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# Scalable ultra-sensitive detection of heterogeneity via coupled bistable dynamics

KAMAL P. SINGH<sup>(a)</sup>, RAJEEV KAPRI<sup>(b)</sup> and SUDESHNA SINHA<sup>(c)</sup>

*Indian Institute of Science Education and Research (IISER) Mohali - SAS Nagar, Sector 81,  
Mohali 140 306, Punjab, India*

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**Abstract** – We demonstrate how the collective response of  $N$  globally coupled bistable elements can strongly reflect the presence of very few non-identical elements in a large network of otherwise identical elements. Counter-intuitively, when there are a small number of elements with natural stable state different from the bulk of the elements, *all* the elements of the system evolve to the stable state of the minority due to strong coupling. The critical fraction of distinct elements needed to produce this swing shows a sharp transition with increasing  $N$ , scaling as  $1/\sqrt{N}$ . Furthermore, one can find a global bias that allows robust *one-bit* sensitivity to heterogeneity. Importantly, the time needed to reach the attracting state does not increase with the system size. We indicate the relevance of this ultra-sensitive generic phenomenon for massively parallelized applications, such as the determination of the existence of a “needle in a haystack” by one measurement.

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The complex interactive systems modelling spatially extended physical, chemical and biological phenomena, has commanded intense research effort in recent years. One of the important issues in such systems is the effect of heterogeneity on spatiotemporal patterns. The role of disorder, such as static or quenched inhomogeneities, and the effect of coherent driving forces, has yielded a host of interesting, often counter-intuitive, behaviours. For instance, stochastic resonance [1] in coupled arrays [2], diversity-induced resonant collective behaviour in ensembles of coupled bistable or excitable systems [3] demonstrated how the response to a sub-threshold input signal is optimized. However, the potential of coupled systems for parallel information processing remains largely unexplored. It is our aim to show the existence of an ultra-sensitive regime of  $N$ -coupled bistable elements whereby small heterogeneity in the system strongly influences its global dynamics.

Here we consider  $N$ -coupled nonlinear systems, where the evolution of the element  $i$  ( $i = 1, \dots, N$ ) is given by

$$\dot{x}_i = F(x_i) + a_i + C(\langle x \rangle - x_i) + b, \quad (1)$$

where  $C$  is the coupling strength,  $b$  is a small global bias, and the mean field  $\langle x \rangle$  [4] is given by

$$\langle x \rangle = \frac{1}{N} \sum_{i=1, N} x_i. \quad (2)$$

The function  $F(x)$  is nonlinear and yields a bistable potential. Specifically, we consider  $F(x) = x_i - x_i^3$ , which gives rise to a double-well potential, with one well centered at  $x_-^* = -1$  (lower well) and another at  $x_+^* = +1$  (upper well).

We consider a situation where  $a_i$  can take either of two sufficiently different values,  $A_0$  and  $A_1$ . With no loss of generality, we set  $A_0 = 0$  and  $A_1 = 1$ , *i.e.*  $a_i$  of the elements  $i = 1, \dots, N$ , can be 0 or 1. The initial conditions on  $N$  elements here are taken to be randomly distributed about zero mean, and in our simulations a very large number of initial states ( $\sim 10^4$ ) are sampled in different trial runs. In order to quantify what fraction of elements have  $a_i = 0$ , we use the following notation:  $N_0$  is the number of elements with  $a_i = 0$ , and  $N_1 = N - N_0$  is the number of elements with  $a_i = 1$ . The principal question is how sensitive to small inhomogeneity collective dynamical features are, such as the ensemble average  $\langle x \rangle$ , which can be considered as the *output* of the system (see fig. 1(a)).

<sup>(a)</sup>E-mail: kpsingh@iisermohali.ac.in

<sup>(b)</sup>E-mail: rkapri@iisermohali.ac.in

<sup>(c)</sup>E-mail: sudeshna@imsc.res.in; sudeshna@iisermohali.ac.in

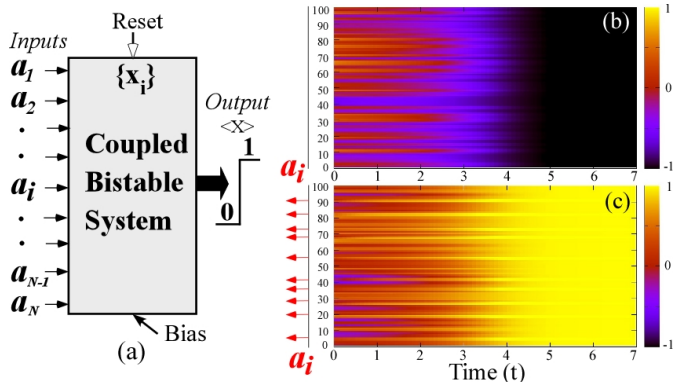


Fig. 1: (Colour on-line) (a) Schematics of coupled nonlinear system with  $N$  inputs, output, bias, and reset for initial conditions. (b) Time evolution of an array of 100 strongly coupled ( $C=1$ ) bistable elements having *all*  $a_i = 0$  in eq. (1), and (c) having 10 elements with  $a_i = 1$  (denoted by arrows) and 90 elements with  $a_i = 0$ .

The values  $A_0$ ,  $A_1$  and bias  $b$  are such that in an uncoupled system, when  $a_i = A_0$ , the system goes rapidly to the lower well  $x_-^* \sim -1$ , while the system with  $a_i = A_1$  is attracted to the upper well  $x_+^* \sim 1$ . When all  $a_i = A_0$ , we have a homogeneous system, and this uniform system is naturally attracted to the lower well  $x_-^*$ . One may wonder, how many  $a_i$  need to be different from 0 in order to make a significant difference in the collective output.

Intuitively, one may expect that the global average will pick up contributions of order  $1/N$  from each element. So a fairly large number of elements need to be different in order to obtain significant deviation in the mean field and drive a different collective response. Alternately, for strong coupling, one may think, for small heterogeneity, the majority of the elements will dictate the nature of the collective field, as the minority should synchronize with the majority population.

However, we will show here that both the expectations above do not hold true. Instead, this system, under sufficiently strong coupling, will evolve to the stable state of the *minority population*. Furthermore, the critical number of elements distinct from the bulk that is needed for this effect, is typically less than  $O(\sqrt{N})$ , and can actually be made as small as *one*.

Figure 1(b) shows the evolution of 100 globally coupled elements, with coupling constant  $C=1$ , to the *lower* well from Gaussian random initial conditions, in the homogeneous case where all  $a_i=0$ . In sharp contrast, fig. 1(c) shows all the elements of the network being attracted to the *upper* well, when a few elements have  $a_i=1$ . So it is clearly evident that even when very few  $a_i$ 's are different from 0, the entire network is pushed to the upper well.

So the collective field sensitively reflects very small deviations from uniformity. In fact, the response to small diversity is a swing from the lower well to the upper one,

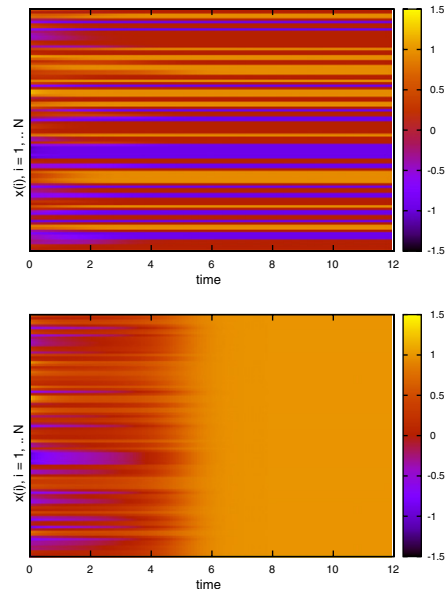


Fig. 2: (Colour on-line) Time evolution of an array of 100 coupled bistable elements having one  $a_i = 1$  in eq. (1) and the rest 0, with coupling strength  $C=0.1$  (top) and  $C=1$  (bottom). Here bias  $b$  is  $-0.0005$  in both cases.

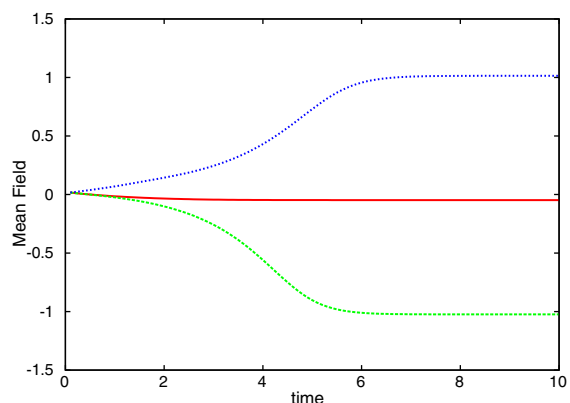


Fig. 3: (Colour on-line) Time evolution of the mean field  $\langle x \rangle$  of a network of 1000 coupled bistable elements for the cases of: i)  $C=0.1$ ,  $N_1/N=0.1$  (red solid line); ii)  $C=1$ ,  $N_1/N=0$  (green dashed line); and iii)  $C=1$ ,  $N_1/N=0.1$  (blue dotted line). Here bias  $b$  is  $-0.05$  in all cases.

for *all* elements in the system. The coupled system then acts like a sensitive detector, as its response to few  $a_i = 1$ , in an otherwise uniform lattice of  $a_i = 0$ , is very large.

Coupling is crucial in this effect. In a weakly coupled system, when a few  $a_i$  are different, the difference in the mean field of the homogeneous and inhomogeneous systems will be proportional to  $N_1/N$ . However, the response of the strongly coupled system to small  $N_1$  is very large (namely  $\sim (x_+^* - x_-^*)$ ) (see figs. 2, 3).

In order to quantify the sensitivity of the collective response, we calculate the minimum  $N_1$  needed to flip the output to the upper well (within a small prescribed accuracy). We call this the *critical population*  $N_{1c}$ .

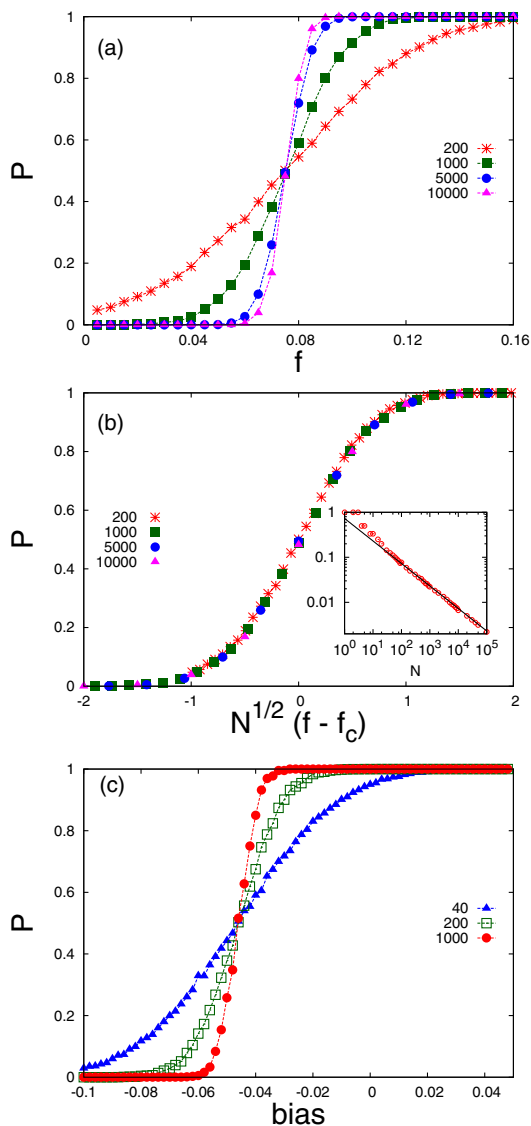


Fig. 4: (Colour on-line) (a) Probability,  $P$ , that all the elements evolve to the upper well, from random initial conditions, as a function of fraction  $f = N_1/N$  for different system sizes. Here bias  $b = -0.05$ , coupling constant  $C = 1$ , and averaged over 10000 runs. (b) Data collapse of probability  $P$  for various  $N$  as obtained by scaling the  $x$ -axis by  $N^{1/2}(f - f_c)$ , indicates that  $f_c$  is  $0.075 \pm 0.001$  for this bias. Inset: scaling of  $f - f_c$  with respect to  $N$ , where  $f$  is the fraction at which  $P \sim 1$ ; solid line:  $1/\sqrt{N}$  fit. (c)  $P$  vs. global bias  $b$ , for different system sizes, with  $f = N_1/N = 0.075$ .

Figure 4 displays the collective response to very small inhomogeneity under varying system size  $N$  and global bias  $b$ . In fig. 4(a), we show the probability,  $P$ , that all the oscillators evolve to the upper well, as a function of  $f = N_1/N$  for different system sizes for a bias  $b = -0.05$  and coupling constant  $C = 1$ . The figure shows that there is a critical fraction above which all the oscillators switch to the upper well. The switching becomes sharper and sharper as the system size increases. To obtain the critical population,  $N_{1c}$  in the large  $N$  limit, we use the finite

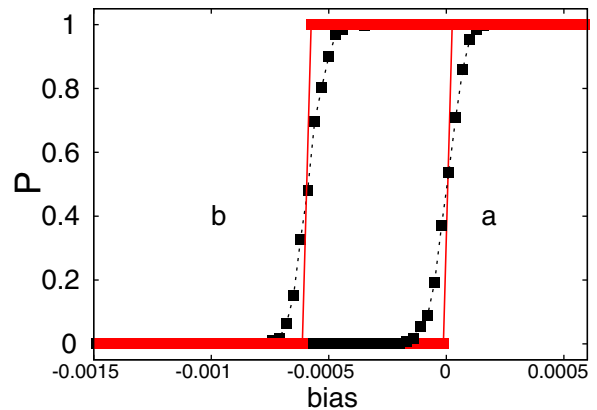


Fig. 5: (Colour on-line) Probability,  $P$ , that all the oscillators evolve to the upper well as a function of global bias, for a system of 1000 elements: curve (a) with no  $a_i = 1$ , namely  $f = N_1/N = 0$  and curve (b) with just *one* element with  $a_i = 1$ , namely  $f = N_1/N = 0.001$ . The red (solid) line shows the deterministic case with all initial  $x = 0$ . The black (dashed) curve shows the evolution from an initial system with states drawn from a Gaussian distribution, with small standard deviation ( $\sim 0.01$ ), centered around zero. Here coupling strength  $C = 1$ .

size scaling. For a given bias and coupling constant, the probability  $P$  satisfies the following scaling form:

$$P \sim \mathcal{G}(N^\phi(f - f_c)), \quad (3)$$

where  $f_c = N_{1c}/N$  when  $N \rightarrow \infty$ ,  $\phi$  is the critical exponent and  $\mathcal{G}$  is the scaling function. A good data collapse, shown in fig. 4(b), is obtained for  $\phi = 1/2$  indicating that

$$|f - f_c| \sim \frac{1}{\sqrt{N}} \Rightarrow |N_1 - N_{1c}| \sim \sqrt{N}. \quad (4)$$

A similar transition is observed under varying bias  $b$ , as displayed in fig. 4(c).

Clearly then, the minority population can pull the strongly coupled bistable system to a final state distinct from the homogeneous case, under suitable bias. Now, one may wonder if the fundamental one-bit detection limit can be achieved in our system. In fig. 5, we show how a large system,  $N = 1000$ , responds to only *one* distinct element in the array. It demonstrates that there exists a range of global bias which allows the system to yield  $P = 0$  for  $N_1 = 0$  and  $P = 1$  when  $N_1 = 1$ . So by tuning the global bias we can obtain a system where a single  $a_i = 1$  can draw the whole system to the upper well.

Specifically then, in the representative example displayed in fig. 6, in a lattice of 100 elements, when all  $a_i = 0$  the mean field is  $\sim -1$ , reflecting the fact that all elements go to the lower well, as expected. However, when *one* of the  $a_i$  is 1 (*i.e.*  $N_1 = 1, N_0 = 99$ ), the mean field evolves to  $\sim 1$ , reflecting the fact that all elements have been attracted to the upper well now, driven by this one different element. So even though only one element in the network would have evolved to the upper well in the uncoupled case, when strongly coupled, all 100 elements are dragged rapidly to the upper well.

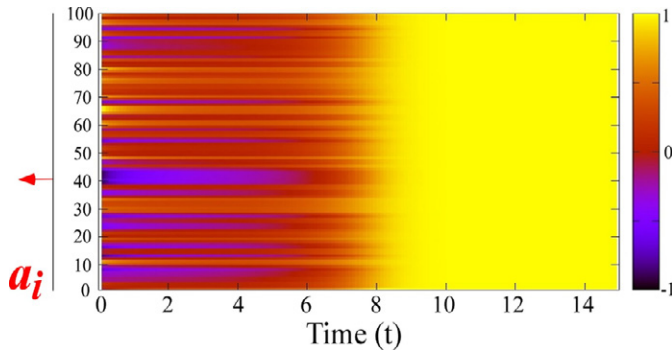


Fig. 6: (Colour on-line) Time evolution of the elements in the array of size  $N = 100$ , where only one element has  $a_i = 1$  (denoted by arrow) and 99 elements have  $a_i = 0$ . Here coupling strength  $C = 1$  and bias  $b = -0.05$ .

One can analyze the dynamics by considering the random fluctuations of  $\langle x \rangle$  about the true thermodynamic average  $x_{av}$  ( $\sim 0$ ), which leads to the following effective dynamics of each element:

$$\begin{aligned} \dot{x}_i &= (1 - C)x_i - x_i^3 + a_i + b + Cx_{av} + D\eta \quad (5) \\ &= F_{eff}(x_i) + D\eta, \end{aligned}$$

where  $\eta$  is unit variance Gaussian noise with strength  $D = C/\sqrt{N}$ . The probability  $P(x)$  of obtaining the system in state  $x$  for the elements, can be analyzed by solving for the steady-state distribution arising from the relevant Fokker Planck equation, namely  $P(x) = A \exp(-2\phi(x)/D)$ , where  $A$  is a normalization constant and  $-\partial\phi(x)/\partial x = F_{eff}(x)$  [5]. Using this we verify that the uncoupled symmetric case, *i.e.* with  $C = 0$  and  $b = 0$ , yields the following: elements with  $a_i = 0$  yield equal probability of residence in either of the two wells (centered around 1 and  $-1$ ), and for elements with  $a_i = 1$  the probability  $P(x)$  shifts entirely to the upper well ( $\sim 1$ ). When there is no coupling or very weak coupling, this is indeed the case in our simulations as well.

However, for strong coupling ( $C \sim 1$ ), we have a very different scenario: when all  $a_i = 0$  (with  $N \rightarrow \infty$ ) and even the slightest negative bias,  $P(x)$  peaks sharply in a well with  $x < 0$ . That is, the entire system is synchronized and attracted to the lower well. Contrast this to the unsynchronized situation in weak coupling, where the elements go to either upper or lower well depending on their initial state. Similarly, for strong coupling, even a slightly positive bias drives all the elements to the upper well.

Now consider the strong-coupling case with a few  $a_i = 1$ . The elements with  $a_i = 1$  have  $P(x)$  centered sharply at a well  $\sim 1$  (as  $a_i$  acts as a positive bias). As these  $N_1$  elements evolve to the upper well,  $x_{av}$  becomes slightly positive, and even elements with  $a_i = 0$  experience a positive bias:  $b + Cx_{av} > 0$ , which shifts  $P(x)$  entirely to a well at  $x > 0$ . Following the small initial positive push, there is a strong positive feedback effect that drives the  $x_{av}$  to more and more positive values, and consequently the stable attracting well shifts rapidly towards  $\sim x_+^*$ .

One can also rationalize this mechanism intuitively as follows: when the initial system has  $x \sim 0$ , namely the system is poised on the “barrier” between the two wells, the state is tipped to the well at  $x_+^*$  if  $\dot{x} > 0$  and to the lower well at  $x_-^*$  if  $\dot{x} < 0$ . Now, initial  $F(x) \sim 0$  as the system is at the unstable maximum of the potential, and  $\dot{x}_i \sim a_i + b + (\langle x \rangle - x_i)$ , where  $b$  is close to 0, and  $\langle x \rangle - x_i$  is small in magnitude. So for elements with  $a_i = 1$ ,  $\dot{x} \sim 1$ , and for  $a_i = 0$ ,  $\dot{x}$  is also positive, though small in magnitude, as  $x_i < \langle x \rangle$ . After this infinitesimal initial push towards  $x_+^*$ , all elements evolve rapidly towards that stable upper well, as  $F(x)$  gets increasingly positive.

*Robustness of the phenomena:* In order to gauge the generality of our observations, we have considered different nonlinear functions  $F(x)$  in eq. (1). For example, we explored a system of considerable biological interest, namely, a system of coupled synthetic gene networks. We used the quantitative model, developed in [5], describing the regulation of the operator region of  $\lambda$  phase, whose promoter region consists of three operator sites. The chemical reactions describing this network, given by suitable rescaling yields [5]

$$F_{gene}(x) = \frac{m(1 + x^2 + \alpha\sigma_1 x^4)}{1 + x^2 + \sigma_1 x^4 + \sigma_1 \sigma_2 x^6} - \gamma_x x,$$

where  $x$  is the concentration of the repressor. The nonlinearity in this  $F_{gene}(x)$  leads to a double-well potential, and different  $\gamma$  introduces varying degrees of asymmetry in the potential. We studied a system of coupled genetic oscillators given by:  $\dot{x}_i = F_{gene}(x_i) + C(\langle x \rangle - x_i) + a_i + b$ , where  $C$  is the coupling strength, and  $b$  is a small global bias. We observe similar features in this system as well.

In addition, we studied various different coupling forms. For instance, a system of  $N$ -coupled nonlinear systems, where the evolution of element  $i$  is given by

$$\dot{x}_i = F(x_i) + a_i + C\langle x \rangle + b, \quad (6)$$

where  $C$  is the coupling strength and  $\langle x \rangle$  is the mean field given by eq. (2), and  $F(x)$  is a suitable nonlinear function. Furthermore, we considered small-world networks, where varying sets of regular links were replaced by random connections. Lastly, we explored networks with different ranges of coupling, namely the coupling occurred over increasingly large subsets of neighbours, up to the global coupling limit. Qualitatively, the same ultra-sensitivity to heterogeneity has been observed for all these different dynamical systems and coupling forms.

*Potential application:* Lastly, this unexpected central observation of scalable ultra-sensitivity may find potential applications in tackling problems dealing with a very large number of variables. For instance, consider the following difficult general question: in a large unsorted database of items does there exist even a single special item, namely, posed in layman’s language (following [6]): “In a haystack, does there exist even a single needle?”. We answer this question without having to go through the



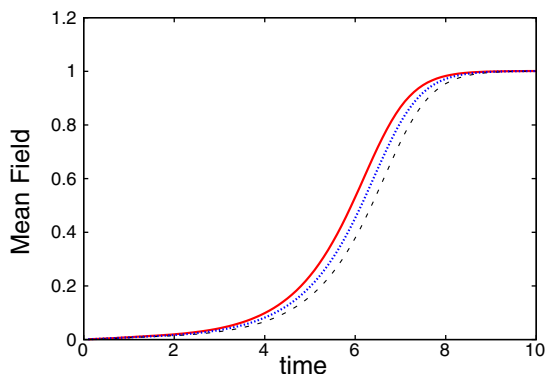


Fig. 7: (Colour on-line) Evolution of the mean field as a function of time for different system sizes: 100 (red solid), 1000 (black dashed) and 10000 (blue dotted), with  $N_1/N=0.01$  and bias  $b=-0.005$ . Clearly, the time needed to reach the attracting state does not depend on  $N$ .

entire “haystack” (namely, scan the full database). Rather, we have to make only one measurement to obtain the answer, as we explain below.

Without loss of generality, we use the bistable elements to stably encode  $N$  binary items (0 or 1) by setting  $a_i$  ( $i=1,\dots,N$ ) to take values 0 or 1, respectively (see fig. 1(a)). This creates a (unsorted) binary database. Then, using the scalable ultra-sensitivity demonstrated above, one can search this arbitrarily large database for the existence of a single different bit (say a single 1 in a string of 0’s) by making just one measurement of the evolved mean field of the whole array. That is, a single global operation can determine the existence of very few special items in a given, arbitrarily large, unsorted database of general items.

Additionally, we observed that the special element with  $a_i=1$  always reaches the upper well much faster than the other elements, when the initial state is centered closely around the barrier. For instance, a network of 1000 elements, with only *one*  $a_i=1$  ( $b=-0.0001$ ,  $C=1$ ), evolving from states drawn from a gaussian distribution with standard deviation  $\sim 0.1$  centered around zero, sampled over  $10^6$  random initial realizations yields the following: the average time taken for the element with  $a_1=1$  to reach the upper well (within accuracy of  $\sim 0.1$ ) is  $\sim 1$ , while the time taken by all other elements is  $\sim 4$ . So in the context of search, the first element that crosses a predetermined threshold will be the item being searched for. This is loosely analogous to a “time-of-flight” scenario, where the first element to reach the prescribed state triggers the answer. So one can also determine the exact element  $i$  that has  $a_i=1$  in the array dominated by  $a_i=0$ .

Furthermore, we have a look-up table relating critical  $N_1$  to global bias  $b$  (cf. fig. 5). So by sweeping  $b$  we can find where the crossover to the upper well occurs. This average critical value can be used to gauge the *number of ones* present in the system as well.

The significant feature here that allows this massive parallelization, is the fact that the time taken to reach the attracting mean-field value *does not scale with system size* (see fig. 7). In fact, the time taken to reach the mean field that encodes the output is *independent* of  $N$ .

Another important feature of this scheme is that it employs a *single* simple global operation, and does not entail accessing each item separately at any stage. In comparison, for example, a conventional algorithm can take up to  $\sim N$  steps to answer this question [6].

In summary, the collective response of  $N$  globally coupled bistable elements can strongly reflect the presence of very few non-identical elements in a very large array of otherwise identical elements. Counter-intuitively, the mean field evolves to the stable state of the minority population, rather than that of the bulk of the array. Adjusting the global bias enables us to observe robust *one-bit* sensitivity to diversity in this array. Further, the time needed to reach the attracting state does not increase with system size. Thus, this phenomenon has much relevance to the problem of massively parallelized search. Lastly, this scalable ultra-sensitivity is a generic and robust phenomenon, and can potentially be observed in social and biological networks [7], coupled nano-mechanical resonators [8], and coupled laser arrays [9].

## REFERENCES

- [1] GAMMAITONI L., HANGGI P., JUNG P. and MARCHESONI F., *Rev. Mod. Phys.*, **70** (1998) 223.
- [2] ROY R. *et al.*, *Phys. Rev. Lett.*, **68** (1992) 1259; JUNG P., BEHN U., PANTAZELOU E. and MOSS F., *Phys. Rev. A*, **46** (1992) R1709; BULSARA A. R. and SCHEMERA G., *Phys. Rev. E*, **47** (1993) 3734; GANG HU, HAKEN H. and FAGEN X., *Phys. Rev. Lett.*, **77** (1996) 1925; LOECHER M., CIGNA D. and HUNT E. R., *Phys. Rev. Lett.*, **80** (1998) 5212; LINDNER J. F., MEADOWS B. K., DITTO W. L., INCHIOSA M. E. and BULSARA A. R., *Phys. Rev. Lett.*, **75** (1995) 3; ZHOU C., KURTHS J. and HU B., *Phys. Rev. Lett.*, **87** (2001) 098101; MARCHESONI F., GAMMAITONI L. and BULSARA A. R., *Phys. Rev. Lett.*, **76** (1996) 2609; LOECHER M. *et al.*, *Chaos*, **8** (1998) 604.
- [3] TESSONE C. J., MIRASSO C. R., TORAL R. and GUNTON J. D., *Phys. Rev. Lett.*, **97** (2006) 194101; XIE J. *et al.*, *Phys. Rev. E*, **84** (2011) 011130.
- [4] Global interactions have been considered in the context of Kuramoto oscillators, in papers such as ACEBRON J. A., *Rev. Mod. Phys.*, **77** (2005) 137; UM J. *et al.*, *Phys. Rev. Lett.*, **108** (2012) 060601.
- [5] HASTY J. *et al.*, *Chaos*, **11** (2001) 207.
- [6] Alternate ideas to implement the increasingly important problem of search have included the use of quantum computers, which involves scaling of time steps as  $O(\sqrt{N})$ : see GROVER L., *Phys. Rev. Lett.*, **79** (1997) 325; **80** (1998) 4329; **95** (2005) 150501.
- [7] SCHEFFER M., *Nature*, **467** (2010) 411.
- [8] SHIM S.-BO, IMBODEN M. and MOHANTY P., *Science*, **316** (2007) 95; MAHBOOB I. *et al.*, *Nat. Commun.*, **2** (2011) 198.
- [9] NIXON M. *et al.*, *Phys. Rev. Lett.*, **106** (2011) 223901.