

Molecular Weights by Computer from Gel Permeation Data on Punched Tape

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Synopsis

A Fortran IV program has been written that reduces digitized data from gel permeation chromatography to number and weight average molecular weights. This computer program is suitable for routine calculations whenever corrections are unnecessary for axial diffusion and branching effects.

INTRODUCTION

Manual computation of molecular size and weight data from raw molecular weight distribution (MWD) curves obtained by gel permeation chromatography (GPC) is tedious and subject to error. Accuracy in such calculations is essential when interpreting effects of experimental treatments on polymer molecular weight or structure from GPC data.

Computer processing of GPC data automatically recorded on teletype punched tape greatly increases the accuracy of molecular weight calculations because many more data points can be used than are practical manually and because errors in determining baselines and curve heights are reduced. Most programs for processing taped GPC data are designed to

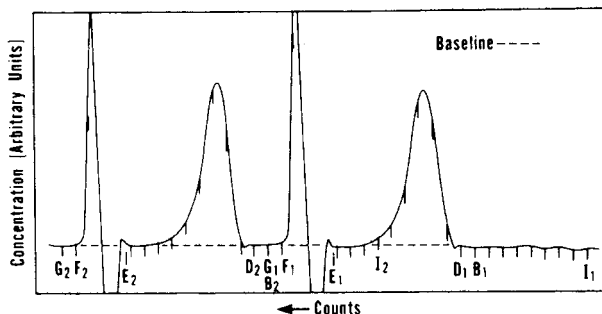


Fig. 1. Gel permeation chromatography (GPC) elution profiles showing curve segments ($\overline{B_i D_i}$ and $\overline{F_i G_i}$) selected for baseline determination and a segment ($\overline{D_i E_i}$) for calculation of molecular weight data. I_i indicates sample injection, and each count is indicated by a small vertical line under the curve.

GPC Input Form

Data Card No. 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45

1 0 1 0 7 7 2 2 3

Mo., Day, Yr. Number of Samples Number of Comments

2 SAMPLE IS POLY(ACRYLONITRILE) Comments (up to 5)

3 SOLVENT IS DIMETHYLFORMAMIDE

4 COLUMNS ARE 10EXP7 AND 1.5X10EXP4

5 3 0 . 0 7 3 1 0 . 6 0 5 - . 4 4 5 7 1

Data Interval Oven Temp., °C Intercept of Standard Curve Slope of Standard Curve

6 9 4 6 4 2 8 6 0 . 0 9 0 1 0 0 1 8 3 2 2 0 2 3 0 2 5

7 9 4 6 4 2 8 2 0 . 0 8 6 9 6 1 8 3 2 2 0 2 3 0 2 5

Notebook Number Page Number Sample Number B_i D_i E_i F_i G_i Q

See Figure 1

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45

Fig. 2. Raw data input form showing statements that control sorting of the taped data. Data cards are keypunched in these formats.

plot MWD after correcting for axial spreading, other chromatographic phenomena, or long- and short-chain branching effects.¹⁻⁵ Such complex procedures are often unwarranted in routine polymer characterizations. Other programs compute number-average molecular weight (\bar{M}_n), weight-average molecular weight (\bar{M}_w), viscosity-average molecular weight, z -average molecular weight, viscosity, and differential and integral MWD's, but are designed for data input from card decks rather than teletype tape.⁶ Our program computes \bar{M}_n , \bar{M}_w , and d values directly from taped GPC curve data in the output form provided by the digital translator of Waters Associates, Inc. Computations follow the example of Harmon.⁷

PROGRAM DESIGN

Data on each tape include the gross curve heights measured at uniform data intervals (DI 's) and the times of each volume count (C) or sample injection event (percentage of DI elapsed since preceding height measurement) along with their respective identifying codes. A strip chart record of typical data is shown in Figure 1. Note that the baseline drifts and must be redetermined for each new curve; solvent impurity data follow each sample's data and must be excluded from calculations; and the succeeding sample may be injected before the preceding sample is completely eluted, provided the elution curve can return to the baseline between peaks.

Specific details required for sorting and computing the data on each tape are supplied to the computer by an input subdeck (Fig. 2) that lists both the number of samples on the tape (NS) and their sample identifying codes; the count intervals where baseline and peak data are to be calculated ($B_i D_i$ and $F_i G_i$ for baseline and $D_i E_i$ for peak, Fig. 1); the DI ; the weight of a unit length of polymer (Q); and the slope and intercept fo the equation that relates molecular contour length (A) to C . The general subscript i assumes the value 1 for the first sample injected, 2 for the second sample,

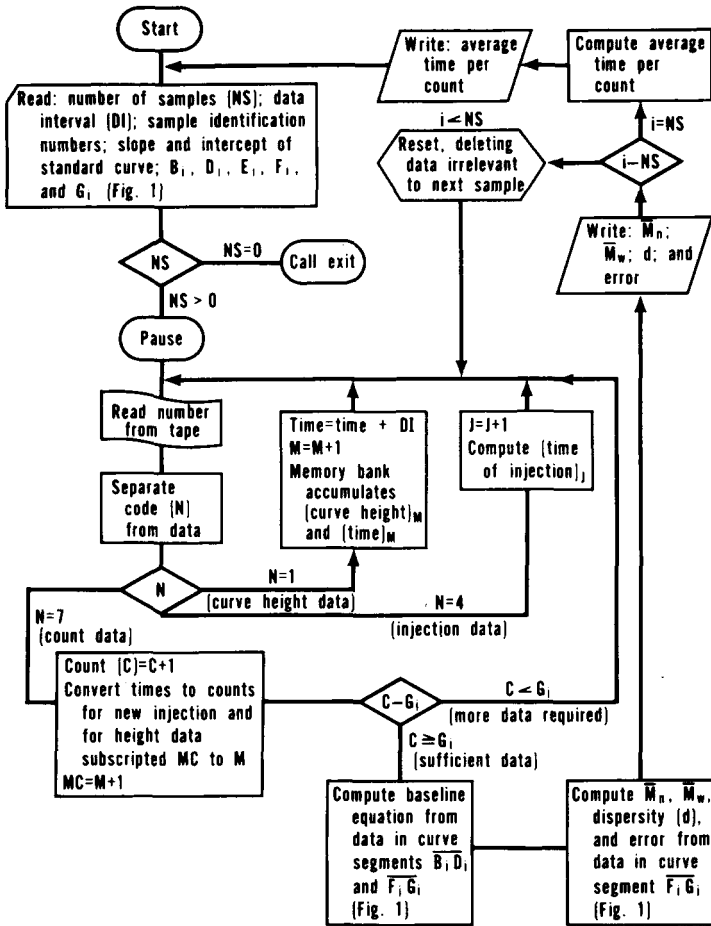


Fig. 3. GPC program flow chart. Subscript i corresponds to the position of a sample in the sequence of injections (e.g., i equals 3 for the third sample).

etc. Data on the tape are sorted as outlined in the abbreviated flow chart (Fig. 3) until count G_1 is located. Then the equation of the baseline is computed by the method of least squares. From this baseline equation, the equation of the standard curve ($\log A_{std} = mC + b$) and the height and count data in the computer memory for curve segment $\overline{D_1E_1}$, the computer determines the sum of the net curve height (ΣH) and the sums $\Sigma(H/A)$ and $\Sigma(H \cdot A)$ for the sample. From these sums it computes

$$A_n = \Sigma H / \Sigma (H/A)$$

$$A_w = \Sigma (H \cdot A) / \Sigma H$$

$$\overline{M}_n = Q \cdot A_n$$

$$\overline{M}_w = Q \cdot A_w$$

and

$$d = A_w / A_n.$$

After printing the molecular weight data for the sample, the computer discards information that is irrelevant to the succeeding sample and continues. When calculations for the first tape are completed, the computer reads another card subdeck and pauses until a new tape is loaded onto the reader. The program continues until the computer finds $NS = 0$ (a blank #1 card).

```
// JOB
LOG DRIVE   CART SPEC   CART AVAIL  PHY DRIVE
0000       1816       1816       0000

V2 M06   ACTUAL 8K   CONFIG 8K

// FOR
* LIST SOURCE PROGRAM
* ONE WORD INTEGERS
* IOCS ( CARD , 1132 PRINTER , TYPEWRITER )
  DIMENSION M1(350),CTH1(350),CNT1(3),NBN(20),NPN(20),SPL(20),CBL1(2
  10),CBL2(20),CSP(20),CBL3(20),CBL4(20),JIC(3),IALPH(30,5),Q(20)
  M1MAX=350
  J1MAX=3
  100 KL=0
  M1=0
  M2=0
  IX=1
  IDP=0
  TIMEC=0
  TIMED=0.
  TPC=0
  J1=0
  JC=0
  K=1
  KLM=1
  JK=1
  TTPC=0.
  READ (2,120) MO,MDAY,MYR,NS,NC
  120 FORMAT (3I2,14,15)
  IF(NS)130,130,140
  130 CALL EXIT
  140 WRITE (3,160) MO,MDAY,MYR
  160 FORMAT (' MOLECULAR SIZE BY GEL PERMEATION CHROMATOGRAPHY'4X12/'1
  12/'12/'0')
  READ (2,200) ((IALPH(I,J),I=1,30),J=1,NC)
  200 FORMAT (30A2)
  WRITE (3,220) ((IALPH(I,J),I=1,30),J=1,NC)
  220 FORMAT (1X,30A2)
  READ (2,260) DI, OVT,YSTD,SLSTD
  260 FORMAT (2F5.0,2F10.0)
  WRITE (3,270) YSTD,SLSTD
  270 FORMAT (' STANDARD CURVE IS LOG(A)='F10.4,F10.4'(C'))
  WRITE (3,280) OVT
  280 FORMAT (' OVEN TEMPERATURE IS 'F5.1' DEGREES CENTIGRADE')
  WRITE (3,320)
  320 FORMAT ('0 SAMPLE M-SUB=N M-SUB=W D ERR
  10R INTERCEPT SLOPE Q')
  READ (2,360) (NBN(I),NPN(I),SPL(I),CBL1(I),CBL2(I),CSP(I),CBL3(I),
  1CBL4(I),Q(I),I=1,NS)
  360 FORMAT (2I5,6F5.1,F6.1)
  PAUSE 3001
  LIN=-1
  400 CALL TLTAP (NO,NUMBR)
  IF(NO=4)420,500,460
  420 IF(NO=3)460,440,460
  460 WRITE (1,480) LIN,NO,NUMBR
  PAUSE 3003
  GO TO 400
  440 LIN=NUMBR
```

(8)

Fig. 4 (continued)

PROGRAM OPERATION

An input subdeck (Fig. 2) must be prepared for each tape. Each input subdeck includes (in the order listed): A card giving the date, the number of samples on the tape, and the number of informational comments (up to five) to be read and printed in the output; the comment cards (each contain-

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GO TO 400
480 FORMAT (' ERROR LINE='I6' NO='I2' VALUE='I6')
500 N=NUMBR/1000
    NUM=NUMBR-1000*N
    IF(N-1)460,600,520
520 IF(N-4)460,690,540
540 IF(N-7)460,740,560
560 IF(N-9)460,980,460
600 IDP=IDP+1
    TIME=IDP*D1
    IF(J1-1)400,660,660
660 M1=M1+1
    IF(M1=M1MAX)680,680,460
680 M1(M1)=NUM/10.
    CTH1(M1)=TIME
    GO TO 400
690 IF(J1)695,695,700
695 IF(TPC)696,696,701
696 WRITE (3,697)
697 FORMAT (' SAMPLE WAS INJECTED WITHOUT TWO PRIOR COUNTS')
    JK=2
    GO TO 400
700 IF(JIC(J1)-JC)701,400,400
701 J1=J1+1
    IF(J1-J1MAX)720,720,460
720 CNT1(J1)=TIME+NUM*D1/100.
    JIC(J1)=JC
    COAJ=1-(CNT1(J1)-TIMEC)/TPC
    M2=M1
    GO TO 400
740 JC=JC+1
    K1=M1
    TIMEC=TIME+NUM*D1/100.
    IF(TIMED)815,815,760
760 TPC=TIMEC-TIMED
    TTPC=TTPC+TPC
    IF(K1)815,815,764
815 TIMED=TIMEC
    IX=M1+1
    GO TO 400
764 IF(KL-1)782,765,765
782 DO 783 MX=IX,K1
783 CTH1(MX)=(CTH1(MX)-CNT1(1))/TPC
    CAJ=(TIMEC-CNT1(1))/TPC
    CNT1(1)=0
    KL=1
    GO TO 815
765 DO 780 MX=IX,K1
780 CTH1(MX)=(CTH1(MX)-TIMED)/TPC+JC-2.-JIC(1)+CAJ
    KMI=JIC(J1)+1
    IF(KMI-JC)820,810,820
810 CNT1(J1)=(CNT1(J1)-TIMED)/TPC+JC-2.-JIC(1)+CAJ
820 TIMED=TIMEC
    IX=M1+1
    CNT=CTH1(M1)
    CB4=CBL4(JK)
    IF (CNT-CB4) 400,830,830
830 MIX=M1
    CB1=CBL1(JK)
    CB2=CBL2(JK)
    CB3=CBL3(JK)

```

(b)

Fig. 4 (continued)

ing up to 60 characters and spaces); a card listing the data interval, oven temperature, and the intercept and the slope of the standard equation; a card for each sample, which lists its identification (notebook number, page number, and sample number), B_i , D_i , E_i , F_i , and G_i (from the GPC

```

DO 877 M=1,MIX
COUNT=CTH1(M)
IF (COUNT-CB1) 840,850,850
840 MLOW=M+1
GO TO 877
850 IF (COUNT-CB2) 860,860,870
860 MMID=M
GO TO 877
870 IF (COUNT-CS) 875,880,880
875 MMHIGH=M
877 CONTINUE
880 DO 890 M=1,MIX
COUNT=CTH1(M)
IF (COUNT-CB3) 881,881,887
881 MLB1=M+1
GO TO 890
887 IF (COUNT-CB4) 888,888,900
888 MLB2=M
890 CONTINUE
900 SCNT=0.
SH=0.
SCNTH=0.
SCNT2=0.
DO 910 M=MLOW,MMID
SCNT=SCNT+CTH1(M)
SH=SH+H1(M)
SCNTH=SCNTH+CTH1(M)*H1(M)
910 SCNT2=SCNT2+CTH1(M)**2
DO 915 M=MLB1,MLB2
SCNT=SCNT+CTH1(M)
SH=SH+H1(M)
SCNTH=SCNTH+CTH1(M)*H1(M)
915 SCNT2=SCNT2+CTH1(M)**2
Z=MMID+MLB2+2-MLB1-MLOW
SLOPE=(SCNT*SH-Z*SCNTH)/(SCNT*SCNT-Z*SCNT2)
YCEPT=(SH-SLOPE*SCNT)/Z
SHXA=0.
SHDA=0.
SHCRV=0.
DO 940 M=MMID,MMHIGH
HCRV=H1(M)-SLOPE*CTH1(M)-YCEPT
IF (HCRV) 920,930,930
920 HCRV=0.
930 ASTD=SLSTD*CTH1(M)+YSTD
ASTD=EXP(ASTD*2.30258509)
SHXA=SHXA+ASTD*HCRV
SHDA=SHDA+HCRV/ASTD
940 SHCRV=SHCRV+HCRV
ABARN=SHCRV/SHDA
ABARW=SHXA/SHCRV
HBARN=Q(JK)*ABARN
HBARW=Q(JK)*ABARW
DSPTY=ABARW/ABARN
ERROR=H1(MHIGH)-SLOPE*CTH1(MHIGH)-YCEPT
WRITE (3,950) NBN(JK),NPN(JK),SPL(JK),HBARN,HBARW,DSPTY,ERROR,YCEPT,
17,SLOPE,Q(JK)
950 FORMAT (1X I5,' -' I3,' -' F6.1,2F10.0,2F10.2,F10.4,F10.3,F6.1)
IF (JK=NS) 960,980,980
960 IF (M2) 964,964,968
964 M1=0
J1=0
KL=0

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(c)

Fig. 4 (continued)

```

IX=1
JK=JK+1
GO TO 400
968 L2=M1-M2
    L3=M2+1
    DO 970 IM=1,L2
    CTH1(IM)=CTH1(L3)-CNT1(2)
    M1(IM)=M1(L3)
970 L3=L3+1
    IX=IX-M2
    M1=M1-M2
    M2=0
    CNT1(1)=CNT1(2)
    JIC(1)=JIC(2)
    JI=1
    KL=2
    CAJ=COAJ
    JK=JK+1
    GO TO 400
980 AVTPC=TTPC/(JC-1)
    WRITE (3,990) AVTPC
990 FORMAT (// 'O AVERAGE TIME PER COUNT IS 'F6.2,' SEC')
    GO TO 100
    END

FEATURES SUPPORTED
ONE WORD INTEGERS
IOCS

CORE REQUIREMENTS FOR
COMMON      0 VARIABLES      2002 PROGRAM      1656

END OF COMPILATION

// XEQ

```

(d)

Fig. 4. GPC program listing.

strip chart, Fig. 1), and the Q factor to be used in the calculations. All numbers must be right-justified integers unless shown in floating point (decimal) form.

For computation, the input subdecks are loaded into an IBM card reader on top of the program deck (listed in Fig. 4) in the order that the tapes will be processed, and two blank cards are put on the back of the entire deck. The first tape is loaded onto an IBM 1134 paper tape reader. Each tape must be loaded so that the computer finds two counts before it locates the first injection since the time of the first injection is calculated from the time between the preceding two counts. (If less than two counts are observed before injection, the computer will indicate this fact on the printer and proceed to the next sample.)

After the program is loaded, the computer reads the first subdeck, prints the date and comments (Fig. 5), and pauses until the "program start" button is pushed. As \bar{M}_n , \bar{M}_w , and d are calculated for each sample, they are listed along with error, baseline, intercept, slope, and Q factor according to the format in Figure 5. Error is the difference in heights of the baseline and sample curve at count E_i . Deviation of this residual from zero by more than 0.5 unit for a sample implies nonvalidity of its molecular weight data. Intercept and slope define the equation of the baseline for that sample. After all samples on a tape have been processed, the average time

MOLECULAR SIZE BY GEL PERMEATION CHROMATOGRAPHY 10/20/72

SAMPLE IS POLY(ACRYLONITRILE)
 SOLVENT IS DIMETHYLFORMAMIDE
 DATA INTERVAL IS 30 SEC.
 COLUMNS ARE 10EXP7 AND 1.5X10EXP4
 STANDARD CURVE IS LOG(A)= 10.6050 -0.4457(C)
 OVEN TEMPERATURE IS 73.0 DEGREES CENTIGRADE

SAMPLE	M-SUB-N	M-SUB-W	D	ERROR	INTERCEPT	SLOPE	Q
9535 - 5 -	1.1	2479055.	8030165.	3.23	-0.81	15.7993	0.066 25.0
9535 - 6 -	1.0	2162225.	7020786.	3.24	-0.18	16.6738	0.044 25.0

AVERAGE TIME PER COUNT IS 289.68 SEC

Fig. 5. Computer output from GPC program.

elapsed per count is computed and printed, and the card reader processes another input subdeck. The computer then pauses until a new tape is loaded onto the tape reader and the program start button is depressed again.

DISCUSSION

The program can be modified readily to process information from three GPC units recorded on a single tape. Only slight modification is required to use a nonlinear relationship between A or M and C as the standard equation. Calibration of GPC with samples of the test polymer that have small d values and known peak M 's would remove the uncertainties associated with use of the Q factor.

TLTAP (statement 400, Fig. 4) refers to a tape reading subroutine. Specific inquiries about this subroutine can be directed to the Northern Regional Research Laboratory in care of J. O. Ernst.

The mention of firm names or trade products does not imply that they are endorsed or recommended by the U.S. Department of Agriculture over other firms or similar products not mentioned.

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Received November 2, 1973

Revised November 13, 1973