


Killing versus branching: Unexplored facets of diffusive relaxation

Piotr Garbaczewski  and Mariusz Żaba 
Institute of Physics, University of Opole, 45-052 Opole, Poland

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We analyze the relaxation dynamics of Feynman-Kac path integral kernel functions, in terms of branching diffusion processes with killing. This amounts to the killing versus branching approach to path integration, which seems to be a novelty in the pathwise description of conditioned Brownian motions and diffusion processes with absorbing boundaries. There, Feynman-Kac kernels appear as building blocks of inferred (Fokker-Planck) transition probability density functions. A consistent probabilistic meaning is hereby provided (killing versus branching time rate) to bounded from below Feynman-Kac potential functions, which instead of being positive-definite (a standard killing paradigm), may take negative values on bounded spatial subdomains (that inflicts trajectory branching).

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I. MOTIVATION

The familiar Feynman-Kac formula [1–3] for nonnegative potential functions has received a canonical probabilistic interpretation in terms of diffusion processes with killing [4,5], ultimately resulting in the asymptotic decay of the related F-K kernel function. It has been noticed, that for renormalized potentials (“potentials with subtraction” [3,6]), the killing can be tamed [1] but no probabilistic interpretation has been associated with the pertinent “tamed dynamics.” Basically, in view of the obvious “proliferation” of involved sample trajectories, whose surplus (sometimes named “mass creation” in the mathematical literature) seems to invalidate a customary probabilistic reasoning.

We assign a direct probabilistic meaning to the relaxation dynamics (when in existence) of Feynman-Kac path integral kernel functions, in terms of the tamed-killing-diffusion process, in which killing is (over)compensated by branching of still alive sample paths. We explain a probabilistic origin of the compensation effect.

To this end we follow a strict logical route, beginning from conditioned diffusion processes, with a built-in killing mechanism, investigate the decay of the “probability mass” (its loss), and propose a decay-prohibiting solution in the form of the taming mechanism. The relaxation property is hereby enforced by the branching of not yet killed paths.

The present endeavor departs directly from the discussion of various aspects of the relaxation versus killing intertwine in the pathwise analysis of the Brownian motion in trapping enclosures, cf. Refs. [1,7,8]. That actually stems from the pseudo-Schrödinger reformulation of the Fokker-Planck dynamics [9,10] and the validity of the Feynman (respectively, Feynman-Kac) path integration route in the derivation of integral kernels of closely related motion operators $\exp(tL^*)$ and $\exp(-tH)$ [2,3,11,12], cf. also Refs. [13–15].

Here L^* stands for the Fokker-Planck generator, while H for the associated Schrödinger-type Hamiltonian, [1,10,12]. We point out that the integral kernels in question are transition probability densities $p(y, s, x, t) = [\exp(tL^*)](y, x)$,

$0 \leq s < t$ of the diffusion process and (Euclidean) propagators $k(y, s, x, t) = [\exp(-tH)](y, x)$ of the generalized Schrödinger equation, where $H = -(1/2)\Delta + \mathcal{V}$, and the potential function $\mathcal{V}(x)$ may take negative values on bounded domains, while being bounded from below.

We focus on Markovian diffusion processes driven by conservative (gradient) time-independent drift fields. Let us consider a diffusion process $X(t)$, associated with the stochastic differential equation of the Langevin-type (here interpreted in terms of infinitesimal time increments)

$$dX(t) = b(X(t))dt + \sqrt{2\nu}dW(t), \quad (1)$$

where $b(x)$ stands for a forward drift, ν is a diffusion constant (2ν is interpreted as the variance parameter), and $W(t)$ is the normalized Wiener noise in R , defined by expectation values $\langle W \rangle = 0$ and $\langle W(s)W(t) \rangle = \delta(s - t)$.

From now on we rescale the diffusion coefficient to the value $\nu = 1/2$ to conform with the notation of Refs. [1,2,12]. Accordingly, if an initial probability density function $\rho_0(x)$ is given, then its time evolution $\rho_0(x) = \rho(x, 0) \rightarrow \rho(x, t) = [\exp(tL^*)\rho_0](x)$ follows the Fokker-Planck equation:

$$\partial_t \rho = \frac{1}{2} \Delta \rho - \nabla(b\rho) = L^* \rho, \quad (2)$$

where the operator $L^* = \nu \Delta - \nabla(b \cdot)$ is a Hermitian $L^2(R)$ adjoint of the, traditionally favored by mathematicians, diffusion generator $L = \nu \Delta + b \nabla$ [10].

We anticipate the existence of a transition probability density function $p(y, s, x, t)$, $0 \leq s < t \leq T$, ($T \rightarrow \infty$ is admissible) for the diffusion process Eqs. (1) and (2): $\rho(x, t) = \int p(y, s, x, t) \rho(y, s) dy$. We presume $p(y, s, x, t)$ to be a (possibly fundamental) solution of the Fokker-Planck equation, with respect to variables x and t , i.e., $\partial_t p(y, s, x, t) = L_x^* p(y, s, x, t)$.

A. Relaxation regime

Given $\rho(x, t)$ solving Eq. (2). Let us introduce an osmotic velocity field $u = \nabla \ln \rho^{1/2}$ and the current velocity field $v = b - u$, with $b = -\nabla \phi$, where $\phi = \phi(x)$ is time-independent.

We can readily rewrite the Fokker-Planck equation as the continuity equation $\partial_t \rho = -\nabla j$, where $j = v \cdot \rho$ has a standard interpretation of a probability current.

We assume that the diffusion process asymptotically relaxes to the stationary (invariant) strictly positive probability density function (pdf), $\rho(x, t) \rightarrow \rho_*(x)$ as $t \rightarrow \infty$. In the stationary regime we have $j \rightarrow j_* = 0$ and thence $v \rightarrow v_* = 0$. Since b is time-independent, the drift field potential (presumed to be confining) $\phi(x)$ becomes correlated with ρ_* : $b = u_* = \nabla \ln \rho_*^{1/2} = -\nabla \phi$. Accordingly, a stationary solution of the Fokker-Planck equation actually appears in the form (Gibbs-Boltzmann by provenance [1]) $\rho_*(x) = (1/Z) \exp[-U(x)]$, with the normalization constant $Z = \int_R \exp(-U) dx$, where $U(x) = 2\phi(x)$.

Following a standard procedure [9,10], given a stationary density $\rho_*(x)$, one can transform the Fokker-Planck dynamics into an associated Hermitian (Schrödinger-type) dynamical problem in $L^2(R)$, by means of a factorization:

$$\rho(x, t) = \Psi(x, t) \rho_*^{1/2}(x). \quad (3)$$

Indeed, the Fokker-Planck evolution of $\rho(x, t)$ implies the validity of the generalized diffusion (Schrödinger-type) equation

$$\partial_t \Psi = \frac{1}{2} \Delta \Psi - \mathcal{V} \Psi = -H \Psi, \quad (4)$$

for $\Psi(x, t) = [e^{(-tH)} \Psi](x)$, with $\Psi(x, 0) = \rho(x, 0) / \rho_*^{1/2}(x)$.

Note that the $\rho(x, t) \rightarrow \rho_*(x)$ as $t \rightarrow \infty$ needs to be paralleled by $\Psi(x, t) \rightarrow \rho_*^{1/2}(x)$; hence, $\Psi(x, t)$ itself exhibits the relaxation behavior (its pathwise implementation is actually the main focus of the present paper).

We demand that $H \rho_*^{1/2} = 0$, which implies that the admissible functional form of the potential function $\mathcal{V}(x)$ derives as a function of $\rho_*^{1/2}(x)$ [1]:

$$\mathcal{V}(x) = \frac{1}{2} \frac{\Delta \rho_*^{1/2}}{\rho_*^{1/2}} = \frac{1}{2} (b^2 + \nabla b) = \frac{1}{2} [(\nabla \phi)^2 - \Delta \phi], \quad (5)$$

with $b(x) = -\nabla \phi(x)$. Note that proceeding in reverse, the functional form (5) of the potential function $\mathcal{V}(x)$ is a guarantee for the existence of the bottom eigenvalue zero of the Hermitian operator $H = -\frac{1}{2} \Delta + \mathcal{V}$, associated with a strictly positive ground state $\rho_*^{1/2}(x)$.

We note that by its very derivation, the potential function $\mathcal{V}(x)$ is not necessarily positive definite, nor nonnegative, but surely is bounded from below and continuous (this is secured by the properties of $\rho_*(x)$ and thence $\phi(x) = \nabla \ln \rho_*^{1/2}$). This admissible negativity property of $\mathcal{V}(x)$ on bounded subsets of R will be of relevance in our further discussion. We shall relate it to the concept of trajectory cloning (branching) for killed diffusion processes.

B. Path integration hints

Let us notice that by employing the identity $\nabla(b\rho) = (b\nabla)\rho + \rho(\nabla b)$ we can rewrite the Fokker-Planck operator L^* , Eq. (2), as follows:

$$L^* = \frac{1}{2} \Delta - b\nabla - (\nabla b) = \frac{1}{2} (\nabla - b)^2 - \mathcal{V}, \quad (6)$$

where \mathcal{V} has been previously defined in Eq. (5), cf. Ref. [12].

It is known [2,11,12] that the transition probability densities of the diffusion processes in question, actually coincides with the integral kernel of the motion operator $\exp(tL^*)$:

$$p(\vec{y}, s, \vec{x}, t) = [e^{L^*(t-s)}](\vec{y}, \vec{x}). \quad (7)$$

Moreover [11], Fokker-Planck transition probability density functions and probability densities, for diffusions with (non)conservative drifts, are known to be amenable to Feynman's path integration routines. In case of conservative drifts, this can be achieved by means of a multiplicative (Doob-like) conditioning of the related (strictly positive) Feynman-Kac kernels, [1,3,7,8,11,12,16], provided the existence of stationary pdfs is granted.

The path integral context for drifted diffusion processes has been revived in Refs. [2,11,12], through the formula “for the propagator associated with the Langevin system” (1) [e.g., the integral kernel of the operator $\exp(tL^*)$]:

$$\begin{aligned} p(y, 0, x, t) &= \exp(L^*t)(y, x) \\ &= \int_{x(\tau=0)=y}^{x(\tau=t)=x} \mathcal{D}x(\tau) \exp \left[- \int_0^t d\tau \mathcal{L}(x(\tau), \dot{x}(\tau)) \right], \end{aligned} \quad (8)$$

where the τ -dynamics stems from the (actually Euclidean) Lagrangian \mathcal{L} :

$$\begin{aligned} \mathcal{L}(x(\tau), \dot{x}(\tau)) &= \frac{1}{2} [\dot{x}(\tau) - b(x(\tau))]^2 + \frac{1}{2} \nabla b(x(\tau)) \\ &= \frac{1}{2} \dot{x}^2(\tau) - \dot{x}(\tau) b(x(\tau)) + \mathcal{V}(x(\tau)), \end{aligned} \quad (9)$$

with $\mathcal{V}(x)$ given by Eq. (5).

Remark 1: We recall that the “normal” (e.g., non-Euclidean) classical Lagrangian would have the form $L = T - V$ with $T = \dot{x}^2/2$ and $V(x, x, t) = \mathcal{V} - \dot{x}b$. The diffusion-induced Lagrangian (9) clearly has the Euclidean form $\mathcal{L} = \mathcal{T} + V$.

Let us consider the action functional (e.g., minus exponent) in Eq. (8), in association with the drift field $b = -\nabla \phi = \nabla \ln \rho_*^{1/2}$. We readily infer that the term $\dot{x}(\tau) b(x(\tau))$ in the Lagrangian (9) contributes

$$\begin{aligned} \int_0^t \dot{x}[-\nabla \phi(x(\tau))] d\tau &= - \int_0^t \frac{d}{d\tau} \phi(x(\tau)) d\tau \\ &= \phi(x(0)) - \phi(x(t)) \end{aligned} \quad (10)$$

to the action functional.

Therefore, the related probability density function [path integral kernel of $\exp(tL^*)$] can be rewritten in the form

$$p(y, 0, x, t) = e^{\phi(y) - \phi(x)} k(y, 0, x, t), \quad (11)$$

where the new function $k(y, 0, x, t)$ is no longer a transition probability density (does not integrate to one) but an integral kernel of another motion operator [actually $\exp(-tH)$, cf. Eq. (4)]:

$$k(y, 0, x, t) = \int_{x(\tau=0)=y}^{x(\tau=t)=x} \mathcal{D}x(\tau) \exp \left[- \int_0^t d\tau \mathcal{L}_{st}(x(\tau), \dot{x}(\tau)) \right], \quad (12)$$

where

$$\mathcal{L}_{st}(x(\tau), \dot{x}(\tau)) = \frac{1}{2}\dot{x}^2(\tau) + \mathcal{V}(x(\tau)), \quad (13)$$

and \mathcal{V} is given by Eq. (5).

On the operator level, the passage from the transition kernel p of Eq. (8) to k of Eq. (12) amounts to the similarity transformation [1,2,10,12]:

$$H = e^\phi L^* e^{-\phi} = -\frac{1}{2}\Delta + \mathcal{V}, \quad (14)$$

which in fact “stays behind” the transformation (3), mapping the Fokker-Plack equation into the generalized heat (Schrödinger-type) equation. The outcome can be readily verified by resorting to the operator identity $e^\phi \nabla e^{-\phi} = \nabla - (\nabla\phi)$.

Accordingly, we have $[\exp(-tH)](y, x) = k(y, 0, x, t)$, whose path integral evaluation reduces to the Feynman-Kac formula (12) [3,4,16].

Concerning the generalized diffusion equation (4), we clearly have $\Psi(x, t) = [e^{(-tH)}\Psi](x)$ with H , Eq. (14). It is useful to mention that for an undisputable validity of the formalism, we need to impose some assumptions upon the potential function \mathcal{V} : to be continuous and bounded from below function, plus an implicit technical assumption that H is not merely Hermitian, but a selfadjoint operator [3,4]. Then, we know that $k(y, 0, x, t) = k(x, 0, y, t)$ is positive symmetric integral kernel of the semigroup operator $\exp(-tH)$, given by the Feynman-Kac formula with an explicit \mathcal{V} entry, cf. Refs. [4,6–8]. We emphasize that \mathcal{V} may take negative values, while being bounded from below.

C. What does the Feynman-Kac formula tell us about the trajectories fate and destiny?

While in the path integral vein, we recall that the Feynman-Kac formula can be redefined as a weighted integral over sample paths of the Wiener process (colloquially, the free Brownian motion), with the conditional Wiener path measure $\mu_{(y,0,x,t)}(\omega)$ being involved [3,4,6]:

$$k(y, 0, x, t) = [\exp(-tH)](y, x) = \int \exp\left[-\int_0^t \mathcal{V}(\omega(\tau))d\tau\right] d\mu_{(y,0,x,t)}(\omega). \quad (15)$$

Here paths ω originate from y at time $t = 0$ and their destination is x to be reached at time $t > 0$. In passing we note that in contrast to the kernel function $k(y, 0, x, t)$, transition pdfs $p(y, 0, x, t)$ are not symmetric functions of x and y .

We may here try to imagine a pictorial view of the Brownian motion in potential energy landscapes, as set by Feynman-Kac potential spatial profiles. The Wiener path measure in Eq. (15) refers to paths of the free (undisturbed) Brownian motion, and it is the exponential factor which represents [4] “the distortion of the distribution of free-particle paths, introduced by the potential.” Thus, a possible pathwise

interpretation of the Feynman-Kac formula can be given in terms of a random mover in a potential $\mathcal{V}(x)$, which acts as a mechanism that reinforces or penalizes the random mover tendency to reside or go into specific regions of space. A “responsibility” for a weighted redistribution of random paths in a given time interval, is here transferred from drift fields of Eq. (1) to the spatial variability of potentials $\mathcal{V}(x)$ of Eq. (5), specifically to their curvature and steepness.

There is, however, a problem. For the validity of the above pictorial view, we should presume that once released from y at $t = 0$, a bunch of continuous sample trajectories should be in existence (survive) up to the terminal point x at time t . There should be no loss or gain of the “probability mass,” like, e.g., changes in the overall number of involved sample paths, or surplus and deficit contributions from *a priori* admissible paths with random starting and terminal times [5,17–20].

Essentially, if one accepts the *realistic particle* propagation ansatz, then in the quantum mechanical contexts (the pseudo-Schrödinger equation (5) being tentatively included) nonrelativistic particle paths in a field of a potential should never be terminated [4]. We point out that while taking the “random mover” concept seriously, the killing picture described above might be appropriate when one relates the average to a diffusion process in a medium capable of absorption, like, e.g., the diffusion of neutrons in a nuclear reactor with active moderator materials.

1. Killing alternative

However, we may invoke the *killing* alternative, favored in Refs. [5–20]. Then, the Feynman-Kac formula is interpreted as a weighted average over the Wiener process with weight $\exp[-\int_0^t \mathcal{V}(\omega(\tau))d\tau]$ for each sample path. Let us tentatively assume, [4,5], that $\mathcal{V}(x) \geq 0$, departing for a while from the generic property of the (*a priori*) confining potential $\mathcal{V}(x)$ to be bounded from below [that in principle allows $\mathcal{V}(x)$ to take negative values in bounded subdomains in R].

We may picture a set of Wiener paths in the (x, τ) space in terms of a random *killing* mechanism inflicted by $\mathcal{V}(x)$. Namely, we admit that a particle following one of sample paths gets killed at a point x , in the time interval $\delta\tau$ (infinitesimally $d\tau$) with the probability $\mathcal{V}(x)\delta\tau$.

The killed path is henceforth removed from the ongoing (surviving) ensemble of Wiener paths. That modifies the statistics of paths-in-existence to the extent, that at the final time t , the Feynman-Kac average is taken exclusively with respect to paths, which survive the full period $[0, t]$ to complete their travel from y to x .

The factor $\exp[-\int_0^t \mathcal{V}(\omega(\tau))d\tau]$ in Eq. (18) is a probability that a particle (random mover) completes its path from $(y, 0)$ to (x, t) , cf. Ref. [4].

Denoting $W(\tau)$ the Wiener process, cf. Eq. (1), we can write a formal stochastic differential equation for the diffusion process with the killing rate $\mathcal{V}(x) \geq 0$:

$$X(\tau + d\tau) = \begin{cases} \emptyset & \text{with probability } \mathcal{V}(X(\tau))d\tau, \\ X(\tau) + dW(\tau) & \text{with probability } [1 - \mathcal{V}(X(\tau))d\tau]. \end{cases} \quad (16)$$

Since the operator $H = -(1/2)\Delta + \mathcal{V}$ is the generator of the diffusion process with killing, we recognize Eq. (4), with $\Psi(x, t) = [\exp(-Ht)\Psi](x)$, as the appropriate motion rule (generalized diffusion equation) following directly from Eq. (16) [13]. Surely, $\Psi(x, t)$ does not conserve probability, and for $\mathcal{V} > 0$ asymptotically approaches 0.

2. Branching alternative

We emphasize, that the $\mathcal{V} > 0$ ansatz temporarily excludes from considerations bounded from below potentials, which are negative-valued on finite open subintervals in R .

We shall abandon this restriction below, thus enforcing a compensation of killing via cloning of trajectories, and ultimately by introducing branching diffusion processes in the context set by Eqs. (4), (5), and (15). To this end we shall accomplish the pathwise construction of such processes, in conjunction with simple Hamiltonian model system, naturally associated with Eqs. (1)–(5) and subsequently with Eqs. (8), (12), and (15).

For further analysis, we select exemplary potentials $\mathcal{V}(x)$ for the Hamiltonian (14), in the form of Eq. (5) deriving from the Fokker-Plack drift, $b(x) = -\nabla\phi = \nabla \ln \rho_*^{1/2}$:

(i) the downward shifted harmonic potential

$$\mathcal{V}(x) = \frac{1}{2}(x^2 - 1) = V(x) - \frac{1}{2}, \quad (17)$$

where $1/2$ is the bottom eigenvalue of the standard quantum harmonic oscillator with $V(x) = x^2/2$. The Feynman-Kac potential $\mathcal{V}(x)$, which is negative in $(-1, 1)$, derives from $b(x) = -x$, related to $\rho_*(x) = \pi^{-1/2} \exp(-x^2)$;

(ii) the downward shifted infinite well potential

$$\mathcal{V}(x) = \begin{cases} -\frac{\pi^2}{8}, & x \in (-1, 1), \\ \infty, & x \in R \setminus (-1, 1). \end{cases} \quad (18)$$

This constant potential is negative in $(-1, 1)$, and can be obtained by shifting down (energy renormalization) the standard infinite well potential by the lowest eigenvalue $\pi^2/8$ of the energy operator with potential bottom set at 0, cf. Ref. [1] [the “standard” potential has the form of Eq. (18), but takes the value 0 in $(-1, 1)$]. The emergent $\mathcal{V}(x) = -\pi^2/8$, $x \in (-1, 1)$ derives from the Fokker-Planck drift for the process confined in the interval forever, $b(x) = -(\pi/2) \tan(x\pi/2)$, with $\rho_*(x) = \cos^2(\pi x/2)$; see, e.g., Ref. [1].

We note that our exemplary Hamiltonians have the bottom eigenvalue 0, with $\rho_*^{1/2}$ as the corresponding (ground-state) eigenfunction; compare, e.g., also Refs. [3,6,15].

Our further discussion will refer to a less restrictive conceptual setting, where the sample path notion will not necessarily refer to *realistic* particle trajectories, but to more abstract sample paths to be followed in the course of a stochastic diffusion process (it is useful to remember that the mathematical construct of Wiener paths may be safely termed “unrealistic”). This will ultimately lead us to the “branching alternative” as an appropriate diffusion scenario underlying the dynamics (15) in case of Feynman-Kac potentials with finite negativity domains.

A more detailed pathwise discussion of the branching alternative is relegated to Secs. II B, II C, and II D. Here, we extract from the formulas (17) and (18) the respective branching rates,

born to action if $x(t) \in (-1, 1)$: (i) $-\mathcal{V}(x(t)) = \frac{1}{2}[1 - x^2(t)]$, and (ii) $-\mathcal{V}(x(t)) = +\pi^2/8$.

We recall that the nonnegative Feynman-Kac potential $\mathcal{V}(x(t)) \geq 0$, has been interpreted as the killing rate in (16). Accordingly, $\mathcal{V}(x(t))\delta t$ is used as a killing probability if \mathcal{V} is positive, while $-\mathcal{V}(x(t))\delta t$ is interpreted as the branching probability if \mathcal{V} is negative.

Technical Comment 1: We emphasize that the killing and branching rates turn over into respective killing and branching probabilities, only after multiplying them by properly tuned time increments δt (ultimately infinitesimal, denoted dt). In particular, in reference to the branching simulations, we realize that the harmonic potential (17) has a minimum $-1/2$ for $x \in (-1, 1)$, while the potential (18) takes the constant value ~ -1.23 for $x \in (-1, 1)$. Time increments involved in our simulations are $\delta t \leq 0.001$. In the harmonic case, the killing effect is to occur for $|x| > 1$, where $\mathcal{V}(x) > 0$ and for $|x| > \sqrt{3}$, we have $\mathcal{V}(x) > 1 \rightarrow \infty$. In computer simulations we always impose a spatial cutoff on the admissible domain. Then, the preselected $x_{\max} > 0$ defines the local maximum for the potential (17) in the domain $[-x_{\max}, x_{\max}]$. The value of $\mathcal{V}(\pm x_{\max}) = \mathcal{V}_{\max}$ dictates the fine tuned choice of δt , allowing to secure the consistent killing probability meaning of $\mathcal{V}(x)\delta t \leq 1$ for $x \in (-x_{\max}, x_{\max})$.

These reservations are actually observed in the killing and cloning (trajectory bifurcation) and move-on scenarios employed in the direct pathwise analysis of Sec. III A.

II. DIFFUSION PROCESS WITH KILLING AND CLONING (BRANCHING)

A. Killing can be tamed: Harmonic potential

Since we know [1,7,8] (see below) exact analytic formulas for Feynman-Kac integral kernels with quadratic potentials, we shall consider two options concerning the choice of the potential in Eq. (15): (i) nonnegative, harmonic one $\mathcal{V}(x) \rightarrow V(x) = x^2/2$, and (ii) bounded from below $\mathcal{V}(x) = (x^2 - 1)/2 = V(x) - 1/2$, which is negative in $(-1, 1)$ (e.g., the “harmonic potential with subtraction”, [6]). We keep $y = 0$ as the initial $t = 0$ starting point for all trajectories.

This entails a visualization of the drastic difference in the asymptotic $t \rightarrow \infty$ behavior of $k(0, 0, x, t)$, while set against $k_0(0, 0, x, t)$, which is of major interest in our subsequent discussion, and ultimately will lead us to the concept of *branching* diffusion processes in the context of the dynamics inferred from Eq. (15).

For clarity of discussion, we recall the analytic form of the integral kernel of the motion operator for the killed diffusion process: $[\exp(-tH_0)](y, x)$, where $H_0 = -(1/2)\Delta + V(x)$ and $V(x) = x^2/2$ is the standard harmonic potential. We have [1,3,7,8]

$$\begin{aligned} k_0(y, 0, x, t) &= \exp(-tH_0)(y, x) \\ &= \frac{1}{(2\pi \sinh t)^{1/2}} \exp\left[-\frac{(x^2 + y^2) \cosh t - 2xy}{2 \sinh t}\right]. \end{aligned} \quad (19)$$

On the analytic level of description, the integral kernel of $[\exp(-tH)](y, x)$ with the renormalized harmonic

potential $V(x) = \frac{1}{2}(x^2 - 1)$ has the form looking trivially different from the previous formula, since the tamed killing effect is obtained via a multiplication by $\exp(+t/2)$:

$$\begin{aligned} k(y, 0, x, t) &= \exp(-tH)(y, x) \\ &= \exp(+t/2)k_0(y, 0, x, t) \\ &= [\pi(1 - \exp(-2t))]^{-1/2} \\ &\quad \times \exp\left[\frac{1}{2}(x^2 - y^2) - \frac{(x - e^{-t}y)^2}{1 - e^{-2t}}\right]. \end{aligned} \quad (20)$$

Remark 2: We can here establish a direct relationship of the above propagators with the transition probability density $p(y, 0, x, t)$ of the familiar Ornstein-Uhlenbeck process in R . Namely, we have

$$\begin{aligned} p(y, 0, x, t) &= k(y, 0, x, t) \frac{\rho_*^{1/2}(x)}{\rho_*^{1/2}(y)} \\ &= e^{+t/2}k_0(y, 0, x, t) \frac{\rho_*^{1/2}(x)}{\rho_*^{1/2}(y)} \\ &= (\pi[1 - \exp(-2t)])^{-1/2} \exp\left[-\frac{(x - e^{-t}y)^2}{1 - e^{-2t}}\right], \end{aligned} \quad (21)$$

where the invariant pdf of the OU process reads $\rho_*(x) = (\pi)^{-1/2} \exp(-x^2)$.

Let us make a closer look at the integral kernel (20), which refers to the tamed killing [1]. By its definition, at time $t = 0$, all sample trajectories are being released from $y = 0$. Denoting $k(x, t) = k(0, 0, x, t)$ we get

$$k(x, t) = \frac{1}{\sqrt{\pi(1 - e^{-2t})}} \exp\left[\frac{x^2}{2} - \frac{x^2}{1 - e^{-2t}}\right]. \quad (22)$$

For large-time values, and ultimately $t \rightarrow \infty$, the kernel $k(x, t)$ asymptotically approaches

$$K(x) = \frac{1}{\sqrt{\pi}} \exp\left(\frac{-x^2}{2}\right). \quad (23)$$

We note a subtle difference, namely $(\pi)^{-1/2}$ replacing $(\pi)^{-1/4}$, if compared with the asymptotic form of $\rho_*^{1/2}$, recovered in the OU process.

Let us integrate the kernel (22) over all locations $x \in R$:

$$K(t) = \int_{-\infty}^{\infty} k(t, x) dx = \sqrt{\frac{2}{1 + e^{-2t}}}. \quad (24)$$

Clearly $1 \leq K(t) \leq \sqrt{2}$, and as $t \rightarrow \infty$, the upper bound $K(t) \rightarrow K = \sqrt{2} \approx 1.41421$ is reached. We note that $K(t)$ is a monotonically increasing function, hence $\partial_t K(t) > 0$. To the contrary, we infer from Eq. (20) that $K_0(t) = e^{-t/2}K(t)$, decays exponentially for large t . For completeness, let us add that in the standard lore $K_0(t) \rightarrow 0$, with $K_0(0) = 1$, has the interpretation of the survival probability for finite times t .

Below we shall give computer-assisted arguments to the meaning of $K(t)$ as the quantitative measure of the overall number $N(t)$ of alive sample trajectories, while set against their initial number $N(0)$. Actually, we shall demonstrate that $K(t) \approx N(t)/N(0)$.

We point out, that this interpretation is a straightforward generalization of the properties of $k_0(x, t)$ in case of the pure killing. We have verified that the survival probability $K_0(t) = \int_R k_0(x, t) dx$ provides a measure of the fraction of initially released trajectories, which have survived until time t . Obviously, in the pure killing case, we have $N(t)/N(0) < 1$ for all $t > 0$, followed by an asymptotic decay to 0

Effectively, as confirmed in simulations, the initial number 100 000 of released at $t = 0$ trajectories, in the course of the branching diffusion with killing, increases up to $\approx 141\,421$. This is encoded in the evolution of $K(t)$, which begins from $K(0) = 1$ and approaches the limiting value $K = 1.41421 = 141\,421/100\,000$.

Thus, $K(t)$ is the relative measure of the “net trajectory production surplus” in our branching process with killing.

B. Probabilistic detour: Killing and cloning (branching) may saturate each other

We can legitimately consider $K(t)$ of Eq. (24) as the $L(R)$ normalization of the function $k(x, t)$, Eq. (22). Accordingly, we get a legitimate probability density function

$$\rho(x, t) = \frac{k(x, t)}{K(t)}, \quad (25)$$

whose evolution rule directly follows from the motion rule for $k(0, 0, x, t) = [\exp(-tH)](0, x)$, (22), where $H = (1/2)[- \Delta + (x^2 - 1)]$ and $\partial_t k = -H_x k$. We have

$$\partial_t \rho = \frac{1}{K(t)} \partial_t k(x, t) - k(x, t) \frac{\partial_t K(t)}{K^2(t)} = -\frac{1}{2} \Delta \rho - [\mathcal{V} + \mathcal{K}] \rho, \quad (26)$$

where we encounter a specific time-dependent killing-type contribution $\mathcal{K}(t)$ to the overall expression for the potential term on the right-hand side of Eq. (26), which is positive-valued for all $t > 0$:

$$\mathcal{K}(t) = \partial_t \ln K(t) = +\frac{1}{e^{2t} + 1}. \quad (27)$$

We note that $\rho(x, t)$ is a monotonically increasing function toward the asymptotic shape $K(x)/K$. The “probability mass” $\int_R \rho(x, t) dx$ remains conserved and equals 1 for all times $t \geq 0$.

If we interpret the positivity domain of the original potential $\mathcal{V}(x) = (1/2)(x^2 - 1)$ as responsible for killing, while the negativity domain as responsible for birth (cloning) of trajectories, then we need to interpret the negative-valued “corrector” $\mathcal{K}(t)$ in Eq. (26) as an additional killing term, which reduces the surplus of cloned trajectories. This secures that there is no “probability mass” excess, we have observed in connection with the large-time asymptotic of $K(t) \rightarrow \sqrt{2}$, cf. Eq. (24).

We remind that $\mathcal{V}(x)$ is negative in $(-1, 1)$ and nonnegative in $R \setminus (-1, 1)$. Thus the compensating term \mathcal{K} increases the overall killing effect on R against that of cloning alone in $(-1, 1)$. As a consequence, the random motion $\rho(x, t)$ not only preserves the “probability mass” but sets down at the

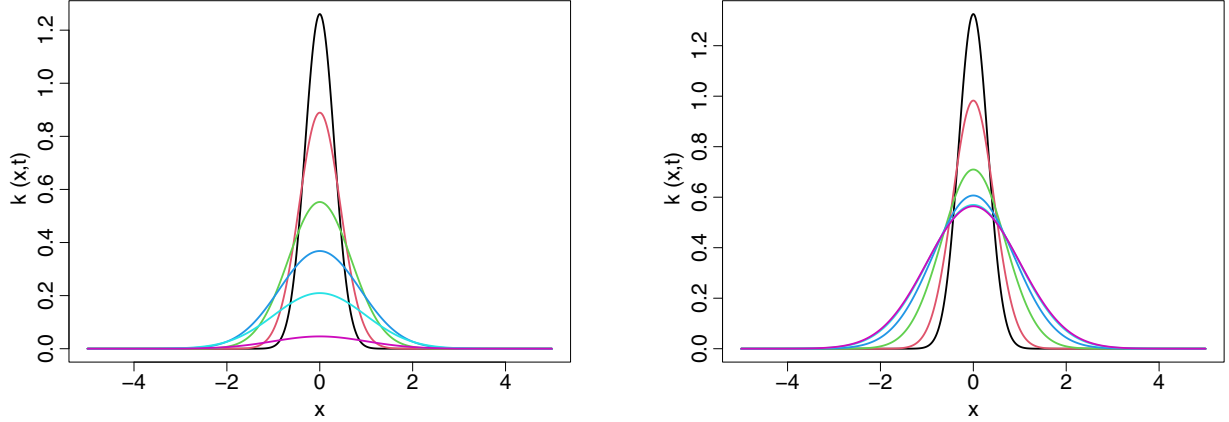


FIG. 1. Left panel: Diffusion with the harmonic $V(x) = x^2/2$ killing rate. An asymptotic decay down to 0; follow the maxima of depicted curves $k(0, 0, x, t) = k(x, t)$ for times $t = 0.1, 0.2, 0.5, 1, 2, 5$. Right panel: Relaxation process with the Feynman-Kac potential $\mathcal{V}(x) = V(x) - 1/2 = (x^2 - 1)/2$ for the same time instants as in the left panel. The asymptotic curve is $K(x) = (\pi)^{-1/2} \exp(-x^2/2)$, with a maximum $\pi^{-1/2} \sim 0,5641$.

asymptotic stationary pdf,

$$\rho(x, t) \rightarrow \rho_*(x) = \frac{K(x)}{K} = \frac{1}{\sqrt{2\pi}} \exp\left(-\frac{x^2}{2}\right), \quad (28)$$

which is a normalized Gaussian, with a maximum $(2\pi)^{-1/2} \sim 0.3989$. This should be compared with the $\pi^{-1/2} \sim 0.5641$ outcome mentioned in the caption of Fig. 1.

We note that the limiting behavior (28) has close links with the concept of quasi-stationary distributions and related Yaglom-type limits [21–28].

C. Direct hint toward the branching scenario

In below we shall give a computer-assisted pathwise argument that by integrating $k(x, t)$ and eventually $K(x)$ over R , we get a quantitative (relative) measure of the number of alive trajectories, if compared with their initial population at $t = 0$.

Surely, the integrals (23) and (24) have no meaning of the “survival” or “whatsoever” probability. Nonetheless, Eq. (24) admits a direct interpretation in terms of the ratio of the number of actually alive trajectories, while set against the initial number 100 000 of released trajectories at time $t = 0$. In the harmonic case, an overall number of alive trajectories increases up to a saturation limit, roughly about 141 421.

This conjecture is easily verifiable by means of our simulation killing and branching and move-on algorithm (detailed in below), for all times of interest. We can literally count all trajectories crossing at t any predefined spatial subinterval Δx in R . For concreteness, we indicate that $\Delta x \approx 0,03$ is employed, while considering the interval of interest $([-3, 3])$ for reference); see, e.g., Fig. 3. In fact, the coarse-graining of the reference $[-3, 3]$ needs a bit more meticulous approach, which we shall explain below in Sec. III, in the subsection devoted to the trajectory counting procedure.

Accordingly, the number of alive trajectories needs to grow in the process in which killing (even if we regard it as tamed) is admitted. And that we can justify only by introducing the trajectory birth (cloning, branching) process. Ultimately, the stable balance between killing and branching (“probability mass generation”) is achieved when we reach (approximately)

the “saturation” number of alive trajectories (like 1.4×10^5 , against the initial number 10^5 at $t = 0$).

However, we can expand $K(t)$ defined in Eq. (24) into power series for small t ,

$$\sqrt{\frac{2}{1 + e^{-2t}}} = 1 + \frac{t}{2} - \frac{t^2}{8} + O(t^3). \quad (29)$$

The coefficient $1/2$ in the linear term may be interpreted as the cloning and creation speed for new trajectories appearing in the branching events, soon after the trajectory release from $y = 0$ at $t = 0$. To justify this interpretation, we note that for small t , all trajectories are still concentrated in the close vicinity of ($y = x(0) = 0$), and they are effectively cloned (alternatively, given birth) with the probability

$$-\mathcal{V}(x(t))\delta t = \frac{1}{2}(1 - x^2(t))\delta t \approx \frac{\delta t}{2}. \quad (30)$$

We recall that in the interval $(-1, 1)$ our potential $\mathcal{V}(x) = (x^2 - 1)/2$ takes negative values, whose sign inversion leads to the above probability notion.

For completeness, let us mention that the potential (18) induces the appropriately modified version of the birth (branching) probability (30):

$$-\mathcal{V}(x(t))\delta t = +\frac{\pi^2}{8}\delta t, \quad (31)$$

which stands for the the birth (cloning, branching) probability for trajectories in the interior $(-1, 1)$ of the interval with absorbing ends. The above mentioned trajectory counting procedure, in this case involves a coarse-graining of the interval $(-1, 1)$.

D. Interval with absorbing boundaries

Let us consider the interval $(-1, 1)$ as a model arena for the diffusion process with absorbing boundaries at points ± 1 , cf. Refs. [1,7,8,29] (we recall that we assign the value $1/2$ to the diffusion coefficient). We reinterpret the original diffusion problem through a useful quantum-like artifice of the infinite well potential, and subsequently a related one, whose well

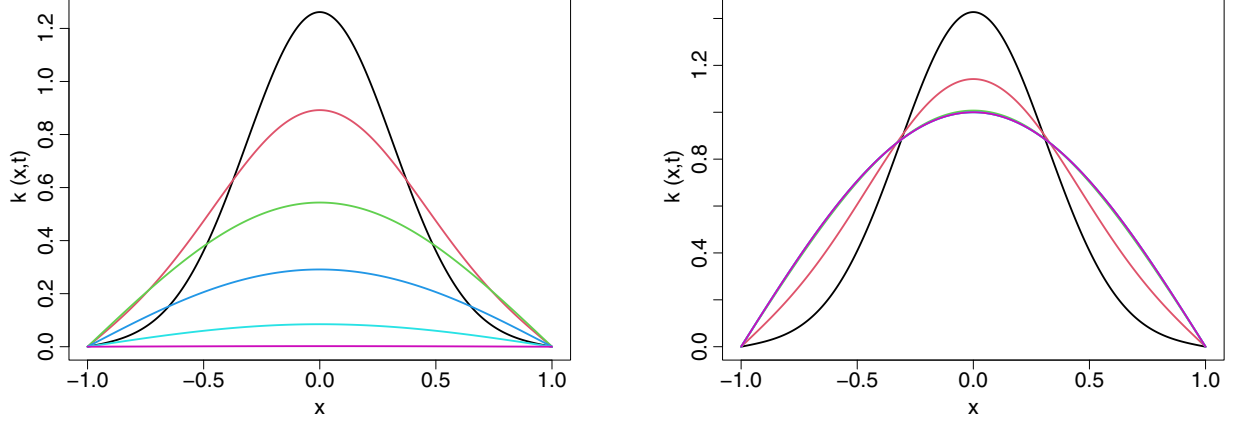


FIG. 2. Left panel: Diffusion with killing (absorption) at the boundaries of the interval $(-1, 1)$. An asymptotic decay to 0; follow the maxima of depicted curves $k(0, 0, x, t) = k(x, t)$ for times $t = 0.1, 0.2, 0.5, 1, 2, 5$. Right panel: Relaxation process with the Feynman-Kac potential (cloning rate) $\mathcal{V}(x) = +\pi^2/8$ in $(-1, 1)$, for the same time instants as in the left panel. The asymptotic curve is $K(x) = \cos(\pi x/2)$, $x \in (-1, 1)$, with a maximum 1.

bottom is shifted down on the energy scale to the negative value $\mathcal{V}(x) = -\pi^2/8$ for all $x \in (-1, 1)$. We note that $+\pi^2/8$ actually is the ground-state eigenvalue of the original quantum infinite well spectral problem, with the well bottom set at 0.

The Feynman-Kac integral kernel corresponding to the related (tamed killing) dynamics has the form [1]:

$$k(y, 0, x, t) = \exp(\pi^2 t/8) k_0(y, 0, x, t), \quad (32)$$

and like in the harmonic case, differs from the standard killing kernel $k_0(y, 0, x, t)$ by the killing taming factor (here, $\exp(\pi^2 t/8)$):

$$k_0(y, 0, x, t) = \sum_{n=1}^{\infty} \exp(-n^2 \pi^2 t/8) \sin \frac{n\pi(x+1)}{2} \times \sin \frac{n\pi(y+1)}{2}. \quad (33)$$

Since $\sin \frac{n\pi(y+1)}{2}$ for $y=0$ equals $\sin \frac{n\pi}{2}$, which vanishes for n even, the kernel $k(0, 0, x, t) = k(x, t)$ can be rewritten as

$$k(x, t) = \sum_{l=0}^{\infty} (-1)^l \exp[(1 - (2l+1)^2) \pi^2 t/8] \times \sin \left(\frac{(2l+1)\pi(x+1)}{2} \right), \quad (34)$$

or equivalently,

$$k(x, t) = \sum_{l=0}^{\infty} (-1)^l \exp[(-l^2 - l) \pi^2 t/2] \times \sin \left(\frac{(2l+1)\pi(x+1)}{2} \right). \quad (35)$$

For large times $k(x, t)$ approaches the asymptotic shape

$$K(x) = \sin \frac{\pi(x+1)}{2} = \cos \left(\frac{\pi x}{2} \right), \quad (36)$$

with $x \in (-1, 1)$.

Let us integrate $k(x, t)$ over x , and interpret the outcome as the quantitative description of the fate (destiny) of a bunch (population) of random trajectories, while propagated from $t=0$ to some $t > 0$. We have

$$\int_{-1}^1 \sin \left(\frac{(2l+1)\pi(x+1)}{2} \right) dx = 4/[(2l+1)\pi], \quad (37)$$

and therefore

$$K(t) = \int_{-1}^1 k(x, t) dx = \sum_{l=0}^{\infty} \frac{(-1)^l 4}{(2l+1)\pi} \exp[-(l^2 + l) \pi^2 t/2]. \quad (38)$$

For large t ($t \rightarrow \infty$) only the $l=0$ term survives in $K(t)$ and we have

$$\lim_{t \rightarrow \infty} K(t) = K = \frac{4}{\pi} \approx 1.2732. \quad (39)$$

Clearly, $\int_{-1}^1 \cos(\pi x/2) dx = 4/\pi$. Therefore, we can proceed analogously to the discussion of Sec. II B and introduce the legitimate probability density function, see, e.g., Eq. (25), with the relaxation behavior manifested as $t \rightarrow \infty$:

$$\rho(x, t) = \frac{k(x, t)}{K(t)} \rightarrow \rho_*(x) = \frac{K(x)}{K} = \frac{\pi}{4} \cos(\pi x/2), \quad (40)$$

where $\rho_*(x)$ has a maximum at $\frac{\pi}{4} \approx 0.7854$.

If we turn back to the untamed killing case, i.e., consider the interval with absorbing ends, then a direct consequence of Eqs. (32) and (33) is an exponential decay of the survival probability $K_0(t) = e^{-i\pi^2/8} K(t) \approx (4/\pi) e^{-i\pi^2/8} \rightarrow 0$ with $t \rightarrow \infty$. For the record, we infer from Eqs. (32) and (33) the large-time behavior of $k_0(x, t) \rightarrow e^{-i\pi^2/8} \cos(\pi x/2) \rightarrow 0$, cf. the left panel of Fig. 2.

In line with the conclusion of Sec. II A, we tentatively interpret the asymptotic K value of $K(t)$ as a quantitative measure of the overall amount of killed and (re)born paths, that ultimately survive. We encounter the same as before signature of the trajectory number increase, due to the excess of cloning (branching) against killing. Would we have begun with the number 100 000 of initially released trajectories, their

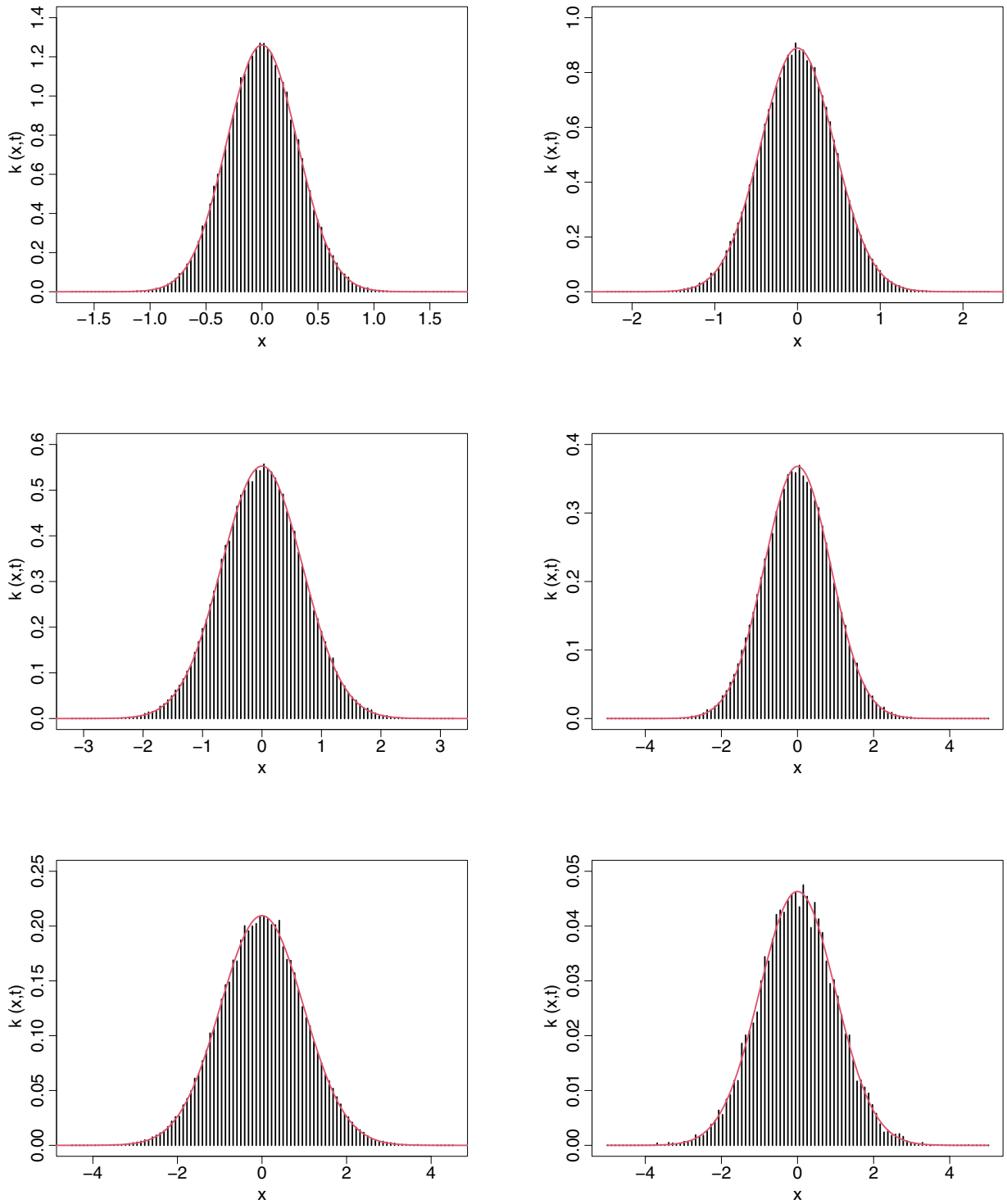


FIG. 3. Effects of the pure killing rate $\mathcal{V}(x) = x^2/2$ in terms of the counting of surviving trajectories [we depict the recorded numbers $N = N(t)$]. Note that scales along the vertical axis change from panel to panel. Time labels stay in correspondence with vertical scales. If read in the decreasing order of scale upper bounds (left to right and next downwards), then we have: $t = 0, 1; N = 99\,766, t = 0.2; N = 98\,981, t = 0.5; N = 94\,085; t = 1; N = 80\,462, t = 2; N = 51\,472, t = 5; N = 11\,565$. Here $N(0) = 10^5$. We realize that $K_0(t) = (\cosh t)^{-1/2} \approx N(t)/N(0) \rightarrow 0$.

net number should increase to about 127 323 as $t \rightarrow \infty$. In terms of $K(t)$ that is encoded in a monotonic growth of $K(t)$ from $K(0) = 1$ to $K = (4/\pi) \approx 1.2732$.

The necessary condition for the validity of the pathwise diffusive implementation of this result, is that (i) the killing (at

the boundaries) is hereby (over)compensated by the trajectory cloning (birth, branching) within the interval $(-1, 1)$, (ii) for large times the killing and cloning rates saturate each other, so that the stable “survival probability” profile $k(x, t) \rightarrow K(x)$ is reached.

A computer-assisted analysis, which confirms the validity of the above killing versus branching trajectory interpretation will be given in below.

III. DIFFUSION WITH KILLING AND BRANCHING: DIRECT PATHWISE ANALYSIS

A. Trajectory generation

The trajectory (sample path) picture stems from the standard Brownian motion $\{X(t), t \geq 0\}$ (e.g., the Wiener process) as introduced in Sec. I, and next incorporating killing via the stochastic differential equation (16). As yet, we have left aside the cloning (branching) scenario.

To implement a computer-assisted trajectory interpretation of the killed diffusion process with branching, as outlined in Secs. I and II, we need to pass from the lore of continuous nowhere differentiable trajectories, to their space and time discretized approximants. The simulation procedure, enabling the trajectories counting, is based on standard assumptions.

Let $t \in [0, T]$, we set $\delta t = T/n$ for a predefined value of $n \in \mathcal{N}$. The notation δt is fairly informal, but presupposes that any finite time interval δt of interest can be made arbitrarily small (we thus bypass the usage of dt). The Brownian walk is defined according to $x(t + \delta t) = x(t) + \sqrt{\delta t} \times u$, where u is the random variable sampled from the normal distribution $N(0, 1)$, $x(0) = 0$.

Our aim is to construct a specific version of the diffusion process (with a link to the broad subject of branching random walks and processes [21–28]), where in the course of time we may have allowed random killing accompanied by random cloning (branching event, giving birth to the, not yet killed trajectory, offspring) of sample paths. Our primary motivation stems from the Feynman-Kac formula, known to be valid for confining potentials $V(x)$, which may not necessarily be nonnegative (the essential restriction is that $V(x)$ is bounded from below and continuous in the area of interest).

Our construction involves the random cloning (branching) option for all sample trajectories in existence, provided they visit (any time) the potential $\mathcal{V}(x)$ negativity area $(-1, 1)$. If the trajectory visits the complement of $(-1, 1)$ in R , then it may be killed (terminated) at random. Trajectories are never killed in $(-1, 1)$.

We discretize time, as mentioned before (while properly adjusting $n \gg 1$ for different test runs). If the simulated random trajectory takes the value $x(t) = x$ for some $t \in [0, T]$, then its subsequent “behavior” admits three instances: killing, cloning, and moving on, whose realization in each simulation step $[t, t + \delta t)$ depends on the concrete value of the potential $\mathcal{V}(x(t)) = \mathcal{V}(x)$, where the sign of $\mathcal{V}(x)$ is of particular importance.

We adopt the following killing and cloning and move-on scenarios:

(1) If $\mathcal{V}(x(t)) \geq 0$, then we interpret $p(t) = \min(1, \delta t \mathcal{V}(x(t)))$ as the probability of the killing event at $x(t) = x$ (no cloning is allowed in this regime). Depending on the killing outcome we admit two options for the step $[t, t + \delta t)$:

(a) the trajectory is killed at $x(t) = x$ with the probability $p(t)$, and thence removed from the trajectory statistics at the

time $t + \delta t$. [For the interval with absorbing endpoints, each trajectory entering the complement of $(-1, 1)$ is killed with the probability one].

(b) if the trajectory is not killed, then it moves-on, by following the evolution rule $x(t + \delta t) = x(t) + \sqrt{\delta t} \times u$, where u a random variable sampled from the normal distribution $N(0, 1)$ [the trajectory survival probability at time t is given by $(1 - p(t))$].

(2) If at $x(t) = x$ the potential is negative-valued, then we consider $|\mathcal{V}(x)| = -\mathcal{V}(x(t))$ as the probability defining factor, while setting $q(t) = \min(1, -\delta t \mathcal{V}(x(t)))$. No killing is allowed in $(-1, 1)$, and we are left with two options:

(a) the cloning (branching) event—the trajectory clones itself (produces an offspring) at $x(t) = x$ with the probability $q(t)$, subsequently both the clone and the parent trajectory independently move on from the branching point, in accordance with the adopted universal rule $x(t + \delta t) = x(t) + \sqrt{\delta t} \times u$, up to time $t + \delta t$. At $t + \delta t$ we thus need to handle two trajectories instead of one.

(b) no offspring—the trajectory follows the evolution $x(t + \delta t) = x(t) + \sqrt{\delta t} \times u$, [that with the probability $(1 - q(t))$].

Technical Comment 2: The above killing versus branching scenarios go beyond the reservations of the Technical Comment 1, and can be adopted to more general confining potentials, bounded from below but admitting negative values. Let us choose *a priori* a certain (small) reference time interval δt . If for some x we have $\mathcal{V}(x) > 1$ and $\delta t \mathcal{V}(x) > 1$, then we may retain a probabilistic interpretation by assuming *per force* that $p = \min(1, \delta t \mathcal{V}(x))$ is the probability of the killing event. In that case the trajectory is killed with the probability 1. Analogously, if $\mathcal{V}(x) < -1$ and $\delta t |\mathcal{V}(x)| > 1$, then we (again and *per force*) assume that $q = \min(1, \delta t |\mathcal{V}(x)|)$ is the branching probability, the trajectory bifurcates (gives birth to a clone) with the probability 1.

We emphasize that killing and branching options are mutually exclusive in our procedure. In the branching literature, cf. Refs. [21–26], one may meet trajectories in which killing and branching occur at the same space-time point. As well, one may consider the option of a multiple offspring (not merely a bifurcation of a trajectory into two) at each branching instant. This is never the case in our procedure. Ultimately, after each simulation time step, we deal with a statistics of all yet alive trajectories.

B. Trajectory counting

In Figs. 3, 4, and 5 we display the outcomes of an explicit trajectory counting for the considered before harmonic variants of the Feynman-Kac potential $\mathcal{V}(x)$. In below we describe the adopted counting and display procedure:

(1) We coarse-grain the spatial axis (x label) by dividing the reference interval of interest into small segments of length Δx .

(a) the reference interval (say $[-3, 3]$ in the harmonic case, or $(-1, 1)$ for killing at boundaries) is selected as follows. At a given time t , for all alive trajectories we choose a minimal value x_{\min} of a trajectory location, and likewise a maximal value x_{\max} ;

(b) the obtained interval $[x_{\min}, x_{\max}]$ is divided into 100 segments, with length $\Delta_t x = (x_{\max} - x_{\min})/100$. We point

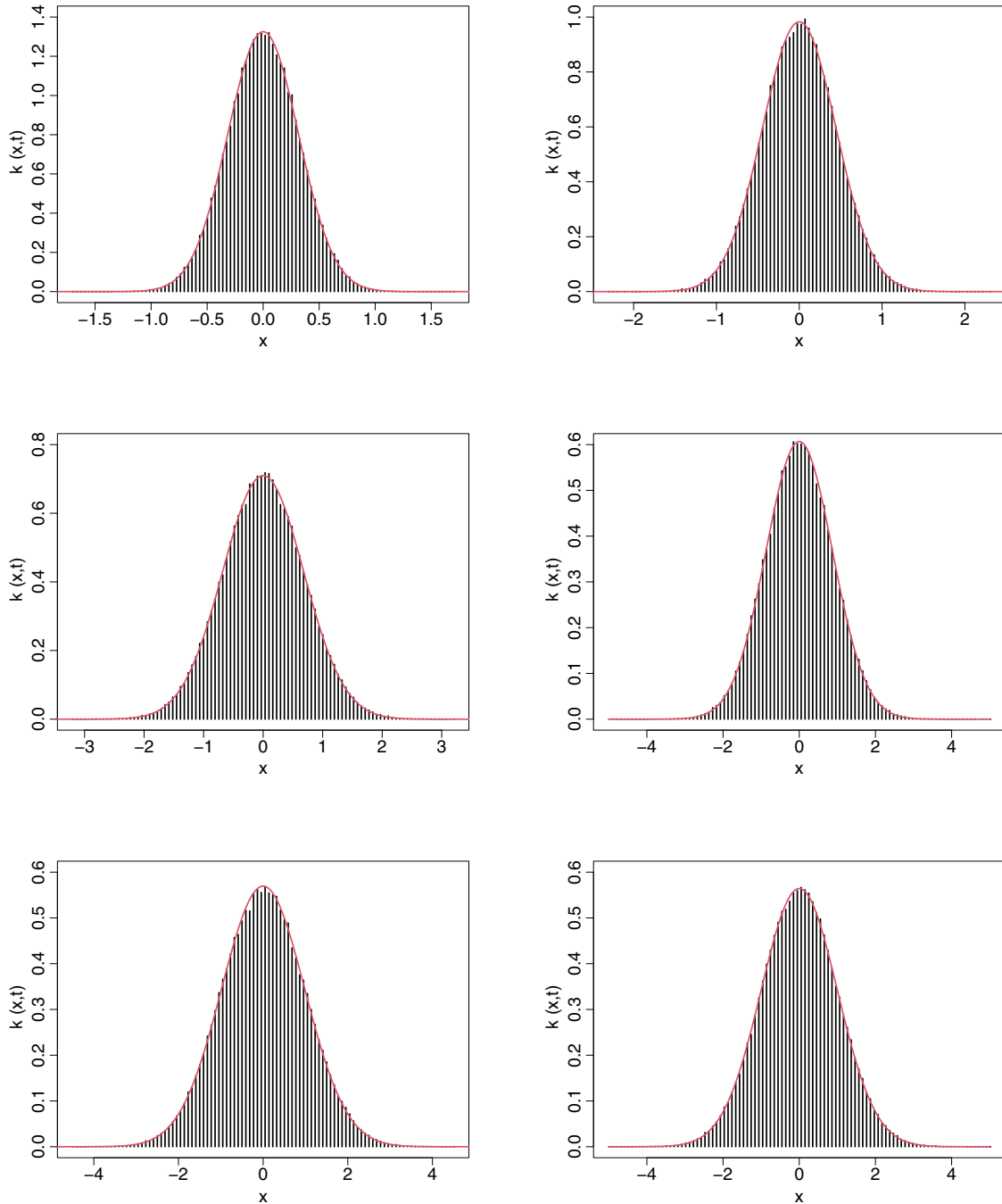


FIG. 4. Effects of the (tamed) killing rate $\mathcal{V}(x) = (x^2 - 1)/2$ in terms of counted alive trajectories [we depict the recorded numbers $N = N(t)$]. In depicted rows, time labels are encoded in the increasing order from left to right, and further downwards. Note that scales along the vertical axis change in first four panels. The envelope (continuous curve) has an exact analytic form $k(x, t)$, as given by Eq. (22). Compare, e.g., the right panel of Fig. 1.

out that $\Delta_t x$ is specific for each chosen time instant $t = 0.1, 0.2, 0.5, 1, 2, 5$ and varies from time to time, cf. Figs. 3 and 4.

(2) Once a time instant is selected, for each consecutive segment Δx covering $[x_{\min}, x_{\max}]$, we count the number $n(\Delta x)$ of simulated trajectories, which reach the pertinent subinterval.

(3) To obtain the relative measure of the trajectory number increase or decrease, we evaluate $h(\Delta x) =$

$n(\Delta x)/(\Delta x \times 10^5)$, which is a quantitative measure of the fraction of counted in a segment Δx trajectories, while set against their initial number 10^5 , per length of the subinterval. The number $h(\Delta x)$ corresponds to the height of the respective vertical bar in Figs. 3 and 4.

(4) We note that $h(\Delta x) \times \Delta x$, is the relative number of alive trajectories in Δx at time t , and summing up over all $h(\Delta x)$ covering $[x_{\min}, x_{\max}]$ gives $N(t)/N(0)$ of Fig. 3, with $N(0) = 10^5$.

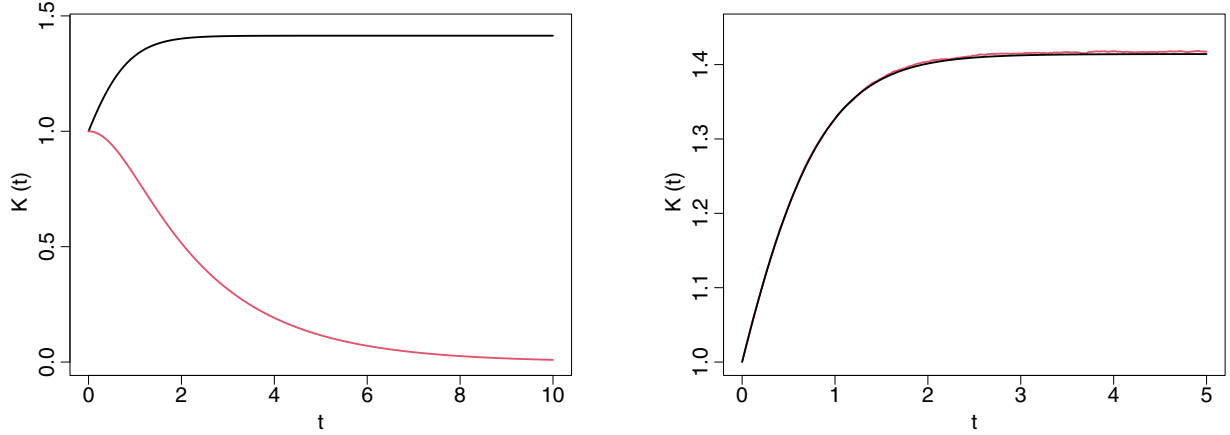


FIG. 5. Left panel: A comparative display of $K_0(t)$ (exponential decay) against $K(t)$ (relaxation). We point out that $K_0(t) = \int_R k_0(x, t) dx$ integrates to $N(t)/N(0) \approx K_0(t) = (\cosh t)^{-1/2}$, cf. Fig. 3. Right panel: A comparison of the analytic formula for $K(t) = e^{(+t/2)}(\cosh t)^{-1/2}$ (black curve), while set against the numerically retrieved curve $N(t)/N(0)$ (red).

(5) The envelope in each drawing of Fig. 3 is given by an exact analytic expression for $k_0(x, t)$, cf. Eqs. (19) and (20), at indicated instants of time. The envelopes in Fig. 4 are given by the analytic expression for $k(x, t)$, Eq. (22).

Remark 3: In our simulations, we choose the reference time $T = 5$ and $n = 50\,000$, hence $\delta t = 0.0001$. The initial number of released trajectories equals 100 000. All simulated trajectories are started at $t = 0$ at the point $x(0) = 0$. The outlined above trajectory counting recipe allows to estimate that in Figs. 3 and 4, the spatial coarse-graining subinterval Δx size varies between 0.01 and 0.05.

C. Harmonic killing versus branching

In Fig. 3 we visualize the pure killing case with the killing rate $\mathcal{V}(x) = x^2/2$. We follow the trajectory generation recipe of Sec. III A.

In Fig. 3 the envelope (continuous curve) has an exact analytic form $k_0(x, t) = \exp(-t/2)k(x, t)$, with $k(x, t)$ given by Eq. (22).

The pathwise description of the interplay between killing (not allowed in $[-1, 1]$) and branching (omnipresent in $(-1, 1)$) is comparatively provided in Figs. 4 and 5, by means of computer-assisted arguments (numerical simulation of trajectories, according to Secs. III A and III B). We consider the Feynman-Kac potential $\mathcal{V}(x) = (x^2 - 1)/2$.

In connection with Fig. 5, we point out that $K(t) \approx N(t)/N(0)$, at the corresponding time instants. In particular, $K(t)$ asymptotically approaches $\sqrt{2}$, and accordingly $N(t) \rightarrow 10^5 \sqrt{2} \approx 141\,421$.

We point out that in the harmonic case, there is no killing in the closed interval $[-1, 1]$. The killing rate gradually increases from 0 to ∞ beyond this interval. The smoothness of the potential results in the perfect agreement of analytic formulas and simulation (pathwise killing versus branching) data in Figs. 4 and 5.

D. Killing versus branching for the interval with absorbing ends

The smoothness of the harmonic potential at ± 1 will be lost for the diffusion in the interval with absorbing ends.

There, each trajectory hitting the boundaries ± 1 is abruptly killed, and the branching alternative becomes operational merely in the open set $(-1, 1)$, where due attention needs to be paid to the close vicinity of the endpoints of the interval.

We begin from the visualization of the pure killing case, e.g., diffusion process in the interval $(-1, 1)$ with absorbing ends ± 1 . In case of $t = 5$, the number of alive trajectories is too small to produce a reliable statistics (compare, e.g., $t = 5$ harmonic killing data in Fig. 3. Note that scales along the vertical axis change from panel to panel. The envelope (continuous curve) has an exact analytic form $k_0(x, t)$ given by Eq. (33). For large times the envelope curve scales down exponentially to 0, while preserving its functional shape:

$$k_0(x, t) \approx e^{-t\pi^2/8} \cos(x\pi/2) \rightarrow 0, \tag{41}$$

cf. also the left panel of Fig. 2.

The taming input of branching upon killing is visualized for the branching rate choice $\mathcal{V}(x) = -\pi^2/8$ in Note that scales along the vertical axis, except for the first panel are the same. The envelope (continuous curve) has an exact analytic form $k(x, t)$, as given by Eq. (35). Compare, e.g., the right panel of Fig. 2.

We note that $K(t) \approx N(t)/N(0)$ asymptotically approaches $4/\pi \approx 1.27$, and accordingly $N(t) \rightarrow 10^5(4/\pi) \approx 127\,000$, which is a definite branching surplus effect, if compared with $N(0) = 10^5$.

In case of the interval with absorbing ends, all simulation runs are accomplished in the open interval $(-1, 1)$, where there is no killing, while branching is allowed at a constant rate. All trajectories passing (reaching) the endpoints ± 1 of the interval are abruptly killed. At the boundaries, we must overcome the singularity of the model (QM by provenance) infinite well potential and the killing versus branching “abruptness” issue for the diffusion problem.

We have found necessary to allow trajectory cloning, which is actually admitted in $(-1, 1)$ with a constant probability $(\pi^2/8)\delta t$, in the slightly reduced domain $[-1 + \epsilon, 1 - \epsilon]$, instead of $(-1, 1)$ proper. Told otherwise, we do not admit cloning in the ϵ vicinity of the endpoints ± 1 .

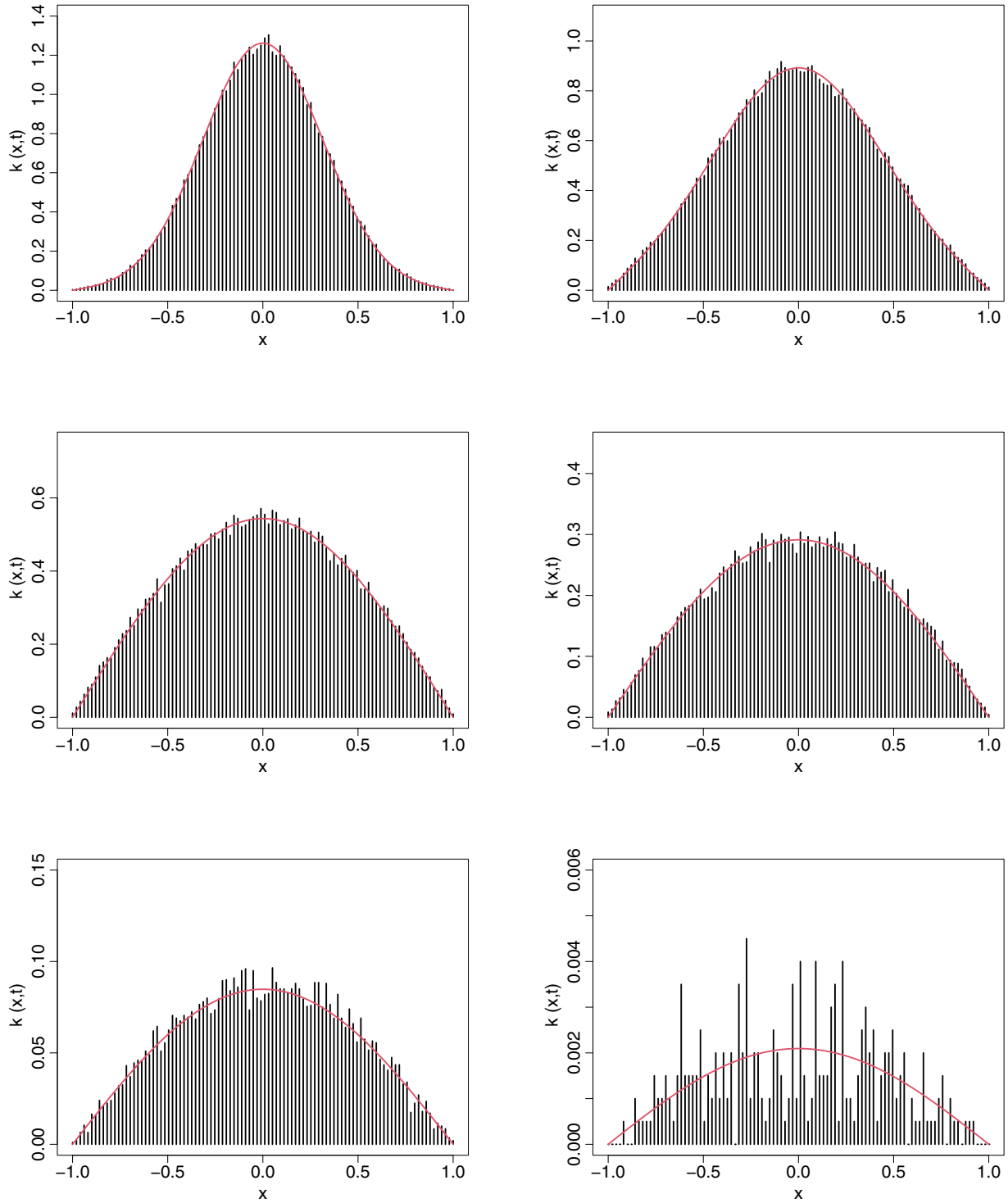


FIG. 6. Effects of the pure killing for the interval with absorbing ends in terms of the counting of surviving trajectories. We depict the recorded numbers $N = N(t)$. In all rows, time labels are encoded in the increasing order from left to right and next downwards. We have $t = 0, 1; N = 99\,732, t = 0.2; N = 95\,138, t = 0.5; N = 69\,086, t = 1; N = 37\,535, t = 2; N = 11\,081, t = 5; N = 258$. We note that at $t = 5$, the number of available trajectories is insufficient for the reliable statistics.

To have some control over the obvious loss of some branching trajectories in the overall trajectory statistics, we test a number of the parameter ϵ adjustments, to get the best fit to the analytical data of Sec. II. We have found that the value of ϵ can be significantly lowered only in strict correlation

with the improving finesse of the timescale coarse-graining ($\delta t = T/n$ with n increasing).

We have comparatively displayed in Figs. 7 and 8 the analytic and computer-retrieved trajectory counting data for the interval with absorbing ends, with the cloning rate

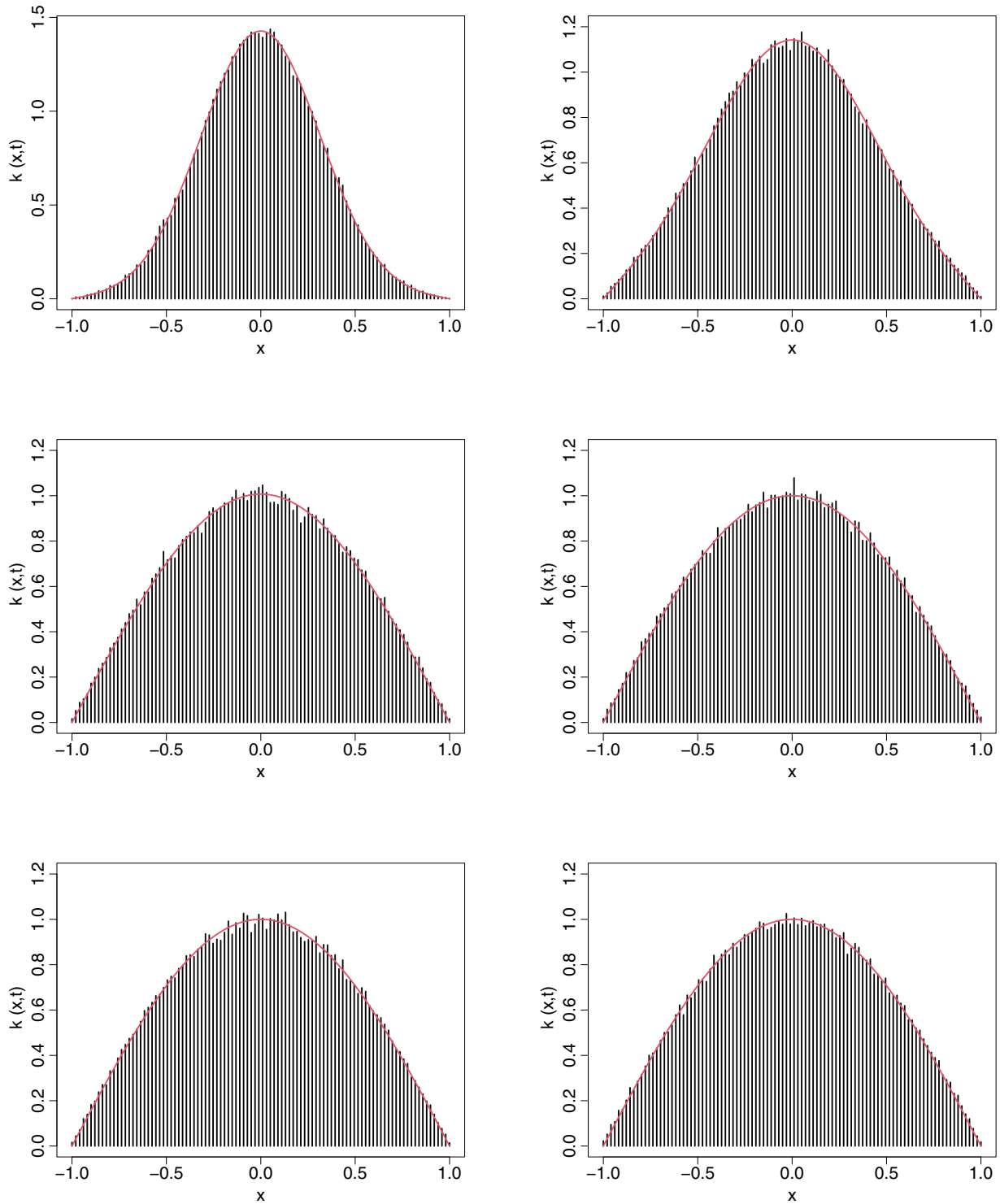


FIG. 7. Effects of the(tamed) killing rate for the interval problem with killing and branching: relaxation with the branching rate $\mathcal{V}(x) = -\pi^2/8$ in terms of alive trajectories counting. Time labels are encoded in the increasing order from left to right, and next downwards, like in Fig. 6.

$\mathcal{V} = -\pi^2/8$. In Fig. 8 the analytic curve $K(t)$ (black) satisfactorily agrees with the computer-assisted data, if the best fit for ϵ is found, given the value of δt . With the choice of $\delta t = 10^{-5}$ the best fit is $\epsilon = 0.0005$, cf. the right panel of Fig. 8.

One can see in both panels of Fig. 8, how slight changes of ϵ , which enlarge or diminish the noncloning area (and thus affect the reproduction of trajectories), lead to quite serious deviations from the analytic prediction $K(t)$. Specifically, we cannot freely minimize ϵ , with δt predefined and fixed.

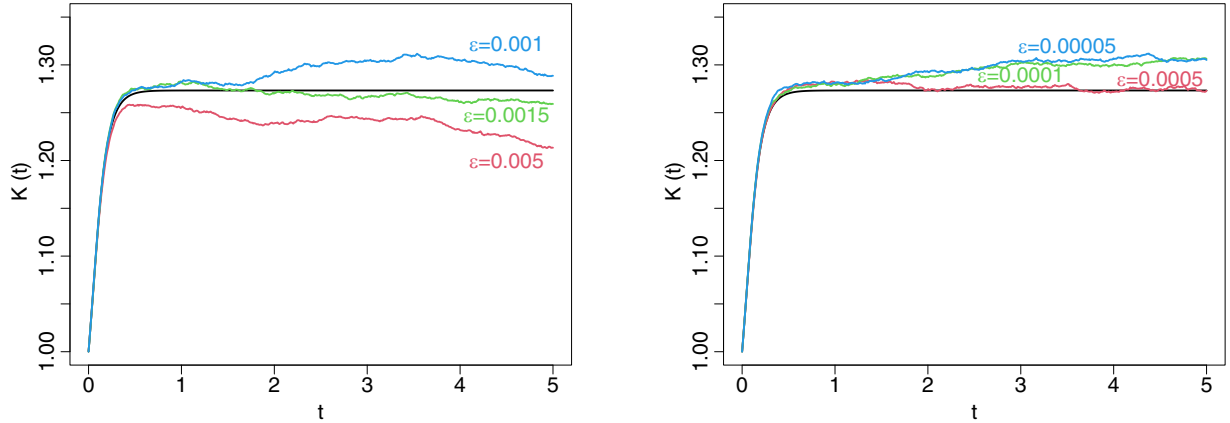


FIG. 8. Interval with absorbing ends. Branching relaxation in terms of $K(t)$, Eq. (38), black curve, set against numerically retrieved data for $N(t)/N(0) \approx K(t)$, with the predefined choice of δt . Left panel: $\delta t = 0.0001$. The best fit corresponds to the noncloning threshold $\epsilon = 0.0015$ (green curve). We display results of the enlargement of this fit to the value 0.005 and its minimization to 0.001. Right panel: $\delta t = 0.00001$. By decreasing 10 times the previous δt we pass from $\epsilon = 0.0015$ to $\epsilon = 0.0005$ (red). We demonstrate that the best fit cannot be arbitrarily minimized with δt predefined and fixed. We display deviations of $N(t)/N(0)$ from $K(t)$, for test thresholds 0.0001 and 0.00005.

In the left panel of Fig. 8, the optimal fit of the noncloning threshold $\epsilon = 0.0015$ has been set for $\delta t = 0.0001$. In the right panel of Fig. 8, where $\delta t = 0.00001$ allows to minimize the optimal threshold value down to $\epsilon = 0.0005$. We expect that with further lowering of δt , the threshold value of ϵ would go down as well, thus increasing the accuracy with which $N(t)/N(0)$ approximates the analytic outcome $K(t)$, Eq. (38).

We have verified what might happen if the noncloning area is narrowed below the optimal value $\epsilon = 0.0005$, while preserving $\delta t = 10^{-5}$. By selecting $\epsilon = 0.0001$ and $\epsilon = 0.00005$, we obtain a definite increase of the number of finally recorded trajectories. This trajectories surplus is clearly identifiable beginning from $t \approx 0.5$, once compared with the analytically known behavior of $K(t)$. We find convincingly confirmed, that the optimal $N(t)/N(0) \approx K(t)$ curve corresponds to $\epsilon \approx 0, 0005$, albeit some (hyper)fine tuning might still be possible.

IV. OUTLOOK

The above discussion, both analytic and computer-assisted, of the branching versus killing pathwise scenario for a continuous passage from y at $t = 0$ to x at $t > 0$ (clearly realizable along the admissible, with dead ends bypassed, branching trajectory) has been motivated out of curiosity. Namely, while the renormalized Hamiltonians, [3,6], with a conspicuous shift-down of the potential function on the energy scale, have been often employed in the literature, due to the inflicted “tamed killing effects” [1] in the behavior of kernel functions $\exp(-tH)(y, x)$, somewhat unexpectedly nothing has been said about the intrinsic stochastic background of that behavior.

Relaxing (conditioned) diffusion processes are described in terms of Fokker-Planck transition probability densities, whose main building blocks actually are the associated Feynman-Kac path integral kernels. These kernels share the relaxation property as well, and that quite often due to the presence in the Feynman-Kac exponent, of *killing rate (potential) functions*

with subtraction [1,6]; check, e.g., Ref. [15] for an alternative viewpoint.

Here, if a nonnegative $V(x)$ would imply a standard killing scenario [4,6], then by performing a potentially trivial subtraction we induce quite nontrivial (branching picture) consequences. The main point here is that $H = -(1/2)\Delta + [V(x)] \rightarrow H = -(1/2)\Delta + [V(x) - E_0]$ places H in the considered before (much broader) family $H = -(1/2)\Delta + \mathcal{V}$ of Hamiltonian operators with the vanishing (equal 0), isolated ground-state eigenvalue, cf. Ref. [15].

In passing we note, that we have extended the original idea of the reconstruction of a random dynamics from the sole eigenstate (ground state) of the Schrödinger Hamiltonian [16,19,30], in a new rather unexpected direction (that, in view of the branching admixture).

We have quite intentionally skipped routine introductory phrases, with a message about an overall relevance and unquestionably broad significance of (i) the killing and mass creation in the Brownian motion [5–20], (ii) branching stochastic processes, (iii) quasistationary distributions, (iv) links with the Feynman-Kac formalism, all that within physics or beyond physics (social sciences, biology etc.), since these can be found in Refs. [2–6] and furthermore in Refs. [21–29].

The trajectory picture we have described in the present paper, effectively reduces each branching event to the trajectory bifurcation at a random time instant. This, to some extent, may be interpreted in terms of the metaphor, [31], concerning an uncontrollable multitude of ways allowing to reach a predefined destiny (here a terminal point x at t), from a predefined beginning (starting point y at $t = 0$), along a continuous path, with branching versus killing events happening randomly on the way. We note that a continuity property of the ultimate (uninterrupted) path, is nonetheless preserved and the terminal point of the trajectory can be always reached by meticulously avoiding path segments with dead ends (“pruned branches”).

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