# NOTES

## Comments on "An Analytical Solution to Tung's Axial Dispersion Equation. Applications in Gel Permeation Chromatography"

We wish to acknowledge the existence of an error in our earlier paper and discuss some of its implications. In addition, we wish to draw attention to some errors and statements made in the paper published under the above title[1] which require further clarification.

The general statistical shape function known as the Gram-Charlier series,[2-4] originally proposed by Provder and Rosen[5] to describe instrument spreading in gel permeation chromatography (GPC), has the form

$$G(v - y) = \phi(v - y) + \sum_{n=3}^{\infty} \left\{ (-1)^n \left( \frac{A_n}{n!} \right) \mu_2^{n/2} \phi^n(v - y) \right\} \tag{1}$$

where

$$\phi(v - y) = (1/2\pi\mu_2)^{1/2} \exp \left[ - \frac{(v - y)^2}{2\mu_2} \right], \tag{2}$$

$\phi^n(v - y)$ are the $n$th order derivatives of $\phi(v - y)$ with respect to $v$, and

$$A_3 = \mu_3/(\mu_2^{3/2}) \tag{3}$$

$$A_4 = (\mu_4/\mu_2^2) - 3. \tag{4}$$

The coefficients $A_3$ and $A_4$ are measures of skewness and kurtosis or flatness, respectively. Practical considerations require the truncation of the Gram-Charlier series to the form known as the Edgeworth series,[6] where

$$A_5 = 0 \tag{5}$$

$$A_6 = 10A_3^2 \tag{6}$$

$$A_n = 0 \text{ for } n \geq 7. \tag{7}$$

Often the series is further truncated[7] by setting $A_6 = 0$.

In general, the instrumental spreading parameters $\mu_2$, $\mu_3$, and $\mu_4$ are functions of the elution volume. As pointed out by Vladimiroff,[8] however, the functional dependence of the $\mu_n$'s in eq. (1) is on $y$, not on $v$ as previously indicated.[7] This leads to several implications. The first implication is that the definition of $\mu_n$'s given[7] as the $n$th order moments about $y$ of the instrumental spreading function is consistent regardless whether the $\mu_n$'s are constant or a function of elution volume:

$$\mu_n(y) = \int_{-\infty}^{\infty} (v - y)^n G(v - y) dv \qquad n = 2,3,4. \tag{8}$$

The second implication arises in the relationships among the moments about the means of the corrected normalized chromatogram $W(y)$ and the uncorrected normalized chromatogram $F(v)$ obtained with the aid of Tung's equation:

$$F(v) = \int_{-\infty}^{\infty} G(v - y) W(y) dy. \tag{9}$$

When the $\mu_n$'s are independent of $y$, then the relationships among the zero to fourth moments of $F(v)$ and $W(y)$ about their means are as indicated in ref. 7.   When the $\mu_n$'s are a function of $y$, however, the relationships indicated in ref. 7, in general, did not hold. However, indeed, it is easy to show that both the zero and first moments are preserved when $G(v - y)$ is defined by eqs. (1) and (2):

$$\int_{-\infty}^{\infty} F(v)dv = \int_{-\infty}^{\infty} W(y)dy \tag{10}$$

$$\int_{-\infty}^{\infty} vF(v)dv = \int_{-\infty}^{\infty} yW(y)dy. \tag{11}$$

In the paper of the above title,[1] Hamielec defines $A_n$ to be functions of $\mu_n$ "the $n$th order moments about the mean eluent volume, $\mu_1$, of the observed GPC chromatogram normalized."   This is incorrect since the correct definition, as given by eq. (8), can be derived as indicated in ref. 7.   This definition also is incorrect on a physical basis, since the $\mu_n$ determined according to Hamielec's definition would contain contributions from the natural skewness, flatness, and dispersion associated with the molecular weight distribution of the standards as well as the corresponding contributions associated with instrumental spreading effects.

As Hamielec pointed out, however, there was a small error in the development of some of the equations in the preliminary version of ref. 5 which appeared in the *ACS Preprints.*[9]   However, this error was corrected, and all the corrected equations can be found in the final paper.[5]   Although noting an error in the formalism in the preliminary version, Hamielec used values of $\mu_2$, $\mu_3$, and $\mu_4$ from Table II of ref. 9 for sample 184–212 to illustrate the difficulty of choosing the proper instrument spreading function for use with Tung's equation for the purpose of correcting the differential molecular weight distribution (DMWD).   Due to the error in the formalism, the values used are incorrect and invalidate his numerical examples.   However, the point Hamielec raised is a valid one and requires further amplification and clarification.

As indicated by Hamielec, negative corrections for values of $\bar{M}_4(t)$ or higher molecular weight averages require the corrected DMWD to have negative heights.   Clearly, this is an unreasonable physical situation, and the shape function giving these results is not valid.   The truncated form of the general shape function, defined by eqs. (3) through (7), was dictated by the fact that in practice only accurate values of $\bar{M}_n$, $\bar{M}_w$, and $[\eta]$ can be obtained.   If sufficiently accurate, higher average molecular weights could be determined, the higher-order coefficients $A_n$, $n \geq 7$, could be obtained.   Then, the higher average molecular weights as well as $\bar{M}_n$ and $\bar{M}_w$ could be satisfactorily corrected with eq. (12) below.   Equation (12) as well as eq. (13) were derived previously by the method of molecular weight averages[5]:

$$\frac{M_k(t)}{M_k(\infty)} = \exp\left[\frac{-(2K - 3)\mu_2 D_2^2}{2}\right] \left\{ \frac{1 + \sum_{n=3}^{\infty} \left(\frac{A_n}{n!}\right)[-(k - 2)D_2\mu_2^{1/2}]^n}{1 + \sum_{n=3}^{\infty} \left(\frac{A_n}{n!}\right)[-(K - 1)D_2\mu_2^{1/2}]^n} \right\} \tag{12}$$

$$\frac{[\eta](t)}{[\eta](\infty)} = \frac{\exp\left[\frac{-\epsilon^2\mu_2 D_2^2}{2}\right]}{\left\{1 + \sum_{n=3}^{\infty} \left(\frac{A_n}{n!}\right)[-\epsilon D_2\mu_2^{1/2}]^n\right\}} \tag{13}$$

where $k = 1, 2, 3$, and 4 correspond to the number-, weight-, $z$-, and $(z + 1)$-average molecular weights, respectively; $\epsilon$ is the exponent in the Mark-Houwink intrinsic viscosity-molecular weight expression; and $D_2$ is the local slope of the $\log_e M$ versus elution

volume calibration curve. Subsequently, the values of $\mu_2$, $\mu_3$, and $\mu_4$ due solely to instrumental spreading were determined by fitting these expressions to standards of known $(\bar{M}_n, \bar{M}_w, [\eta])$ values. If only $(\bar{M}_n, \bar{M}_w)$ or $(\bar{M}_n, [\eta])$ values are available, $\mu_2$ and $\mu_3$ were determined, and the $A_4$ coefficient was set equal to zero.

Since practical considerations limit the form of the general shape function to that defined by eqs. (1) through (7), let us examine the contributions of the terms in $A_3$, $A_4$, and $A_6$ to the overall value of the correction factor term, enclosed by braces in eq. (12), in order to assess the validity of the general shape function for correcting higher molecular weight averages. The correct values[5] of $\mu_2$, $\mu_3$, and $\mu_4$ for sample 182–212 obtained from $\{\bar{M}_n, \bar{M}_w\}$ are $\mu_2 = 0.629$, $\mu_3 = 2.52$, and $\mu_4 = 0$, and the values obtained from $(\bar{M}_n, \bar{M}_w, [\eta])$ are $\mu_2 = 0.629$, $\mu_3 = 2.52$, and $\mu_4 = 0.390$. Using these values in eq. (12) yields values of the correction factors shown in Table I. The column under $A_3$ lists the values of the correction factor obtained when the $A_4$ and $A_6$ terms are neglected. Similarly, the column of values under $A_3 + A_6$ are the correction factors obtained when the $A_4$ term is neglected, and the values under the column $A_3 + A_4 + A_6$ are the correction factors obtained when all terms through $A_6$ are evaluated.

### TABLE I
#### Values of the Correction Factor

$$\left\{\frac{1 + \sum_{n=3}^{\infty}\left(\frac{A_n}{n!}\right)[-(K-2)D_2\mu_2^{1/2}]^n}{1 + \sum_{n=3}^{\infty}\left(\frac{A_n}{n!}\right)[-(K-1)D_2\mu_2^{1/2}]^n}\right\}$$

for Sample 184–212

| $K$ | $A_3$ | $A_3 + A_6$ | $A_3 + A_6 + A_4$ |
|---|---|---|---|
| 1 | 1.049 | 1.051 | 1.049 |
| 2 | 1.052 | 1.051 | 1.053 |
| 3 | 1.570 | 1.393 | 1.455 |
| 4 | −1.831 | 0.965 | 0.964 |
| 5 | 0.154 | 0.251 | 0.290 |
| 6 | 0.418 | 0.204 | 0.185 |

Examination of the values in Table I indicates that the $A_4$ and $A_6$ terms hardly affect the correction factors for $\bar{M}_n(t)$ and $M_w(t)$. However, the correction factors for the higher molecular weight averages are significantly affected by the $A_6$ term and somewhat less by the $A_4$ term. The large difference in the correction factors obtained for $\bar{M}_4(t)$, $\bar{M}_5(t)$, and $\bar{M}_6(t)$ when only the $A_3$ term is evaluated compared to the values obtained when $A_6$ and the $A_4$ and $A_6$ terms are evaluated indicates that the instrument spreading function truncated at the $A_3$ term does not adequately correct higher molecular weight averages. The negative value obtained for the correction factor to $\bar{M}_4(t)$ when only the $A_3$ term is evaluated is physically unrealistic. Therefore, the instrument spreading function truncated at the $A_3$ term is not a valid function and should not be used to correct higher molecular weight averages. If at least the $A_6$ term ($A_6 = 10A_3^2$) is included, the instrument spreading function will be physically reasonable. At low values of $\mu_4$, the $A_4$ term does not significantly affect the value of the correction factor for the higher averages and, to a first approximation, can be neglected. However, to accurately estimate the correction factors to the higher molecular weight averages via eq. (12), the coefficients $A_4$ and $A_n$ for $n \geq 7$ are needed. To obtain corrected higher molecular weight averages, perhaps the best course would be to first find the corrected DMWD and then calculate the higher molecular weight averages from the corrected DMWD.

The corrected DMWD can be found by two methods. In the first method, the corrected $\bar{M}_n(t)$ and $\bar{M}_w(t)$ values obtained from eq. (12) are used to obtain a corrected calibration curve which along with the raw chromatogram is used to obtain the corrected DMWD and, subsequently, the corrected higher molecular weight averages. Hamielec and co-workers[10] have demonstrated the feasibility of this approach by using $\bar{M}_n(t)$ and $\bar{M}_w(t)$ values to fit for the slope and intercept of an effective linear calibration curve. Provder and Rosen[5] have successfully used the hydrodynamic volume concept to obtain linear and/or nonlinear calibration curves by fitting for effective Mark-Houwink parameters $\epsilon$ and $K$.

In the second method, the corrected chromatogram obtained by Tung's integral equation is used along with the calibration curve to obtain the corrected DMWD and the corrected higher average molecular weights. Most of the methods reported in the literature, for solving Tung's integral equation, are inadequate when applied to real data.[5] This is due to (1) the use of an inadequate shape function such as the pure Gaussian, (2) requiring constancy of dispersion or skewing factors with elution volume, and (3) oscillations produced in the corrected chromatogram and, subsequently, in the DMWD because of the problem of distinguishing between the noise and the data in the chromatogram, particularly at the tails of the chromatogram. Recently, a method has been reported by Rosen and Provder[11] which overcomes these problems. Tung's integral equation is approximated by a set of linear algebraic equations. These equations are then solved approximately using singular value decomposition[12] in order to avoid the oscillations introduced owing to the ill-posed mathematical nature of the problem. Rosen and Provder[11] have applied this method successfully to real data using the general shape function containing terms in $A_3$ and $A_4$ which vary with elution volume.

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