

Delay-induced stochastic oscillations in gene regulation

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The small number of reactant molecules involved in gene regulation can lead to significant fluctuations in intracellular mRNA and protein concentrations, and there have been numerous recent studies devoted to the consequences of such noise at the regulatory level. Theoretical and computational work on stochastic gene expression has tended to focus on instantaneous transcriptional and translational events, whereas the role of realistic delay times in these stochastic processes has received little attention. Here, we explore the combined effects of time delay and intrinsic noise on gene regulation. Beginning with a set of biochemical reactions, some of which are delayed, we deduce a truncated master equation for the reactive system and derive an analytical expression for the correlation function and power spectrum. We develop a generalized Gillespie algorithm that accounts for the non-Markovian properties of random biochemical events with delay and compare our analytical findings with simulations. We show how time delay in gene expression can cause a system to be oscillatory even when its deterministic counterpart exhibits no oscillations. We demonstrate how such delay-induced instabilities can compromise the ability of a negative feedback loop to reduce the deleterious effects of noise. Given the prevalence of negative feedback in gene regulation, our findings may lead to new insights related to expression variability at the whole-genome scale.

master equation | stochastic delay equations | noise | time delay | systems biology

There is considerable experimental evidence that noise can play a major role in gene regulation (1–10). These fluctuations can arise from either intrinsic sources, which are related to the small numbers of reactant biomolecules, or extrinsic sources, which are attributable to a noisy cellular environment. Although the importance of fluctuations in gene regulation was stressed >30 years ago (11), recent experimental advances have renewed interest in the stochastic modeling of the biochemical reactions that underlie gene regulatory networks (12–16). The most typical approaches are the utilization of the Gillespie algorithms (17–20), the direct analysis of the master equation, or the development of simplified descriptions based on the Fokker–Planck or Langevin equations (see ref. 21 for a review). A common thread in many of these approaches has been to consider intrinsic noise as the dominant source of variability in gene expression.

One major difficulty often encountered in the analysis of gene regulatory networks is the vast separation of time scales between what are typically the fast reactions (dimerization, protein–DNA binding/unbinding) and the slow reactions (transcription, translation, degradation). There have been many studies devoted to the development of reduced descriptions of these systems using the idea of quasiequilibrium for the fast processes compared with the slow dynamics (cf. ref. 22 and references therein). These approaches have thus far implicitly assumed that all of the reactions (fast and slow) are Markovian processes obeying Poissonian statistics. In this regard, it is important to note that the transcriptional and translational processes are not just slow but also are compound multistage reactions involving the sequential assembly of long molecules. Thus, by virtue of the central limit theorem, these processes should obey Gaussian statistics with a certain characteristic mean delay time.

When delays in biochemical reactions are small compared with other significant time scales characterizing the genetic system, one can safely ignore them in simulations. Furthermore, time delays usually do not affect the quasiequilibrium behavior of gene regulatory networks and mean values of corresponding observables, and the conventional stochastic models without delays work properly here (for a review, see ref. 23). However, if indeed the time delays are of the order of other processes or longer, and the feedback loops associated with these delays are strong, taking the delays into account can be crucial for description of transient processes. This finding implies that when delay times are significant, both analytical and numerical modeling should take into account the non-Markovian nature of gene regulation.

The fact that delayed-induced stochastic oscillations can occur during transcriptional regulation is supported by recent studies of circadian oscillations in *Neurospora*, *Drosophila*, and others. It is widely accepted now that these oscillations are caused by delays in certain elements of gene regulation networks [see recent experimental (24, 25) and modeling (26–29) studies]. It is plausible that the role of time delays in circadian rhythms has come to light because the delays in the corresponding reactions are particularly long (several hours) in comparison with other characteristic times of the system. It would be logical to suppose that shorter delays present in other systems also can have a significant impact on dynamics; however, they may be more difficult to detect with currently available experimental methods.

The behavior of stochastic delay-differential equations (SDDEs) has been extensively studied, and various approximation techniques have been developed and utilized (30–35). For example, delayed differential equations have been reduced to coupled map lattices and perturbed by white noise, demonstrating how the phase space density reaches a limit cycle in the asymptotic regime (30). The stability of the moment equations for linear SDDEs has been explored to elucidate the oscillatory properties of the first and second moments (31), and the master equation approach has been applied to a delayed random walker in an effort to demonstrate the effects of delay in an analytically tractable system (32, 33). The limit of short delay time has been used to show how a univariate nondelayed stochastic differential equation can be used to approximate the original system (34), and, more recently, a noise-driven bistable system with delayed feedback was reduced to a two-state model with delayed transition rates to demonstrate the phenomenon of coherence resonance (35). These important studies have provided many valuable insights, yet little work has been directed toward realistic delay times coupled with intrinsic noise in the context of gene regulation.

In the present work, we develop methodologies for the analysis and simulation of delayed biochemical reactions that describe gene regulation. Specifically, we establish a theoretical approach for reducing and solving master equations that describe gene expres-

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Abbreviation: DG, direct Gillespie.

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delay in that systems can lead to oscillations with a period as large as tens of hours, and stochastic events separated by such time spans become effectively decoupled. In other cases, however, the delay time can be of order or smaller than other characteristic times. Extrinsic processes that are much slower than the time-delayed reactions can be taken into account as adiabatic change of parameters, and the theory developed here would still apply. If, however, there are significant cell processes operating on the time scales of the order of time delay, one has to resort to numerical simulations.

In fact, large τ is a necessary but not a sufficient condition for this theory to hold. We will see below that strong delayed feedback leads to significant correlations over long periods of time, and an additional condition for the applicability of Eq. 4 is to have relatively weak feedback. Adopting this approximation, we obtain

$$\begin{aligned} \frac{dP(n, t)}{dt} &= A(E^{-1} - 1)P(n, t) + B(E - 1)nP(n, t) \\ &+ C \sum_{m=0}^{\infty} mP(m, t - \tau)(E - 1)H(n)P(n, t), \\ &= A(E^{-1} - 1)P(n, t) + B(E - 1)nP(n, t) \\ &+ C\langle n(t - \tau) \rangle (E - 1)H(n)P(n, t), \quad n = 0.. \infty. \quad [5] \end{aligned}$$

Exploiting the same approximation, we can write the autocorrelation function in the following form (see *Supporting Text*, which is published as supporting information on the PNAS web site):

$$K(T) = \sum_{n=0}^{\infty} nP_s(n)\langle n', T|n, 0 \rangle - \langle n \rangle^2,$$

where $P_s(n)$ is the stationary probability and $\langle n', T|n, 0 \rangle$ is the conditional mean number of proteins at time T , given it was n at time 0. By using the generating function method, we can calculate the stationary probability distribution and the conditional mean from the master equation (5) and arrive at the autocorrelation function (see *Supporting Text* for details of this calculation)

$$K(T) = \frac{A}{B} \frac{\sigma(T)}{(1 - \zeta e^{-\lambda T})}, \quad [6]$$

where $\lambda = \sqrt{B^2 - C^2}$, $\zeta = (B - \lambda)/C$, and

$$\sigma(T) = \begin{cases} e^{-\lambda T} - \zeta e^{\lambda(T-\tau)}, & 0 < T < \tau \\ e^{-B(T-N\tau)} (\sigma(N\tau) - C \int_{N\tau}^T \sigma(T' - \tau) e^{B(T'-N\tau)} dT'), & N\tau < T < (N+1)\tau. \end{cases}$$

This solution is defined if $B > C$, i.e., below the deterministic Hopf bifurcation. It has a form of a sequence of peaks of alternating polarity with decaying heights (Fig. 1B). By using Eq. 6 we can calculate the power spectrum $S(\omega)$ (cf. ref. 35)

$$S(\omega) = 2 \frac{A}{B} \operatorname{Re} \frac{1 - C e^{i\omega\tau} I(\omega)}{B + C e^{i\omega\tau} - i\omega}, \quad [7]$$

where

$$I(\omega) = \frac{1}{1 - \zeta e^{-\lambda\tau}} \left(\frac{1 - e^{-(i\omega + \lambda)\tau}}{i\omega + \lambda} + \zeta e^{-\lambda\tau} \frac{1 - e^{-(i\omega - \lambda)\tau}}{i\omega - \lambda} \right).$$

The main difference between the deterministic and stochastic approaches manifests itself in Fig. 2, where the power spectra for the latter are plotted in accordance with Eq. 7. One can see that the stochastic model predicts quasiregular oscillations in the

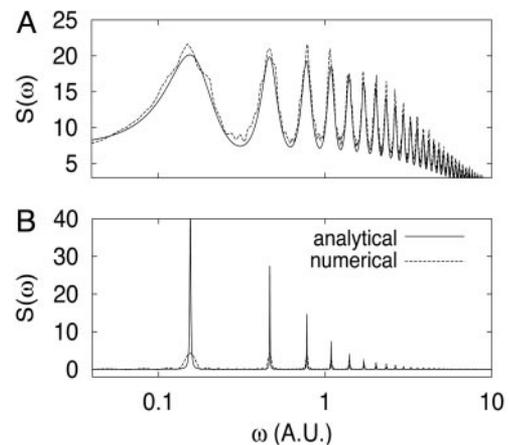


Fig. 2. Comparison of power spectra $S(\omega)$ obtained analytically (solid line) and numerically (dashed line) for the delayed protein degradation model (Eq. 1) with $\tau = 20$, $A = 100$, $B = 4.1$, and two values of C indicated by filled squares in Fig. 1A, $C = 1$ (A) and 4 (B). Insets show the same comparison for the correlation functions normalized by the variance. The frequency ω and time are plotted in arbitrary units (A.U.).

parameter range where the deterministic model shows a stable steady state. Thus, it is evident that the coupling between noise and delay leads to the oscillatory behavior, whereas each element separately does not.

Stochastic Simulations: Modified Gillespie Method

To test the validity of our approximations and analytical results, we performed numerical simulations of the original system of stochastic chemical reactions (1). Here we introduce modifications to the direct Gillespie (DG) algorithm (17), which allow us to incorporate delayed reactions. Suppose the system consists of N components X_i , which react through M elementary reaction channels R_μ . According to the DG algorithm, time is advanced from one elementary reaction to the next. At every “stop” one determines the time of the next reaction and which reaction it will be. For Markovian processes, the distribution of times until the next reaction is exponential

$$P(\tau) = \sum_{\mu} a_{\mu} \exp\left(-\Delta t \sum_{\mu} a_{\mu}\right), \quad [8]$$

where $a_{\mu} = c_{\mu} h_{\mu}$ is the propensity of channel R_{μ} . The choice of the next reaction is made based upon the discrete distribution,

$$P(\mu = \mu') = a_{\mu'} / \sum_{\mu} a_{\mu}. \quad [9]$$

When some of the channels are non-Markovian, it is necessary to modify the original version of the DG algorithm as follows. At each stop we perform the same selection of the next reaction time according to the distributions in Eqs. 8 and 9. If the next reaction time is chosen to be t^* but the selected reaction is delayed, it is placed in a stack, so it will actually be completed at time $t^* + \tau$. If, however, the chosen reaction is Markovian, the time of the next reaction t^* is compared with the times of the previously scheduled delayed reactions. If none of those scheduled reactions are to occur before t^* , the time is advanced to t^* , the numbers of molecules are updated according to the chosen nondelayed reaction, and the process repeats. If, however, there is a delayed reaction scheduled for completion at $t_d < t^*$, the last selection is ignored, time advances to t_d , the scheduled delayed reaction is performed, and the selection process repeats. The formal steps for the algorithm execution are as follows (see Fig. 3 for the illustration):

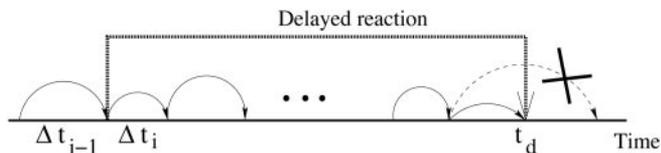


Fig. 3. Illustration to the modified Gillespie algorithm for normal and delayed reactions.

1. Input values for initial state $\mathbf{X} = (X_1, \dots, X_N)$, set time $t = 0$ and reaction counter $i = 1$.
2. Compute propensities of M reactions a_μ , $\mu = 1, \dots, M$.
3. Generate uniform random numbers $u_1, u_2 \in [0, 1]$
4. Compute the time interval until the next reaction $\Delta t_i = -\ln u_1 / \sum_{\mu} a_\mu$.
5. Check whether there are delayed reactions scheduled within time interval $[t, t + \Delta t_i]$. If YES, then steps 2–4 are ignored, time t advances to the time t_d of the next scheduled delayed reaction, \mathbf{X} states are updated according to the delayed reaction channel, and counter is increased $i = i + 1$. Proceed to step 2. If NO, go to step 6.
6. Find the channel of the next reaction μ , namely take μ to be the integer for which $\sum_{\nu=1}^{\mu-1} a_\nu < u_2 a_\mu \leq \sum_{\nu=1}^{\mu} a_\nu$, where $a_t = \sum_{\nu=1}^M a_\nu$ is the total propensity.
7. If the selected reaction μ is not delayed, update \mathbf{X} according to the R_μ , update time $t = t + \Delta t_i$ and increase counter $i = i + 1$. If the selected reaction is delayed, update is postponed until time $t_d = t + \tau$. Go to step 2.

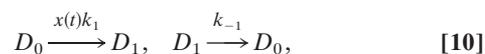
We note that stochastic variations of the delay time itself can be an additional source of genetic noise. Our numerical algorithm can easily incorporate these fluctuations; however, in the present work for simplicity we assume that τ is constant.

The comparison for the power spectra and correlation functions obtained analytically and numerically is shown in Figs. 1B and 2 for $\tau = 20$. The chosen delay time is large compared with the characteristic equilibration time $B^{-1} \approx 0.25$, which is necessary to justify the master Eq. 5. The first peak of the power spectrum in both figures corresponds to the frequency $\omega = 2\pi/2\tau \approx 0.157$.

When the system is far away from the Hopf bifurcation, the influence of the delay term is relatively weak, and the analytical and numerical curves are in excellent agreement (Figs. 1B and 2A). In Fig. 1B *Inset* we plot the height of the secondary peak located near $\tau = 20$ as a function of the parameter τC . Near the Hopf bifurcation (Fig. 2B), the agreement between our analytical approach and the simulations becomes worse because the processes at times t and $t - \tau$ become strongly correlated (the secondary peak of the correlation function is large).

Negative Feedback with Delayed Production

In this section we apply our approach to a system that represents one of the most common motifs in gene regulation (36, 39). Namely, we consider single-gene protein synthesis with negative feedback. The dynamics of this system have been analyzed deterministically (40) and stochastically (21), and experimental findings have demonstrated how negative feedback can dampen the effects of noise (3). Here we generalize this system by allowing for the finite delay time necessary for protein transcription and translation. We postulate that the chemical state of the operator site $D' \in \{D'_0, D'_1\}$ determines the production of protein at time $t + \tau$. If the operator at time t is unoccupied (D'_0), then the protein may be produced at time $t + \tau$ with probability A per unit time. Otherwise, if the operator is occupied (D'_1), the production at time $t + \tau$ is blocked. The transitions between operator states, denoted as D_0 (unoccupied) and D_1 (occupied), occur with rates k_1, k_{-1} , can be written as



where $x(t)$ represents the number of proteins at time t . The protein production and degradation reactions can be written as



Here $S(t) = 1$ for unoccupied operator state D_0 and 0 for occupied state D_1 . Thus, the reactions have negative feedback through the first reaction rate in Eq. 11.

Deterministic Description. We introduce continuous variables $x(t)$ for the average number of proteins and $s(t)$ for the average number of unoccupied operator sites at time t . For a single gene circuit, $s(t) \leq 1$, and the number of occupied sites is $1 - s(t)$. Exploiting the typically large separation of time scales between protein–DNA binding rates and the production/degradation rates, the deterministic rate equations for reactions 10 and 11 can be written as

$$\frac{dx}{dt} = \frac{A}{1 + \varepsilon x(t - \tau)} - Bx, \quad [12]$$

where $\varepsilon = k_1/k_{-1}$. This system has only a single positive stationary solution, which is always stable, so the system does not possess bifurcations (see *Supporting Text*).

Stochastic Description. We introduce two probabilities, $P_n^0(t)$ and $P_n^1(t)$, for the number of proteins to be equal to n at time t , and for the state of the operator at time $t - \tau$ to be $D'_{0-\tau}$ or $D'_{1-\tau}$, respectively. Then the master equations for the reactions in Eqs. 10 and 11 have the form

$$\begin{aligned} \frac{dP^0(n, t)}{dt} &= A(E^{-1} - 1)P^0(n, t) + B(E - 1)nP^0(n, t) \\ &\quad - k_1 \sum_{m=0}^{\infty} m[(P^0(m, t - \tau) + P^1(m, t - \tau))]P^0(n, t) \\ &\quad + k_{-1}P^1(n, t), \end{aligned} \quad [13]$$

$$\begin{aligned} \frac{dP^1(n, t)}{dt} &= B(E - 1)nP^1(n, t) - k_{-1}P^1(n, t) \\ &\quad + k_1 \sum_{m=0}^{\infty} m[(P^0(m, t - \tau) + P^1(m, t - \tau))]P^0(n, t). \end{aligned}$$

We have again made the assumption that the processes at times t and $t - \tau$ are weakly correlated, and to first approximation the two-point probability distribution function factorizes, $P(n, t; m, t - \tau) \approx P(n, t)P(m, t - \tau)$. To calculate the correlation function, we again use generating functions (see *Supporting Text*)

$$\begin{aligned} K(T) &= \left(\frac{A^2(B + k_{-1})}{B((B + k_{-1})(B + \varepsilon A) + k_1 A)} \right. \\ &\quad \left. + \frac{A(B + \varepsilon A - A)}{(B + \varepsilon A)^2} \right) \frac{\sigma(T)}{1 - \zeta e^{-\lambda T}}, \end{aligned} \quad [14]$$

with the same notations as in Eq. 6.

Comparison of Analytical and Numerical Results. We performed DG simulations of the stochastic model for the single-gene negative feedback system. Comparison between our analytical and numer-

The power spectrum, correlation function, and the time series for two particular parameter sets are shown in Fig. 6. One can see that even far below the Hopf bifurcation (Fig. 6*A* and *B*), the correlation function has a remarkably narrow peak, indicating that some periodicity in the stochastic signal exists (Fig. 6*A Inset*). The first peak of the power spectrum corresponds to the frequency $\omega = 2\pi/2\tau \approx 0.159$ ($\tau = 20$). As the system approaches the bifurcation point A^* , the peaks become wider and higher. Above the bifurcation the power spectrum and correlation function are depicted in Fig. 6*C*. They correspond to periodic oscillations above the bifurcation threshold with a period slightly higher than 2τ (Fig. 6*D*).

At first glance, one might expect that within the stochastic approach the bifurcation-like transition from the steady state to a limit cycle is not observed, and the point of such a transition cannot be clearly determined. However, Fig. 5*C* shows that this hypothesis is not the case. If the decay rate of the correlation function peaks as a function of A is plotted on a logarithmic scale, the curve can be approximated well by two lines that intersect at $A \approx 56$. Thus, stochastic fluctuations shift the bifurcation point by ≈ 5 with respect to the deterministic value for A ($A^* = 57.85$). This result appears particularly important from an experimental point of view, because frequently an experimenter needs to define a bifurcation occurring in a stochastic system. As we have shown, relatively simple manipulations with the autocorrelation function can help in defining this bifurcation.

Fig. 5*D* illustrates how the coefficient of variation (CV) changes with transcription rate A in two cases: with (open circles) and without (filled circles) time delay in protein production. If in the former case CV decreases monotonically with transcription rate because the number of molecules increases, in the latter case as the system crosses the bifurcation point the CV increases again and tends to some limiting level.

Finally, delayed feedback strongly affects transient behavior of genetic networks. Unlike nondelayed system, the transition to a new fixed point in the delayed system is accompanied by significant stochastic oscillations (see Fig. 7, which is published as supporting information on the PNAS web site).

Discussion

We have developed both deterministic and stochastic models for transcriptional regulation with delayed feedback and have explored these models both analytically and numerically. Problems with delay are generally difficult because of the non-Markovian nature of the dynamics, yet we have demonstrated that the main features of such systems can be understood using relatively simple models. Assuming significant decorrelation on the time scale of gene transcription, we have deduced a truncated master equation of the reactive system and derived analytical expressions for the correlation function and power spectrum. In addition, we have developed a generalization of the Gillespie algorithm that accounts for delay

and have demonstrated how numerical simulations can be performed and compared with analytical findings. Within the context of negative autoregulation, which is one of the most commonly occurring regulatory motifs (36), we have shown how oscillations can arise from the coupling of noise and delay.

The likely importance of fluctuations arising from the small number of reactant molecules in gene expression was noted by Stuart and Branscomb in 1971 (11). In this prescient work, analytical techniques were applied to a model for the *lac* operon to show how fluctuations could play an important role in gene regulation. Owing mainly to the lack of experimental assays capable of resolving fluctuations at the single-cell level, this work went largely unnoticed, and the role of noise in gene expression received little attention until the late 1990s. More recently, the predicted role of intrinsic noise in the context of developmental pathways ignited widespread interest (12), and there have been numerous subsequent experimental studies that empirically demonstrate the importance of such fluctuations (1–10).

As in the case of intrinsic noise, the generic origin of delay implies a high likelihood that it plays an important role in gene regulation (cf. ref. 41 and references therein). It could be a dominant source of large deterministic variability, as in the case of circadian rhythms (26, 27), or it can play a supportive role as a mechanism that amplifies the effects of random fluctuations. Along these lines, it is interesting to note that our model can be used to demonstrate that the “noise signature” of a system dominated by delay can be similar to a system dominated by intrinsic noise (Fig. 5*D*). This result implies that care must be taken in attributing variability to purely stochastic sources, because delay-induced variability can appear empirically similar to fluctuations arising from intrinsic noise.

Pragmatically, models that use delay could be essential in understanding whole-genome regulation, because it is unrealistic to construct models that incorporate the numerous sequences of biochemical reactions that underlie the complexities of transcribing and translating a single gene. Time-delayed reactions have long been utilized as a natural approximation for the modeling of such a complex sequence of events. This reduction comes at a high cost, because analytical and numerical techniques are more difficult, and there has been little work addressing the coupling of intrinsic noise in biochemical reactions with delay. In this regard, our results provide a framework for analyzing and simulating the interplay of noise and delay. Along the same lines, the generalization of the Gillespie algorithm provided in our work should prove highly useful because large-scale simulation techniques that incorporate time delays should lead to new insights in describing the dynamics of complex gene regulatory networks.

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Supporting Text

Model I: Delayed Protein Degradation

Deterministic Description.

The deterministic dynamics of this system in the rate approximation is described by the following linear delay-differential equation:

$$\frac{dx}{dt} = A - Bx(t) - Cx(t - \tau). \quad [1]$$

It is straightforward to analyze the onset of periodic oscillations in this system. This system has one fixed point $x^* = A/(B + C)$ whose stability determines the transition to oscillations. We look for a solution $x(t)$ in the form $x(t) \sim e^{\lambda t}$, where the eigenvalues are the solutions of

$$(\lambda + B)e^{\lambda\tau} + C = 0. \quad [2]$$

We set $\lambda = \mu + i\omega$. To solve Eq. **2**, we use the Lambert function $W(z)$, which by definition satisfies $W(z)e^{W(z)} = z$

$$\mu = \frac{1}{\tau} \text{Re}(W(-\tau C e^{\tau B})) - B, \quad [3]$$

$$\omega = \frac{1}{\tau} \text{Im}(W(-\tau C e^{\tau B})). \quad [4]$$

By solving Eqs. **3** and **4** for $\mu = 0$ and $\omega \neq 0$ we find the condition for Hopf bifurcation discussed in the main text.

Stochastic Description

Denote $P(n, t)$ as the probability of having n monomers at time t . Then the master equation for $P(n, t)$ can be written as

$$\begin{aligned} \frac{dP(n, t)}{dt} &= A(P(n-1, t) - P(n, t)) + B((n+1)P(n+1, t) - nP(n, t)) \\ &+ C \sum_{m=0}^{\infty} m(P(n, t; m, t-\tau) - \Theta_n P(n, t; m, t-\tau)), \quad n = 0.. \infty, \end{aligned} \quad [5]$$

where $P(n, t; m, t-\tau)$ is the joint probability of having n molecules at time t and m molecules at time $t-\tau$ and the multiplier

$$\Theta_n = \begin{cases} 0, & n = 0 \\ 1, & n > 0 \end{cases}, \quad [6]$$

is added to account for the fact that $P(n, t), P(n, t; m, t-\tau)$ should remain zero for negative n .

Assume that the time delay τ is large compared with other characteristic times of the system, so the events at time t and $t-\tau$ are effectively decoupled, then

$$P(n, t; m, t-\tau) = P(n, t)P(m, t-\tau). \quad [7]$$

Adopting this approximation, we get

$$\begin{aligned} \frac{dP(n, t)}{dt} &= A(P(n-1, t) - P(n, t)) + B((n+1)P(n+1, t) - nP(n, t)) \\ &+ C \sum_{m=0}^{\infty} mP(m, t-\tau) (P(n+1, t) - \Theta_n P(n, t)), \\ &= A(P(n-1, t) - P(n, t)) + B((n+1)P(n+1, t) - nP(n, t)) \\ &+ C \langle n(t-\tau) \rangle (P(n+1, t) - \Theta_n P(n, t)), \quad n = 0.. \infty. \end{aligned} \quad [8]$$

By definition, the autocorrelation function for a random process characterized by $n(t)$ is given by

$$K(T) = \langle n(t)n(t+T) \rangle - \langle n(t) \rangle^2 \quad [9]$$

$$= \sum_{n=0}^{\infty} \sum_{n'=0}^{\infty} nn' P(n, t; n', t+T) - \left[\sum_{n=0}^{\infty} n P_s(n) \right]^2, \quad [10]$$

For a stationary random process, the joint probability density $P(n, t; n', t + T)$ can be written in the following as

$$P(n, t; n', t + T) = P_s(n)P_c(n', T|n, 0), \quad [11]$$

where $P_s(n)$ is the stationary probability, and P_c is the conditional probability for the sample path to pass through the point n' at time $t = T$, given that it passes through n at time $t = 0$. By inserting Eq. 11 into Eq. 10, we obtain the stationary correlation function

$$K(T) = \sum_{n=0}^{\infty} n P_s(n) \langle n', T|n, 0 \rangle - \langle n \rangle^2. \quad [12]$$

The calculation of the correlation function is done in three steps: (i) calculate the conditional mean value of $n(T)$ given $n(0)$, $\langle n', T|n, 0 \rangle$, (ii) find the stationary probability density $P_s(n)$, and (iii) take the sum. Generating functions are particularly useful here. The generating function $G(s, t)$ is defined as

$$G(s, t) = \sum_{n'=0}^{\infty} s^{n'} P(n', t|n, 0). \quad [13]$$

We convert the infinite set of ordinary differential equations 8 to a single partial differential equation for $G(s, t)$

$$\frac{\partial G}{\partial t} = (s - 1) \left(AG(t) - B \frac{\partial G(t)}{\partial s} + C \frac{\langle n(t - \tau) \rangle}{s} (P_0(t) - G(t)) \right). \quad [14]$$

Our numerical simulations show that for a large mean number of molecules, $P_0(t)$ is small and can be neglected in Eq. 14.

The moments of the probability distribution can be found by expanding the generating function near $s = 1$

$$\frac{\partial G}{\partial s} \Big|_{s=1} = \sum_{n'=0}^{\infty} n' s^{n'-1} P(n', t|n, 0) \Big|_{s=1} = \sum_{n'=0}^{\infty} n' P(n', t|n, 0) = \langle n', t|n, 0 \rangle, \quad [15]$$

$$\begin{aligned} \frac{\partial^2 G}{\partial s^2} \Big|_{s=1} &= \sum_{n'=0}^{\infty} n'(n' - 1) s^{n'-2} P(n', t|n, 0) \Big|_{s=1} = \\ &= \sum_{n'=0}^{\infty} n'(n' - 1) P(n', t|n, 0) = \langle n'^2, t|n, 0 \rangle - \langle n', t|n, 0 \rangle. \end{aligned} \quad [16]$$

(only first and second moments are needed). Substituting the expansion

$$G(s-1, t) = 1 + (s-1)\alpha(t) + \frac{1}{2}(s-1)^2\beta(t) + \dots \quad [17]$$

into Eq. 14 we obtain

$$\frac{d\alpha}{dt} = A - B\alpha(t) - C\alpha(t-\tau), \quad [18]$$

$$\frac{1}{2} \frac{d\beta}{dt} = A\alpha(t) - C\alpha(t-\tau) - B\beta(t) + C\alpha(t)\alpha(t-\tau), \quad [19]$$

where the functions $\alpha(t)$ and $\beta(t)$ are Eqs. 15 and 16, respectively. As expected, the equation for mean 18 coincides with Eq. 1, which was obtained within that rate equation approximation. Note that since the autocorrelation function has to be symmetric with respect to the transformation $T \rightarrow -T$, we have to impose an additional symmetry condition $\alpha(t) = \alpha(-t)$ on the solution of Eq. 18. Since it is linear, it can be readily solved with initial condition $\alpha(0) = n$

$$\alpha(t) \equiv \langle n', t | n, 0 \rangle = (n-1) \frac{\sigma(t)}{1 - \zeta e^{-\lambda\tau}} + \left(1 - \frac{A}{B+C}\right) \frac{\sigma(t)}{1 - \zeta e^{-\lambda\tau}} + \frac{A}{B+C}, \quad [20]$$

where

$$\sigma(T) = \begin{cases} e^{-\lambda T} - \zeta e^{\lambda(T-\tau)}, & 0 < T < \tau \\ e^{-B(T-N\tau)}(\sigma(N\tau) - C \int_{N\tau}^T \sigma(T' - \tau) e^{B(T'-N\tau)} dT'), & N\tau < T < (N+1)\tau. \end{cases}$$

$$\lambda = \sqrt{B^2 - C^2}, \quad \zeta = \frac{1}{C}(B - \lambda). \quad [21]$$

The solution of Eqs. 20 and 21 exists if $B > C$, i.e. below the deterministic Hopf bifurcation. The solution for $B < C$ can be derived but it is not as interesting since the amplitude of the oscillations grows without bound.

Substituting Eq. 20 into Eq. 12 we find that only the first two moments of the stationary distribution are needed. The stationary solution for G is derived from Eq. 14:

$$G_s(s) = s^{-\frac{C}{B}\langle n \rangle_s} e^{\frac{A}{B}(s-1)}, \quad [22]$$

where $\langle n \rangle_s$ denotes the stationary mean: $\langle n \rangle_s = \langle n(t \rightarrow \infty) \rangle$ and normalization $G_s(1) = 1$ has been taken into account.

From Eq. **22** we obtain the stationary moments of the distribution

$$\frac{dG_s}{ds}\Big|_{s=1} = \frac{d}{ds} s^{-\frac{C}{B} \langle n \rangle_s} e^{\frac{A}{B}(s-1)}\Big|_{s=1} = \frac{A}{B+C}, \quad [23]$$

$$\frac{d^2G_s}{ds^2}\Big|_{s=1} = \frac{d^2}{ds^2} s^{-\frac{C}{B} \langle n \rangle_s} e^{\frac{A}{B}(s-1)}\Big|_{s=1} = \frac{A(AB+BC+C^2)}{B(B+C)^2} \quad [24]$$

and insert them, along with Eq. **20**, into Eq. **12**. We obtain

$$\begin{aligned} K(T) &= \frac{\sigma(T)}{1-\zeta e^{-\lambda\tau}} \sum_{n=0}^{\infty} n(n-1)P_s(n) + \left(1 - \frac{A}{B+C}\right) \frac{\sigma(T)}{1-\zeta e^{-\lambda\tau}} \sum_{n=0}^{\infty} nP_s(n) = \\ &= \frac{\sigma(T)}{1-\zeta e^{-\lambda\tau}} \frac{d^2G_s(s)}{ds^2}\Big|_{s=1} + \frac{B+C-A}{B+C} \frac{\sigma(T)}{1-\zeta e^{-\lambda\tau}} \frac{dG_s(s)}{ds}\Big|_{s=1} = \frac{A}{B} \frac{\sigma(T)}{(1-\zeta e^{-\lambda\tau})}, \end{aligned} \quad [25]$$

where $T = N\tau + t$.

After calculating the auto-correlation function, we proceed with the power spectrum $S(\omega)$ of the system and obtain

$$S(\omega) = 2\frac{A}{B} \operatorname{Re} \frac{1 - Ce^{i\omega\tau} I(\omega)}{B + Ce^{i\omega\tau} - i\omega}, \quad [26]$$

where

$$I(\omega) = \frac{B}{A} \int_0^\tau K(T) e^{i\omega T} dT = \frac{1}{1-\zeta e^{-\lambda\tau}} \left(\frac{1 - e^{-(i\omega+\lambda)\tau}}{i\omega + \lambda} + \zeta e^{-\lambda\tau} \frac{1 - e^{-(i\omega-\lambda)\tau}}{i\omega - \lambda} \right). \quad [27]$$

Comparison of Analytical and Numerical Results

In applying the numerical technique described in the main text, it is convenient to calculate the auto-correlation function using

$$K(T) = \lim_{t \rightarrow \infty} \frac{1}{t} \int_0^t n(t') n(t' + T) dt' - \left[\lim_{t \rightarrow \infty} \frac{1}{t} \int_0^t n(t') dt' \right]^2. \quad [28]$$

Given the ergodic properties of the system, this method is equivalent to Eq. **10**. The power spectrum $S(\omega)$ of the system has been calculated by numerical integration of Eq. **28**, using $S(\omega) = 2 \int_0^\infty K(T) \cos(\omega T) dT$.

Model II: Negative Feedback with Delayed Production

Deterministic Description

The deterministic rate equations corresponding to reactions **11** and **12** in the main text read

$$\frac{dx}{dt} = As(t - \tau) - Bx(t), \quad [29]$$

$$\frac{ds}{dt} = k_{-1} - k_{-1}s(t)(1 + \varepsilon x(t)), \quad [30]$$

where $\varepsilon = k_1/k_{-1}$. This system has only a positive stationary solution:

$$x^* = \frac{1}{2\varepsilon} \left(\sqrt{1 + 4\varepsilon \frac{A}{B}} - 1 \right). \quad [31]$$

We can show that this solution is always stable, so the system does not possess a Hopf bifurcation.

By linearizing Eqs. **29** and **30** near **31**, and looking for a solution of the form $x \sim e^{\lambda t}$ we obtain

$$\lambda^2 + (B + 1 + \varepsilon x^*)\lambda + \varepsilon B + \varepsilon \frac{A}{1 + \varepsilon x^*} e^{-\lambda\tau} = 0. \quad [32]$$

This equation has no solution for $\lambda = 0$, and so the transcritical Hopf bifurcation cannot occur. Let us check for a Hopf bifurcation when $\lambda = i\omega$. By inserting this into Eq. **32** we obtain two transcendental equations

$$\begin{aligned} -\omega^2 + (1 + \varepsilon x^*)B + \frac{\varepsilon A}{1 + \varepsilon x^*} \cos(\omega\tau) &= 0, \\ B + 1 + \varepsilon x^* - \frac{\varepsilon A}{1 + \varepsilon x^*} \sin(\omega\tau) &= 0, \end{aligned} \quad [33]$$

whose solvability condition yields

$$\omega^2 = \frac{1}{2} \left(-B^2 - (1 + \varepsilon x^*)^2 + \sqrt{(B^2 + (1 + \varepsilon x^*)^2)^2 - 4B^2(1 + \varepsilon x^*)^2 + 4\frac{\varepsilon^2 A^2}{(1 + \varepsilon x^*)^2}} \right). \quad [34]$$

The solution exists only if

$$B^2(1 + \varepsilon x^*)^2 < \frac{\varepsilon^2 A^2}{(1 + \varepsilon x^*)^2}. \quad [35]$$

By inserting Eq. **31** into Eq. **35** we arrive at the following inequality:

$$A > A + \frac{B}{2\varepsilon} \left(1 + \sqrt{1 + 4\varepsilon \frac{A}{B}} \right), \quad [36]$$

We see that for $B > 0, \varepsilon > 0$, this Hopf bifurcation cannot occur either. Thus, the system is linearly stable for any values of the parameters.

Stochastic Description

We introduce two probabilities, $P_n^0(t)$ and $P_n^1(t)$, for the number of proteins to be equal to n at time t and for the state of the operator at time $t - \tau$ to be D_0 or D_1 , respectively. Then the master equations for the reactions **11** and **12** in the main text have the form

$$\begin{aligned} \frac{dP^0(n, t)}{dt} &= A(P^0(n-1, t) - P^0(n, t)) + B((n+1)P^0(n+1, t) - nP^0(n, t)) - \\ &\quad - k_1 \sum_{m=0}^{\infty} m[(P^0(m, t-\tau) + P^1(m, t-\tau)]P^0(n, t) + k_{-1}P^1(n, t), \\ \frac{dP^1(n, t)}{dt} &= B((n+1)P^1(n+1, t) - nP^1(n, t)) + \\ &\quad + k_1 \sum_{m=0}^{\infty} m[(P^0(m, t-\tau) + P^1(m, t-\tau)]P^0(n, t) - k_{-1}P^1(n, t). \end{aligned} \quad [37]$$

Again, we have made the assumption that the processes at times t and $t - \tau$ are weakly correlated, and to first approximation the two-point probability distribution functions $P(n, t; m, t - \tau) \approx P(n, t)P(m, t - \tau)$. To calculate the correlation function we again utilize generating functions. We introduce two generating functions

$$G_i(s, t) = \sum_{n=0}^{\infty} s^n P_n^i(t), \quad i = 1, 2, \quad [38]$$

which correspond to the two operator states. Their sum gives the full generating function $G(s, t) = G_0(s, t) + G_1(s, t)$. Then the equations are given by

$$\begin{aligned}\frac{\partial G_0}{\partial t} &= (s-1) \left(AG_0 - B \frac{\partial G_0}{\partial s} \right) - k_1 \langle n(t-\tau) \rangle G_0 + k_{-1} G_1, \\ \frac{\partial G_1}{\partial t} &= -(s-1) B \frac{\partial G_1}{\partial s} + k_1 \langle n(t-\tau) \rangle G_0 - k_{-1} G_1.\end{aligned}\quad [39]$$

Let us introduce the hierarchy of marginal moments

$$M_i^0(t) = \sum_{n=0}^{\infty} n^i P_n^0(t), \quad M_i^1(t) = \sum_{n=0}^{\infty} n^i P_n^1(t).\quad [40]$$

The zeroth moments $M_0^s(t)$ characterize the probabilities to find the operator in an unoccupied/occupied state at time $t - \tau$ ($M_0^0(t) + M_0^1(t) = 1$), and the first moments $M_1^s(t)$ characterize the mean number of proteins at time t given the state s of the operator at time $t - \tau$. Hence,

$$M_1^0(t) + M_1^1(t) \equiv \alpha(t) = \langle n(t) \rangle.$$

The equations for the zeroth moment M_0^0 read

$$\frac{dM_0^0}{dt} = k_{-1} - (k_1 \alpha(t-\tau) + k_{-1}) M_0^0.\quad [41]$$

The equations for the first moments read

$$\begin{aligned}\frac{dM_1^0}{dt} &= AM_0^0 - BM_1^0 - k_1 \alpha(t-\tau) M_1^0 + k_{-1} M_1^1, \\ \frac{dM_1^1}{dt} &= BM_1^1 + k_1 \alpha(t-\tau) M_1^0 - k_{-1} M_1^1.\end{aligned}\quad [42]$$

Summing these, we obtain

$$\frac{d\alpha}{dt} = AM_0^0 - B\alpha(t).\quad [43]$$

As before, the equations for the nonstationary mean number of proteins $\alpha(t)$ and the probability to find the operator in the unoccupied state $s(t)$ coincide with Eqs. **29** and **30**, which were obtained directly within the deterministic description.

To proceed further we simplify the system by assuming that operator fluctuations are much faster than protein transcription and degradation. Then the operator state s reaches equilibrium much faster than the protein concentration, and we write

$$M_0^0 \approx \frac{1}{1 + \varepsilon\alpha(t - \tau)}, \quad [44]$$

and obtain

$$\frac{d\alpha}{dt} = \frac{A}{1 + \varepsilon\alpha(t - \tau)} - B\alpha(t). \quad [45]$$

Unfortunately, Eq. 45 has no general analytical solution. We can solve it approximately for $\varepsilon \ll 1$. Under this approximation, Eq. 45 reads

$$\frac{d\alpha}{dt} = A - B\alpha(t) - A\varepsilon\alpha(t - \tau). \quad [46]$$

The solution of Eq. 46 was obtained above (sf. Eqs. 20 and 21). The fixed point of Eq. 46 gives the stationary mean value $\langle n \rangle_s = A/(B + \varepsilon A)$. Given the linearity of Eq. 46, only the two first moments of the stationary probability distribution $P_s(n)$ are required to compute the autocorrelation function.

The stationary solution of Eqs. 39 is described by the equations

$$\frac{B}{A} \frac{dG^s}{d\gamma} = G_0^s, \quad [47]$$

$$B\gamma \frac{d^2 G_0^s}{d\gamma^2} + (\delta_1 - A\gamma) \frac{dG_0^s}{d\gamma} - \delta_2 G_0^s = 0, \quad [48]$$

where $\gamma \equiv s - 1$, $\delta_1 \equiv B + k_1 \langle n \rangle_s + k_{-1}$, $\delta_2 \equiv A(1 + k_{-1}/B)$. In fact, we do not need the complete solution of Eqs. 39. Rather we need to compute the first and second derivatives of G^s at $\gamma = 0$, as was shown in previous section (see Eqs. 23 and 24). To find the value of $dG_0^s/d\gamma$ at $\gamma = 0$, we apply the Frobenius method to Eq. 48. The solution of $G_0^s(\gamma)$ can be written as

$$G_0^s(\omega) = \sum_{m=0}^{\infty} a_m \gamma^{\mu+m}, \quad [49]$$

where μ and a_m are to be determined. By substituting it in Eq. 48, we obtain

$$a_0\mu(B(\mu - 1) + \delta_1) = 0,$$

$$a_{m+1} = a_m \frac{A(\mu + m) + \delta_2}{(\mu + m + 1)(B(\mu + m) + \delta_1)}.$$

It is evident that $a_0 \neq 0$ and $\mu = 0$. In this case

$$\frac{dG_0^s}{d\gamma}|_{\gamma=0} = a_1 = a_0 \frac{\delta_2}{\delta_1} = \frac{A(B + k_{-1})}{((B + k_{-1})(B + \varepsilon A) + k_1 A)}. \quad [50]$$

Thus, the derivatives are

$$\frac{dG^s}{ds}|_{s=1} = \frac{A}{B} G_{s0}|_{s=1} = \langle n \rangle_s, \quad [51]$$

$$\frac{d^2 G^s}{ds^2}|_{s=1} = \frac{A}{B} \frac{dG_{s0}}{ds}|_{s=1} = \frac{A^2(B + k_{-1})}{B((B + k_{-1})(B + \varepsilon A) + k_1 A)}. \quad [52]$$

We next proceed to the calculation of the auto-correlation function. Substituting the solution of Eq. 46 and Eqs. 51 and 52 into Eq. 12, we obtain

$$K(T) = \frac{\sigma(T)}{1 - \zeta e^{-\lambda\tau}} \frac{d^2 G_s}{ds^2}|_{s=1} + \left(1 - \frac{A}{B + \varepsilon A}\right) \frac{\sigma(T)}{1 - \zeta e^{-\lambda\tau}} \frac{dG_s}{ds}|_{s=1} =$$

$$= \left(\frac{A^2(B + k_{-1})}{B((B + k_{-1})(B + \varepsilon A) + k_1 A)} + \frac{A(B + \varepsilon A - A)}{(B + \varepsilon A)^2} \right) \frac{\sigma(T)}{1 - \zeta e^{-\lambda\tau}},$$

with the same $\sigma(T)$ as in Eq. 21.

Transient Behavior

The delayed feedback does not change the stationary state of the system, but it affects strongly its transient behavior. As an example, we show here the response of the negative feedback model with dimerization to a sudden change of one of the system parameters (degradation rate B). A comparison of the stochastic dynamics of the system without (Fig. 1A) and with (Fig. 1B) time delay demonstrates that the transition to a new fixed point in the delayed system is accompanied by significant stochastic oscillations, whereas the nondelayed system exhibit a more rapid nonoscillatory transition.

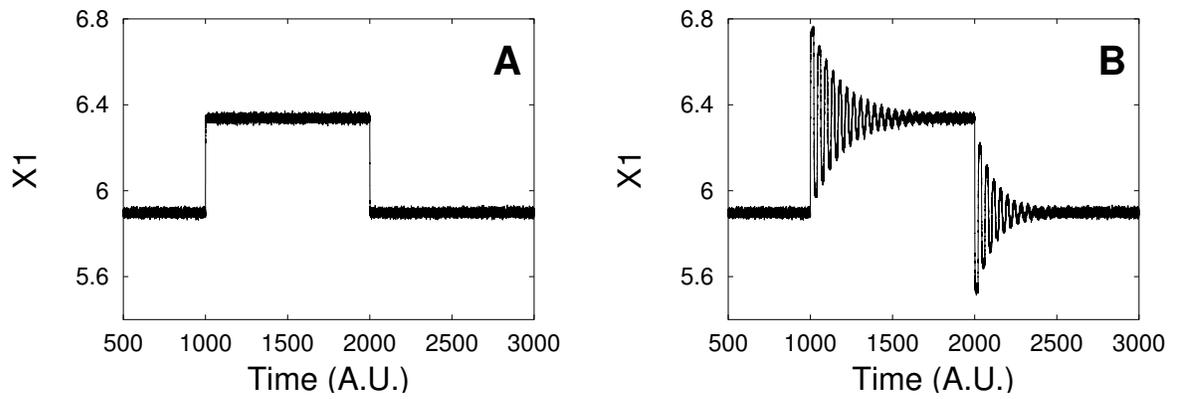


Figure 1: Time series obtained in stochastic simulations without (A) and with (B) delay. In both cases the sudden decrease of the degradation rate from $B = 4$ to $B = 3.5$ was applied in the range $1000 < t < 2000$. The trajectories are averaged over 100 samples. The fixed parameters are $A = 40$, $\tau = 20$, $k_1 = 100$, $k_{-1} = 1000$, $k_2 = 200$, $k_{-2} = 1000$.