

Monte Carlo Simulations of the Hyaluronan-Aggrecan Complex in the Pericellular Matrix

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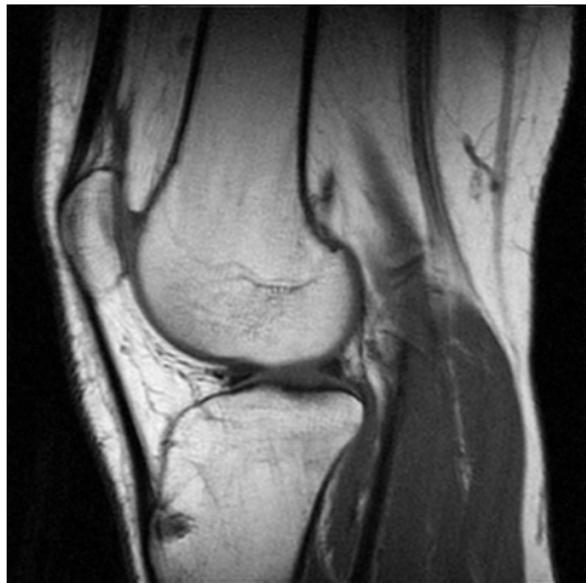
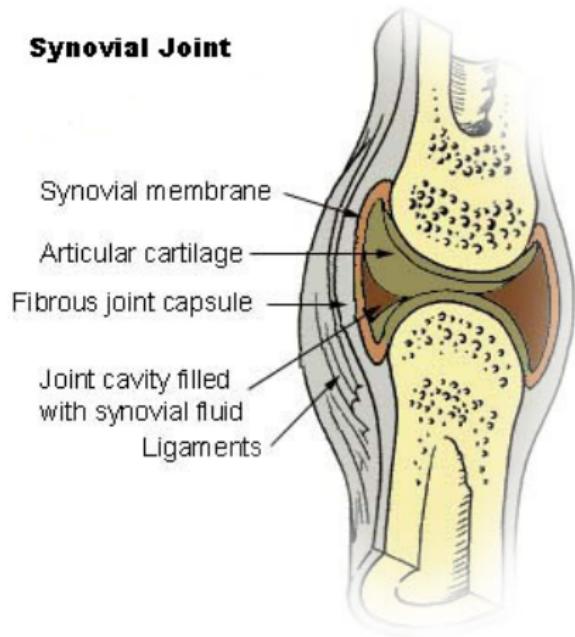
DELTA'07 Meeting, 11/15/2007

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 - Modelling and Simulations
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The Human Knee Joint

Synovial Joint



www.wikipedia.org

Articular Cartilage

macroscopic observations:

- articular cartilage forms *menisci* in synovial joints
- highly elastic cushion
- serves as a rampart against pressure (e.g. during movements)
- damage results in disease (e.g. osteoarthritis)

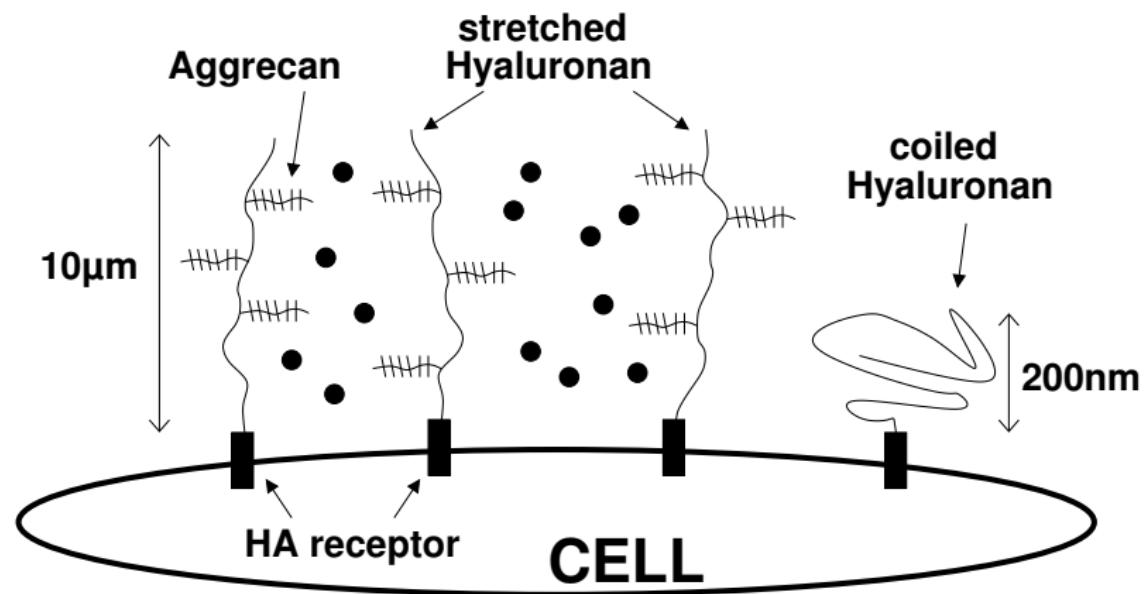
microscopic nature:

- highly entangled polymer network
- origin of synthesis: **pericellular matrix** around specialized cells
(fibroblasts)

How do the macroscopic properties emerge from the microscopic structure?

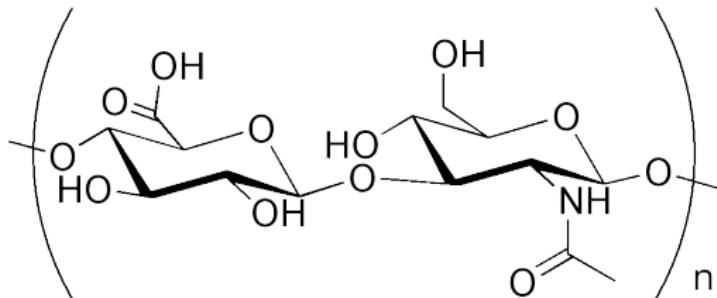
The Pericellular Matrix - A Simple Model

A simplified model of the pericellular matrix (PCM) around a fibroblast¹



¹Lee et al. 1993

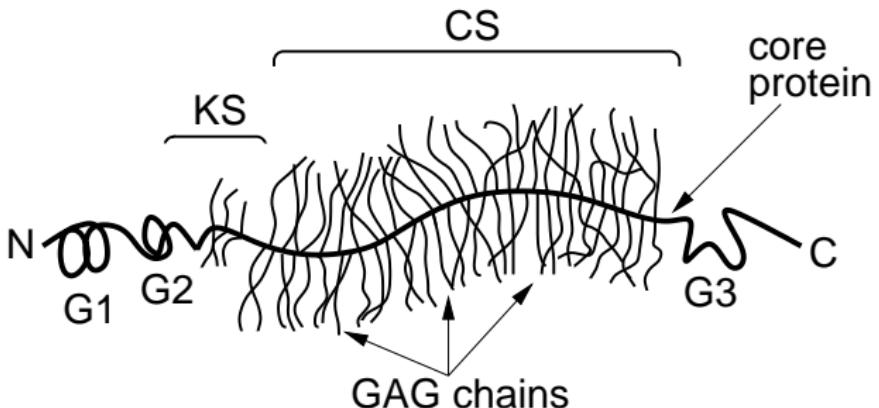
Hyaluronan (hyaluronic acid, HA)



- chain of sugars, total molecular weight: $\sim 10^6$ u
- contour length: $\sim 10\mu\text{m}$; persistence length: $\sim 8\text{ nm}$
- can be tethered to the membran by HA receptor protein

⇒ **HA is a long, flexible polymer chain**

Aggrecan ('large aggregating proteoglycan')



- ~ 300 ku core protein with ~ 100 side chains attached
- contour length: ~ 400 nm; persistence length: ~ 110 nm
- core protein can bind to HA via linker protein

⇒ **Aggrecan is a rather rigid 'polymer comb'**

Model Characteristics

- backbone (HA) fully flexible with length N ; end-grafted on flat substrate (cell)
- side chain (Aggrecan) fully rigid with length S
- branching site b

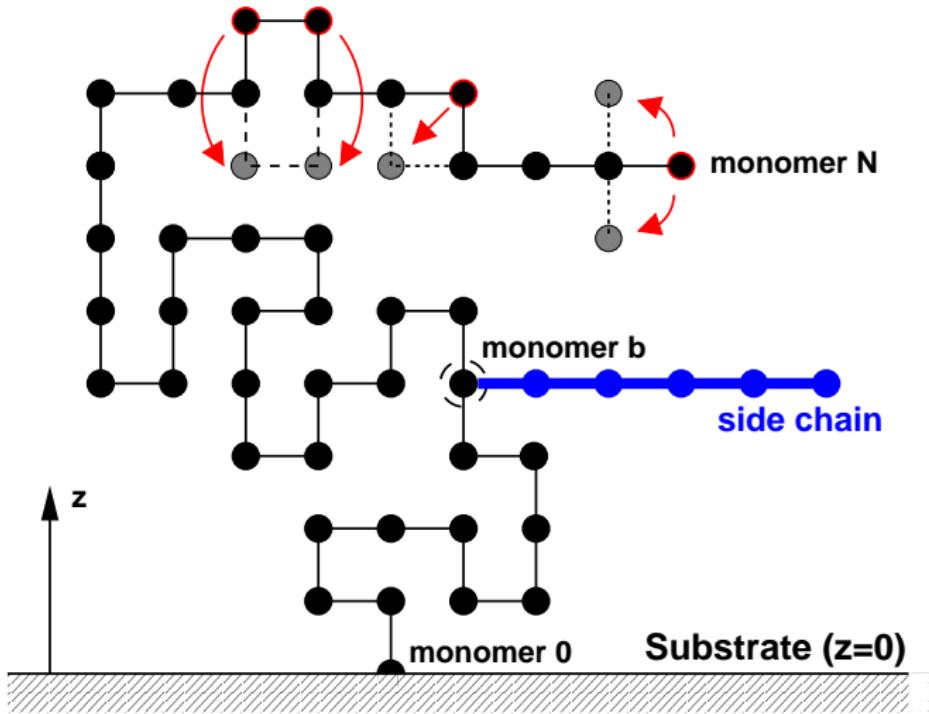
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- simple **cubic lattice**, prohibit multiple occupations of one lattice site
⇒ **self-avoidance**
- **good athermal solvent** ⇔ no interactions between monomers besides self-avoidance; no adsorbtion

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- **Dynamical Monte Carlo** to generate independent configuartions:
Verdier-Stockmayer-type algorithm and random rotations of side chain

Simulation Model, 2D-sketch



Shape of a Polymer

polymer shape described by gyration tensor²:

$$S_{mn} = \frac{1}{N} \sum_{i=1}^N r_m^{(i)} r_n^{(i)}$$

- diagonalisation yields principle axes of gyration, $\mathbf{v}_1, \mathbf{v}_2, \mathbf{v}_3$ defining the triaxial gyration ellipsoid

²Šolc & Stockmayer 1971

³Bruns 1992

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- ratios between the lengths of these axes ($L_1 \leq L_2 \leq L_3$) quantify the asphericity
- MC simulations reveal³

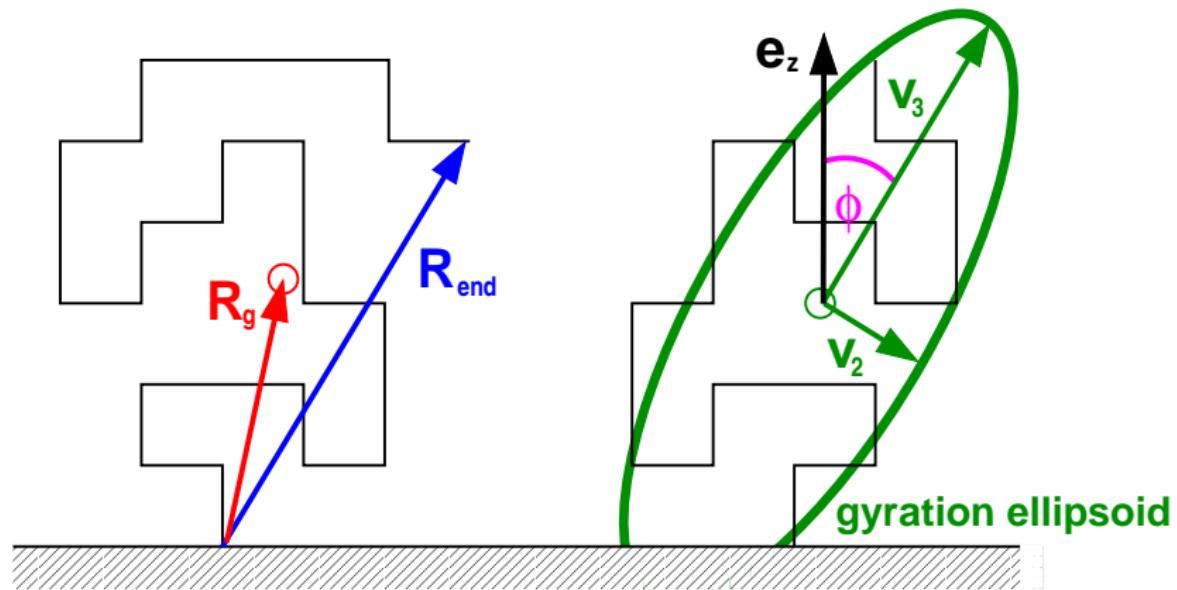
$$\begin{array}{lll} \text{RW: } & \langle L_1^2 \rangle : \langle L_2^2 \rangle : \langle L_3^2 \rangle & \xrightarrow{N \rightarrow \infty} 1 : 2.7 : 12 \\ \text{SAW: } & \langle L_1^2 \rangle : \langle L_2^2 \rangle : \langle L_3^2 \rangle & \xrightarrow{N \rightarrow \infty} 1 : 3.0 : 14 \end{array}$$

²Šolc & Stockmayer 1971

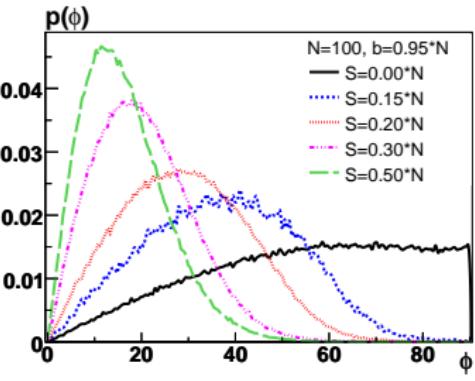
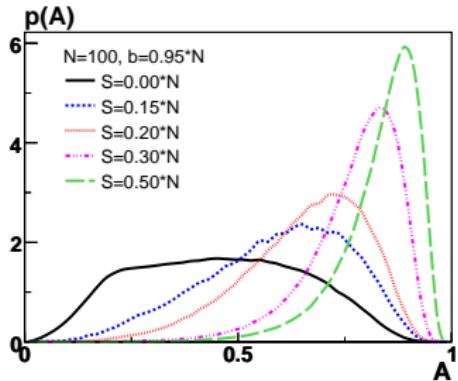
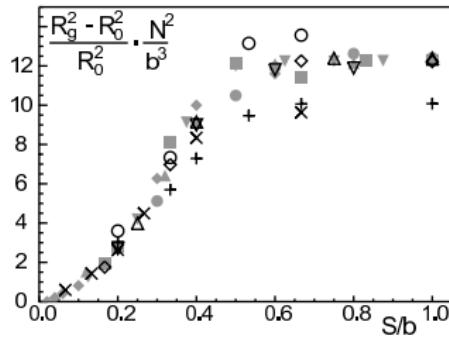
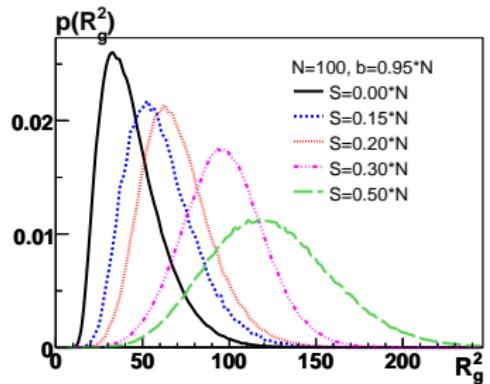
³Bruns 1992

Read Outs

only backbone monomers are used for calculations!



Simulation Results



Summary: Isolated HA-aggregcan Complex

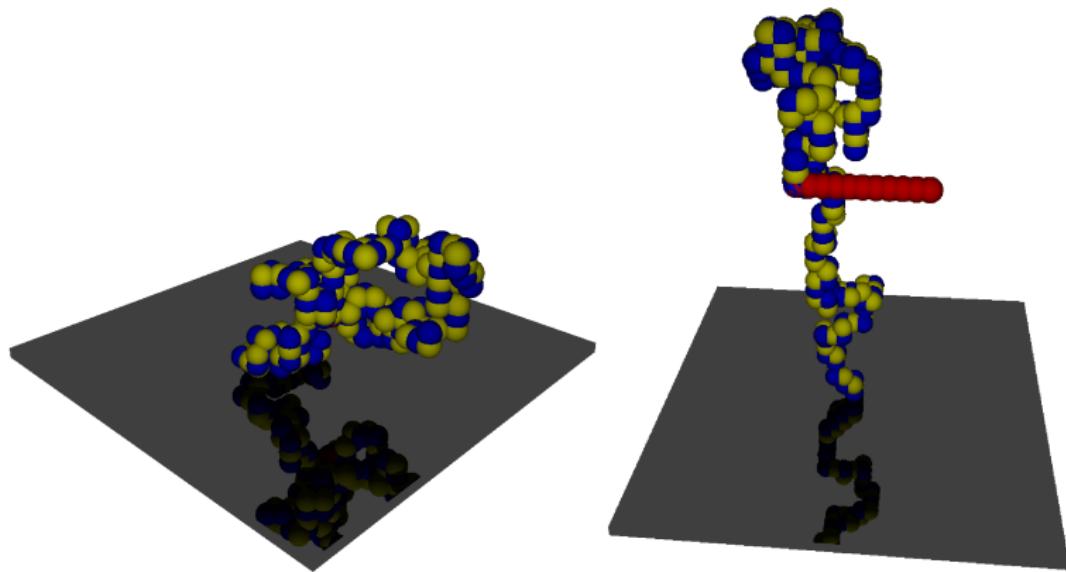
Conformational changes due to rigid side chain:

- ① $R_g, R_{end} \Rightarrow$ increase in size
 - ② asphericity \Rightarrow pronounced rod-like shape
 - ③ angle $\phi \Rightarrow$ backbone orientates towards z -axis
 - ④ increased persistency below side chain
 - ⑤ additional side chains \Rightarrow straightening largely caused by uppermost side chain
-
- all changes depend on b and S
 - strongest effect for $b \approx N, S \geq 0.5 \cdot N$

M. H., M. Weiss, and D. W. Heermann, *Phys. Rev. E* **76**, 021802

Isolated HA-aggregcan Complex: 3D-Representation

Conformational changes due to rigid side chain:



Towards Dense Systems

observed straightening not sufficient to explain full extension of PCM

next: account for interactions between neighbouring complexes

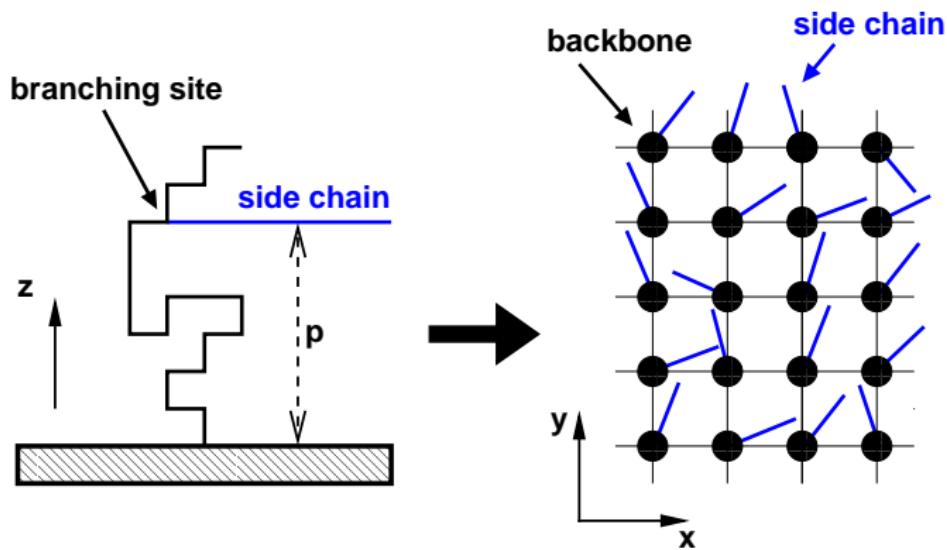
tasks/problems:

- simulations with single chain resolution are much too expensive!
- new model necessary: only account for 'most important' degrees of freedom

⇒ *physically interesting side project*

New Model

idea: polymer with side chain → rotating rods



New Model

- account for height p above the substrate: only side chains on the same level may interact → **Potts model**

$$\mathcal{H}_{Potts} = -J_P \sum_{\langle i,j \rangle} \delta_{p_i p_j} \quad \text{with } p_i \in \{0, 1, \dots, q-1\}$$

- particular interaction between side chains unknown

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- particular interaction between side chains unknown
- consider NN-ferromagnetic interaction (prefers parallel alignment)
→ **planar rotator model (XY-model)**

$$\mathcal{H}_{XY} = -J_{XY} \sum_{\langle i,j \rangle} \mathbf{S}_i \cdot \mathbf{S}_j = -J \sum_{\langle i,j \rangle} S_i S_j \cos \theta_{i,j}$$

New Model

⇒ hybrid model:

$$\mathcal{H}_{\text{Hybrid}} = -J_H \sum_{\langle i,j \rangle} \delta_{p_i p_j} \cdot S_i S_j \cos \theta_{i,j} \quad \text{with } p_i \in \{0, 1, \dots, q-1\}$$

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- parameters:

- rotator length S_i fix: $S_i = 1$,
- number of Potts levels q fix: $q = 3$,
- system size $N = L \times L$ vary,
- interaction strength J_H (\Leftrightarrow temperature T) vary.

New Model

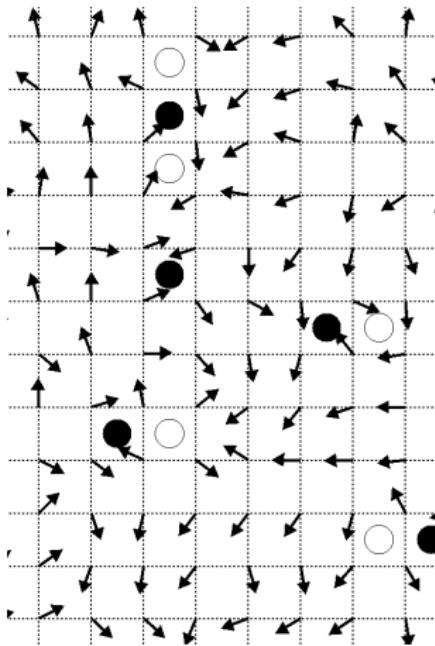
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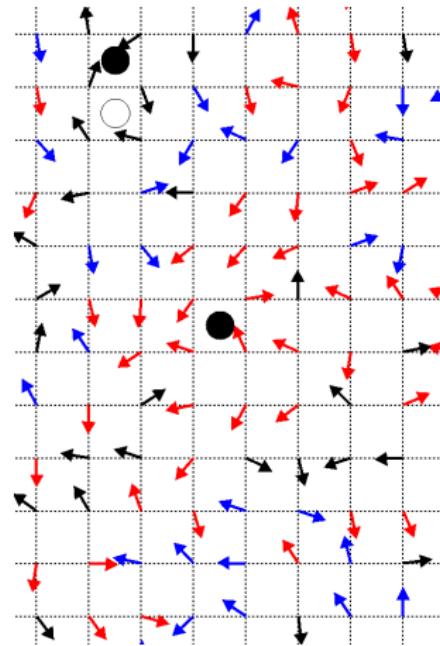
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 - interaction strength J_H (\Leftrightarrow temperature T) vary.
- behaviour in dependence on temperature and system size?
 - ① XY model, NN-ferromagnetic → KT-transition
 - ② 2D q -state Potts model: $q \leq 4 \rightarrow$ 2nd order
 - ③ hybrid: KT, 1st or 2nd order?

Vorticity: XY model and hybrid model

a) $q = 1$ (XY model, $T > T_{KT}$)

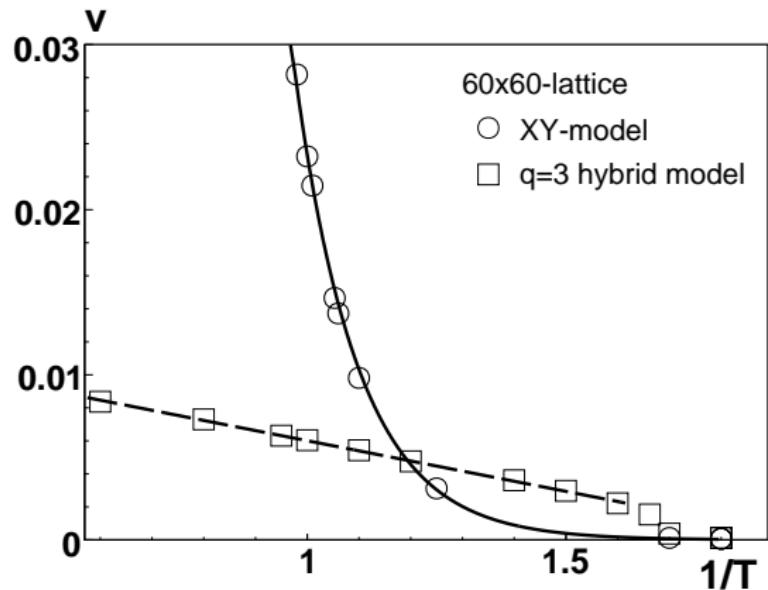


b) $q = 3$ (hybrid model)



Vortex Density

Vortex density $\equiv (\# \text{vortices} + \# \text{antivortices}) / \text{lattice size}$



- XY model:

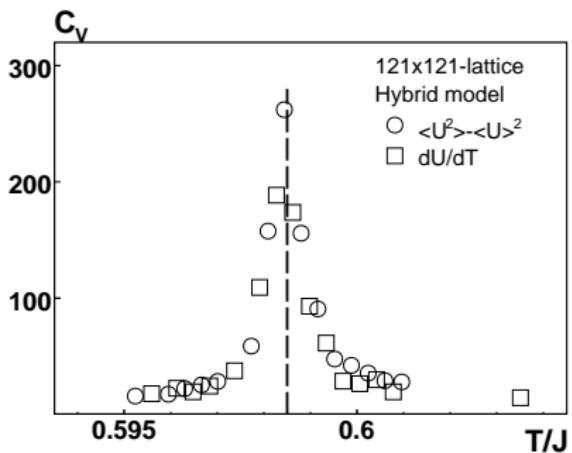
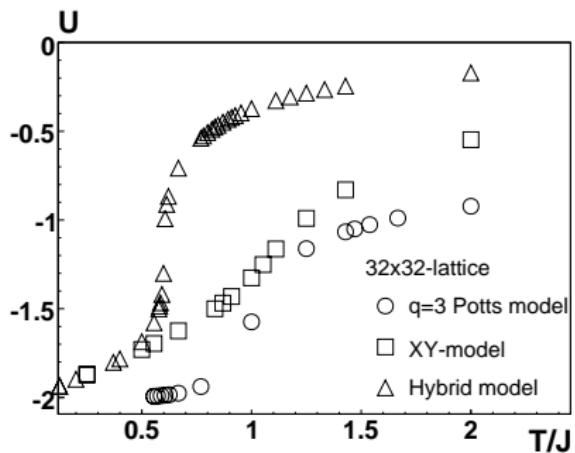
$$v \sim \exp(-2\mu/T)$$

- hybrid:

$$v \sim -6.14 \cdot 10^{-3}/T$$

Thermodynamics: Inner Energy and Specific Heat

results of Metropolis MC



⇒ transition temperature: $T_c \approx 0.5985$

Wolff's Cluster Algorithm⁴

Wolff Cluster Flipping

- randomly choose a lattice site
- draw bonds to all nearest neighbours with probability

$$P = 1 - \exp(-K\delta_{p_i, p_j})$$

(with $K \equiv J/k_B T$)

- proceed recursively until no more new bonds are created
- flip all spins in the cluster

hybrid model has two *dof*: p (discrete) and θ (continuous)

⇒ flip cluster with respect to **embedded variables**

⁴Wolff, 1989

Embedding I

XY degree of freedom

embedding procedure for XY model well known (**Wolff Embedding Trick**)

- consider **projection** of spin vector onto x -axis
⇒ **Ising model** of projected spins
- add bond between nearest neighbour sites with

$$P = 1 - \exp\left(\delta_{p_i, p_j} \cdot \min[0, 2K \cdot S_i^x \cdot S_j^x]\right)$$

- invert the x -component of all spins in the cluster
- to provide ergodicity rotate all spins by the same angle

Embedding II

Potts degree of freedom

- choose randomly a pair of p -values: (0,1), (0,2), (1,2)
- calculate effective interaction strength:

$$J_{\text{eff}} = J_H \cdot S_i S_j \cos \theta_{i,j}$$

- if $J_{\text{eff}} > 0 \Rightarrow$ ferromagnetic coupling:

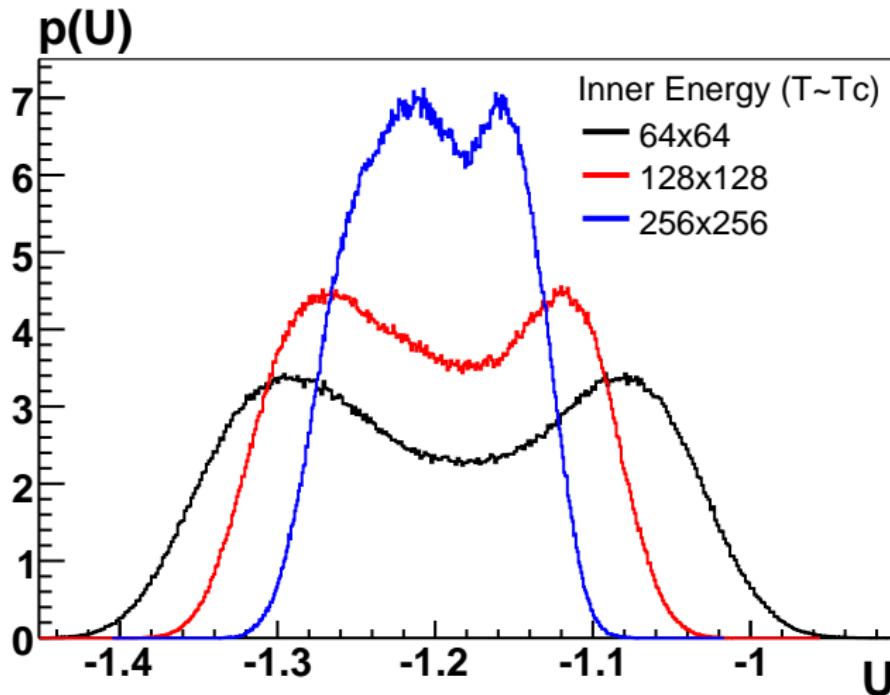
$$P = 1 - \exp(-K_{\text{eff}} \delta_{p_i=p_j})$$

- if $J_{\text{eff}} < 0 \Rightarrow$ anti-ferromagnetic coupling:

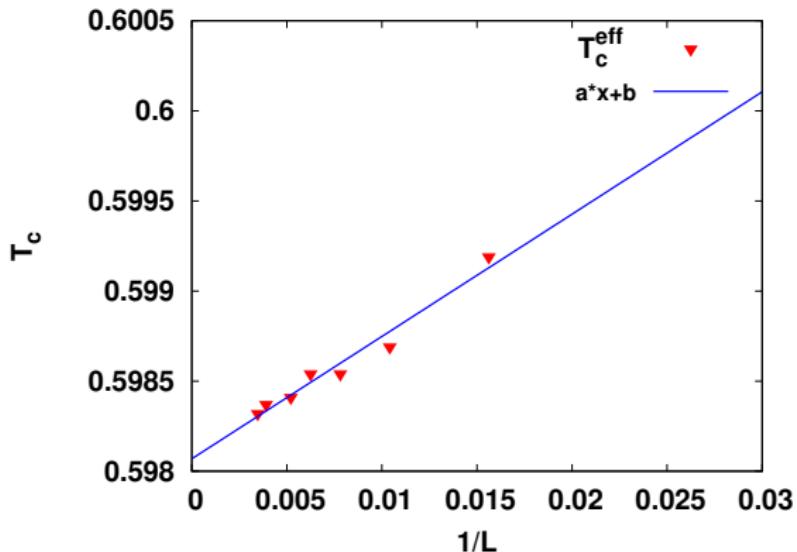
$$P = 1 - \exp(K_{\text{eff}} \delta_{p_i \neq p_j})$$

- switch all Potts spins in the cluster

Recent Results: Inner Energy Distribution



Recent Results: Transition Temperature



linear fit \Rightarrow $T_c^{eff}(L \rightarrow \infty) = 0.598069$

Open Questions/Problems/Ideas

- character/order of phase transition? Weak 1st order or 2nd order?
- order parameter?
- use results obtained for isolated complex (distribution for p)
- biologically motivated interaction (e.g. steric, electrostatic)?
- obtain macroscopic quantities (e.g. disjoining force)
- biological/biophysical implications?

Thank You for Your Attention!

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