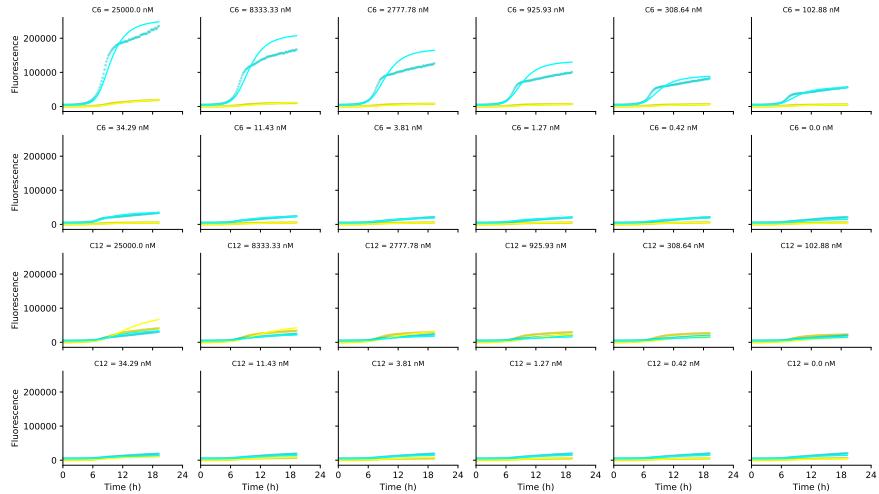
**Supplementary Table 5:** Priors for version 2 of the Receiver circuit characterization. In the unit column,  $M_R$  and  $M_S$  denote the normalised mass units for LuxR and LasR, and Fl denotes fluorescence units. The scaling column refers to the proposal distribution used to generate new parameters during MCMC.

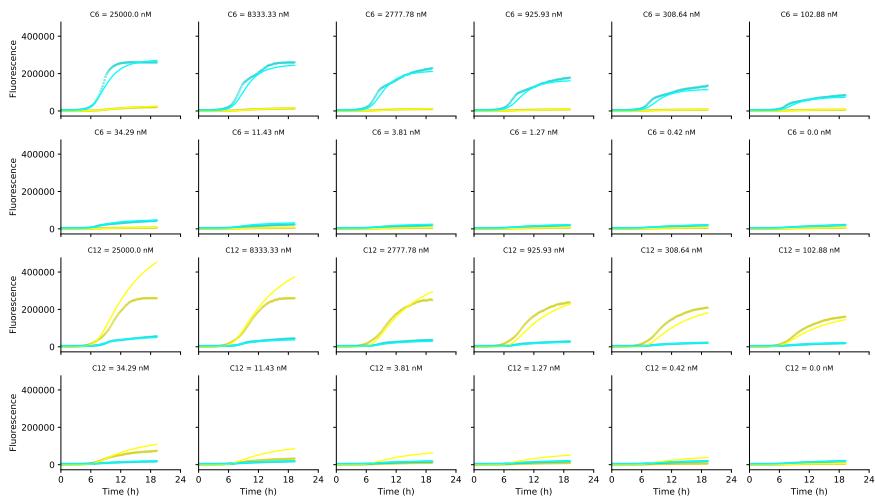
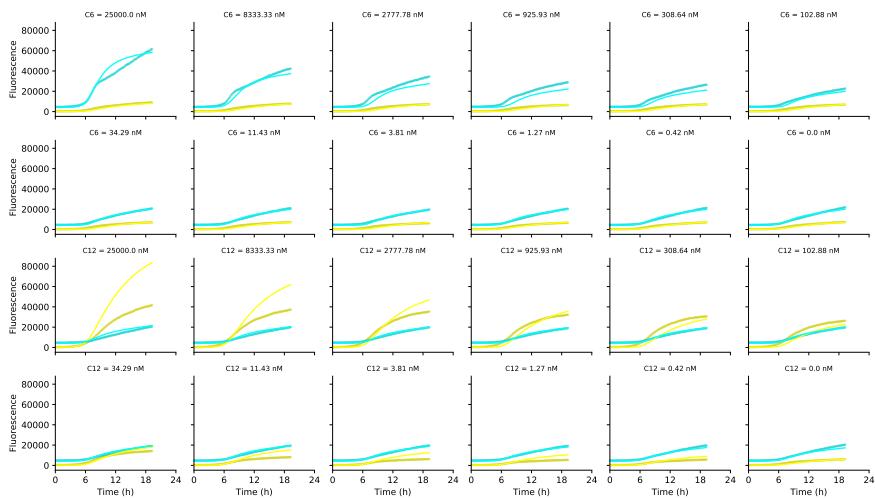
Parameter	Description	Unit	Distribution	Scaling
$a_{R100}$	LuxR synthesis	$M_R \cdot h^{-1}$	$U(1, 10^2)$	Log
$a_{R33}$	LuxR synthesis	$M_R \cdot h^{-1}$	$U(1, 10^2)$	Log
$a_{S32}$	LasR synthesis	$M_S \cdot h^{-1}$	$U(1, 10^2)$	Log
$a_{S175}$	LasR synthesis	$M_S \cdot h^{-1}$	$U(1, 10^2)$	Log
$d_R$	LuxR degradation	$h^{-1}$	$U(10^{-2}, 10^2)$	Log
$d_S$	LasR degradation	$h^{-1}$	$U(10^{-2}, 10^2)$	Log
$e_{R12}$	Chemical crosstalk (LuxR)	-	$U(10^{-8}, 1)$	Log
$e_{S6}$	Chemical crosstalk (LasR)	-	$U(10^{-8}, 1)$	Log
$K_{GR}^{(76)}$	Dissociation (P76-LuxR)	$M_R^{-(2+n_R)}$	$U(10^{-4}, 10^3)$	Log
$K_{GS}^{(76)}$	Dissociation (P76-LasR)	$M_S^{-(2+n_S)}$	$U(10^{-8}, 10^3)$	Log
$K_{GR}^{(81)}$	Dissociation (P81-LuxR)	$M_R^{-(2+n_R)}$	$U(10^{-8}, 10^3)$	Log
$K_{GS}^{(81)}$	Dissociation (P81-LasR)	$M_S^{-(2+n_S)}$	$U(10^{-4}, 10^3)$	Log
$n_R$	Hill constant (LuxR-HSL)	-	$U(0.2, 2)$	Real
$n_S$	Hill constant (LasR-HSL)	-	$U(0.2, 2)$	Real
$e^{(76)}$	Leak production (P76)	-	$U(10^{-4}, 1)$	Log
$e^{(81)}$	Leak production (P81)	-	$U(10^{-4}, 1)$	Log
$a_{CFP}$	CFP synthesis	$Fl \cdot cell^{-1} \cdot h^{-1}$	$U(10^2, 10^6)$	Log
$a_{YFP}$	YFP synthesis	$Fl \cdot cell^{-1} \cdot h^{-1}$	$U(10^2, 10^6)$	Log
$B_{480}$	Background fluorescence (CFP)	Fl	$U(0, 10^4)$	Real
$B_{530}$	Background fluorescence (YFP)	Fl	$U(0, 5 \times 10^3)$	Real

The marginal posterior estimates are shown in Figure 21. Simulation of the maximum likelihood estimate is shown in Figure 22.



**Supplementary Figure 21: Marginal parameter posterior estimates of the Receiver model (version 2) parameters.** The marginal distributions are computed from 20 independent MCMC chains.

**A Pcat circuit****B R100S32 circuit**

**C R33S32 circuit****D R33S175 circuit**

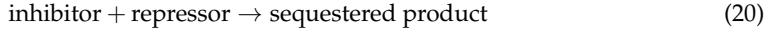
**Supplementary Figure 22: Comparison of Receiver models with fluorescence measurements.** Simulations are of bulk CFP (cyan lines) and YFP (yellow lines) fluorescence, evaluated with the maximum likelihood parameter set. Measurements of bulk culture fluorescence are shown in for CFP (cyan circles) and YFP (yellow circles). C6 and C12 treatment concentrations are indicated atop each panel.

### Exclusive Receiver model

To model the Exclusive Receiver, we consider the inhibition of PTet by TetR and PLac by LacI, and the mechanism of chemical inhibition by IPTG and ATC. For promoter regulation, we use the inhibition Hill function

$$H_I(x, n) := \frac{1}{1 + x^n} \quad (19)$$

Typically, these functions would include a parameter for the half-saturation concentration, but we omit that here because, without loss of generality, [LacI] and [TetR] can be arbitrarily scaled by those half-saturation concentrations. In such a rescaling, the half-saturation constants get embedded within the maximal production rates,  $a_L$  and  $a_T$ . For the chemical inhibitors, we assume a reaction of the form



Correspondingly, the action of IPTG and ATC is proportional to the product of its concentration and its target repressor protein concentration.

$$\frac{d\rho}{dt} = \gamma(\rho).\rho \quad (21a)$$

$$\frac{dc_{YFP}}{dt} = a_{YFP}.f_{81}(c_6, c_{12}, c_R, c_S) - (\gamma(\rho) + d_{YFP})c_{YFP} \quad (21b)$$

$$\frac{dc_{CFP}}{dt} = a_{CFP}.f_{76}(c_6, c_{12}, c_R, c_S) - (\gamma(\rho) + d_{CFP})c_{CFP} \quad (21c)$$

$$\frac{dc_{530}}{dt} = b_Y - \gamma(\rho).c_{530} \quad (21d)$$

$$\frac{dc_{480}}{dt} = b_C - \gamma(\rho).c_{480} \quad (21e)$$

$$\frac{dc_R}{dt} = a_R.H_I(c_T, n_T) - (\gamma(\rho) + d_R).c_R \quad (21f)$$

$$\frac{dc_S}{dt} = a_S.H_I(c_L, n_L) - (\gamma(\rho) + d_S).c_S \quad (21g)$$

$$\frac{dc_L}{dt} = a_L.P_{76}(c_6, c_{12}, c_R, c_S) - (\gamma(\rho) + d_L + i_I.c_I).c_L \quad (21h)$$

$$\frac{dc_T}{dt} = a_T.P_{81}(c_6, c_{12}, c_R, c_S) - (\gamma(\rho) + d_T + i_A.c_A).c_T \quad (21i)$$

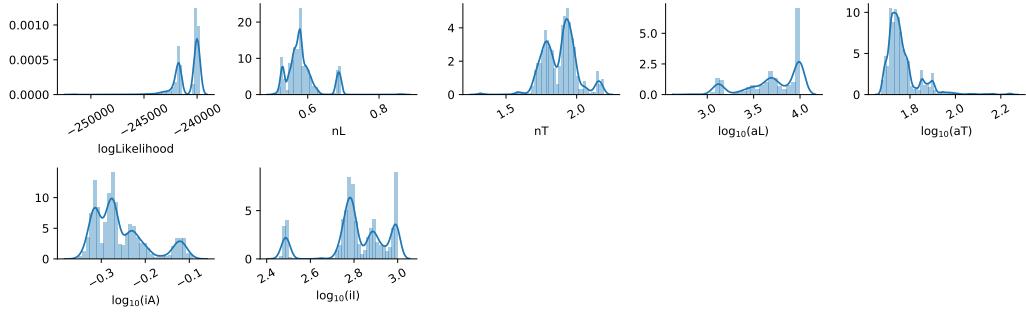
where  $P_{76}$  and  $P_{81}$  are defined in (15).

**Inference for version 1 (uniform degradation).** The inference procedure was less robust for the Exclusive Receiver, as compared with upstream circuits in the inference graph. In particular, we found it was not possible to identify a unique mode within the parameter space when all parameters were allowed to be flexible. Specifically, there was strong interdependency within the triplet  $\{a_L, d_L, i_I\}$  and the triplet  $\{a_T, d_T, i_A\}$ . Our interpretation is that we are unable to fully recover the time-scales of variations in  $c_L$  and  $c_T$ , as they are likely to not vary much during the experiments we used for characterization. It's likely that  $c_L$  and  $c_T$  quickly stabilise to equilibria when the cells are transferred to the media containing the treatments (specific concentrations of C6, C12, IPTG and ATC). In which case, only those equilibrium values will be identifiable, and not the production and degradation rates separately. Therefore, in the final version of the inference results presented here, we have fixed the degradation rates of LacI and TetR to  $1 \text{ h}^{-1}$ .

Even when running the inference with  $d_L$  and  $d_T$  fixed, we found that chain convergence was not perfect, and some chains got stuck in local optima. Therefore, in our marginal posterior estimates, we have only included chains that converged to relatively good likelihood scores Figure 23. The marginals clearly indicate some additional flexibility in the inferred parameter values, possibly resulting from the larger parameter space being navigated, which includes uninformative priors for the parameters listed in Table 6, but also some flexibility in all of the parameters associated with the Receiver module, despite them having a strong prior.

**Supplementary Table 6:** Priors for the Exclusive Receiver circuit characterization. In the unit column,  $M_L$  and  $M_T$  denote the normalised mass units for LacI and TetR, and Fl denotes fluorescence units. The scaling column refers to the proposal distribution used to generate new parameters during MCMC.

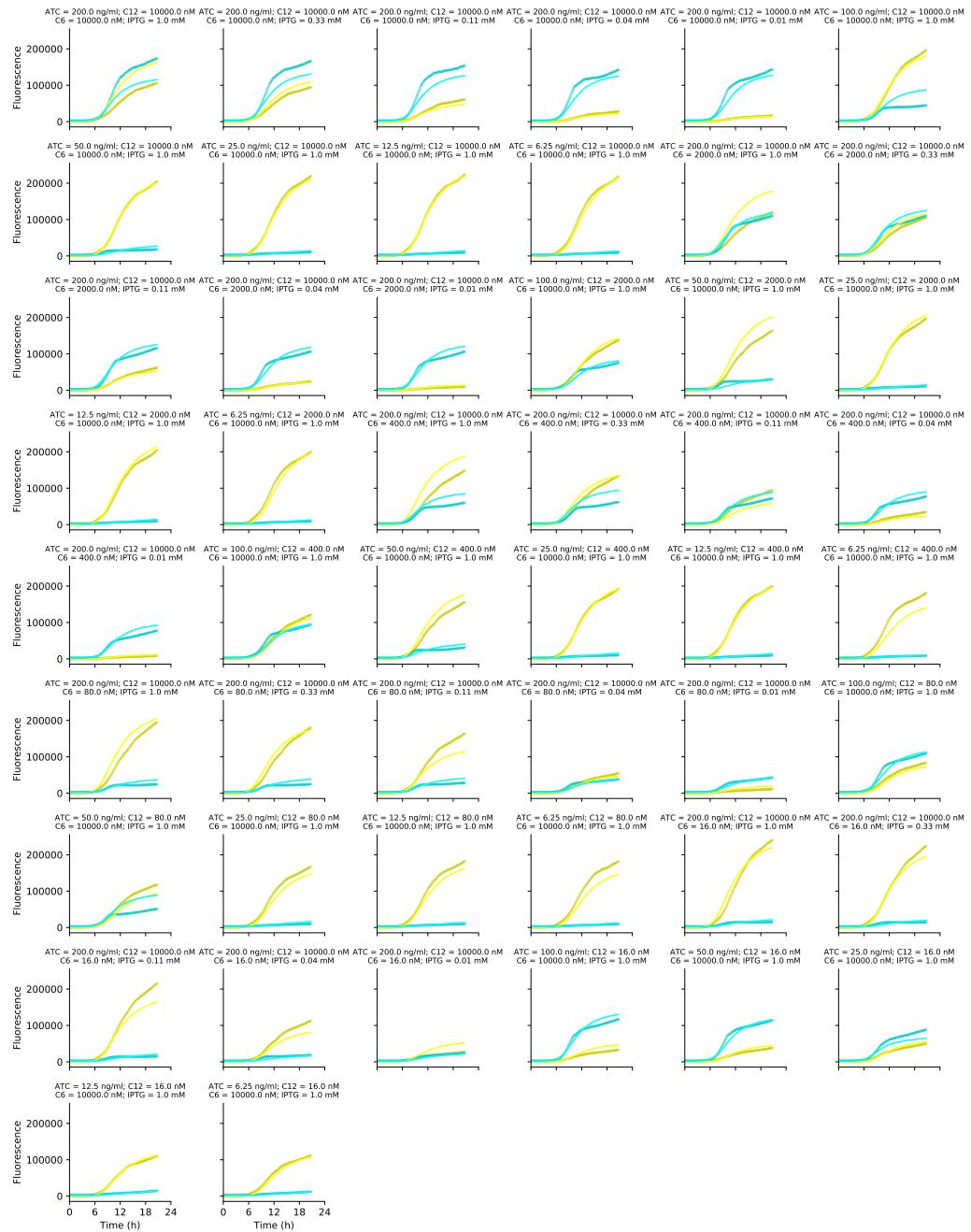
Parameter	Description	Unit	Distribution	Scaling
$a_L$	LacI synthesis	$M_L \cdot h^{-1}$	$U(1, 10^4)$	Log
$a_T$	TetR synthesis	$M_T \cdot h^{-1}$	$U(1, 10^4)$	Log
$d_L$	LacI degradation	$h^{-1}$	1 (Fixed)	N/A
$d_T$	TetR degradation	$h^{-1}$	1 (Fixed)	N/A
$n_L$	Hill constant (Laci)	-	$U(0.5, 4.0)$	Real
$n_T$	Hill constant (TetR)	-	$U(0.5, 4.0)$	Real
$i_A$	ATC inhibition of TetR	$M_T^{-1} \cdot (\text{ng/ml ATC})^{-1} \cdot h^{-1}$	$U(10^{-2}, 10^3)$	Log
$i_I$	IPTG inhibition of LacI	$M_L^{-1} \cdot (\text{mM IPTG})^{-1} \cdot h^{-1}$	$U(10^{-2}, 10^3)$	Log
$B_{480}$	Background fluor. (CFP)	Fl	$U(0, 10^4)$	Real
$B_{530}$	Background fluor. (YFP)	Fl	$U(0, 5 \times 10^3)$	Real



**Supplementary Figure 23: Marginal parameter posterior estimates of the Exclusive Receiver model (version 1) parameters.** The marginal distributions are computed from 9 of 20 independent MCMC chains. Chains were discarded that did not converge to high log-likelihood regions.

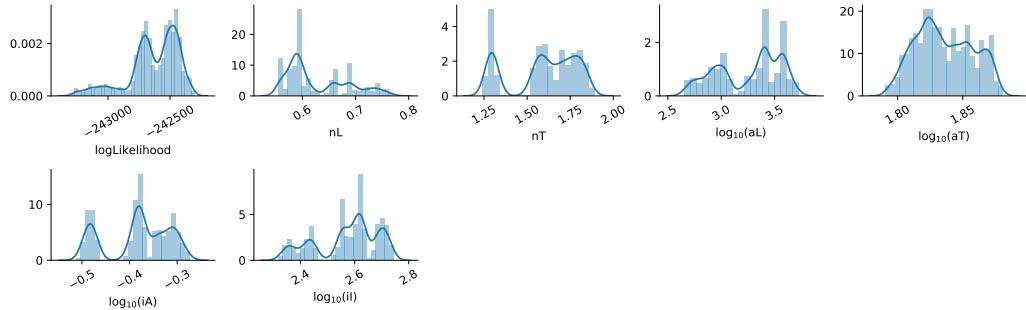
Simulation of the maximum likelihood estimate is shown in Figure 23.

**A 2d dilution of  $C_6$  and  $C_{12}$** 

**B Characterization of IPTG and ATC**

**Supplementary Figure 23: Comparison of Exclusive Receiver model (version 1) with fluorescence measurements.** Simulations are of bulk CFP (cyan lines) and YFP (yellow lines) fluorescence, evaluated with the maximum likelihood parameter set. Measurements of bulk culture fluorescence are shown in for CFP (cyan circles) and YFP (yellow circles). C6, C12, ATC and IPTG treatment concentrations are indicated atop each panel.

**Inference for version 2 (Protected degradation).** The inference procedure was also not completely robust for version 2 of the Exclusive Receiver model. We used the same uninformative priors for the parameters specific to the Exclusive Receiver model as in version 1, including fixing  $d_L$  and  $d_T$ . Again, in our marginal posterior estimates, we have only included chains that converged to relatively good likelihood scores Figure 24.



**Supplementary Figure 24: Marginal parameter posterior estimates of the Exclusive Receiver model (version 2) parameters.** The marginal distributions are computed from 8 of 20 independent MCMC chains. Chains were discarded that did not converge to high log-likelihood regions.

Simulation of the maximum likelihood estimate is shown in Extended Data Figure 2.

## 2.2 Bistability Analysis

In this section we outline computations used to create Figure 2b in the main text which compares regions of bistability indicated by hysteresis experiments in flow cytometry to that given by the differential equation model for the exclusive receiver circuit.

To characterize the region in the  $(c_{12}, c_6)$  plane where bistability occurs, we used numerical continuation to calculate a co-dimension two limit curve. The code in `get_bifurcations.jl` in our repository takes advantage of the Julia package `PseudoArcLengthContinuation.jl` [7]. To calculate the bifurcations, we only need consider the steady states of the model. The auto-fluorescence equations are independent of the others and CFP and YFP are simply readouts of  $c_L$  and  $c_T$  respectively, leaving only four coupled equations to solve, defined by state vector  $\mathbf{c} = (c_R, c_S, c_L, c_T)$ . For simplicity of analysis, we assume that cell density  $\rho$  is constant, and consequently the specific growth rate  $\gamma(\rho) =: \gamma_0$  is constant. Later, we check this assumption in Figure 26. With this simplification, the model given by (21) can be represented compactly as

$$\frac{d\mathbf{c}}{dt} = \mathbf{F}_\theta(\mathbf{c}, \mathbf{u}) \quad (22)$$

where  $\mathbf{u} = (c_6, c_{12}, c_I, c_A)$  are the experimental control parameters,  $\theta$  is the vector containing the inferred parameters from Section S1 and  $\gamma_0$ .

To improve the numerical stability of numerical continuation, we transform the model into  $\log_{10}$  coordinates via the element-wise transformations  $\mathbf{c} \rightarrow 10^\mathbf{c}$  and  $\mathbf{u} \rightarrow 10^\mathbf{u}$  yielding

$$\frac{d\mathbf{c}}{dt} = \frac{\mathbf{F}_\theta(10^\mathbf{c}, 10^\mathbf{u}) 10^{-\mathbf{c}}}{\ln(10)} \quad (23)$$

The steady states are defined by zeros of the numerator of the right-hand side. We can immediately see that this transformation induced a zero at  $\mathbf{c} \rightarrow \infty$  which we are not interested in and thus simply seek to solve

$$\mathbf{F}_\theta(10^\mathbf{c}, 10^\mathbf{u}) = 0 \quad (24)$$

To further increase numerical stability of finding 24 we explicitly calculate the Jacobian in the log coordinate system. Luckily the Jacobian in the new coordinates can be expressed in terms of the matrix product between the Jacobian in the original coordinates and the Jacobian of the coordinate transformation

$$\frac{\partial \mathbf{F}_\theta}{\partial \mathbf{c}} \rightarrow \ln(10) \frac{\partial \mathbf{F}_\theta}{\partial \mathbf{c}} \Big|_{\mathbf{c} \rightarrow 10^\mathbf{c}} \text{Diag}[10^\mathbf{c}] \quad (25)$$

where  $\text{Diag}[\mathbf{v}]$  is a diagonal matrix with the vector components of  $\mathbf{v}$  along the diagonal. The Jacobian in the original coordinates is

$$\frac{\partial \mathbf{F}_\theta}{\partial \mathbf{c}} = \begin{pmatrix} 0 & 0 & 0 & a_{R33} \frac{\partial H_T}{\partial T} \\ 0 & 0 & a_{S175} \frac{\partial H_L}{\partial L} & 0 \\ a_L \frac{\partial P_{76}}{\partial R} & a_L \frac{\partial P_{76}}{\partial S} & 0 & 0 \\ a_T \frac{\partial P_{81}}{\partial R} & a_T \frac{\partial P_{81}}{\partial S} & 0 & 0 \end{pmatrix} - \text{Diag} \left[ \gamma_0 + \begin{pmatrix} d_R \\ d_S \\ d_L \\ d_T \end{pmatrix} + \begin{pmatrix} 0 \\ 0 \\ i_I c_I \\ i_A c_A \end{pmatrix} \right] \quad (26)$$

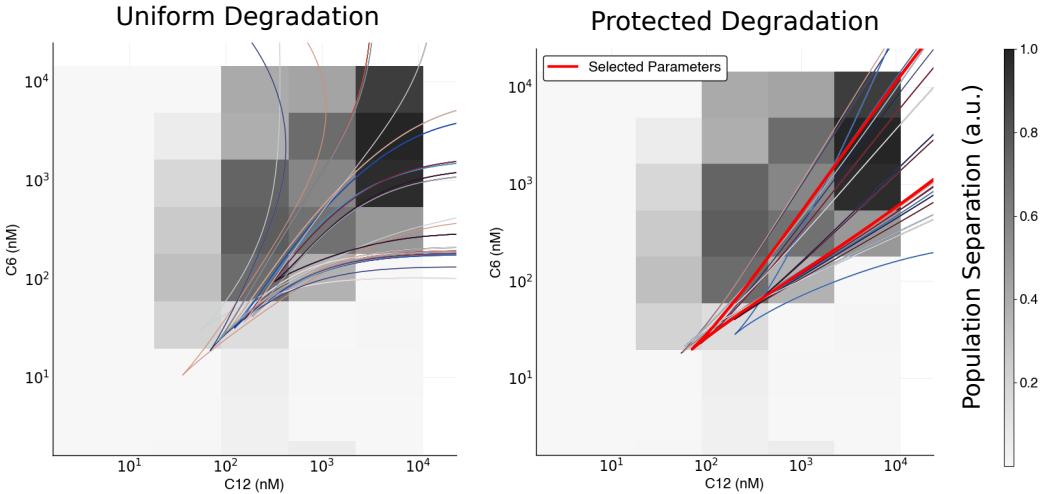
where partials of inhibitory hill functions and promoter activities are

$$\frac{\partial H_X}{\partial X} = \frac{-n_X c_X^{(n_X-1)}}{(1+c_X^{n_X})^2} \quad \frac{\partial P_N}{\partial X} = \frac{K_{GX}^N (1-e_N)}{[1+K_{GR}^N B_R(c_R) + K_{GS}^N B_S(c_S)]^2} \frac{\partial B_X}{\partial X} \quad (27)$$

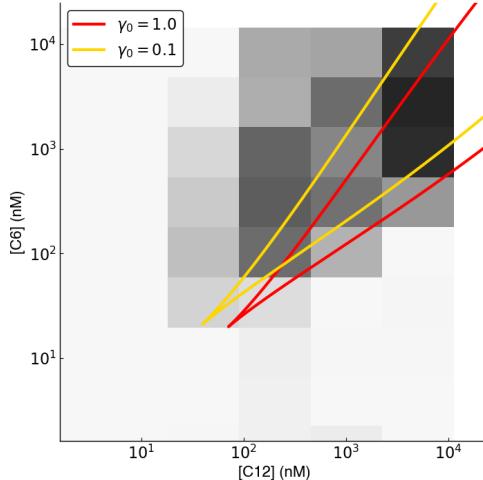
and partial bound molecules for uniform and protected degradation models are respectively

$$\frac{\partial B_X}{\partial X} = 2c_X \frac{(K_{X6}c_6)^{n_X} + (K_{X12}c_{12})^{n_X}}{(1+K_{X6}c_6 + K_{X12}c_{12})^{n_X}} \quad \frac{\partial B_X}{\partial X} = 2c_X \begin{cases} c_6^{n_X} + (E_{R12}c_{12})^{n_X} & X = R \\ c_{12}^{n_X} + (E_{S6}c_6)^{n_X} & X = S \end{cases}$$

Given the rate function  $\mathbf{F}_\theta$  and its Jacobian  $\frac{\partial \mathbf{F}_\theta}{\partial c}$  in log coordinates we can perform a co-dimension one parameter continuation for a fixed value of  $c_{12}$  along the  $c_6$  direction to find a limit point. Then the solution can be continued along a limit curve in the  $(c_6, c_{12})$  plane along both directions until the limits of the observation region are met. Figure 25 reveals these curves for different models and inferred maximum likelihood parameter sets  $\theta$  and Figure 26 reveals that the chosen model for the main text is insensitive to changes in growth  $\gamma_0$  and therefore we can safely assume that the qualitative behaviour of the model will not change if the cell density is constant. For simplicity, this is what is done in the spatial simulations in Sections 2.3 and 2.4.



**Supplementary Figure 25: Bifurcation curves for uniform and protected degradation models.** Curves are plotted on top of bimodal population separation heatmaps generated from flow cytometry data. The selected maximum likelihood parameters are used in the main text.



**Supplementary Figure 26: Bifurcation curve insensitivity specific growth rate  $\gamma_0$ .** The cell density is a monotonically increasing function of time that saturates at the carrying capacity. Concomitantly, the specific growth rate declines towards 0. By evaluating the bifurcation diagram at different values of  $\gamma_0$ , we can see how the cusp would move over time. Here the maximum likelihood parameters from the main text reveal that the cusp does not move much as the cell density increases over time.

## 2.3 Boundary Experiments

### Simulation and local equilibria

For spatial simulations a simple forward-Euler method is implemented in `get_movie.py`. The bacterial colonies for the spatial experiments were placed on top of agar with no signalling molecules inside it. Then additional volumes of agar were attached either side of the width of the experiment with different concentrations of  $c_6$  and  $c_{12}$ . The signalling molecules then diffuse in the agar and established a cross-gradient felt by the bacterial colonies. These are governed by diffusion

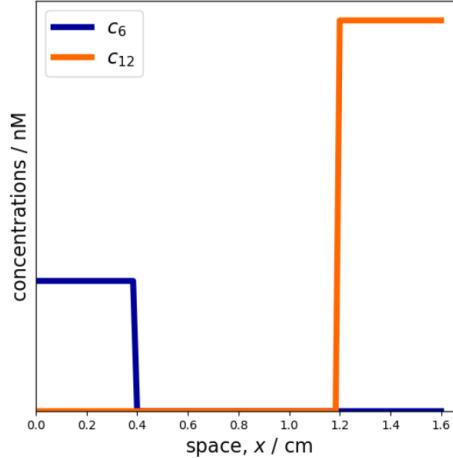
$$\frac{\partial c_X(x, t)}{\partial t} = D_X \frac{\partial^2 c_X(x, t)}{\partial x^2} \quad (28)$$

where  $D_6 = 1.8 \cdot 10^{-6} \text{ m}^2 \cdot \text{h}^{-1}$  and  $D_{12} = 0.9 \cdot 10^{-6} \text{ m}^2 \cdot \text{h}^{-1}$ .

The initial conditions for spatial simulations are zero everywhere except for  $c_6(x, t)|_{t=0}$  and  $c_{12}(x, t)|_{t=0}$  initialised in small regions widths  $w$  on opposite sides of the experiment of width  $W$  at concentrations such that the homogeneous equilibrium after diffusion would be  $c_6(x, t)|_{t \rightarrow \infty} = \bar{C}_6$  and  $c_{12}(x, t)|_{t \rightarrow \infty} = \bar{C}_{12}$  with zero-flux boundary conditions. Therefore

$$c_6(x, t)|_{t=0} = \frac{W\bar{C}_6}{w} H(w - x) \quad c_{12}(x, t)|_{t=0} = \frac{W\bar{C}_{12}}{w} H(x - W + w) \quad (29)$$

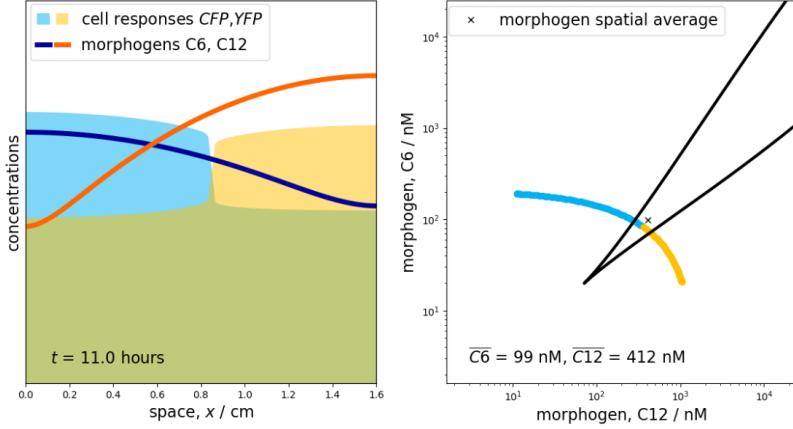
where  $H(x)$  is a unit step function.



**Supplementary Figure 27:** Initial conditions  $c_6(x, t)|_{t=0}$  and  $c_{12}(x, t)|_{t=0}$  with  $W = 1.6 \text{ cm}$  and  $w = 0.4 \text{ cm}$

Each location  $x$  experiences concentrations  $c_6, c_{12}$  which define a local equilibrium for the remaining state variables. These local equilibria evolve over time and are chased by the actual concentrations of protein in the cells at that location. As shown by Figure 25, at some concentrations  $c_6, c_{12}$  there may two stable equilibria rather than one. Therefore it becomes useful to not only display the dynamics in the one dimensional spatial domain but also in the  $(c_6, c_{12})$  plane. How and when local equilibria bifurcate reveals the eventual fate of the spatial pattern.

Figure 28 shows a snapshot of the dynamics in the spatial domain  $x$  and the  $(c_6, c_{12})$  plane. A sharp boundary in space forms when the state density in  $(c_6, c_{12})$  moves into the bistable region enclosed by the limit point curve. This means that, given the cross-gradient initial conditions 29, if the homogeneous equilibrium  $\bar{C}_6, \bar{C}_{12}$  lies within the bistable region, a sharp stationary boundary will form. If  $\bar{C}_6, \bar{C}_{12}$  lies below the cusp of the limit point curve, only soft boundaries will form. In other regions outside the bistable cone the sharp boundary has a finite velocity and will eventually leave the experimental region. See supplementary movies 2-5 for examples of the above. This motivated the experimental exploration of the space of  $\bar{C}_6, \bar{C}_{12}$  and measurements of boundary velocity, which are described in the following section.



**Supplementary Figure 28:** Dynamics in the spatial domain  $x$  on the left and  $(c_6, c_{12})$  plane on the right. Spatial averages of morphogens  $\bar{C}_6, \bar{C}_{12}$  are 99 nM and 412 nM respectively for both panels

### Computation of the boundary velocity

The velocity of the boundary is determined using `get_movement.py` from the TIFF image stack  $M[t, x, y, s]$  obtained by the fluorescence microscope from one experiment, set up with a chosen  $\bar{C}_6, \bar{C}_{12}$  combination. Here  $t$  indexes the time point,  $x$  and  $y$  index the width and height and  $s$  indexes the three channels: CFP, YFP and RFP.

First the data are normalised by the RFP channel. This way the location of the boundary can be defined by comparing the pixel values of one channel against the other. The pixels are masked for the colony grid squares  $(x, y) \in \Omega$  which are otherwise surrounded by hydrophobic ink filter paper, on which no colonies grow. The grid squares are detected by thresholding the constituent RFP channel at the `end` time point.

$$X[t, x, y, s] := \frac{M[t, x, y, s]}{M[t, x, y, \bullet]} \quad \text{where } (x, y) \in \Omega \quad (30)$$

$$\text{where } \Omega := \left\{ (x, y) : M[\text{end}, x, y, \bullet] > \frac{1}{2} \right\} \quad (31)$$

Next, a sigmoidal basis function Bayesian Ridge regressor is applied to each channel and time point along the width  $x$  of the preprocessed data  $X[t, x, y, s]$ . Sigmoidal basis functions are used because they satisfy the zero-flux boundary conditions as well as our expectations that the fluorescence profile across the width of the experiment will mostly be flat with a transient step due to the cross-gradient. The unknown weights  $\phi$  of the basis functions are obtained by minimising the objective

$$J_\phi[t, s] := \sum_{(x, y) \in \Omega} ||X[t, x, y, s] - f_\phi(x)[t, s]||^2 \quad (32)$$

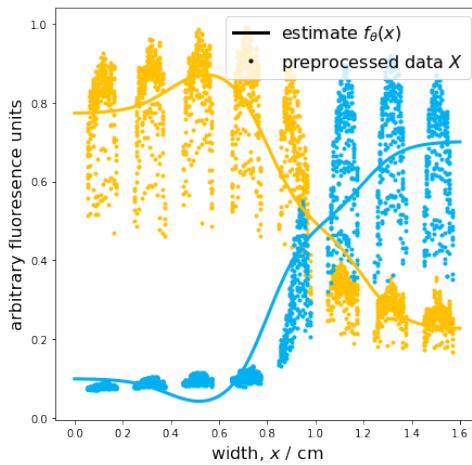
$$\text{where } f_\phi(x) := \sum_{(\alpha, \mu, \sigma) \in \phi} \frac{\alpha}{1 + e^{-\frac{x-\mu}{\sigma}}} \quad (33)$$

With the continuous estimate  $f_{\phi^*}(x)$  for each  $[t, s]$ , the location of the boundary can be obtained even if it was estimated to lie between two colonies as seen in Figure 29. Since this continuous estimate is obtained for each point in time, the position of the boundary can be tracked in a smooth kymograph as shown in Figure 30. We define the boundary location  $\beta[t]$  to be where the estimate of the CFP channel  $\bullet$  is equal to that of the YFP channel  $\circ$ ,

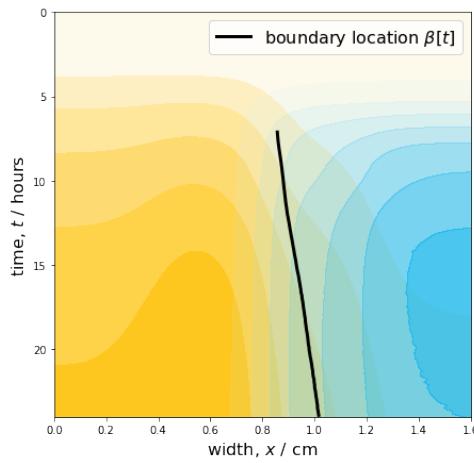
$$f_{\phi^*}(\beta)[t, \bullet] = f_{\phi^*}(\beta)[t, \bullet] \quad (34)$$

The distance travelled by the boundary  $\Delta\beta$  from its formation time  $t^*$  to the end as a fraction of the size of the experiment  $W$  can now be computed. The formation time  $t^*$  was judged by eye and seems to lie between 3 – 5 h, at which fluorescence values are sufficiently steep to form a sharp boundary. The boundary should have travelled at least 10% along the width - which is the approximate size of one colony grid square - in order to be classified as moving.

$$\Delta\beta = \frac{\beta[t^*] - \beta[\text{end}]}{W} \quad (35)$$

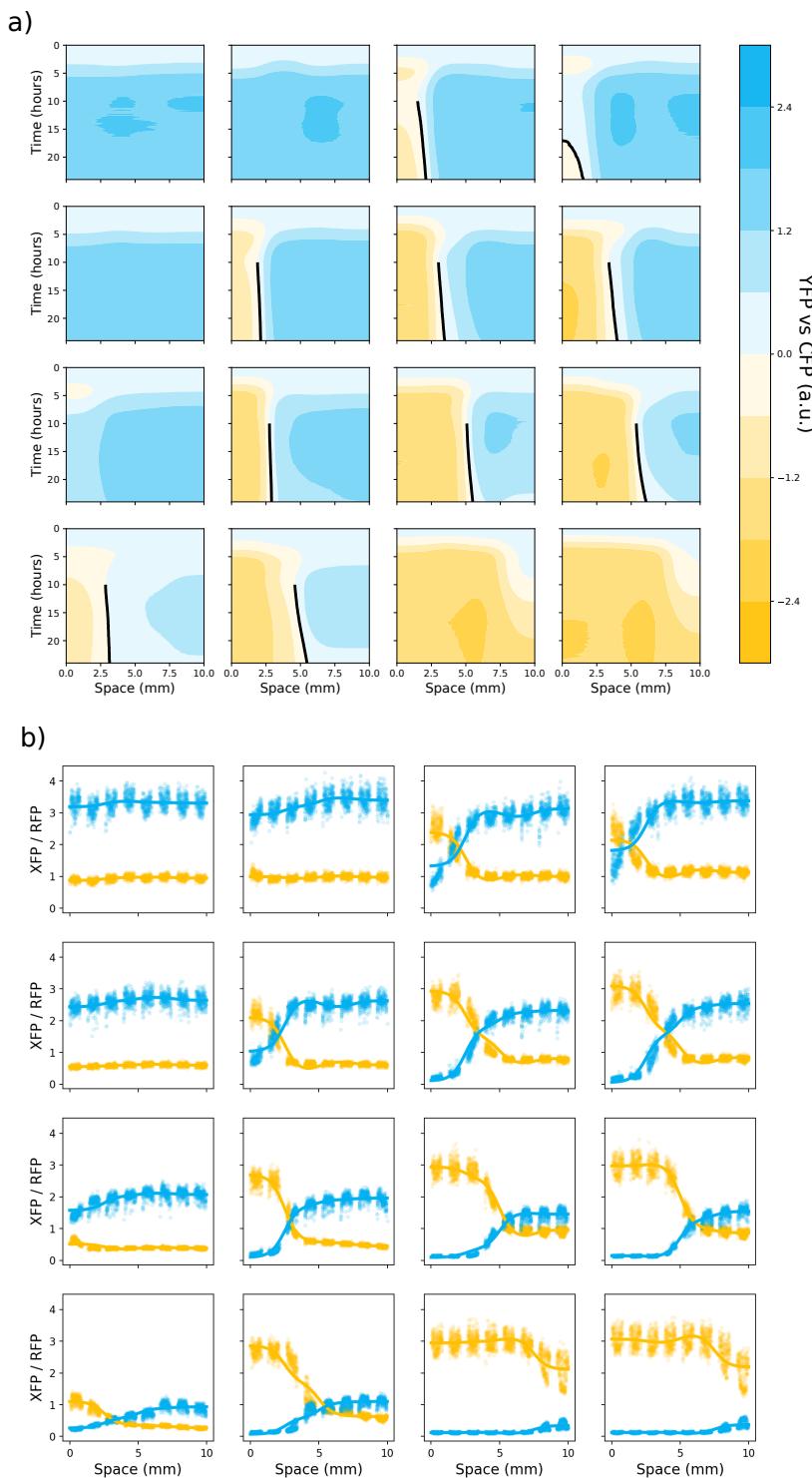


**Supplementary Figure 29:** Bayesian Ridge regression estimate  $f_{\phi}(x)$  from preprocessed data  $X$

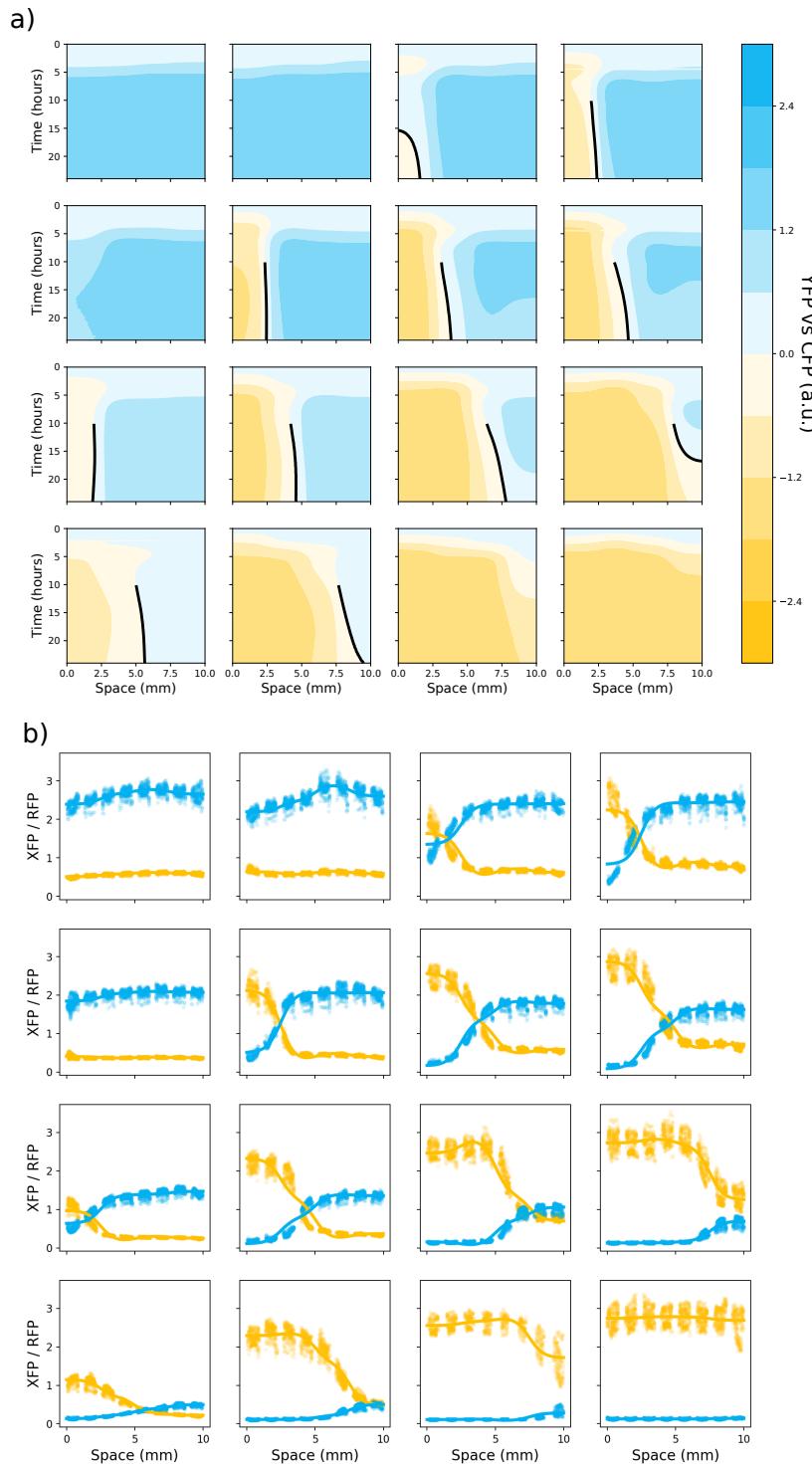


**Supplementary Figure 30:** Boundary location  $\beta[t]$  by equating estimates from two channels

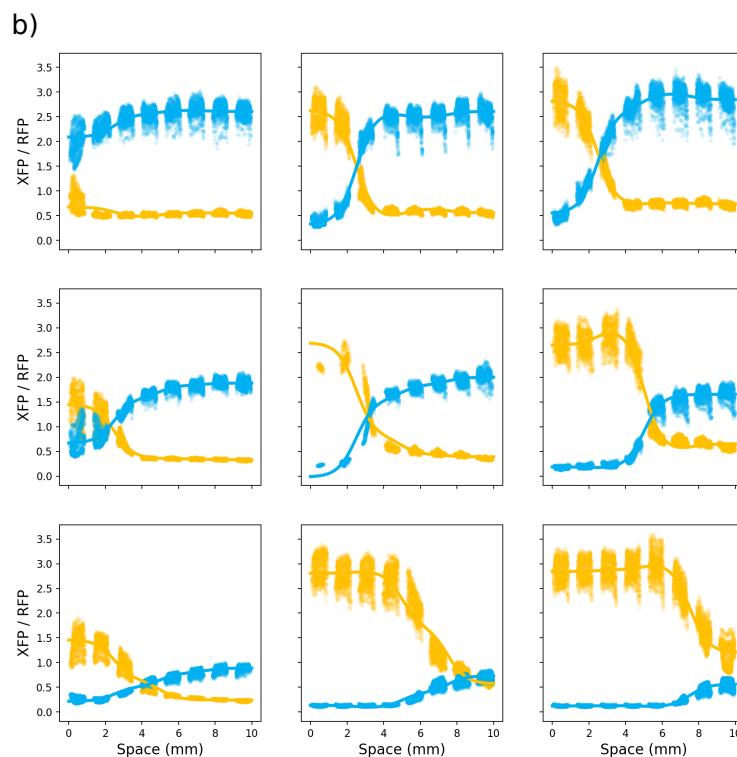
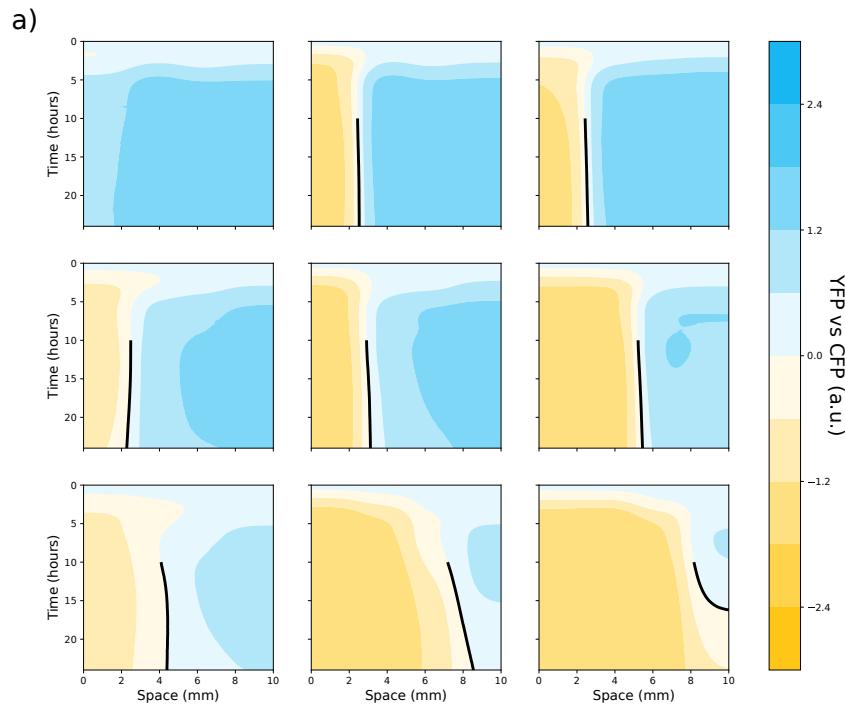
The distance travelled  $\Delta\beta$  can be investigated for different equilibrium concentrations  $\overline{C6}$  and  $\overline{C12}$ . Figure 31 shows results for a two dimensional dilution between 5 nM and 25000 nM and fixed 10  $\mu$ M IPTG. The subsequent classification using  $\Delta\beta$  is shown as Figure 3c in the main text.



**Supplementary Figure 31:** a) Boundary movements  $\beta[t]$  for a grid of equilibrium concentrations  $\overline{C}_6, \overline{C}_{12}$  and fixed  $10 \mu\text{M}$  IPTG. This is an expanded version of Figure 3c in the main text, showing the kymographs that were used for classification. b) Bayesian Ridge regression estimates for final time points of preprocessed data  $X$



**Supplementary Figure 32:** a) Replicate of Figure 31 for a two dimensional dilution of  $\overline{C}_6, \overline{C}_{12}$  between 5 nM and 25000 nM and fixed 10  $\mu$ M IPTG. b) Bayesian Ridge estimates for final time points of preprocessed data  $X$

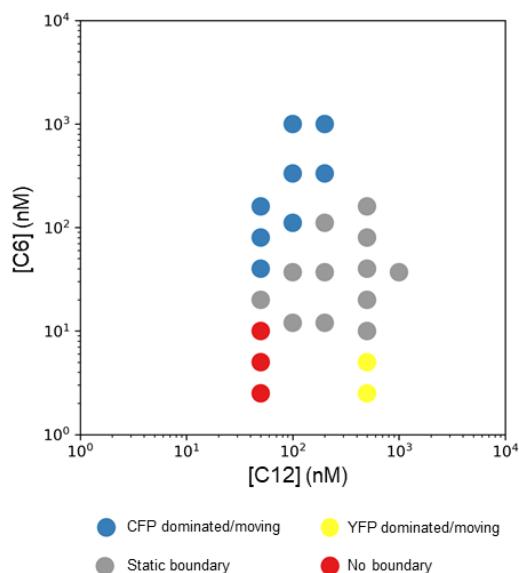


**Supplementary Figure 33:** a) Replicate of Figure 31 for a two dimensional dilution of  $\overline{C6}, \overline{C12}$  between 20 nM and 2000 nM and fixed 10  $\mu$ M IPTG. b) Bayesian Ridge estimates for final time points of preprocessed data  $X$

### Use of IPTG to influence bifurcation curve

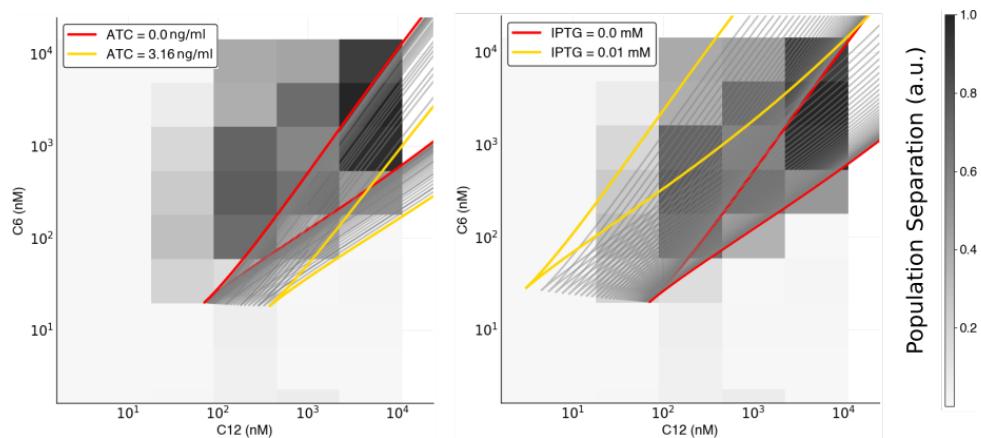
Solid culture experiments on boundary movement were initially performed in the absence of IPTG. We observed stationary boundaries at the concentrations labelled as grey points (Figure S24). The shape of the region encompassing the grey points was qualitatively similar to the conical bistability region we observed in previous experiments and in our models, but was quantitatively shifted such that even very low concentrations of C6 enabled bistability. We hypothesized that this was due to minor differences in culture conditions between solid and liquid cultures. We hypothesized that the addition of a low concentration of IPTG would partially derepress LacI, thereby making the YFP-dominant region larger and more like that seen in liquid culture. We used IPTG to shift the bistability region back (Figure S25) to coincide with the region in liquid culture. This allowed us to perform the solid culture experiments in a regime in which we could observe the transition from stable boundary to moving boundary with YFP dominance, by using higher concentrations of C12 while keeping C6 constant.

Experiments with the relay circuit (Fig. 4b) performed as expected without the need for addition of IPTG or ATC.



**Supplementary Figure 34: Boundary movement in the absence of IPTG** Boundaries were classified by eye at the spatial average concentrations indicated.

Experiments with the relay circuit (4a) performed as expected without the addition of IPTG or ATC.



**Supplementary Figure 35: Bifurcation curve dependence on ATC and IPTG.** Increasing the concentrations  $c_A$  or  $c_I$  shifts the cusp point keeping the general shape of the bistable region. Here the maximum likelihood parameters from the main text are used as the reference cusp.

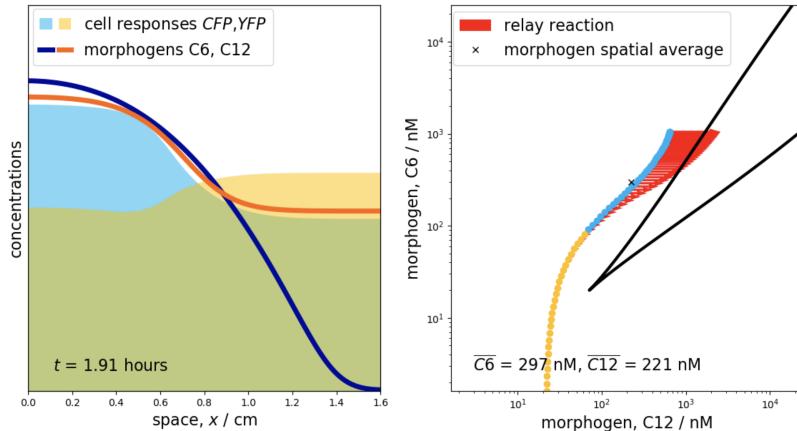
## 2.4 Models of the Exclusive Receiver Relay Circuits

The Exclusive Receiver Relay circuits were described in Figure 4 of the main text. The models for these circuits are simple extensions of the constant density model of the Exclusive Receiver circuit (22) with  $\rho = \rho_0$ ,  $\gamma = \gamma_0$  and production terms in the signal diffusion equations

$$\frac{\partial c_6(x, t)}{\partial t} = D_6 \frac{\partial^2 c_6(x, t)}{\partial x^2} + k_{C6}\rho_0 c_{\text{luxI}} \quad \frac{\partial c_{12}(x, t)}{\partial t} = D_{12} \frac{\partial^2 c_{12}(x, t)}{\partial x^2} + k_{C12}\rho_0 c_{\text{lasI}} \quad (36)$$

$$\frac{dc_{\text{luxI}}}{dt} = P_{81} - (\gamma_0 + d_{\text{luxI}})c_{\text{luxI}} \quad \frac{dc_{\text{lasI}}}{dt} = P_{76} - (\gamma_0 + d_{\text{lasI}})c_{\text{lasI}} \quad (37)$$

Here, the additional production terms  $k_{C6}\rho_0 c_{\text{luxI}}$  and  $k_{C12}\rho_0 c_{\text{lasI}}$  break mass conservation of the signalling molecules and thus may increase the spatial averages  $\bar{C}_6$ ,  $\bar{C}_{12}$ . These terms can be visualised as vertical and horizontal vector fields components in the  $(c_6, c_{12})$  plane respectively, which induce a drift on the local equilibria and the spatial average  $\bar{C}_6$ ,  $\bar{C}_{12}$ . Since there is no saturation of signal production, the spatial average  $\bar{C}_6$ ,  $\bar{C}_{12}$  will eventually always move outside of the bistable region, giving rise to a uniform dominant CFP or YFP profile. Within the finite observation time  $t < 24$  h however, we may observe sharp boundaries forming, as the spatial average  $\bar{C}_6$ ,  $\bar{C}_{12}$  passes through the bistable region. Figure 36 shows how even monotonic gradients can facilitate boundary formation.



**Supplementary Figure 36:** Dynamics of the relay circuit for  $k_{C12} > 0$ ,  $k_{C6} = 0$  in the spatial domain  $x$  on the left and  $(c_6, c_{12})$  plane on the right, showing additional reaction terms as red vectors driving the dynamics. This way even monotonic gradients can facilitate boundary formation

The additional parameters  $k_{C6}, k_{C12}, d_{\text{luxI}}, d_{\text{lasI}}$  are tuned by hand. Simulations in Section 2.3 suggest that local cellular responses approach local equilibria faster than the diffusion timescales of signalling molecules. This means we can reasonably assume that our system is diffusion-limited and so reactive dynamics (37) are much faster than diffusive dynamics (36) and we can apply the quasi-steady state assumption to (36) yielding

$$\frac{\partial c_6(x, t)}{\partial t} = D_6 \frac{\partial^2 c_6(x, t)}{\partial x^2} + \frac{k_{C6}\rho_0 P_{81}}{\gamma_0 + d_{\text{luxI}}}, \quad \frac{\partial c_{12}(x, t)}{\partial t} = D_{12} \frac{\partial^2 c_{12}(x, t)}{\partial x^2} + \frac{k_{C12}\rho_0 P_{76}}{\gamma_0 + d_{\text{lasI}}}, \quad (38)$$

and therefore in effect only two ratio parameter ratios need to be tuned. These ratios determine the magnitude of the relay reactions in the  $(c_6, c_{12})$  plane, which determine whether diffusion had contracted the local equilibria to the spatial average  $\bar{C}_6$ ,  $\bar{C}_{12}$  before or after having crossed into bistable region. Boundaries only form if contraction to  $\bar{C}_6$ ,  $\bar{C}_{12}$  occurred after entering the bistable region. See supplementary movies 6-7 for examples of these cases.

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## **Appendix B**

# **Parameter Inference with Bifurcation Diagrams**

## Appendix

### A Bifurcation Diagrams as Tangent Fields

Let each component of the vector function  $F_\theta$  in the model (1) implicitly define a surface embedded in  $\mathbb{R}^{N+1}$ . Let's assume that the intersection of these  $N$  surfaces exists and is not null or degenerate, then the steady states of (1) must be a set of one dimensional space curves in  $z \in \mathbb{R}^{N+1}$  defined by

$$F_\theta(z) = 0 \quad (14)$$

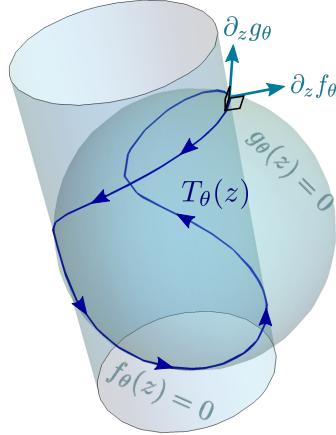


Figure 6: Two implicit surfaces  $f_\theta(z) = 0$  and  $g_\theta(z) = 0$  in  $\mathbb{R}^3$  intersecting to form a space curve which is tangent to field  $T_\theta(z)$  and perpendicular to gradients  $\partial_z f_\theta$  and  $\partial_z g_\theta$

An expression for the field  $T_\theta(z)$  tangent to the set of curves would allow us to take derivatives and integrals along the bifurcation curve. This is exactly what we need to do to evaluate our cost function 8. Fortunately the tangent field can be constructed by ensuring it is perpendicular to the gradient  $\partial_z$  of each component of  $F_\theta$  as illustrated by an example two component system in Figure 6. The tangent field  $T_\theta(z)$  can be constructed perpendicular to all gradient vectors using the properties of the determinant [32]

$$T_\theta(z) := \begin{vmatrix} \hat{z} \\ \partial_z F_\theta \end{vmatrix} \quad T_\theta : \mathbb{R}^{N+1} \rightarrow \mathbb{R}^{N+1} \quad (15)$$

$$= \sum_{i=1}^{N+1} \hat{z}_i (-1)^{i+1} \begin{vmatrix} \frac{\partial F_\theta}{\partial (z \setminus z_i)} \end{vmatrix} \quad (16)$$

where  $\hat{z}$  is a collection of unit basis vectors in the  $\mathbb{R}^{N+1}$  space and  $\partial_z F_\theta$  is an  $N \times (N+1)$  rectangular Jacobian matrix of partial derivatives and  $z \setminus z_i$  denotes the  $N$  dimensional vector  $z$  with component  $z_i$  removed. This construction ensures perpendicularity to any gradients of  $F_\theta$

$$T_\theta(z) \cdot \partial_z f_\theta = \begin{vmatrix} \partial_z f_\theta \\ \partial_z F_\theta \end{vmatrix} = 0 \quad \forall f_\theta \in F_\theta \quad (17)$$

since the determinant of any matrix with two identical rows or columns is zero. Note that the tangent field  $T_\theta(z)$  is actually defined for all values of  $z$  where adjacent field lines trace out other level sets where  $F_\theta(z) \neq 0$ . Furthermore deformations with respect to  $\theta$  are always orthogonal to the tangent

$$T_\theta(z) \cdot \frac{dT_\theta}{d\theta} = 0 \quad (18)$$

Figure 7 shows how the bifurcation curve defined by  $F_\theta(z) = 0$  picks out one of many level sets or traces in tangent field  $T_\theta(z)$  for the saddle and pitchfork. The tangent field  $T_\theta(z)$  can always be

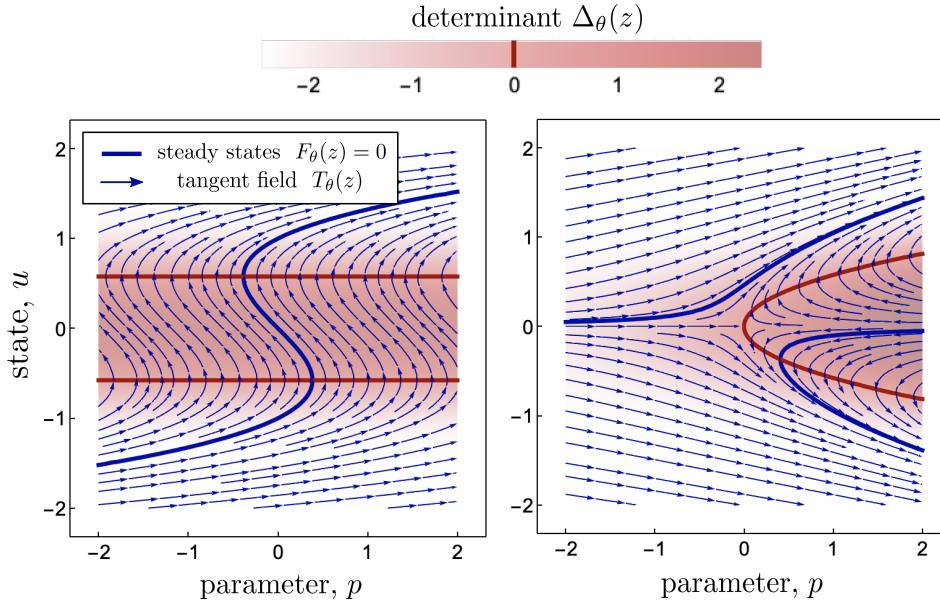


Figure 7: Left/Right : Determinant  $|\frac{\partial F_\theta}{\partial u}|$  and tangent field  $T_\theta(z)$  for the saddle-node/pitchfork models for some set values of  $\theta$  revealing that  $|\frac{\partial F_\theta}{\partial u}| = 0$  defines bifurcations

analytically evaluated by taking the determinant in (15). We will proceed with calculations on  $T_\theta(z)$  in the whole space  $z$  and pick out a single trace by solving  $F_\theta(z) = 0$  later. For our two models

$$\begin{aligned} T_\theta(z) &= \hat{u} - (3\theta_2 u^2 + \theta_1) \hat{p} & T_\theta(z) &= u\hat{u} - (3\theta_2 u^2 + p) \hat{p} \\ &\text{saddle-node model} & &\text{pitchfork model} \end{aligned} \quad (19)$$

Figure 7 reveals that  $|\frac{\partial F_\theta}{\partial u}| = 0$  is also a level set and that the intersection with level set  $F_\theta(z) = 0$  defines the bifurcations at specific parameter  $\theta$ . In this particular setting we can see that the tangent field  $T_\theta(z)$  only folds when  $|\frac{\partial F_\theta}{\partial u}| = 0$ . Plotting the value of the determinant along  $F_\theta(z) = 0$  from Figure 7 would give rise to Figures 1. The directional derivative of the determinant  $|\frac{\partial F_\theta}{\partial u}|$  along the tangent field  $T_\theta(z)$  is defined as

$$\frac{d}{ds} \left| \frac{\partial F_\theta}{\partial u} \right| := \hat{T}_\theta(z) \cdot \frac{\partial}{\partial z} \left| \frac{\partial F_\theta}{\partial u} \right| \quad (20)$$

where  $\hat{T}_\theta(z)$  is the unit tangent field.

## B Conditions for Bifurcations

The conditions for bifurcations (2) are expressed at a parametrised location  $s \in \mathbb{R}$  on the equilibrium manifold. A local bifurcation *not involving limit cycles* can be defined as a change of sign of the real part of an eigenvalue of the state-space Jacobian. In this section we show that the conditions

$$\left| \frac{\partial F_\theta}{\partial u} \right|_{s=s^*} = 0 \quad \frac{d}{ds} \left| \frac{\partial F_\theta}{\partial u} \right|_{s=s^*} \neq 0 \quad (21)$$

are sufficient for a local bifurcation to occur at a specific location  $s^*$  along the equilibrium manifold. Here we denote  $|\frac{\partial F_\theta}{\partial u}|$  as the determinant of the state-space Jacobian. We begin by expressing the determinant is the product of eigenvalues

$$\left| \frac{\partial F_\theta}{\partial u} \right| = \prod_{n=1}^N \lambda_n(s) \quad (22)$$

Applying the product rule when differentiating yields

$$\frac{d}{ds} \left| \frac{\partial F_\theta}{\partial u} \right| = \sum_{n=1}^N \frac{d\lambda_n}{ds} \prod_{n' \neq n} \lambda_{n'}(s) \quad (23)$$

As  $\left| \frac{\partial F_\theta}{\partial u} \right|_{s=s^*} = 0$  then by (22) one of the eigenvalues must vanish, say  $\lambda^*(s)$  at  $s = s^*$  then

$$\frac{d}{ds} \left| \frac{\partial F_\theta}{\partial u} \right|_{s=s^*} = \frac{d\lambda^*}{ds} \prod_{\lambda \neq \lambda^*} \lambda(s) \Big|_{s=s^*} \quad (24)$$

which implies the following conditions on the eigenvalues

$$\lambda^*(s)|_{s=s^*} = 0 \quad \frac{d\lambda^*}{ds} \Big|_{s=s^*} \neq 0 \quad (25)$$

$$\lambda(s^*) \neq 0 \quad \forall \lambda \neq \lambda^* \quad (26)$$

Conditions (25) guarantee that eigenvalue  $\lambda^*(s)$  crosses zero at  $s^*$  with a finite slope and are therefore sufficient and necessary for a local non-degenerate bifurcation not involving limit cycles. Condition (26) restricts the bifurcation at  $s^*$  to be such that only one eigenvalue may vanish with all others being finite. Therefore conditions (21) are sufficient *but not necessary* for local non-degenerate bifurcations at  $s^*$  not involving limit cycles.

In the case where more than one eigenvalue vanishes at the bifurcation the second condition (21) is broken. This is because the determinant scales like  $(s - s^*)^k$  where  $k$  is the number of eigenvalues crossing zero. When the second condition (21) is broken the measure (5) becomes zero. This means that the unsupervised term does not encourage bifurcations which have more than one eigenvalue crossing zero.

## C Leibniz Rule for Space Curves

Suppose there exists a one dimensional space curve  $\mathcal{C}(\theta)$  embedded in  $z \in \mathbb{R}^{N+1}$  whose geometry changes depending on input parameters  $\theta \in \mathbb{R}^M$ . This curve could be open or closed and changes in  $\theta$  could change the curve topology as well. Let the function  $\gamma_\theta : \mathbb{R} \rightarrow \mathbb{R}^{N+1}$  be a parameterisation of the position vector along the curve within a fixed domain  $s \in \mathcal{S}$ . Note that the choice of parameterisation is arbitrary and our results should not depend on this choice. Furthermore, if we parametrise the curve  $\mathcal{C}(\theta)$  with respect to a fixed domain  $\mathcal{S}$  the dependence on  $\theta$  is picked up by the parameterisation  $\gamma_\theta(s)$ . We can write a line integral of any scalar function  $L_\theta : \mathbb{R}^{N+1} \rightarrow \mathbb{R}$  on the curve as

$$L(\theta) := \int_{\mathcal{C}(\theta)} L_\theta(z) dz = \int_{\mathcal{S}} L_\theta(z) \left| \frac{d\gamma_\theta}{ds} \right| ds \Big|_{z=\gamma_\theta(s)} \quad (27)$$

where  $\left| \frac{d\gamma_\theta}{ds} \right|$  is the magnitude of tangent vectors to the space curve and we remind ourselves that the integrand is evaluated at  $z = \gamma_\theta(s)$ . We would like to track how this integral changes with respect to  $\theta$ . The total derivative with respect to  $\theta$  can be propagated into the integrand [31] as long as we keep track of implicit dependencies

$$\frac{dL}{d\theta} = \int_{\mathcal{S}} \left| \frac{d\gamma_\theta}{ds} \right| \left( \frac{\partial L}{\partial \theta} + \frac{\partial L}{\partial z} \cdot \frac{dz}{d\theta} \right) + L_\theta(z) \frac{d}{d\theta} \left| \frac{d\gamma_\theta}{ds} \right| ds \Big|_{z=\gamma_\theta(s)} \quad (28)$$

Here we applied the total derivative rule in the first term due to the implicit dependence of  $z$  on  $\theta$  through  $z = \gamma_\theta(s)$ . Applying the chain rule to the second term

$$\frac{d}{d\theta} \left| \frac{d\gamma_\theta}{ds} \right| = \left| \frac{d\gamma_\theta}{ds} \right|^{-1} \frac{d\gamma_\theta}{ds} \cdot \frac{d}{d\theta} \left( \frac{d\gamma_\theta}{ds} \right) \quad (29)$$

By choosing an  $s$  that has no implicit  $\theta$  dependence we can commute derivatives

$$\frac{d}{d\theta} \left( \frac{d\gamma_\theta}{ds} \right) = \frac{d}{ds} \left( \frac{d\gamma_\theta}{d\theta} \right) \Rightarrow \frac{d}{d\theta} \left| \frac{d\gamma_\theta}{ds} \right| = \left| \frac{d\gamma_\theta}{ds} \right|^{-1} \frac{d\gamma_\theta}{ds} \cdot \frac{d}{ds} \left( \frac{d\gamma_\theta}{d\theta} \right) \quad (30)$$

To proceed we note that the unit tangent vector can be written as an evaluation of a tangent field  $\hat{T}_\theta(z)$  defined in the whole domain  $z \in \mathbb{R}^{N+1}$  along the parametric curve  $z = \gamma_\theta(s)$ . The unit tangent field may disagree with the tangent given by  $\frac{d\gamma_\theta}{ds}$  up to a sign

$$\hat{T}_\theta(z) \Big|_{z=\gamma_\theta(s)} = \pm \left| \frac{d\gamma_\theta}{ds} \right|^{-1} \frac{d\gamma_\theta}{ds} \quad (31)$$

this leads to

$$\frac{d}{d\theta} \left| \frac{d\gamma_\theta}{ds} \right| = \left| \frac{d\gamma_\theta}{ds} \right| \left( \hat{T}_\theta(z) \cdot \frac{\partial}{\partial z} \left( \frac{d\Gamma_\theta}{d\theta} \right) \cdot \hat{T}_\theta(z) \right)_{z=\gamma_\theta(s)} \quad (32)$$

It is possible to find the normal deformation of the implicit space curves due to changes in  $\theta$ . This can be done by taking the total derivative of the implicit equation defining the level set

$$\frac{dF_\theta(z)}{d\theta} = \frac{\partial F}{\partial \theta} + \frac{\partial F}{\partial z} \cdot \frac{dz}{d\theta} \quad (33)$$

We can rearrange for  $\frac{dz}{d\theta}$  using the Moore-Penrose inverse of the rectangular Jacobian matrix  $\frac{\partial F}{\partial z}$  which appeared in equation (15). Since the level set is defined by  $F_\theta(z) = 0$  the total derivative along the level set  $dF_\theta(z) = 0$  and we arrive at an expression for the deformation field [26]

$$\frac{dz}{d\theta} = -\frac{\partial F^\top}{\partial z} \left( \frac{\partial F}{\partial z} \frac{\partial F^\top}{\partial z} \right)^{-1} \frac{\partial F}{\partial \theta} \quad (34)$$

The tangential component of the deformation field is not uniquely determined because there is no unique way of parameterising a surface. This is the subject of many computer graphics papers [26, 33, 34]. We are however not interested in the continuous propagation of a mesh - as is the subject of those papers. In fact we are looking for a deformation field that is orthogonal to the tangent vector  $\hat{T}_\theta(z) \cdot \frac{dz}{d\theta} = 0$  for the space curve, and therefore letting the tangential component of the deformation equal zero is a valid choice and we can it instead of the parameterised deformation

$$\frac{d\gamma_\theta}{d\theta} \rightarrow \frac{dz}{d\theta} \quad (35)$$

To summarise we now have the gradient of our line integral only in terms of the implicit function defining the integration region.

$$\frac{dL}{d\theta} = \int_{F_\theta(z)=0} \frac{\partial L}{\partial \theta} + \frac{\partial L}{\partial z} \cdot \varphi_\theta(z) + L_\theta(z) \hat{T}_\theta(z) \cdot \frac{\partial \varphi}{\partial z} \cdot \hat{T}_\theta(z) dz \quad (36)$$

$$\text{where } \hat{T}_\theta(z) := \frac{T_\theta(z)}{|T_\theta(z)|} \quad T_\theta(z) := \left| \frac{\hat{z}}{\partial_z F_\theta} \right| \quad \varphi_\theta(z) := -\frac{\partial F^\top}{\partial z} \left( \frac{\partial F}{\partial z} \frac{\partial F^\top}{\partial z} \right)^{-1} \frac{\partial F}{\partial \theta} \quad (37)$$

We have settled on choosing normal deformations which we will call  $\varphi_\theta(z)$ . The above result can be seen a the generalised Leibniz rule [31] for the case of line integration regions. The last integrand term can be seen as the divergence the vector field  $\varphi_\theta(z)$  projected onto the one dimensional space curve.

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