
Simulations of polymers with a new Monte-Carlo algorithm

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Joint work with

Jaroslaw Krawczyk, TU Clausthal, and A. Rechnitzer, Uni Melbourne

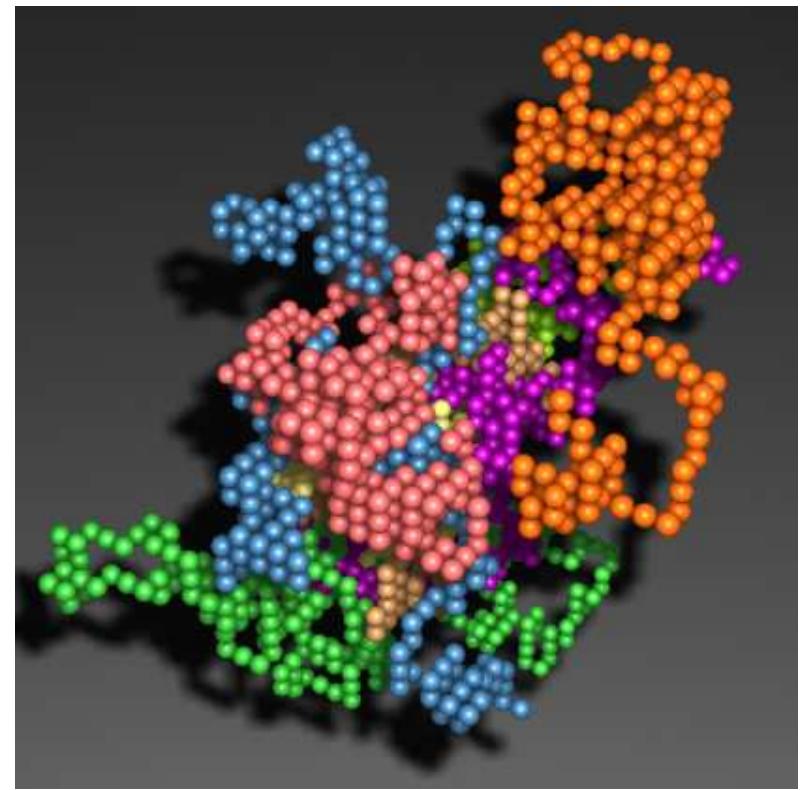


Introduction



Modelling of Polymers in Solution

- Polymers:
long chains of monomers
- “Coarse-Graining”:
beads on a chain
- “Excluded Volume”:
minimal distance
- Contact with solvent:
effective short-range interaction
- Good/bad solvent:
repelling/attracting interaction
- Consequence:
chains clump together



Eight polymers in a bad solvent
(Grassberger, FZ Jülich)

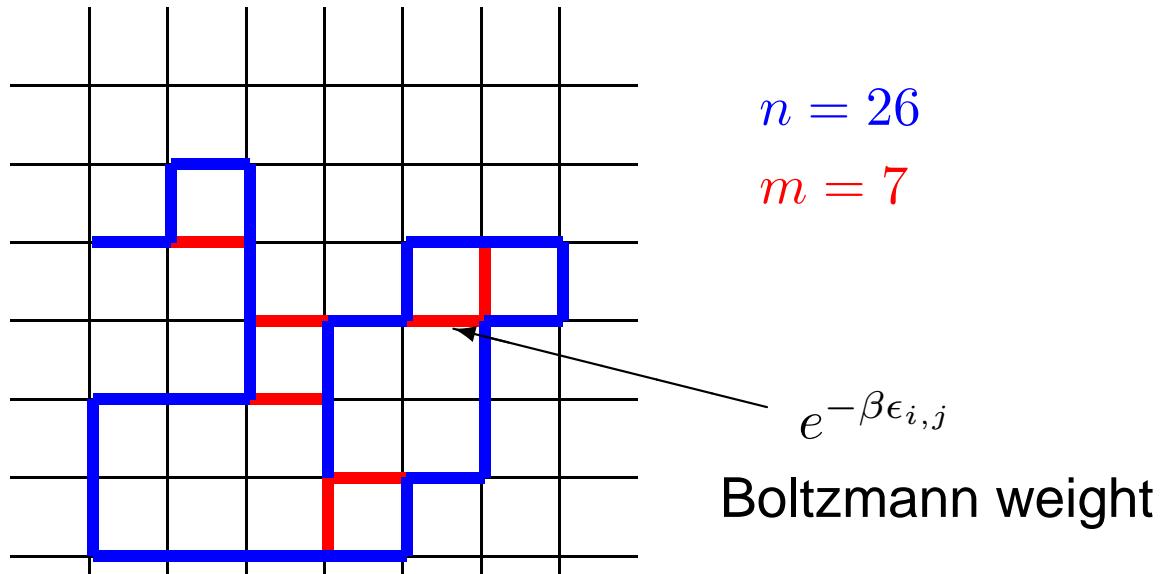
Self-Avoiding Walks with Interactions

- Physical space → lattice \mathbb{Z}^3 (or \mathbb{Z}^d)
- Polymer in solution → random walk with self-avoidance
- Quality of solvent → short-range interaction ϵ
- Properties of monomers i, j → interaction $\epsilon = \epsilon_{i,j}$

Self-Avoiding Walks with Interactions

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- Properties of monomers i, j → interaction $\epsilon = \epsilon_{i,j}$
- Three examples:
 - SAW in a strip: interaction $\epsilon_{i,j} = 0$, restricted geometry
 - HP model: two types of monomers H and P: $\epsilon_{HH}, \epsilon_{HP}, \epsilon_{PP}$
of interest: fixed finite sequence, density of states
 - ISAW model: interaction $\epsilon_{i,j} = -1$
of interest: thermodynamic limit ($V = \infty$ and $n \rightarrow \infty$)

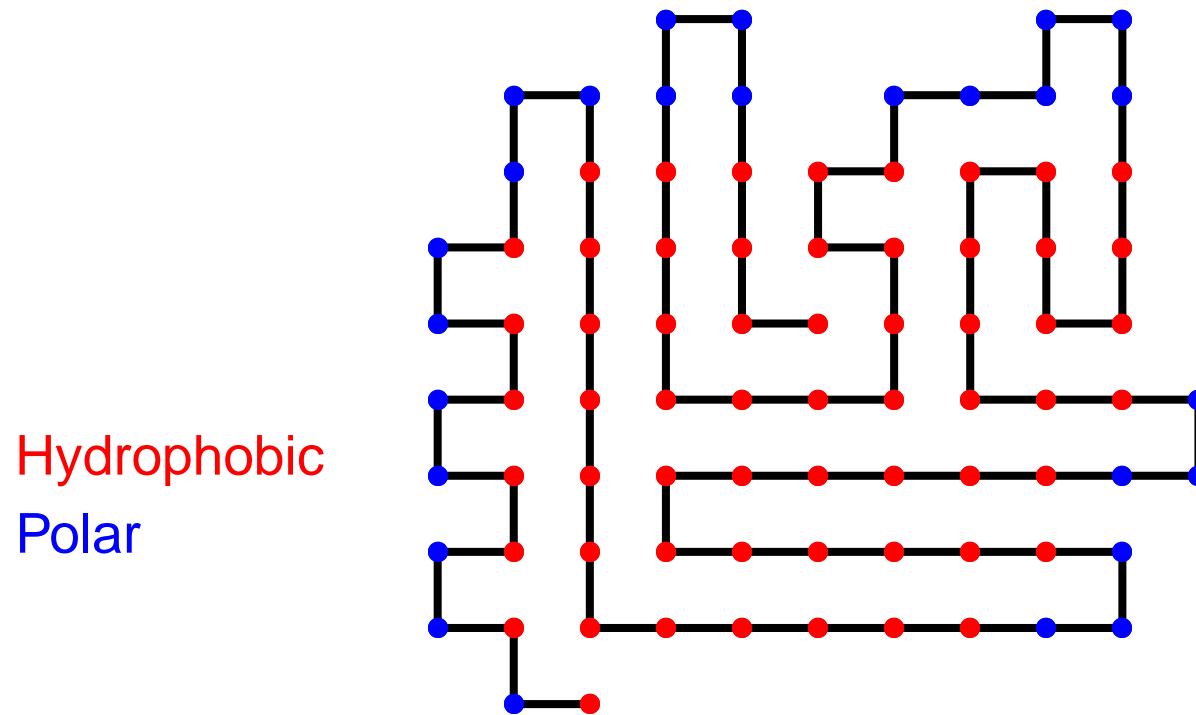
Lattice Model: (I)SAW



- ISAW model: interaction $\epsilon_{i,j} = -1$
- Partition function: $Z_n(\beta) = \sum_m C_{n,m} e^{\beta m}$
- $C_{n,m}$ number of SAW with length n and m interactions
- SAW: $C_n = \sum_m C_{n,m}$ number of SAW with length n ($\beta = 0$)

Lattice Model: HP model

- HP model: interaction $\epsilon_{HH} = -1$, $\epsilon_{HP} = \epsilon_{PH} = \epsilon_{PP} = 0$



- Groundstate of sequence with 85 monomers ($d = 2$)

Why Simulations?

- ISAW model:
 - Tricritical phase transition, $d_u = 3$
 - In principle understood, however surprising details
e.g. “pseudo-first-order transition” for $d > 3$
 - No good understanding of collapsed regime

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 - Toy model for proteins
 - Design of sequences with specific ground state structure
 - Density of states – folding dynamics

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 - Design of sequences with specific ground state structure
 - Density of states – folding dynamics
- Most interesting open questions in collapsed regime

Collapsed regime is notoriously difficult to simulate

Stochastic Growth Algorithms



PERM: “Go With The Winners”

PERM = Pruned and Enriched Rosenbluth Method

Grassberger, Phys Rev E 56 (1997) 3682

- **Rosenbluth Method: kinetic growth**



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Grassberger, Phys Rev E 56 (1997) 3682

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- **Enrichment:** weight too large → make copies of configuration
- **Pruning:** weight too small → remove configuration occasionally

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- **Rosenbluth Method:** kinetic growth



- **Enrichment:** weight too large → make copies of configuration
- **Pruning:** weight too small → remove configuration occasionally

Observation: kinetic growth weights and interactions balance each other at suitable temperatures (in the collapse region)

PERM – further developments

- A significant improvement: nPERM = “new” PERM

Hsu et al, J Chem Phys 118 (2003) 444

- Enforce distinct enrichment steps
- Crossover to exact enumeration



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- Current work: flatPERM = “flat histogram” PERM

TP and JK, PRL 92 (2004) 120602

TP, JK, and AR, cond-mat/0402549

- flatPERM samples a generalised multicanonical ensemble
- Covers the whole temperature range in *one* simulation!

Related: multicanonical chain growth algorithm

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Applications:

- linear and branched polymers, proteins, percolation, . . .

Algorithm details - kinetic growth

View kinetic growth as approximate enumeration



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- Exact enumeration: choose *all* a continuations with equal weight
- Kinetic growth: chose *one* continuation with a -fold weight (a may be zero).



Algorithm details - kinetic growth

View kinetic growth as approximate enumeration

- Exact enumeration: choose *all* a continuations with equal weight
- Kinetic growth: chose *one* continuation with a -fold weight (a may be zero).
- An n step configuration gets assigned a weight

$$W = \prod_{k=0}^{n-1} a_k$$

- S growth chains with weights $W_n^{(i)}$ give estimate

$$C_n^{\text{est}} = \langle W \rangle_n = \frac{1}{S} \sum_i W_n^{(i)}$$

Why does this work?

- The sum is normalized with the number S of *started* growth chains

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(not all of these growth chains reach length n)

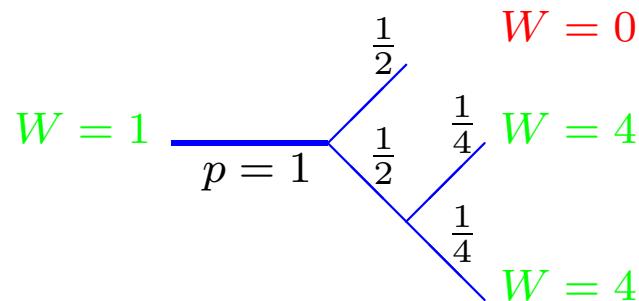
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- ➋ Example:



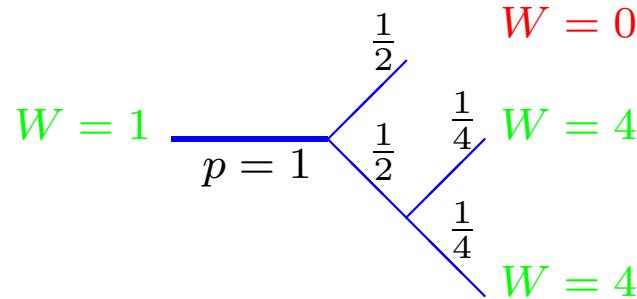
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- Example:



$$\langle W \rangle_2 = \frac{1}{2}0 + \frac{1}{4}4 + \frac{1}{4}4 = 2$$

Algorithm details - pruning/enrichment

- $W_n^{(i)}$ is estimate of C_n
- Consider ratio $r = W_n^{(i)} / C_n^{est}$
 - $r > 1 \rightarrow$ enrichment step:
make $c = \min(\lfloor r \rfloor, a_n)$ distinct copies with weight $\frac{1}{c} W_n^{(i)}$
 - $r < 1 \rightarrow$ pruning step:
continue growing with probability r and weight C_n^{est}

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 - $r < 1 \rightarrow$ pruning step:
continue growing with probability r and weight C_n^{est}
- Consequences
 - Number of samples generated for each n is roughly constant
 - Ideally, unbiased random walk in configuration size
 - We have a flat histogram algorithm

From PERM to flatPERM

- PERM: estimate number of configurations C_n
 - $C_n^{est} = \langle W \rangle_n$
 - $r = W_n^{(i)} / C_n^{est}$



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Consider energy $E_m = \epsilon m$, temperature $\beta = 1/k_B T$

- thermal PERM: estimate partition function $Z_n(\beta)$
 - $Z_n^{est}(\beta) = \langle W \exp(-\beta E) \rangle_n$
 - $r = W_n^{(i)} \exp(-\beta E_m^{(i)}) / Z_n^{est}(\beta)$

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- flatPERM: estimate density of states $C_{n,m}$

- $C_{n,m}^{est} = \langle W \rangle_{n,m}$
- $r = W_{n,m}^{(i)} / C_{n,m}^{est}$

From PERM to flatPERM

- PERM: estimate number of configurations C_n

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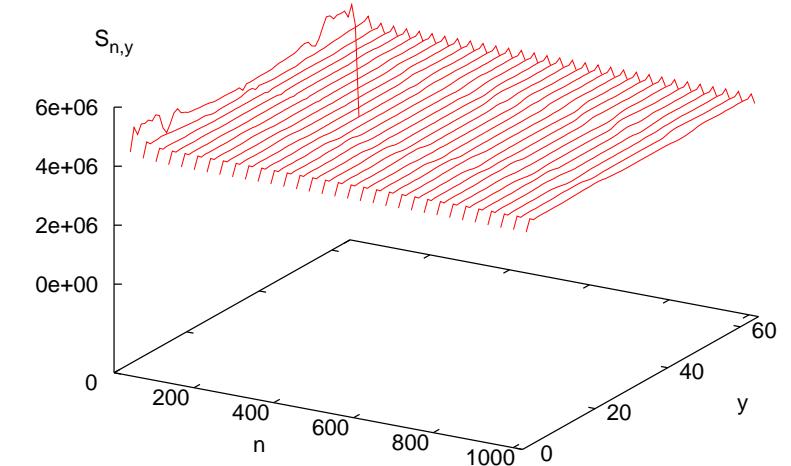
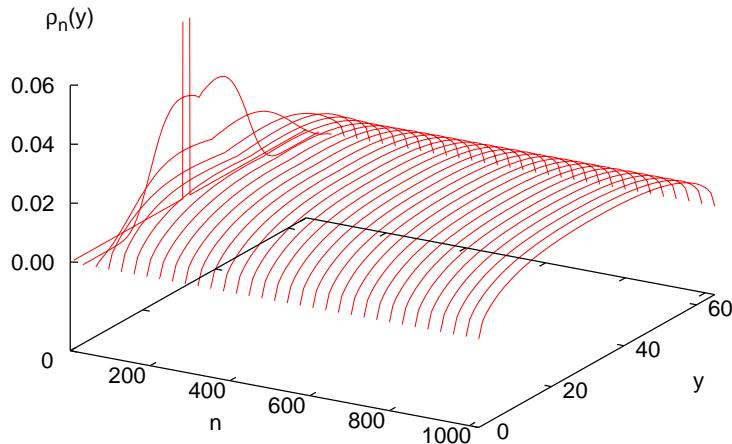
- $C_{n,m}^{est} = \langle W \rangle_{n,m}$
 - $r = W_{n,m}^{(i)} / C_{n,m}^{est}$

- Generalization to more microcanonical parameters possible

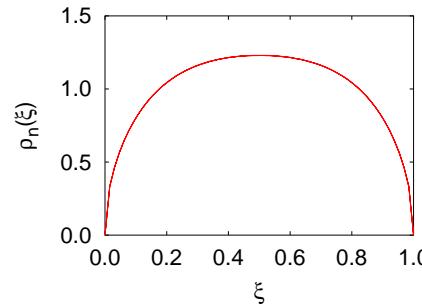
Simulation Results

Simulational results: SAW in a strip

- 2d SAW in a strip: strip width 64, up to $n = 1024$



- Endpoint density

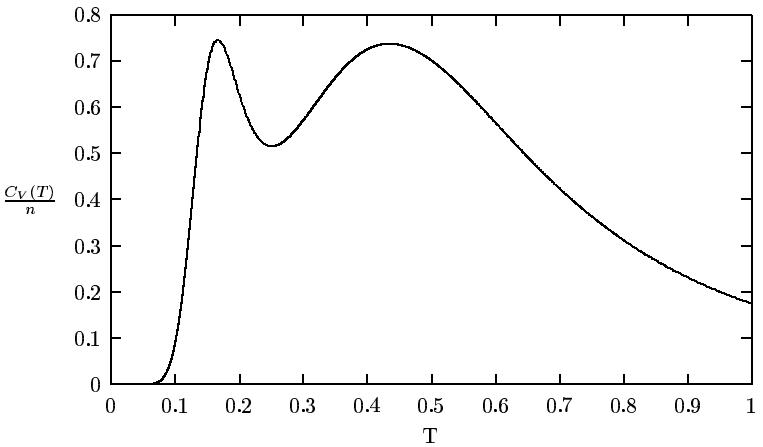
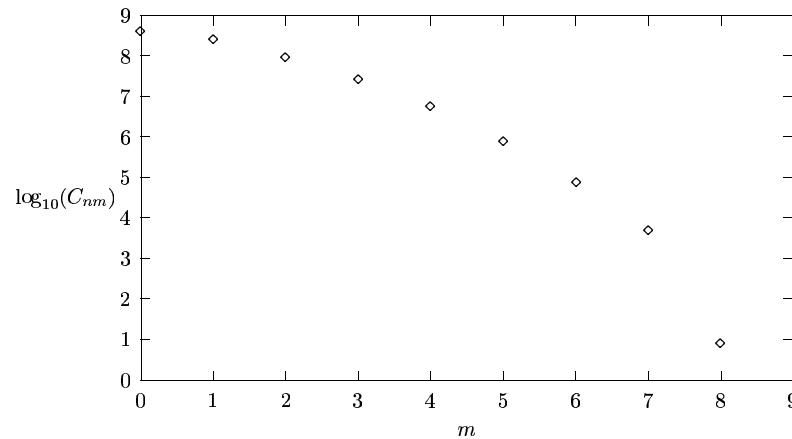


- Compares favorably with “Markovian anticipation”–PERM

Hsu and Grassberger, Eur Phys J 36 (2003) 209

Simulation results: HP model

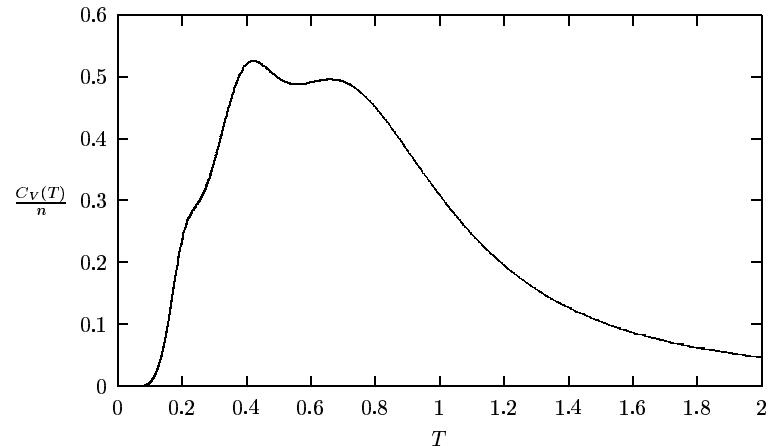
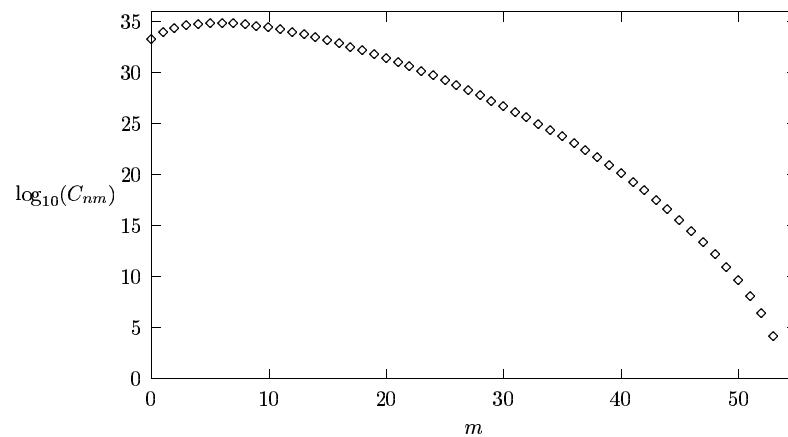
- Sequence I (14 Monomers, HPHPHHPPHPPH, $d = 3$):



- Pedagogical example, engineered for native ground state
- Perfect agreement with exact enumeration

Simulation results: HP model

- Sequence II (85 Monomers, $d = 2$):



- Investigated several other sequences in $d = 2$ and $d = 3$
- Collapsed regime accessible
- Reproduced known ground state energies
- Obtained $C_{n,m}$ over large range

Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

- To stabilize algorithm (avoid initial overflow/underflow):
Delay growth of large configurations
- Here: after t tours growth up to length $10t$

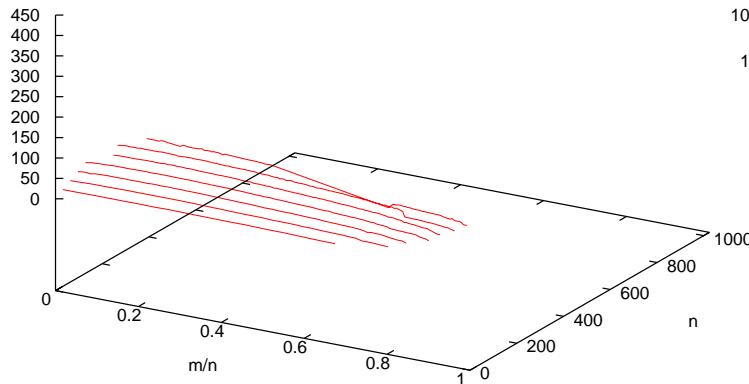


Simulation: dynamics of the algorithm

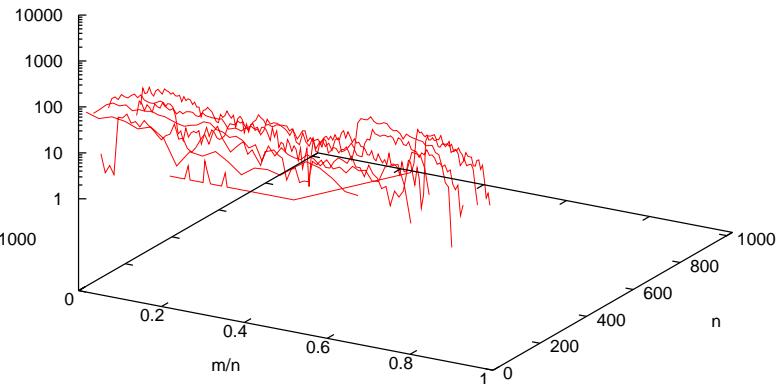
2d ISAW simulation up to $n = 1024$

- Total sample size: 1,000,000

$\log_{10}(C_{nm})$



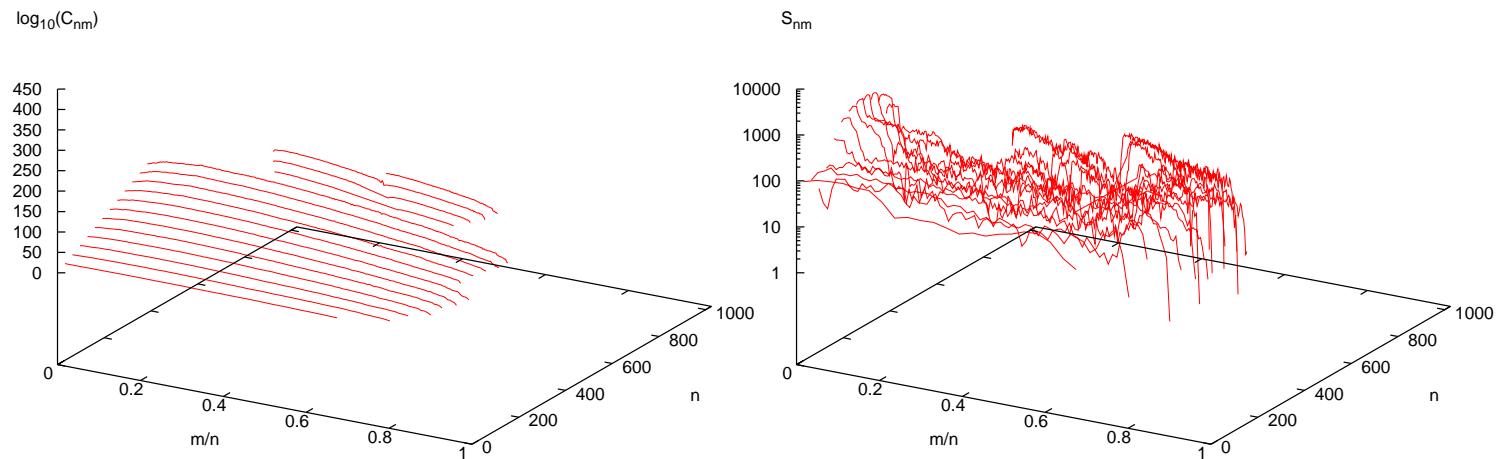
S_{nm}



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

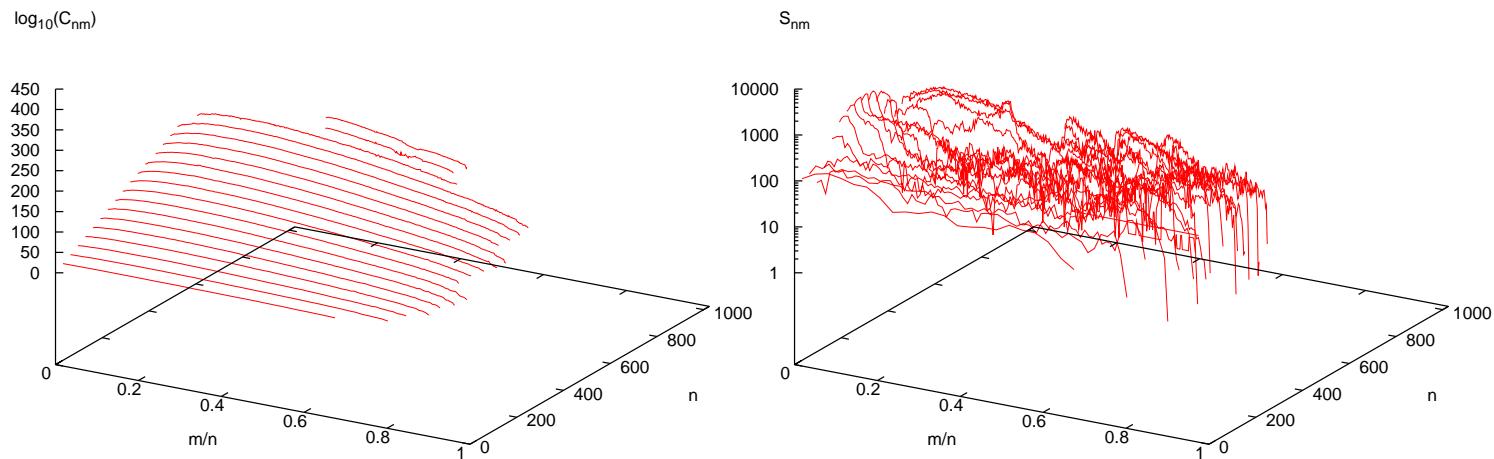
- Total sample size: 10,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

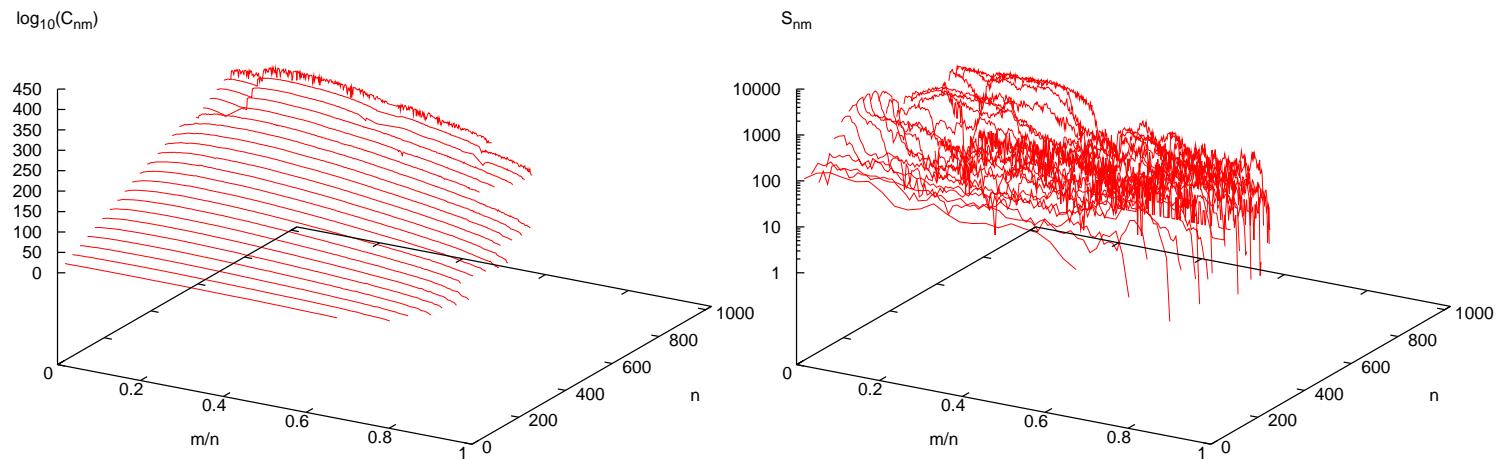
- Total sample size: 20,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

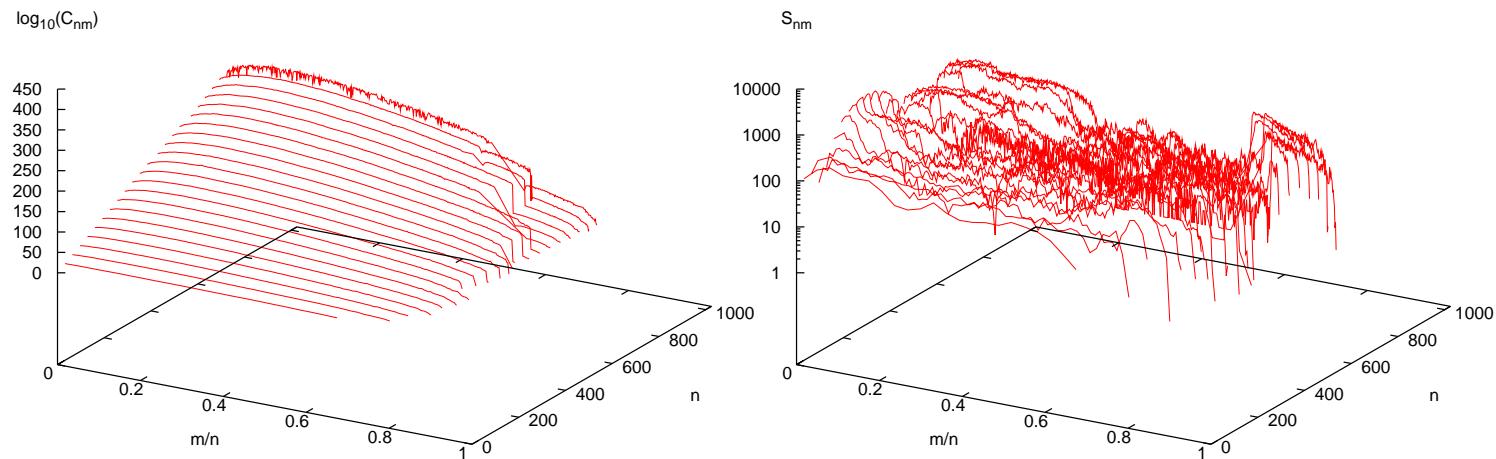
- Total sample size: 30,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

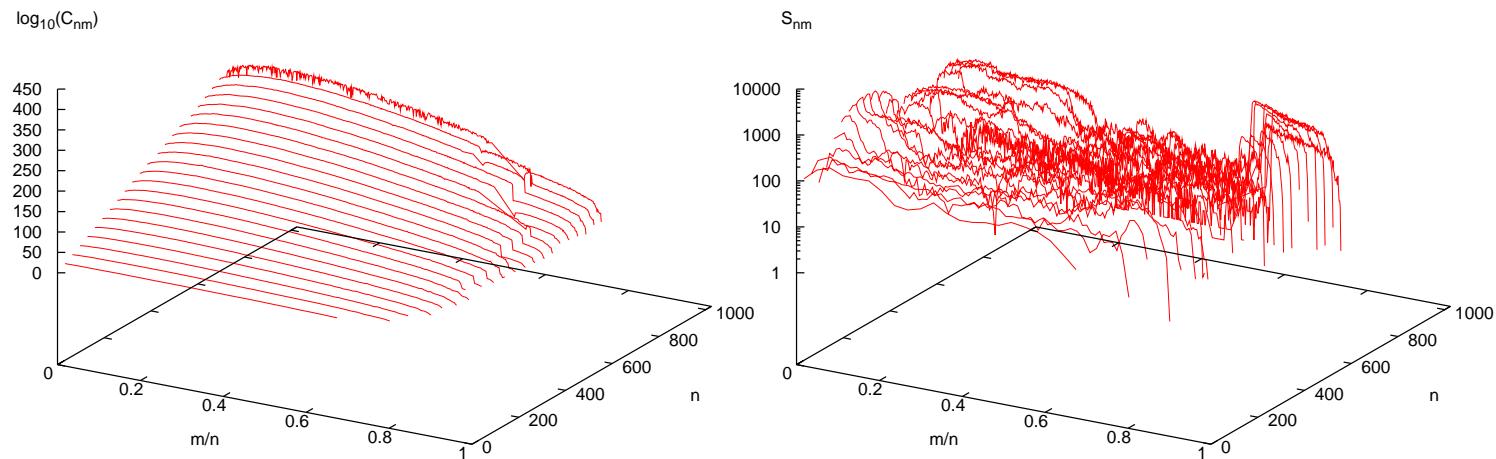
- Total sample size: 40,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

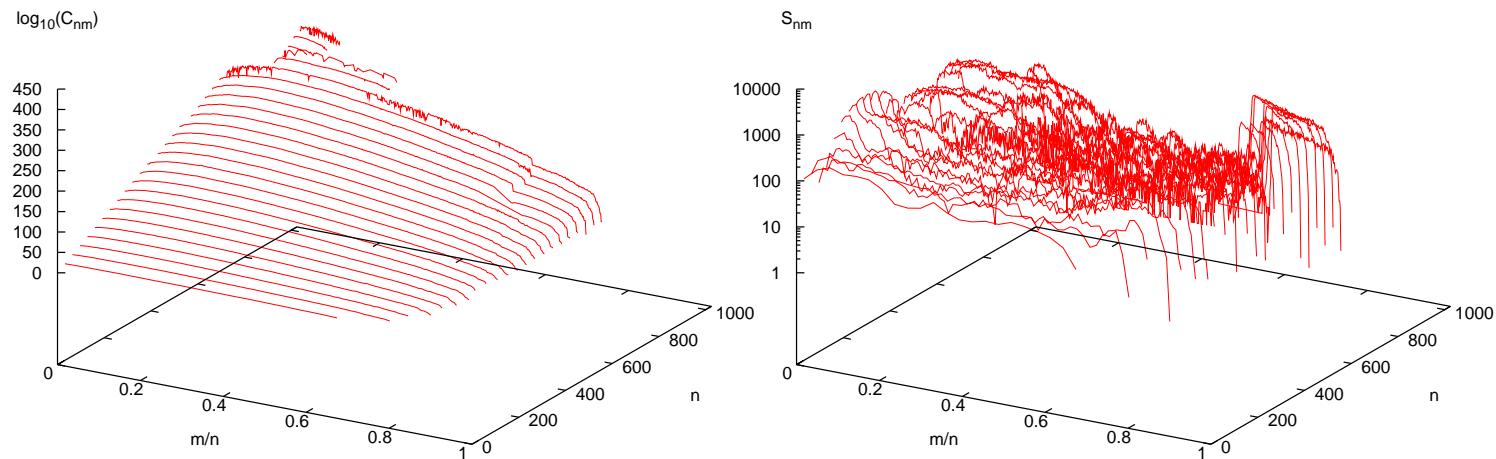
- Total sample size: 50,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

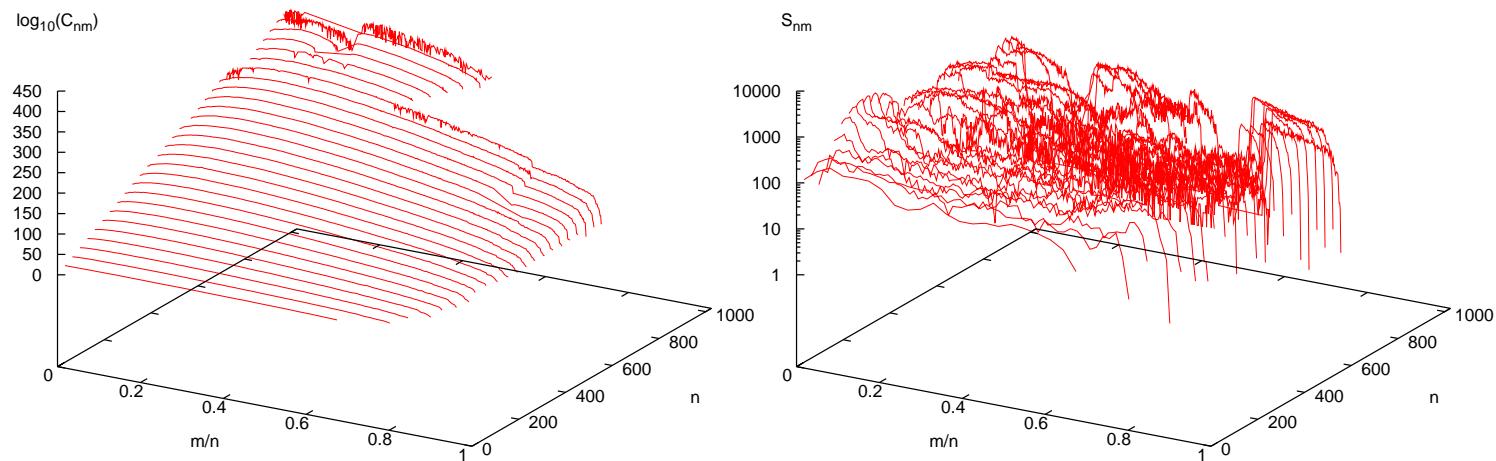
- Total sample size: 60,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

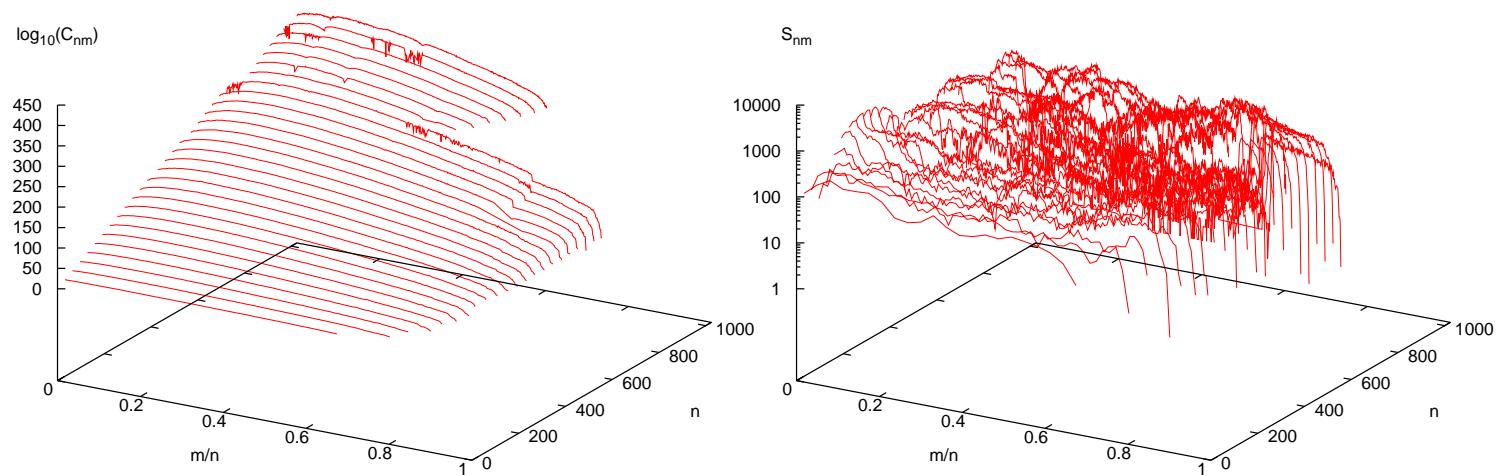
- Total sample size: 70,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

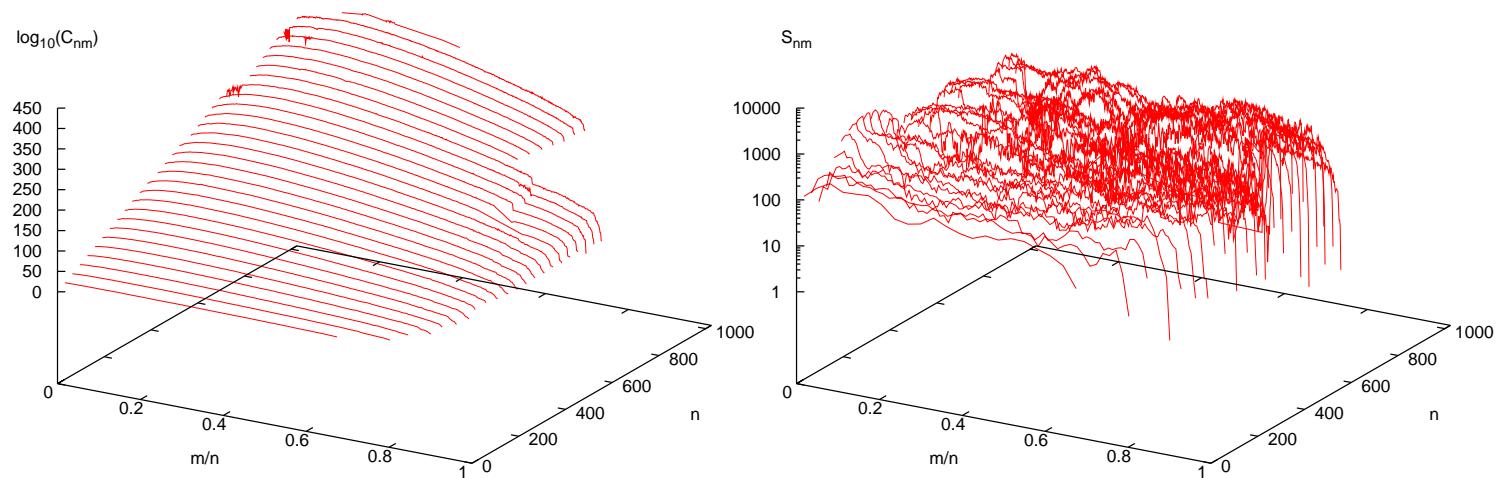
- Total sample size: 80,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

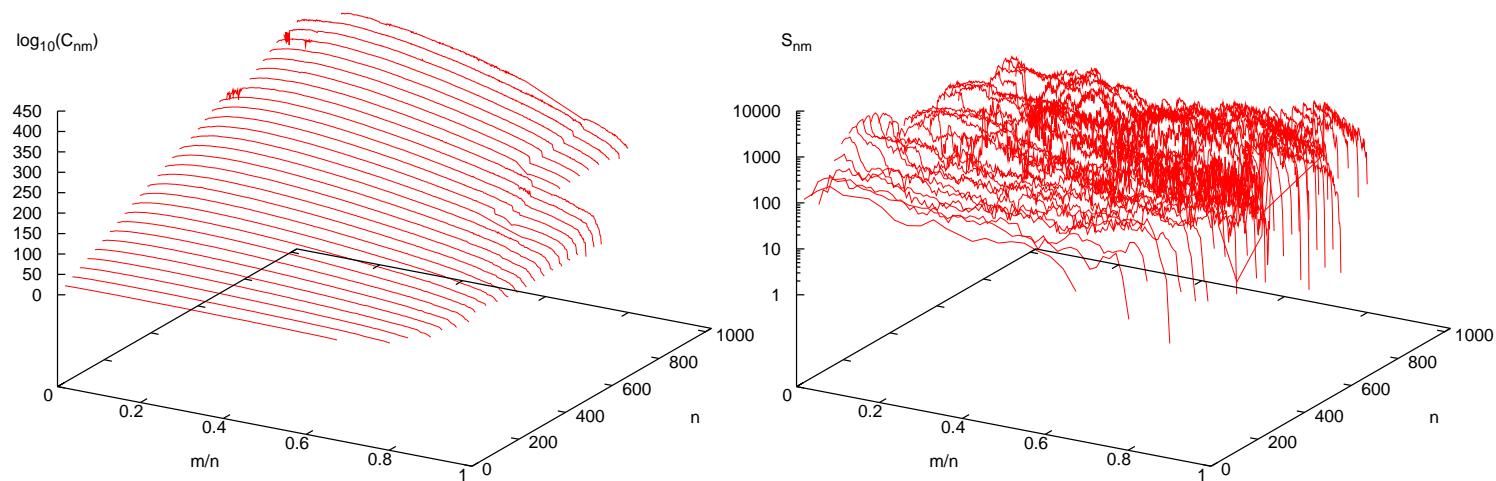
- Total sample size: 90,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

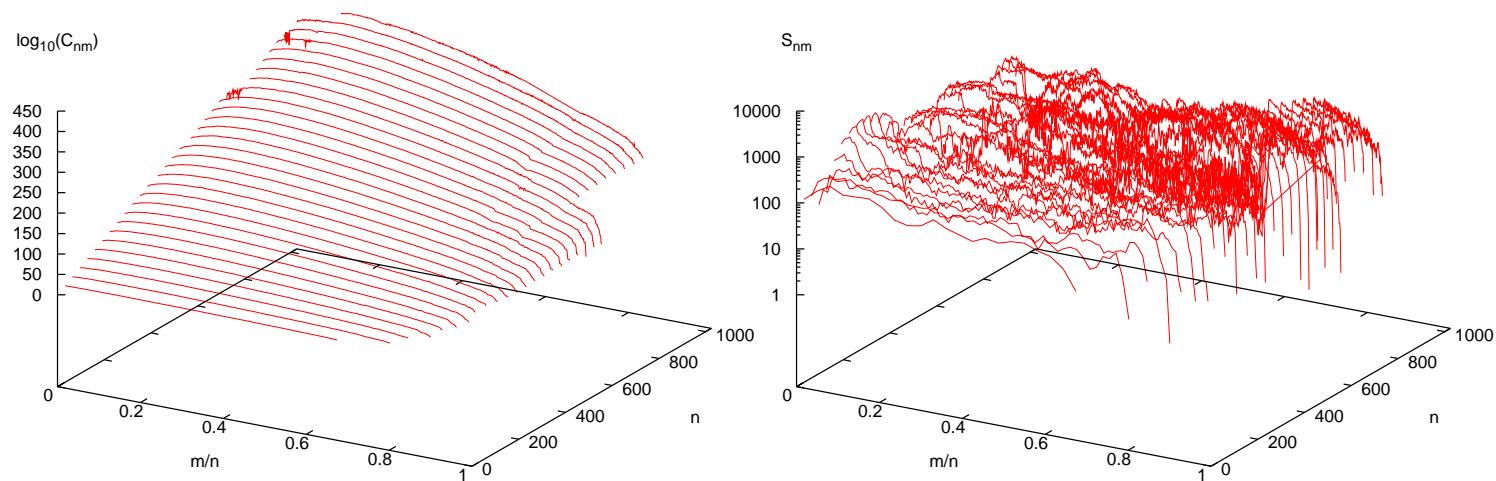
- Total sample size: 100,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

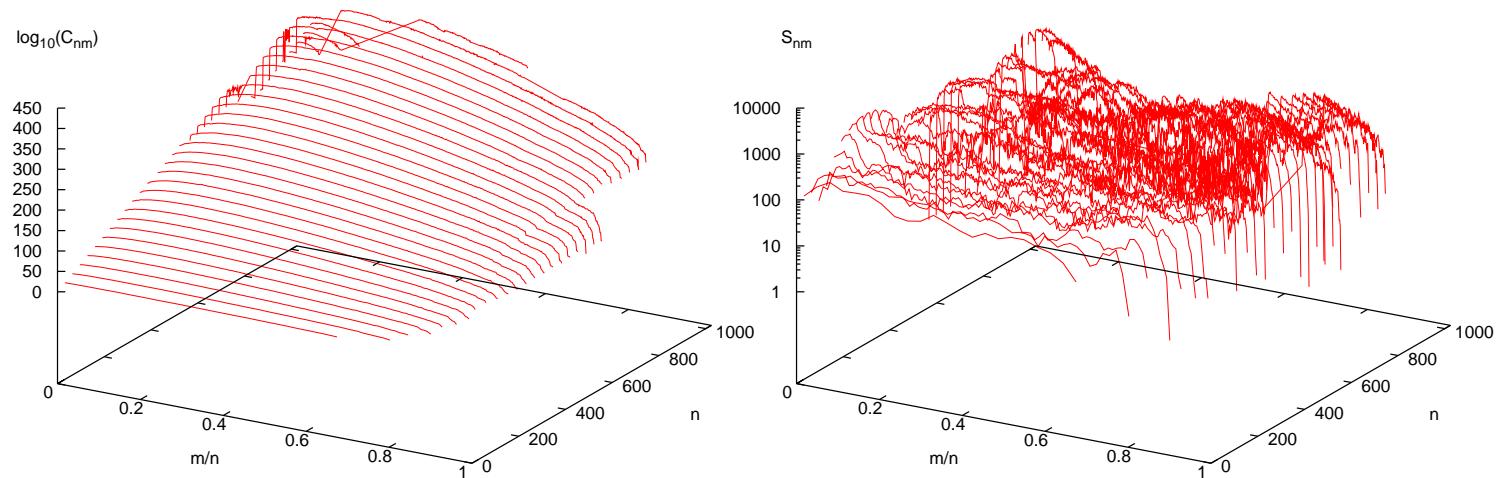
- Total sample size: 110,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

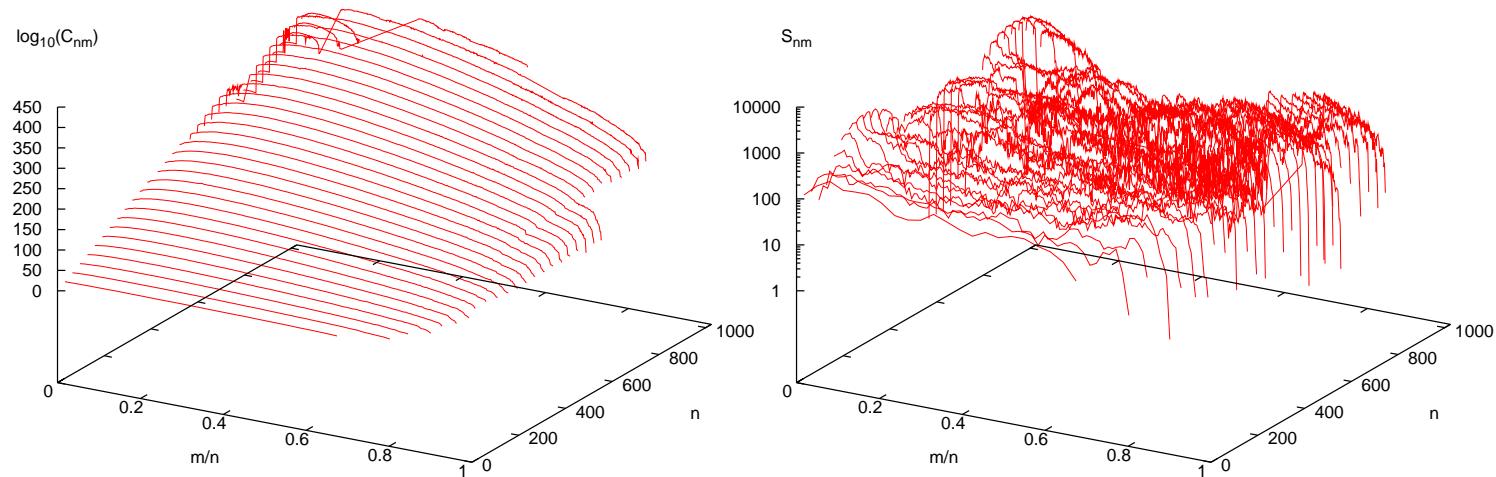
- Total sample size: 120,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

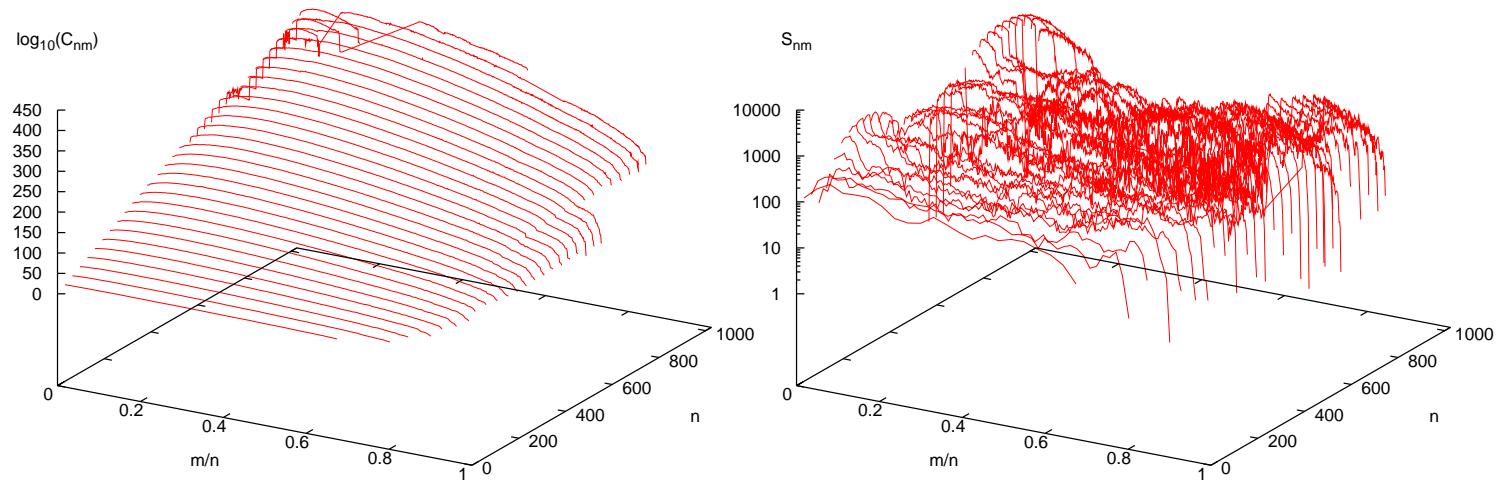
- Total sample size: 130,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

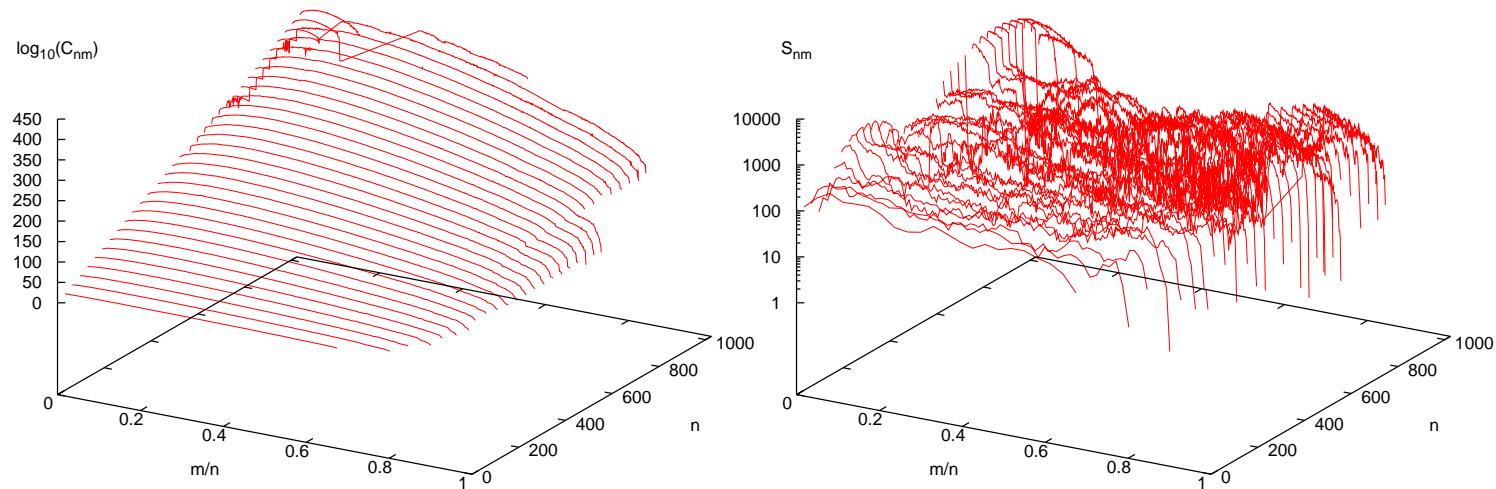
- Total sample size: 140,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

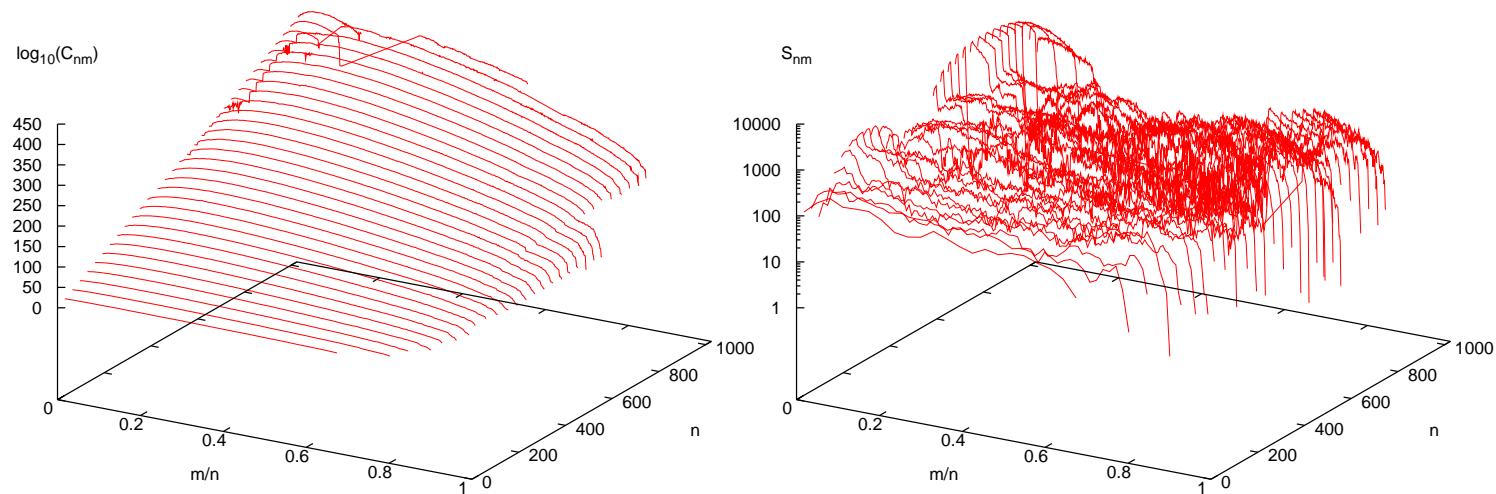
- Total sample size: 150,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

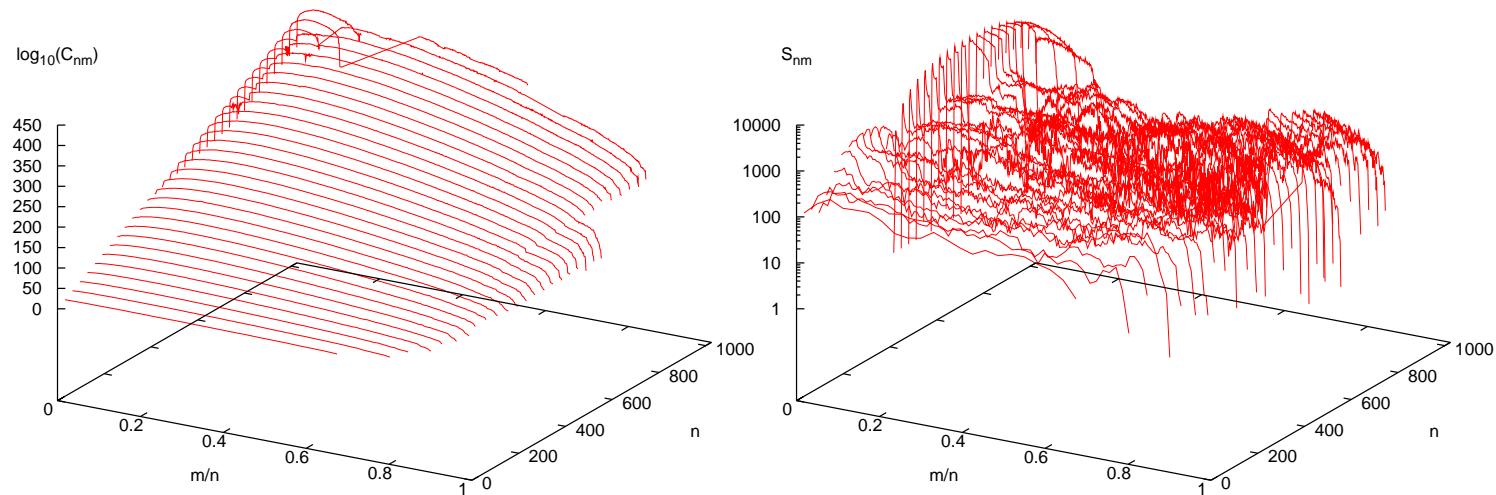
- Total sample size: 160,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

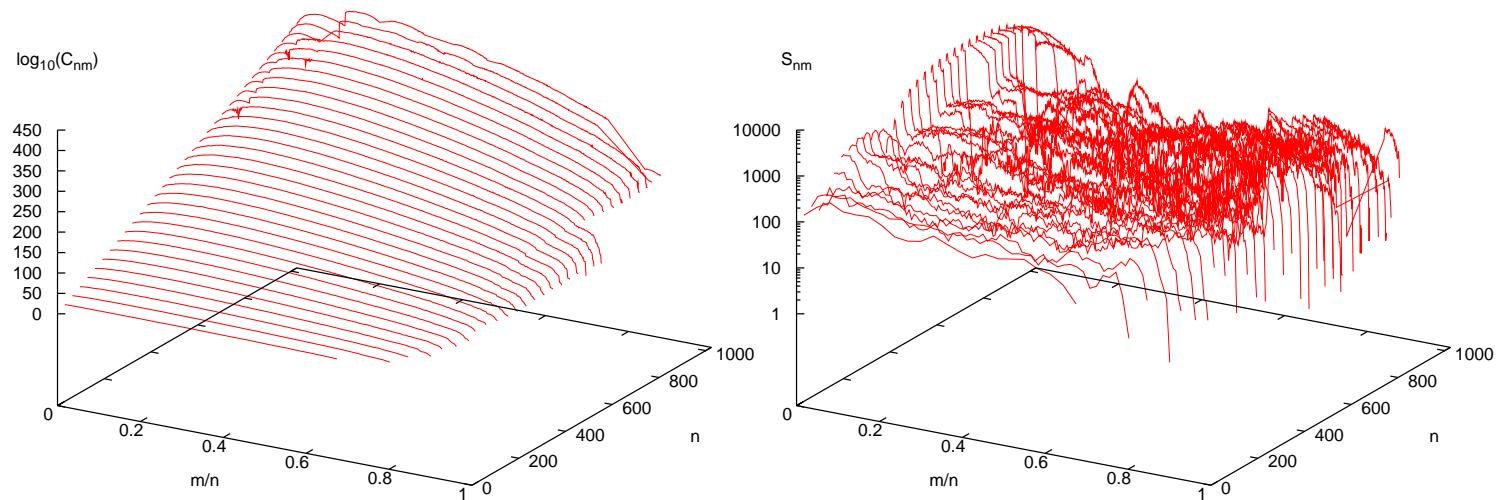
- Total sample size: 170,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

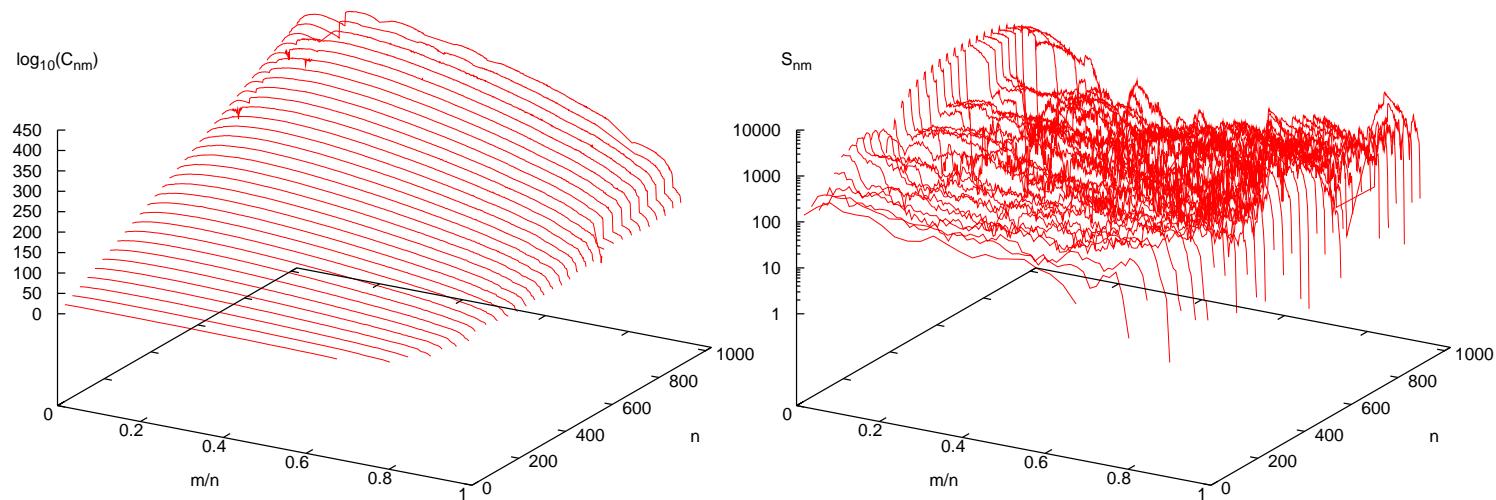
- Total sample size: 180,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

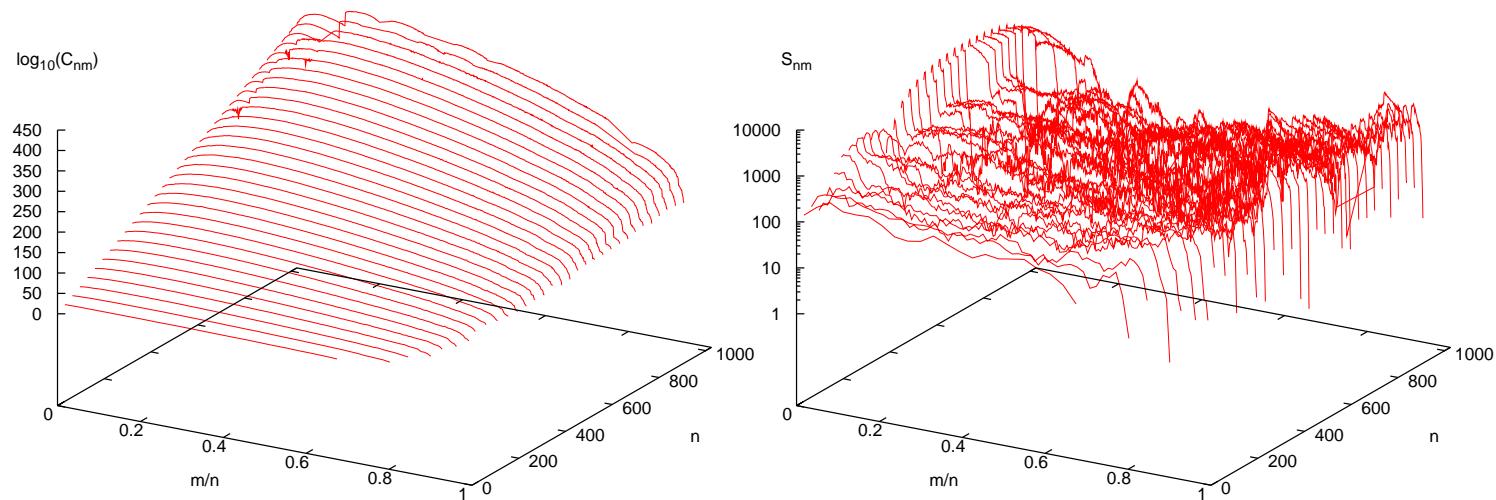
- Total sample size: 190,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

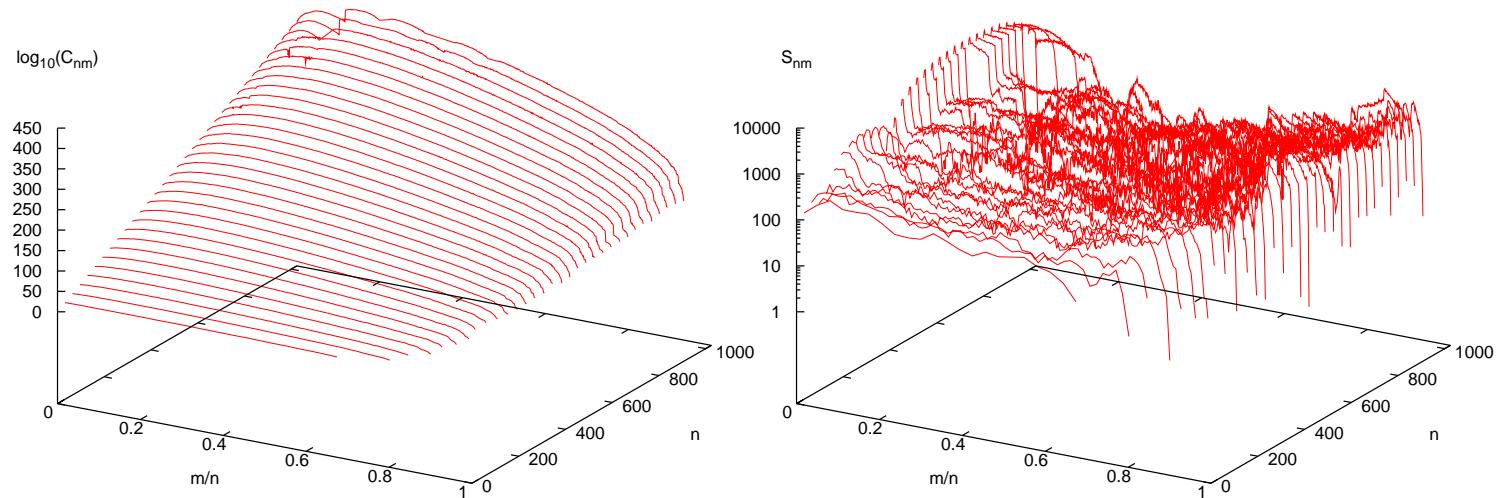
- Total sample size: 200,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

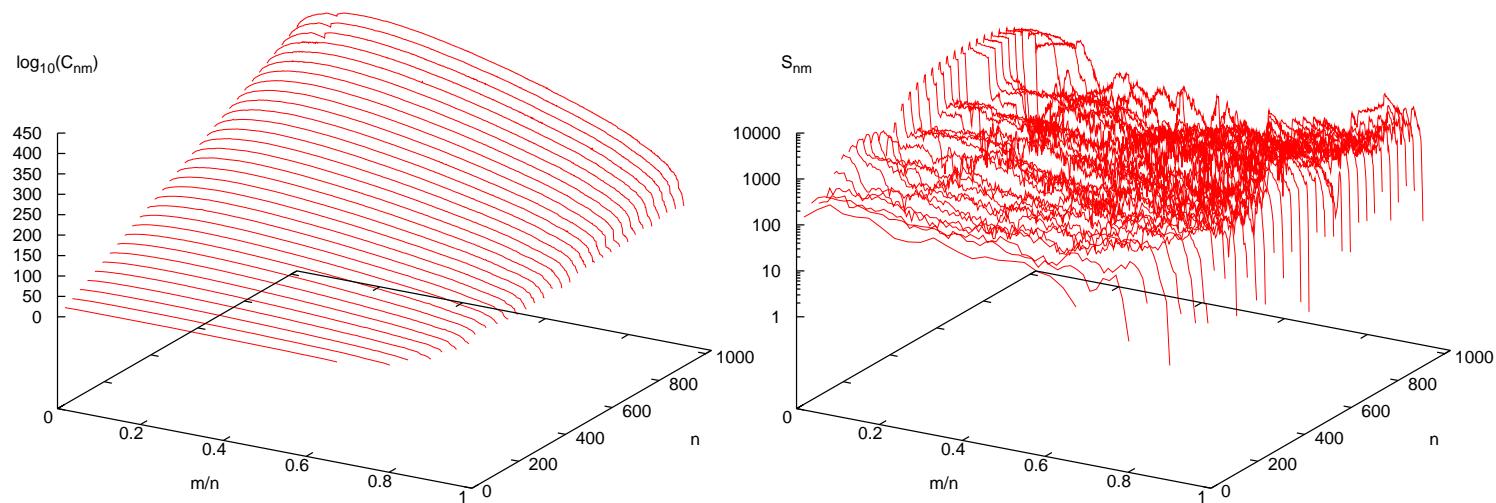
- Total sample size: 210,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

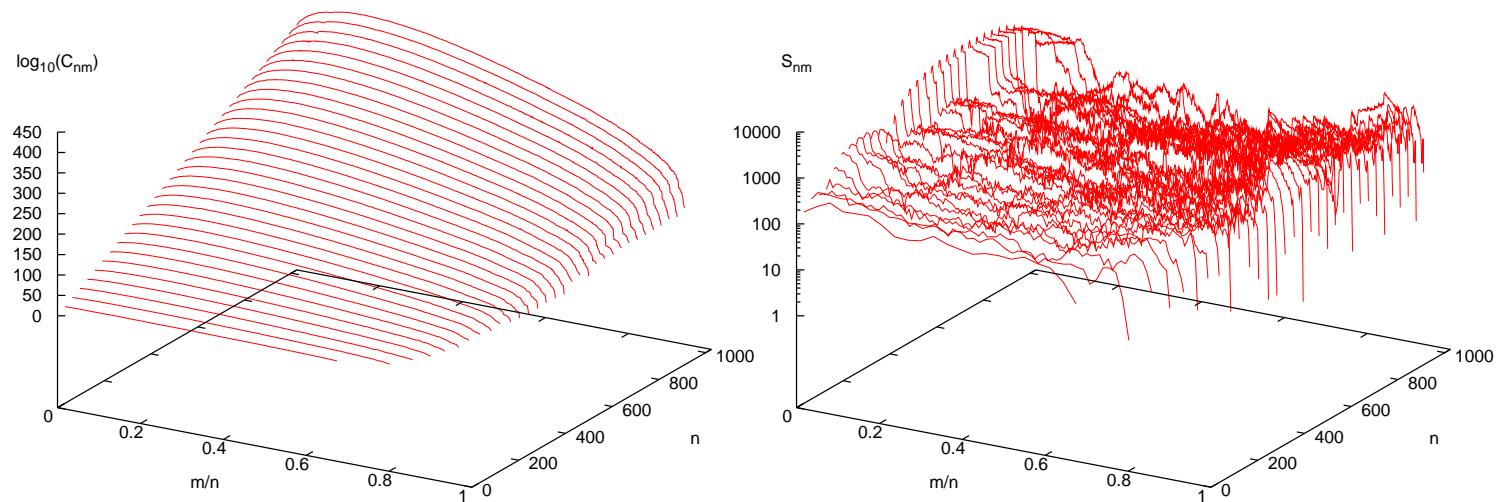
- Total sample size: 220,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

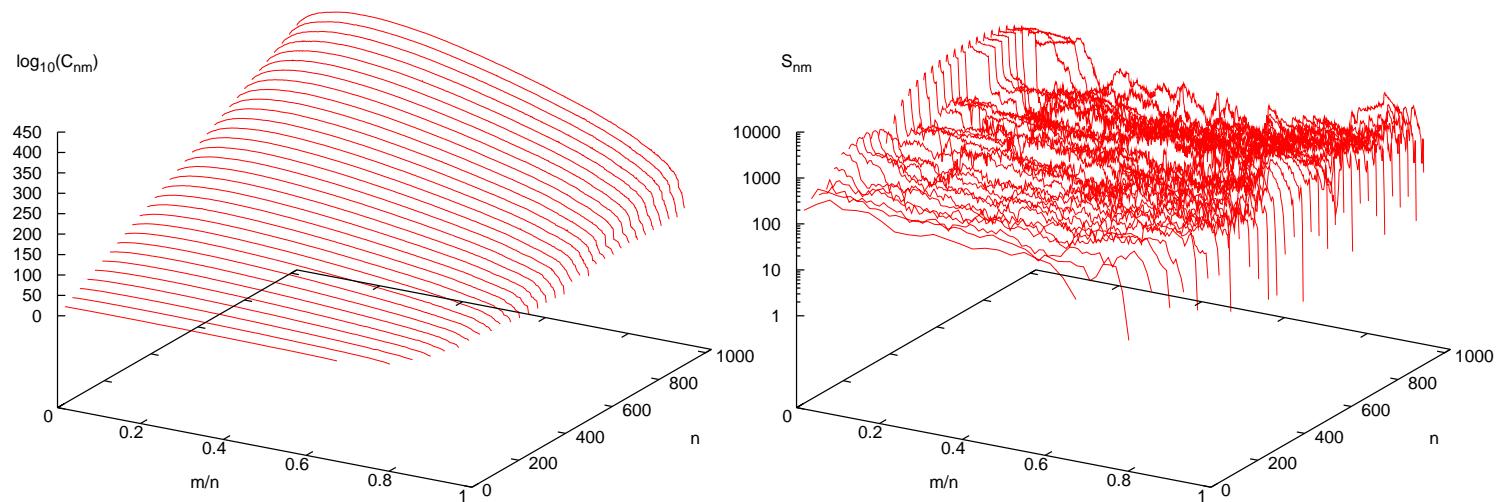
- Total sample size: 230,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

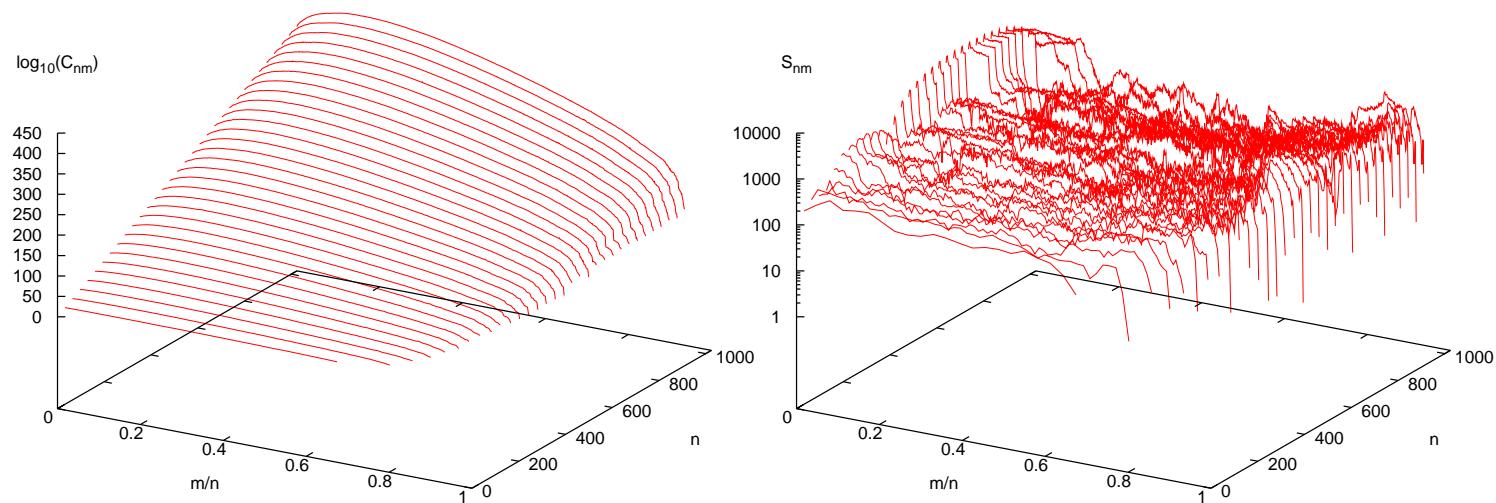
- Total sample size: 240,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

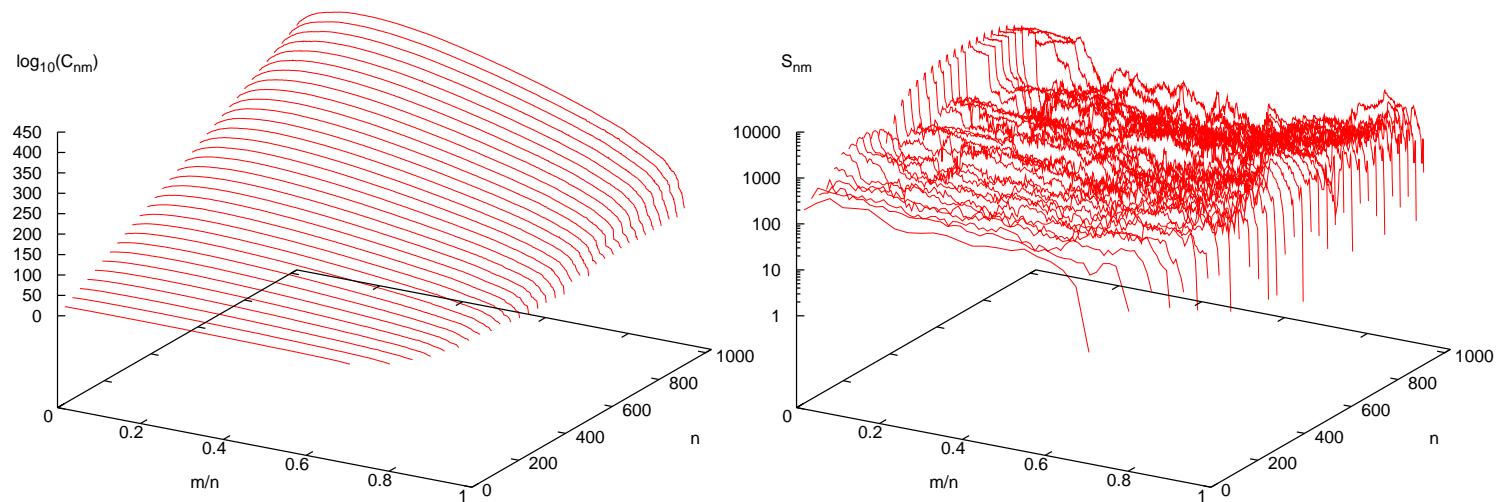
- Total sample size: 250,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

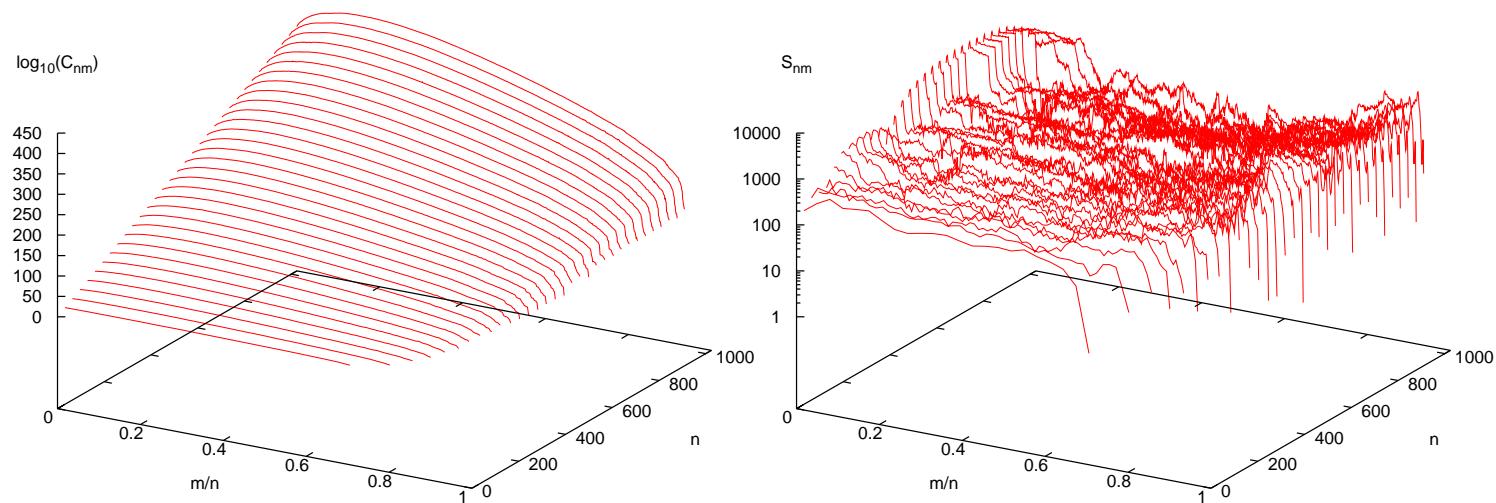
- Total sample size: 260,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

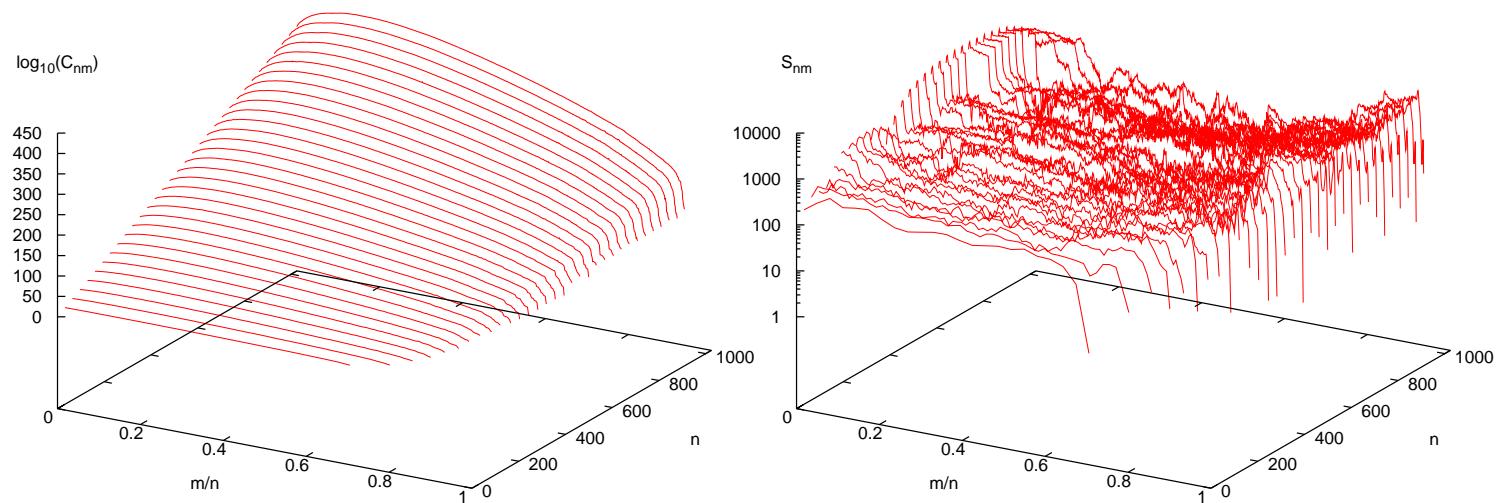
- Total sample size: 270,000,000



Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

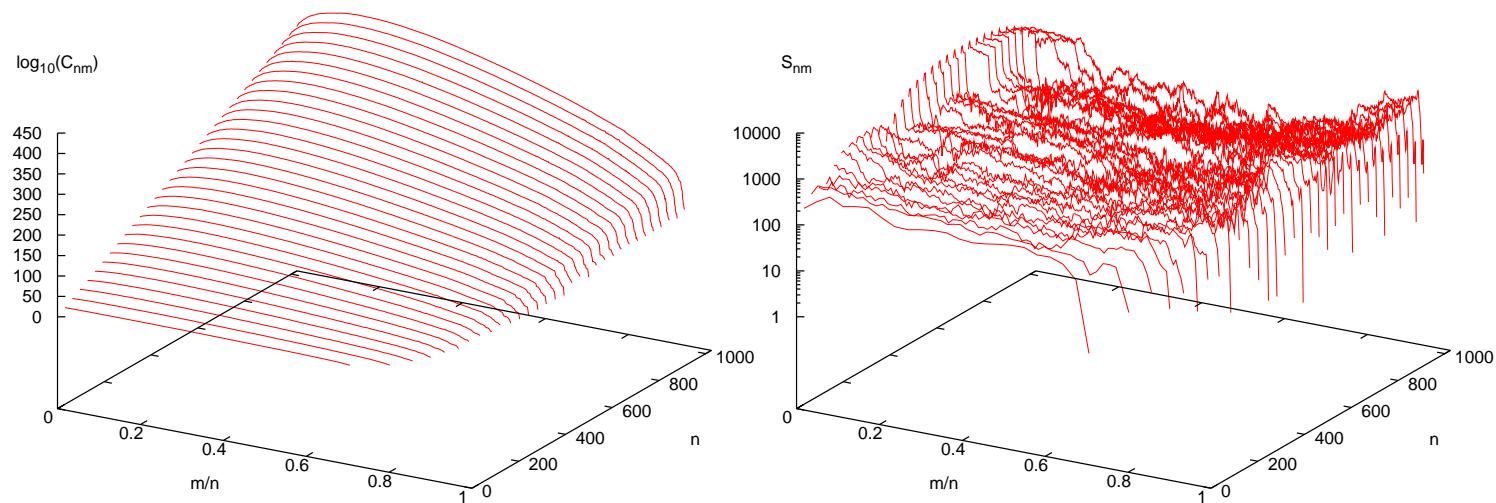
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Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

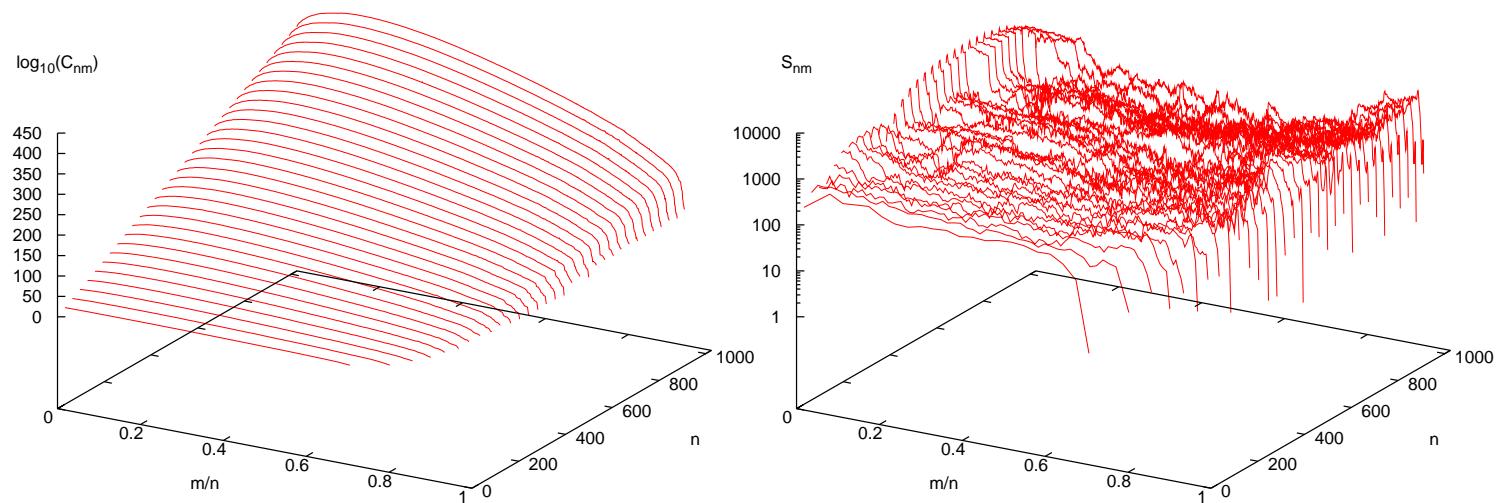
- Total sample size: 290,000,000



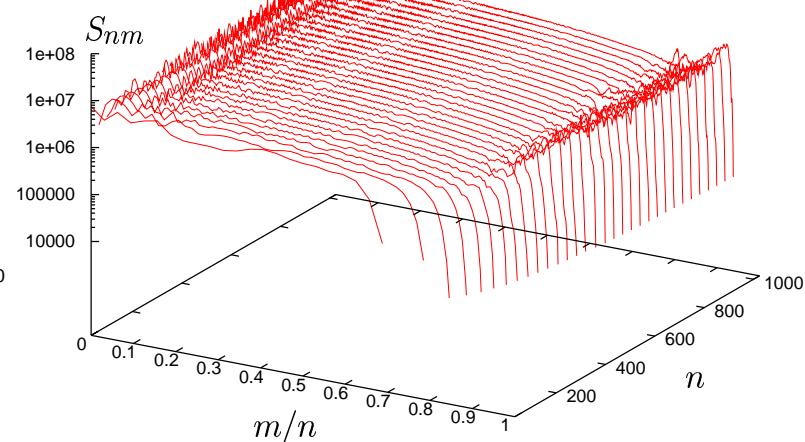
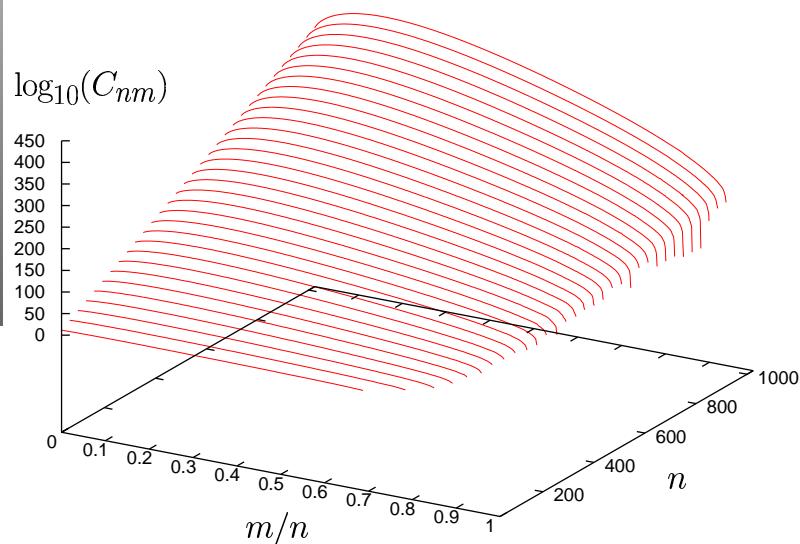
Simulation: dynamics of the algorithm

2d ISAW simulation up to $n = 1024$

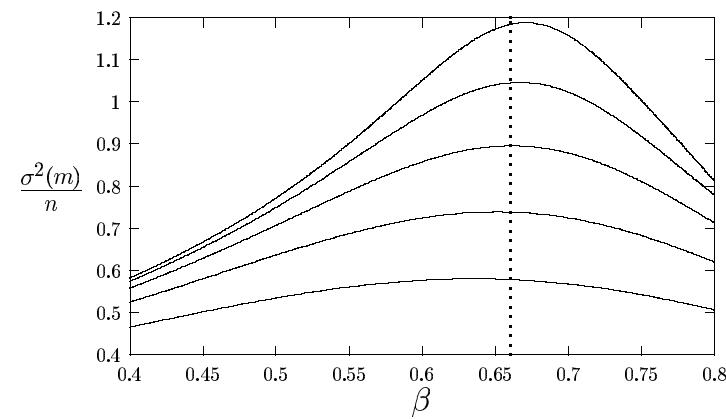
- Total sample size: 300,000,000



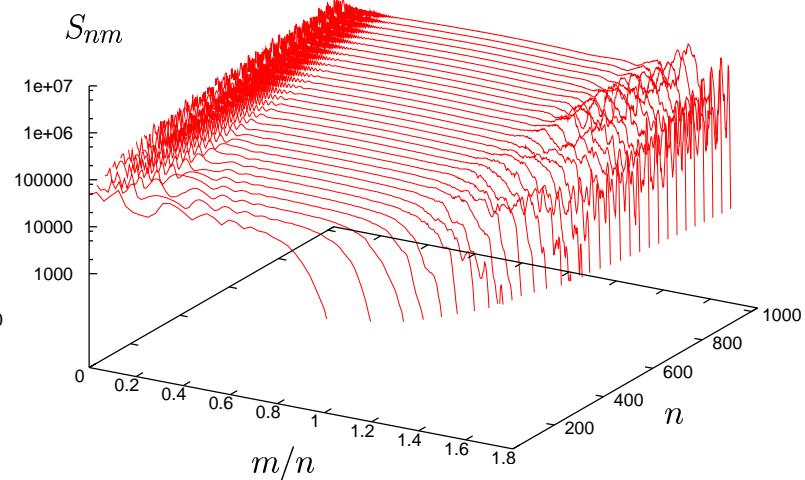
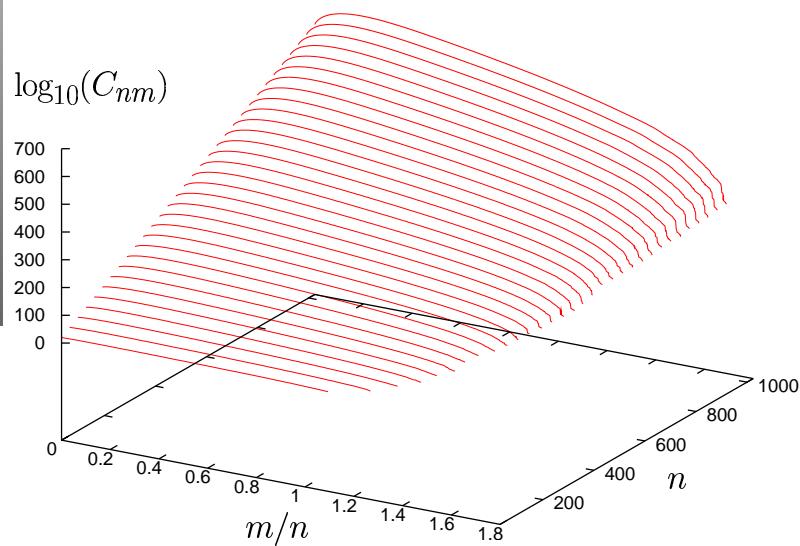
Simulation results: 2d ISAW



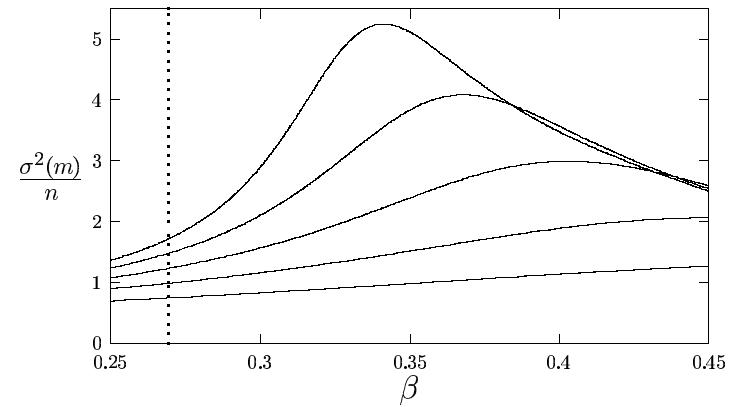
- 2d ISAW up to $n = 1024$
- One simulation suffices
- 300 orders of magnitude



Simulation results: 3d ISAW



- 3d ISAW up to $n = 1024$
- One simulation suffices
- 400 orders of magnitude



Summary and Outlook



Conclusion: A Promising New Algorithm

- Reviewed Stochastic Growth Algorithms for Polymers
- Presented “flat histogram” version of PERM
 - One simulation for complete density of states!
(the range can also be selectively restricted)
- Applications: SAW in a strip, HP model, ISAW



Conclusion: A Promising New Algorithm

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Outlook: applications to further models, e.g.

- Square lattice trees / branched polymers: with A. Rechnitzer
 - Connective constant estimate $5.1435(5)$
(compare to $5.1434(7)$ with Pivot algorithm)
- Full two/three-dimensional density of states with *one* simulation
 - Extended Domb-Joyce model: with J. Krawczyk
 - Pulling adsorbing and collapsing polymers: with A. Owczarek

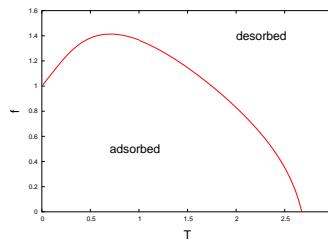
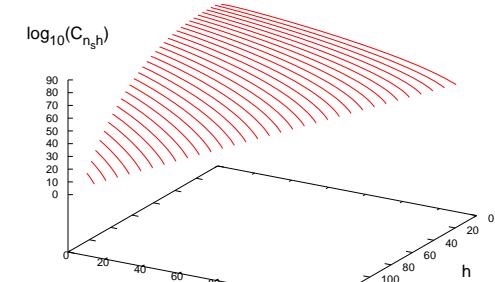
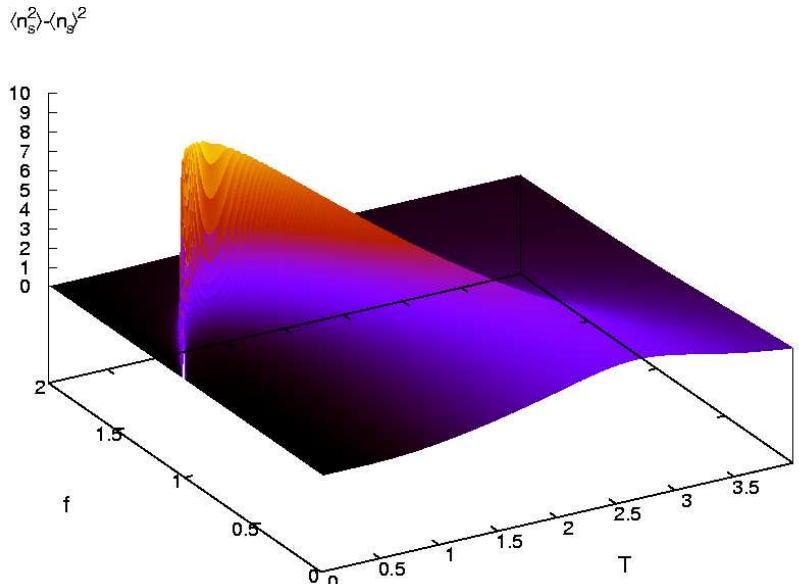
Outlook: 2-Dimensional Density of States

- Force-induced desorption of adsorbed polymers: with J. Krawczyk
 - Relevance: optical tweezers, AFM; related to DNA unzipping



Outlook: 2-Dimensional Density of States

- Force-induced desorption of adsorbed polymers: with J. Krawczyk
 - Relevance: optical tweezers, AFM; related to DNA unzipping
- 3-dim polymer in a half space, one simulation, up to $n = 256$



Marenduzzo et al, PRL 82 (2002) 828102; Orlandini et al, J Phys A (2004) 1535;

Mishra et al, cond-mat/0404191

Thomas Prellberg, Applied Mathematics Seminar, Open University, July 13, 2004 – p.24/25

The End

