Molecular Weight Distributions of Imperfect Dendrimers

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ABSTRACT: We consider the molecular weight distribution of dendrimer macromolecules when some segments do not survive to produce "offspring". The Fourier transform of the molecular weight distribution, and therefore the number- and weight-average molecular weights, can be computed using numerically exact recursion formulas. We examine a few special cases and find, for example, that very narrow molecular weight distributions are obtainable by making the molecule as perfect as possible in the early generations and that it is theoretically possible to construct large dendrimers with arbitrary molecular weights different from the values expected for perfect dendrimers, that nevertheless have effectively monodisperse molecular weight distributions.

1. Introduction

Dendrimers[1-6] are regularly branched, treelike macromolecules. Obviously, perfectly formed dendrimers, in which the number of segments in one generation is an exact multiple of the number of segments in the previous generation, have molecular weights proportional to R^k, where k is the total number of generations, and have monodisperse molecular weight distributions.

It has always been assumed that synthetic dendrimers are sufficiently perfect that questions of molecular weight distribution have not been raised. However, precise mass measurements of the higher generation poly(amido amine) (PAMAM) dendrimers indicate that molecular weights increase by factors less that R from one generation to the next, which obviously indicates that the dendrimers are less than perfect.[7] This naturally leads to questions of molecular weight distribution. The question is of fundamental importance since excessive polydispersities could compromise the use of these molecules as molecular weight standards. On the other hand, a good understanding of the problem might permit precise molecular weight control and the ability to obtain narrow molecular weight distributions at values of the molecular weight intermediate between those values provided by perfect dendrimers.

We assume that a dendrimer begins with a single core segment in generation 0. We let N_j designate the population of segments in generation j, so that $N_0 = 1$. We then assume that, in the addition of generation $j+1$, each of the N_j segments in generation j dies out with probability $1-p_j$ and that each surviving segment receives R_j daughter segments. Then, generally, each of the N_j's, for $j > 0$, will not be monodisperse. We show below that it is possible to compute, in the form of exact recursion formulas, the Fourier transform of the distribution function of the total number of segments in the molecule. The Fourier transform either can be transformed numerically to obtain the distribution function or can be expanded in series to provide exact recursion formulas for the lower moments of the distribution, which of course provides the number-average and weight-average molecular weights.

2. General Formalism

Let generation j contain N_j segments. Each of these segments survives or dies out with probability p_j and $1-p_j$, respectively. Then the number surviving, m, is given by the binomial distribution:

$$\binom{N_j}{m}(1-p_j)^{(N_j-m)}p_j^{\,m}$$

where $\binom{n}{r}$ represents the usual combinational factor $n!/(n-r)!r!$. Each of these m surviving segments then receives R_j daughter segments in the creation of generation $j+1$, and $N_{j+1} = mR_j$ is the number of segments present in the $(j+1)$th generation. Therefore define

$$G(N_j,N_{j+1}) = \binom{N_j}{N_{j+1}/R_j}(1-p_j)^{(N_j-N_{j+1}/R_j)}p_j^{\,(N_{j+1}/R_j)} \quad (1a)$$

whenever $N_{j+1} \bmod R_j = 0$ and $0 \le N_{j+1} \le R_jN_j$, and

$$G(N_j,N_{j+1}) = 0 \quad (1b)$$

otherwise. $G(N_j,N_{j+1})$ represents the probability that generation $j+1$ contains N_{j+1} segments given that generation j contains N_j segments. Then, the probability that the molecule contains a total of N segments after being built up to k generations is

$$P_T(N) = \sum_{N_1}\sum_{N_2}\cdots\sum_{N_k}\delta\Big(\sum_{j=0}^{k}N_j - N\Big)\prod_{j=1}^{k}G(N_{j-1},N_j) \quad (2)$$

where the subscript "T" indicates the distribution for the total molecule. Hereafter, we assume the index k always refers to the terminal generation. We introduce the Fourier representation of the Dirac δ function:

$$P_T(N) = \int_{-\infty}^{+\infty}dq\, e^{-iqN}e^{iqN_0}\sum_{N_1}\sum_{N_2}\cdots\sum_{N_k}\prod_{j=1}^{k}[e^{iqN_j}G(N_{j-1},N_j)] \quad (3)$$

(In this step and in what follows, we neglect multiplicative constants and remedy this neglect with a renormalization at the end.)

It proves possible to evaluate eq 3 through a repeated application of the binomial theorem. We begin by defining recursively a set of functions $U_0, U_1, \ldots, U_k$ as follows:

$$U_0 = 1 \quad (4)$$

$$U_j = p_{k-j}(e^{iq}U_{j-1})^{R_{k-j}} + 1 - p_{k-j} \quad (5)$$

Then we assert the following:

$$P_T(N) = \int_{-\infty}^{+\infty}dq\, e^{-iqN}e^{iqN_0}\sum_{N_1}\sum_{N_2}\cdots\sum_{N_{k-m}}\prod_{j=1}^{k-m}[e^{iqN_j}G(N_{j-1},N_j)]U_m^{\,N_{k-m}} \quad (6)$$

Equation 6 can be proven by mathematical induction. First note that the $m = 0$ form of eq 6 is equivalent to eq 3 since $U_0 = 1$. Then, the $m+1$ form of eq 6 can be obtained from

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the m form by executing the $\sum_{N_{k-m}}$ sum:

$$\sum_{N_{k-m}} G(N_{k-m-1},N_{k-m})\, e^{iqN_{k-m}} U_m^{N_{k-m}} = (U_{m+1})^{N_{k-m-1}} \quad (7)$$

(Equation 7 follows directly from the binomial theorem.) Finally, setting $m = k$ in eq 6 yields

$$P_T(N) = \int_{-\infty}^{+\infty} dq\, e^{-iqN} e^{iqN_0} U_k^{N_0} \quad (8)$$

Therefore, $C_T(q)$, where

$$C_T(q) = e^{iq} U_k(q) \quad (9)$$

is the Fourier transform of $P_T(N)$, since we are assuming that $N_0 = 1$. This Fourier transform may be computed directly, using eqs 4 and 5.

Additionally, it is well-known that $C_T(q)$ is a generating function for the moments of the distribution function. Ultimately, this implies that if we expand to second order in q:

$$C_T = Q_0 + iqQ_1 - \frac{Q_2}{2}q^2 + O(q^3) \quad (10)$$

then the number- and weight-average populations are given exactly by:

$$\langle N\rangle_n = Q_1/Q_0 \quad (11)$$

$$\langle N\rangle_w = Q_2/Q_1 \quad (12)$$

Additionally, all higher molecular weight averages are given by similar ratios. Assume that U_j is given to second order in q by

$$U_j = \alpha_j + i\beta_j q - \frac{\gamma_j}{2}q^2 \quad (13)$$

Inserting this into eq 5 yields the following recursion formulas:

$$\alpha_j = 1 \text{ for all } j \quad (14)$$

$$\beta_{j+1} = S_{k-j-1}(1 + \beta_j);\ \ \beta_0 = 0 \quad (15)$$

$$\gamma_{j+1} = S_{k-j-1}[\gamma_j - \beta_j^2 + 2R_{k-j-1}\beta_j + R_{k-j-1} + R_{k-j-1}\beta_j^2];\ \ \gamma_0 = 0 \quad (16)$$

where $S_i = R_i p_i$.

The number- and weight-average molecular weights are given as:

$$\langle N\rangle_n = (1 + \beta_k) \quad (17)$$

$$\langle N\rangle_w = \langle N\rangle_n + \frac{(\gamma_k - \beta_k^2)}{(1 + \beta_k)} \quad (18)$$

A simpler version of the recursion formulas is obtained if we set $w_j = \gamma_j - \beta_j^2$. Then we obtain

$$w_{j+1} = S_{k-j-1}[w_j + (R_{k-j-1} - S_{k-j-1})(1 + \beta_j)^2] \quad (19)$$

and

$$\langle N\rangle_w = \langle N\rangle_n + \frac{w_k}{1 + \beta_k} \quad (20)$$

3. Special Cases

An interesting special case is obtained by assuming that all the p_j's are equal. However, since actual dendrimers are undoubtedly perfect, or at least nearly so, in the initial generations, we chose to examine a slightly more general special case, namely, one for which $p_0 = p_1 = \ldots = p_{n-1} = 1$ and $p_n = p_{n+1} = \ldots = p_{k-1} = p$. We also assume that $R_0 = R_1 = \ldots = R_{k-1} \equiv R$ and adapt the notation $S \equiv pR$.

With these assumptions, we obtain

$$\beta_j = \sum_{l=1}^{j} S^l \qquad if\ j \le k-n \quad (21)$$

$$\beta_j = \sum_{i=1}^{j-k+n-1} R^i + R^{j-k+n}\sum_{l=0}^{k-n} S^l \qquad if\ j > k-n \quad (22)$$

and

$$\beta_k = \sum_{i=1}^{n-1} R^i + R^n \sum_{l=0}^{k-n} S^l \quad (23)$$

Furthermore, we obtain

$$w_j = (R - S)SZ_{j-1}(S) \qquad if\ j \le k-n \quad (24)$$

where $Z_{j-1}(S)$ represents one of the polynomials defined in the appendix. Equation 24 follows directly from eqs 19, 21, and A4 by mathematical induction. We also obtain

$$w_j = R^{j-k+n} w_{k-n} \qquad if\ j > k-n \quad (25)$$

The number-average molecular weight becomes

$$\langle N\rangle_n = \frac{R^n - 1}{R - 1} + R^n\left(\frac{S^{k-n+1} - 1}{S - 1}\right) \quad (26)$$

where the first term is obviously the contribution from the $n - 1$ perfect generations. For the weight-average molecular weight, we obtain

$$\langle N\rangle_w = \langle N\rangle_n + \frac{R^{n+1}S(1-p)Z_{k-n-1}(S)}{\langle N\rangle_n} \quad (27)$$

In this particular case, we can obviously write

$$U_k = \exp[iq\sum_{l=1}^{n} R^l](U_{k-n})^{R^n} \quad (28)$$

Since its Fourier transform is written as a product of a phase factor and a function taken to a large power, we conclude that P_T can be well represented by a Gaussian distribution whenever R^n, the population of the last perfect generation, is large.

It is interesting to evaluate the above averages in the $k \to \infty$ limit. These have two forms, depending on whether $S < 1$ or $S > 1$. First, for $S > 1$, we obtain

$$\langle N\rangle_n \to \frac{R^n S^{k+1-n}}{(S-1)} \qquad as\ k \to \infty \quad (29)$$

$$\frac{\langle N\rangle_w}{\langle N\rangle_n} - 1 \to \frac{R^{1-n}(1-p)}{(S-1)} \qquad as\ k \to \infty \quad (30)$$

If $S < 1$:

$$\langle N\rangle_n \to \frac{(R^n - 1)}{(R-1)} + \frac{R^n}{(1-S)} \qquad as\ k \to \infty \quad (31)$$

$$\frac{\langle N\rangle_w}{\langle N\rangle_n} - 1 \to \frac{R^{n+1}S(1-p)}{(1-S)^3\langle N\rangle_n} \qquad as\ k \to \infty \quad (32)$$

These results imply a number of things. Contrary to what one might think, the polydispersity of this constant p model generally does not increase without limit as more generations are added. Rather it levels off to a specific asymptotic limit except when $S = 1$. When $S > 1$, one minimizes the polydispersity either by keeping the molecule perfect for as long as possible (making the population of the last perfect generation, R^n, very large) or by making p near 1, which keeps all generations nearly perfect. When $S < 1$, one minimizes the polydispersity by making S small,

meaning that the molecule completely dies out shortly after the last perfect generation. We also observe that the molecular weight distribution is Gaussian if the population of the last perfect generation is much larger than 1.

4. Minimum Polydispersity at Any Given Molecular Weight

The use of dendrimer macromolecules as molecular weight standards has been suggested.[3] Assuming it is possible to construct perfect dendrimers, then we are able to obtain molecules of monodisperse molecular weight, but only at certain discrete molecular weights: $1, 1 + R, 1 + R + R^2$, etc. The ability to construct imperfect dendrimers through control of the probabilities $p_0, p_1, p_2, \ldots$, etc., presents the advantage of obtaining molecular weights of any desired value, albeit with polydispersity. This suggests one more problem: Determine the values of $p_0, p_1, p_2, \ldots$ that minimize the polydispersity ratio $\langle N\rangle_w/\langle N\rangle_n$ subject to the constraint that $\langle N\rangle_n$ is fixed. This lets us compute the theoretical lower bound to the polydispersity at any given value of $\langle N\rangle_n$. We have examined this problem by the minimization procedure known as simulated annealing[8] and have demonstrated that the sequence of p_j's that solves this problem is the one that satisfies $p_0 = p_1 = p_2 = \ldots p_{k-2} = 1$; i.e., to obtain the lowest possible polydispersity, the molecule must be perfect through generations $k - 1$. (Given the results of the previous section, this result is not surprising.) Then the final probability p_{k-1} is selected to produce the desired molecular weight. The results of the previous section apply directly, as long as we set $n = k - 1$. Then we obtain

$$\langle N\rangle_n = \frac{R^k - 1}{R - 1} + pR^k \tag{33}$$

The first term on the right accounts for the populations of the $k - 1$ perfect generations, and the second term, for the last, imperfect generation. As p changes from 0 to 1 we progress from a completely empty k generation to a completely full one. The polydispersity index proves to be

$$\frac{\langle N\rangle_w}{\langle N\rangle_n} - 1 = \frac{R^k p(1-p)}{\langle N\rangle_n^2} \tag{34}$$

This expression is the lowest possible polydispersity achievable for a given $\langle N\rangle_n$ and occurs under the conditions laid out above. It is 0 in either of the two limits $p \to 0$ or $p \to 1$, as expected, and since $\langle N\rangle_n \sim R^k$, it also predicts that the polydispersity index is approximately inversely proportional to the total molecular weight.

We conclude that, in principle, large dendrimers of arbitrary molecular weight can be formed with an effectively monodisperse molecular weight distribution. It only suffices to grow the dendrimer perfectly through all but the last generation and then short the last generation by precisely the amount needed to yield the desired molecular weight. If the resulting dendrimers are large, then they will be effectively monodisperse, having polydispersities inversely proportional to the total number of segments.

5. Summary and Conclusions

We have shown how to compute the Fourier transform of the molecular weight distribution and thereby the number- and weight-average molecular weights, of imperfect dendrimers, i.e., dendrimers for which reaction conditions prevent specific generations from adding completely. The formalism takes the form of numerically exact recursion formulas, eqs 4, 5, and 9 for the Fourier transform of the molecular weight distribution and eqs 15, 17, 19, and 20 for the number- and weight-average molecular weights. We have also specialized this argument to the case in which the molecule forms perfectly in the first few generations and then has a constant survival probability in all later generations.

From these calculations, we can draw a few conclusions:

1. Polydispersities may be suppressed by keeping the molecule as perfect as possible in all generations (e.g., keeping p near 1 in eq 30) and, most especially, by keeping it perfect in the early generations (e.g., making n large in eq 30).

2. On the other hand, relatively large polydispersities may be obtained either by introducing imperfections in the early generations or by adjusting the survival probability so that successive generations contain, on average, the same number of segments, i.e., by making S near 1 in eqs 30 or 32.

3. In the case for which the survival probability is constant in later generations, the polydispersity tends to a well-defined constant, neither increasing nor decreasing indefinitely (except, of course, when $S = 1$).

4. The molecular weight distribution is Gaussian if the molecule is sufficiently perfect in the initial generations. It suffices that the last perfect generation have a segment population much greater than unity.

5. The lowest possible polydispersity at a given arbitrary value of the number-average molecular weight is achieved by making all generations but the last one perfect and by adjusting the survival probability of the last generation to yield the desired number-average molecular weight. The ensuing polydispersity index is inversely proportional to the molecular weight for large dendrimers. Therefore, it is theoretically possible to prepare large dendrimers having arbitrary molecular weights, i.e., with molecular weights apart from those values expected for perfect dendrimers, and yet that are effectively monodisperse.

Appendix

In this appendix, we define a set of polynomials and explore some of their properties. Consider the polynomials

$$Z_0(S) = 1$$

$$Z_1(S) = 1 + 3S + S^2$$

$$Z_2(S) = 1 + 3S + 6S^2 + 3S^3 + S^4$$

$$Z_3(S) = 1 + 3S + 6S^2 + 10S^3 + 6S^4 + 3S^5 + S^6$$

etc.

In general:

$$Z_j = \sum_{l=0}^{2j} C_{jl} S^l \tag{A1}$$

with

$$C_{jl} = (l + 1)(l + 2)/2 \qquad \text{if } l \le j \tag{A2}$$

and

$$C_{jl} = C_{j,2j-l} \qquad \text{if } l > j \tag{A3}$$

We now prove this expression:

$$\left(\sum_{l=0}^{j} S^l\right)^2 + SZ_{j-1}(S) = Z_j(S) \tag{A4}$$

Observe that the coefficients of

$$\left(\sum_{l=0}^{j} S^l\right)^2$$

define a vector of order $(2j + 1)$:

$$(1, 2, 3, ..., l + 1, ..., j, j + 1, j, ..., 3, 2, 1)$$

The central element of this vector is $j + 1$; entries to the left of center have the general form $l + 1$, and entries to the right of center are assigned by symmetry about the center. The coefficients of SZ_{j-1} define a similar centrosymmetric vector:

$$(0, 1, 3, ..., l(l + 1)/2, ..., j(j + 1)/2, ...)$$

The central element here is $j(j + 1)/2$, and entries left of center are $l(l + 1)/2$. So the sum of these two vectors is also centrosymmetric, with the left-side entries equal to $(l + 1) + l(l + 1)/2 = (l + 1)(l + 2)/2$. But this is precisely the vector of coefficients of Z_j, which concludes the proof.

At large j, $Z_j(S)$ is dominated either by the low-order or the high-order terms in S, depending on whether $S < 1$ or $S > 1$. Therefore, in the large j limit we obtain

$$Z_j \simeq S^{2j}\sum_{l=0}^{\infty}\frac{(l + 1)(l + 2)}{2}\left(\frac{1}{S}\right)^l = S^{2j}\left(\frac{S}{S-1}\right)^3 \quad \text{if } S > 1 \quad \text{(A5)}$$

$$Z_j \simeq \sum_{l=0}^{\infty}\frac{(l + 1)(l + 2)}{2}S^l = (1 - S)^{-3} \quad \text{if } S < 1 \quad \text{(A6)}$$

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Noted Added in Proof: Kallos et al.[9] have presented mass spectroscopic data on PAMAM dendrimers, including some discussion of molecular weight distributions.

References and Notes

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