

Hollow-Core Dendrimers Revisited

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In revisiting the original argument of de Gennes and Hervet [J. Phys. (Paris) **44**, L351 (1983)] leading to “hollow-core” dendrimers, we show that a self-consistent application of their model leads to the “filled-core” model first elucidated by Lescanec and Muthukumar [Macromolecules **23**, 2280 (1990)]. The monomer density falls off parabolically from the center of the dendrimer, and the tips are distributed throughout the molecule.

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Dendrimers have received much attention since their invention [1], and today offer single-molecule smart materials for temperature-gated catalysis [2], and drug delivery [3,4]. The location and profusion of functional tips, with a distinctive, selective core cavity provide many avenues for harnessing self-assembled structures [5,6].

Much of the initial interest in dendrimers focused on their application as drug delivery agents, prompted by the “hollow-core” model of de Gennes and Hervet [7] [see Fig. 1(a)]. Based on an analysis of the Edwards self-consistent field model, it was shown that for G generations of trifunctional junctions joined by flexible polymer in a good solvent, the chain tips spontaneously segregate to the spherical edge of the molecule, creating a dense shell enclosing a diffuse core that could be filled with small molecules.

Shortly after this prediction, in dynamic simulations on dendrimers with very short spacers, Lescanec and Muthukumar [8] found a very different behavior, that of the “filled core.” The chain tips were not segregated to an extremal zone but were distributed throughout the molecule. Very near the core of the dendrimer, a usable region of lower polymer density exists at some generations. This physical core region little resembles the one originally predicted and is suited mainly for steric-controlled catalysis [9–11]. All of the theoretical and simulation approaches to the problem uniformly support the filled-core picture, with the single exception of the initial work in Ref. [7]. Even still, the experimental picture is not clear [12], at least as far as the distribution of chain tips is concerned.

The clash between the filled- and hollow-core pictures has not impeded the development of dendrimers for specific applications. The differing predictions, after all, operate in different regimes (with the hollow-core model depending on flexible Gaussian spacers, while the filled-core simulations modeled spacers only one or two monomers in length). A large step toward resolving the controversy was taken by Boris and Rubinstein [13], who applied a numerical self-consistent field (SCF) method to the flexible-spacer problem and found that high- G den-

drimers are densest in their cores, with distributed tips. This calculation began a shift in the application of SCF methods from collective many-chain physics [14,15] to single-chain physics [16,17]. The only weakness, and it is certainly not a crippling one, of Ref. [13] is that it is not directly comparable to that in Ref. [7], as it rests on a different set of approximations.

We propose here to follow the de Gennes model, correcting its major flaw, and show that the properly predicted dendrimer conformation in *all models* is that of the filled-core. The hollow-core prediction in Ref. [7] rests upon a reasonable, through incorrect, assumption that a single conformation of the dendrimer dominates all statistical averages in the thermodynamic limit. Fixing the flaw fills in the dendrimer core.

The essential problem is to determine the consequence of the connectivity of the dendrimer, which naturally tends to contract the overall spread of the molecule, and the consequence of hard-core excluded-volume interactions between the monomers. To be specific, let the dendrimer consist of flexible polymer spacers composed of N spheres of diameter $a = 1$. As in Fig. 1, the dendrimer has a regularly branched structure, with 2^G free tips. For each

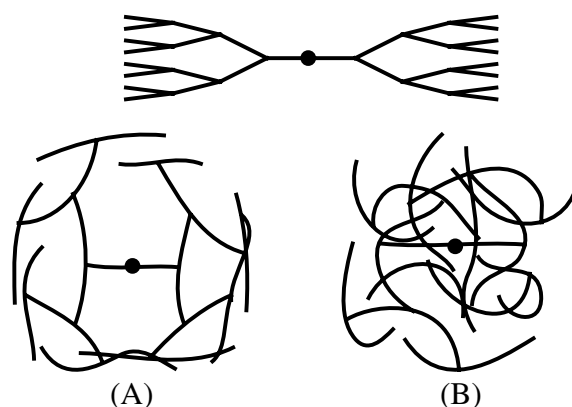


FIG. 1. (a) The hollow core conformation of a G_4 dendrimer polymer. (b) The filled core conformation. The central monomer of the dendrimer is marked by the filled circle.

monomer in the molecule let the chemical index, n , be the fewest number of monomers connecting the given monomer to any of the tips. Thus, each of the free ends has $n = 0$, and the central monomer on the dendrimer has $n = GN$. Each monomer with the same n is statistically equivalent. Following Ref. [7], we consider each of the flexible strands to be essentially Gaussian, but interacting with a position-dependent concentration of monomers within the chain. The local concentration of monomers biases these random walks to seek lower monomer concentrations, thus swelling the overall size of the dendrimer. We take a second virial approach to the excluded-volume interactions:

$$U(r) = v_o \phi(r), \quad (1)$$

where $U(r)$ is the free energy required to insert a monomer at the position r in the dendrimer, while $\phi(r)$ is the average volume fraction at the position r given that the center monomer on the dendrimer is held at $r = 0$, and v_o is related to the excluded volume. Unless $U(r) = \text{const}$, each strand in the dendrimer is not an ideal Gaussian random walk but rather displays fluctuations around a systematically varying path $R(n) = r(n) + \delta(n)$. For the moment, we focus on the mean path, $r(n)$, for the strand, and ignore the fluctuations, $\delta(n)$. Let the m th monomer on a linear substrand have its mean position in the dendrimer be $r(m)$. This monomer is subject to two average tensile forces from the chain segments on either side, these forces being in magnitude approximately

$$F_{\text{out}} = \left. \frac{dr}{dm} \right|_{r(m-1)} \quad (2)$$

and

$$F_{\text{in}} = - \left. \frac{dr}{dm} \right|_{r(m+1)}. \quad (3)$$

The difference in these tensions must be balanced by a gradient in the monomer potential

$$\frac{d^2 r}{dm^2} = \nabla U(r), \quad (4)$$

the continuum limit linear response force balance equation. Equation (4) holds at each nonjunction monomer in the dendrimer, supplemented by $\left. \frac{dr}{dm} \right|_{m=0} = 0$ holding for each of the 2^G chain tips.

The junction points have two statistically equivalent incoming chains leading outward to the free tips of the dendrimer and one chain leading inward toward the central monomer. Mechanical equilibrium then requires

$$\left. \frac{dr}{dm} \right|_{r(m+1)} = 2 \left. \frac{dr}{dm} \right|_{r(m-1)} \quad (5)$$

so that the chain extension is discontinuous at the junctions.

This set of equations enforcing mechanical equilibrium on each chain segment and junction actually arises from a variational principle on the overall dendrimer free energy [18]. Indeed, mechanical equilibrium is essentially enforced through

$$- \frac{d}{dn} \left[f(n) \frac{dr}{dn} \right] + f(n) \nabla U(r) = 0, \quad (6)$$

where the weighting function $f(n)$ imposes the doubling of the chain tension at each of the junction points. We let

$$\begin{aligned} f(n) &= 2^G \quad \text{when } 0 < n < N, \\ &\vdots \\ f(n) &= 2 \quad \text{when } (G-1)N < n < GN. \end{aligned} \quad (7)$$

Thus, $f(n)$ counts the number of statistically equivalent monomers at each n . A further approximation can be made, as in Ref. [7],

$$f(n) = 2^G 2^{(1-G)n/(GN)}, \quad (9)$$

smoothing out the discontinuities of $f(n)$.

Equation (6) is thus generated as the classical equation of motion for the action

$$S[r(n)] = \int_0^{GN} dn f(n) \left[\frac{1}{2} \left| \frac{dz}{dn} \right|^2 + U[r(n)] \right]. \quad (10)$$

$S[r(n)]$ is the Edwards single-chain free energy, and a polymer obeying Eq. (6) represents the saddle-point approximation to the full partition function. If the value of this saddle-point free energy evaluated self-consistently is much larger than unity, then $\delta(n)$ above may be safely ignored. This approach has been successful in determining the microsegregation of dendrimer-dendrimer copolymers [19,20] and the behavior of dendrimer polymer brushes [18].

Thus, the heart of the matter is the determination of the self-consistent monomer potential, or in light of Eq. (1), simply the monomer density as a function of distance from the core. The calculation of Ref. [7] starts with the force balance in Eq. (6) and further assumes that *there is a unique "typical" trajectory $r(n)$ which dominates all statistical averages*, and from which the self-consistent $U(r)$ can be determined. This program of calculation was highly successful in determining the properties of a strongly absorbed polymer layer [21], and rests on the physically reasonable assumption that a unique ground-state, self-consistent trajectory can be found for the action $S[r]$. If a degeneracy develops, then more of these monotonic trajectories have to be considered in the statistical averages. Up to the assumption that the ground state is unique, Hervet and de Gennes were led directly to the hollow-core scenario, and this model still carries significant weight as an *a priori* prediction of flexible dendrimer conformations.

The reality, as below, is that there are *infinitely many* degenerate trajectories for the true self-consistent potential, $U(r)$. The situation mirrors that between the Alexander polymer brush and the parabolic brush of Refs. [22,23]. Following the development for the linear polymer brush, let us suppose that the correct potential is harmonic (so that each trajectory will arrive at $r = 0$ after the proper “time” = GN has been played out):

$$U(r) \equiv \frac{\omega^2}{2N^2}(R^2 - r^2), \quad (11)$$

where we introduce the dimensionless angular frequency of the oscillator ω and the overall size of the dendrimer R . Using a dimensionless measure of “time” (i.e., chemical index), $\mu = n/N$, the equation of motion for the polymer trajectory becomes [Eq. (6) with Eqs. (9)–(11)]

$$\frac{d^2r}{d\mu^2} - b \frac{dr}{d\mu} + \omega^2 r(\mu) = 0, \quad (12)$$

the equation for a curiously damped linear oscillator. In this case, the drag coefficient $b = \log 2(1 - 1/G)$ serves to *further accelerate* the motion. The fact that Eq. (11) represents an equal-time potential is easy to show. Subject to the initial conditions, $r(0) = r_o$ and $\frac{dr}{d\mu}|_0 = 0$, we have

$$r(\mu) = r_o e^{b\mu/2} \left[\cosh \frac{\mu\nu}{2} - \frac{b}{\nu} \sinh \frac{\mu\nu}{2} \right], \quad (13)$$

where we have introduced the discriminant of Eq. (12), $\nu^2 = b^2 - 4\omega^2$. The equal-time property is maintained when $r(\mu = G) = 0$ for any choice of r_o , which for this linear equation and solution is therefore $b = \nu \cot G\nu/2$, which may be nearly analytically inverted [24]. The resulting $\omega(G)$ is shown in Fig. 2. $S[r]$ evaluated for Eq. (13) with $\omega(G)$ as in Fig. 2 has the single-chain free energy independent of r_o . Thus, *chains with each and every $0 < r_o < R$ contribute to all statistical averages*, filling in the dendrimer core.

The physical size of the dendrimer can easily be determined once $\omega(G)$ is known. The maximum value taken by the monomer volume fraction ϕ_o satisfies $\phi_o = b \frac{\omega^2 R^2}{2N^2}$. As all of the monomers on the chain are to be accounted for, the overall size of the dendrimer is

$$R = \left| \frac{15(2^G - 1)}{2\pi\omega} \right|^{1/5} \nu_o^{1/5} N^{3/5}. \quad (14)$$

The G dependence of the prefactor in Eq. (14) is shown in the inset to Fig. 2.

It would seem that the self-consistent potential is necessarily parabolic for all G , resulting in a parabolic *density* profile for the dendrimer molecule, a novel prediction agreeing well with numerical studies [11,13]. The proviso is that chain tips must exist in all regions $0 < r < R$, and the overall saddle-point free energy must be large. If self-consistency requires that ends be excluded

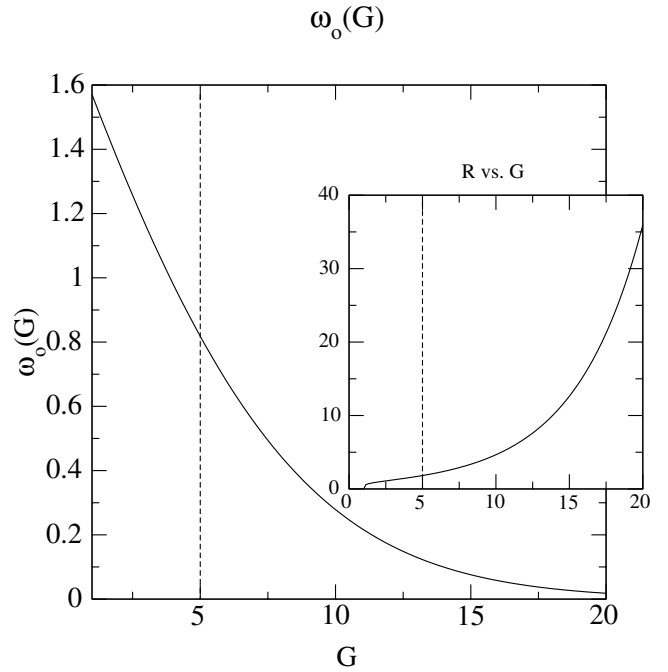


FIG. 2. $\omega(G)$ for $G = 1, \dots, 20$. The inset is the dimensionless size of the dendrimer, up to a prefactor scaling as $N^{3/5}b^{1/5}$. $G \geq 5$ (marked as the vertical dashed line) is the physical region of the calculation for which the end density is non-negative at all r .

from some zone (“dead” zones, or end-exclusion zones), then another self-consistent potential must be sought [25]. We have carried this out numerically and show in Fig. 3 that as long as $G \geq 5$ the required end distribution is non-negative. Also shown in Fig. 3 is the end distribution calculated in a Scheutjens and Fler lattice self-consistent calculation for $G = 10$ dendrimers with $N = 60$ flexible spacers, and the inset is the overall monomer density for a $G = 8$ dendrimer with highly stretched, short spacers, $N = 4$. The small dip in monomer density at the core of the molecule is characteristic of small-spacer, high generation dendrimers as in Ref. [11], explicitly *not the limit considered by Ref. [7]* or this work.

Thus, for large G , and long enough N for Gaussian statistics to hold for individual chain lengths, the cross section density profile for flexible dendrimer molecules is parabolic and achieves its maximum value at the center, decreasing toward the edge of the dendrimer. Our conclusions are drawn almost completely without resorting to numerical work.

We have appropriately generalized the original de Gennes and Hervet hollow-core dendrimer model and come to the conclusion that their model analyzed consistently agrees with the simulations of Lescanec and Muthukumar. This argument can now be placed to rest, or rather back into the context of *how to force* the technologically intriguing Alexander-like packing of chain ends. This is not a new conclusion [8,13], but now it

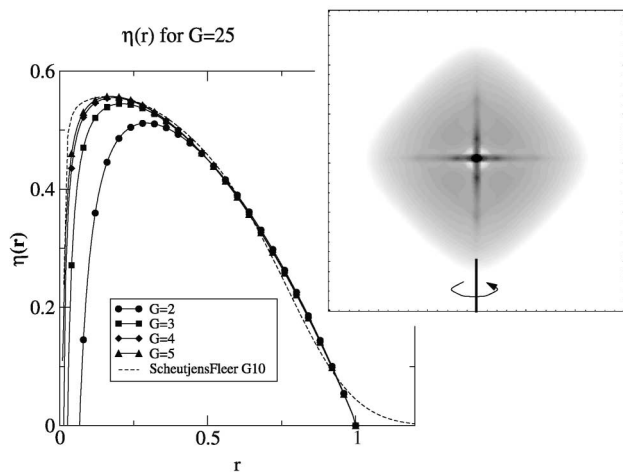


FIG. 3. The distribution of free ends for a dendrimer of $G = 2-5$ are plotted. Only at $G = 5$ and higher does the end-density profile become non-negative at all r . Thus, for $G \geq 5$ the concentration profiles are parabolic. The end distribution for $G = 10$ dendrimers with flexible $N = 60$ spacers has been calculated in a lattice self-consistent field and agrees well with the present model. Shown in the inset is the density distribution for a $G = 8$ dendrimer with $N = 4$ spacers, again as calculated in the self-consistent lattice model. The axis of revolution for the full three-dimensional structure is shown and compares well with the characteristics of short-spacer, high generation dendrimers as in Ref. [11]. Only at high N does the parabolic picture hold, precisely the limit originally conceived in Ref. [7].

appears that *all* theoretical notions about flexible dendrimers lead to the same filled-core conclusion.

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