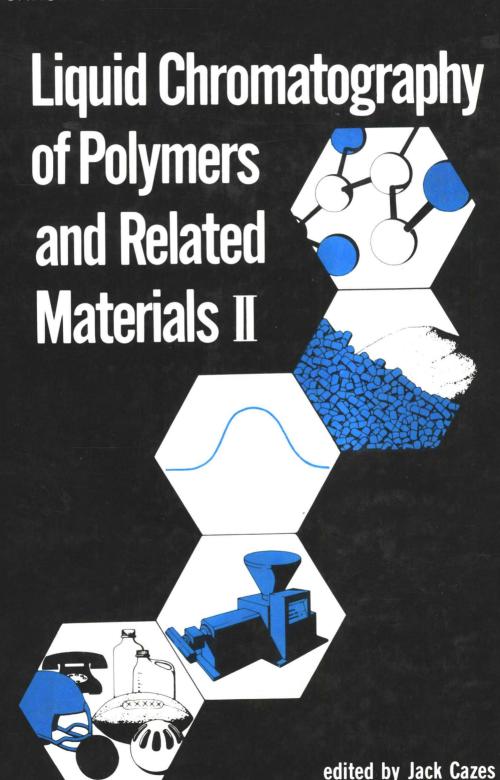
and Xavier Delamare



# Liquid Chromatography of Polymers and Related Materials II

edited by

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MARCEL DEKKER, INC. New York and Basel

Library of Congress Cataloging in Publication Data

International Liquid Chromatography Symposium, Palais des congres et de la musique, 1979. Liquid chromatography of polymers and related materials II.

(Chromatographic science; v. 13) Includes indexes.

1. Polymers and polymerization--Analysis--

Congresses. 2. Liquid chromatography—Congresses. I. Cazes, Jack II. Delamare, Xavier

III. Title.

QD139.P6155 1979 547.8'4046 80-16061 ISBN 0-8247-6985-6

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MARCEL DEKKER, INC.

270 Madison Avenue, New York, New York 10016

Current printing (last digit):

10 9 8 7 6 5 4 3 2 1

PRINTED IN THE UNITED STATES OF AMERICA

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## PREFACE

Published in this volume are selected papers presented at the Fourth International Liquid Chromatography Symposium: Liquid Chromatography of Polymers and Related Materials, which was held on October 24-25, 1979 at the Palais des Congres et de la Musique, Strasbourg, France. Included are thirteen papers covering a range of topics of interest to those involved in the fractionation and characterization of polymeric substances.

We thank the authors of these contributed papers for the fine work they have done and reported here, and also for their patience in the preparation of their manuscripts.

Special thanks are extended to Mrs. Cecile Daly for her valuable assistance, patience, and understanding at all stages of the preperation of this volume.

Lastly, thanks to Waters Associates, Inc., for sponsoring the symposium and for making their facilities available during the preparation of the final manuscript.

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# PROBLEMS ENCOUNTERED IN THE DETERMINATION OF AVERAGE MOLECULAR WEIGHTS BY GPC VISCOMETRY

#### J. Lesec

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## ABSTRACT

This paper deals with problems that are encountered in modern GPC with dual detection (refractometer-viscometer) when calculating average molecular weights, that can lead to incorrect values. Three main problems are developed: axial dispersion in columns, dependence of elution volumes upon solute concentration, and application of the hydrodynamic volume concept. In each case, we have tried to emphasize the best method that takes into account these different effects, avoiding data treatment errors and that leads, thus, to the best accuracy in the determination of average molecular weights of polymers.

## INTRODUCTION

Gel Permeation Chromatography is a modern method of polymer characterization which can be used in two different ways. One can only try to obtain a representation of the polymer molecular distribution. The GPC chromatogram is then directly recorded to compare polymers with different molecular distributions. Calculations can then be performed on the chromatographic data to determine average molecular weight values. In this case, GPC can be considered as a real measurement system which is going to take the place of traditional methods of average molecular weight determination and, consequently, as with every technique leading to numerical evaluation of physical values, must withstand a critical analysis. For this

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reason, it seems important to take stock of the measurement method's validity and the accuracy that we can expect from calculations performed with chromatographic data.

We will consider the situation where only the steric exclusion process arises without perturbing phenomena such as adsorption or partition whose effects were recently described  $^{(1)}$ , and we will discuss the different errors that can affect molecular weight values given by GPC. We can thus classify two kinds of errors  $^{(2)}$ :

- typical chromatographic errors
- data treatment errors.

Typical chromatographic errors are directly related to instrumentation and chemicals. They can lead to very wrong molecular weight values when a chromatographic analysis is not performed under very well defined conditions. The main reasons are: the molecular weight accuracy of standards used for calibration, the problem of sample dissolution, the determination of exact elution volumes in relation to the mobile phase flow rate stability, the accuracy of the substance amount which is injected into the column set and peak shifts resulting from solute concentration and column temperature effects.

But we will assume here that our chromatographic instrumentation is perfect and we will only examine the problems encountered in GPC data treatment when calculating polymer average molecular weights: correction of solute concentration, correction of axial dispersion and application of universal calibration. We will consider only modern GPC using microgels whose analysis time is about 20 minutes.

## PRINCIPLE OF AVERAGE MOLECULAR WEIGHT DETERMINATION

Macromolecular compounds are mainly characterized by a molecular distribution function which depends upon the synthesis process. Therefore, their physical and mechanical properties are directly related to this distribution which can be discribed by average molecular weight:  $\overline{M}_n$ ,  $\overline{M}_v$ ,  $\overline{M}_w$ ,  $\overline{M}_z$ . These molecular weights are usually determined by classical methods (osmometry, viscometry, light scat-

tering, and ultra-centrifugation). But GPC is the only method which can simultaneously lead to all of these parameters. The principle of chromatogram analysis  $^{(3)}$  is represented in Figure 1. It consists in digitizing the refractometric peak into equal fractions, located at the elution volume Vi and whose surfaces are is proportional to solute concentration Ci. The calibration equation Log Mi = f(Vi) gives the relation between Mi and Vi; therefore, summation throughout the peak leads to the average molecular weights.

$$\overline{M}_{n} = \frac{\Sigma C_{i}}{\frac{\Sigma C_{i}}{M_{i}}}, \overline{M}_{v} = (\frac{\Sigma C_{i}M_{i}}{\Sigma C_{i}})^{\alpha}, \overline{M}_{w} = \frac{\Sigma C_{i}M_{i}}{\Sigma C_{i}}, \overline{M}_{z} = \frac{\Sigma C_{i}M_{i}}{\Sigma C_{i}M_{i}}^{2}$$

But, if universal calibration (4) Log  $[n_i]$ .  $M_i = f(V_i)$  is used, we have to simultaneeously analyse a second chromatogram, given by a viscometric detector (5-7). In addition, molecular weight distribution curves can be plotted (8), since the relative ratio of each species  $M_i$  can be calculated.

In actual fact, the principle of calculation is less evident than it appears. The chromatogram is a very distorted representation of the molecular weight distribution because of the logarithmic nature of the elution  $^{(9-10)}$ . If C(M) and W(V), respectively, represent the real distribution and the experimental chromatogram, we can represent the total weight of solute by:

$$\int_{M_1}^{M_2} C(M) . dM = \int_{V_1}^{V_2} W(V) . dV$$
 (1)

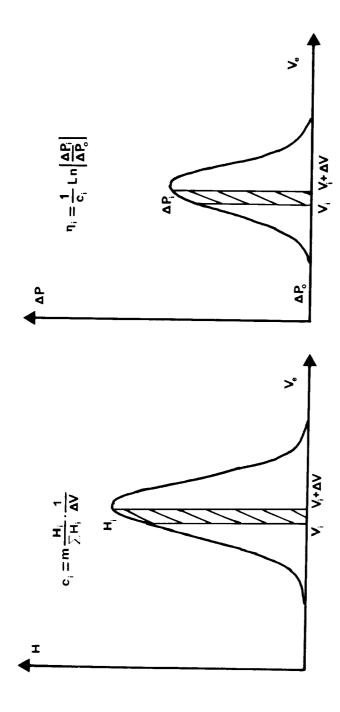
Considering the general equation of a calibration curve:

$$V = F(M) \tag{2}$$

and its derivative:  $F'(M) = \frac{dV}{dM}$  (3)

by using (2) and (3), (1) becomes:

$$\int_{V_{1}}^{V_{2}} \frac{C(M)}{F'(M)} \cdot dV = \int_{V_{1}}^{V_{2}} W(V) \cdot dV$$
 (4)



Principle of Calculation in Double Detection GPC. (Refractometer-Viscometer). m is the Weight of Solute. FIGURE 1

The relationship (4) being true whatever the limits we obtain:

$$C(M) = W(V) \cdot F'(M)$$
 (5)

In GPC, the logarithmic nature of the elution leads to:

$$W_{\underline{i}}(V) = M_{\underline{i}}C_{\underline{i}}(M) \cdot \frac{1}{Log_{\underline{e}}} \cdot \frac{dLogM}{dV}$$
(6)

Relationship (6) represents the polymer distribution deformation by the GPC phenomenon and gives a correspondance, point by point, between the chromatogram and the real distribution and, consequently, allows its determination (11).

Fortunately, in the calculation of molecular weights, this deformation is balanced by the detection system which analyses equal volumes. For example, by using (3) and (5), we can write:

$$\int M.C(M).dM = \int M.F'(M).W(V).dM = \int M.W(V).dV$$
 (7)

and carrying (1) and (7) in the definition of  $\overline{\mathbf{M}}_{\mathbf{W}}$ , we see that:

$$\overline{M}_{W} = \frac{\int M \cdot C(M) \cdot dM}{\int C(M) \cdot dM} = \frac{\int M \cdot W(V) \cdot dV}{\int W(V) \cdot dV}$$

The same holds true for  $\overline{M}_n$ ,  $\overline{M}_v$ , and  $\overline{M}_z$ . This very interesting result points out that we can calculate an average molecular weight by two different ways, both of which lead to an identical result: either by digitizing in dM the real distribution C(M) or by using directly the chromatogram W(V) digitized in dV, whatever the calibration curve. This demonstration makes the correction of calibration curve slope, included in some authors' calculation methods, not justified.

In fact, the simple method described previously can only be strictly applied with an infinite resolution column set, since molecules  $\mathbf{M_i}$ , eluted at the elution volume  $\mathbf{V_i}$ , are contaminated by their neighbors  $(\mathbf{M_{i-1}},\ \mathbf{M_{i+1}},\ \mathbf{M_{i-2}},\ \mathbf{M_{i+2}},\ \text{etc...})$  that have diffused in the mobile phase. This is an axial dispersion phenomenon.

## THE AXIAL DISPERSION PHENOMENON

Axial dispersion depends upon the column set efficiency. An abundant literature has been devoted to this effect when column efficiencies are poor. With modern columns, axial dispersion is

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less important, and we can hope that it will become negligible in the near future. Tung  $^{(12)}$  showed that the experimental chromatogram F(V) and the ideal chromatogram W(V) are linked by the general relationship:

$$F(V) = \int_{-\infty}^{+\infty} W(y) \cdot G(v - y) \cdot dy$$
 (8)

where G(v-y) is the axial dispersion function, which is generally assumed to be guassian  $^{(13)}$ . Many solutions were proposed to resolve Equation 8: Fourier transform  $^{(14)}$ , polynomial methods  $^{(12,15)}$ , and minimisation method  $^{(16)}$ . These methods are not easy to apply and generally require involved computation treatments.

A simple method was recently developed by Marais $^{(17)}$ . Assuming a guassian dispersion function, Equation 8 becomes:

$$F(V_e) = \int_{-\infty}^{+\infty} W(V) \cdot \exp{-\frac{(V - V_e)^2}{2\sigma^2}} \cdot dV$$
 (9)

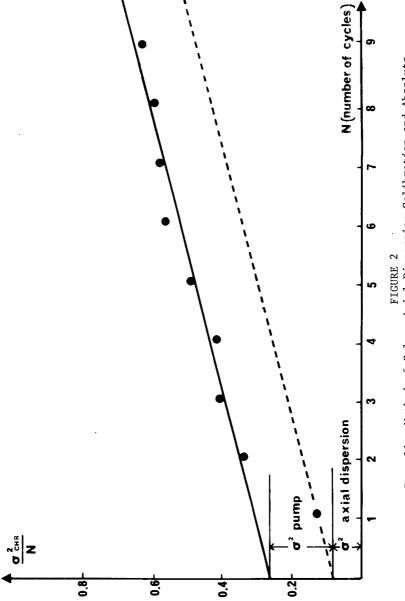
where  $V_{\rm e}$  is the elution volume of the peak apex and  $\sigma$  the axial dispersion parameter of the guassian dispersion function. A sophisticated resolution of (9) leads to the simple result:

$$\overline{M}_{\beta \dot{1}} = M_{\dot{1}} \left[ \exp \frac{\beta \tau^2}{2} \right] \cdot \left[ 1 + \tau^2 \frac{C'}{C} \right]$$
 (10)

 $(\overline{M}_{\beta i} = M_{ni} \text{ for } \beta = -1, \overline{M}_{vi} \text{ for } \beta = \alpha, \overline{M}_{wi} \text{ for } \beta = 1)$  where  $\tau = \sigma/a$  (a = slope of the calibration curve), C the distribution curve and C' its derivative. As ratio C'/C is unknown, it can be approximately expressed through H'/H, ratio of the experimental chromatogram derivative on itself:

$$\frac{C'}{C} \approx \frac{H'}{H}$$
. a (11)

Relationship 10 permits the calculation of average molecular weights when the parameter  $\tau$  is determined throughout the chromatogram. The calibration of the parameter  $\sigma$  can be performed by the Waters' recycle method <sup>(18)</sup> (Fig. 2) which leads to the precise determination of the polydispersity of the polystyrene standards used <sup>(19)</sup>. We could thus obtain <sup>(2)</sup> (Fig. 3) a calibration of  $\tau$  for a



Recycling Method of Column Axial Dispersion Calibration and Absolute Polydispersity Determination (Polystyrene Standard 20,500).

