

A flat histogram stochastic growth algorithm (with application to polymers and proteins)

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Joint work with Jaroslaw Krawczyk, TU Clausthal

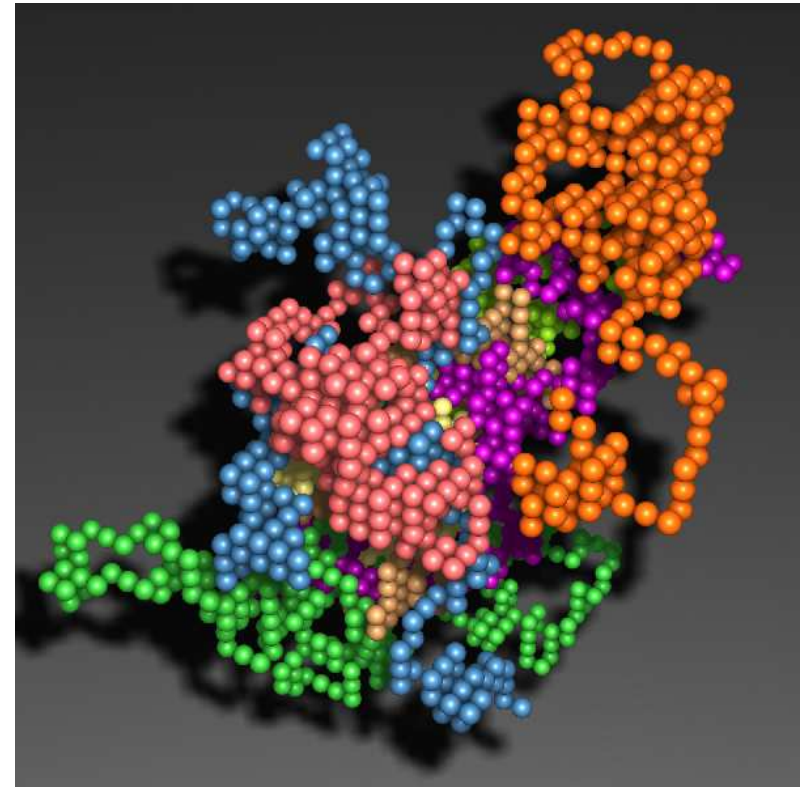


Introduction



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)

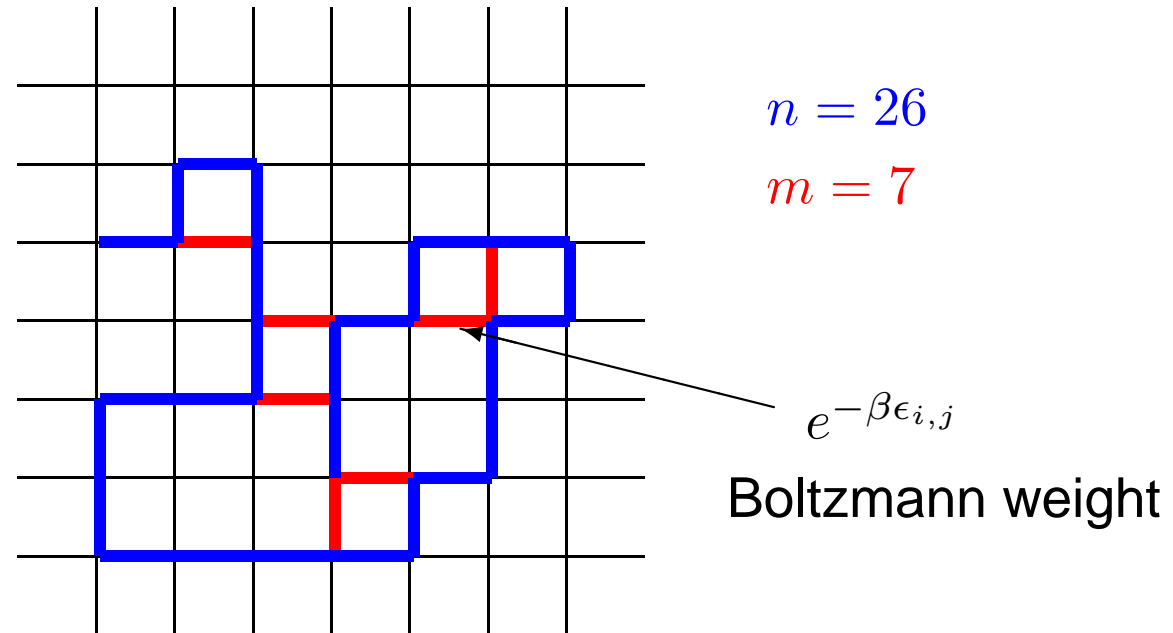
Self-Avoiding Walks with Interactions

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

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

Lattice Model: ISAW

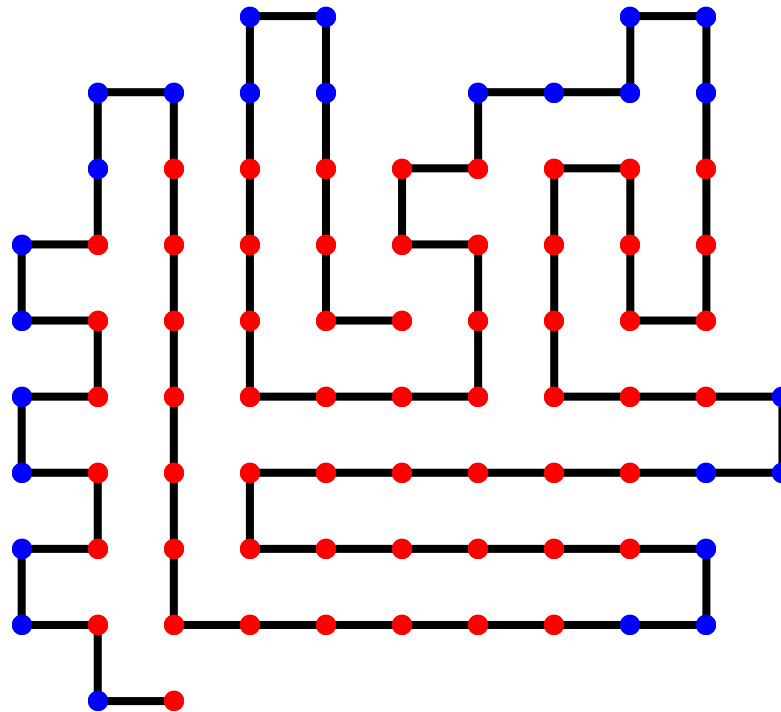


- ISAW model: interaction $\epsilon_{i,j} = -1$, $\omega = e^\beta$
- Partition function: $Z_n(\omega) = \sum_m C_{n,m} \omega^m$
- $C_{n,m}$ number of SAW with length n and m interactions

Lattice Model: HP model

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

Hydrophobic
Polar



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

Collapsed regime is notoriously difficult to simulate

Stochastic Growth Algorithms

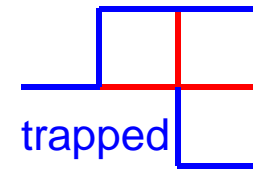
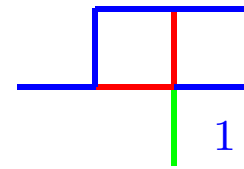
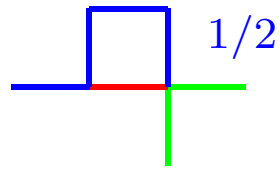
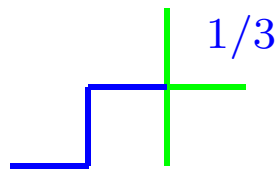


PERM: “Go With The Winners”

PERM = Pruned and Enriched Rosenbluth Method

Grassberger, Phys Rev E 56 (1997) 3682

- Rosenbluth Method: kinetic growth

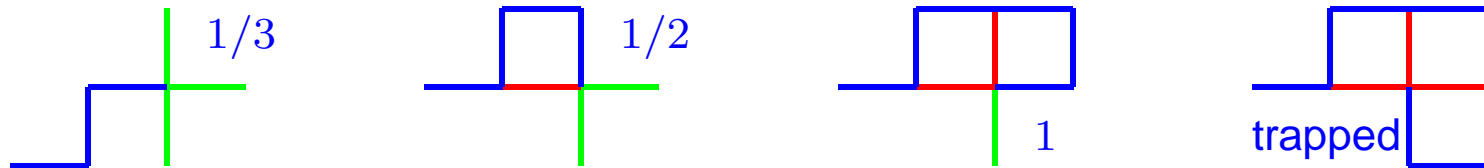


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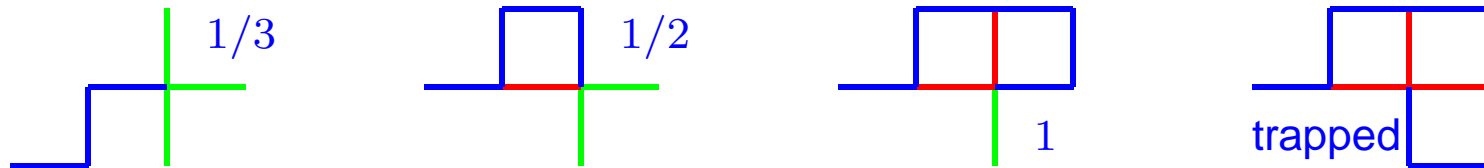
- Enrichment: weight too large \rightarrow make copies of configuration
- Pruning: weight too small \rightarrow remove configuration occasionally

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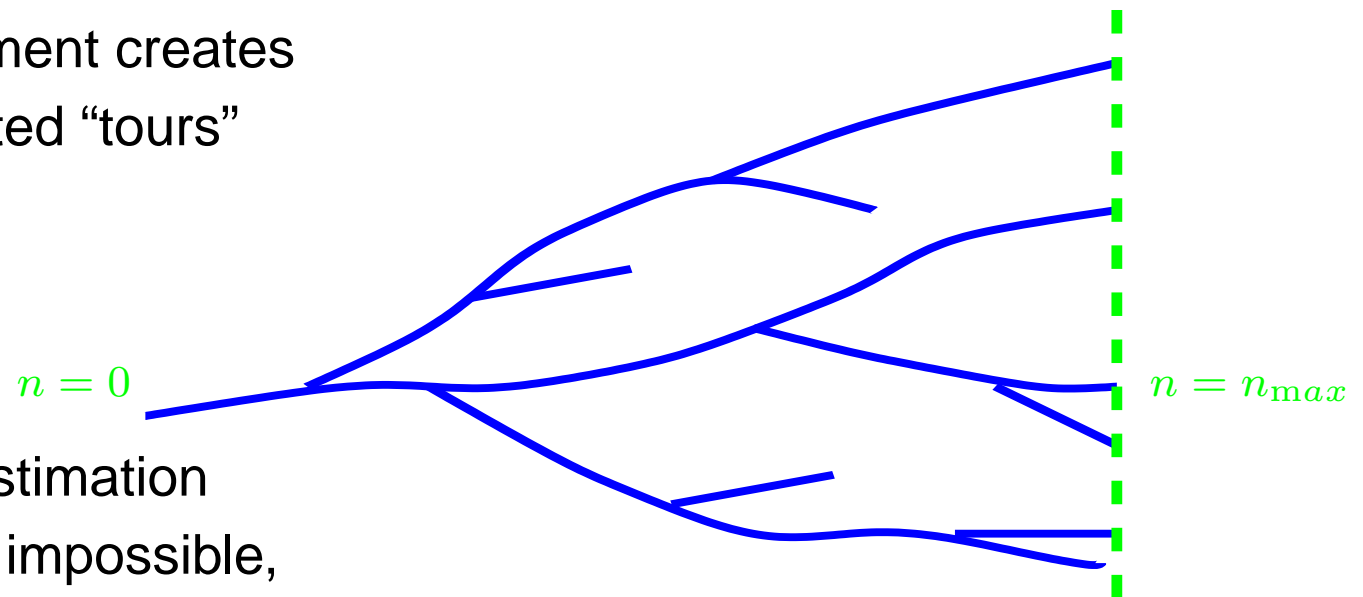


- Enrichment: weight too large → make copies of configuration
- Pruning: weight too small → remove configuration occasionally

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

PERM – continued

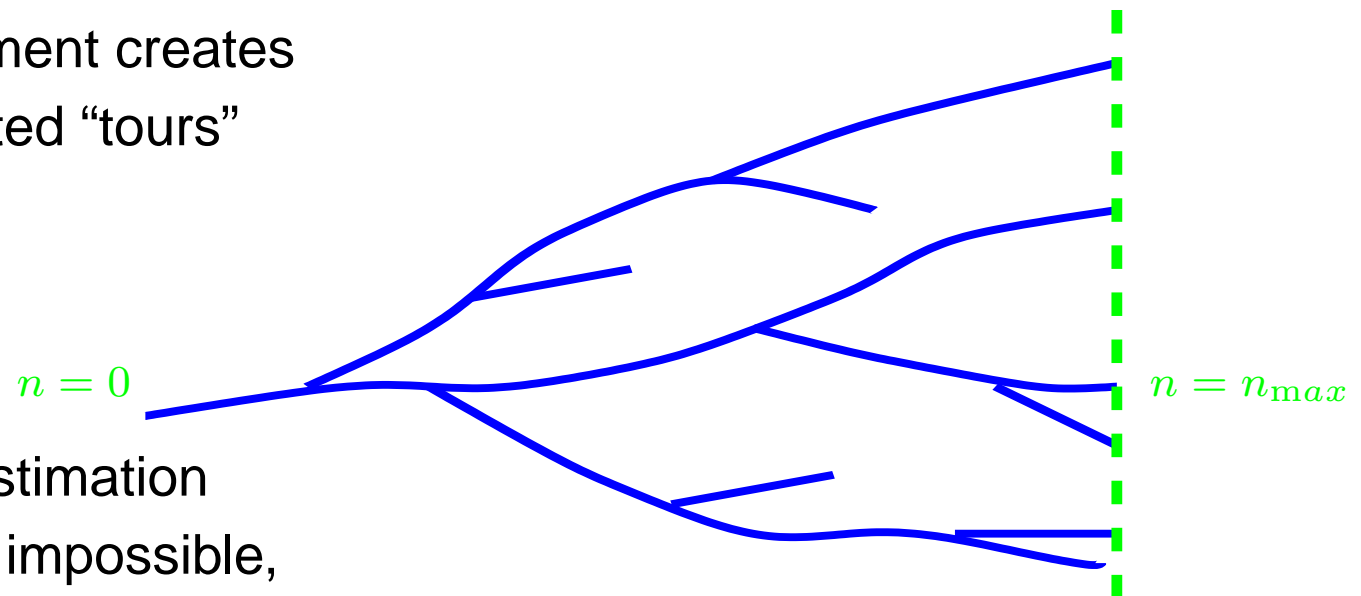
- PERM well suited for simulation of collapsing polymers
- Enrichment creates correlated “tours”



- Error estimation
a priori impossible,
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PERM is “blind” - it benefits from “visual aids”, such as

- Markovian anticipation (learning from experience)

PERM – further developments

- A significant improvement: nPERM = “new” PERM

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

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- Current work: flatPERM = “flat histogram” PERM

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- 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

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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).
- 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

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



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 $\frac{1}{c} W_n^{(i)}$
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- 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

● $C_n^{est} = \langle W \rangle_n$

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

- thermal PERM: estimate partition function $Z_n(\beta)$

- $Z_n^{est}(\beta) = \langle W \exp(-\beta E) \rangle_n$

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- Generalization to more microcanonical parameters possible



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- What if we don't need the whole histogram?
 - Restriction of histogram possible
 - e.g. impose internal energy restriction $m/n < u_{cutoff}$

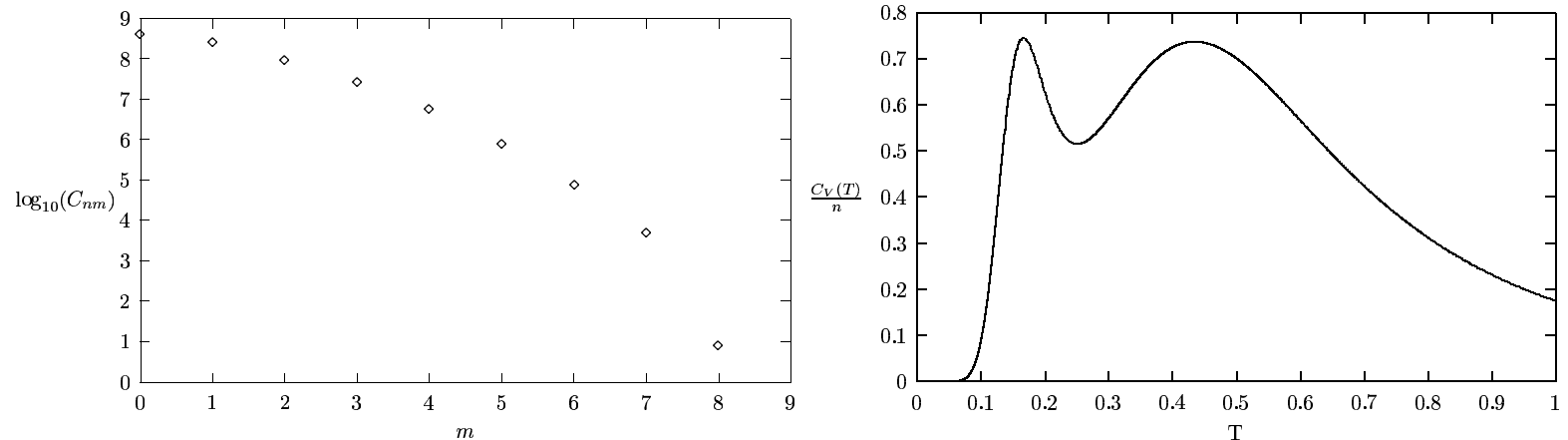
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- What if we don’t need the whole histogram?
 - Restriction of histogram possible
 - e.g. impose internal energy restriction $m/n < u_{cutoff}$
- What if we don’t want a “flat” histogram?
 - Sample profile can be tuned
 - Selectively perform pruning/enrichment with respect to profile shape $f_{n,m}$

Simulation Results



Simulation results: HP model

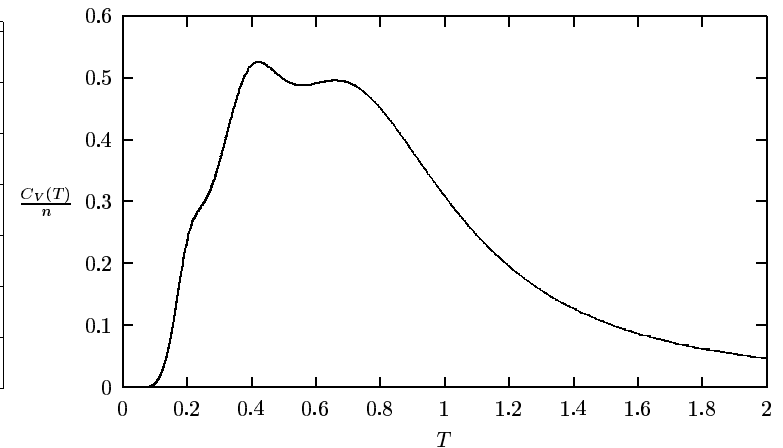
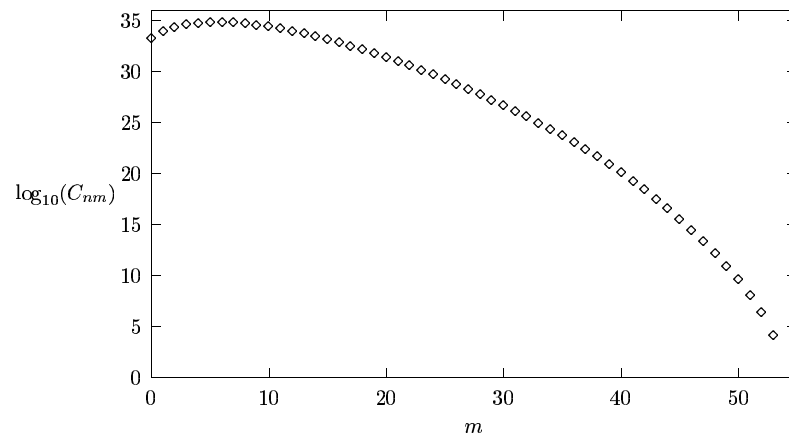
- Sequence I (14 Monomers, HPHPHHPHHPH, $d = 3$):



- 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: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

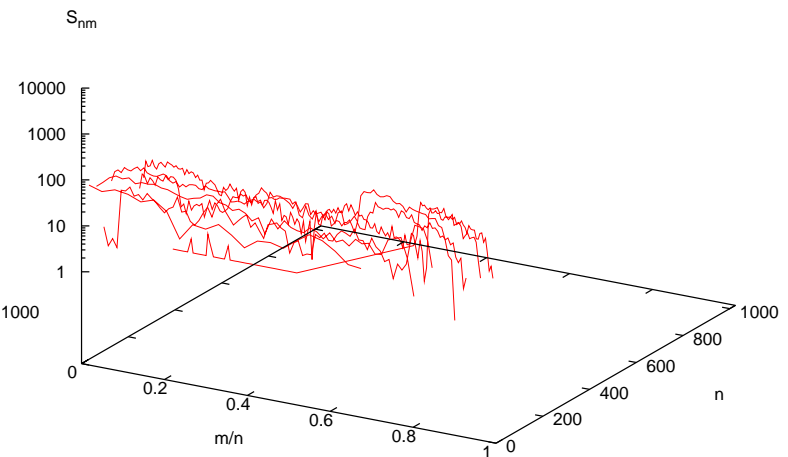
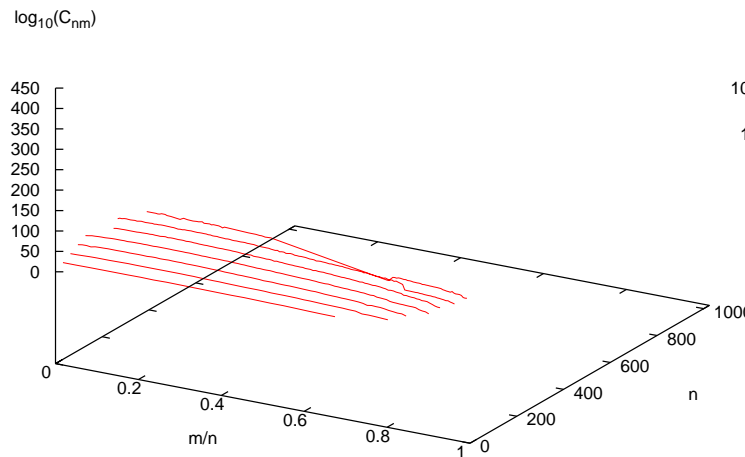
- Equilibration with delay 0.1:
after t tours growth up to length $10t$



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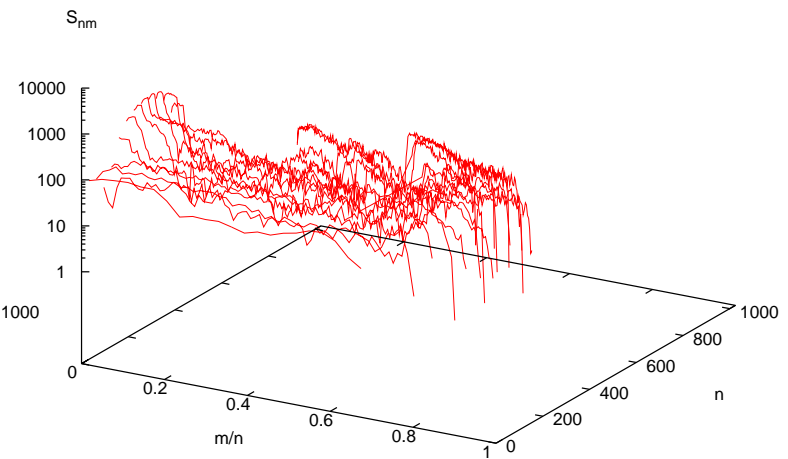
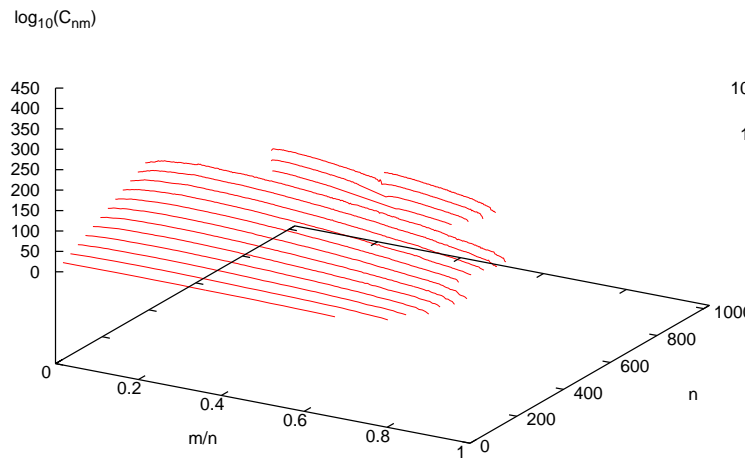
- Total sample size: 1,000,000



Simulation: Equilibration for 2d ISAW

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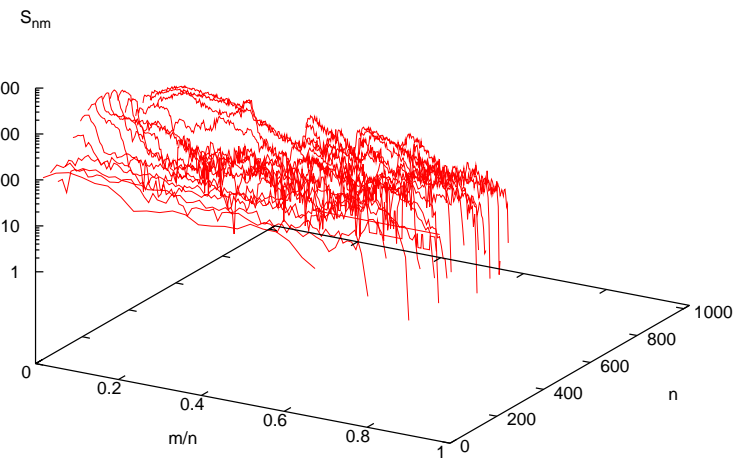
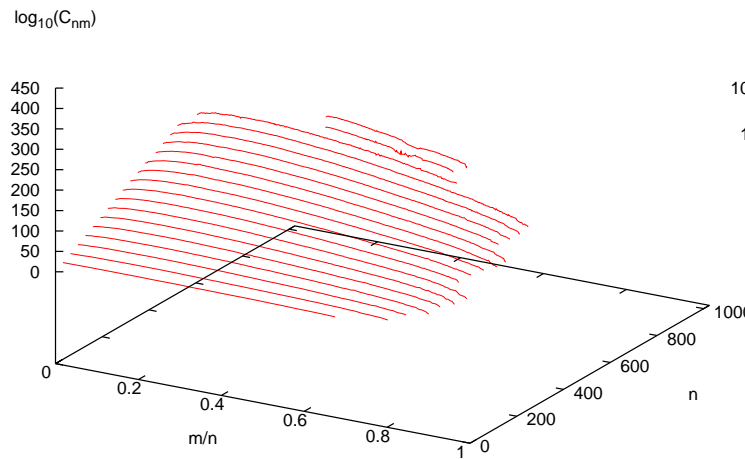
- Total sample size: 10,000,000



Simulation: Equilibration for 2d ISAW

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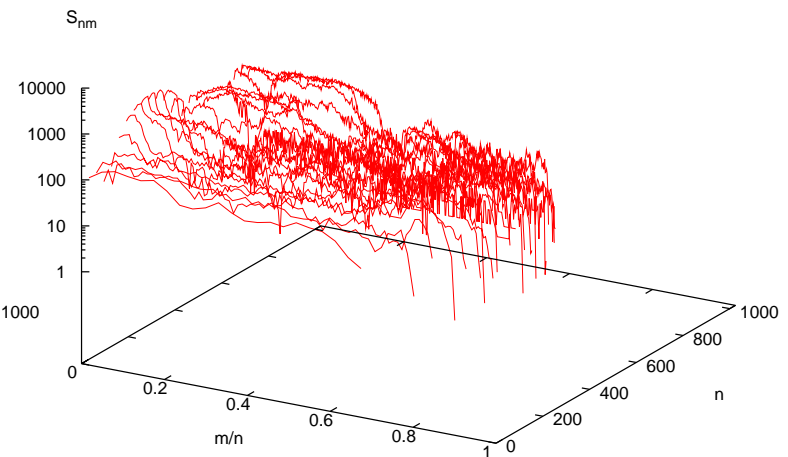
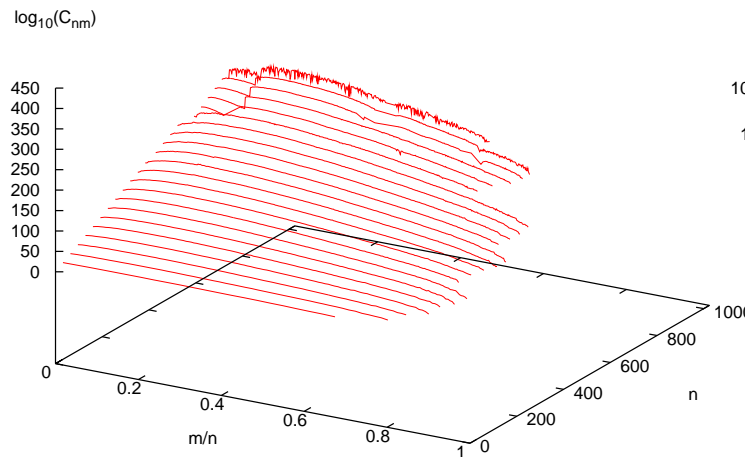
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Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

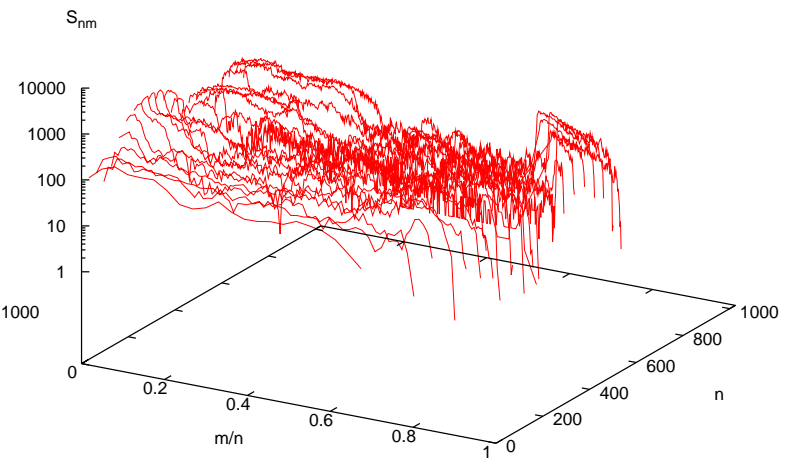
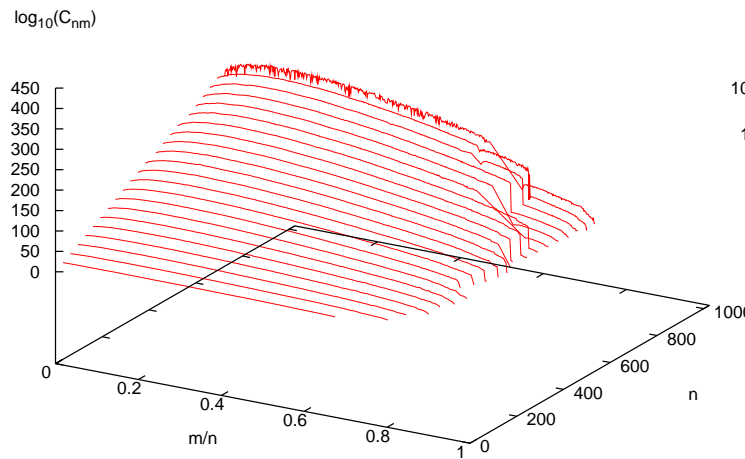
● Total sample size: 30,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

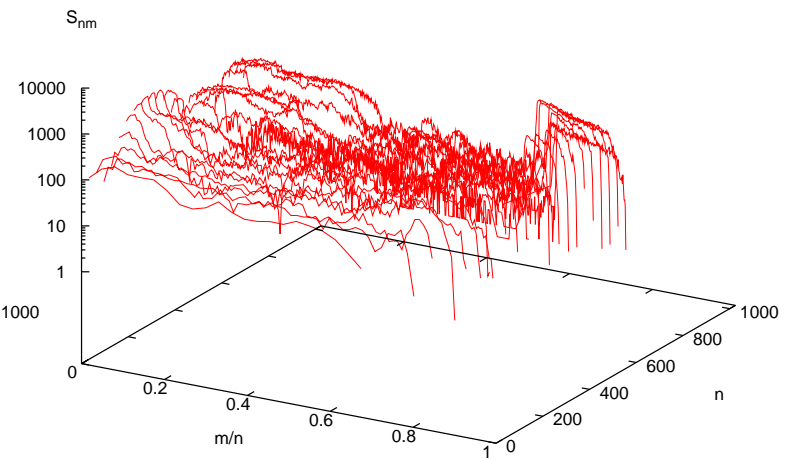
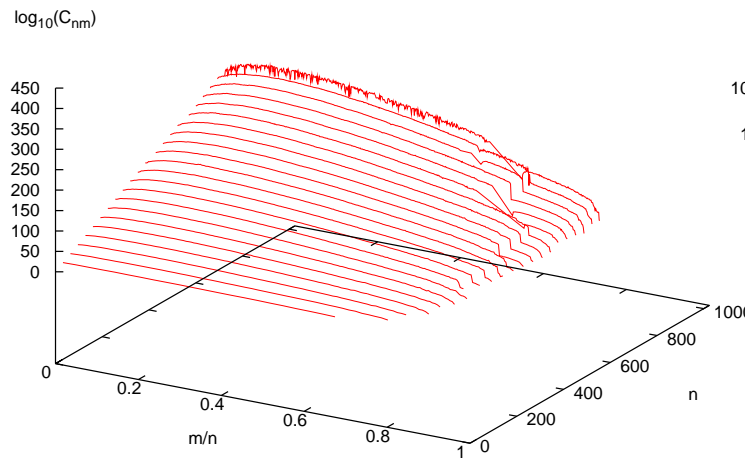
● Total sample size: 40,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

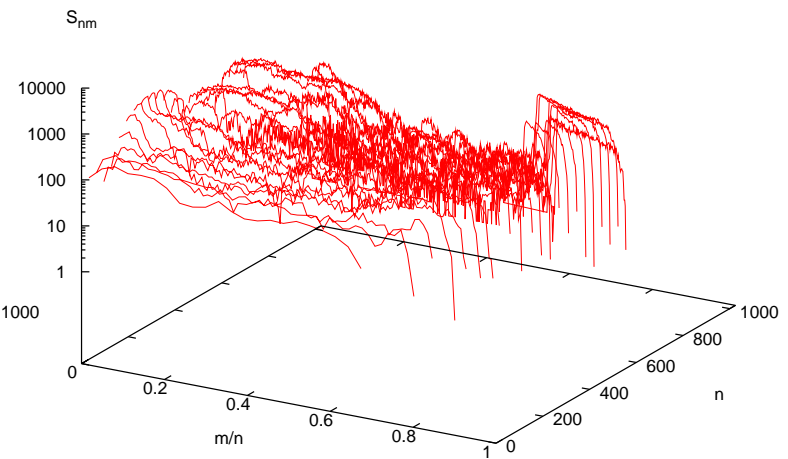
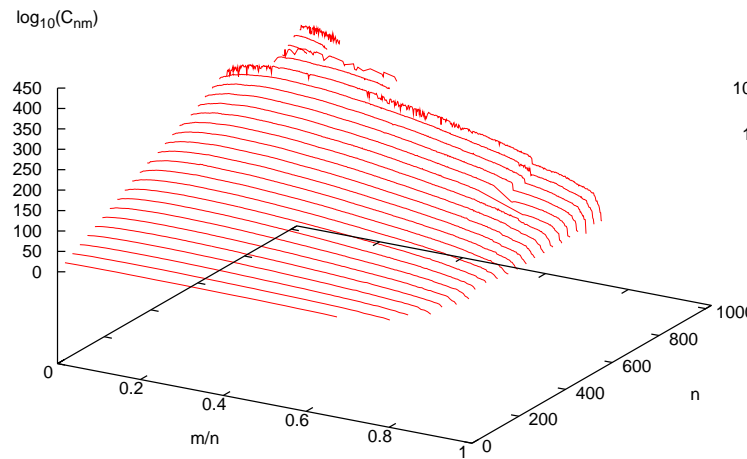
● Total sample size: 50,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

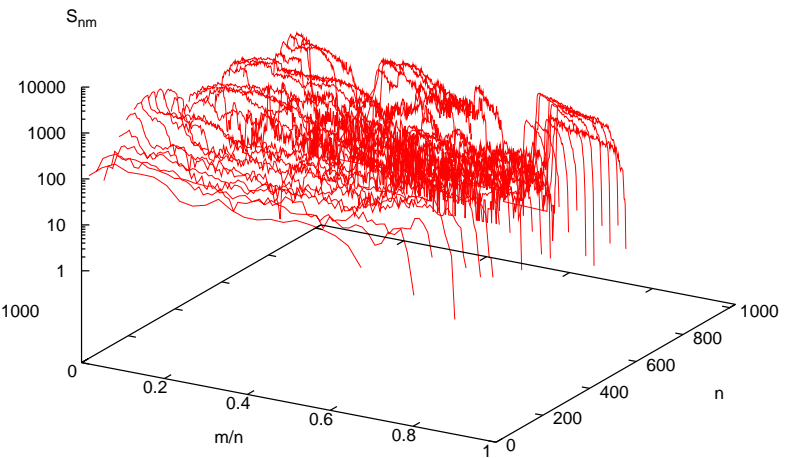
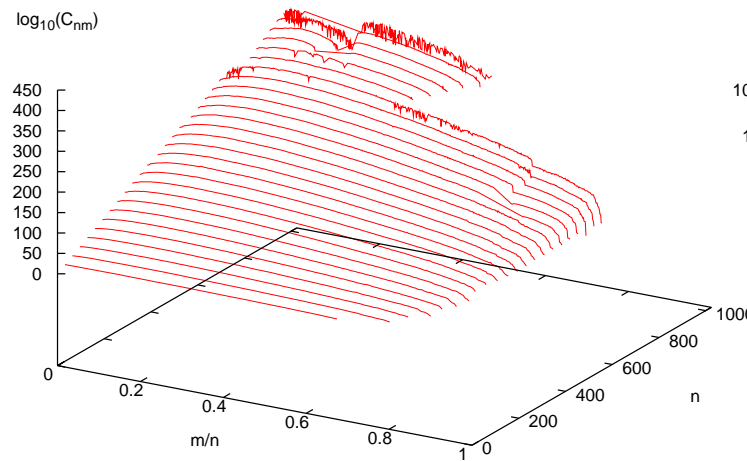
- Total sample size: 60,000,000



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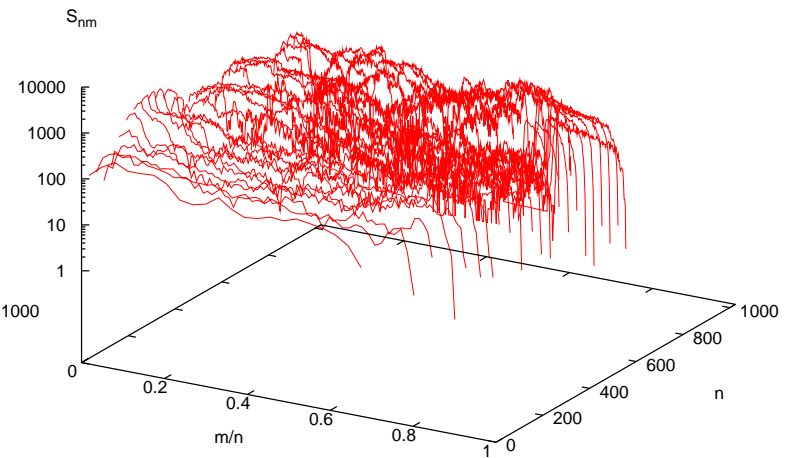
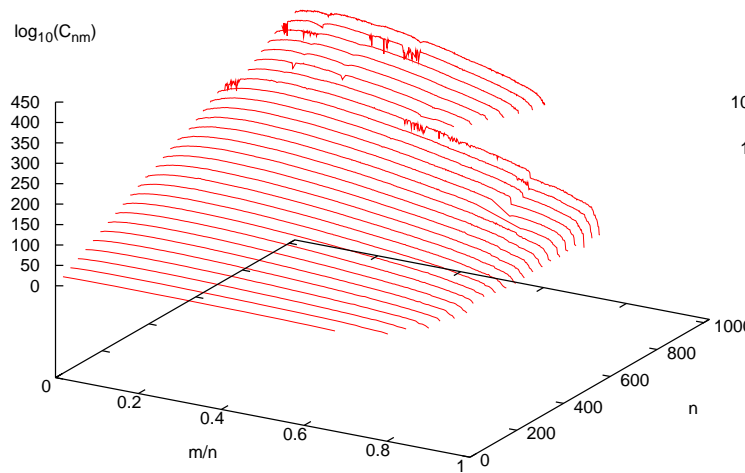
- Total sample size: 70,000,000



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2d ISAW simulation up to $n = 1024$

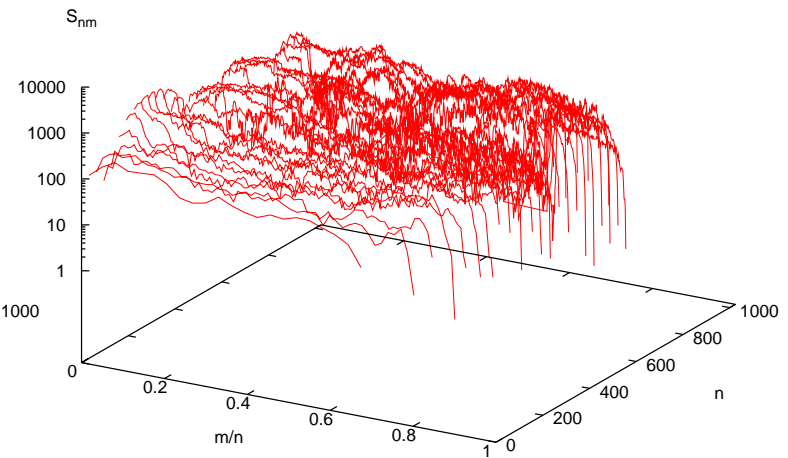
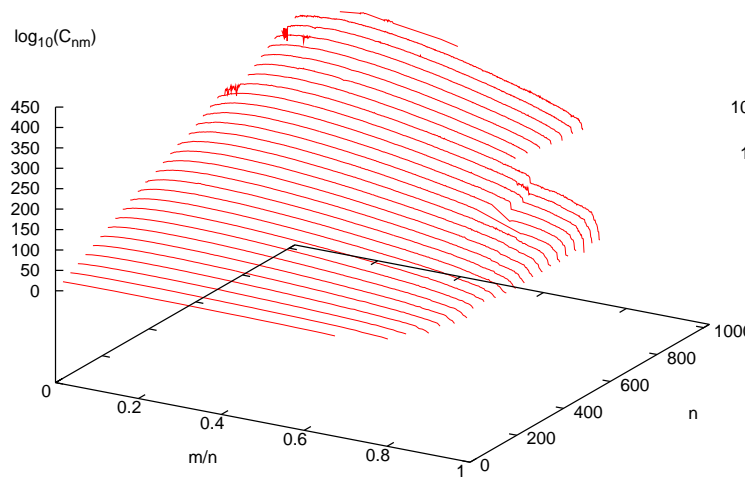
- Total sample size: 80,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

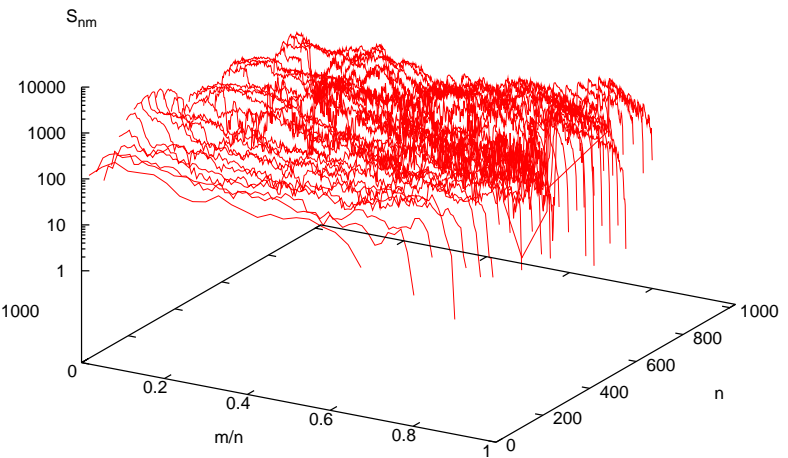
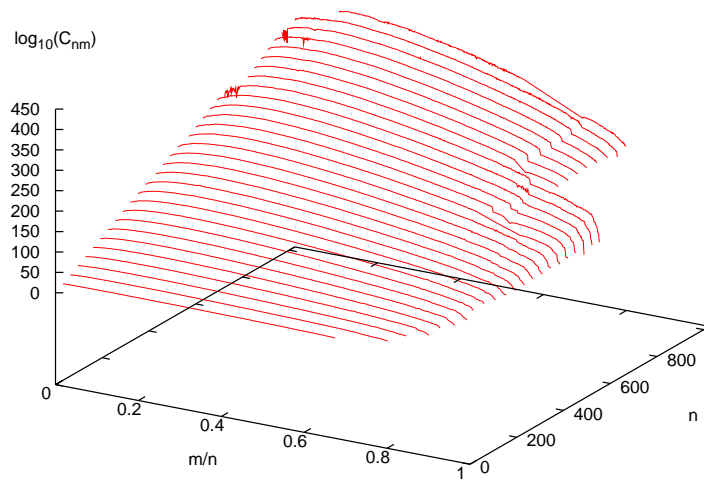
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Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

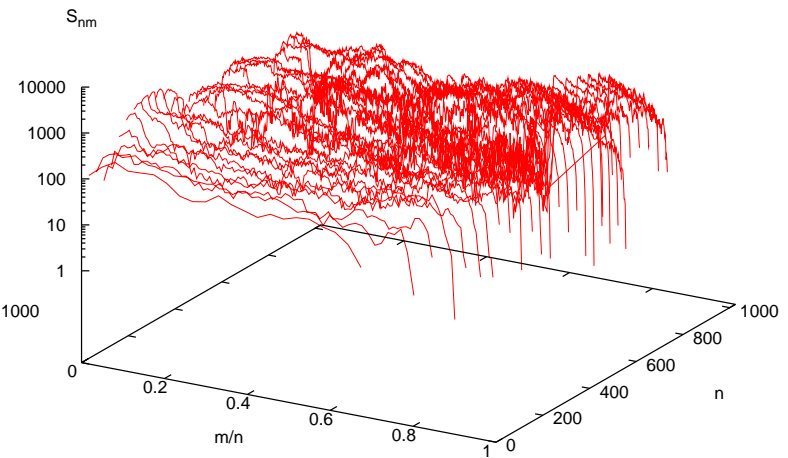
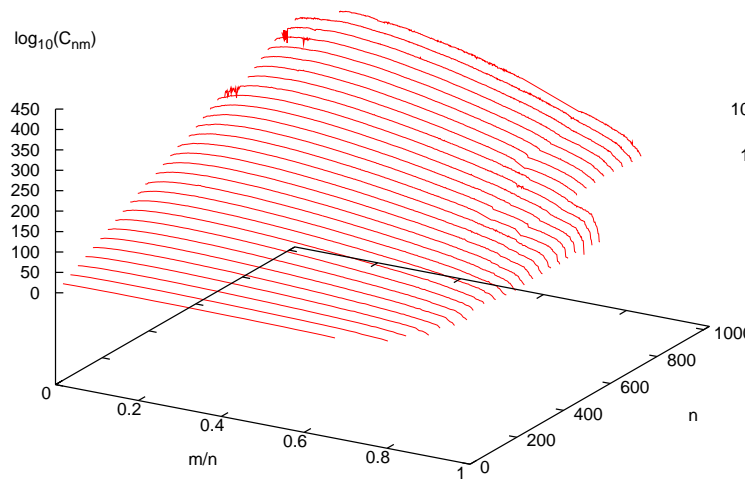
- Total sample size: 100,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

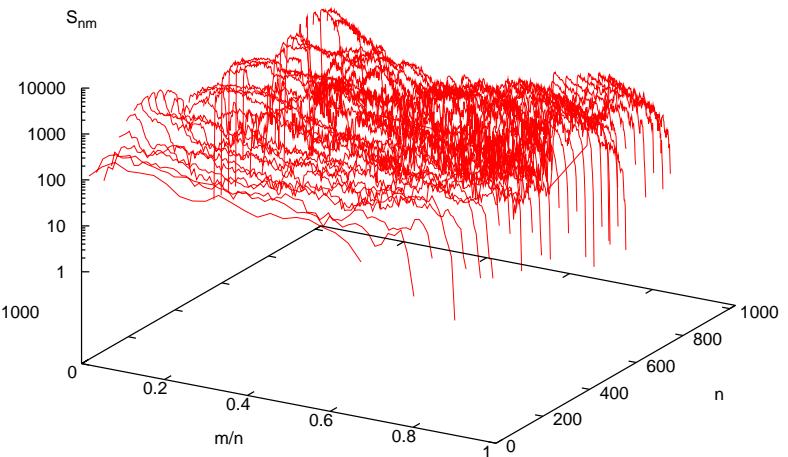
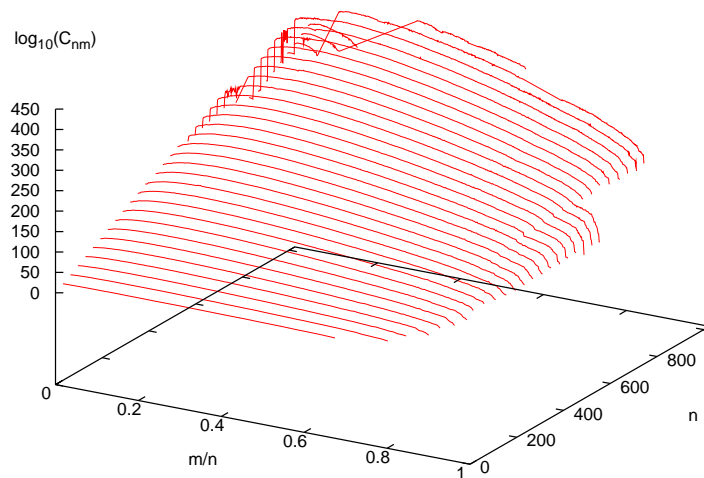
● Total sample size: 110,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

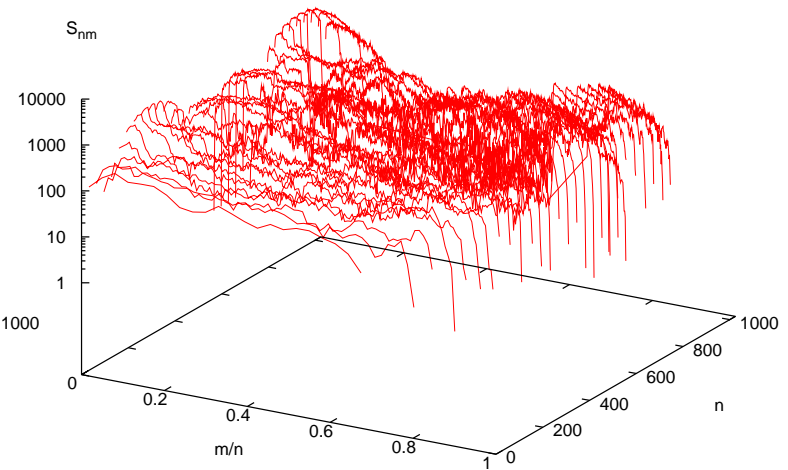
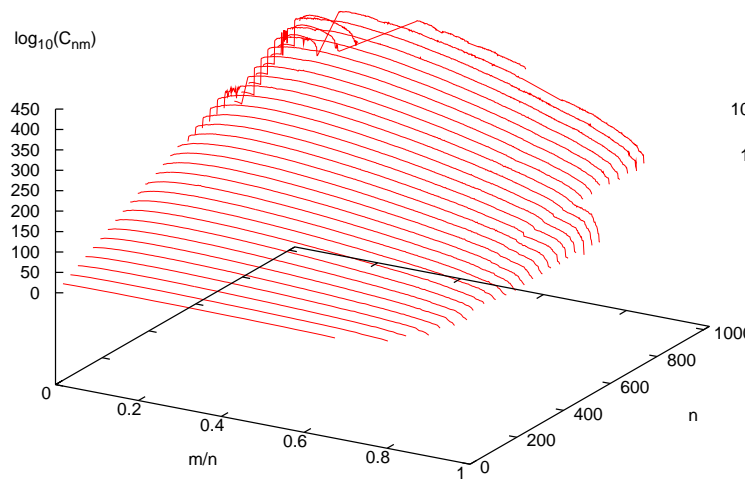
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Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

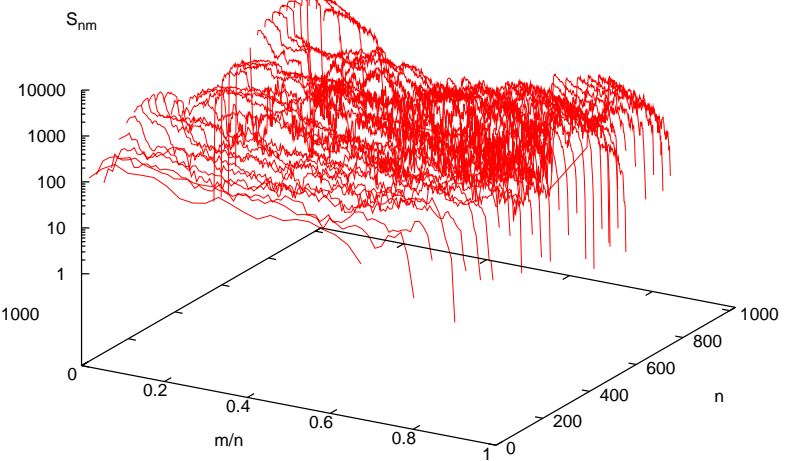
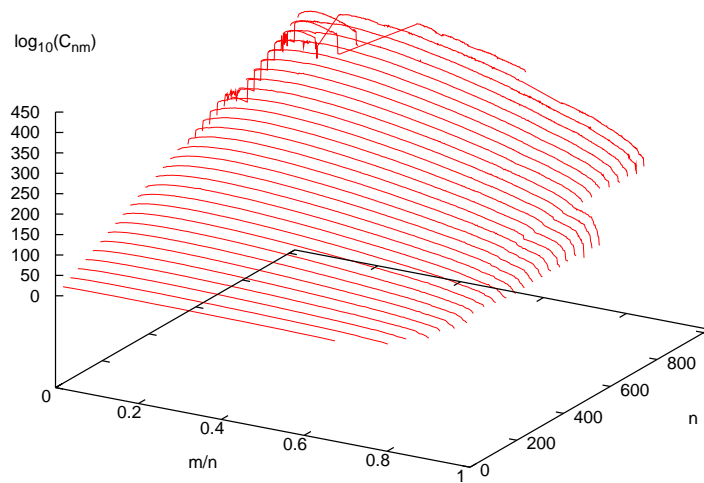
- Total sample size: 130,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

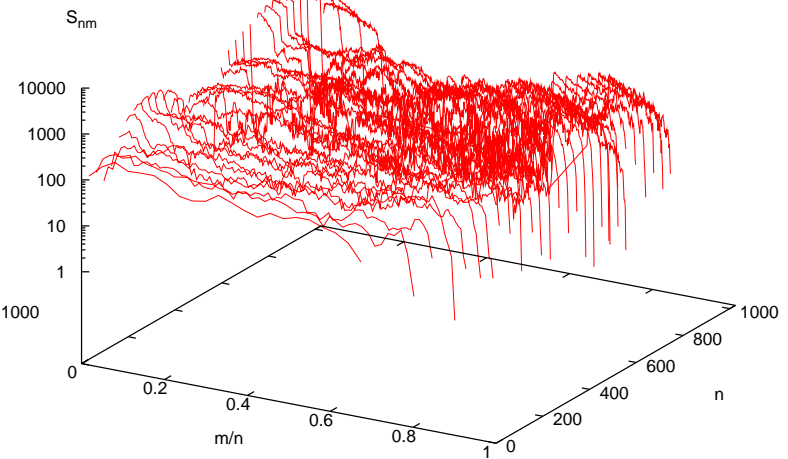
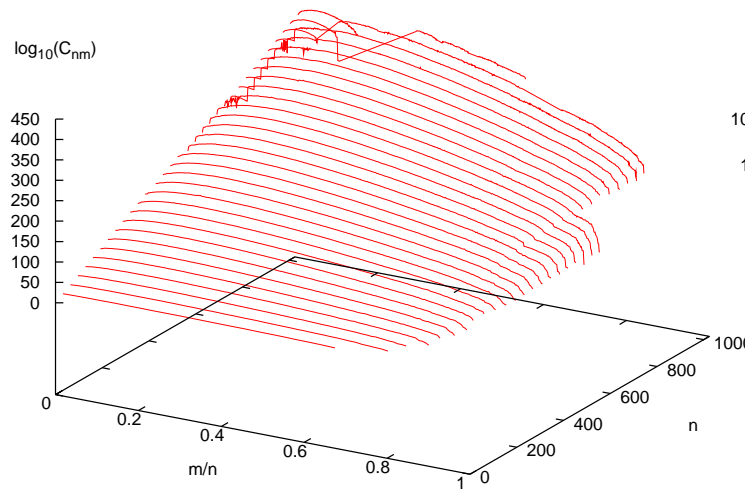
● Total sample size: 140,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

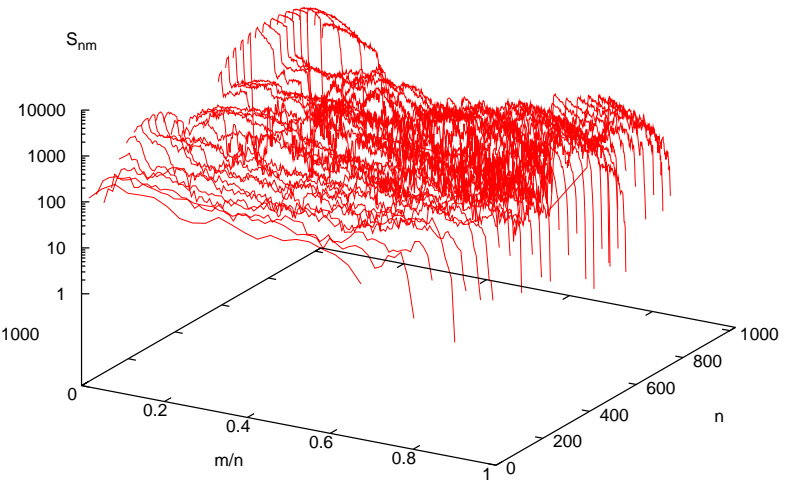
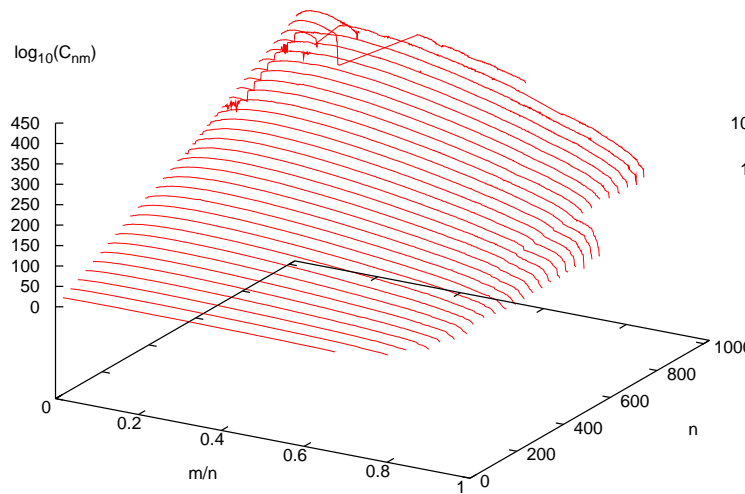
● Total sample size: 150,000,000



Simulation: Equilibration for 2d ISAW

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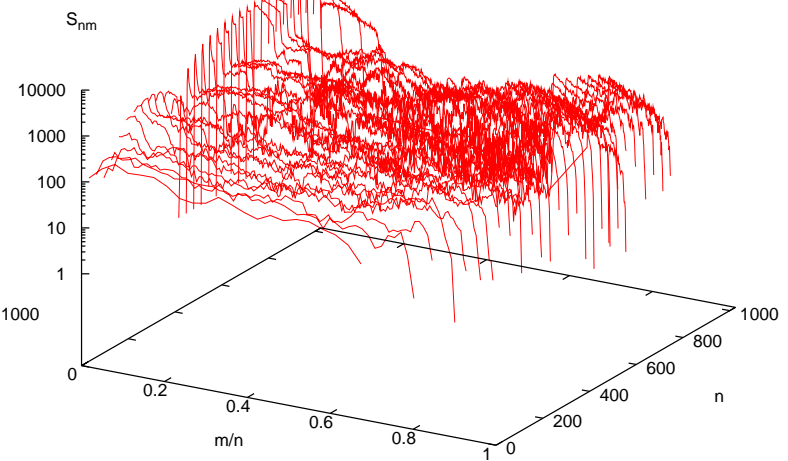
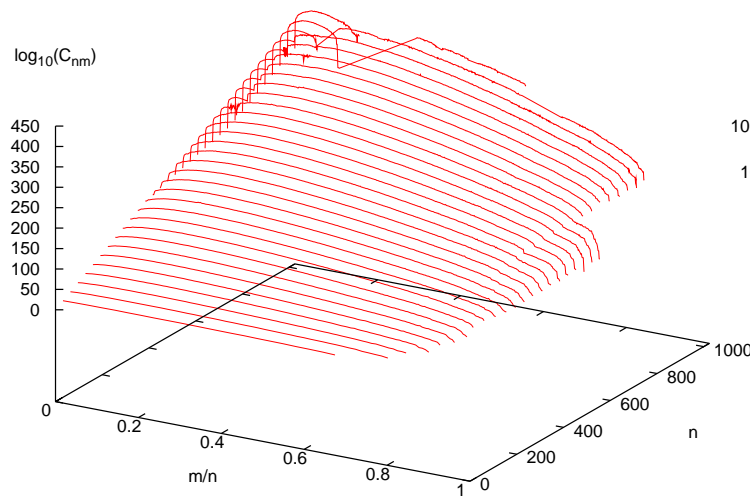
● Total sample size: 160,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

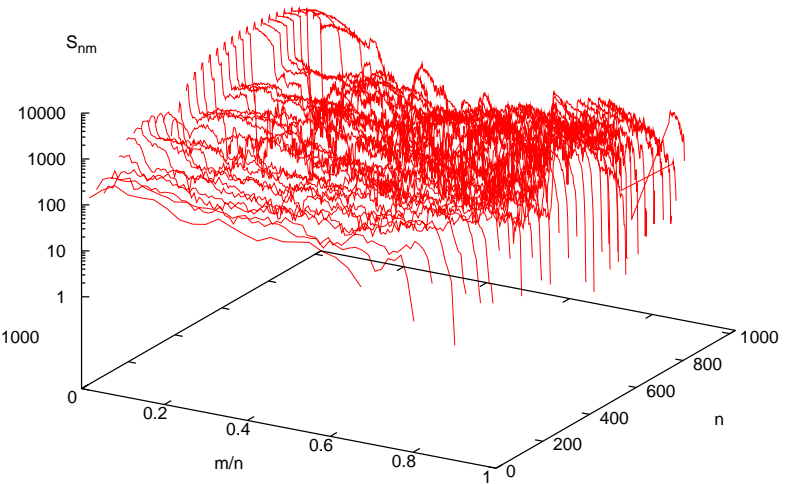
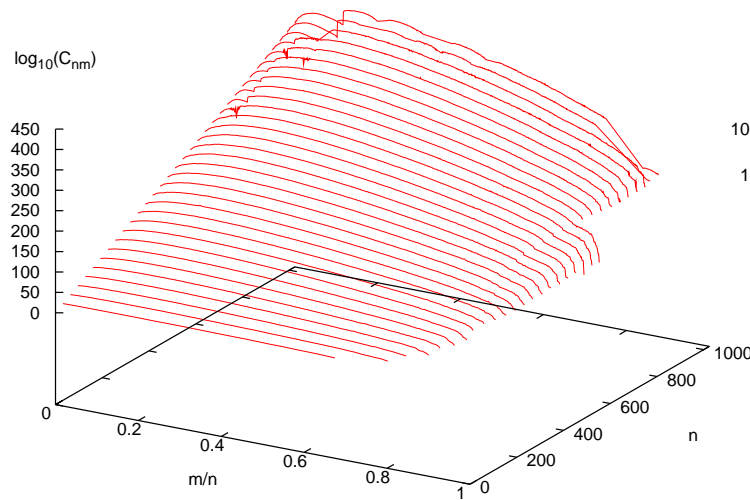
● Total sample size: 170,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

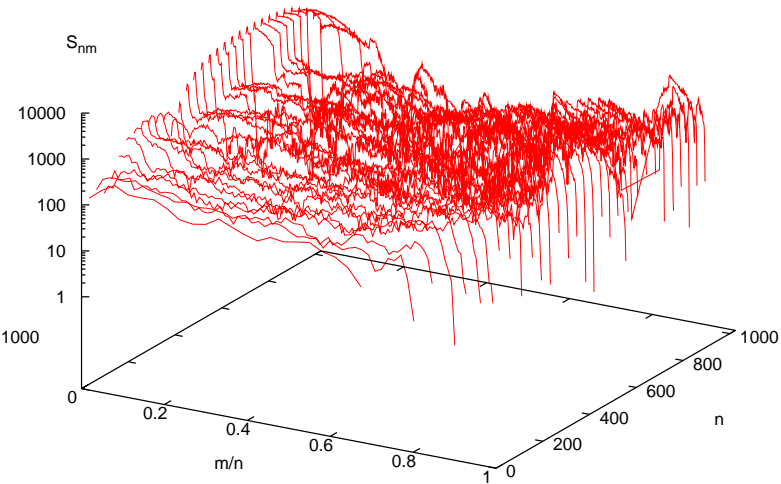
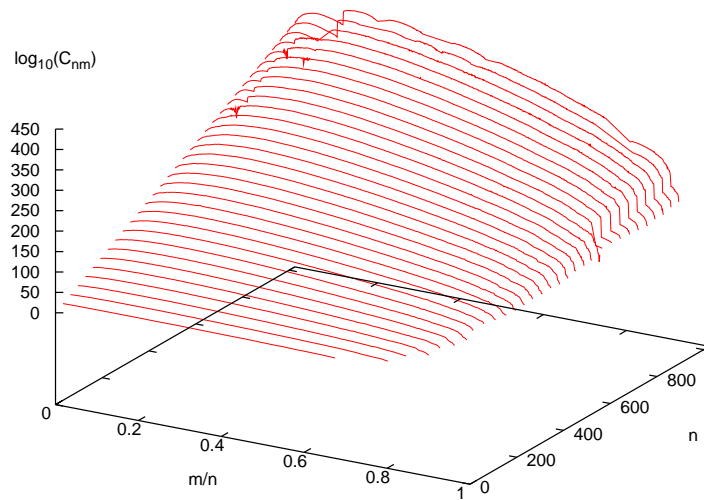
- Total sample size: 180,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

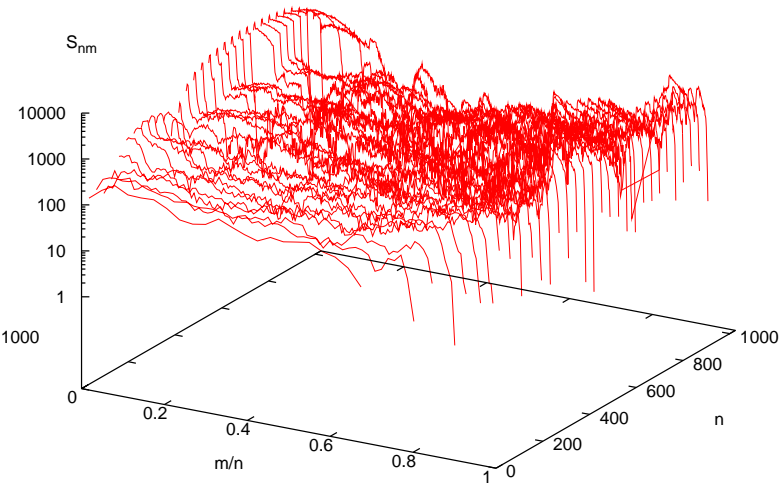
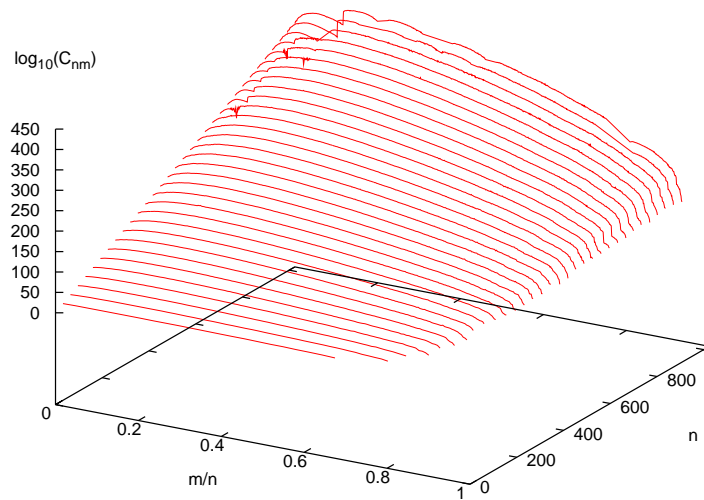
- Total sample size: 190,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

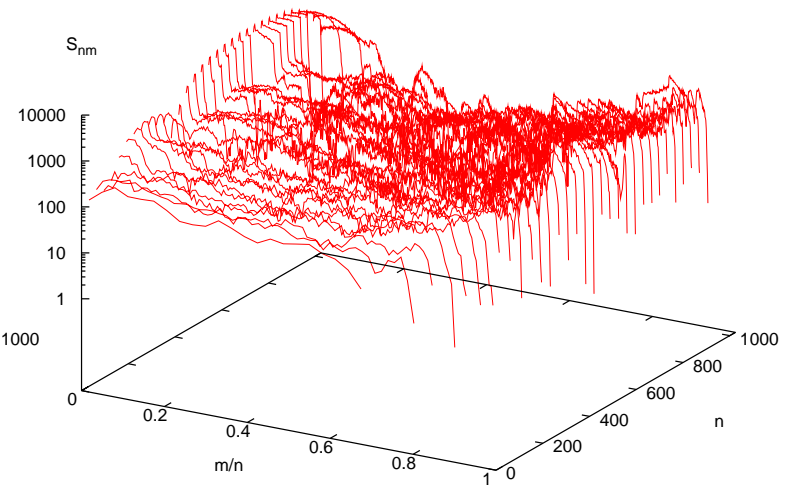
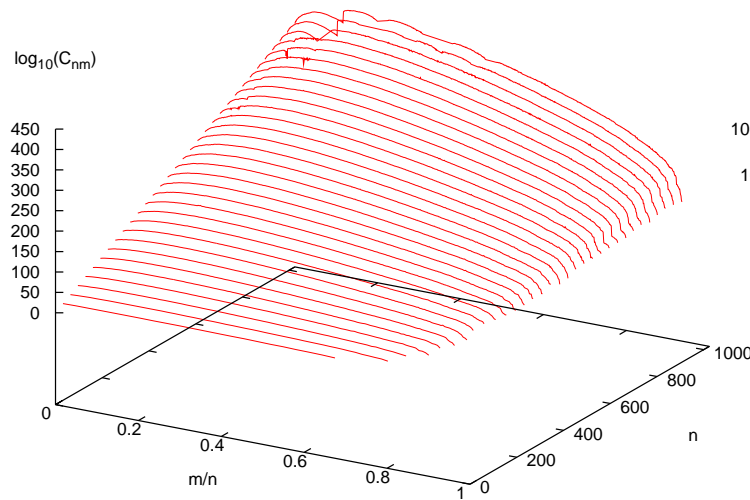
- Total sample size: 200,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

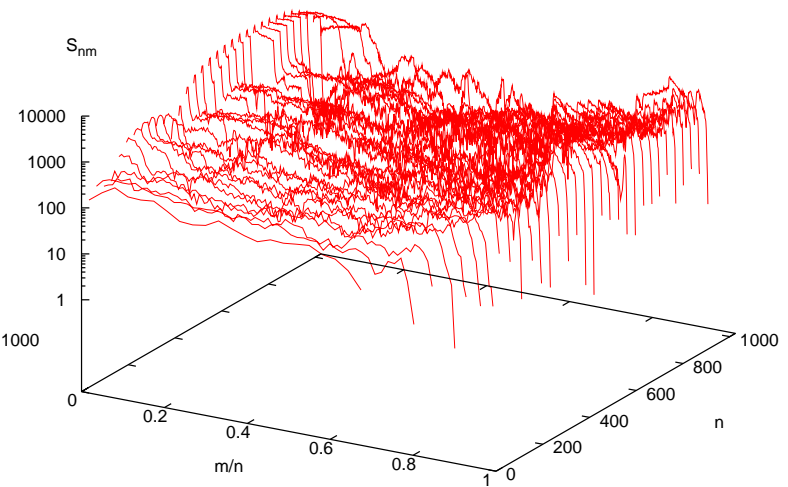
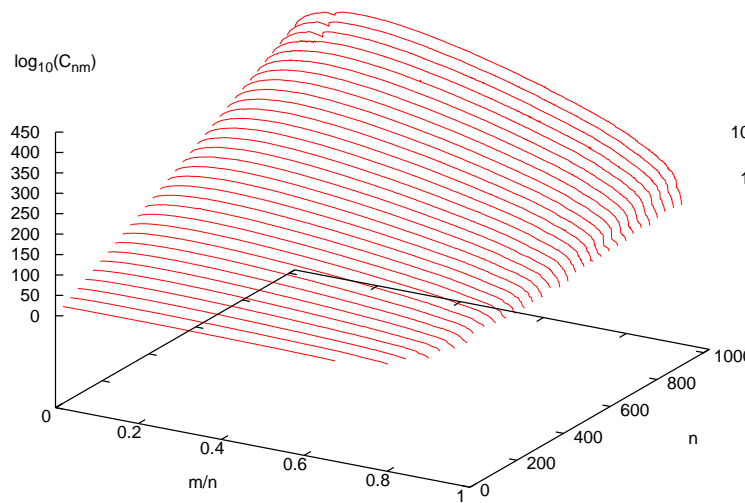
- Total sample size: 210,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

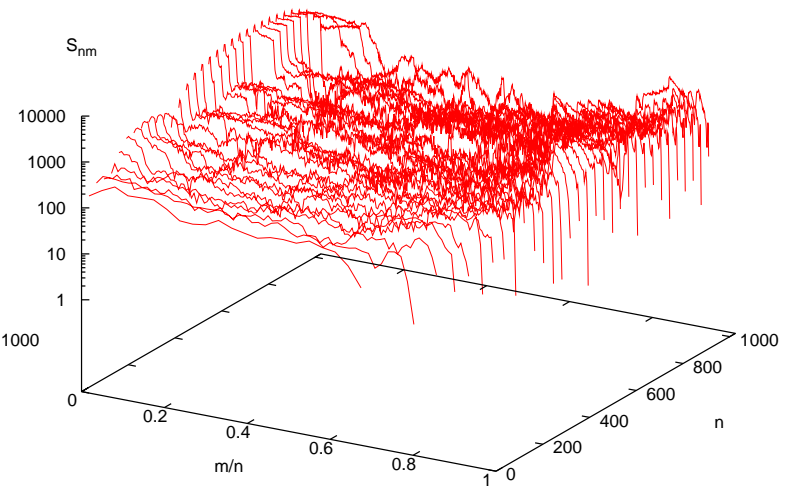
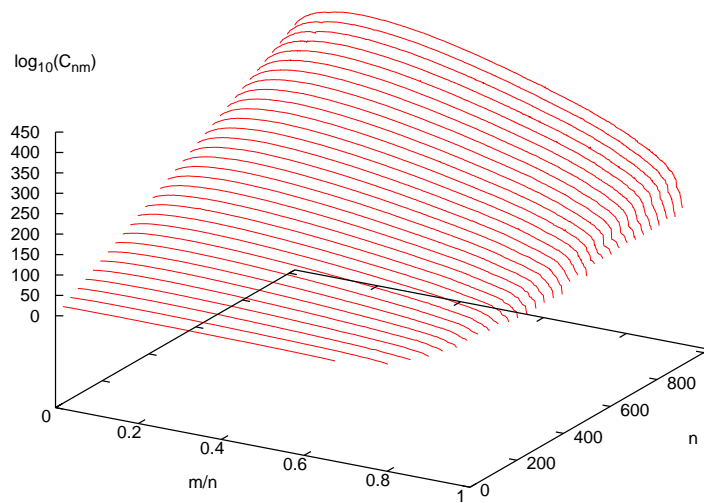
● Total sample size: 220,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

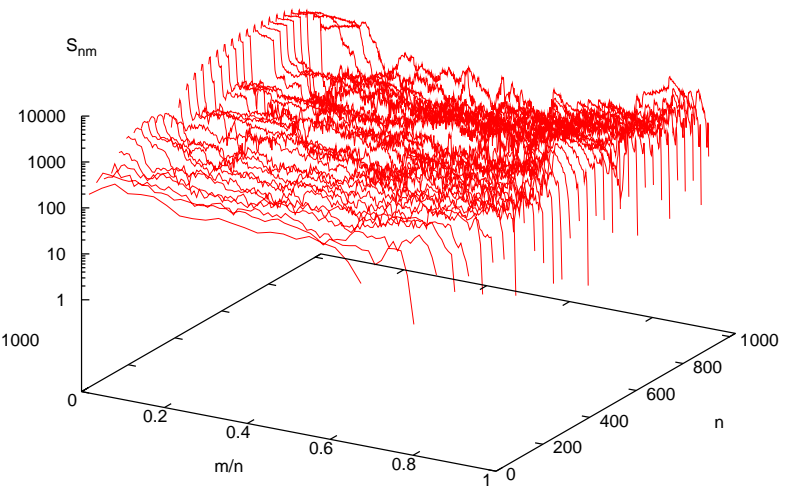
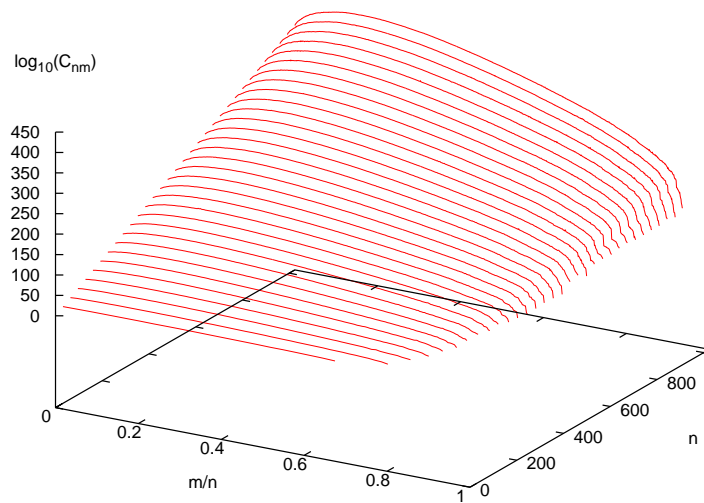
- Total sample size: 230,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

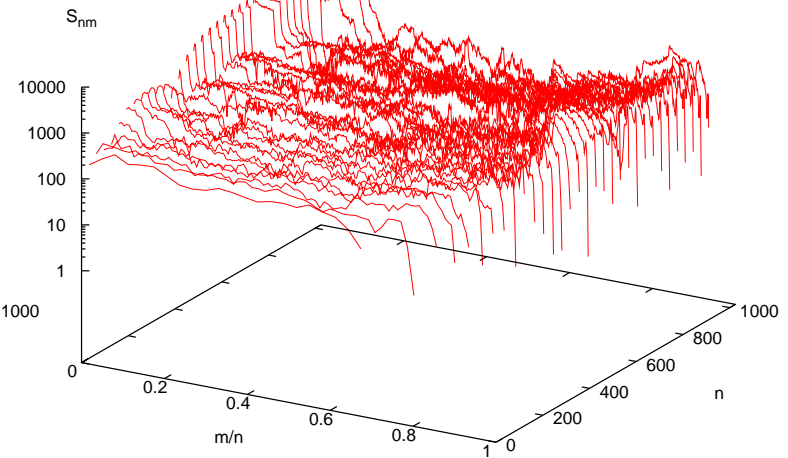
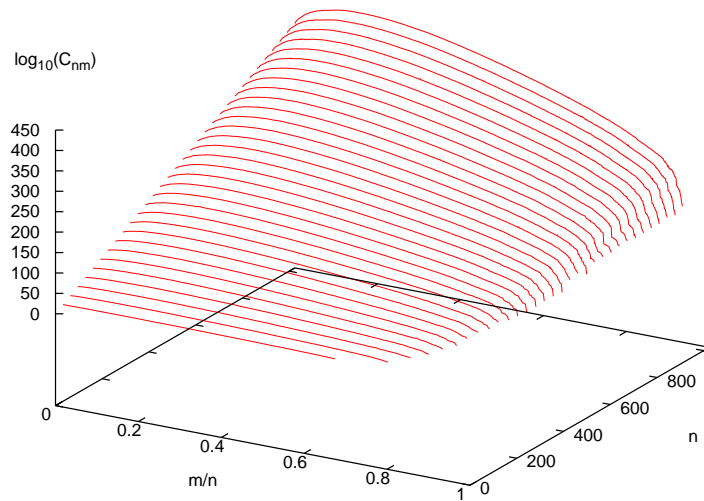
- Total sample size: 240,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

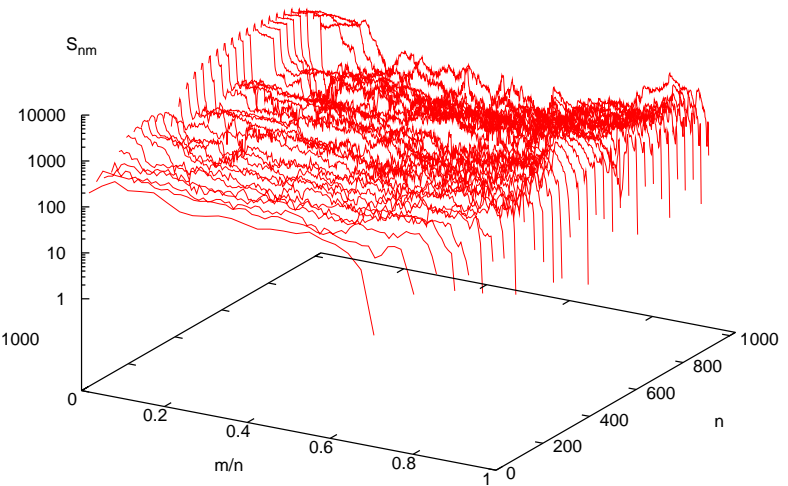
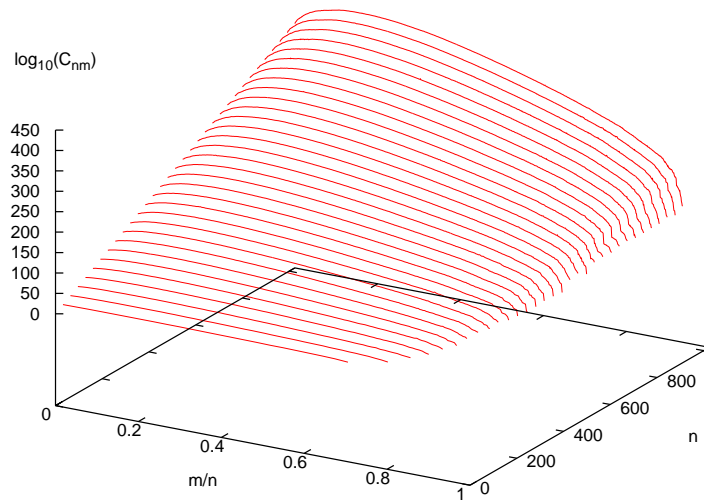
- Total sample size: 250,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

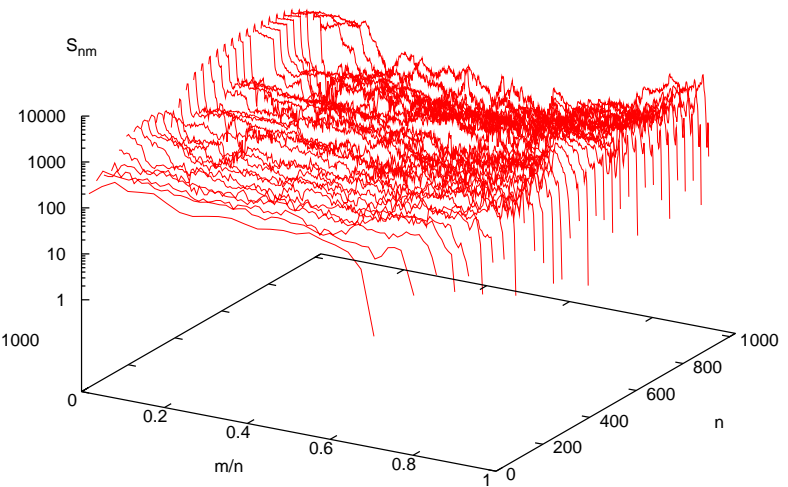
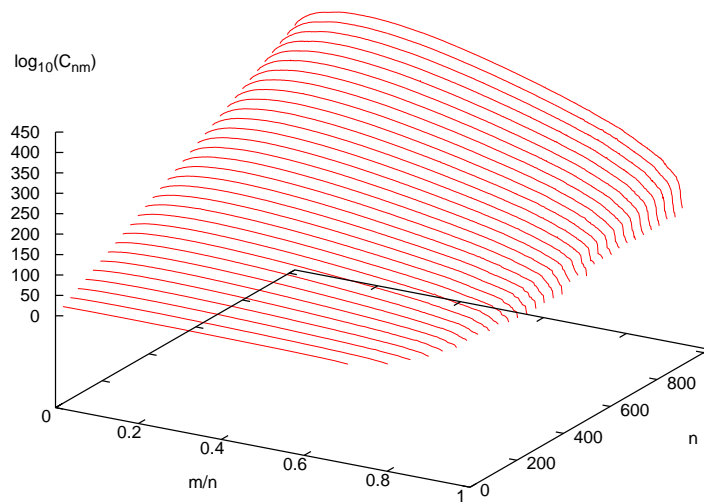
- Total sample size: 260,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

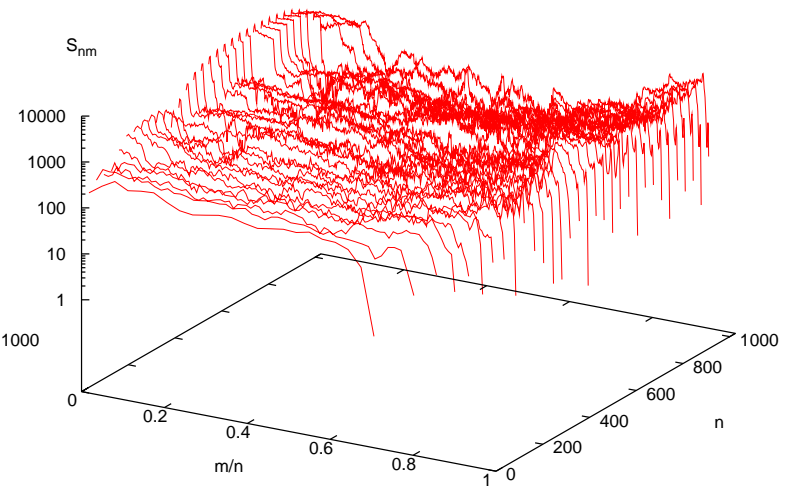
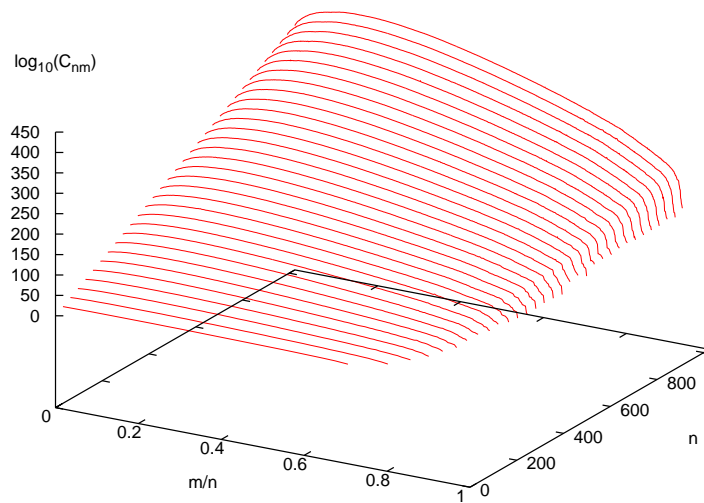
● Total sample size: 270,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

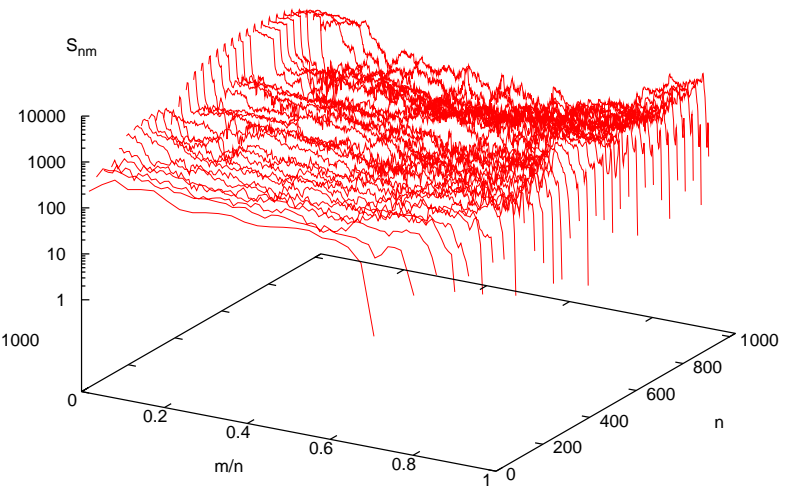
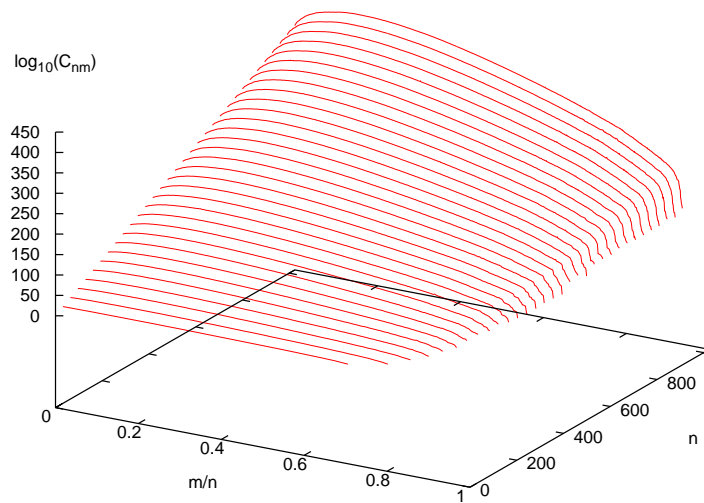
- Total sample size: 280,000,000



Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

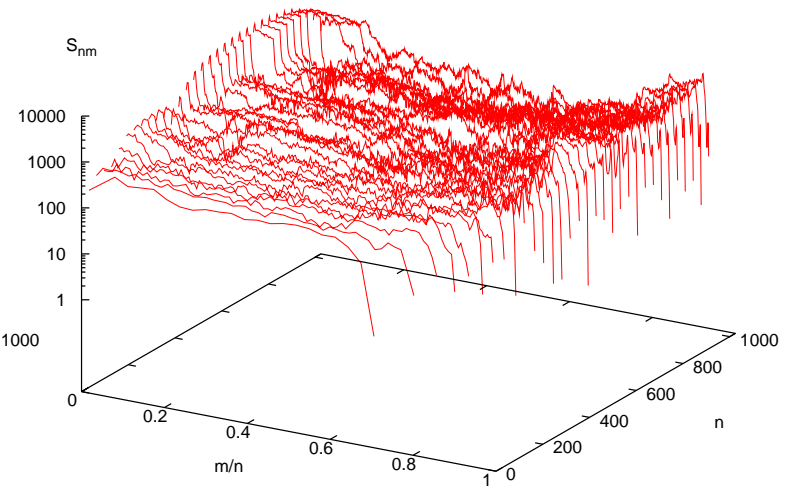
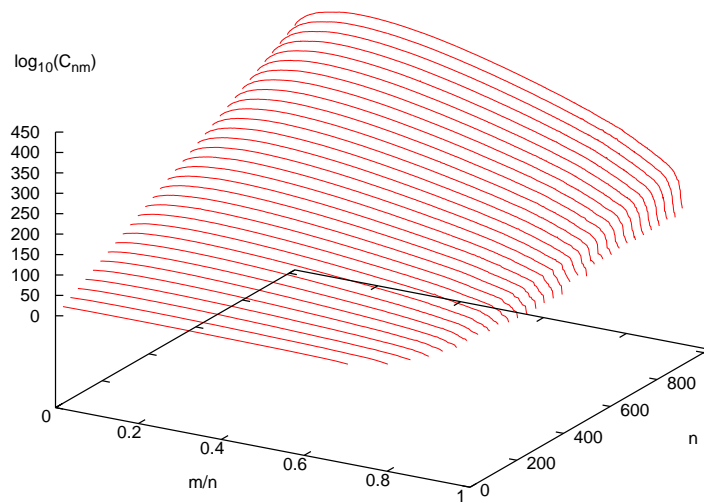
- Total sample size: 290,000,000



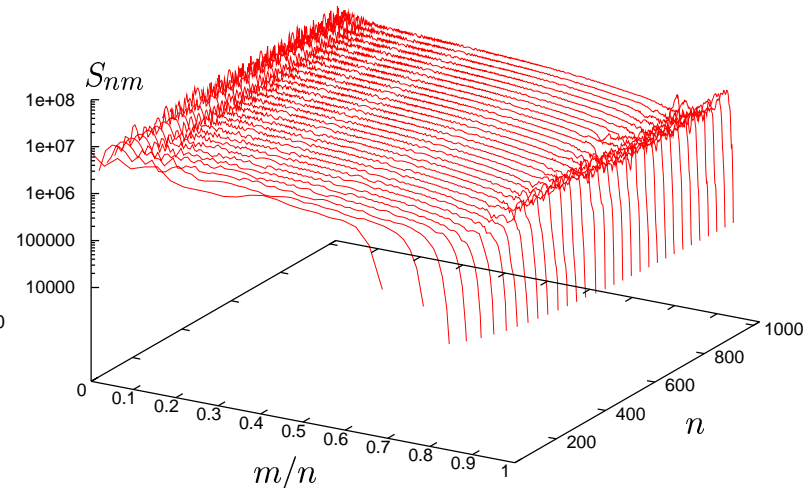
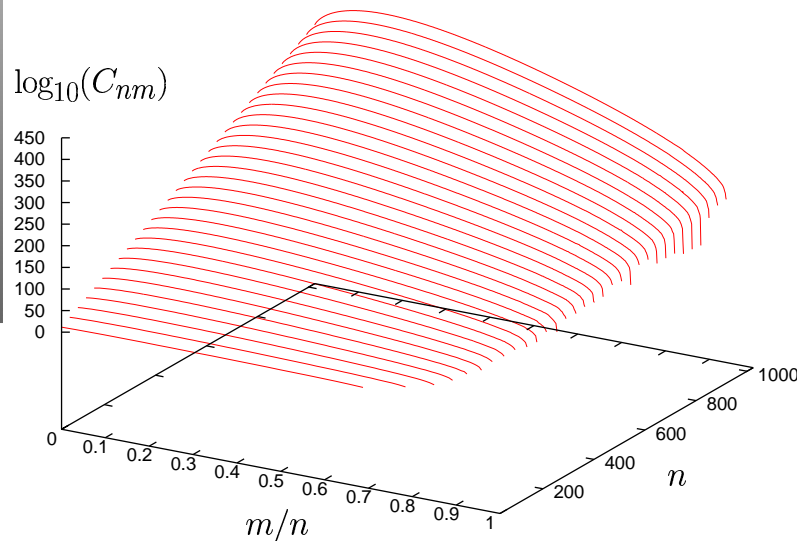
Simulation: Equilibration for 2d ISAW

2d ISAW simulation up to $n = 1024$

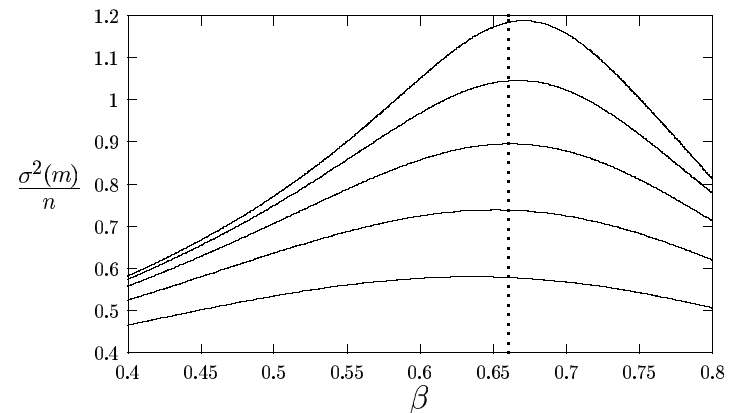
- Total sample size: 300,000,000



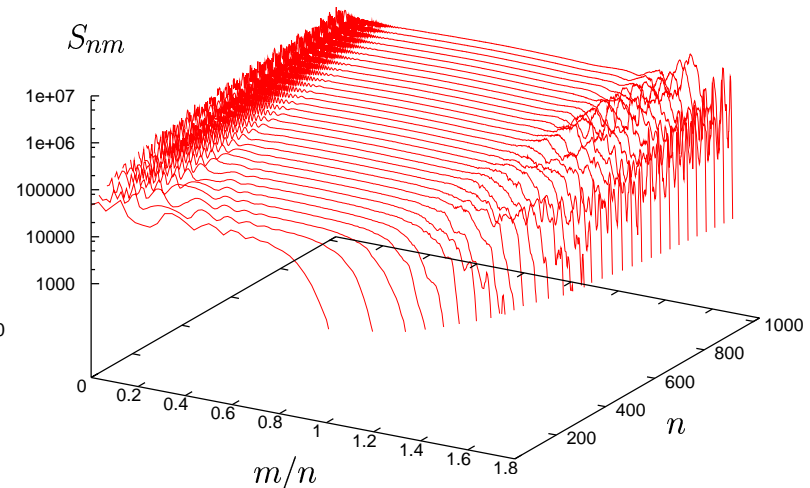
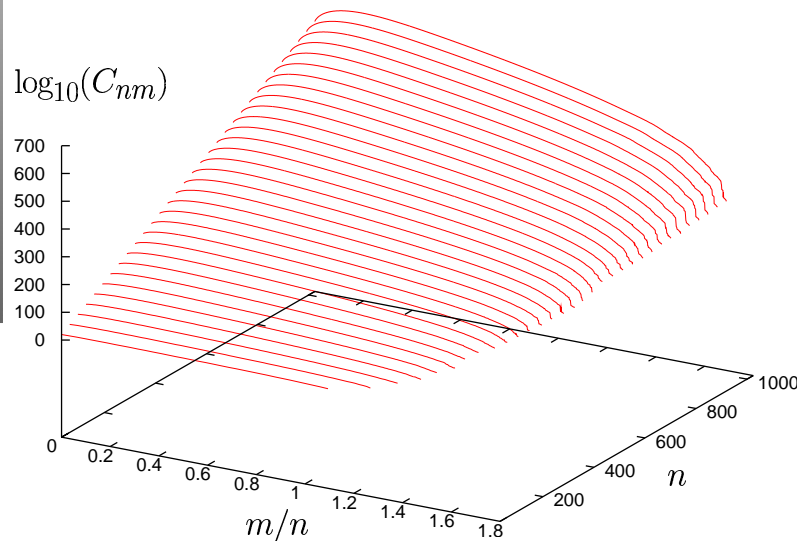
Simulation results: 2d ISAW



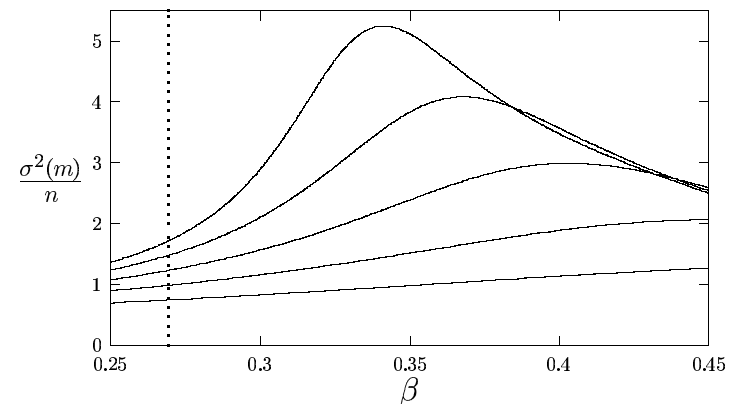
- 2d ISAW up to $n = 1024$
- One simulation suffices
- 300 orders of magnitude



Simulation results: 3d ISAW



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



Summary



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: HP model, ISAW

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: HP model, ISAW

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)
- Two-dimensional density of states with *one* simulation
 - Absorbing collapsing polymers: with A. Owczarek
 - Extended Domb-Joyce model: with J. Krawczyk



The End

