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# Scaling theory of polymer solutions trapped in small pores: the $\theta$ -solvent case

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**Abstract.** — We study theoretically the behavior of a single macromolecular chain dissolved in a  $\theta$ -solvent and confined in a tube with a diameter D comparable to the natural size  $(R_0 = N^{1/2}a)$  of the chain (Nbeing the number of monomers of the chain). We find that for  $D \ll R_0$  the longitudinal dimension  $R_1$  of the chain increases as  $R_1 \cong Na$  (a/D), in contrast with the longitudinal behavior of an ideal chain which is unaffected by the confinement. We show that this extension of the chain is a consequence of the three-body interactions which are still present at the Flory temperature. We then generalize these results to semi-dilute solutions where the overlap between different chains is significant.

#### 1. Introduction.

The properties of flexible polymer chains moving inside porous structures are relevant to many practical problems such as filtration, gel permeation chromatography, oil recovery etc. [1]. Recently a large number of studies have been devoted to the properties of polymers in confined geometry [1-5]. In particular, Daoud and de Gennes [1] have analyzed in detail the theoretical behavior of macromolecular chains dissolved in a *good solvent* and confined into tubes of diameter D comparable to the coil radius. The case of macromolecular chains dissolved in a  $\theta$ -solvent and squeezed in a tube has (to the best of our knowledge) not yet been addressed in the literature [6]. The problem is interesting because we know that : (1) the behavior of a single, unconfined chain at the Flory temperature is similar to the behavior of an ideal chain (i.e. a random walk), and (2) the longitudinal dimension of an ideal chain trapped in a tube is unperturbed by the confinement [7]. Since for very small tubes the real chain (dissolved in the  $\theta$ -solvent) must be fully extended, its behavior must at some point depart from that of an ideal chain.

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In section 2, we discuss the single chain problem. In section 3, we consider the semi-dilute case where the overlap between different chains is significant. Our analysis is restricted to scaling laws; the exact prefactors in all our formulas remain unknown.

## 2. The single chain problem.

Let us start from a single chain immersed in a  $\theta$ -solvent. The coil behaves like an ideal chain with a radius of the form :

$$R_{,} \cong N^{1/2} a \tag{1}$$

where N is the polymerization index and a the monomer size [8].

We now confine the chain in a cylindrical pore of diameter D (the precise shape of the cross-section is not important for our scaling arguments). We assume that polymer adsorption on the solid wall is negligible. If  $D \gg R_0 = N^{1/2}a$  no change in the hehavior of the chain is expected: the chain remains ideal. But if D < R, the chain is squeezed into a « cigar » of length  $R_{\parallel}$ . The Flory free energy of the confined chain is then given by

$$\frac{F}{kT} \simeq \frac{R_{\parallel}^2}{a^2 N} + \frac{w^2 N^3}{(R_{\parallel} D^2)^2} \tag{2}$$

where  $w^2 (\approx a^6)$  is the third virial coefficient. The first term of equation (2) is an elastic deformation energy. The second term is a repulsive term due to three-body interactions. (The usual repulsive term  $vN^2/(R_\parallel D^2)$  is absent since the two-body interactions vanish at the Flory temperature).

From equation (2) one can define a perturbation parameter as  $\zeta = w^2 N^3 / (R_0 D^2)^2 - N^2 (a/D)^4$ . For  $D < R_0$  the perturbation parameter  $\zeta$  is large and the chain is swollen  $(R_{\parallel} > \mathcal{P}_{I})$ . The length  $R_{\parallel}$  of the chain can be derived directly by minimizing the free energy (2). This leads to:

$$R_{\parallel} \cong Na\left(\frac{a}{D}\right) \qquad (D < R_0) \tag{3}$$

The result (3) can also be derived from scaling arguments by writing

$$R_{\parallel} \cong R_0 \, h\left(\frac{R_0}{D}\right) \tag{4}$$

where the dimensionless function h(x) has the following features:  $h(x) \to 1$  for  $x \to 0$  and  $h(x) \to x^m$  when  $x \to +\infty$ . The value of m is obtained from the requirement that  $R_{\parallel}$  is a linear function of N for a thin tube  $(x \to +\infty)$ :

$$R_0(R_0/D)^m = N^{(m+1)/2}(a/D)^m$$
  
 $(m+1)/2 = 1$   
 $R_{\parallel} \cong aN(a/D)$  (5)

in agreement with equation (3).

Another derivation of equation (3) is based on a  $\times$  blob  $\times$  picture. The chain can be pictured as a sequence of blob of diameter D (see Fig. 1). At scales smaller than D the effects of the boundaries are weak and the chain behaves as an unconstrained chain. At scales greater than D the chain can be described as a sequence of blobs of size D, each containing

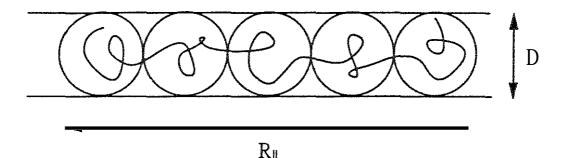


Fig. 1. — Conformation of a single chain immersed in a  $\theta$ -solvent and trapped in a capillary of diameter  $D (\ll R_0)$ . The chain can be described as a linear sequence of blob of size D each containing N/g monomers. Within one blob the behavior is ideal  $(g \approx (D/a)^2)$ . At larger scales the N/g blobs repel each other leading to an overall size  $R_{\parallel} = (N/g)D$ .

 $g = (D/a)^2$  monomers. The Nig blobs repel each other, leading to an overall length:

$$R_{\parallel} \cong (N/g) D . \tag{6}$$

One can check that equations (6) and (3) do coincide.

Let us now consider the confinement energy F. It must be of the form :

$$\frac{F}{kT} \cong s \left(\frac{R_0}{D}\right) \tag{7}$$

where  $s(x) \to 1$  for  $n \to 0$  and  $s(x) \to x^n$  when  $x \to +\infty$ . The value of n is obtained from the requirement that F he an extensive function of N:

$$(R_0/D)^n \cong N^{n/2}(a/D)^n$$

$$\frac{F}{kT} \stackrel{ni2}{=} N \left(\frac{a}{D}\right)^{2}$$
(8)

equation (8) can be rewritten as  $F \cong kT(N/g)$ : the energy F corresponds to the loss of entropy due to the confinement of N/g blobs. Note that equation (8) is identical (**up** to numerical prefactors) to the confinement energy of an ideal chain [7], despite the fact that their respective hehaviors are very different.

The free energy F can be obtained by measuring the partition coefficient (i.e. the ratio of concentration inside the **pore** to the concentration outside) for a pore exchanging chains with a hulk solution:

$$\frac{C_{\text{pore}}}{C_{\text{bulk}}} \cong \exp - (F/kT) \tag{9}$$

It is also of some interest to consider the internal filling fraction  $f = Na^3/R_{\parallel}D^2$ . It scales according to :

$$f \cong a/D \tag{10}$$

and is independent of N. Note that f is smaller than the ideal value  $f_0 \cong N^{1/2} (a/D)^2$  and reaches a value of order unity only when  $D \cong a$ .

### 3. The semi-dilute solution.

We now increase the number of chains inside the tube (we assume  $D < R_0$ ). Above the critical concentration:

$$\Phi^* = Na^3/R_{\parallel} D^2 \cong a/D \tag{11}$$

the different chains overlap. **As** in the case of a good solvent [7], the transition from  $\Phi < \Phi^*$  to  $\Phi > \Phi^*$  is very different from what happens in three dimensions. If one tries to define a correlation length of the form

$$\xi' = R_{\parallel} (\Phi/\Phi^*)^p \tag{12}$$

one finds that no value of the exponent p would lead to  $\xi'$  which is independent of N (since  $\Phi^*$  is independent of N). The physical answer is the following [7]: as soon as  $\Phi > \Phi^*$  the three dimensional correlation length  $\xi = a\Phi^{-1}$  becomes smaller than the tube diameter D and all local correlation properties return to their three dimensional value. In particular, the osmotic pressure is given by:

$$\Pi \cong \frac{kT}{a^3} \Phi^3 \qquad (\Phi^* \lessdot \Phi \lessdot 1).$$
(13)

### 4. Conclusion.

We have extended the analysis of Daoud and de Gennes [1] to the case of macromolecular chains dissolved in a  $\theta$ -solvent and confined in tubes of diameter D. For  $D \gg R_0$  the longitudinal dimension  $R_{\parallel}$  of the chain is unperturbed  $(R_{\parallel} \cong R_0)$ . For  $D \ll R_n$ , the size  $R_{\parallel}$  increases as  $R_{\parallel} \cong Na(a/D)$ . We have shown that this extension of the chain is a consequence of the three-body interactions.

It is of some interest to compare these results with the conformations of individual chains for a monodisperse melt (N monomers per chain) confined in a tube of diameter D [2], since in both cases the unconfined chain is ideal. In the melt case the two-body interactions are screened out. **As** shown by Brochard and de Gennes [2], this phenomena leads to the following results: as long as  $D \gg aN^{1/4}$  the longitudinal dimension  $R_{\parallel}$  of the chain is unperturbed ( $R_{\parallel} \cong R_0$ ). For  $D \ll aN^{1/4}$ , the size  $R_{\parallel}$  increases as  $R_{\parallel} \cong Na^3/D^2$ .

It is hoped that future experiments (e.g. in ternary solutions: lipid + water + polymer) and computer simulations will allow a test of the predictions presented in this work.

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