Zusammenfassung der wissenschaftlichen Ergebnisse zur Dissertation

Structural Behavior of Polymers from Monte Carlo Studies of Coarse-Grained Models

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Polymers and polymeric materials are present in everyday life and fundamental components in biology. Hence, they are among the most interesting substances in science in general and in particular subject of numberless studies in experimental, theoretical and computational physics. In my doctoral thesis, I present new results on different generic aspects of polymer science, obtained by means of sophisticated Monte Carlo computer simulations. More precisely, I focus on the phase behavior of polymers described by different coarse-grained models.

Motivation and Overview   Polymers are chemical compounds consisting of equal or similar molecules, forming a molecular chain. They are therefore often also called macromolecules. Two of the most important examples of polymers in life are synthetic carbon-based homopolymers, such as polyethylene, and biopolymers, like proteins or DNA. The first mentioned homopolymers consists of (a large number of) identical (simple) components and are the basis of a multitude of macroscopic products in everyday life. In the case of polyethylene, these components are ethene molecules simply consisting of two carbon and four hydrogen atoms (see Fig. 1).

Biopolymers consist, generally, of more complex and different molecules. In the case of proteins, these are the amino acids, in the case of DNA for example the so-called nucleotides. Since proteins are the basic building blocks of cells and involved in the majority of the biological processes, for example, transport of substances, catalysis of chemical reactions or recognition of messengers, a general as well as specific understanding of these macromolecules, in particular of their structure is highly desirable. It is widely assumed, that the primary structure of proteins, i.e., their amino-acid sequence, determines uniquely the three-dimensional native conformation and hence the biological function [1]. Unfortunately, the major question,
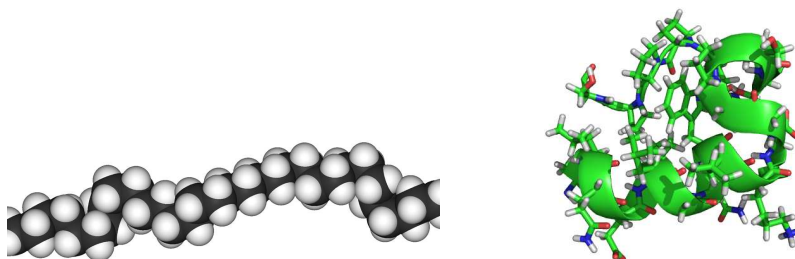

Figure 1: Left: All-atom visualization of a part of a polyethylene chain (space-filling model). Right: A miniprotein in the all-atom stick representation. Additionally emphasized is the helical secondary structure.

how a protein exactly finds or folds into its native state is still open, though extensively studied since decades. Hence, theoretical and computational efforts should be made studying the behavior of single polymers with respect to their structure and structural behavior.

Generally, as every other substance, polymers can be found in different states depending on external conditions like temperature or solvent quality. At high temperatures, polymers are known to be in the swollen random coil state. Cooling them down, they collapse at the so-called Θ-temperature into much more compact globules. At very low temperatures, they freeze into glassy or crystalline solids [2–4]. In the case of proteins, by definition finite systems, one speaks also of the "folding" transition.

All this leads to the general structure of this work. In the first part, I study lattice polymers using the interacting self-avoiding walk model. Special attention has been paid to the scaling of the collapse and the freezing transition. The interesting question is, if the intermediate amorphous phase is stable or vanishes in the thermodynamic limit. In the second part, I study an off-lattice tube model for polymers with the emphasis on the different low-temperature pseudo-phases for finite systems depending on the thickness of the tube and the folded secondary structures therein.

Methods All results in this work have been obtained by means of computer simulations [5, 6], a third cornerstone of physics beside experiments and theoretical work, of simplified, coarse-grained models. The simplicity of these models results from "integrating out" nonrelevant, microscopic degrees of freedom and replacing them by a few effective parameters. By studying polymer *models*, several restrictions imposed on "real" experimental studies do not exist. Furthermore, as physical conditions of the system and the environment can be varied freely and rapidly, theories could be verified and statistical analyses could be carried out more easily in general.

For the study of lattice polymers, in particular for the low temperature freezing regime, I applied sophisticated chain growth algorithms [7, 8], where the polymer chain is created, i.e, grows, during the simulation. By a clever population control through pruning and enriching the simulated sample, the simulation can be forced to perform a random walk in the energy space and system size and one can hence estimate the entire density of states of the system over many orders of magnitude within one single simulation (see Fig. 2). For the simulation of the off-lattice systems, I used mainly generalized ensemble Monte Carlo methods, like the multicanonical recursion or the Wang–Landau algorithm. These methods base on conformational updates of the chain which are accepted with a certain probability depending on statistical weights. Rather than sampling, for example, the canonical ensemble using just the Boltzmann weights, these weights are here adapted such
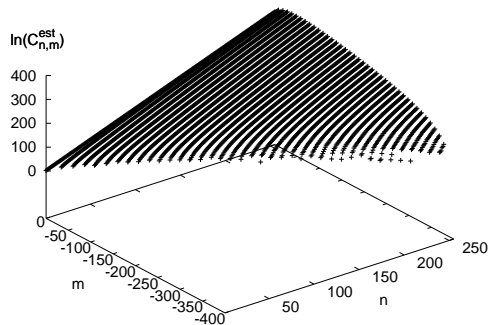

Figure 2: The logarithm of the estimated density of states, i.e., the estimated number of configurations, $C_{n,m}^{est}$ versus the number of nearest neighbor contacts $-m$ and system size n of lattice polymers resulting from a single flat-histogram chain-growth simulation is shown. The density of states is obtained with high quality over many orders of magnitude.

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that the simulated system performs a random walk through the energy space. For reliability reasons, cross-checks have been made using further different simulational techniques, as well as independent data from previous studies. Ground states have been refined using deterministic minimization techniques.

Lattice Polymers   In the study of lattice polymers, I considered monomer chains on the simple cubic (sc) and the face centered cubic (fcc) lattice, whereas non-bonded nearest neighbors interact between each other via a local attractive potential. I studied conformational transitions of these systems, namely the collapse (or coil–globule transition) at the so-called Θ-temperature and the freezing transition at very low temperatures, i.e., well below the Θ-temperature. A question of particular interest deals with the coincidence of these transitions, i.e., with the stability or instability of intermediate phases between the random coil (vapor) phase and the frozen (solid) phase, in the thermodynamic limit. Both scenarios have been found for polymeric systems and were explained by different ranges of interaction between the single monomers [9]. This behavior can be described introducing an interaction-range parameter R. It is known for colloidal systems, that for very small R-values different solid phases can coexist and that there is a stable liquid phase for large R [10]. As I used here a potential with $R \to 0$, and with the implicit understanding that polymeric systems behave similarly, one would expect a two-stage collapse from random-coil conformations at high temperatures to the ground states of the system.

   The thermodynamic behavior of the polymer systems was studied considering peaks in the specific heat as indicators of structural activity. Figure 3 (left) shows specific-heat peak positions [1] of polymers on the sc lattice with lengths $8 \leq N \leq 125$ [O1, O2]. In contrast to similar studies for other polymer models [9], the freezing peaks seem not to behave in any regular way at first view. Unraveling the non-uniform peak structure, it became rather clear, that the finite-size low temperature behavior is strongly superposed by systematic lattice effects (see Fig. 3, right). Due to the high precision of my simulations, it was possible to
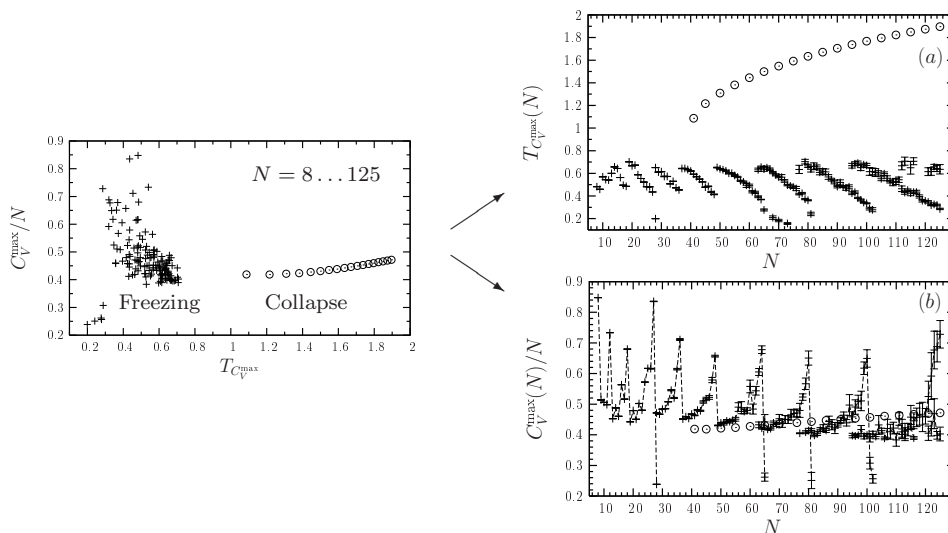

Figure 3: Left: Map of specific-heat maxima for several chain lengths $N \in [8, 125]$. Right: The same data in dependence of the chain length N. (a) Collapse ($\odot$) and freezing ($+$) peak temperatures of the specific heat, (b) values of the specific-heat maxima.
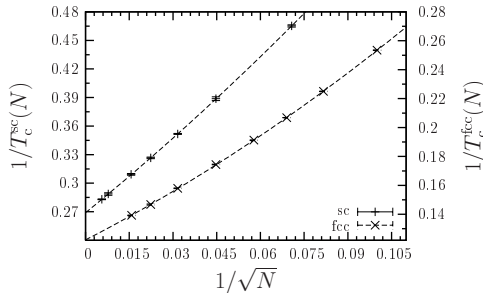
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Figure 4: Inverse collapse temperatures for several chain lengths on sc ($N \leq 32\,000$) and fcc lattices ($N \leq 4\,000$). Dashed lines are fits to $1/T_c(N) - 1/T_\Theta = \tilde{a}_1/\sqrt{N} + \tilde{a}_2/N$.

explain this behavior also quantitatively. One notes for example, that the freezing temperature fluctuates systematically. In particular, there are "magic" lengths where the ground-state conformations fit into compact cuboid shapes (see [O3] for similar considerations) and where the transition temperature jumps between almost fixed boundaries. Generally, the low-temperature transition can be interpreted as the "freezing" of compact globular shapes into polymer crystals.

To estimate the scaling of the finite size collapse transition temperature, I simulated much longer polymers with lengths up to $N = 32\,000$. This task is by no means trivial, as the upper critical dimension is just $d_c = 3$ and hence logarithmic corrections to the leading order scaling $T_c(N) - T_\Theta \sim 1/\sqrt{N}$ are expected. By fitting my data to various scaling functions motivated by field-theoretic studies (see, for example, Fig. 4), it was not possible to uniquely identify the nature of these corrections. It rather turned out that even these apparently large systems are still to short to determine the type of corrections and hence verify theoretical predictions. Still, the value of the infinite length Θ temperature seems not to be affected seriously by the explicit type of scaling corrections, as they can mimic each other effectively to a certain degree. Beside a very well agreement of my estimates on the sc lattice with the most precise estimates from the literature, my data confirm, to my best knowledge, the only numerical value existing so far for the fcc lattice [O1, O2].

Concerning the question of the stability of the structural phases, it can be concluded from my results, that both transitions, the collapse and the freezing remain well separated also in the extrapolation towards the thermodynamic limit. This may be explained by the expected stable "solid" phase due to the very short attractive interaction in the model. Hence, a qualitative agreement between the behavior or polymers and colloids has been found.

The Tube Model In the presented analysis of the tube model, I concentrated on the formation of secondary structures of short systems. Similar to previously studied tube models [11], the polymer is modeled as an off-lattice chain consisting of monomers, which interact between each other by means of a Lennard–Jones potential. The chain itself is coated by a tube, mimicking the three-dimensional extension of polymers due to steric constraints introduced, for example, by amino-acid side chains in the case of proteins. Its diameter was introduced using the concept of the global radius of curvature, a mathematical concept which has been proven to provide a concise characterization of the thickness of a curve [12].

The main task of this work was, to take this simple coarse-grained model and to show, to which degree secondary structure formation as observed in nature can be understood already with this approach. The other way around one may ask: Which level of coarse graining is necessary, to observe secondary structure formation including helices, sheets, etc. Therefore, I first studied systematically the ground-state structures depending on the thickness parameter ρ. It turned out that, driven by
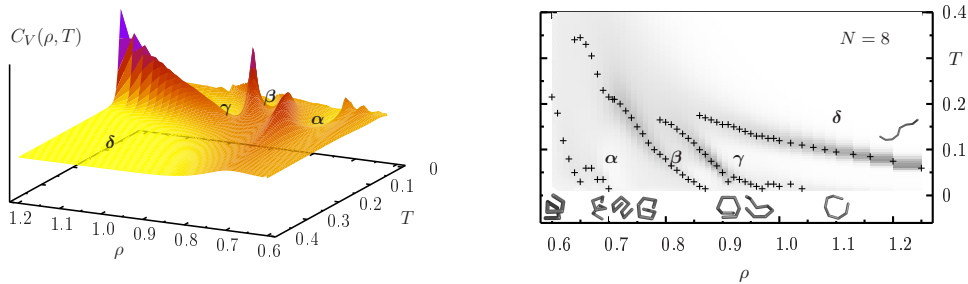
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Figure 5: Phase diagram of the homopolymer with $N = 8$ monomers. The labels α, β, γ, and δ indicate the different pseudophases at finite temperature. The left picture shows the perspective view of the specific-heat landscape, in the right one the top-view is plotted with marked peak positions for various thickness parameters ρ. The specific-heat values are encoded in gray scale. The pictures in the inset in correspond to the ground-state conformations.

the variation of the thickness parameter, several different conformations occur as ground states. In particular, I could show that the exact α-helix and planar β-sheets are amongst them [O4, O5]. For examples, see inset of Fig. 5 at $\rho \approx 0.68$ and $\rho \lesssim 1.0$. [2] This is remarkable as the model consists of nothing but Lennard–Jones interaction and an additional length scale, the tube diameter.[3] This is of course just a first step in the understanding of the model. Subsequently, in detailed and elaborate studies I could develop the full conformational phase diagrams depending on the thickness constraint and temperature for short polymers and unravel the internal structure of the pseudo phases of folded conformations (Fig. 5 shows exemplarily the phase diagram for the tubes with length $N = 9$). Independently of the polymer length, I identified four major structural phases, where helices, sheet-like planar structures, bended rings and sprawled random coils are the dominant conformations [O4, O6]. As a by-product, I found special regions in the parameter space, where conformations crystallized into regular lattices dominate.

After introducing finally the AB tube model for heteropolymers, I studied a special protein in this model, which has been subject of several preceding works without thickness. As a key result, I showed that special sequences of different monomers, involving different intramolecular interactions, can stabilize the secondary structures of tube polymers. In particular, I found a broad and stable ground-state region of a β-sheet structure for that protein [O6].

To conclude, I could resolve the complete (pseudo)phase behavior of the Lennard–Jones tube model for polymers with respect to the thickness constraint and temperature, including the formation of the native states for $T \to 0$. This allowed, for example, for the classification of thermodynamic conformational phases. Hence, I have identified the generic structure of the conformational phase space for classes of polymers, parameterized by their thickness. Although a mesoscopic model for flexible polymers was employed, I found that the thickness constraint is an intrinsic source of an effective stiffness and enhances the capability of a polymer to form secondary structures which are stable against thermal fluctuations.

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[1] The observables in Figs. 3–5 are given in a dimensionless form, where the Boltzmann constant k_B and the energy scale of the model ϵ are set to 1 for convenience. Alternatively, the dimensionless temperature and specific heat would read $T k_B \epsilon^{-1}$ and $C_V k_B^{-1}$, respectively.

[2] The thickness parameter ρ is measured in terms of the unit length of the model, i.e., the bond length between two monomers, which is set to 1 as well.

[3] Doubtlessly, secondary structures can be stabilized by further interactions, for example due to special primary structures (see below).

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