

Large deviations and population dynamics

Vivien Lecomte⁽¹⁾, Julien Tailleur⁽²⁾

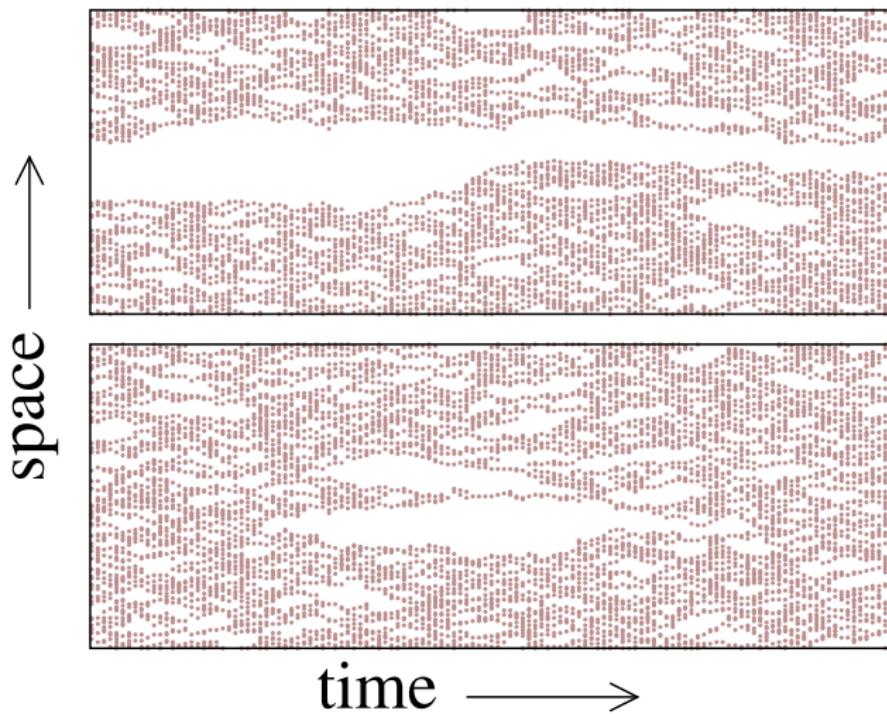
Freddy Bouchet⁽³⁾, Rob Jack⁽⁴⁾, Takahiro Nemoto^(1,3)

Esteban Guevara⁽⁵⁾

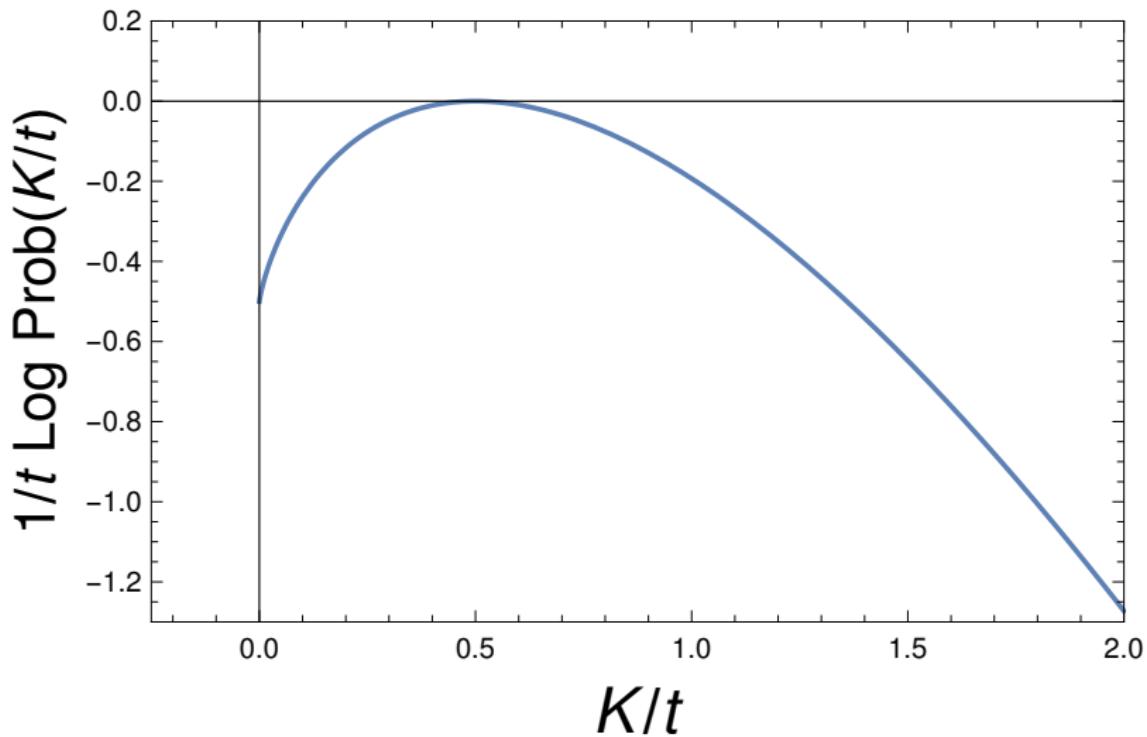
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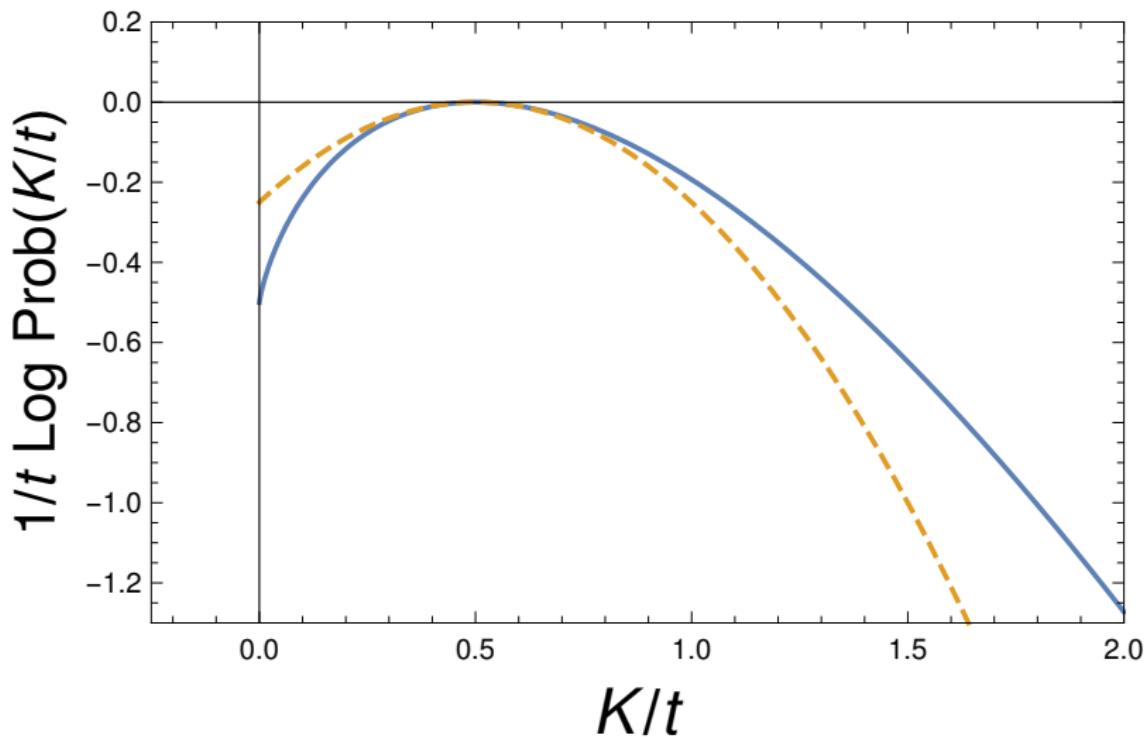
Princeton — November 17th, 2015



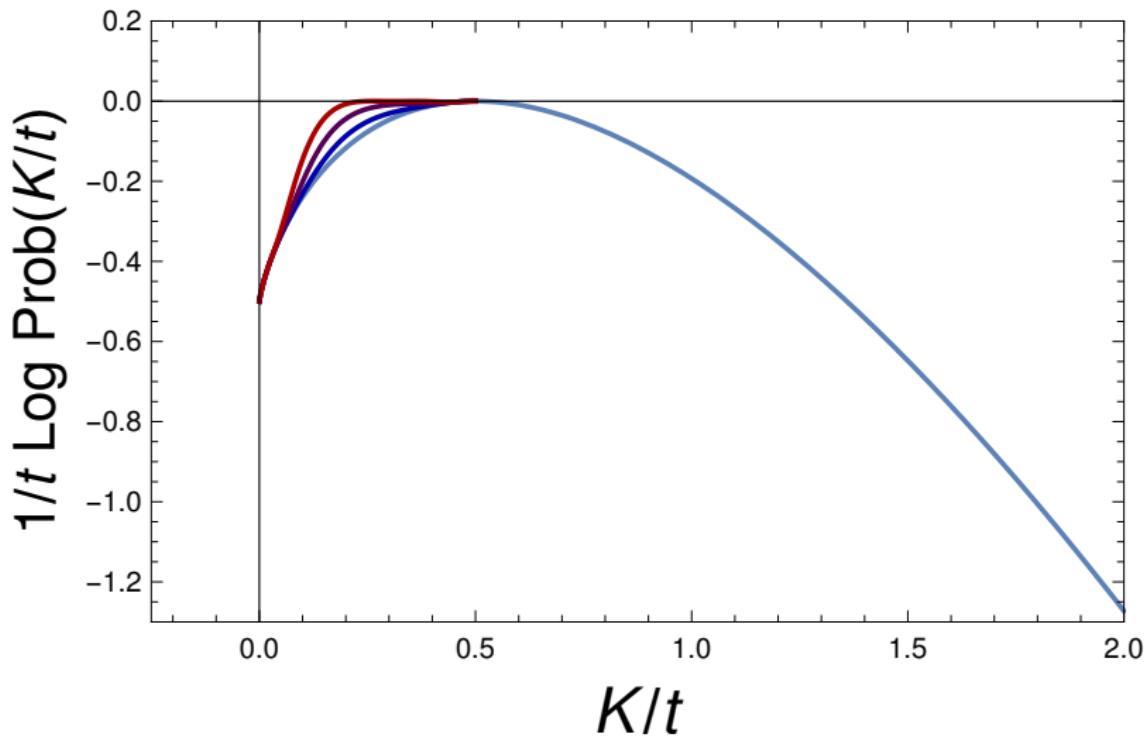
[Merolle, Garrahan and Chandler, 2005]



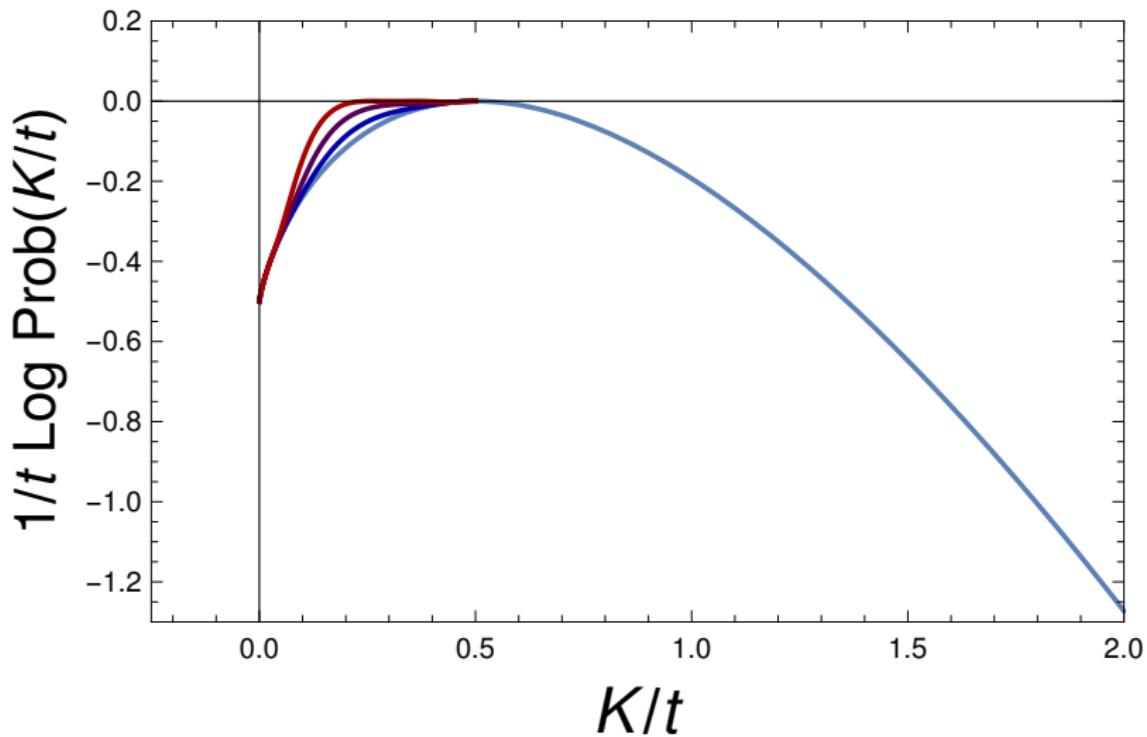
$$\text{Prob}[K] \sim e^{t\varphi(K/t)}$$



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Finite-time & -size scalings matter.

s-modified dynamics

- Markov processes:

$$\partial_t P(\mathcal{C}, t) = \sum_{\mathcal{C}'} \left\{ \underbrace{W(\mathcal{C}' \rightarrow \mathcal{C}) P(\mathcal{C}', t)}_{\text{gain term}} - \underbrace{W(\mathcal{C} \rightarrow \mathcal{C}') P(\mathcal{C}, t)}_{\text{loss term}} \right\}$$

s-modified dynamics

K = activity

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- More detailed dynamics for $P(\mathcal{C}, K, t)$:

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s-modified dynamics*K*=activity

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- Canonical description: s conjugated to K

$$\hat{P}(\mathcal{C}, s, t) = \sum_K e^{-sK} P(\mathcal{C}, K, t)$$

s -modified dynamics $K = \text{activity}$

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- s -modified dynamics [probability non-conserving]

$$\partial_t \hat{P}(\mathcal{C}, s, t) = \sum_{\mathcal{C}'} \left\{ e^{-s} W(\mathcal{C}' \rightarrow \mathcal{C}) \hat{P}(\mathcal{C}', s, t) - W(\mathcal{C} \rightarrow \mathcal{C}') \hat{P}(\mathcal{C}, s, t) \right\}$$

Numerical method

[with J. Tailleur]

Evaluation of large deviation functions

[à la Monte-Carlo diffusion]

$$Z(s, t) = \sum_{\mathcal{C}} \hat{P}(\mathcal{C}, s, t) = \langle e^{-s K} \rangle \sim e^{-t \psi(s)}$$

- discrete time: Giardinà, Kurchan, Peliti [PRL **96**, 120603 (2006)]
- continuous time: Lecomte, Tailleur [JSTAT P03004 (2007)]

Cloning dynamics

$$\partial_t \hat{P}(\mathcal{C}, s) = \underbrace{\sum_{\mathcal{C}'} W_s(\mathcal{C}' \rightarrow \mathcal{C}) \hat{P}(\mathcal{C}', s) - r_s(\mathcal{C}) \hat{P}(\mathcal{C}, s)}_{\text{modified dynamics}} + \underbrace{\delta r_s(\mathcal{C}) \hat{P}(\mathcal{C}, s)}_{\text{cloning term}}$$

- $W_s(\mathcal{C}' \rightarrow \mathcal{C}) = e^{-s} W(\mathcal{C}' \rightarrow \mathcal{C})$
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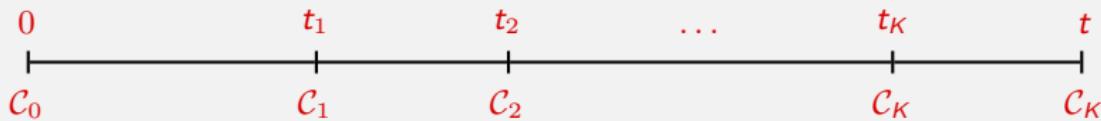
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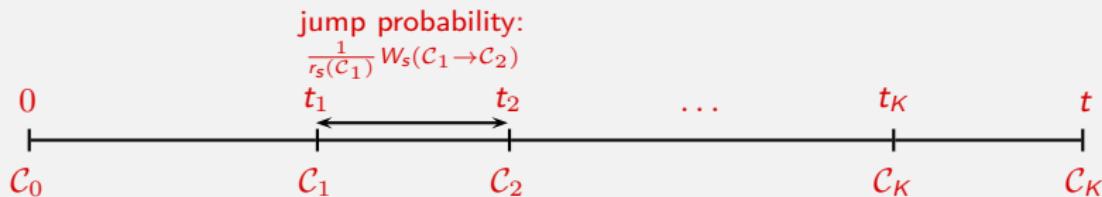
Explicit construction (1/3)



Probability-preserving contribution

$$\partial_t \hat{P}(\mathcal{C}, t) = \sum_{\mathcal{C}'} \left\{ \underbrace{W_s(\mathcal{C}' \rightarrow \mathcal{C}) \hat{P}(\mathcal{C}', t)}_{\text{gain term}} - \underbrace{W_s(\mathcal{C} \rightarrow \mathcal{C}') \hat{P}(\mathcal{C}, t)}_{\text{loss term}} \right\}$$

Explicit construction (1/3)



Which configurations will be visited?

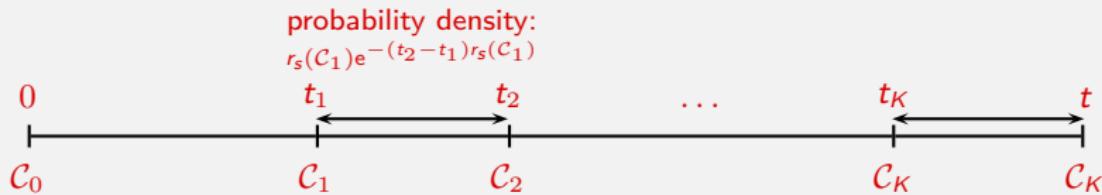
Configurational part of the trajectory: $\mathcal{C}_0 \rightarrow \dots \rightarrow \mathcal{C}_K$

$$\text{Prob}\{\text{hist}\} = \prod_{n=0}^{K-1} \frac{W_s(\mathcal{C}_n \rightarrow \mathcal{C}_{n+1})}{r_s(\mathcal{C}_n)}$$

where

$$r_s(\mathcal{C}) = \sum_{\mathcal{C}'} W_s(\mathcal{C} \rightarrow \mathcal{C}')$$

Explicit construction (2/3)

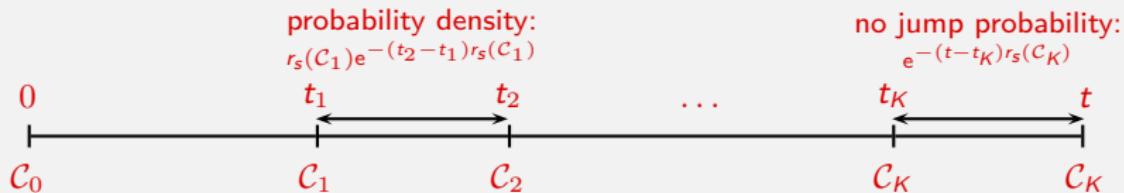


When shall the system jump from one configuration to the next one?

- probability density for the time interval $t_n - t_{n-1}$

$$r_s(\mathcal{C}_{n-1})e^{-(t_n-t_{n-1})r_s(\mathcal{C}_{n-1})}$$

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- probability not to leave \mathcal{C}_K during the time interval $t - t_K$

$$e^{-(t-t_K)r_s(\mathcal{C}_K)}$$

Explicit construction (3/3)

$$\partial_t \hat{P}(\mathcal{C}, s) = \underbrace{\sum_{\mathcal{C}'} W_s(\mathcal{C}' \rightarrow \mathcal{C}) \hat{P}(\mathcal{C}', s) - r_s(\mathcal{C}) \hat{P}(\mathcal{C}, s)}_{\text{modified dynamics}} + \underbrace{\delta r_s(\mathcal{C}) \hat{P}(\mathcal{C}, s)}_{\text{cloning term}}$$

How to take into account loss/gain of probability?

- handle a large number of copies of the system
- implement a **selection** rule: on a time interval Δt
a copy in config \mathcal{C} is replaced by $e^{\Delta t \delta r_s(\mathcal{C})}$ copies
- $\psi(s)$ = the rate of exponential growth/decay of the total population
- optionally: keep population constant by un-biased pruning/cloning

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Biological interpretation

- copy in configuration $\mathcal{C} \equiv$ organism or **genome** \mathcal{C}
- dynamics of rates $W_s \equiv$ **mutations**
- cloning at rates $\delta r_s \equiv$ **selection** rendering atypical histories typical

How to perform averages?

[with R Jack, F Bouchet, T Nemoto]

- ★ Final-time distribution: *proportion* of copies in \mathcal{C} at t

$$\langle N_{\text{nc}}(t) \rangle_s$$

$$\langle N_{\text{nc}}(\mathcal{C}, t) \rangle_s$$

$$p_{\text{end}}(\mathcal{C}, t) = \frac{\langle N_{\text{nc}}(\mathcal{C}, t) \rangle_s}{\langle N_{\text{nc}}(t) \rangle_s}$$

[N_{nc} = number in non-constant population dynamics]

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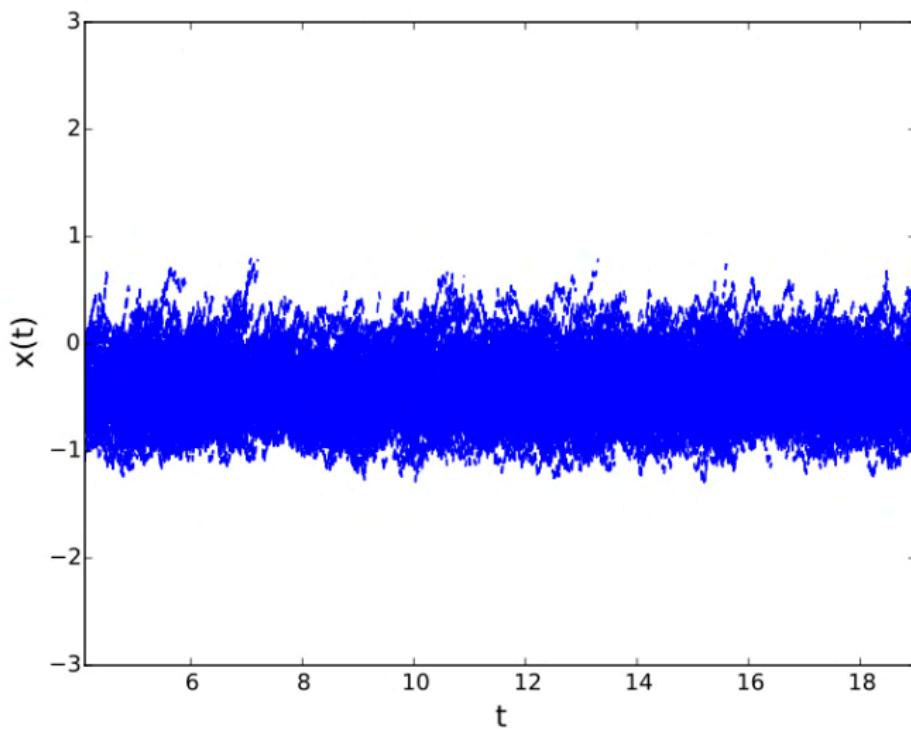
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Final-time distribution governed by **right** eigenvector.



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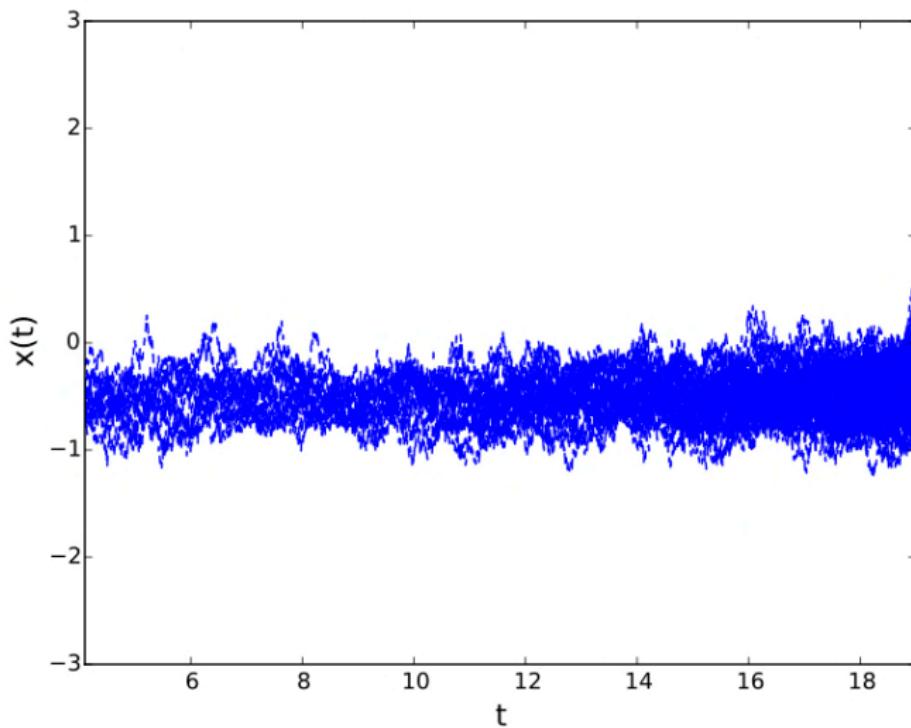
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Mid-time distribution governed by **left** and **right** eigenvectors.



Huge sampling issue

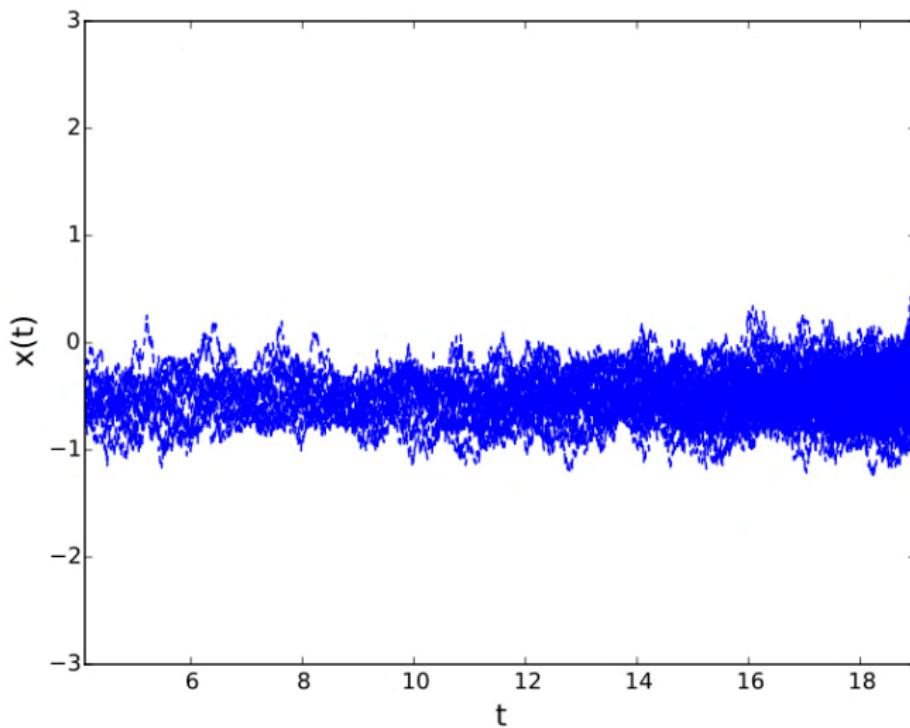
How to perform averages?

- ★ Mid-time ancestor distribution:

fraction of copies (at time t_1) which were in configuration \mathcal{C} , knowing that there are in configuration \mathcal{C}_f at final time t_f :

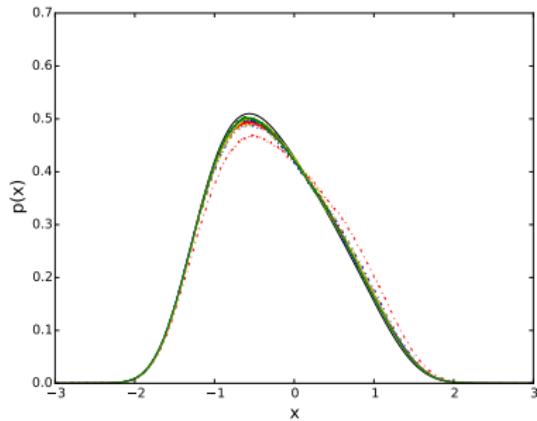
$$p_{\text{anc}}(\mathcal{C}, t_1; \mathcal{C}_f, t_f) = \frac{\langle N_{\text{nc}}(\mathcal{C}_f, t_f | \mathcal{C}, t_1) \rangle_s}{\sum_{\mathcal{C}'} \langle N_{\text{nc}}(\mathcal{C}_f, t_f | \mathcal{C}', t_1) \rangle_s} \underset{t_{f,1} \rightarrow \infty}{\sim} \langle L | \mathcal{C} \rangle \langle \mathcal{C} | R \rangle = p_{\text{ave}}(\mathcal{C})$$

The “ancestor statistics” of a configuration \mathcal{C}_f is thus independent (far enough in the past) of the configuration \mathcal{C}_f .

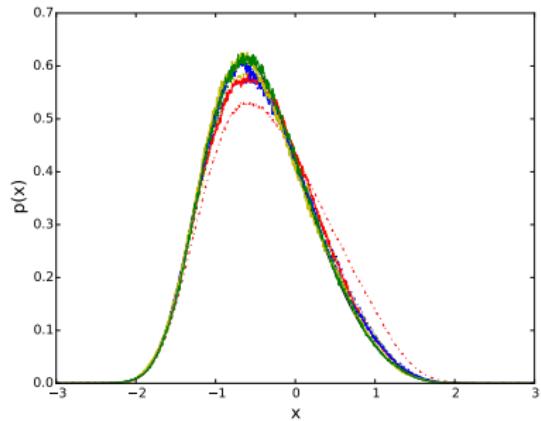


Still huge sampling issue

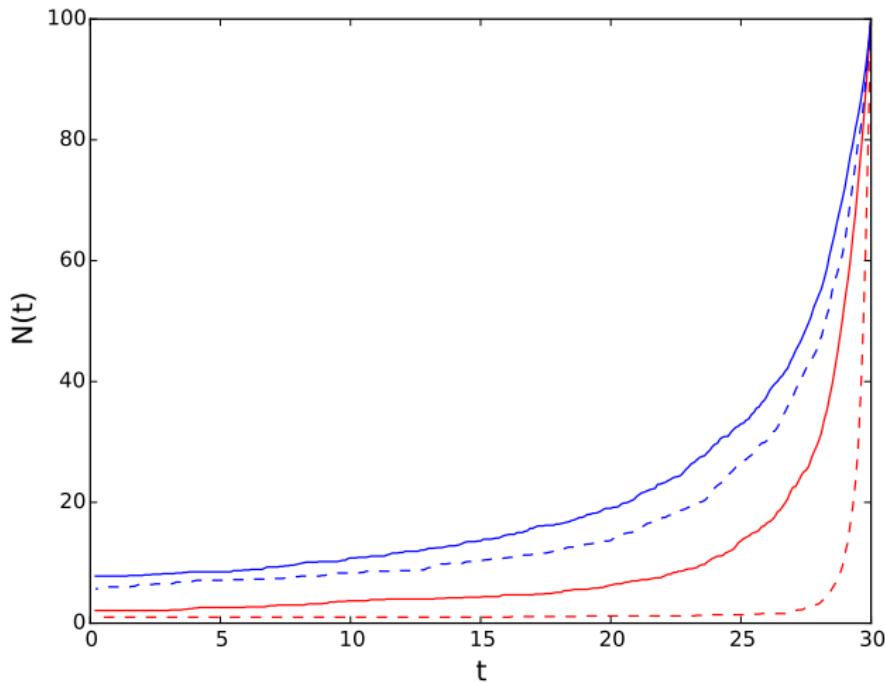
Example distributions for a simple Langevin dynamics



$$p_{\text{end}}(x)$$



$$p_{\text{ave}}(x)$$



Decrease of the number $N(t)$ of surviving trajectories on $[t_f - t, t_f]$

How to make mid- and final-time distribution closer?

Driven/auxiliary dynamics:

[Maes, Jack&Sollich, Touchette&Chetrite]

- Probability preserving
- No mismatch between p_{ave} and p_{end}
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- Issue: determining L is difficult
- Solution: evaluate L as L_{test} on the fly and simulate

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- Whichever L_{test} , the simulation is still correct.

How to make mid- and final-time distribution closer?

Driven/auxiliary dynamics: [Maes, Jack&Sollich, Touchette&Chetrite]

- Probability preserving
- No mismatch between p_{ave} and p_{end}
- Constructed as

$$\mathbb{W}_s^{\text{aux}} = L \mathbb{W}_s L^{-1} - \psi(s) \mathbf{1}$$

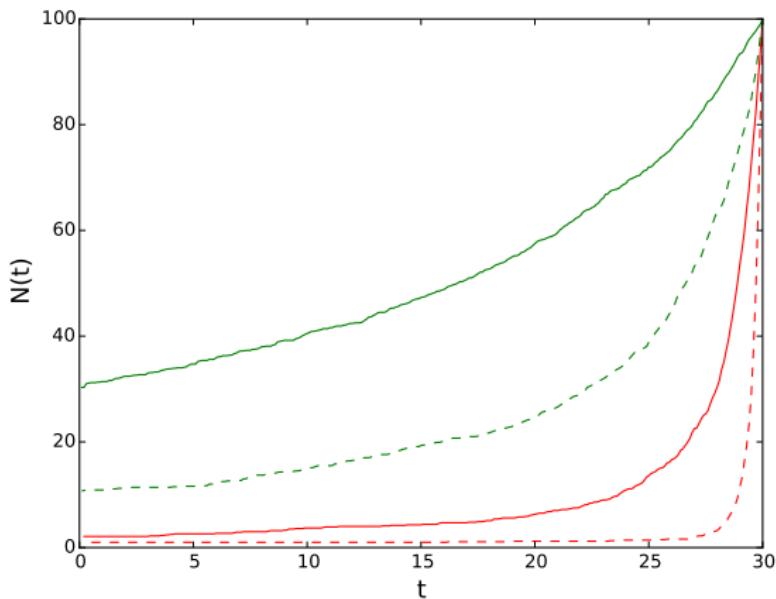
- Issue: determining L is difficult
- Solution: evaluate L as L_{test} on the fly and simulate

$$\mathbb{W}_s^{\text{test}} = L_{\text{test}} \mathbb{W}_s L_{\text{test}}^{-1}$$

- Whichever L_{test} , the simulation is still correct.

Similar in spirit to **multi-canonical** (e.g. Wang-Landau) approach in static thermodynamics

Improvement of the depletion-of-ancestors problem:

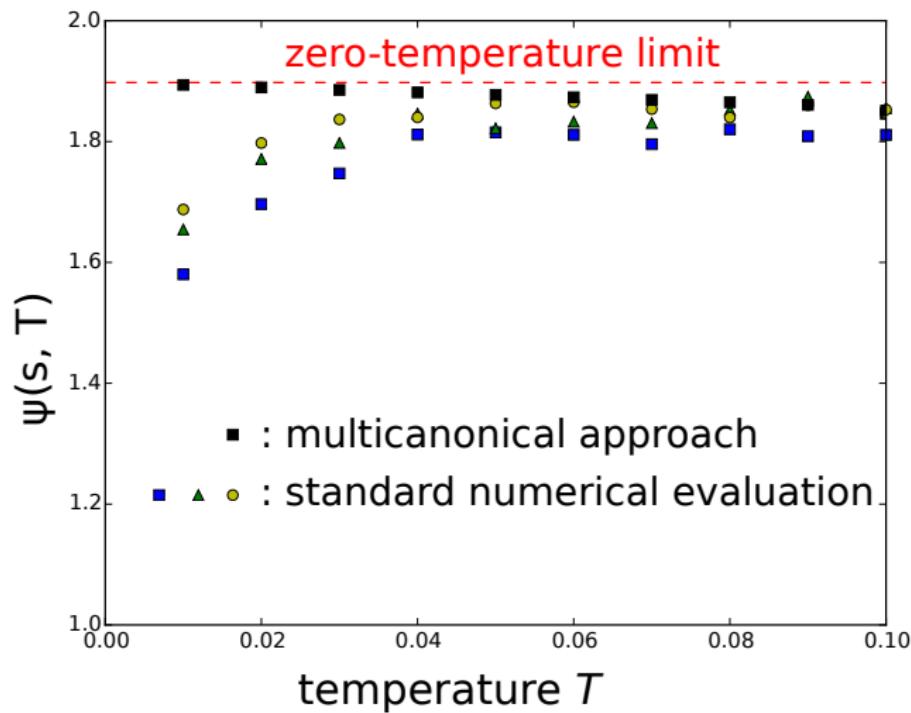


Red: without multicanonical sampling.

Green: with multicanonical sampling (L_{test} evaluated on the fly)

Dashed: lower temperature

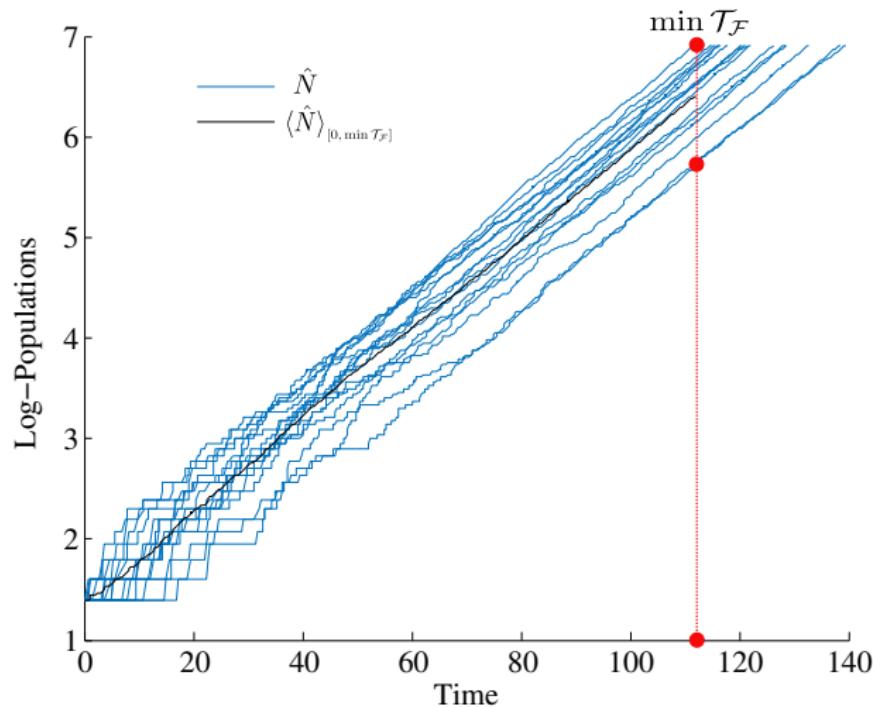
Improvement of the small-noise crisis:



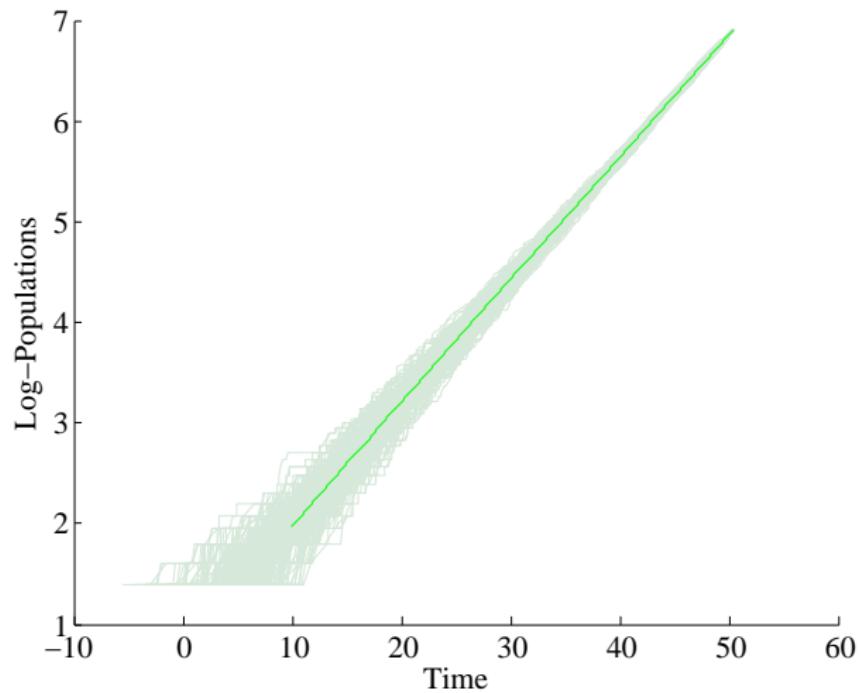
Initial transient regime

[with E. Guevara]

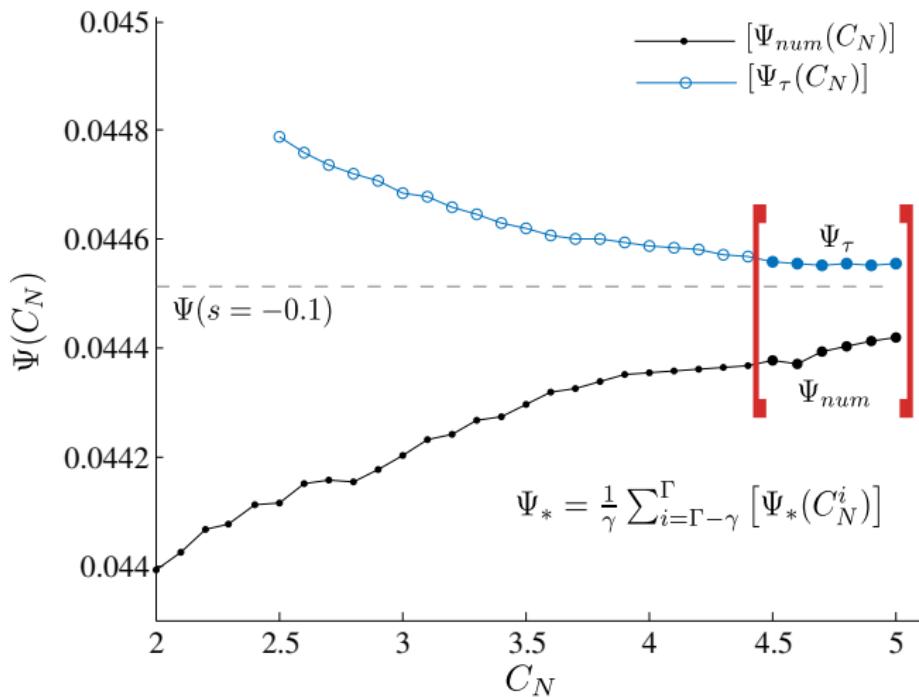
Non-constant population dynamics



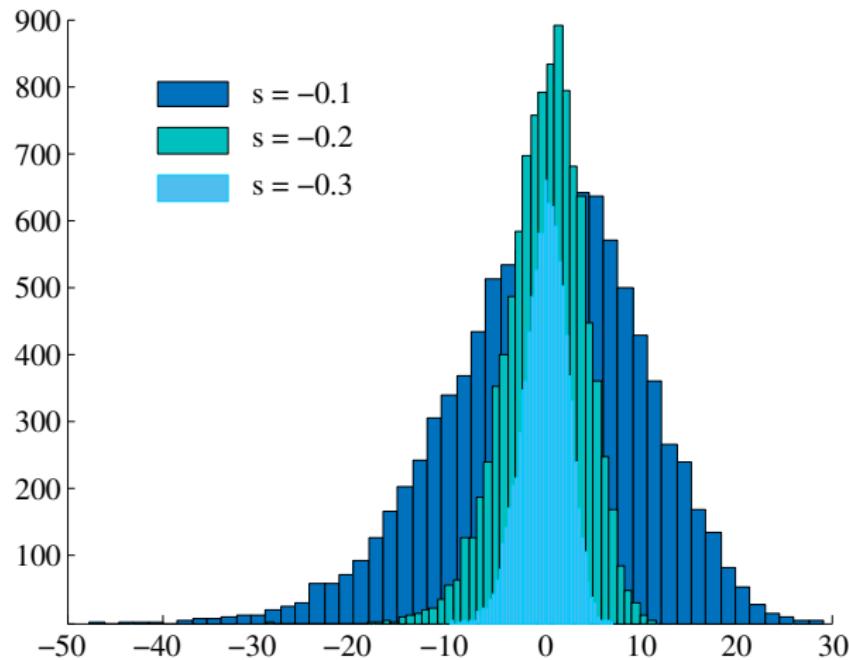
Time-delay



Improvement of the numerical evaluation of $\psi(s)$



Distribution of time delays



Summary and questions

Multicanonical approach

[with F Bouchet, R Jack, T Nemoto]

- Sampling problem (depletion of ancestors)
- On-the-fly evaluated auxiliary dynamics
- Solution to the small-noise crisis
- Systems with large number of degrees of freedom?

Summary and questions

Multicanonical approach

[with F Bouchet, R Jack, T Nemoto]

- Sampling problem (depletion of ancestors)
- On-the-fly evaluated auxiliary dynamics
- Solution to the small-noise crisis
- Systems with large number of degrees of freedom?

Non-constant population dynamics

[with E Guevara]

- Sampling problem (depletion of ancestors)
- Initial transient regime due to small population
- Procedure: time-delay
- Analogy with biology: many small islands vs. few large islands?