

Heteropolymers in a solvent at an interface

This article has been downloaded from IOPscience. Please scroll down to see the full text article.

1999 J. Phys. A: Math. Gen. 32 L275

(<http://iopscience.iop.org/0305-4470/32/25/102>)

View [the table of contents for this issue](#), or go to the [journal homepage](#) for more

Download details:

IP Address: 171.66.16.105

The article was downloaded on 02/06/2010 at 07:34

Please note that [terms and conditions apply](#).

LETTER TO THE EDITOR

Heteropolymers in a solvent at an interface

A Maritan, M P Riva and A Trovato

International School for Advanced Studies (SISSA), and Istituto Nazionale di Fisica della
Materia, Via Beirut 2–4, 34014 Trieste, Italy
The Abdus Salam International Center for Theoretical Physics, Strada Costiera 11, 34100 Trieste,
Italy

Received 23 April 1999, in final form 14 May 1999

Abstract. Exact bounds are obtained for the quenched free energy of a polymer with random hydrophobicities in the presence of an interface separating a polar from a non-polar solvent. The polymer may be ideal or have steric self-interactions. The bounds allow one to prove that a ‘neutral’ random polymer is localized near the interface at any temperature, whereas a ‘non-neutral’ chain is shown to undergo a delocalization transition at a finite temperature. These results are valid for a quite general *a priori* probability distribution for both independent and correlated hydrophobic charges. As a particular case we consider random *AB*-copolymers and confirm recent numerical studies.

The statistical behaviour of heteropolymers has been intensively studied in recent years [1–7]. They model random copolymers [2, 3] and to some extent protein folding [1]. For example, a chain composed of hydrophobic and hydrophilic (polar or charged) components in a polar (aqueous) solvent evolves toward conformations where the hydrophobic part is buried in order to avoid water, whereas the polar part is mainly exposed to the solvent [8]. This is what commonly happens to proteins and it makes them soluble in aqueous solutions. However, other proteins (e.g. structural proteins) are almost insoluble under physiological conditions and prefer to form aggregates [8]. Many of the proteins which are insoluble in water are segregated into membranes which have a lipid bilayer structure [8]. Membrane proteins have a biological importance at least as great as those which are water soluble. Usually one distinguishes integral and non-integral membrane proteins according to whether the protein is most immersed in the lipid bilayers or simply anchored to the membrane, respectively (in the latter case the protein is essentially water soluble) [8]. An analogous situation occurs for copolymers at interfaces separating two immiscible fluids. If the solvents are selective (i.e. poor for one of the two species and good for another), *AB*-copolymers are found to stabilize the interface [9]. Moreover, random copolymers have been claimed to be more effective in carrying out this re-enforcement action [10].

The simplest theoretical approach to the above problems has been proposed by Garel *et al* [2]. In the case of membrane proteins the finite layer of lipidic environment is modelled as an infinite semi-space. Though a quite rough approximation, this is the simplest attempt in capturing the relevant features due to the competition of different selective effects [11].

We study a lattice discretized version of their model. The nodes of an N links chain occupy the sites $\vec{r}_i = (x_{i1}, \dots, x_{id})$, $i = 0, \dots, N$ of a d -dimensional hypercubic lattice. A flat interface passing through the origin and perpendicular to the $\vec{u} = (1, \dots, 1)$ direction

separates a polar (e.g. water), on the $\vec{u} \cdot \vec{r} > 0$ side, from a nonpolar (e.g. oil or air), on the $\vec{u} \cdot \vec{r} < 0$ side, solvent. The i th monomer interacts with the solvent through its charge q_i (the monomer is hydrophilic if $q_i > 0$, hydrophobic if $q_i < 0$) and contributes to the energy with a term $-q_i \operatorname{sgn}(\vec{u} \cdot \vec{r}_i)$ †. For simplicity we can associate the charge to the link between adjacent positions on the chain instead of that to the single monomer.

The partition function of the model for a chain W starting at position $\vec{r}_0 \equiv \vec{r}$ is

$$\mathcal{Z}(\vec{r}, \{q_i\}) = \sum_{W: \vec{r} \rightarrow \cdot} \exp \left\{ \beta \sum_{i=1}^N q_i \operatorname{sgn}(\vec{u} \cdot \vec{r}_i) \right\} \quad (1)$$

where $\beta^{-1} = k_B T$. If one sums over non-interacting (ideal) chains, then the lattice version of the model introduced in [2] is recovered. We also consider the more physical case where steric interaction among monomers does not allow for multiple occupancy of lattice nodes, studied for a particular case in [3].

The free-energy density of the system reads $f(\vec{r}, \beta) = -\lim_{N \rightarrow \infty} \frac{1}{\beta N} \overline{\ln \mathcal{Z}(\vec{r}, \{q_i\})}$, where $\overline{\cdot}$ denotes the quenched average over the distribution of the charges $\{q_i\}$. In the following we assume that $\{q_i\}$ are independent random variables having a Gaussian distribution of the form

$$P(q_i) = \frac{1}{\sqrt{2\pi} \Delta} \exp \left[-\frac{(q_i - q_0)^2}{2\Delta^2} \right]. \quad (2)$$

More general cases will be treated at the end. In particular, considering charges not independently distributed is of interest for *designed* sequences, as occurs for real proteins.

We show that for a neutral chain ($q_0 = 0$) $f(0, \beta) < f(\vec{r}, \beta)$ with $|\vec{r}| \geq N$, in the large N limit, and for all β . The same holds also for $q_0 \neq 0$ if $\beta > \beta_{upper}(|q_0|, \Delta)$ with $\beta_{upper} \rightarrow 0$ if $\frac{|q_0|}{\Delta} \rightarrow 0$. This implies that the chain is localized around the interface at any temperature if $q_0 = 0$, and at sufficiently low temperature if $q_0 \neq 0$. The proof is rigorous for the ideal chain, whereas for the self-avoiding case only a mild and well accepted hypothesis on the asymptotic behaviour of the entropy is needed. When $q_0 \neq 0$ a rigorous lower bound on the free energy for both the ideal and the self-avoiding chain allows one to determine a $\beta_{lower}(|q_0|, \Delta)$ below which the chain is delocalized.

We first consider the ideal chain case and then explain the modifications necessary to extend the results to self-avoiding chains.

Ideal chain. For clarity we derive the bounds in the $d = 1$ case. The general case does not contain any further difficulty‡. Let us first consider initial positions far from the interface in the favourable solvent, $x \geq N$ if $q_0 > 0$ or $x \leq -N$ if $q_0 < 0$. Under these assumptions all chains remain on the same side, implying that $\operatorname{sgn}(x_i) = 1$ (or $\operatorname{sgn}(x_i) = -1$ respectively) for all i . Upon averaging over the charge distribution, we obtain the free-energy density of a walk in the favourable solvent:

$$f^* = -\frac{1}{\beta} \ln 2 - |q_0|. \quad (3)$$

We give an upper bound to the free energy as follows. Consider only chains made up of blobs of k steps, with k even. Bringing a blob in its globally favoured side leads to an energy

† The case where the energy is $-\lambda_+ q_i$ and $\lambda_- q_i$ ($\lambda_{+,-} > 0$) when $\vec{u} \cdot \vec{r}_i > 0$ and $\vec{u} \cdot \vec{r}_i < 0$, respectively, is readily reduced to the one treated here apart from an additive constant and a redefinition of the ‘charges’ $q'_i = \frac{\lambda_+ + \lambda_-}{2} q_i$.

‡ Notice that in the off-lattice model of [2] the entropy has only a harmonic term (Edwards functional) and thus the d -dimensional case reduces trivially to the $d = 1$ case. In the lattice model considered here this is no longer true.

contribution of the form $H_{j^{\text{th blob}}} = -|\sum_{i=1}^k q_{k(j-1)+i}|$, so that

$$\mathcal{Z}(x = 0, \{q_i\}) \geq (C_k)^{\frac{N}{k}} \exp \left\{ \beta \sum_{j=1}^{\frac{N}{k}} \left| \sum_{i=1}^k q_{k(j-1)+i} \right| \right\}$$

where C_k is the number of k -step chains starting and ending in the origin and remaining on the same side. In the one-dimensional case it is easy to exactly determine C_k . It turns out $C_k = \frac{1}{\frac{k}{2}+1} \binom{k}{\frac{k}{2}}$, so that, by using the Stirling formula, the asymptotic result $C_k \sim 2^k k^{-\frac{3}{2}}$ is found (in d dimensions $C_k \sim (2d)^k k^{-\frac{d+2}{2}}$ [12]). The upper bound on the free energy is then:

$$f(0, \beta) \leq -\frac{1}{\beta} \frac{\ln C_k}{k} - \frac{1}{k} \left| \sum_{i=1}^k q_i \right| \tag{4}$$

and, by using equation (2), we obtain:

$$\Delta f = f(0, \beta) - f^* \leq h_{q_0}(k, \beta) \equiv \frac{1}{\beta} \left[\ln 2 - \frac{\ln C_k}{k} \right] - |q_0| G \left(\frac{\sqrt{k}|q_0|}{\sqrt{2}\Delta} \right) \tag{5}$$

where the scaling function G is given by

$$G(x) = \frac{1}{\sqrt{\pi}} \frac{1}{x} e^{-x^2} - [1 - \text{erf}(x)]. \tag{6}$$

$G(x)$ is a positive decreasing monotonic function for positive arguments.

We consider, separately, the neutral and the $q_0 \neq 0$ cases. In the neutral case it turns out that the chain is always localized at the interface. In fact, if $q_0 = 0$ we have

$$\Delta f \leq h_0(k, \beta) = \frac{1}{\beta} \left[\ln 2 - \frac{\ln C_k}{k} \right] - \sqrt{\frac{2}{\pi}} \Delta \frac{1}{\sqrt{k}}. \tag{7}$$

It is easy to see that for any β there exists a value $k(\beta)$ such that $h_0(k, \beta) < 0$ for $k > k(\beta)$. For example, at high temperature $k(\beta) \sim [\ln(\beta\Delta)]^2 (\beta\Delta)^{-2}$. This shows that at any temperature a neutral random chain is always adsorbed by the interface.

In the non-neutral case with $k = 2$, one has $\Delta f < 0$ if

$$\beta > \beta_{upper} = \frac{\ln 2}{|q_0| G \left(\frac{|q_0|}{\Delta} \right)}. \tag{8}$$

The limit $\lim_{k \rightarrow \infty} h_{q_0}(k, \beta) = 0_+$ does not allow one to deduce the existence of a negative minimum in k , so that the previous argument, showing that the neutral chain is always localized, does not hold for $q_0 \neq 0$. Equation (8) proves localization at sufficiently low temperatures. For $|q_0| \ll \Delta$, it yields $\beta_{upper} = \frac{\sqrt{\pi} \ln 2}{\Delta}$, and in the opposite regime $\Delta \ll |q_0|$, $\beta_{upper} = 2\sqrt{\pi} \ln 2 e^{\frac{|q_0|^2}{\Delta^2}} \frac{|q_0|^2}{\Delta^3}$. In the limit $|q_0|/\Delta \ll 1$ we can give a better estimate for β_{upper} , such that $\beta_{upper} \rightarrow 0$ as $|q_0| \rightarrow 0$, by considering a larger blob size $k = 2x_0^2 (\Delta/|q_0|)^2$, where $x_0 \gg |q_0|/\Delta$ is fixed:

$$\beta_{upper} = \frac{3}{2x_0^2 G(x_0)} \ln(\sqrt{2}x_0\Delta/|q_0|) \frac{|q_0|}{\Delta^2}. \tag{9}$$

We now look for a lower bound on f for all chain initial positions. If, for example, $q_0 > 0$, the preferred side is the right one. Consider then the starting point at $x = N - k$ ($0 < k \leq N$) and let g_E , with E some subset of the last k steps of the walk ($0 < |E| \leq k$ with $|E|$ the number

of elements in E), be the number of walks having the steps belonging to E in the unfavourable side. Upon defining $G_k = \sum_E g_E (G_k < 2^k)$ one has

$$\mathcal{Z}(x = N - k, \{q_i\}) = (2^N - G_k) e^{\beta \sum_{i=1}^N q_i} + e^{\beta \sum_{i=1}^N q_i} \sum_E g_E e^{-2\beta \sum_{i \in E} q_i} \quad (10)$$

so that, by using the inequality $\ln \bar{x} \geq \overline{\ln x}$ and averaging over the charge distribution, one obtains

$$f(N - k) \geq f^* - \frac{1}{\beta N} \ln \left[1 + \sum_E g_E \frac{a(\Delta, q_0, \beta)^{|E|} - 1}{2^N} \right]$$

with $a(\Delta, q_0, \beta) = \exp[2\Delta^2\beta^2 - 2\beta q_0]$. This equation and its analogue in the $q_0 < 0$ case show that there is a delocalization temperature

$$\beta_{lower} = \frac{|q_0|}{\Delta^2} \quad (11)$$

such that, if $\beta < \beta_{lower}$, $f(|N - k|) \geq f^*$ for all k and the chain delocalizes. This argument can be extended to the d -dimensional case, in which $1 \leq G_k < (2d)^k$, $\mathcal{Z}_d^*(q_i) = (2d)^N e^{\beta \sum_{i=1}^N q_i}$ and $f_d^* = -\frac{1}{\beta} \ln 2d - |q_0|$.

The bounds we have proved above allow one to conclude that there is a critical value β_c such that for values of β smaller than β_c the chain is delocalized in the favourable solvent, while for larger values it is adsorbed by the interface, with the estimates $\beta_{lower} < \beta_c < \beta_{upper}$ (it is easy to verify that $\beta_{lower} < \beta_{upper}$). The lower bound (11) and the upper bound (9), in the limit $|q_0|/\Delta \ll 1$, show the same behaviour found by using both an Imry–Ma-type argument [2] and variational approaches [5, 7].

Self-avoiding chain. All the results shown for a random chain can be readily generalized for a self-avoiding chain. Namely, a neutral chain is localized at all temperatures, whereas a non-neutral chain undergoes a localization transition at some critical temperature β_c .

The delocalization temperature, β_{lower} , can be derived in exactly the same way, since the division of walks into classes according to the number of steps made in the unfavourable solvent does not depend on the self-avoidance constraint.

The upper bounds on the free energy, which allow one to prove chain localization, instead requires some refinements with respect to the previous case. While the energy term is computed in the same way as before, the entropy term is different. First, the connective constant ($\kappa = 2d$ for a random walk in d dimensions) is different. We recall that the existence of the connective constant, $\kappa = \lim_{N \rightarrow \infty} \ln S_N/N$, for self-avoiding walks (SAW) has been rigorously established [13] (S_N is the total number of N -steps SAW starting from the same site). The subleading correction of the form $S_N \simeq \kappa^N N^{\gamma-1}$ is widely agreed upon, although not rigorously proved [12]. Secondly, we introduce the notion of *loop*, following e.g. [14], and consider only walks made up of N/k blobs, each blob being a k -loop, in such a way that different blobs can be embedded independently, as well as for a random chain. An N -loop is an N -steps SAW, starting and ending on the interface, which always remains in the same half-space, with the further condition $x_{01} - x_{02} \leq x_{i1} - x_{i2} < x_{N1} - x_{N2} \forall i$. It has been proved [15] that the free-energy density of loops is the same as for SAW, $\kappa_l \equiv \lim_{N \rightarrow \infty} \ln L_N/N = \kappa$, where L_N is the number of N -loops. The subleading correction is usually assumed in the same form as for the number of SAW:

$$L_N \simeq \kappa^N N^{\gamma_s-1}. \quad (12)$$

These considerations are sufficient to generalize the previous results to the self-avoiding case, yielding the following bounds for the critical temperature:

$$\frac{\ln \kappa}{|q_0|G\left(\frac{\sqrt{2}|q_0|}{\Delta}\right)} \leq \beta_c \leq \frac{|q_0|}{\Delta^2} \tag{13}$$

which do not depend on the assumption (12) and is therefore rigorous. Again, in the limit $|q_0|/\Delta \ll 1$ a better estimate β_{upper} can be derived by using equation (12):

$$\beta_{upper} = \frac{1 - \gamma_s}{x_0^2 G(x_0)} \ln(\sqrt{2}x_0\Delta/|q_0|) \frac{|q_0|}{\Delta^2}. \tag{14}$$

Generic probability distribution. Up to now we have considered the hydrophobic charges as independently distributed Gaussian random variables. Actually, the results we have proved do not depend on this assumption. We will briefly sketch this in a few cases [12].

The argument showing localization at any temperature for a neutral chain holds true, both for random and self-avoiding chains, if $|\sum_{i=1}^k q_i| \simeq \sqrt{k}$ as $k \rightarrow \infty$. The central limit theorem ensures this for independent random variables having a generic probability distribution with finite variance and null mean. In the non-neutral case, the existence of a delocalization transition can be proved e.g. for a bimodal distribution. This corresponds to the more realistic case of two kinds of monomers, one hydrophilic and the other hydrophobic. We thus consider the generic bimodal distribution [16]†:

$$P(q_i) = \alpha\delta(q_i - q_+) + (1 - \alpha)\delta(q_i + q_-) \tag{15}$$

with $q_+, q_- > 0$. The probability distribution (15) has three independent parameters, and fixing the average charge $q_0 = \alpha(q_+ + q_-) - q_-$ and the variance $\Delta = \sqrt{\alpha(1 - \alpha)}(q_+ + q_-)$ we are left with one free parameter. It is interesting to report the delocalization temperature β_{lower} , which provides a good estimate for the critical temperature in the previous cases:

$$\beta_{lower}^{bim} = \frac{\sqrt{\alpha(1 - \alpha)}}{2\Delta} \left| \ln \left[1 + \frac{q_0}{\sqrt{\alpha(1 - \alpha)}\Delta - (1 - \alpha)q_0} \right] \right|.$$

Notice that in the limit of nearly neutral chain ($|q_0| \ll \Delta$) we get $\beta_c^d \simeq \frac{|q_0|}{2\Delta^2}$, which is the same function of $|q_0|$ and Δ as in the Gaussian case, suggesting the existence of a universal behaviour. In the limit of nearly homogeneous chain ($\Delta \ll |q_0|$ which implies $\alpha \simeq 0$ or $\alpha \simeq 1$) instead $\beta_{lower}^{bim} = \frac{1}{2(q_+ + q_-)} \left| \ln \left[\frac{\alpha}{1 - \alpha} \frac{q_+}{q_-} \right] \right|$ diverges logarithmically in contrast with the Gaussian case.

We now consider the case in which the hydrophobic charges $\{q_i\}$ are not independent random variables, but are Gaussianly distributed with $\overline{q_i} = q_0 \forall i$, $\overline{q_i q_j} - \overline{q_i} \overline{q_j} = M_{ij}^{-1}$. We assume $M_{ii}^{-1} = \Delta^2 \forall i$, in analogy with the non-correlated case, and also translational invariance along the chain for the correlation matrix: $M_{ij} = b(|i - j|)$. One can prove that if long-range correlations decay exponentially or even algebraically the neutral chain is again localized at all temperatures. In fact, by assuming an algebraic decay, $b(r) \simeq r^{-\eta}$, it turns out that $|\sum_{i=1}^k \overline{q_i}| \simeq k^{\delta/2}$ with $\delta = \min(\eta, 1)$. Only if correlations are so strong that they do not vanish along the chain ($\eta = 0$), does the chain not localize at all temperatures.

In the non-neutral case the existence of the transition can be proved. For example the estimate of the delocalization temperature is

$$\beta_{lower}^{corr} = \min_E \left\{ \frac{|E||q_0|}{\sum_{i,j \in E} M_{ij}^{-1}} \right\}. \tag{16}$$

† Some previous exact results for the bimodal distribution and only for ideal chains were also obtained by Sinai and Bolthausen and den Hollander [16].

If the charges are positively correlated ($M_{ij}^{-1} > 0$ for $i \neq j$), chain localization is more favoured than in the non-correlated case, whereas if charges are anti-correlated ($M_{ij}^{-1} < 0$ for $i \neq j$) it is less favoured.

Asymmetric interface potentials. Finally, we extend our demonstrations to the random *AB*-copolymers studied by Sommer *et al* [3]. Their model corresponds to consider the following Hamiltonian:

$$\mathcal{H} = \sum_i |q_i| [\lambda \theta(q_i) \theta(-\vec{u} \cdot \vec{r}_i) + \theta(-q_i) \theta(\vec{u} \cdot \vec{r}_i)] \quad (17)$$

with the charges distributed according to equation (15) with $\alpha = \frac{1}{2}$ and $q_+ = q_-$ ($|\lambda - 1|$ measures the potential asymmetry). Such an *AB*-copolymer (equation (17)) is equivalent to a non-neutral chain in symmetric potentials ($\lambda = 1$), a case that we have already discussed. We have proved the existence of a delocalization transition for a neutral chain also in the Gaussian case. For both distributions, the delocalization temperature shows the behaviour $\beta_{lower} \simeq \frac{|\lambda-1|}{\Delta}$ in the limit of nearly symmetric potentials ($\lambda \simeq 1$), in agreement with the scaling law and the numerical results found in [3]. In contrast, in the highly asymmetric cases (small and large λ) different asymptotic behaviours for β_{lower} occur[†].

To conclude, in this letter we have proved several exact results on random heteropolymers in the presence of an interface. Namely, a neutral chain is localized at all temperatures, whereas a charged chain delocalizes at a finite temperature. The results are quite general and hold for ideal and self-avoiding chains, Gaussian and bimodal distribution with independent and correlated charges. Furthermore, our lower bounds for the transition temperature confirm previous estimates.

We would like to thank Jayanth Banavar, Cristian Micheletti and Flavio Seno for useful discussion and ongoing collaboration, and Enzo Orlandini for bringing [16] to our attention.

References

- [1] Garel T, Orland H and Thirumalai D Analytical theories of protein folding *New Developments in Theoretical Studies of Proteins* ed R Elber (Singapore: World Scientific) and references therein
- [2] Garel T, Huse D A, Leibler L and Orland H 1989 *Europhys. Lett.* **8** 9
- [3] Sommer J-U, Peng G and Blumen A 1996 *J. Chem. Phys.* **105** 8376
- [4] Kantor Y and Golding I 1997 *Phys. Rev. E* **56** R1318
- [5] Stepanow S, Sommer J-U and Erukhimovich I Y 1998 *Phys. Rev. Lett.* **81** 4412
- [6] Monari P and Stella A L 1999 *Phys. Rev. E* **59** 1887
- [7] Trovato A and Maritan A 1998 *Preprint cond-mat/9812321 Europhys. Lett.* to be published
- [8] Creighton T E 1992 *Proteins: Structures and Molecular Properties* (New York: Freeman)
- [9] Brown H R, Deline V R and Green P F 1989 *Nature* **341** 221
- [10] Dai C-A, Dair B J, Dai K H, Ober C K, Kramer E J, Hui C-Y and Jelinsky L W 1994 *Phys. Rev. Lett.* **73** 2472
- [11] See e.g. R Bonaccini and F Seno 1998 For a more refined model *Preprint*
- [12] Hughes B D 1995 *Random Walks and Random Environments* vol I (Oxford: Clarendon)
- [13] Hammersley J M 1957 *Proc. Camb. Phil. Soc.* **53** 642
- [14] Whittington S G 1998 *J. Phys. A: Math. Gen.* **31** 3769
- [15] Hammersley J M, Torrie G M and Whittington S G 1982 *J. Phys. A: Math. Gen.* **15** 539
- [16] Sinai Ya G 1993 *Theory Prob. Appl.* **38** 382
Bolthausen E and den Hollander F 1997 *Ann. Prob.* **25** 1334

[†] Details will be published elsewhere.