

SISSA

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## Stochastic resetting from an interval

Model: one dimensional Brownian motion resetting at space dependent rate $r_{c}(x)=r \theta(a-|x|)$ to a prescribed resetting point $x_{r}$.


Master Equation: $\partial_{t} P\left(x, t \mid x_{0}\right)=$ $D \partial_{x}^{2} P\left(x, t \mid x_{0}\right)-r_{c}(x) P\left(x, t \mid x_{0}\right)+\delta\left(x-x_{r}\right) \int d y r_{c}(y) P\left(y, t \mid x_{0}\right)$.

DIFFUSION
LOSS DUE TO RESETTING
 GAIN DUE TO RESETTING
) Resetting induces a cusp at $x_{r}$ at all times
ii) Diffusion is responsible for Gaussian tails

Brownian yet non-Gaussian: non-Gaussian distribution but
ii) $\longrightarrow \sigma^{2}(t) \simeq D_{\text {eff }} t \quad$ for $t \gg 1$, with
i) $\longrightarrow 1-\frac{2}{\pi}<\frac{D_{\text {eff }}}{D} \leq 1$.


## Resetting on a ring

Model: Brownian particle resetting at space dependent rate $r_{c}(x)$ on ( $-L, L$ ) with periodic boundary conditions; this ensures the existence of a stationary state.


Particles can reset both clockwise and conterclockwise: this is fixed by Resetting is instantaneous a protocol.


The total current $J$ is composed by two contributions
i) $J_{\text {diff }}$ independent of the protocol;
ii) $J_{\text {res }}$ dependent of the protocol.


Application: Modelling backtrack recovery of RNA polymerase


Distribution of the length of cleaved RNA
$Q_{r e s}\left(x=a y \mid x_{0}=a y_{0}\right)$
$=\rho \frac{\sinh \left(y_{<} \rho\right)}{a \cosh \rho}\left\{1-\theta\left(1-y_{0}\right)\left[1-\cosh \left(\left(1-y_{>}\right) \rho\right)\right]\right\}$

## Cleavage efficiency

$\eta_{r e s}\left(y_{0}\right) \equiv \eta\left(x_{0}=a y_{0}\right)$
$=1-\frac{\cosh \left(\left(1-y_{0}\right) \rho\right)+\theta\left(y_{0}-1\right)\left[1+\cosh \left(\left(1-y_{0}\right) \rho\right)\right]}{\cosh \rho}$
with $\rho=a \sqrt{r / D}, y_{<}=\min \left(y, y_{0}\right)$, and $y_{>}=\max \left(y, y_{0}\right)$.

RNA polymerases along a DNA template during transcriptional pauses. Two recovery mechanisms from the inactive state ("backtracking"): i) Brownian diffusion, and ii) active cleavage of the backtracked RNA. Model : evolution of the backtrack depth $x \geq 0, \mathbf{i})$ diffusion in $\mathrm{d}=1$ starting from $x_{0}>0$ with an absorbing boundary in the origin, $\mathbf{i i}$ ) resetting of the backtrack depth $x \rightarrow x_{r}=0$ at a rate $r$ from the region $(0, a)$.



