Multi-component random model of diffusion in chaotic systems

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Abstract.   We extend our recent study (Robnik *et al* 1997 *J. Phys. A: Math. Gen.* **30** L803) of diffusion in strongly chaotic systems (*'the random model'*) to systems composed of several weakly coupled ergodic components. By this we mean that the system as a whole is ergodic, but the typical time for the transition from one to another component is very long, much longer than the ergodic time inside each individual component. Thus for short times the system behaves like a single component ergodic system and the random model applies (neglecting the coupling to other components). At times much longer than the transition time the system behaves like an ergodic system without internal structure (without decomposition into several components) and the random model applies again (with different parameters). At intermediate times there is the crossover regime which we describe in detail analytically for a two-component system and test it numerically in a double billiard system (butterfly billiard).

1. Introduction

In a recent work (Robnik *et al* 1997) we have demonstrated some general scaling laws in the behaviour of stochastic diffusion in strongly chaotic systems (ergodic, mixing and K with a large Lyapunov coefficient, i.e. large KS entropy), mainly in Hamiltonian systems, or in the strange attractors of dissipative systems. The so-called *random model* that we developed describes very well the diffusion on chaotic components, in the sense that the relative (invariant) measure $\rho(j)$ as a function of the discrete time[*] j approaches unity exponentially as

$$\rho(j) = 1 - \exp(-j/N) \tag{1}$$

where N is the number of cells of equal size (relative invariant measure) $q = 1/N$ into which the whole ergodic component is decomposed, provided N is sufficiently large, say $N > 100$ or so. This *random model* rests upon the assumption that there are absolutely no correlations, not even between two consecutive steps, so that at each step (of filling the N cells) we have the same *a priori probability* $q = 1/N$ of visiting any of the cells, irrespective of whether

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[*] We work either with mappings or with Poincaré mappings on the surface of section. In each case j is the number of iterations of the map. Here, $\rho(j) = \rho_2(j)/\rho_2(j = \infty)$, where $\rho_2(j)$ is the actual Lebesgue measure of the occupied territory (cells) of the chaotic component labelled by index 2.

they are already occupied or not. Such absence of correlations can be implied and expected in particular by the large Lyapunov exponents, which in turn imply strong stretching and folding (of a phase space element) even after one iteration, meaning that such a phase element will be evenly distributed (in the coarse grained sense) over the entire phase space (or surface of the section). At first sight such a situation seems to be very exceptional, but in fact, we quote below a number of real dynamical systems which we have checked to obey the model, even though their Lyapunov exponents are not very large, or even when they are zero.

The process of filling the discretized phase space is obviously a Poissonian process (no correlations) and can be described in terms of a Bernoulli chain, because the transition probabilities of the Markov chain are independent of the initial state and are just equal to $q = 1/N$ (Gaspard and Wang 1993). Therefore, the process will be completely specified by calculating the probability, denoted $P_j(k)$, that at time j there are precisely k cells occupied (i.e. exactly $(N-k)$ cells empty). This problem was solved exactly in (Robnik *et al* 1997), and thus the average measure of the occupied domain on the grid of cells is $\langle kq \rangle = \rho(j)$, which in the case of sufficiently large N reduces to the exponential law (1). The universal scaling property is reflected in the fact that $\rho(j)$ is only a function of the ratio (j/N), and does not depend on j and N separately.

Such an assumption of absence of all correlations appears to be strong at first sight, and therefore it is quite surprising that the model describes many deterministic dynamical systems for which we can expect large Lyapunov coefficients, namely a 2D billiard (Robnik 1983, $\lambda = 0.375$), 3D billiard (Prosen 1997a, b, in his notation $a = -\frac{1}{5}$, $b = -\frac{12}{5}$), ergodic logistic map (tent map), hydrogen atom in a strong magnetic field ($\epsilon = -0.05$) (Robnik 1981, 1982, Hasegawa *et al* 1989), and standard map (see e.g. Ott 1993, Chirikov 1979) at ($K = 400$), in which the agreement is almost perfect, except for the last two systems where we see some long-time deviations on very small scales. However, in the standard map at $K = 3$, and in Hénon–Heiles (1964) system at $E = \frac{1}{6}$ the deviations are noticeable though not very big (about only 1%).

It is also quite astonishing that the random model applies very well even to *ergodic-only* systems, with strictly zero Lyapunov exponents, namely in case of the triangle billiards (Artuso *et al* 1997), where the deviations from the exponential law (1) on the largest scale are within only a few per cent. It is a well known result (Sinai 1976) that polygonal billiards have exactly zero Lypunov exponents, easy to understand since all periodic orbits are marginally stable (parabolic), and since they are dense everywhere, we conclude that the Lyapunov exponents must be zero everywhere.

The random model developed in Robnik *et al* (1997) is a statistical model, and $P_j(k)$ is used to predict not only the average relative measure of occupied cells $\rho(j) = \langle kq \rangle$, the average taken over k, resulting in (1), but also the standard deviation $\sigma(j)$, under which the same assumption of sufficiently large N is equal to, to the leading order,

$$\sigma(j) = \sqrt{\langle (kq)^2 \rangle - \langle (kq) \rangle^2} = \sqrt{\frac{1 - \rho(j)}{N}} \tag{2}$$

and gives us an estimate of the size of expected statistical fluctuations in $\rho(j)$.

The random model (Robnik *et al* 1997) has been subsequently generalized in an important direction (Prosen and Robnik 1998), namely to describe the diffusion on chaotic components in systems of mixed dynamics, with divided phase space, having regular regions (invariant tori) coexisting in the phase space with chaotic regions, a typical KAM scenario (Kolmogorov 1954, Arnold 1963, Moser 1962, Benettin *et al* 1984, Gutzwiller 1990). Such systems in two degrees of freedom can have the fractal boundary between the regular and irregular component and thus the convergence to the theoretically expected results can be very slow, mimicking a

departure from the random model, although ultimately it conforms to this model. In three or more degrees of freedom there is no boundary between the regular and chaotic regions, because we have the Arnold web (Chirikov 1979), which is dense everywhere in the phase space, and thus a naive box-counting would always imply that the relative invariant measure of the chaotic component is equal to the measure of the entire phase space, so $\rho_2(j) = 1$, which is wrong, because the KAM theorem rigorously gives that the relative measure of the regular component ρ_1 is strictly positive, $\rho_1 > 1$, moreover it is close to unity with the perturbation parameter. We assume that the invariant measure of the chaotic component is positive, although strictly speaking this is a major open theoretical problem in the mathematics of nonlinear systems, the so-called coexistence problem (Strelcyn 1991). Therefore, in such case one must introduce the possibility of different *a priori probabilities*, which are now no longer just the same and equal to $q = 1/N$, but have a certain distribution described by the so-called greyness distribution $w(g)$, where g is a continuous variable on the interval $[0, 1]$: $g = 0$ means no visits (white cells), $g = 1$ are the most frequently occupied cells (black cells), and those cells with $0 < g < 1$ have intermediate number of visits (grey cells). With this model (Prosen and Robnik 1998) we have shown how by measuring (numerically calculating) $w(g)$ we can determine the relative invariant measure ω of the chaotic component. The result is

$$\omega = \int_0^1 g w(g) \, \mathrm{d}g \tag{3}$$

and the time dependent relative measure of the occupied domain is equal to

$$\rho(j) = 1 - \int_0^1 \mathrm{d}g \, w(g) \exp\left(-\frac{gj}{\omega N}\right) \tag{4}$$

and the standard deviation is still given precisely by the equation (2). The greyness distribution can be numerically calculated quite easily by noticing that the greyness g is proportional to the average occupancy number $n(g)$, namely $n(g) = g/\omega$, so by measuring $n(g)$ in the limit $j \to \infty$ and after normalizing the g of the peak of $n(g)$ to unity, we get the g's, and then by binning them into bins of suitably small size Δg we get the histogram for $w(g)$.

In the case of ergodicity (only one chaotic component) we have $w(g) = \delta(g - 1)$, the Dirac delta function at $g = 1$, and then from equations (3) and (4) follows the random model, with exponential behaviour (1).

In this work we deal with *ergodic* systems, but each having several components, each of them also ergodic, but weakly coupled, by which we mean that the transition probability for going from one to another component is very small and the typical transition time ($=$ mean first passage time) j^* is very long. Obviously, at small times we shall find the random model (1) with N being equal to the number of cells of the starting component, $N = N_1$, whilst for very large times j, bigger than the typical transition time j^*, so $j \gg j^*$, we shall find again the random model (1), but now with N being equal to the number of all cells in the system, $N = N_s$. In between, when $j \approx j^*$, we have the crossover regime which we analyse in this work. Examples for applications of the multi-component model in physics are all situations where we have weakly coupled ergodic Hamiltonian oscillators. One special case is ergodic 2-dim billiards coupled/connected by small holes or channels.

This paper is organized as follows. In section 2 we describe the analytical derivation of the two-component model, in section 3 we show the numerical results on the so-called butterfly billiard (double cardioid billiard at $\lambda = 0.5$, Robnik 1983), in section 4 we describe the generalization to many components, and in section 5 we make some general conclusions and discuss the results in a broader perspective.

2. The two-component random model

We consider a two-component ergodic system, composed of the left and right component, denoted by L and R respectively, or also by indices 1 and 2, respectively. The system is characterized by the number N_1 of cells of equal relative invariant measure $q = 1/N$ in the left component, and N_2 cells of equal size $q = 1/N$ in the right component, where $N = N_1 + N_2$. (In the random one-component model $N_2 = 0$, and $a = q = 1/N_1 = 1/N$.) By definition the probability for a ball in L to fall again in L is just aN_1, and similarly, the probability of a ball in R to fall again in R is equal to cN_2. Now the cross-transitions are allowed, and by b_{12} we denote the transition probability (for transition $1 \rightarrow 2$, i.e. $L \rightarrow R$) per cell in R of falling into one of its N_2 cells, and conversely b_{21} is the probability per cell in L to fall into one of N_1 cells in L.

In fact, considering the precise details of our model, we deal here with a Markov model, where the $N \times N$ transition matrix has a block structure: the $N_1 \times N_1$ diagonal block has all elements equal to a, the $N_2 \times N_2$ diagonal block has all elements equal to c, whilst the off-diagonal blocks have elements equal to b_{12} and b_{21}, respectively. (See e.g., Gaspard and Wang 1993, Durrett 1996, Feller 1968, Gnedenko 1997.) In this section we work out the two-component model in detail, first, because here we can solve the most general case, and secondly, we can show the way how to proceed in the multi-component model with more than two components, although the explicit closed form results cannot be generally obtained there.

From these definitions it follows, by the conservation of probabilities,

$$aN_1 + b_{12}N_2 = 1$$
$$cN_2 + b_{21}N_1 = 1 \tag{5}$$
$$N_1 + N_2 = N$$

where, as mentioned above, N is now defined as the total number of cells. Now by $\tilde{l}_j$ and $\tilde{r}_j$ we denote the probabilities for the current ball (at the jth step) to fall into an L or R component, respectively. Of course, at every step/time j, we must have the probability normalization

$$\tilde{l}_j + \tilde{r}_j = 1. \tag{6}$$

From the above definitions of (transition) probabilities (for transitions LL, LR, RL and RR) we have

$$\tilde{l}_{j+1} = \tilde{l}_j aN_1 + \tilde{r}_j b_{21}N_1$$
$$\tilde{r}_{j+1} = \tilde{l}_j b_{12}N_2 + \tilde{r}_j cN_2. \tag{7}$$

Obviously, (6) is always satisfied simply due to (5). Now, if the cells are of equal relative measure $q = 1/N$ and so have equal *a priori* probabilities, then on the average and in the limit $j \rightarrow \infty$ we must have the same relative occupancy which implies the existence of and the approach to the equilibrium situation. Therefore,

$$\tilde{l}_\infty = \frac{N_1}{N} \qquad \tilde{r}_\infty = \frac{N_2}{N}. \tag{8}$$

By setting $j = \infty$ in (7) we obtain

$$\tilde{l}_\infty = \tilde{r}_\infty \frac{b_{21}N_1}{b_{12}N_2}. \tag{9}$$

Because, due to (6), $\tilde{l}_\infty + \tilde{r}_\infty = 1$, it follows

$$\tilde{l}_\infty = \frac{b_{21}N_1}{b_{21}N_1 + b_{12}N_2}$$
$$\tilde{r}_\infty = \frac{b_{12}N_2}{b_{12}N_2 + b_{21}N_1}. \tag{10}$$

This result, however, is compatible with equation (9) only if

$$b_{12} = b_{21} \tag{11}$$

which should be considered as the detailed balance equivalent to the hypothesis of the existence of the equilibrium (8) in the limit $j \to \infty$. Henceforth we shall denote the transition probability (per cell) just by $b = b_{12} = b_{21}$.

After this preliminary analysis we can write down the probability evolution (recursion) relations (7) simply as

$$\begin{pmatrix} \tilde{l}_{j+1} \\ \tilde{r}_{j+1} \end{pmatrix} = \mathbf{M} \begin{pmatrix} \tilde{l}_j \\ \tilde{r}_j \end{pmatrix} \tag{12}$$

where $\mathbf{M}$ is the simple 2×2 matrix

$$\mathbf{M} = \begin{pmatrix} aN_1 & bN_1 \\ bN_2 & cN_2 \end{pmatrix}. \tag{13}$$

Due to the linearity of the above recursion relations we can write down the explicit solution as follows:

$$\begin{pmatrix} \tilde{l}_j \\ \tilde{r}_j \end{pmatrix} = \mathbf{M}^j \begin{pmatrix} \tilde{l}_0 \\ \tilde{r}_0 \end{pmatrix} \tag{14}$$

where $(\tilde{l}_0, \tilde{r}_0)$ is the initial condition (initial state). After diagonalizing the matrix $\mathbf{M}$ by a similarity transformation with matrix $\mathbf{O}$, so that

$$\mathbf{M} = \mathbf{O}^{-1} \begin{pmatrix} \lambda_1 & 0 \\ 0 & \lambda_2 \end{pmatrix} \mathbf{O} \tag{15}$$

we have simply

$$\mathbf{M}^j = \mathbf{O}^T \begin{pmatrix} \lambda_1^j & 0 \\ 0 & \lambda_2^j \end{pmatrix} \mathbf{O}. \tag{16}$$

Thus we need the eigenvalues λ_1 and λ_2 of $\mathbf{M}$, equation (13) which (after a short calculation) are

$$\lambda_1 = 1 \qquad \lambda_2 = 1 - bN. \tag{17}$$

Therefore,

$$\mathbf{M}^j = \mathbf{O}^T \begin{pmatrix} 1 & 0 \\ 0 & (1 - bN)^j \end{pmatrix} \mathbf{O}. \tag{18}$$

Now as for the initial conditions we must start in one of the two components, and let us assume without loss of generality, of course, that $\tilde{l}_0 = 1$ and $\tilde{r}_0 = 0$, i.e. we start in the left component L, i.e. in 1. Then, due to the linearity of the evolution equations, without explicitly knowing the matrix $\mathbf{O}$ we have

$$\begin{pmatrix} \tilde{l}_j \\ \tilde{r}_j \end{pmatrix} = \begin{pmatrix} a_{11} + (1 - bN)^j a_{12} \\ a_{21} + (1 - bN)^j a_{22} \end{pmatrix}. \tag{19}$$

The final condition (8) immediately implies

$$a_{11} = \tilde{l}_\infty = \frac{N_1}{N} \qquad a_{21} = \tilde{r}_\infty = \frac{N_2}{N} \tag{20}$$

and the initial condition $(\tilde{l}_0, \tilde{r}_0) = (1, 0)$ implies

$$a_{12} = \frac{N_2}{N} \qquad a_{22} = -\frac{N_2}{N}. \tag{21}$$

Thus we arrive at the explicit solution in closed form

$$\tilde{l}_j = \frac{N_1}{N} + \frac{N_2}{N}(1 - bN)^j$$
$$\tilde{r}_j = \frac{N_2}{N} - \frac{N_2}{N}(1 - bN)^j$$

(22)

for the probabilities of being in L or in R at the jth step, which simply follows from the previous three equations (19)–(21)

We now have to define the probability $P_j(l, r)$ of having precisely l cells occupied in L and precisely r cells in R at the jth step. Of course, multiple occupancy is allowed, so that precisely $N_1 - l$ and $N_2 - r$ cells are empty in L and R, respectively. This probability satisfies the following quite obvious recursion relation:

$$P_{j+1}(l, r) = P_j(l, r)[\tilde{l}_j\{al + br\} + \tilde{r}_j\{cr + bl\}] + P_j(l, r - 1)[b\tilde{l}_j + c\tilde{r}_j](N_2 - r + 1)$$
$$+ P_j(l - 1, r)[a\tilde{l}_j + b\tilde{r}_j](N_1 - l + 1).$$

(23)

Let us define the two quantities

$$A_j = a\tilde{l}_j + b\tilde{r}_j \qquad C_j = b\tilde{l}_j + c\tilde{r}_j$$

(24)

which are the probabilities to jump into the L and R component, respectively, at the $(j+1)$-step. With this interpretation in mind, the equation (23) is indeed quite obvious and can be rewritten in compact form

$$P_{j+1}(l, r) = P_j(l, r)[lA_j + rC_j] + P_j(l, r - 1)(N_2 - r + 1)C_j$$
$$+ P_j(l - 1, r)(N_1 - l + 1)A_j.$$

(25)

The probability $P_j(k)$ is defined as the probability of having occupied precisely k cells in the whole system, i.e. in L and R together. Obviously, we have

$$P_j(k) = \sum_{l+r=k} P_j(l, r).$$

(26)

The main quantity we seek is the average (expected) measure of occupied cells at step j, denoted by ρ_j, and by assuming the same relative invariant measure equal to $q = 1/N$ for all of them, in L and in R, we find

$$\rho_j = \sum_{k=1}^{N} \frac{k}{N} P_j(k) = \sum_{l,r} \frac{l+r}{N} P_j(l, r).$$

(27)

This can be split into the L-component contribution ρ_j^L and R-component contribution ρ_j^R, namely

$$\rho_j^L = \sum_{l,r} \frac{l}{N} P_j(l, r) \qquad \rho_j^R = \sum_{l,r} \frac{r}{N} P_j(l, r)$$

(28)

and of course

$$\rho_j = \rho_j^L + \rho_j^R.$$

(29)

The solution for ρ_j^L and ρ_j^R can be found by the following trick: multiply the equation (25) by l/N on both sides and sum up over all l and r. Do the same, symmetrically, for ρ_j^R. After a straightforward calculation we obtain the exact linear recursion relations

$$\rho_{j+1}^L = (1 - q - \beta^L \lambda^j)\rho_j^L + qN_1(q + \beta^L \lambda^j)$$
$$\rho_{j+1}^R = (1 - q - \beta^R \lambda^j)\rho_j^R + qN_2(q + \beta^R \lambda^j)$$

(30)

where

$$q = \frac{1}{N} \qquad \lambda = 1 - bN \qquad \beta^L = q N_2(a - b) \qquad \beta^R = q N_2(b - c). \qquad (31)$$

In order to solve equations (30) we observe that for the L-equation N_1/N is the particular solution, and N_2/N for the R-equation. Thus, we can write the solution in the form, here for the L-part,

$$\rho_j^L = q N_1 + h_j^L \qquad (32)$$

whence

$$h_{j+1}^L = (1 - q - \beta^L \lambda^j) h_j^L. \qquad (33)$$

This equation, unfortunately, cannot be solved exactly in closed form, but only formally as a j-fold product. Therefore, we make the approximation of treating the discrete time j as a continuous variable. In doing this we arrive, after a straightforward calculation, at the expression

$$h_j^L = h_0^L \exp\left[-\left(qj + q N_2(a - b)\frac{(1 - bN)^j - 1}{\ln(1 - bN)}\right)\right] \qquad (34)$$

and by considering the initial condition $\rho_0^L = q N_1 + h_0^L = 0$, we have $h_0^L = -q N_1$, which yields the final result for the L-equation, and also in complete analogy to the R-equation, namely

$$\rho_j^L = \frac{N_1}{N}\left(1 - \exp\left[-\frac{j}{N} - \frac{N_2(a - b)}{N \ln(1 - bN)}((1 - bN)^j - 1)\right]\right)$$
$$\rho_j^R = \frac{N_2}{N}\left(1 - \exp\left[-\frac{j}{N} - \frac{N_2(b - c)}{N \ln(1 - bN)}((1 - bN)^j - 1)\right]\right). \qquad (35)$$

Let us assume that the coupling between L and R is very small, assuming $bN \ll 1$, or equivalently $j^* = 1/(bN) \gg 1$. Then we make the aproximations $\ln(1 - bN) \approx -bN$, and $(1 - bN)^j - 1 \approx -jbN$, and in the limit $j \ll j^*$ find

$$\rho_j^L = \frac{N_1}{N}(1 - e^{-aj})$$
$$\rho_j^R = \frac{N_2}{N}(1 - e^{-bj}). \qquad (36)$$

Thus in L (where we start) the filling of cells behaves precisely as in the random model in the limit $b = 0$, whilst the filling in R is much slower, namely with coefficient b instead of a, where by assumption $b \ll a$.

Let us return to the 'exact' expressions (35), which are 'exact' in the sense that there is no other approximation than merely $j \gg 1$, justifying the treatment of the evolution or recursion equations as the differential rather than the difference equations. See the transition from equation (33) to (34). This condition is certainly very well satisfied for all j at which we study a variety of dynamics systems, with j as big as from 10^2 to 10^9 or so. These equations are *the solution of the problem*, when dealing with one initial condition, starting, say, in L. (Unfortunately, we cannot easily calculate the expected fluctuations of $\rho_j = \rho_j^L + \rho_j^R$, so this is one of the open problems for the future.)

In numerical calculations with specific dynamical systems we can perform the calculation of ρ_j for many different initial conditions, somehow evenly (possibly randomly) distributed over the phase space. For the two-component random model this means that we take the average over initial conditions in L and R. Their number must be proportional to N_1 and N_2, respectively. So, their statistical weight must be just N_1/N and N_2/N, respectively. The exact

results (35) are calculated by assuming a start in L, therefore we shall denote them now by ρ_j^{LL} and ρ_j^{RL}. In analogy and symmetrically we can then calculate the corresponding exact results by assuming a start in R. The results are

$$\rho_j^{LL} = \frac{N_1}{N} \left(1 - \exp\left[-\frac{j}{N} - \frac{N_2(a-b)}{N \ln \lambda}(\lambda^j - 1) \right] \right)$$

$$\rho_j^{RL} = \frac{N_2}{N} \left(1 - \exp\left[-\frac{j}{N} - \frac{N_2(b-c)}{N \ln \lambda}(\lambda^j - 1) \right] \right)$$

$$\rho_j^{LR} = \frac{N_1}{N} \left(1 - \exp\left[-\frac{j}{N} - \frac{N_1(b-a)}{N \ln \lambda}(\lambda^j - 1) \right] \right) \tag{37}$$

$$\rho_j^{RR} = \frac{N_2}{N} \left(1 - \exp\left[-\frac{j}{N} - \frac{N_1(c-b)}{N \ln \lambda}(\lambda^j - 1) \right] \right).$$

Thus, after performing the averaging of the results over the initial conditions in proportion with the invariant measures of L and R, as explained above, we define

$$\bar{\rho}_j = \frac{N_1}{N}(\rho_j^{LL} + \rho_j^{RL}) + \frac{N_2}{N}(\rho_j^{LR} + \rho_j^{RR}) \tag{38}$$

and calculate

$$\bar{\rho}_j = 1 - e^{-j/N} \left\{ \frac{N_1^2}{N^2} \exp\left[-\frac{N_2(a-b)}{N \ln \lambda}(\lambda^j - 1) \right] + \frac{N_1 N_2}{N^2} \exp\left[-\frac{N_2(b-c)}{N \ln \lambda}(\lambda^j - 1) \right] \right.$$

$$\left. + \frac{N_1 N_2}{N^2} \exp\left[-\frac{N_1(b-a)}{N \ln \lambda}(\lambda^j - 1) \right] + \frac{N_2^2}{N^2} \exp\left[-\frac{N_1(c-b)}{N \ln \lambda}(\lambda^j - 1) \right] \right\}. \tag{39}$$

A special interesting model is the symmetric model consisting of two identical components, so that $a = c$ and $N_1 = N_2 = N/2$. The above exact result (39) assumes the simple form

$$\bar{\rho}_j = 1 - e^{-j/N} \cosh\left(\frac{a-b}{2 \ln \lambda}(\lambda^j - 1) \right). \tag{40}$$

Again, the only approximating condition for the validity of this result is $j \gg 1$. Now we assume $j^* = 1/(bN) \gg 1$, which means that the typical transition time for $L \to R$ transition is very long (bN very small), so that according to equation (5) $a = c \approx 2/N$. Then the result (40) reduces to the simple form

$$1 - \bar{\rho}_j = \cosh\left(\frac{j^*}{N}(1 - e^{-j/j^*}) \right) e^{-j/N}. \tag{41}$$

Please observe that $\bar{\rho}_j$ is a function only of two scaled times, namely j/N and j^*/N, and does not depend on N separately. Let us examine the behaviour of such a system. There are two cases. First when $j^* \gg N$ (A) and the second one when $j^* \ll N$ (B).

The case (A): $j^* \gg N$. If $j < N$ we get

$$1 - \bar{\rho}_j \approx 1 - j/N \approx e^{-j/N} \tag{42}$$

which is similar to the random model.

If $N < j < j^*$ we have

$$1 - \bar{\rho}_j \approx \tfrac{1}{2} \tag{43}$$

i.e. locally almost constant value.

If $j^* < j$ then we have

$$1 - \bar{\rho}_j \approx \tfrac{1}{2} e^{-\frac{(j-j^*)}{N}} \tag{44}$$

which means exponential behaviour as in the random model but with the shifted argument (a prefactor which is not unity).
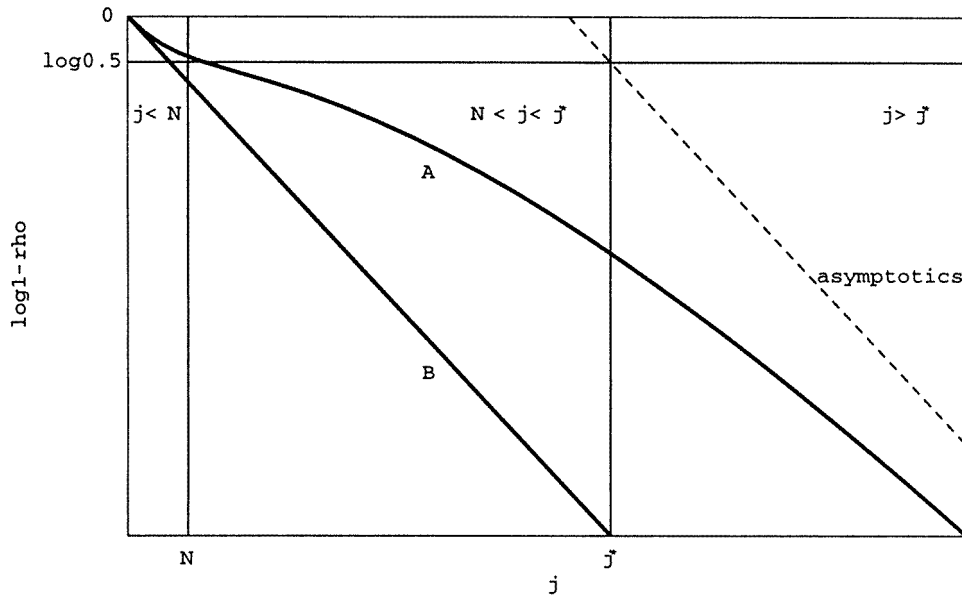
Figure 1. The three regimes of case (A) and of case (B) are qualitatively illustrated. Here, in case (B) we plot the symmetric theoretical distribution (41) with $j^*/N = 8$.

The case (B): $j^* \ll N$. In this case (41) reduces to the simple exponential law of the random model, namely

$$1 - \bar{\rho}_j \approx e^{-j/N}. \tag{45}$$

The three regimes of case (A) and of case (B) are qualitatively illustrated in figure 1.

3. Numerical results on the butterfly billiard

In this section we report on our numerical calculations for the billiard system which consists of two identical ergodic components, in order to test and analyse the (conditions of validity) theory expounded in section 2. We have chosen the quadratic conformal billiard (Robnik 1983), usually called the *'Robnik billiard'* in the literature, defined by the complex conformal map $w(z) = z + \lambda z^2$ from the unit disc in the z-plane onto the physical w-plane. The properties and the wide applications have been recently described in Robnik *et al* (1997) and will not be listed here again. We simply mention that the cardioid billiard is obtained for the shape parameter $\lambda = 0.5$. It is known rigorously to be ergodic (Markarian 1993).

Now we design the billiard shape composed of two such billiards, joined with a small opening, created by the overlap of the boundaries, of size ϵ. The geometry is sketched in figure 2. We shall call such a double billiard the *butterfly billiard* whose geometry is fully specified with two parameters, λ and ϵ.

Due to the ergodicity the escape probability is just equal to the ratio const.$\epsilon/\mathcal{L}$, where $\mathcal{L}$ is the perimeter of the half-billiard, i.e. the perimeter of the Robnik billiard. Thus by this the system is fully specified for the study of diffusion on the surface of section.

In figures 3(a)–(c) we show the results for $\bar{\rho}_j$ versus j/N for three different values of N, for $\lambda = 0.5$ and $\epsilon = 0.000\,05$. For small j/N we see quite good agreement with the theoretical prediction (figure 3(a)), at intermediate j/N the deviations become more
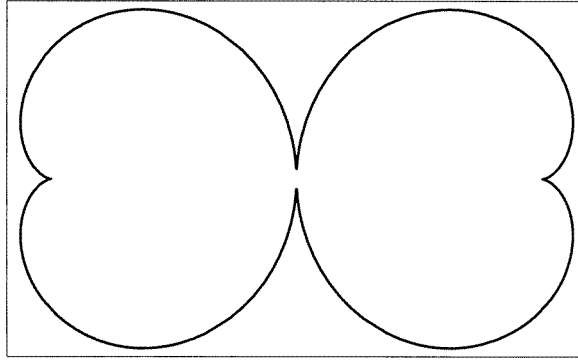
Figure 2. We show the geometry of the butterfly billiard with $\lambda = 0.5$ and $\epsilon = 0.03$.

pronounced (figure 3(*b*)), and for large j/N in (figure 3(*c*)) the deviations are very significant. They can be clearly understood by the departures from the two-component random model: when in one of the components, say in L, the probability to jump into a cell in R is, in our dynamical system, certainly not the same for all cells in R, but the cells closer to the small opening have greater chances to be visited. Nevertheless, qualitatively we see the agreement with theory. We believe that this is certainly a good starting point for even more general theories of diffusion, statistics of classical motion and transport in conservative dynamical systems (MacKay *et al* 1984), especially in the framework of the extensive work by Garspard and Wang (1993).

4. The multi-component random model

In this section we sketch the general multi-component model, which, however, cannot be worked out explicitly in closed form results, as we shall see.

We assume we have M ergodic components, with index μ, $1 \leqslant \mu \leqslant M$, and each of them having N_μ cells of equal (relative invariant) measure equal to $q = 1/N$, where $N = N_1 + \cdots + N_M$ is the total number of cells. By $b_{\mu\nu}$ we denote the probability for transition from component μ to component ν, per cell in ν-component, so the probability to jump from the μ-component to the ν-component is, by definition, equal to $b_{\mu\nu} N_\nu$. The diagonal elements of the matrix $b_{\mu\nu}$ will be occasionally denoted by $a_\mu = b_{\mu\mu}$.

We again therefore have a Markov model, with N cells on the fine-grained scale, with $N \times N$ transition matrix, which has the block structure: each diagonal block μ, of size $N_\mu \times N_\mu$, has all elements equal to $a_\mu = b_{\mu\mu}$, whilst the off-diagonal blocks have equal elements $b_{\mu\nu}$, in exact correspondence and generalization of the two-component model of section 2.

Now, by a vector $\tilde{p}_\mu$ we denote the probabilities of residing in the μ-component. Therefore, by the normalization of total probability

$$\sum_{\mu=1}^{M} \tilde{p}_\mu = 1. \tag{46}$$

By $\tilde{p}_\mu^0$ we shall denote the initial state, and by $\tilde{p}_\mu^j$ the jth state, i.e. the state at time j, where $j = 1, 2, 3, \ldots$. Therefore, we can write the evolution equation as

$$\tilde{p}_\nu^{j+1} = \sum_{\mu=1}^{M} b_{\nu\mu} N_\nu \tilde{p}_\mu^j \qquad j = 0, 1, 2, \ldots. \tag{47}$$
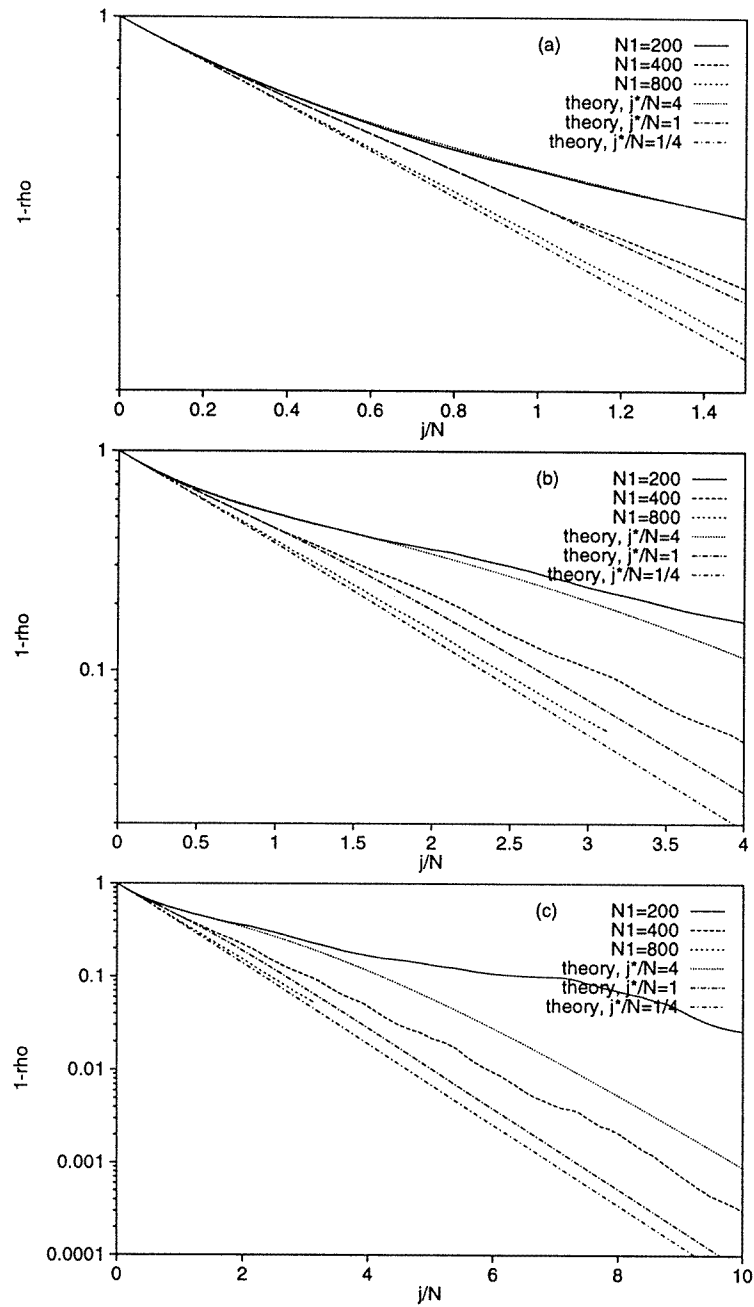
Figure 3. We show the results for the butterfly billiard of figure 2 but with $\epsilon = 0.000\,05$, for three different values of $N = N_1^2 = 40\,000,\ 160\,000,\ 640\,000$. In (*a*) we have $j/N \leqslant 1.5$, in (*b*) the intermediate timescales $0 \leqslant j/N \leqslant 4$ and in (*c*) for long timescales $0 \leqslant j/N \leqslant 10$. In (*a*) and (*b*) the agreement with theory is satisfactory, whilst in (*c*) we see large and significant departures. See text for details.

Thus we have the finite-dimensional Markov chains (Feller 1968), which describe the coarse-grained structure (transitions between the components/blocks), with the transition matrix $\mathbf{T} = T_{\mu\nu} = b_{\nu\mu}N_\nu$. If the probability should be conserved for any $\tilde{p}_\mu$, equation (46), then the rows of the matrix $\mathbf{T}$ must necessarily add to unity,

$$\sum_{\nu=1}^{M} T_{\mu\nu} = \sum_{\nu=1}^{M} b_{\nu\mu}N_\nu = 1. \tag{48}$$

Another property, which must be obeyed, because our model is a physical model and not a general abstract Markov process, is the existence of a unique stationary state† (equilibrium state), which is the microcanonical equilibrium, where the probabilities $\tilde{p}_\mu^\infty$ are just equal to the relative (normalized) invariant ergodic measure of each μ-component, namely

$$\tilde{p}_\mu^\infty = N_\mu/N \qquad \mu = 1, 2, \ldots, M. \tag{49}$$

Assuming the existence of such an equilibrium also implies (Feller 1968, Durrett 1996) its uniqueness and also that any initial state $\tilde{p}_\mu^0$ should asymptotically approach the equilibrium (stationary) state. Inserting (49) in equation (47) we conclude that also the columns of $b_{\mu\nu}N_\mu$ must add to unity,

$$\sum_{\mu=1}^{M} T_{\mu\nu}N_\mu N_\nu^{-1} = \sum_{\mu=1}^{M} b_{\nu\mu}N_\mu = 1. \tag{50}$$

We therefore have $2M$ linear equations that must be satisfied by $\mathbf{T}$. This is not enough, in general, to conclude that $b_{\nu\mu}$ is a real symmetric matrix. We need in general $M(M-1)/2$ equations. Thus, only in two-component model, $M = 2$, of section 2, we can conclude that necessarily $b_{12} = b_{21}$. To the best of our knowledge we cannot, in general, further reduce the properties of $b_{\nu\mu}$ (Gaspard and Wang 1993), and therefore the general case is described by an asymmetric matrix $b_{\nu\mu}$.

We would like to comment on this important observation. Gaspard and Wang (1993) give the example of a baker-type map, which is a strongly chaotic system, in fact a Bernoulli dynamical system, where the transition matrix $\mathbf{T}$ is asymmetric, while $b_{\nu\mu}$ (= transition probability per unit invariant measure of the n-component) is *symmetric*. Nevertheless, even the asymmetry of $b_{\nu\mu}$ is the typical case. One general argument is the following, when we again go to the fine-grained level of discretization (cells): as we make the cells smaller and smaller by increasing N (so that their size (invariant measure) $q = 1/N$ is smaller and smaller), the transition matrix will in general remain irreducible, just due to the ergodicity of the underlying dynamical system, with the unique (microcanonical) equilibrium state, and will describe the microscopic dynamics (the pointwise description of the orbits) better and better. (After all, in computers we work always with some, although very fine, discretization of the phase space!) Such a mapping and its corresponding Markov chain will of course generally map a state x to the state x' in the phase space, but generally not *directly* x' into x, although x' and x of course do communicate due to the ergodicity (irreducibility), but not necessarily directly (in one direct transition). Of course, if this observation is correct on the fine-grained level (cells) then it also holds true on the coarse-grained level of discretization (components/blocks).

One specific elementary example for the asymmetry of both $\mathbf{T}$ and $b_{\nu\mu}$ is the irrational rotation on a circle, which is an ergodic (but not mixing) dynamical system, defined by the map

$$x_{n+1} = x_n + r \,(\mathrm{mod}\ 1) \qquad 0 < r < 1 \tag{51}$$

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† Such a hypothesis is justified if the dynamical system is an ergodic system, and technically, in the framework of the fine-grained and the coarse-grained block/component system, the corresponding Markov model satisfies such a condition if all cells communicate, i.e. a transition from any cell to any other cell is possible (Durrett 1996). Such a Markov process (chain) is called irreducible (Feller 1968).

where r is the irrational number, implying the ergodicity of the map on $[0, 1)$. Let us assume that this interval is divided into M equal intervals (cells) and $r < 1/M$, and let us describe it by our Markov model. Then it is obvious that only the following elements of $b_{\nu\mu}$ are non-zero: $b_{n,n}$ and $b_{n,n+1}$, for all $n = 1, 2, \ldots, M$ where $n = M + 1 = 1$. The matrix $b_{\nu\mu}$ is thus obviously manifestly asymmetric, and so is **T**, because the invariant measure of all cells is the same and equal to $q = 1/M$.

However, it is still our opinion that it is an interesting open problem to precisely characterize the interesting class of dynamical systems, in which we can and should expect the symmetry of $b_{\mu\nu}$, based on physical arguments (some version of detailed balance considerations).

The symmetry of $b_{\nu\mu}$ is not a necessary but certainly sufficient condition for the property of **T** 'rows-add-to-unity' which also implies the property of $b_{\nu\mu}N_\mu$ 'columns-add-to-unity', the latter being a necessary condition for the existence of a unique equilibrium state, see equations (48) and (50).

In principle, having the evolution equation (47), we can calculate everything. First, we must diagonalize the matrix **T**. Since **T** in general is a real but not symmetric matrix (even if $b_{\nu\mu}$ is symmetric!), the diagonalization cannot be done generally (only a reduction to the Jordan canonical form is possible), but if it exists, then it is achieved by a similarity matrix **U** and the eigenvalues λ_μ, $\mu = 1, 2, \ldots, M$ are, in general, complex. However, since the stationary equilibrium state (49) is an eigenvector of **T** with eigenvalue unity, at least one eigenvalue, denoted by λ_1, must be unity $\lambda_1 = 1$. Also, since the existence of the equilibrium implies not only its uniqueness but also its approach to it starting from any initial state $\tilde{p}_\mu^0$, all other eigenvalues must have an absolute value less than unity. After calculating **U** and $\lambda_\mu, \mu = 2, 3, \ldots, M$, and assuming without loss of generality that we start in component $\mu = 1$, such that $\tilde{p}_\mu^0 = 1$ for $\mu = 1$ and $\tilde{p}_\mu^0 = 0$ for $\mu \geqslant 2$, we can completely describe the evolution (47). Then let us denote by **M** the diagonal matrix of **T** with diagonal elements λ_μ, related to **T** by

$$\mathbf{T} = \mathbf{U}^{-1}\mathbf{M}\mathbf{U}. \tag{52}$$

The solution $\tilde{p}_\mu^j$, denoted compactly by p_j (which must always be real) of the evolution equation with the above mentioned initial state ($\tilde{p}_\mu^0 = 1$ for $\mu = 1$ and 0 otherwise, denoted compactly as p_0) can be written as

$$p^j = \mathbf{U}^{-1}\mathbf{M}^j\mathbf{U}p^0 \tag{53}$$

or by writing in components

$$\tilde{p}_\mu^j = \tilde{p}_\mu^\infty + \sum_{\nu=2}^{M} \alpha_{\mu\nu}\lambda_\nu^j$$

$$= \frac{N_\mu}{N} + \sum_{\nu=2}^{M} \alpha_{\mu\nu}\lambda_\nu^j \tag{54}$$

where the quantities $\alpha_{\mu\nu}$ and the eigenvalues λ_μ are in general complex, and fully determined by the knowledge of the matrix **T**, through the diagonalization procedure (52). The solution obviously converges to the asymptotic equilibrium state (49), since $|\lambda_\mu| < 1$ for all $\mu \geqslant 2$. Of course, the initial condition must be satisfied, and therefore the quantities $\alpha_{\mu\nu}$ must obey the following equations

$$\sum_{\mu=2}^{M} \alpha_{1\mu} = 1 - \frac{N_1}{N} \qquad \sum_{\mu=2}^{M} \alpha_{\nu\mu} = -\frac{N_\nu}{N} \qquad \nu = 2, 3, \ldots, M. \tag{55}$$

The procedure is now, in analogy with the two-component model, to define the probabilities $P_j(l_1, l_2, \ldots, l_M)$ of having exactly $l_1, l_2, \ldots, l_M$ occupied cells in the $\mu = 1, 2, \ldots, M$ component. Also, we define the probability $P_j(k)$ of having exactly k occupied cells in the entire system (all components). Of course

$$P_j(k) = \sum_{l_1+l_2+\cdots+l_M=k} P_j(l_1, l_2, \ldots, l_M). \tag{56}$$

What we seek (mainly) is the total occupied measure of all components together, denoted by ρ_j, and equal to

$$\rho_j = \sum_{k=1}^{N} \frac{k}{N} P_j(k) = \sum_{l_1,l_2,\ldots,l_M} \frac{l_1 + l_2 + \cdots + l_M}{N} P_j(l_1, l_2, \ldots, l_M). \tag{57}$$

It can be split into partial contributions

$$\rho_j^{\mu} = \sum_{l_1,l_2,\ldots,l_M} \frac{l_{\mu}}{N} P_j(l_1, l_2, \ldots, l_M) \qquad \mu = 1, 2, \ldots, M \tag{58}$$

so that, according to (57),

$$\rho_j = \sum_{\mu=1}^{M} \rho_j^{\mu}. \tag{59}$$

The next step is, in analogy with (23), to write down the evolution (recursion) equation for $P_j(l_1, l_2, \ldots, l_M)$ and then by the trick of multiplication and summation to arrive at a one-step recursion relation for each partial measure (58), which can be hopefully solved in a similar way as the two-component model. By summing the partial contributions, equation (59), we get the final expression for ρ_j. This can by no means be written down in a closed form because the diagonalization (52) cannot be done analytically and thus the quantities $\alpha_{\mu\nu}$ and the eigenvalues λ_{μ} of the transition probability matrix **T** cannot be expressed in a closed form. Any possible further developments in this direction, especially seeking some powerful analytical approximations, is left for our future project.

5. Discussion and conclusions

In this work we have generalized our *random model* of diffusion in strongly chaotic ergodic systems to ergodic systems consisting of several weakly communicating (coupled) ergodic components, which is (a coarse grained picture of) a Markov model with a $N \times N$ transition matrix having the block structure. Thus the system as a whole is supposed to be ergodic, however, the time of diffusion inside each component is much smaller than the typical transition time to jump from one to another component. A simple but powerful example is a billiard system consisting of several ergodic components, interconnected by small holes or channels. The ergodic dynamical system under consideration is analysed in the phase space, moreover, on the surface of section, and we study the properties of the Poincaré mapping on the surface of section, which we discretize into a grid system of N cells of equal (relative) invariant measure $q = 1/N$.

We have completely analysed the two-component model, giving the explicit analytical results, and tested it in the case of the symmetric butterfly billiard (two cardioid billiards (Robnik 1983) connected by a small hole). The results are very good.

In the general multi-component model the occupancy probability for each component naturally leads to the Markovian model and its coarse grained structure. The results cannot be written in an analytical closed form, because the diagonalizations of the transition probability

matrix cannot be explicitly performed. The development of suitable analytical approximations is one of our future projects. Also, we perhaps need a deeper understanding of how the physics determines the transition matrix **T** and its properties. This matrix is generally not symmetric, and neither is the matrix $b_{\mu\nu}$ (see section 4).

Finally, we should comment on the physical interpretations and applications of our formalism. The multi-component ergodic system has been already mentioned, for example weakly connected ergodic billiards. But we can also equally well study a coupling between an integrable† and an ergodic system, and furthermore, anything in between, such as KAM systems. If a given generic system of KAM type has strongly pronounced cantori, or regions bounded by cantori, then we can again use our multi-component model to describe the statistical features of classical dynamics. This leads us to refine our understanding of the transport and statistical problems in Hamiltonian dynamical systems (MacKay *et al* 1984), especially in the perspective of the extended study by Gaspard and Wang (1993). To look more carefully into such systems, also in higher degrees of freedom, and especially in smooth dynamical systems, such as a hydrogen atom in a strong magnetic field (Robnik 1981, 1982, Hasegawa *et al* 1989) and the Hénon–Heiles system (Hénon and Heiles 1964) is one of our future goals (Robnik and Rapisarda 1998).

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† Because an integrable system can be decomposed, in general, into an infinity (continuum) of invariant tori *on* each of which the motion is ergodic, and after a discretization of the phase space into small equally large cells we can decompose an integrable system in a finite but large number of ergodic components, all of them being coupled to the ergodic system but not among each other.

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