

1980

Computer simulation of polymer dynamics

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COMPUTER SIMULATION OF
"
POLYMER DYNAMICS

A thesis
Presented to
The Faculty of the Department of Chemistry
The College of William and Mary in Virginia

In Partial Fulfillment
Of the requirements for the degree of
Master of Arts

by
Rebecca L. Smithson
1980

APPROVAL SHEET

This thesis is submitted in partial fulfillment of
the requirements for the degree of

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ABSTRACT

The concentration dependence of the equilibrium and dynamic properties of random coil polymer chains was studied using Monte Carlo simulations. Chains of 10, 20, and 30 beads were studied at densities ranging from 0.04 to 0.80. Simulations were performed using two types of bead motions. The equilibrium properties sampled were the second and fourth moments of the end-to-end length and the diffusion constant. Relaxation behavior of the chains was studied by sampling the autocorrelation functions of end-to-end length and square end-to-end length.

The effect of concentration on the equilibrium properties agrees with previous studies and theoretical predictions. The faster relaxation modes of the chain appear to be less affected by concentration than the slower modes. The critical density, at which the onset of entangled behavior begins, was found to decrease with increasing concentration. The dependence of relaxation on polymer volume fraction agrees with the free volume theories.

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CHAPTER 1

The Rouse Model

The Rouse Model has been used successfully to describe linear viscoelastic properties of random coil polymer chains in dilute solution'. The polymer chain is pictured as being composed of a number of submolecules. Each submolecule is a part of the polymer chain which must be of sufficient length to approximate a gaussian distribution for the separation of end-to-end length. Hydrodynamic interactions, which are the effects of one segment on other segments caused by its motion through the viscous medium, are not included in this model. Excluded volume effects, or the obstruction of a segment by any other segments are also not included. As a result, the Rouse Model is valid only in solutions where these effects are small.

Model of the Polymer Chain

Each polymer molecule is divided up into N identical submolecules. The probability that the end of one of these submolecules is located in the region x to $x+dx$, y to $y+dy$, and z to $z+dz$ given that the other end of the molecule is fixed at the origin of this coordinate system is

$$\Psi(x,y,z)dxdydz = (\beta/\pi)^{3/2} \exp(-\beta(x^2 + y^2 + z^2))dxdydz. \quad (1.1)$$

The constant β is given by $(3/2l^2)$ where l^2 is the average square length of the submolecules¹. The number of configurations available to the chain is proportional to $\int \Psi(x,y,z)dxdydz$. The relative number of configurations thus depends only on $x^2 + y^2 + z^2 = r^2$ and is given by

$$\exp(-\beta r^2). \quad (1.2)$$

This model is equivalent to one of N beads connected by $N-1$ Hookean springs. Treloar² shows this by calculating the amount of work required to move an end of the submolecule from r to $r+dr$. For reversible processes it is known from thermodynamics that at constant temperature and volume

$$dE = TdS + dW \quad \text{and} \quad dA = dE - TdS.$$

Combining these two equations gives $dA = dW$.

The Helmholtz free energy, A , may be found by the equation $A = E - TS$, where E is the internal energy of the polymer. Therefore, at constant volume and temperature

$$dW/dr = (\partial E/\partial r) - T\partial S/\partial r. \quad (1.3)$$

By considering a freely jointed chain, or one that is

subjected to no internal energy barriers, $dE/dr = 0$, since the internal energy will be the same for all configurations. With this, equation 1.2 becomes

$$dW/dr = -T \left(\frac{dS}{dr} \right)_{T, V} \quad (1.4)$$

The entropy, S , may be found by Boltzmann's equation, $S = k \ln \Omega$, where k is the Boltzmann constant and Ω is the number of possible configurations. Using equation 1.2, together with the Boltzmann equation gives

$$S = c - k \beta r^2 \quad (1.5)$$

The constant c includes the size of the volume element $dx dy dz$ and is used to indicate that only differences in entropy are of interest, but not absolute values of entropy.

Substituting equation 1.5 into 1.4 gives $dW = 2kT r dr$. Because work had to be done to move the end of the subchain from r to $r+dr$, there is a restoring force acting on the chain such that $dW = f dr = 2kT \beta r dr$, or $f = 2kT \beta r$. The tension is proportional to the length, each submolecule may be thought of as a Hookean spring of equilibrium length zero and spring constant $2kT = 3kT/l^2$ since $\beta = (3/2)l^2$.

In all forthcoming discussion, polymer molecules will be thought of as consisting of N beads connected by $N-1$ Hookean springs with these properties.

The $3N$ coordinates of the system will be obtained by assigning a Cartesian Coordinate system to each bead. The coordinate system assigned to the j th bead is (x_j, y_j, z_j) where x_j is the displacement in the x

direction of the j th bead from its equilibrium position. The coordinates y and z describe similar displacements in the y and z directions.

Motion of the Polymer Molecule.

The equations of motion for the polymer molecules will be set up in a manner analogous to the method used by Zimm³, but without his inclusion of hydrodynamic interactions. The general equation used to describe the forces acting on the j th bead of the polymer chain upon application of an external force is the Langevin equation⁴,

$$m(dv_{x_j}/dt) = -\rho v_{x_j} + X + A(t). \quad (1.6)$$

Similar equations may be written for the y and z dimensions.

The right hand side of the Langevin equation is the sum of the forces acting on the beads. These are

(1) A frictional force, ρv_{x_j} , with friction constant ρ caused by motion of the bead through the solvent. The velocity of the solvent in the x -direction at the j th bead is v_{x_j} .

(2) the term X represents the external, systematic forces exerted on bead j by the springs. The force exerted on bead j by the $(j-1)$ st spring is $-(3kt/l^2)(x_j - x_{j-1})$. The force exerted on this bead by the j th spring is $(-3kt/l^2)(x_j - x_{j+1})$. The total force from the springs on the j th bead is

$$-(3kt/l^2)(-x_{j-1} + 2x_j - x_{j+1}) \text{ for } 0 < j < N. \quad (1.7a)$$

Because beads 1 and N are only affected by springs 1 and N - 1 the force on these beads is

$$-(3kt/l^2)(x_1 - x_2) \text{ for } j = 0 \quad (1.7b)$$

$$\text{and } -(3kt/l^2)(x_N - x_{N-1}) \text{ for } j = N. \quad (1.7c)$$

(3) The force given by A(t) in the Langevin equation is a fluctuating force resulting from the Brownian motion of the solvent. This brownian motion causes the beads to diffuse from regions of high concentration to regions of low concentration. The driving force behind this movement may be written as the change in the Helmholtz free energy⁶, $\partial A / \partial x_i$. Expanding this gives

$$A(t) = \partial A / \partial x = \partial / \partial x_i (E - TS) = T(\partial S / \partial x_i).$$

The entropy may be written according to Boltzmann's relations, $S = k \ln \Psi$ with k being Boltzmann's constant. The unknown function Ψ is a function of the coordinates x_1, x_2, \dots, x_N . It is to be interpreted as the probability of finding each bead with coordinates between x_i to $x_i + dx_i$, y_i to $y_i + dy_i$ and z_i to $z_i + dz_i$, so is proportional to the number of possible configurations of the system. This leads to

$$A(t) = -kT \partial \ln \Psi / \partial x_i. \quad (1.8)$$

The quantity ρ/m is a very high frequency on the order of 10^{13} sec^{-1} . Since only the low frequency response of the chain is of interest and $m(dv_{x_j}/dt) \ll \rho v_{x_j}$ the left hand side of equation (1.6) may be set to zero.

Substituting equations (1.7) and (1.8) into equation (1.6) gives

$$\dot{x}_1 = v_{x_1} - D \frac{\partial \ln \Psi}{\partial x_1} - \sigma (x_1 - x_2),$$

$$\dot{x}_j = v_{x_j} - D \frac{\partial \ln \Psi}{\partial x_j} - \sigma (-x_{j-1} + 2x_j - x_{j+1}) \quad \text{for } 1 < j < N,$$

$$\dot{x}_N = v_{x_N} - D \frac{\partial \ln \Psi}{\partial x_N} - \sigma (x_N - x_{N-1}),$$

where $D = kT/\rho$ and $\sigma = 3kT/l^2\rho$.

These equations may be written more compactly in matrix form

$$\frac{\partial \underline{x}}{\partial t} = \underline{v}_x - D \left(\frac{\partial}{\partial \underline{x}} \right) \ln \Psi - \sigma A \underline{x}. \quad (1.9)$$

In this equation

$$\underline{x} = \begin{pmatrix} x_1 \\ x_2 \\ \vdots \\ x_N \end{pmatrix} \quad \underline{v}_x = \begin{pmatrix} v_{x_1} \\ v_{x_2} \\ \vdots \\ v_{x_N} \end{pmatrix} \quad \left(\frac{\partial}{\partial \underline{x}} \right) = \begin{pmatrix} \partial/\partial x_1 \\ \partial/\partial x_2 \\ \vdots \\ \partial/\partial x_N \end{pmatrix}$$

and

$$A = \begin{pmatrix} -1 & -1 & 0 & 0 & \dots & \dots & 0 & 0 & 0 \\ -1 & 2 & -1 & 0 & \dots & \dots & 0 & 0 & 0 \\ 0 & -1 & 2 & -1 & \dots & \dots & 0 & 0 & 0 \\ 0 & 0 & -1 & 2 & \dots & \dots & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \ddots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & 0 & \dots & \dots & -1 & 2 & 1 \\ 0 & 0 & 0 & 0 & \dots & \dots & -1 & 2 & 1 \\ 0 & 0 & 0 & 0 & \dots & \dots & 0 & -1 & 1 \end{pmatrix}$$

Equations for the y and z dimensions may be written in a similar way.

These equations may now be written in terms of ψ by use of the equation of continuity,

$$\partial\psi/\partial t = -\text{div } \psi [(\partial\tilde{x}/\partial t) + (\partial\tilde{y}/\partial t) + (\partial\tilde{z}/\partial t)]$$

with the divergence operator given by

$$\text{div} = \left(\frac{\partial}{\partial\tilde{x}}\right)^T + \left(\frac{\partial}{\partial\tilde{y}}\right)^T + \left(\frac{\partial}{\partial\tilde{z}}\right)^T.$$

The superscript T is used to indicate the transpose of a vector or matrix. This equation is a statement of the conservation of mass, that the rate at which beads enter some volume element must be equal to the rate at which they leave⁸. Substitution into the equation of continuity for $\partial\tilde{x}/\partial t$, $\partial\tilde{y}/\partial t$, and $\partial\tilde{z}/\partial t$ as given by equation 1.9 yields

$$\begin{aligned} \partial\psi/\partial t = \sum_{q=x,y,z} \left\{ -\left(\frac{\partial\psi}{\partial q}\right)^T \cdot \underline{v}_q - \psi \cdot \left(\frac{\partial}{\partial q}\right)^T \cdot \underline{v}_q + D \left(\frac{\partial}{\partial q}\right)^T \cdot \left(\frac{\partial\psi}{\partial q}\right) \right. \\ \left. + \sigma \left(\frac{\partial\psi}{\partial q}\right)^T \cdot A \cdot \underline{q} + \sigma \cdot \psi \left(\frac{\partial}{\partial q}\right)^T \cdot A \cdot \underline{q} \right\} \end{aligned} \quad (1.10)$$

Transformation to Normal Coordinates

Solution of equation 1.10 is simplified by a transformation to normal coordinates. These new coordinates are defined by the equations

$$\underline{u} = R^{-1} \underline{x}, \quad (1.11a)$$

$$\underline{v} = R^{-1} \underline{y}, \quad \text{and} \quad (1.11b)$$

$$\underline{w} = R^{-1} \underline{z}. \quad (1.11c)$$

The matrix R in these equations is the orthogonal matrix which diagonalizes the A matrix, or

$$R^{-1} A R = \Lambda = (\lambda_p \delta_{pq}). \quad (1.12)$$

The p th eigenvalue of A is given by λ_p and δ_{pq} is the Kronecker delta.

The rules for transformation of partial derivatives are found by use of the chain rule⁸:

$$\begin{aligned} \frac{\partial}{\partial x_j} &= \sum_k \left(\frac{\partial u_k}{\partial x_j} \right) \left(\frac{\partial}{\partial u_k} \right) = \sum_k \sum_i \left[\frac{\partial}{\partial x_j} (R_{ki}^{-1} x_i) \right] \frac{\partial}{\partial u_k} \\ &= \sum_k \sum_i \left[\frac{\partial}{\partial x_j} (R_{ik} x_i) \right] \frac{\partial}{\partial u_k} \\ &= \sum_k \sum_i \left[R_{ki} \delta_{ji} \frac{\partial}{\partial u_k} \right] \\ &= \sum_k R_{jk} \frac{\partial}{\partial u_k}. \end{aligned}$$

In matrix notation this becomes

$$\left(\frac{\partial}{\partial \underline{x}} \right) = R \left(\frac{\partial}{\partial \underline{u}} \right). \quad (1.13)$$

It may be shown in a similar manner that

$$\left(\frac{\partial}{\partial \underline{u}} \right) = R^{-1} \left(\frac{\partial}{\partial \underline{x}} \right). \quad (1.14)$$

The transformation of partial derivatives in the y and z dimensions are of the same form.

Before it is possible to transform the first term of equation 1.10 to normal coordinates, it is necessary to know more about the velocities \underline{v}_q . Application of a shearing

stress to the solution in the $x y$ plane causes the velocity of the solvent to be non zero only in the x direction, as shown in Figure 1.1. Therefore,

$$v_{xj} = \alpha z_j \quad , \quad v_{yj} = v_{zj} = 0. \quad (1.15a)$$

The shear rate α is

$$\alpha = \alpha_0 \exp(i\omega t). \quad (1.15b)$$

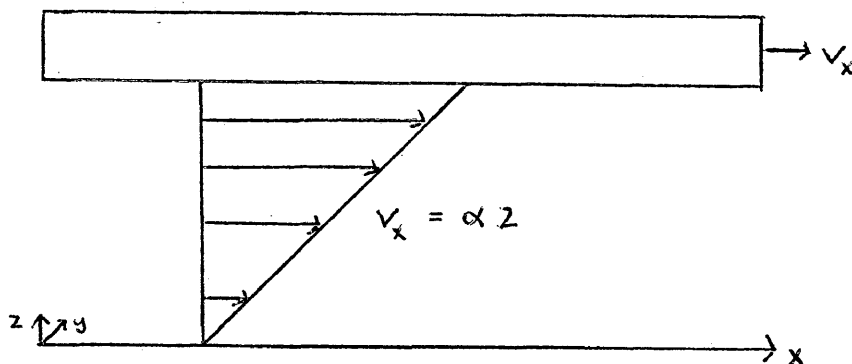


Figure 1.1.
Velocity gradient caused by a shearing motion
in the $x-y$ plane.

The velocity gradient is assumed to be constant over the dimensions of a molecule. This assumption will be good except for solvents of low viscosities at high frequencies¹.

The first two terms of equation 1.10 now become

$$- (\partial \Psi / \partial x)^\top \cdot \underline{v}_x - \Psi (\partial / \partial x)^\top \cdot \underline{v}_x = -\alpha (\partial \Psi / \partial x)^\top \cdot \underline{z}_j .$$

This may be written in terms of the coordinates u, v, w by multiplying by $R^{-1} R = E$, where E is the unit matrix as follows :

$$\begin{aligned} -\alpha (\partial \Psi / \partial x)^\top \cdot \underline{z} &= -\alpha (\underline{z})^\top \cdot (\partial \Psi / \partial x) \\ &= -\alpha \underline{z}^\top \cdot R R^{-1} \cdot (\partial \Psi / \partial x) = -\alpha \underline{z}^\top \cdot R \cdot (\partial \Psi / \partial u) . \end{aligned}$$

Taking the transpose of both sides of equation 1.11c gives⁹

$$(\underline{w})^T = (R^{-1} \underline{z})^T = \underline{z}^T R^{-1T}.$$

Because R is an orthogonal matrix, $R^{-1} = R^T$ giving

$$(\underline{w})^T = \underline{z}^T \cdot R, \quad (1.16)$$

with similar equations for $(\underline{u})^T$ and $(\underline{y})^T$. Using equation 1.13 gives the first term as

$$-\alpha \underline{w}^T \cdot (\partial \psi / \partial \underline{u}) = -\alpha \sum_i w_i \partial \psi / \partial u_i. \quad (1.17)$$

The third term of equation 1.10, the Brownian motion term, may be transformed as follows :

$$\begin{aligned} D(\partial / \partial \underline{x})^T \cdot (\partial \psi / \partial \underline{x}) &= (\partial / \partial \underline{x})^T \cdot R R^{-1} \cdot (\partial \psi / \partial \underline{x}) \\ &= (\partial / \partial \underline{x})^T (\partial \psi / \partial \underline{x}) \\ &= D \sum_i \partial^2 \psi / \partial u_i^2 \end{aligned} \quad (1.18)$$

Transformation of the spring terms is similar :

$$\begin{aligned} &\sigma [(\partial \psi / \partial \underline{x})^T \cdot A \cdot \underline{x} + \psi (\partial / \partial \underline{x})^T \cdot A \cdot \underline{x}] \\ &= \sigma [(\partial \psi / \partial \underline{x})^T \cdot R R^{-1} \cdot A \cdot R R^{-1} \cdot \underline{x} + \psi (\partial / \partial \underline{x})^T \cdot R R^{-1} \cdot A \cdot R R^{-1} \cdot \underline{x}] \\ &= \sigma [(\partial \psi / \partial \underline{u})^T \cdot \lambda_k \cdot \underline{u} + \psi (\partial / \partial \underline{u}) \lambda_k \underline{u}] \\ &= \sigma [(\partial \psi / \partial \underline{u})^T \cdot \lambda_k \cdot \underline{u} + \sigma \lambda_k \psi] \\ &= \sum_i \sigma \lambda_i [u_i \partial \psi / \partial u_i + \psi]. \end{aligned}$$

(1.19)

Combination of equations 1.17, 1.18, 1.19 and their counterparts for the y and z dimensions gives the diffusion equation for the polymer in the coordinates \underline{u} , \underline{v} , and \underline{w} , as

$$\frac{\partial \Psi}{\partial t} = \sum_i \left\{ -\alpha w_i \frac{\partial \Psi}{\partial u_i} + \sum_{g=u,v,w} \left[D \frac{\partial^2 \Psi}{\partial g_i^2} + \sigma \lambda_k \left[g_i \frac{\partial \Psi}{\partial g_i} + \Psi \right] \right] \right\}. \quad (1.20)$$

Solution of the Differential Equation

Equation 1.20 is easily solved when no shearing motion is involved. In this case, the first term is zero, and the unnormalized solution, Ψ_0 is

$$\Psi_0 = \exp(-\sigma/D) \left[\sum_{k=1}^N (u_k^2 + v_k^2 + w_k^2) \right]. \quad (1.21)$$

Differentiating gives

$$\frac{\partial \Psi_0}{\partial t} = (-\sigma/D) g_k \Psi_0 \quad g = u, v, w. \quad (1.22)$$

The solution of 1.20 may be written as a power series in α ,

$$\Psi = \Psi_0 \sum_{n=0}^{\infty} \Psi_n \alpha^n, \quad (1.23)$$

$\Psi_0 = 1$ and α given by equation 1.15b. Substituting 1.19 into 1.16 and equating the coefficients of α^n gives the recursion equations for Ψ_n

$$i\omega \Psi_n = \sum_{k=1}^N \left[(\sigma/D) u_k v_k \Psi_{n-1} - w_k \frac{\partial \Psi_{n-1}}{\partial u_k} \right] + \sum_{g=u,v,w} \left[D \frac{\partial^2 \Psi_n}{\partial g_k^2} - \sigma \lambda_k g_k \frac{\partial \Psi_n}{\partial g_k} \right] \quad (1.24)$$

Solving this equation for Ψ_n will then permit use of

equation 1.25 as a recursion relation from which

$\psi_2, \psi_3, \psi_4 \dots$ may be found.

The equation for ψ_i is

$$i\omega\psi_i = \sum_{k=1}^i \left\{ (\sigma/D) u_k \omega_k + \sum_{g=u, v, w} \left(D \frac{\partial^2 \psi}{\partial g^2} - \sigma \lambda_k g_{ik} \frac{\partial \psi}{\partial g_k} \right) \right\}.$$

A solution for ψ_i is given by

$$\psi_i = \sum_{k=1}^i c_k u_k \omega_k, \quad \text{with}$$

$$c_k = \left(\frac{1}{2D} \right)_k \left(1 + (i\omega/2\sigma\lambda) \right).$$

For small ω , only this first term will be of importance and the relaxation times for the normal modes of vibration of the polymer are then given by

$$\tau_k = 1/(2\sigma\lambda_k) = l^2 P / 6KT\lambda_k. \quad (1.27)$$

The λ_k are the eigenvalues of the A matrix. These are shown in Appendix A to be

$$\lambda_k = 4 \sin^2(\pi k/2N) \quad \text{for } k = 0, 1, \dots, N-1. \quad (1.28)$$

Each of the normal coordinates represents a mode of motion of the polymer chain. These modes are independent of one another, so that superposition or combination of them gives vibrations that are not normal vibrations. All possible vibrations of the molecule can be represented by combinations of the normal vibrations.

Different types of experiments will excite certain modes of motion. For example, mechanical measurements will

predominantly excite the lower modes of motion, whereas dielectric type experiments will excite higher frequencies¹⁰.

CHAPTER 2

Monte Carlo Studies of Random Coil Polymer Chains.

A second approach used in investigating both the equilibrium and dynamic properties of polymers is the computer simulation of lattice model polymer chains based on Monte Carlo techniques. This approach makes it possible to study the effects of excluded volume conflicts which are not easily treated analytically.

The Model

A polymer chain is represented in this model as a series of points or beads on a cubic lattice. Each bead lies on one of the cubes vertices and they are connected along the cube sides. Each connection, called a bond, is of unit length. The initial chain configurations are generated randomly. Movement of the chain due to Brownian motion is

then simulated by picking either a bead or a bond at random and moving it according to the rules to be given later. Each movement of a bead or a bond is called a bead cycle. Without excluded volume more than one bead may occupy a lattice site at a given time. The excluded volume condition is realized by allowing only one bead per lattice site at any one time.

The beads of a chain are indexed from 1 to N. Let \vec{r}_j be the vector pointing from bead j to bead j + 1. The movement of a bead that is not an endbead is accomplished by an interchange of vectors. This interchange for bead j is

$$\vec{r}'_j = \vec{r}_{j-1} \quad \text{and} \quad \vec{r}'_{j-1} = \vec{r}_j \quad \text{for } 2 \leq j \leq N-1, \quad (2.1)$$

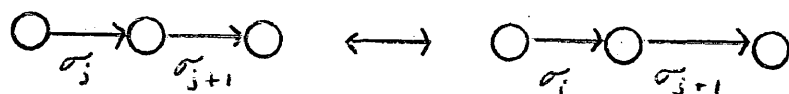
where the prime denotes the vector after the move. This type of vector exchange, which involves the movement of only one bead is pictured in Figure 2.1. It is called a single bead movement. The endbeads, numbered 1 and N are moved by replacing \vec{r}_1 and \vec{r}_{N-1} by a vector chosen at random from one of the six vectors originating at beads 2 or N-1, respectively.

The second type of bead movement, pictured in Figure 2.2, is called a crankshaft bead movement. It results in the movement of two beads instead of just one. The bond connecting bead j and bead j + 1 is moved by the following

Figure 2.1

The possible Single Bead Moves for Midbeads
in the Presence of Excluded Volume.

a) no move possible if the angle between beads is 180° .



b) move across the diagonal if angle is 90° between beads.

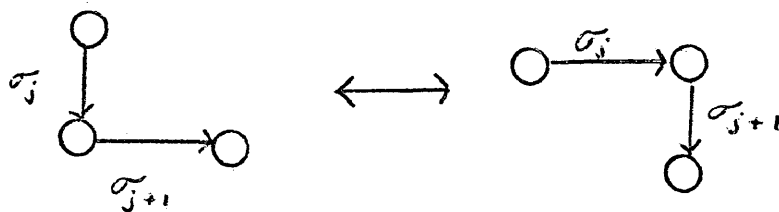
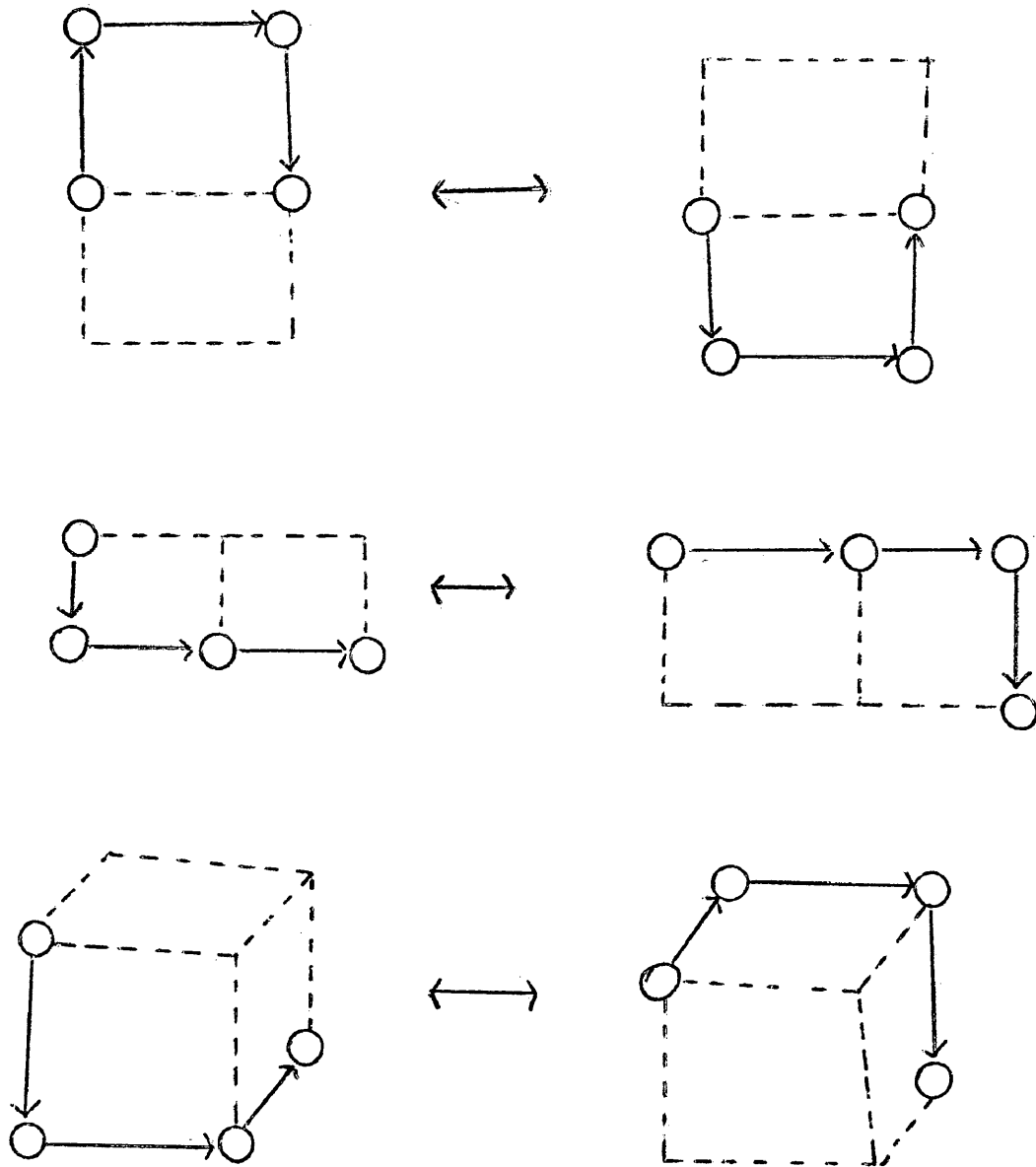


Figure 2.2
 The Possible Crankshaft bead moves for midbonds in the
 Presence of Excluded Volume.



rules :

$$\begin{aligned} \tilde{r}'_{j-1} &= \tilde{r}_{j+1} , \\ \tilde{r}'_j &= \tilde{r}_j , \\ \tilde{r}'_{j+1} &= \tilde{r}_{j-1} \end{aligned} \quad \text{for } 1 \leq j \leq N-1. \quad (2.2)$$

The subscripts 0, 1, N and N - 1 label vectors that are chosen at random from the six possible vectors.

The time interval, in bead cycles, over which the dynamics of the chains are observed is called a frame. Each frame is further divided into samples. The number of bead cycles in each sample varies, and is controlled by input to the program.

At the start of each frame the initial end-to-end length, l_0 , of each chain is calculated, as well as l_0^2 and the position of the center of mass. For each subsequent sample, l_t , l_t^2 , l_t^4 , and the position of the center of mass are again sampled. The products $l_0 \cdot l_t$ and $l_0^2 \cdot l_t^2$ are calculated. This procedure is repeated for some number of frames that is defined by input to the program. This group of frames is called a run.

The products $l_0 \cdot l_t$ and $l_0^2 \cdot l_t^2$ are summed over all the frames for each time, t . The values of l , l^2 , l^4 and the change in the position of the center of mass from the proceeding sample, d , are added into running sums at the end of each sample. At the end of a run the sums are averaged to the quantities

$$\langle l_0 \cdot l_t \rangle, \langle l_0^2 \cdot l_t^2 \rangle, \langle l^2 \rangle, \langle l^4 \rangle \text{ and } \langle d^2 \rangle.$$

From this the correlation functions for each chain as a function of time may be computed as

$$\begin{aligned} \rho(1,1,t) &= \langle l_0 \cdot l_t \rangle / \langle l^2 \rangle, \\ \rho(l^2, l^2, t) &= (\langle l_0^2 \cdot l_t^2 \rangle - \langle l^2 \rangle^2) / (\langle l^4 \rangle - \langle l^2 \rangle^2). \end{aligned} \quad (2.3)$$

This procedure is repeated for a number of runs, again defined by input. The final configurations of each run are used as the initial configuration of the next. Final averages are obtained over all runs for each chain, and then over all the chains. The standard deviation of the final averages is used as a measure of the uncertainty in the results.

It is evident that this model emphasizes the chain connectivity properties of a real polymer chain. It is not possible to look at effects due to short range forces within the polymer. Its utility comes, however in looking at the long range, longtime cooperative motions of the chain'' .

CHAPTER 3

Comparison of Monte Carlo Techniques with the Rouse Model
model polymer chains without excluded volume have shown
remarkable agreement with the Rouse statistical bead
model^{12,13}. In particular, a lattice model chain of N beads
behave svery much like a Rouse chain of N statistical
segments. Theoretical explanations for this have been given
by various arthors^{14,15,16}. The method used by Verdier¹⁶ will
be used here to show the similarities in the relaxation
times and correlation functions for the two models.
Although only single bead moves are considered here, this
method may be extended to include either pure crandshaft or
a mixture of crankshaft and single moves¹⁷.

The Relaxation Times

For single bead moves there are two types of bond
exchanges which result in bead moves. The first is given by

equation 2.1 which is a simple exchange of vectors. The second is one in which an end bond is lost and replaced by one created at random. Calculation of the relaxation of quantities linear in the bond vectors may be accomplished by finding the expectation $\langle \sigma_j(t) \rangle$. This is just the expectation that the i th vector in the initial set of vectors $\{\sigma_1(0), \sigma_2(0) \dots \sigma_{N-1}(0)\}$ will migrate in t moves to the j th position. The angular brackets are used to denote the average over all possible motions of the chain for t steps. Any vector that is absorbed by being replaced at the end, or any vector created at the end will not contribute to this expectation. It can be written then as

$$\langle \sigma_j(t) \rangle = \sum_{i=1}^{N-1} \sigma_i(0) p_{ij}^{(t)} \quad (3.1)$$

The $p_{ij}^{(t)}$ are the probabilities of a vector moving from position i to position j in t bead cycles.

Calculation of the $p_{ij}^{(t)}$ for this case is very similar to that of the t -step transition probabilities for a random walk on a line with two absorbing barriers¹⁸. These t -step probabilities may be calculated with only the knowledge of the one step transition probabilities, $p_{ij}^{(1)} = p_{i,j}$.

The probability that an interior bond will move one step to the right or one step to the left is given by $p_{j,j+1} = 1/N$ or $p_{j,j-1} = 1/N$. The probability that the bond will not move is $p_{i,i} = (N-2)/N$. The matrix of these transition probabilities then looks like

$$\Pi = \begin{pmatrix} K & 1/N & 0 & \dots & 0 & 0 & 0 \\ 1/N & K & 1/N & \dots & 0 & 0 & 0 \\ 0 & 1/N & K & \dots & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & 1/N & K & 1/N \\ 0 & 0 & 0 & \dots & 0 & 1/N & K \end{pmatrix}$$

Here the constant K is used to denote $(N-2)/N$, and Π is a matrix of order $N-1$.

Diagonalization of this matrix yields the t step transition probabilities. Then, by expressing the bond vectors as normal coordinates which are similar to the Rouse normal coordinates, Verdier¹⁶ shows that the relaxation of these normal coordinates is simple exponential and independent of initial configuration.

The relaxation times are therefore of the form $\exp(-t/\tau_{NK})$ where

$$\tau_{NK} = -\ln(1 - (4/N)\sin^2(k\pi/2N)). \quad (3.2)$$

Comparison of the relaxation times for the two models requires rewriting equations 1.23 and 3.2 so that they can be expressed in terms of the same unit of time. This is done by computing the translational diffusion constant, D_{cm} , for both models. For the lattice model, Einstein's relation gives $D_{cm} = 1/6 \cdot \nu \sigma^2$, where ν is the number of times a bead is moved per unit time and σ is the rms magnitude of each displacement¹⁹. Only one bead is moved each bead cycle, so $\nu = 1$ and $\sigma = 2/N$. The diffusion constant is then $D_{cm} = 2/N^2 \cdot 1/6 = 1/3N^2$.

For the Rouse Model, the diffusion constant of a single bead, D , in equation 1.5 is equal to kT/ρ . This is related to the diffusion of the center of mass by $D = D_{cm}N$.

The relaxation times for the two models may now be written as $\tau_{NK} = (3N^2 D_{cm} \ln(1 - (4/N)\sin^2(k\pi/2N)))$ (3.3) for the lattice model, and

$$\tau_{NK} = [24N D_{cm} \sin^2(K\pi/2N)]^{-1} \quad K=0,1,\dots,N-1 \quad (3.4)$$

for the Rouse Model. In writing 3.4 the mean square extension of a submolecule, l^2 is taken as unity.

Both expressions exhibit the same general behavior. The longest relaxation time is for $k = 1$. Spacing between relaxation times is large for small values of k , but decreases as k increases. The relaxation times for both models approach the same value for large N . Even for $N = 8$ the difference in the longest relaxation times for the two models is less than 3%¹⁶.

The Correlation Functions

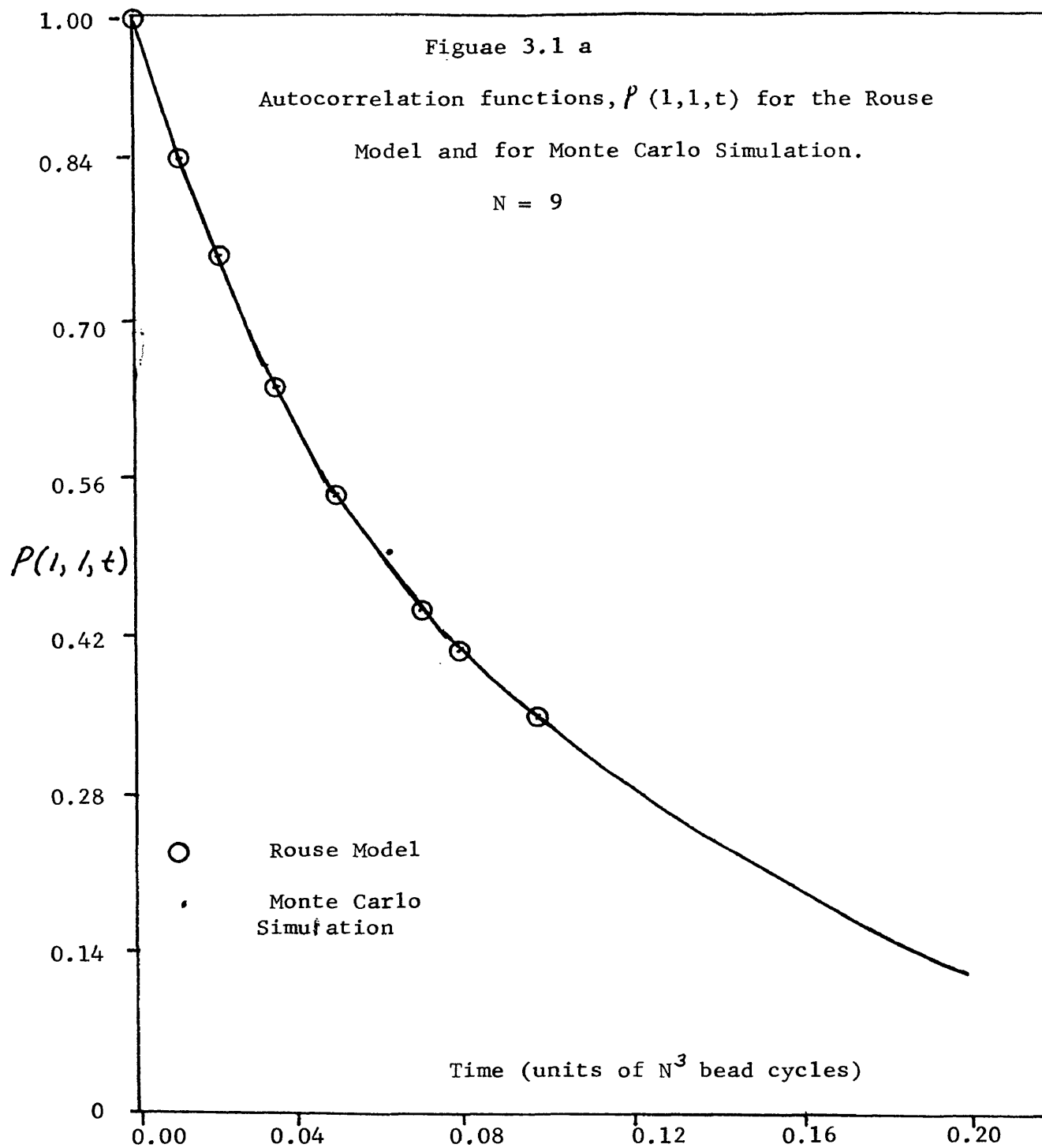
Direct comparison between the Rouse model and computer simulations may be made by calculating the correlation functions of equations 2.3 for the Rouse model. In particular, $\rho(1,1,t) = \langle l_0 \cdot l_x \rangle / \langle l^2 \rangle$ may be calculated as follows.

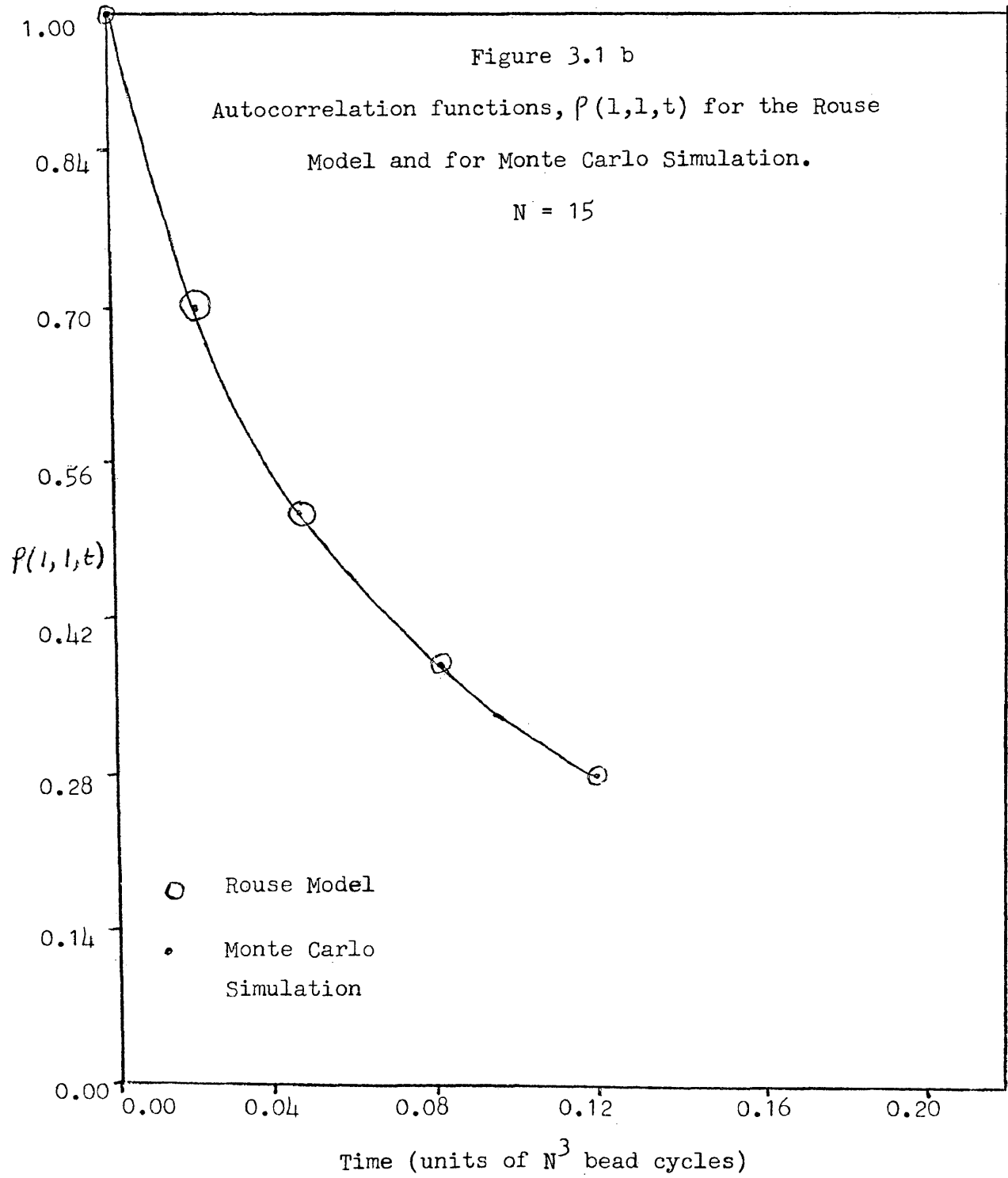
The vector end-to-end length, l may be written as $\underline{l} = \underline{r}_N - \underline{r}_1$ where $r = (x_i, y_i, z_i)$ for bead i . Also, let \underline{u}_m be

the normal coordinates of the Rouse Model. Then by a simple extension of equation 1.11 the \tilde{r}_i may be written as $\tilde{r}_i = \sum_{m=0}^{N-1} R_{jm} \underline{u}_m$. Since R is an orthogonal matrix, its inverse is equal to its transpose and $R_{jm}^{-1} = R_{mj} = (2/N)^{1/2} \cos(n\pi(j - 1/2)/N)$. Let $B_m = R_{Nm} - R_{0m} = (2/N)^{1/2} \cos(\pi n(N - 1/2)/N) - (2/N)^{1/2} \cos(-1/2n\pi/N)$. The correlation functions for vector l may now be written as

$$\rho(l, l, t) = \langle l(t) \cdot l(0) \rangle / \langle l^2 \rangle = \sum_{\lambda=0}^{N-1} \langle B_{\lambda}^2 \underline{u}_{\lambda}(t) \underline{u}_{\lambda}(0) \rangle / \sum_{\lambda=0}^{N-1} \langle B_{\lambda}^2 \underline{u}_{\lambda}(0) \rangle.$$

The normal coordinates, \underline{u}_K may be written as $\underline{u}_K = \langle u_K^2 \rangle \exp(-t/\tau_K)$ where τ_K is the relaxation time of the kth normal mode of vibration and $\langle u_n^2 \rangle_e$ is the mean square of the coordinate at equilibrium. Verdier shows that $\langle u_i^2 \rangle_e = (1/4)N \sin^2(i\pi/2N) = 1/\lambda_i$. This gives $\rho(l, l, t) = \sum_{\lambda=0}^{N-1} (B_{\lambda}^2 / \lambda_i^2) \exp(-t/\tau_{\lambda}) / \sum_{\lambda=0}^{N-1} (B_{\lambda}^2 / \lambda_{\lambda}^2)$. These correlation functions were calculated by computer. The graphical results of these calculations for $N = 9$ and 15 are shown in figures 3.1a and b. Also shown are the results for Monte Carlo simulations for the same chain lengths.





CHAPTER 4

Computer Simulation of the Equilibrium and Dynamic Properties of Random Coil Polymer Chains.

The concentration dependence of both the equilibrium and dynamic properties of polymer chains was studied. Computer experiments for chain lengths of 10, 20 and 30 were performed with concentrations ranging up to 0.8. Both single bead movement rules and mixed rules were used. In order to minimize box edge effects, boxes the size of the chains were used in as many simulations as possible. Smaller boxes were used in some of the runs at higher concentrations because of limitations imposed by computer time. Previous experiments have been performed by Bellemans for equilibrium properties only, and for chains of the same lengths. Kranbuehl and Schardt studied the concentration dependence for both the equilibrium and dynamic properties for chain lengths of 10 and 20 for concentrations of up to 0.6 using single bead movement rules and smaller boxes than were used in this study.

Equilibrium Properties

The equilibrium data sampled in each simulation are $\langle l^2 \rangle$, $\langle l^4 \rangle$ and $\langle d^2/\text{frame} \rangle$. Also of interest is the expansion factor, α . This quantity may be defined by the equation

$$\langle l^2 \rangle = \alpha^2 \langle l_0^2 \rangle.$$

The average end-to-end length squared of the unperturbed chain is given by l_0^2 . By unperturbed is meant the dimensions of the random flight or gaussian chain, in which the end-to-end length is affected only by bond angles and bond lengths. A polymer molecule will assume unperturbed dimensions at the theta temperature, where deviations from ideality vanish. However, in a good solvent at non-theta conditions the attraction of the polymer to the solvent is greater than the attraction of the polymer segments for each other. The polymer will tend to expand so as to minimize these less favorable contacts. Similarly, in a poor solvent at non-theta conditions polymer-polymer contacts are favored over polymer-segment contacts and the chain will contract²⁰.

An expression for $\langle l_0^2 \rangle$ may be obtained from equation 1.1 by performing the integration as described by Flory²⁰. The result is $\langle l_0^2 \rangle = x$, where x is the number of bonds in the chain, and $\langle l_0^2 \rangle$ is expressed in units of the bond length. This gives $\alpha = \langle l^2 \rangle / (N - 1)$, where N is the number of beads in the chain. The expansion factor is expected to be unity under ideal conditions. Fixman and Peterson²¹ have

derived an analytical expression which describes the concentration dependence of α in a good solvent. Initially, α will be greater than one. As the concentration increases in dilute solutions, α decreases rapidly. This decrease slows at higher concentrations, and α approaches unity as ρ^{-1} where ρ is the concentration of the solution.

Studies by Bishop et al²², Wall et al²³, Okamoto²⁴, Kranbuehl and Schardt²⁵, De Vos and Bellemans^{26,27}, and Curro^{28,29,30}, have shown that for chains in dilute solution $\langle l^2 \rangle \propto (N - 1)^{1.2}$. As the solution becomes more concentrated the chains contract and the polymer sizes approach a proportionality of $(N - 1)^{1.0}$ in the bulk phase. This implies that $\alpha > 1$ for dilute solution and becomes one in bulk. This is in line with Flory's reasoning that in the bulk phase the inter-chain repulsions are exactly balanced by the intra-chain repulsions. Therefore the chain will not contract or expand, and $\langle l^2 \rangle$ will be proportional to $(N - 1)^{1.0}$. An $(N - 1)^{1.0}$ dependence in the bulk phase has been observed by Cotton et al³¹ by neutron scattering experiments on bulk polystyrene.

The average squared distance traveled per frame, $\langle D^2 \rangle / \text{frame}$, is another property sampled by the program. This is used to calculate the translational diffusion constant, D_t , given by $D_t = (1/6) \langle D^2 \rangle / t$. The time t is the number of bead cycles in a frame divided by the total number of beads cubed. This time was chosen because a frame

length, whenever possible was one relaxation time. It is not known if this time interval is of sufficient length for the longest range motions of the chain to occur. Data for diffusion over longer time intervals would help to answer this question.

The actual calculation of the chains diffusion became complex because the chain was allowed to penetrate the box walls. This means that when a bead hit a box wall it was moved to the other side of the box. The continuity of the chain was always preserved. Each such hit had to be recorded and used to calculate the diffusion for each chain. Details of this procedure are discussed in Appendix B.

Two factors were found to affect the diffusion of the chains. The first of these is the frame length, the diffusion being greater for greater frame lengths. The second is concentration. Figures 4.1a and 4.1b show the effect of concentration on diffusion for 20 and 30 bead chains. These are graphs of the probability distribution of the average square diffusion of the center of mass of the chain with diffusion measured in the number of lattice sites traveled. As can be seen in these plots, increasing concentration causes the distribution to become sharper and the chains to travel less distance.

Exact calculation of diffusion was not possible using our algorithm if the number of beads in the chain was greater than the box length. However, because of computer

time restrictions it became necessary to go to smaller boxes for the higher concentrations of the 20 and 30 bead chains. The diffusion of chains in these smaller boxes was calculated by assuming that the chain would travel no more than half the box length. Selection of a box size for which this condition would be met was made using Figures 4.1a and 4.1b.

The approach used in calculating the box size and frame length for these smaller boxes is exemplified by the method used in calculating these quantities for concentrations of 0.5 and greater for the 20 bead chains. Analysis of Figure 4.1a indicates that by choosing a box size of 10 and not increasing the frame length no chain should travel more than 5 lattice sites when the density is increased to 0.5.

This box size of 10 was used for all concentrations of 0.5 and higher. The frame length for the density of $\rho = 0.6$ was chosen by multiplying the frame length used at $\rho = 0.5$ by the quantity $D(\rho = 0.4)/D(\rho = 0.5)$. This allows the frame length to increase within safe limits by taking into account the fact that as density increases the diffusion will be less. Frame lengths for densities of 0.7 and 0.8 were chosen in the same way. A similar analysis of Fig. 4.1b led to the the use of a box size of 14 for 30 bead chains.

Dynamic Properties

As a measure of the dynamics of the system, the autocorrelation function,

$$\rho(1,1,t) = \langle 1_0 \cdot 1_t \rangle / \langle 1^2 \rangle, \quad \text{and}$$

$$\rho(1^2,1^2,t) = (\langle 1_0^2 \cdot 1_t^2 \rangle - \langle 1^2 \rangle^2) / (\langle 1^4 \rangle - \langle 1^2 \rangle^2)$$

were obtained from the program. The time, t , is measured in N bead cycles, where N is the total number of beads. These autocorrelation functions are normalized so that they have a value of one at $t=0$ and decrease to zero as time increases. This relaxation behavior of the autocorrelation functions is characteristic of the overall relaxation behavior of the chain. It is not simple exponential. However, for times after which the autocorrelation function has dropped to about $1/2$, it is nearly simple exponential and may be fitted to a function of the form $\rho(t) = \exp(-t/\tau_s)$. This part of the graph is fitted to a function of the form $\ln \rho(1,1,t) = \ln A - t/\tau_s$. The relaxation time, τ_s , may then be calculated from the limiting slope. This relaxation time should be representative of the longest relaxation time found in the Rouse Model. It will therefore involve the long range motions of the chain.

A second relaxation time, $\tau_{1/e}$, is defined as the time it takes $\rho(1,1,t)$ to relax to a value of $1/e$. This

relaxation time is characteristic of the overall relaxation of the chain.

Results and Discussion

The results for the equilibrium properties are shown in tables 4.1 and 4.2. Previous studies of the concentration effects on the equilibrium dimensions were made by De Vos and Bellemans^{26,27}. For low concentration Bellemans used the same model as in the present study, with crankshaft bead movement rules. Samples of $\langle l^2 \rangle$ were made about every 200 bead moves. Because this model has a large number of excluded volume conflicts at high concentrations resulting in large amounts of computer time needed, a different approach was taken. Bellemans approach was to use single bead rules but to pick an empty lattice site at random. If an adjacent bead could move to this site it was moved. Bellemans data is summarized in Table 4.3. Figure 4.2 shows a graphical comparison of our model to Bellemans. Mixed bead movement results are shown, the results of the single bead movements are very similar. All points are within one standard deviation of Bellemans results. This data shows that $\langle l^2 \rangle$ decreases with increasing density. The last four points fit better to $\rho^{-.32}$ than ρ^{-1} .

The dependence of end-to-end length on chain length may be found by taking the slope of lines generated by a log-log plot of $N - 1$ vs $\langle l^2 \rangle$. The results are shown in Table 4.4

The parameter a is the exponent in the equation $\langle l^2 \rangle \propto (N - 1)^a$. It is simply the slope of the plot of $\log \langle l^2 \rangle$ vs $\log(N - 1)$. Results compare with those of Bishop *et al*²² and Bellemans^{26,27}. They show a decrease in the exponent a from 1.2 for a single chain to a value approaching 1 in bulk.

That chains in concentrated solutions show the behavior of $\langle l^2 \rangle \propto (N - 1)^{1.0}$ means that they behave as Gaussian or ideal chains. This does not mean that the complete distribution of chain segments is gaussian, since the distribution is uniquely determined by all even moments, not just the second.

The average end-to-end length squared vs density is plotted in Fig 4.3. The results have been extrapolated to a density of 1. The theoretical results for $\langle l^2 \rangle$ from second order (5 choice) random wald calculations on a cubic lattice at this density are given by Curro³⁰ as

$$\langle r^2 \rangle = ((1 + \delta)/(1 - \delta))n - 2(1 - \delta^m)/(1 - \delta^m)$$

where $\delta = 1/(q - 1)$ and q is the coordination number of the lattice (6 for a cubic lattice). The extrapolated results are close for all three chain lengths, as expected. No exact expression was readily available for $\langle l^4 \rangle$, but the theoretical values for $\langle l^4 \rangle / \langle l^2 \rangle^2$ were obtained from Curro as 1.47, 1.51 and 1.55 for chain lengths of 10, 20 and 30 respectively. Plots of $\langle l^4 \rangle / \langle l^2 \rangle^2$ for all three chain lengths vs density are given in Fig 4.4. They are again

extrapolated to a density of 1, and the agreement is good with the results for a gaussian chain.

The distribution function $W(r)$ is completely determined by the even moments. It is a slowly converging series, however, so it can only be written in terms of just the second and fourth moments as a rough approximation. Curro gives this as

$$W(r) \sim \pi^{-3/2} \exp(-\rho^2) \left((1 + 15g_4) - 20g_4\rho^2 + 4g_4\rho^4 \right)$$

$$\text{where } \rho^2 = 3r^2 / 2\langle r^2 \rangle \text{ and}$$

$$g_4 = 0.125 \left((3/5) \langle r^4 \rangle / \langle r^2 \rangle^2 - 1 \right).$$

The concentration dependence of $\langle l^2 \rangle$ and $\langle l^4 \rangle / \langle l^2 \rangle^2$ with the ideal chain values suggests that this approximate distribution is the same for all chain lengths for the bulk system and the gaussian chain. Data for the higher even moments would be necessary to show with a higher certainty that the two distributions are the same.

The concentration dependence of $\langle l^2 \rangle$ is predicted by theory³¹ to be $\langle l^2 \rangle \sim \rho^{-\gamma}$ with $\gamma = 0.25$ in three dimensions. Least squares fits of the plots of $\log \langle l^2 \rangle$ vs $\log \rho$, shown in Figure 4.5, gave values of γ to be 0.07 ± 0.005 , 0.12 ± 0.05 and 0.13 ± 0.04 for chain lengths of 10, 20, and 30. Table 4.4b shows a comparison of those of Curro³⁰ and Bishop et al²². Our results are within one standard deviation of both sets of data. The exponents for

the small chain lengths are less than predicted by theory. For the longer chain lengths used by Bishop et al²², the exponents did approach the expected result of 0.25.

Plots of D_z vs. bead density are shown in Fig. 4.6a for mixed bead movements and in Fig. 4.6b for single bead movements. The diffusion constant appears to be independent of chain length. D_z decreases linearly with increasing concentration. This decrease might be expected to be less pronounced because frame lengths of less than one relaxation time were used for the higher concentrations of the 20 and 30 bead chains. This length of time is most likely not sufficient for the long range motions of the chain to have occurred, with the result that D_z is too small.

Plots of $\ln \rho(1,1,t)$ vs. time are shown in Figures 4.7a through 4.7h. The time is measured in N^3 bead cycles, with N being the total number of beads in the box. The error bars correspond to one standard deviation of the mean.

The Dynamic results are shown in tables 4.5 and 4.6. Figure 4.8 is a plot of τ_s vs. bead density. The behavior of τ_s is different for the mixed and single bead movement rules. It is the same, however, for the three chain lengths using a given rule. τ_s varies much more slowly at low concentrations for the mixed plots than for the single ones. Behavior is similar for the two bead movement rules for concentrations above about 0.5.

For the mixed moves, τ_s changes very little at the low

densities, but increases very rapidly at the high densities. This effect is much less pronounced for the single moves. A behavior was seen by Kranbuehl and Verdier¹⁷ in the study of the effect of bead movement rules on isolated chains of various lengths. They found that τ_3 increased much more slowly for mixed moves at small chain lengths (10 to 20 beads) than for either pure single or pure crankshaft moves. They also found that the increase in τ_3 with chain length was similar for all bead movement rules at longer chain lengths.

The smaller dependence of τ_3 on density at low densities than at high densities may be explained as follows. At low densities each chain is isolated from the others, each chain forming a cluster. As chains are added this situation does not change until some critical density, ρ^* is reached. At this point the chains become entangled and the relaxation is slowed by these interchain excluded volume effects. At this density τ_3 begins to rise sharply with increasing density.

Figures 4.9a and b are log-log plots of τ_3 vs density. The concentration, ρ^* , at which entanglement begins is the concentration at which the two lines intersect. These concentrations are given in Table 4.7. Schaefer, Joanny and Pincus have predicted that ρ^* is proportional to $1/(N-1)^{4/5}$. As expected, the critical density decreases with increasing chain length. It does not decrease as

rapidly as expected, however. Little can be seen from the runs using single bead moves because runs were not taken to high enough densities.

Figures 4.10a and 4.10b are plots of $\ln \tau_s$ vs. $\ln(N)$ for the various densities. Table 4.8 shows the slopes for each of these lines. For both types of bead movement rule the dependence on chain length increases with increasing density. This dependence is much larger in the single bead movement rules than for the mixed ones.

Figures 4.10c and 4.10d are similar plots of $\ln \tau_{1/2}$ vs. $\ln(N)$. The overall relaxation of the chain shows little change in its N-dependence with increasing densities until a density of $\rho = 0.6$, at which point it also begins to increase.

The dimensionless quantity $\tau_s D_t / \langle l^2 \rangle$ has been found to be nearly linear, as shown in Table 4.5. This gives

$$D_t \propto \tau_s / \langle l^2 \rangle. \quad (4.1)$$

Einstein's equation relates D to the viscosity, η , by the equation

$$D_t \propto 1/\eta. \quad (4.2)$$

Combining equations 4.1 and 4.2 gives

$$\eta \propto \langle l^2 \rangle / \tau_s. \quad (4.3)$$

Cohen and Turnbull derived a relation between the diffusion and free volume by considering transport in a liquid of hard spheres. The molecules are pictured as traveling in a cage consisting of their nearest neighbors.

Diffusion occurs when a hole large enough for the molecule to move through opens up in the cage and another molecule occupies its original position before it is able to return. Using this approach they found that

$$D = D(v^*) \exp(-\gamma v^*/v_f). \quad (4.4)$$

In this equation v^* is a critical volume just large enough to allow another molecule to jump in after the displacement. The average free volume per molecule, v_f , is the volume within the cage minus the volume of the molecule. The contribution of the molecule to the diffusion coefficient is $D(v^*)$, as $D(v)$ is zero if $v < v^*$. $D(v^*)$ is equal to ga^*u with a^* being the molecular diameter, u the velocity of the molecule and g is a geometrical factor. The final quantity, γ is a numerical factor introduced to include the overlap of free volume between molecules and should lie between 1/2 and 1.

An empirical relation of the same form, $\eta = A \exp(Bv_f/v_0)$ was found by Doolittle for simple hydrocarbons³⁶. Here v_f is the free volume of the molecular unit or bead and v_0 is the volume of the bead.

Combining equations 4.2, 4.3, and 4.4 gives

$$\langle l^2 \rangle / \tau_3 \propto D(v^*) \exp(\gamma v^*/v_f). \quad (4.5)$$

The quantity γv^* must be nearly equal to the molecular volume, giving

$$\langle l^2 \rangle / \tau_3 \propto \exp(1/v_f).$$

The free volume, v_f , is the total free volume divided by the number of beads, N . Letting V be the total volume, $v_f = (V - N)/N = (1 - \rho)/\rho$. Therefore $\langle l^2 \rangle / \tau_s \propto (\rho / (1 - \rho))$. A plot of $\ln \langle l^2 \rangle / \tau_s$ vs. $\rho / (1 - \rho)$ is given in Figure 4.11. As predicted it is a linear graph. Also $\langle l^2 \rangle / \tau_s$, which is proportional to D_t is independent of chain length.

Table 4.9 shows the values for $\tau_{1/e}(l^2)$ and $\tau_s(l^2)$ for the correlation functions $\rho(l^2, l^2, t)$. Plots of $\rho(l^2, l^2, t)$ vs time are shown in Figures 4.12a and b. The dependence of $\tau_s(l^2)$ on concentration is shown in figure 4.13. There appears to be no difference based on chain lengths. Figure 4.14 shows that a break point occurs at a density of 0.46. This is comparable to the density at which the break point occurred in τ_s for the longest chain length studied.

The effect of concentration on equilibrium properties agrees with previous studies. $\langle l^2 \rangle$ is proportional to $(N - 1)^a$ where the exponent a is near 1.2 for the single chain and approaches an extrapolated value of 1.0 in bulk. Agreement of $\langle l^2 \rangle$ and $\langle l^4 \rangle / \langle l^2 \rangle^2$ at high concentrations with random walk calculations in bulk is good. This suggests that the distribution of end-to-end length for the bulk system is consistent with that of the gaussian chain. The exponent in the equation $\langle l^2 \rangle \propto (N - 1)^a$ was found to be lower than predicted by theory. The exponent agrees with previous simulations, which show that the theoretical value

is approached as chain length is increased. Diffusion decreases linearly with concentration and is not dependent on chain length.

The behavior of the longtime relaxation, τ_s , is different for mixed and single bead movement rules at low concentration. Behavior is similar at high concentrations. The critical density was found to decrease with increasing chain length, but at a much slower rate than predicted by theory. The N dependence of τ_s increases with increasing density. This increase appears to be stronger for the single bead movement rules than for the mixed ones. The slope of $\ln(\tau_s)$ vs. N increases by a factor of 1.33 for the mixed moves vs. 1.73 for the single moves in the concentration range 0.04 to 0.5. The N dependence of $\tau_{1/e}$ is less pronounced for low concentrations than high ones. Again this increase is larger for single moves. For single moves the slope of $\ln(\tau_{1/e})$ vs. N increases by a factor of 1.45 vs. an increase of 1.08 for the mixed moves in the concentration range 0.04 to 0.5. The overall increase in the N dependence of the long-time relaxation is less than that of the overall relaxation. This suggests that the short range, faster relaxation modes are less affected by concentration changes than the long range cooperative relaxation modes.

The quantity $\ln \langle l^2 \rangle / \tau_s$ vs $(\rho / (1 - \rho))$ is linear as predicted by the free volume theories of Doolittle and

Williams, Landel, and Ferry. The free volume theory provides a good description of the dependence of the relaxation time on polymer volume fraction.

Table 4.1

Mixed Bead Movements. Equilibrium Data.

Length	#Runs	#Frames	Box	Dens	$\langle D^2 \rangle$	Std	$\langle D \rangle$	$\langle L^2 \rangle$	Std	$\langle L \rangle$	Std	χ^2	Std
9	40	200	32	----	2.95	0.17	3.28	13.31	0.39	224	12	0.41	0.04
10	50	100	10	.04	2.38	0.12	3.30	14.70	0.09	297	3	1.63	0.01
10	10	100	10	0.20	2.58	0.10	2.39	14.29	0.20	280	8	1.59	0.02
10	8	100	10	0.40	2.46	0.13	1.33	13.87	0.21	286	7	1.54	0.02
10	6	50	10	0.50	2.20	0.17	0.93	13.63	0.54	256	19	1.49	0.06
10	10	20	10	0.60	1.93	0.26	0.36	13.43	0.54	253	19	1.49	0.06
10	6	20	10	0.70	1.44	0.22	0.34	13.10	0.68	244	24	1.46	0.08
10	8	8	10	0.80	1.53	0.26	0.12	13.30	0.63	252	21	1.48	0.07
15	40	100	32	----	5.00	0.52	4.63	25.23	1.1	887	69	1.80	0.08
20	10	25	20	0.04	5.86	0.59	4.65	36.1	0.9	1848	81	1.90	0.05
20	6	10	20	0.20	4.36	1.40	2.91	34.7	2.0	1727	287	1.69	0.17
20	4	4	20	0.40	4.09	1.13	1.79	31.9	3.2	1506	287	1.68	0.17
20	12	15	20	0.50	4.32	0.28	1.19	31.8	1.3	1447	110	1.67	0.07
20	12	10	20	0.60	4.57	8.00	1.26	30.5	2.0	1389	1.61	1.61	0.11
20	4	15	20	0.70	1.56	0.17	0.42	30.5	3.5	1425	331	1.61	0.18
20	4	15	20	0.80	0.27	0.13	0.05	28.6	13	1212	564	1.51	0.68
32	20	25	32	----	12.5	3.08	6.94	66.01	5.7	6239	1068	2.13	0.18
30	4	20	30	0.06	9.00	1.90	5.74	58.90	3.0	4994	498	2.03	0.10
30	8	15	30	0.20	8.06	3.06	3.60	55.61	7.0	4569	1105	1.92	0.24
30	6	6	14	0.40	5.22	0.69	2.07	51.60	5.0	4040	814	1.78	0.17
30	4	4	14	0.50	4.19	0.50	1.44	50.39	4.5	3817	690	2.68	0.16
30	4	5	14	0.60	2.83	0.44	0.86	49.20	6.3	3633	837	1.70	0.22
30	3	4	14	0.70	2.02	0.38	0.60	52.14	12	4259	2049	1.80	0.41
30	2	5	14	0.80	1.24	0.28	0.19	56.19	15	4845	2708	1.94	0.52

Table 4.2

Single Bead Movements. Equilibrium Data.

Length	#Runs	#Frames	Box	Dens	$\langle D^2 \rangle$	Std	D_t	$\langle L^2 \rangle$	Std	$\langle L^4 \rangle$	Std	α^2	Std
9	30	90	32	-----	2.53	0.28	1.28	12.92	0.88	3.07	475	1.62	0.22
*10	10	500	8	0.02	-----	-----	0.93	14.81	0.21	297	8	1.654	0.02
*10	10	500	6	0.19	-----	-----	0.51	14.37	0.19	282	7	1.597	0.02
*10	10	400	6	0.42	-----	-----	0.26	13.89	0.28	267	9	1.543	0.03
10	8	20	10	0.50	3.47	0.40	0.32	13.74	0.38	264.60	14	1.53	0.40
10	6	20	10	0.50	-----	-----	0.24	13.55	0.32	257	20	1.50	0.06
*10	10	400	6	0.60	-----	-----	0.24	13.55	0.32	257	11	1.506	0.06
*20	10	200	8	0.04	-----	-----	1.45	35.75	0.90	1082	74	1.892	0.05
*20	5	100	8	0.20	-----	-----	0.92	34.07	1.45	1661	135	1.793	0.08
*20	5	100	7	0.41	-----	-----	0.50	31.63	1.53	1446	129	1.665	0.08
*20	5	100	7	0.52	-----	-----	0.32	30.69	1.65	1387	132	1.613	0.09
15	10	100	32	-----	4.32	0.63	1.38	25.02	0.86	879	51	1.79	0.06
20	8	25	20	0.04	5.40	0.64	1.36	35.90	0.74	1829	68.5	1.89	0.04
20	2	4	20	0.20	3.49	2.82	0.59	35.44	4.90	1791	282	1.87	0.20
20	2	2	10	0.40	2.71	7.50	0.50	31.53	4.00	14.67	349	1.66	0.21
20	3	20	10	0.50	3.63	0.40	0.28	31.10	2.50	1438	213	1.64	0.13
20	3	6	10	0.60	4.32	0.70	0.16	31.54	1.73	14386	386	1.66	0.09
32	20	25	32	-----	10.35	4.81	1.44	67.25	6.4	6467	1214	2.17	0.21
30	20	25	14	0.04	6.61	0.64	1.41	59.17	0.6	5056	109	2.04	0.02
30	4	4	14	0.20	4.27	2.00	0.76	53.95	7.0	4216	1080	1.86	0.24
30	2	2	14	0.40	4.33	1.70	0.33	49.87	9.9	3665	1482	1.72	0.34
30	2	2	14	0.50	4.81	2.12	0.18	50.96	12	4023	1840	1.76	0.41

Table 4.3

Concentration dependence of the end to end
Length. Data from A. Bellemans and E. De Vos

ρ	N=10			N=20			N=30		
	$\langle l^2 \rangle$	α^2	ρ	$\langle l^2 \rangle$	α^2	ρ	$\langle l^2 \rangle$	α^2	ρ
0.0000	14.7806	1.642	0.0000	36.32	1.910	0.0000	60.40	1.910	0.0000
0.0930	14.587 ± .027	1.621	0.1006	35.37	1.860	0.1111	57.40	1.860	0.1111
0.2015	14.312	1.590	0.2138	34.22	1.801	0.1901	55.94	1.801	0.1901
.2933	14.111	1.568	0.2975	33.35	1.755	0.3053	52.88	1.755	0.3053
0.3608	13.988	1.544	0.3975	32.49	1.710	0.3884	52.17	1.710	0.3884
0.4506	13.786	1.532	0.4975	31.73	1.670			1.670	
0.4858	13.707	1.528	0.5975	30.71	1.616			1.616	
0.5729	13.519	1.502							
0.5867	13.515	1.502	0.5957	31.06 ± .32	1.635	0.5957	48.812 ± .32	1.635	0.5957
0.7262	13.218	1.476	0.6982	30.57	1.609	0.6982	49.17	1.609	0.6982
0.7438	13.199	1.467	0.6982	30.36	1.598	0.6982	47.76	1.598	0.6982
0.8695	13.018	1.446	0.7910	29.50	1.553	0.7910	44.70 ± .97	1.553	0.7910
			0.7910	29.13	1.533	0.7910		1.533	
0.7983	13.122 ± .090	1.458	0.8495	28.17	1.483	0.8495		1.483	
0.8423	13.084	1.545	0.8496	30.79	1.621	0.8496		1.621	
0.8986	12.896	1.433	0.8984	27.04	1.530	0.8984		1.530	
0.9497	12.924	1.436							
1.0000	12.79 ± .02	1.421	1.0000	28.34 ± .19	1.492	1.0000		1.492	

--The first set of data at each chain length (up to the first blank line) was obtained using a computer model the same as in the present studies.

--The second set of data was obtained by use of a model in which empty lattice sites are moved instead of beads.

--The data given for polymer volume fraction of one was obtained by extrapolation of the computer results.

Table 4.4

a. The dependence of $\langle l^2 \rangle$ on chain length

density	a	
0.04	1.18	$\langle l^2 \rangle \propto (N-1)^a$
0.20	1.16	
0.40	1.11	
0.50	1.12	
0.60	1.06	
0.70	1.12	
0.80	1.17	

b. The dependence of $\langle l^2 \rangle$ on density

l	γ	γ (Curro)	γ (Bishop)	
5			.06 ± .01	$\langle l^2 \rangle \propto \rho^{-\gamma}$
10	.07 ± .005		.13 ± .02	
15		.076		
20	.12 ± .005	.077	.163 ± .02	
30	.13 ± .04			
32			.20 ± .03	
50			.22 ± .02	
70			.23 ± .02	

Table 4.5

Mixed bead movements. Dynamic Properties.

Length	Density	Fr.Len.	#Frames	#Chains	$\tau_{1/e}$	Δf	τ_3	$1/\tau_3$	$\tau_3 D_2 / k_{127}$
9	----	0.150	8000	1	0.14	0.035	$0.15 \pm .02$	-1.88	0.04
10	0.04	0.120	5000	4	0.15	0.002	0.19	-1.66	0.04
10	0.20	0.180	1000	20	0.19	0.01	0.21	-1.56	0.04
10	0.40	0.310	800	40	0.30	0.02	0.36	-1.02	0.03
10	0.50	0.395	300	50	0.41	0.04	$0.50 \pm .08$	-0.70	0.03
10	0.60	0.650	200	60	0.59	0.04	$0.68 \pm .31$	-0.39	0.03
10	0.70	0.700	120	70	1.00	0.05	$1.20 \pm .21$	0.25	0.03
10	0.80	2.100	128	80	2.13	0.04	$3.23 \pm .36$	1.17	0.03
15	----	0.18	4000	1	0.16	0.05	0.23	-1.46	0.04
20	0.04	0.210	250	16	0.20	0.05	$0.26 \pm .01$	-1.35	0.03
20	0.20	0.25	60	80	0.27	0.06	$0.30 \pm .05$	-1.20	0.03
20	0.40	0.38	32	160	0.45	0.10	$0.65 \pm .06$	-0.43	0.04
20	0.50	0.606	180	25	0.65	0.04	$1.02 \pm .18$	0.02	0.05
20	0.60	0.696	120	30	1.04	0.05	$1.43 \pm .15$	0.36	0.06
20	0.70	0.623	120	35	1.90	0.07	$3.09 \pm .32$	1.13	0.04
20	0.80	0.720	240	40	4.61	0.07	$7.46 \pm .3$	2.01	0.01
32	----	0.300	500	1	0.26	0.06	0.32	-1.13	0.03
30	0.06	0.36	80	36	0.29	0.06	$0.41 \pm .01$	-0.89	0.04
30	0.20	0.450	120	17	0.37	0.04	0.45	-0.80	0.03
30	0.40	0.420	36	18	0.565	0.07	0.83	-0.19	0.01
30	0.50	0.487	32	46	0.734	0.07	1.13	0.12	0.03
30	0.60	0.540	40	55	1.239	0.09	$1.79 \pm .38$	0.58	0.03
30	0.70	0.676	24	64	2.86	0.1	4.30 ± 1.4	1.469	0.40
30	0.80	1.10	20	73	4.91	0.1	11.1 ± 4.9	2.411	0.04

Table 4.6

Single bead movements. Dynamic Properties

Length	Density	Fr.Len.	#Frames	#Chains	$\tau_{1/e}$	$\Delta\rho$	$\bar{\tau}_s$	$10\bar{\tau}_s$	$\bar{\tau}_s \rho_c / k_{1,2}$
9	----	0.33	2700	1	0.33	0.04	0.37	-0.99	0.04
*10	0.02	1.00	5000	1	0.33	----	0.44	-0.82	0.036
*10	0.19	1.00	5000	4	0.44	----	0.56	-0.58	0.036
*10	0.42	1.00	4000	9	0.73	----	0.96	-0.04	0.035
10	0.50	1.80	160	50	1.28	0.04	1.28	0.25	0.03
10	0.60	1.40	120	60	1.36	0.50	1.31	0.27	0.02
*10	0.60	1.25	400	13	1.36	----	1.76	0.57	0.034
*20	0.04	1.25	2000	1	0.71	----	1.13	0.12	0.046
*20	0.20	1.25	500	5	1.00	----	1.45	0.37	0.039
*20	0.41	1.25	500	7	1.57	----	2.06	0.72	0.032
*20	0.52	1.25	500	9	2.15	----	2.77	1.02	0.029
15	----	0.50	1000	1	0.50	0.04	0.65	-0.43	0.04
20	0.04	0.71	200	16	0.70	0.04	0.91 \pm .17	-0.09	0.03
20	0.20	1.00	8	80	0.95	0.17	1.32	0.28	0.02
20	0.40	1.57	4	160	1.40	0.14	2.13	0.76	0.04
20	0.50	2.15	60	25	2.34	0.07	4.20 \pm .9	1.44	0.04
20	0.60	4.80	18	30	3.43	0.07	7.58 \pm .12	2.03	0.04
32	----	1.20	500	1	1.18	0.06	1.40 \pm .12	0.40	0.03
30	0.04	0.788	300	4	1.08	0.02	1.55	0.44	0.04
30	0.20	1.30	24	18	1.38	0.10	2.63 \pm 1	0.97	0.04
30	0.40	2.80	8	37	2.93	4.57	4.17	1.43	0.03
30	0.50	4.60	8	46	4.69	7.69	7.14 \pm 3	1.97	0.03

Table 4.7

Densities at which chain entanglements begin
Mixed Moves

Chain Length	ρ^*	
10	0.54	Ratio 1 : .91 : .86
20	0.49	Predicted Ratio 1 : .6 : .4
30	0.42	

Table 4.8

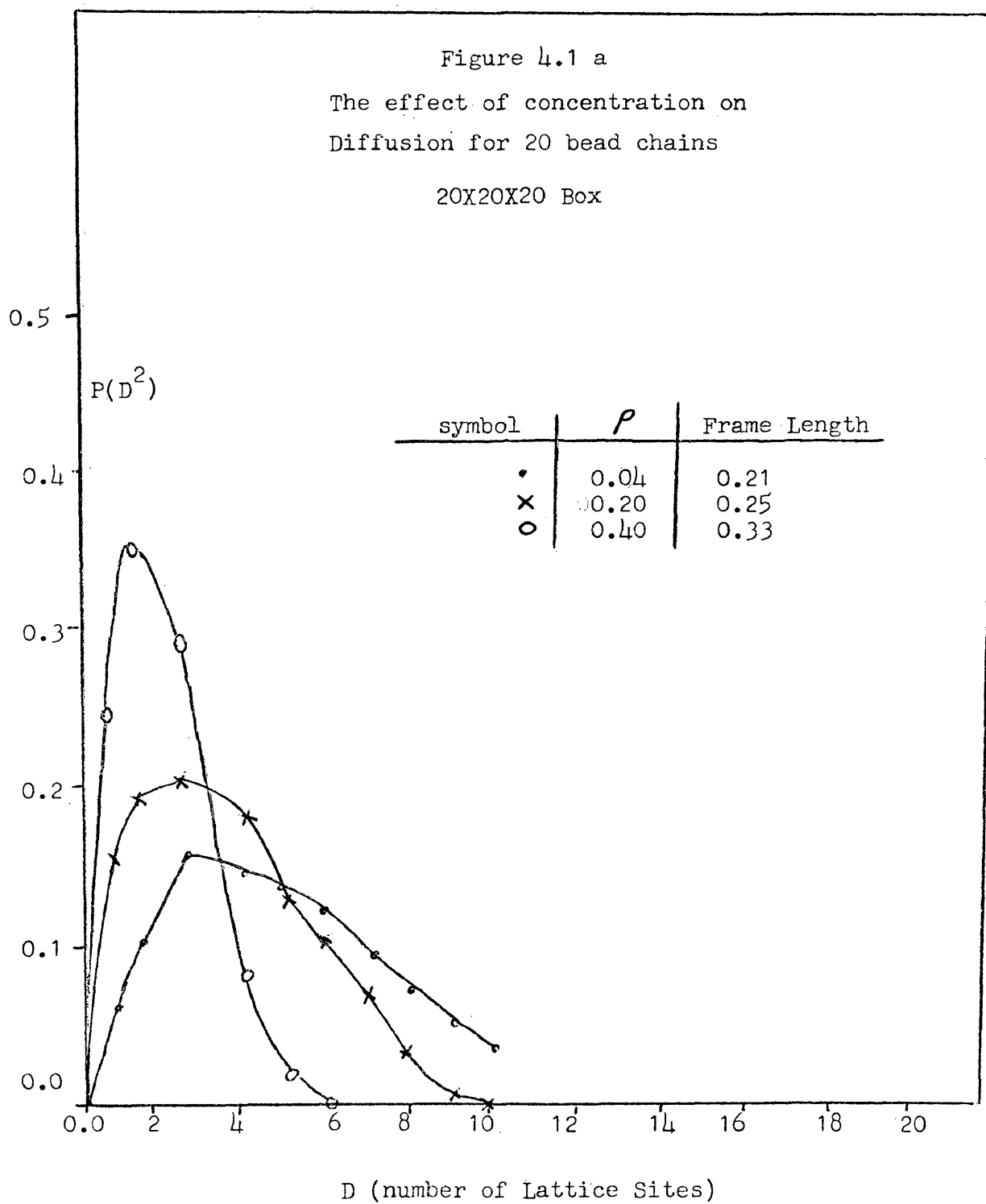
The dependence of relaxation times on chain length

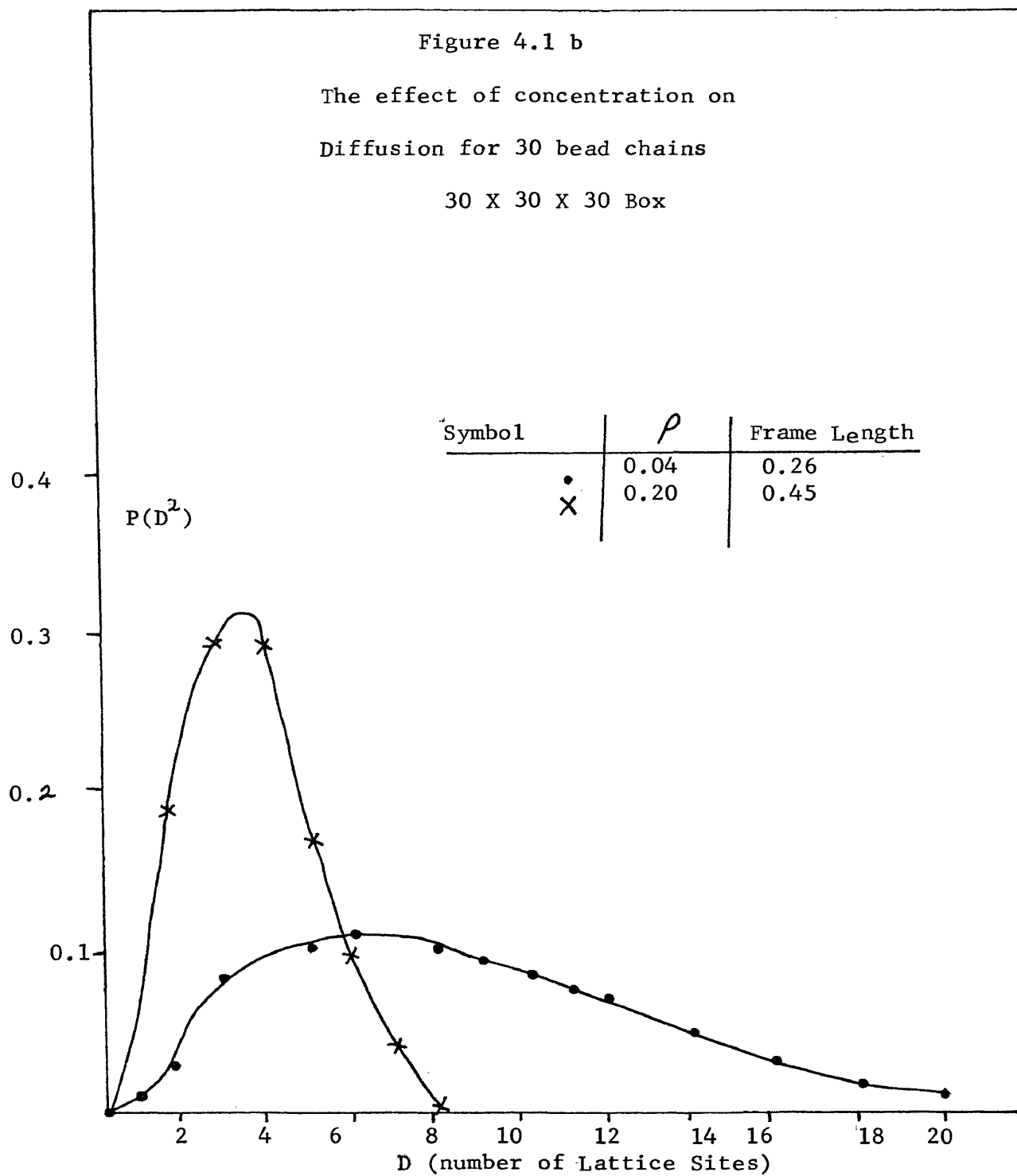
Density	Slope of $\ln \tau_r$ vs $\ln(N)$		Slope of $\ln \tau_{re}$ vs $\ln(N)$	
	Mixed	Single	Mixed	Single
1 chain	0.58	1.18	0.50	1.09
0.04	0.68	1.17	0.58	1.13
0.2	0.67	1.40	0.60	1.39
0.4	0.76	1.18	0.57	1.31
0.5	0.77	2.04	0.54	1.58
0.6	0.90		0.70	2.09
0.7	1.13		0.95	
0.8	1.16		0.79	

Table 4.9

Relaxation of $\rho(L^2, L^2, T)$

Length	Density	τ_{ye}	ΔP	T_s	ΔT_s
10	0.04	0.03	0.04	0.04	0.01
10	0.20	0.04	0.04	0.05	0.01
10	0.40	0.07	0.07	0.11	0.02
10	0.50	0.07	0.11	0.17	0.05
10	0.60	0.09	0.15	0.13	0.08
10	0.70	0.17	0.15	0.23	0.14
10	0.80	0.26	0.32	0.56	0.15
20	0.04	0.03	0.80	0.05	0.01
20	0.20	0.03	0.21	0.08	0.01
20	0.40	0.04	0.43	0.06	0.01
20	0.50	0.09	0.13	0.09	0.02
20	0.60	0.11	0.35	0.16	0.16
20	0.70	0.26	0.22	0.52	0.19
20	0.80	0.41	0.26	0.74	0.25
30	0.04	0.04	0.24	0.07	0.01
30	0.20	0.03	0.17	0.07	0.02
30	0.40	0.07	0.30	0.13	0.13
30	0.50	0.08	0.21	0.21	0.19
30	0.60	0.04	0.25	0.21	0.20
30	0.70	0.12	0.19	0.26	0.20
30	0.80	0.20	0.42	0.65	0.25





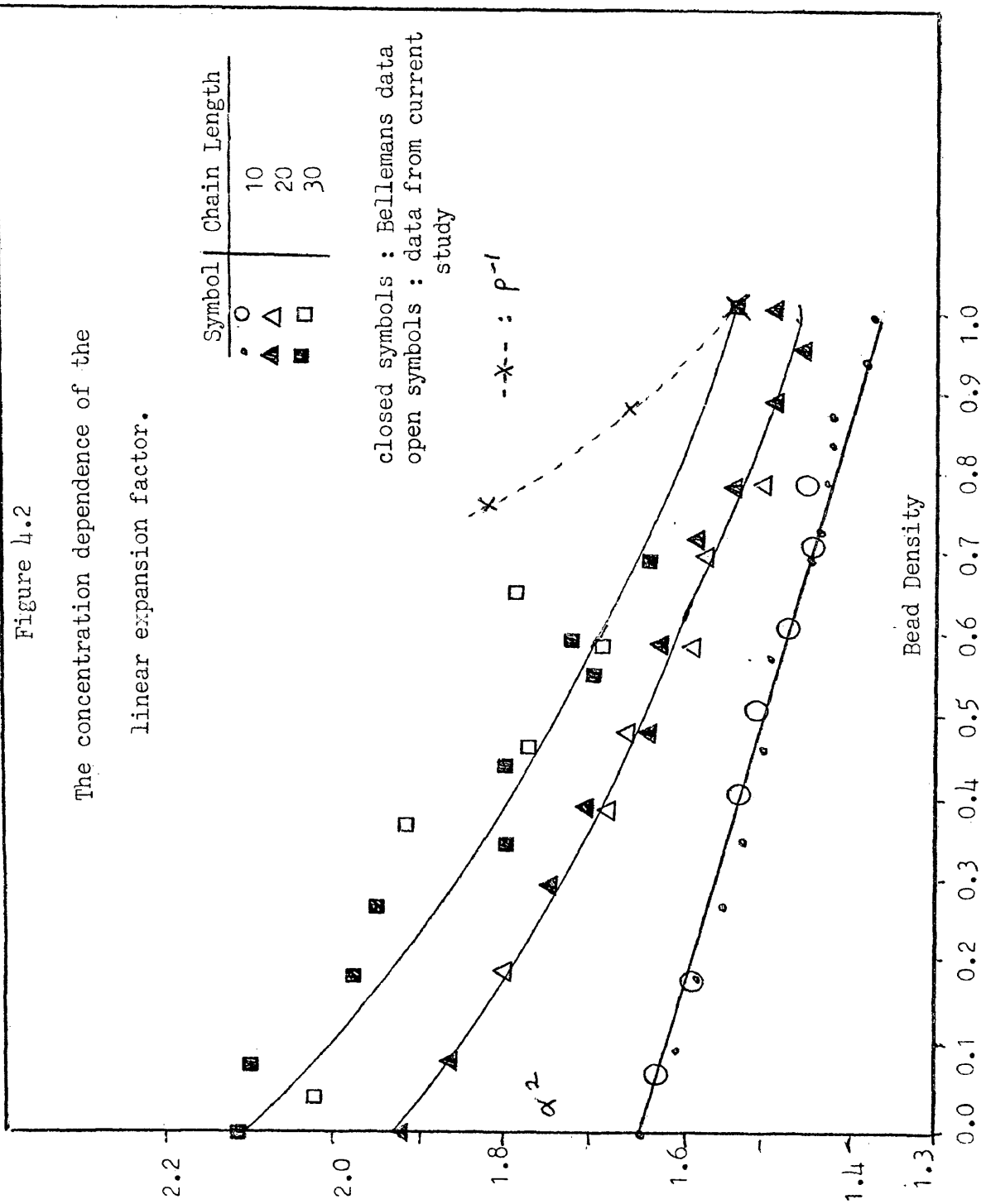
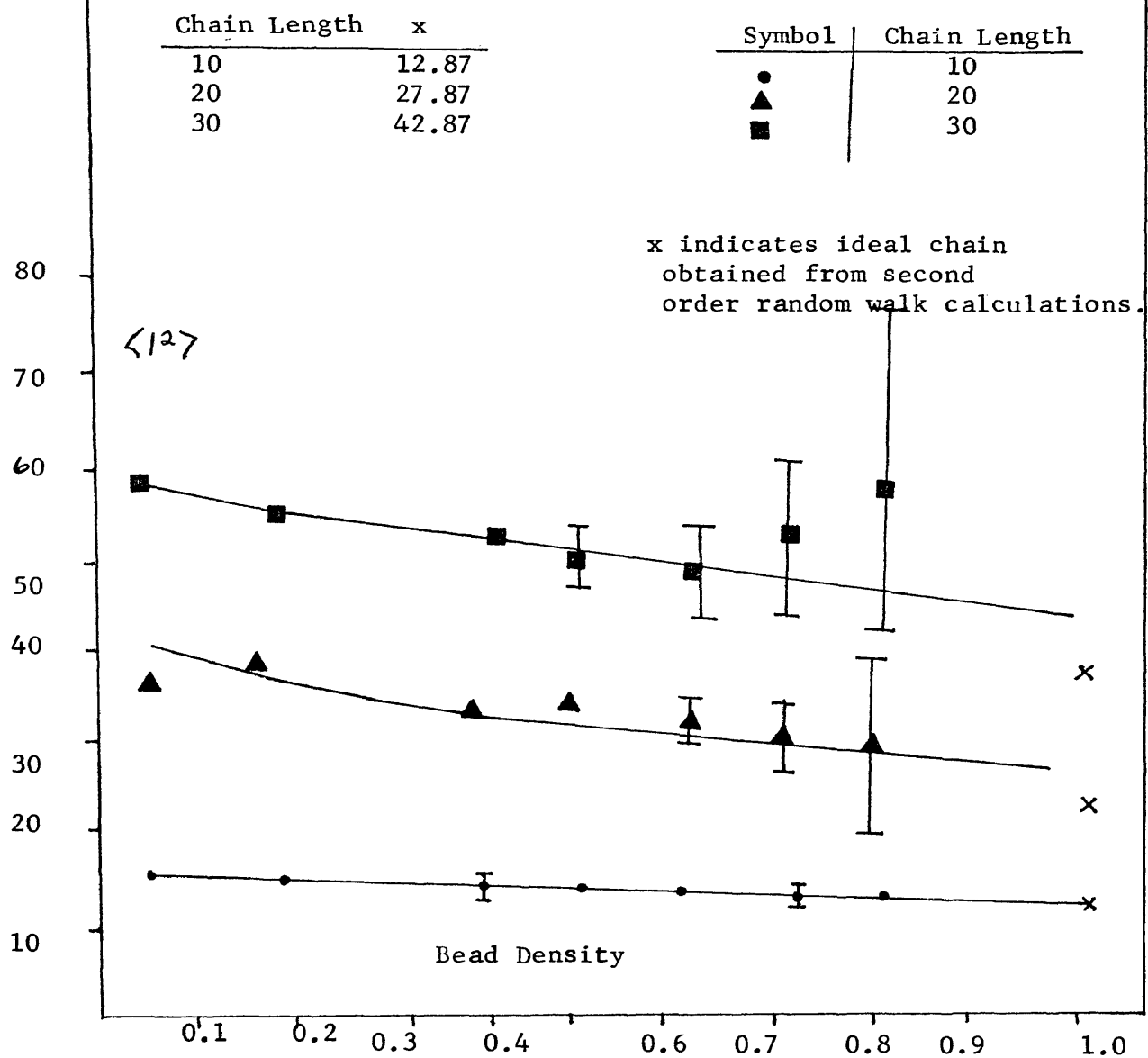
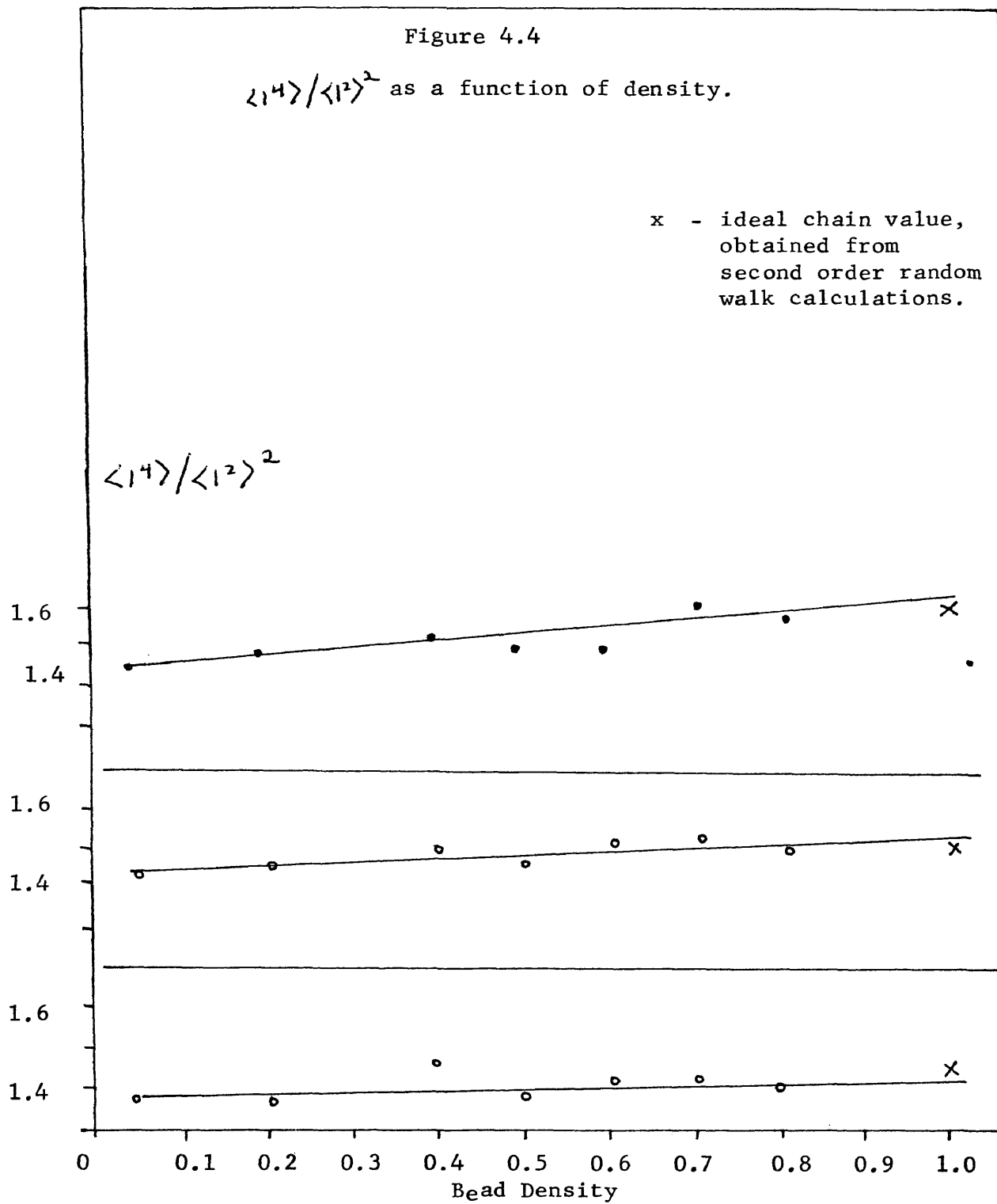
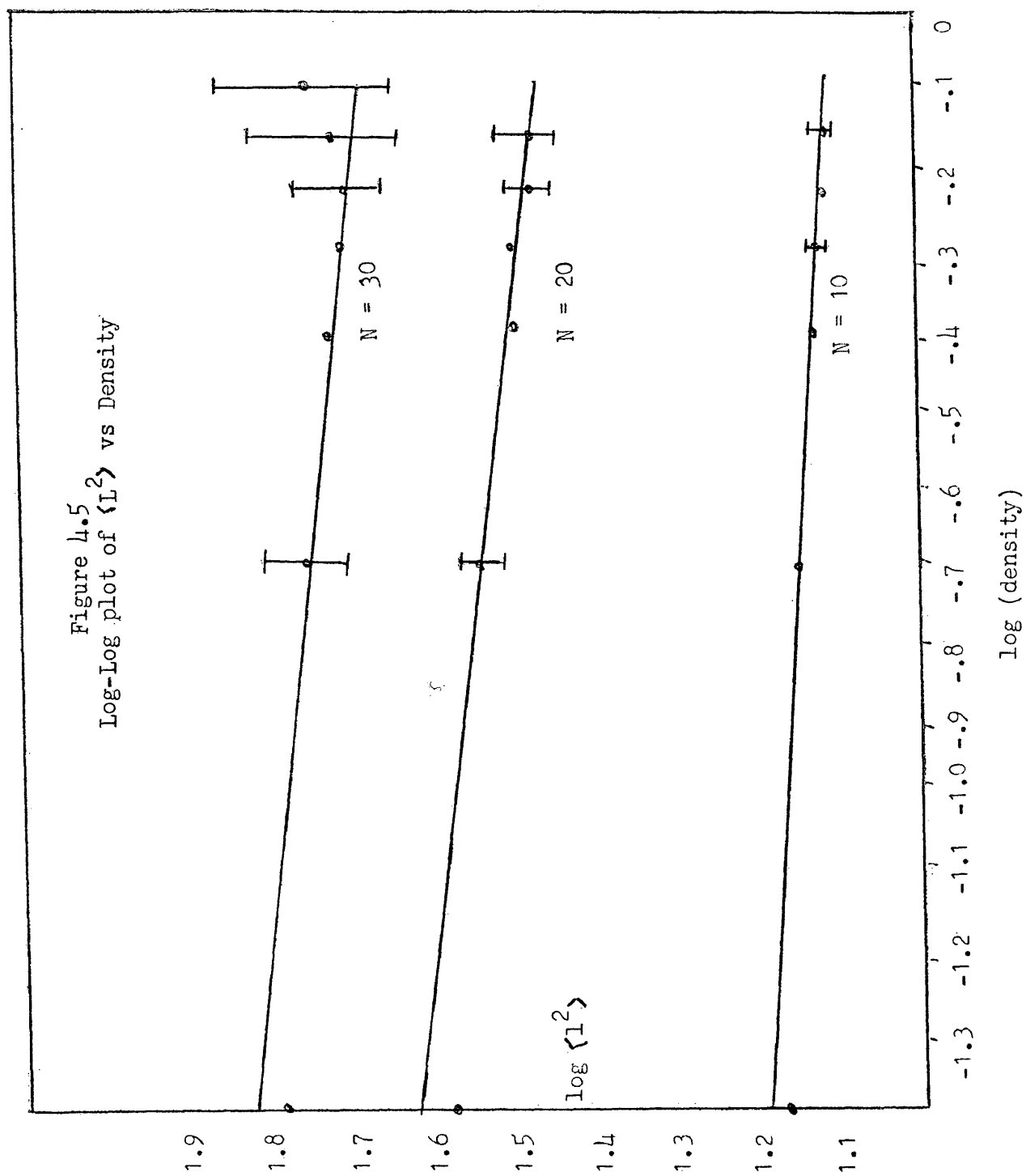
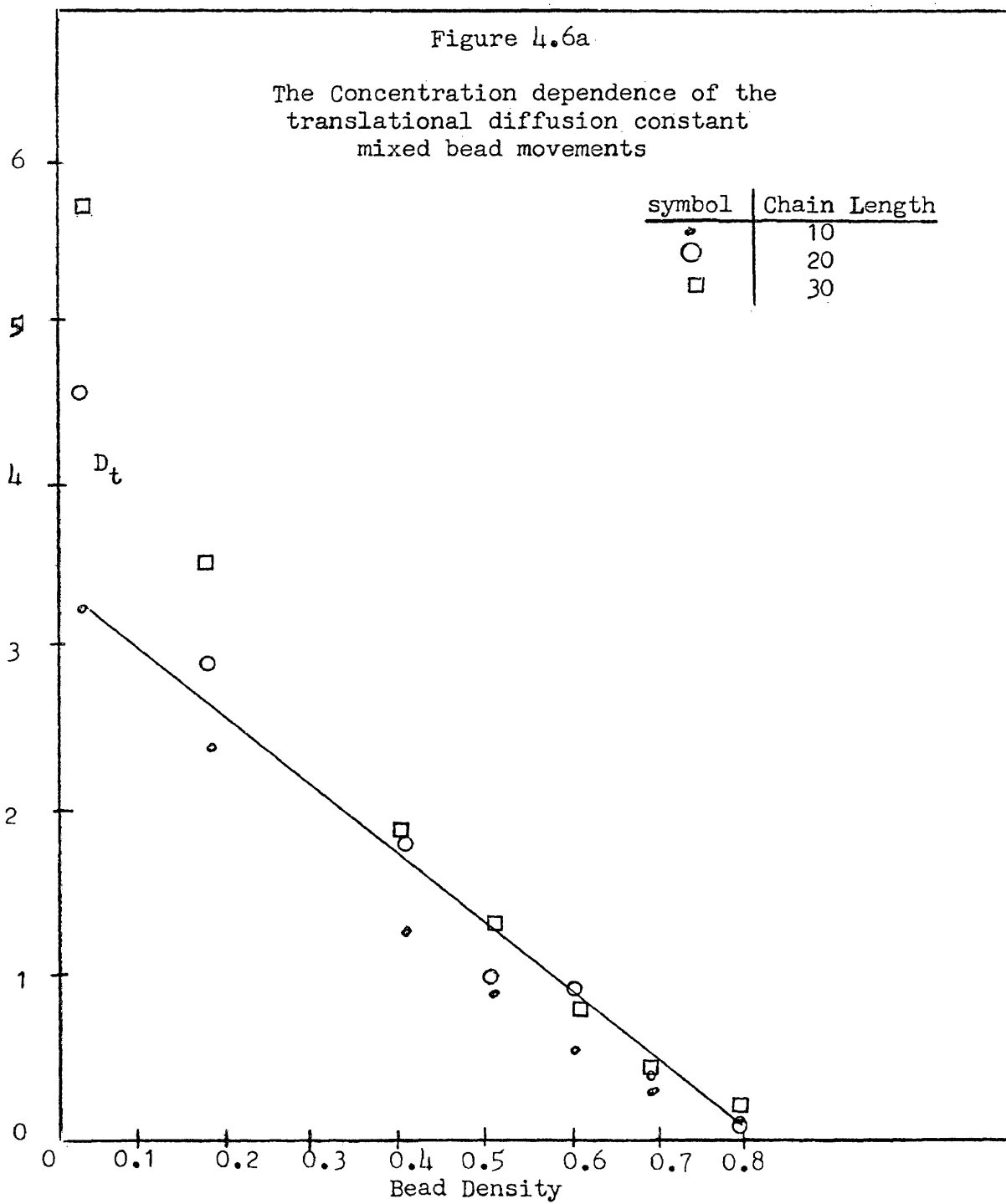


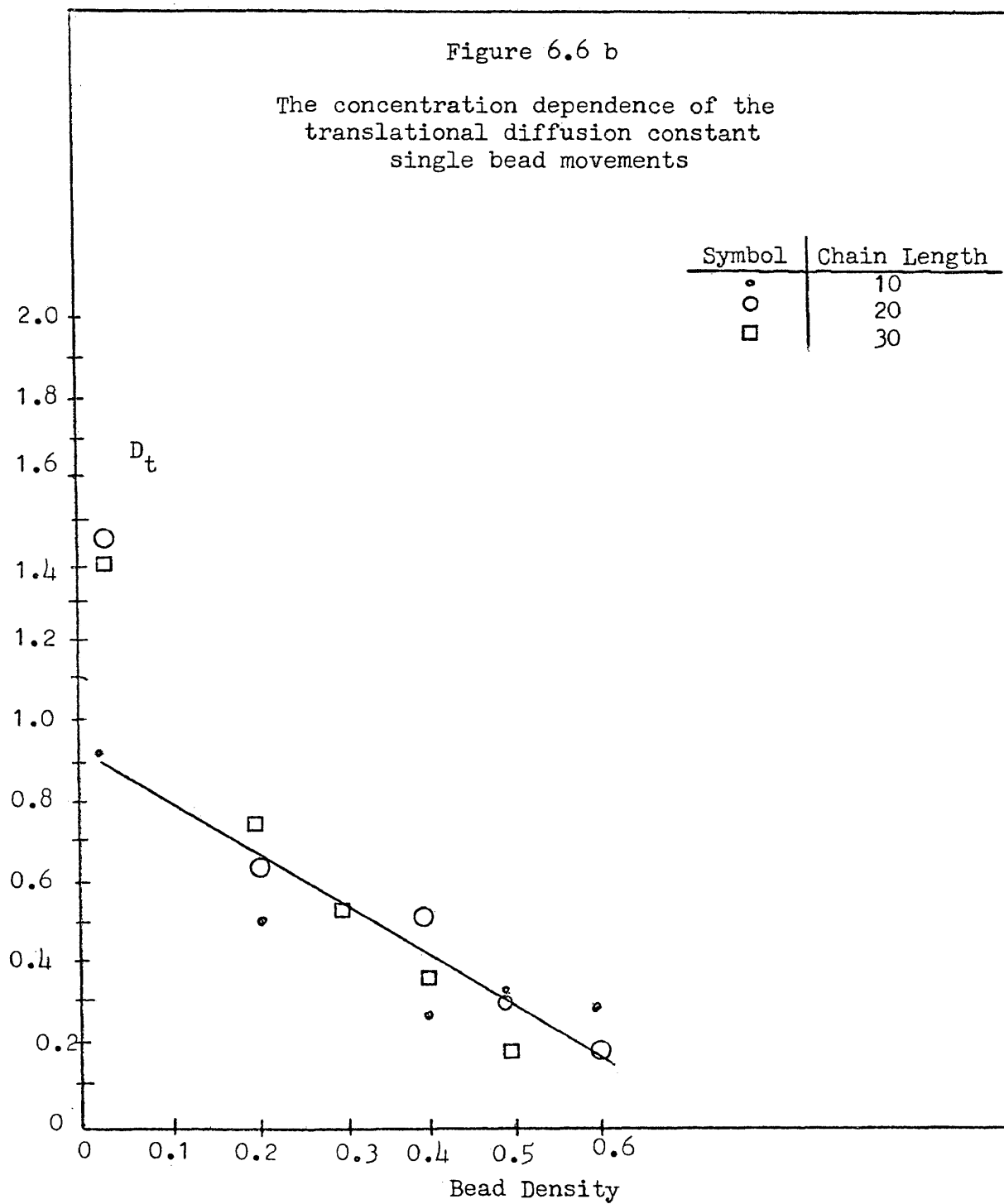
Figure 4.3

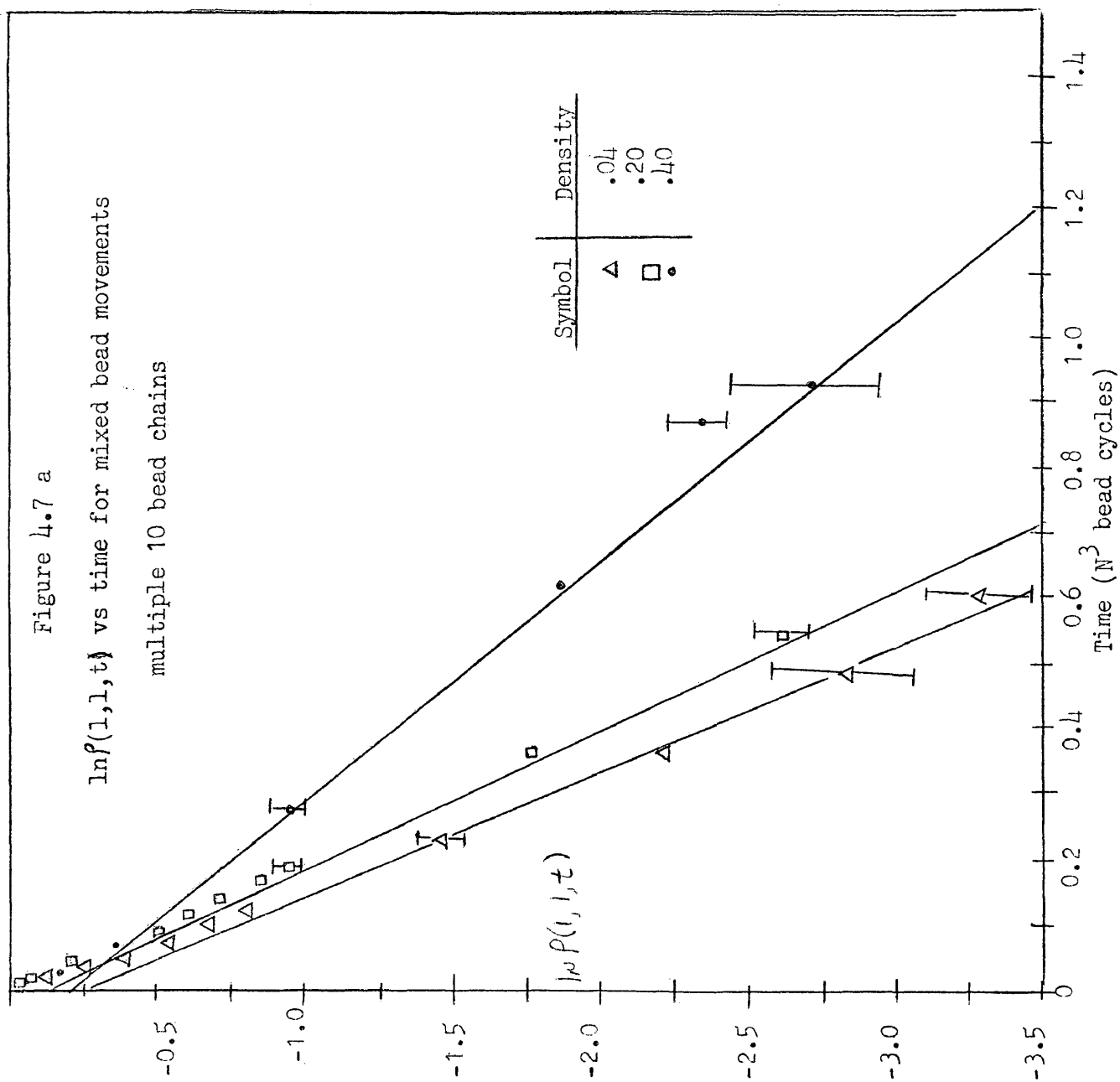
 $\langle l^2 \rangle$ as a function of density.

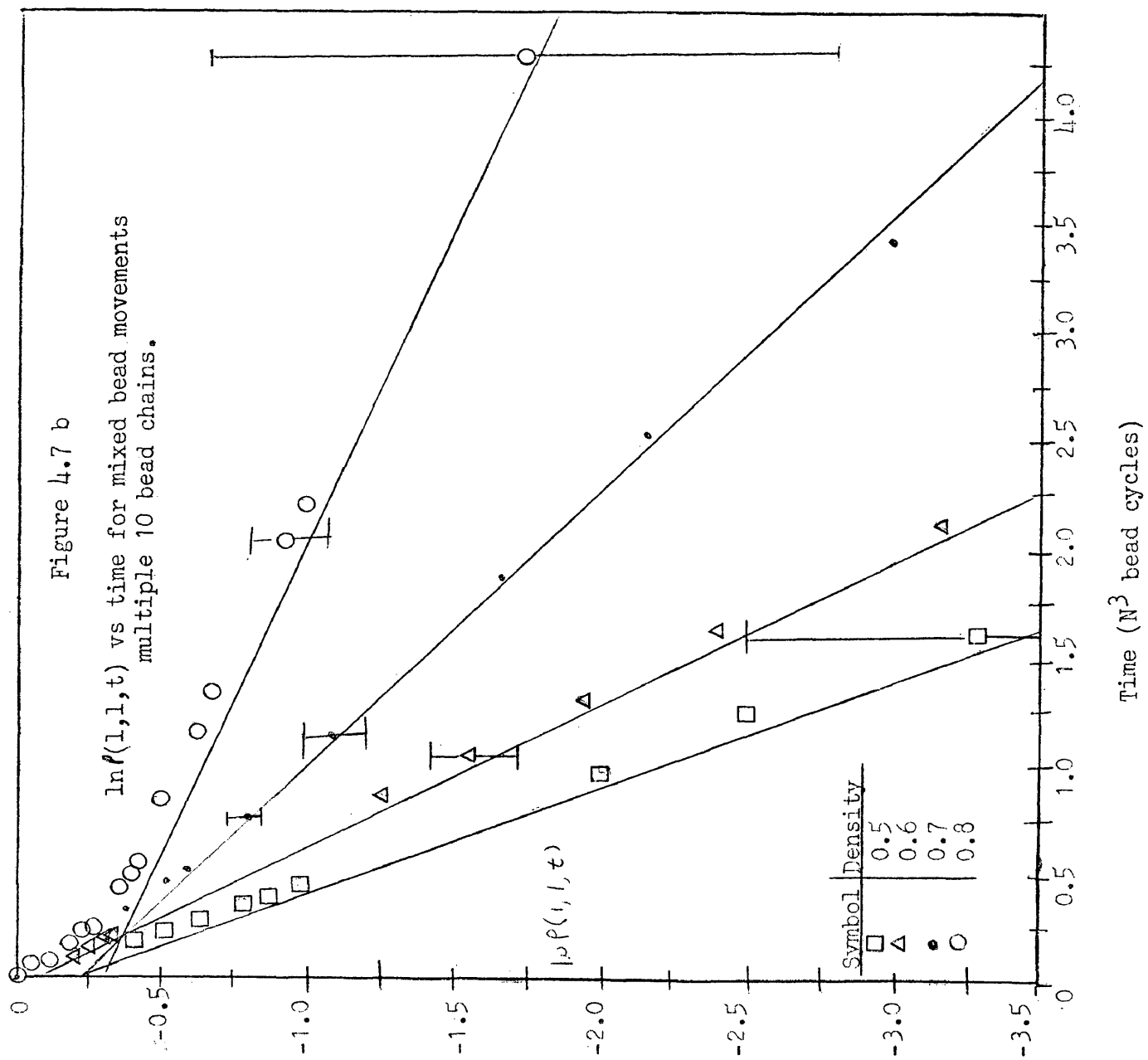


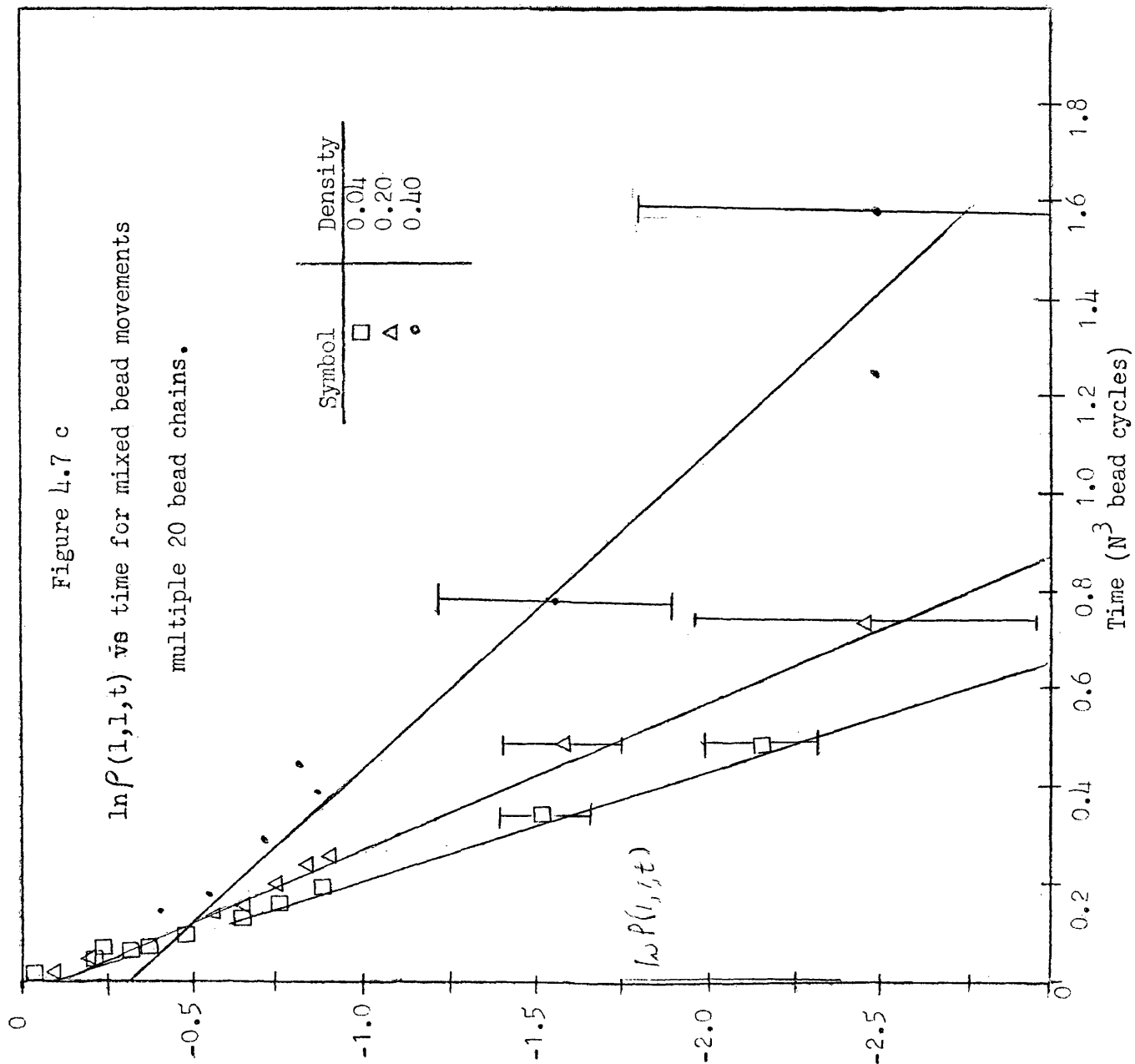


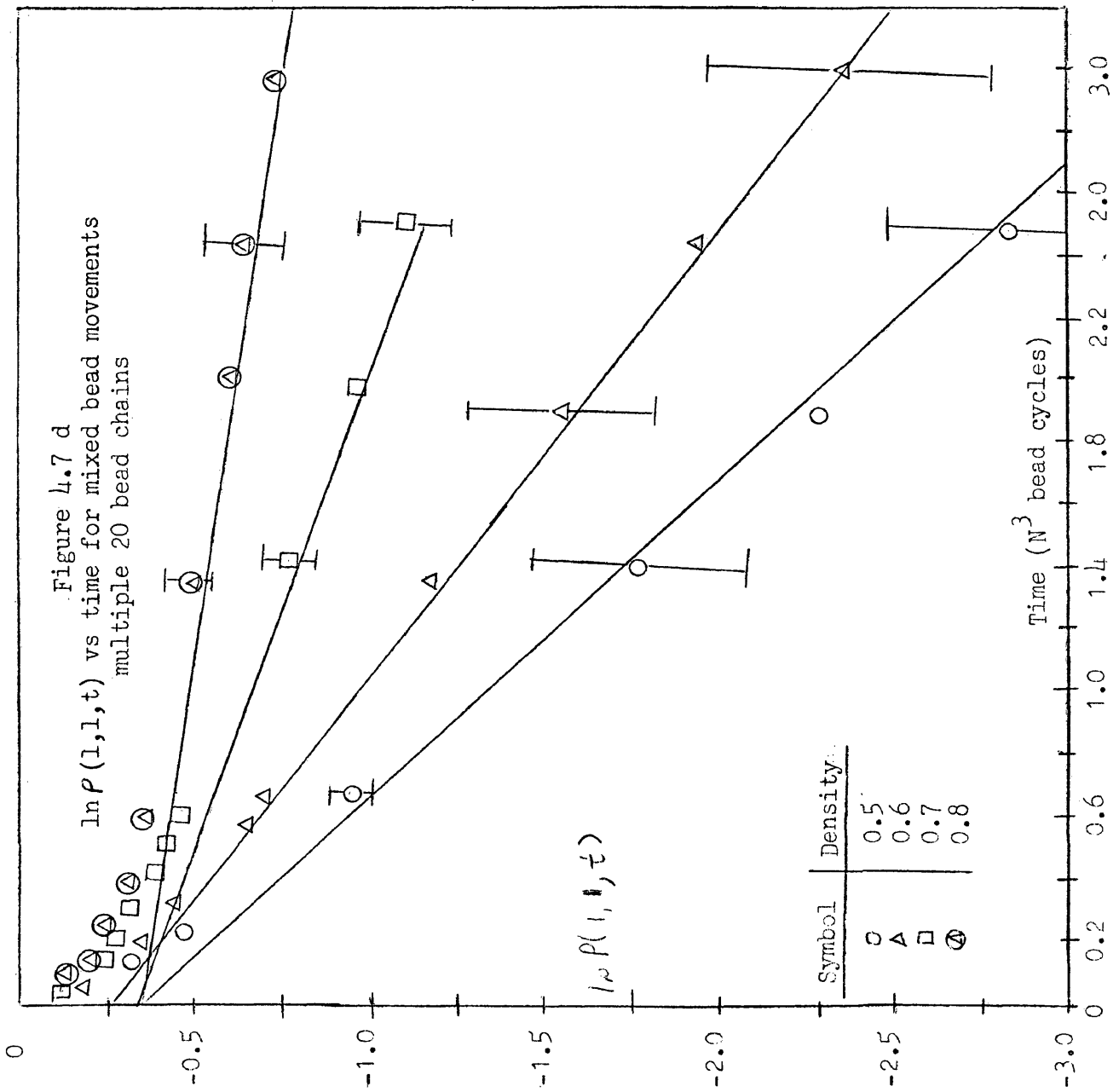


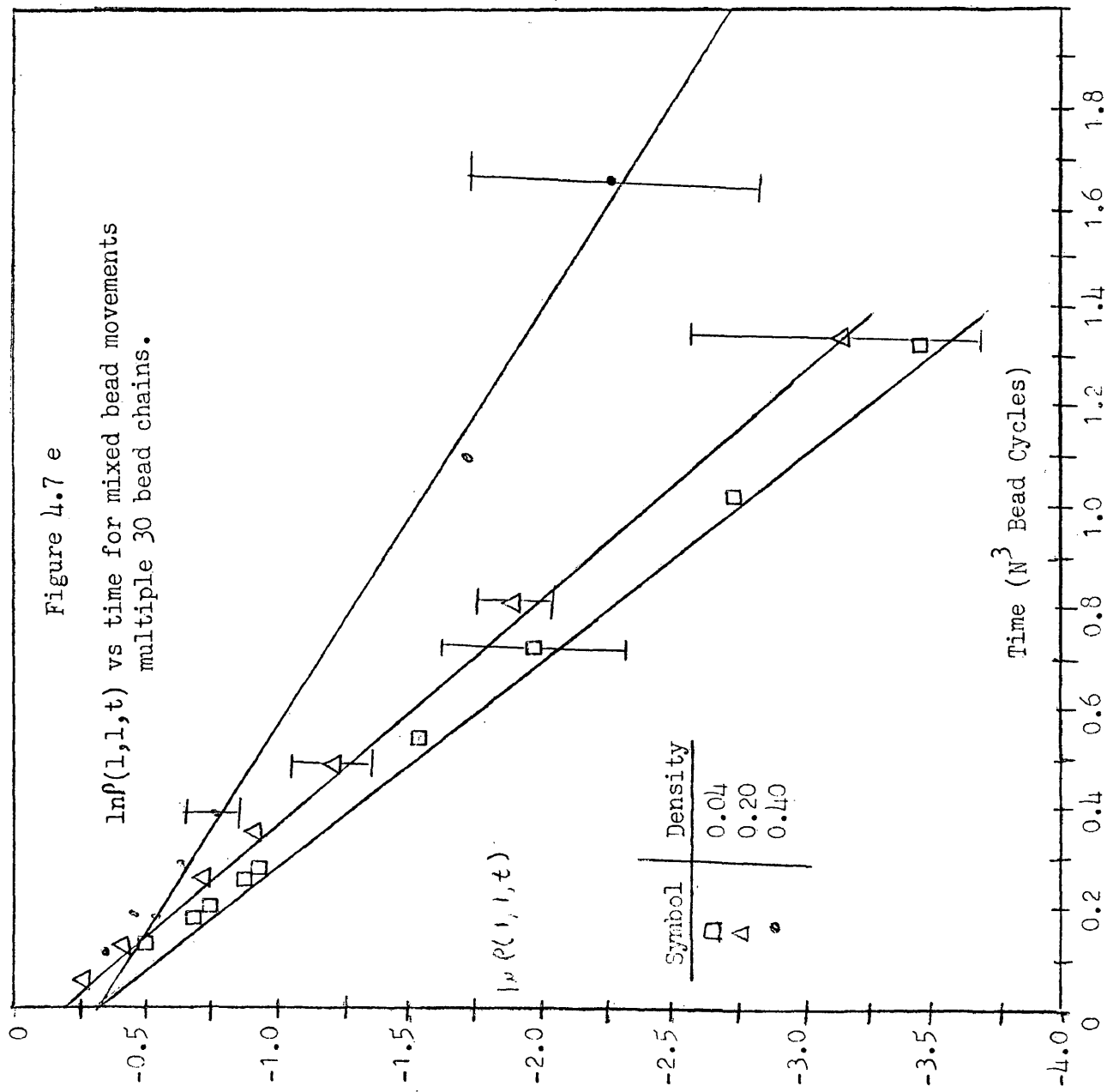


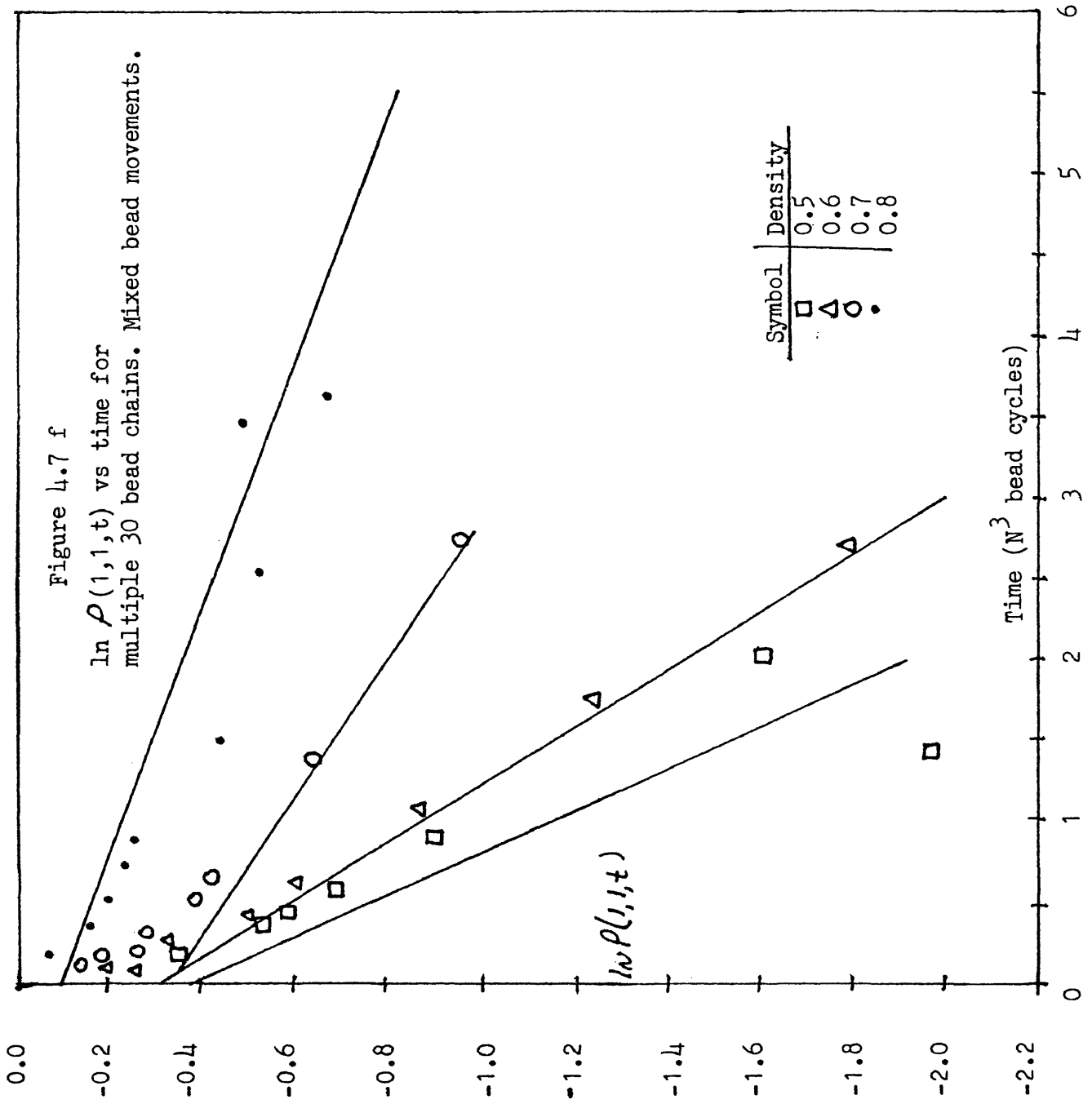


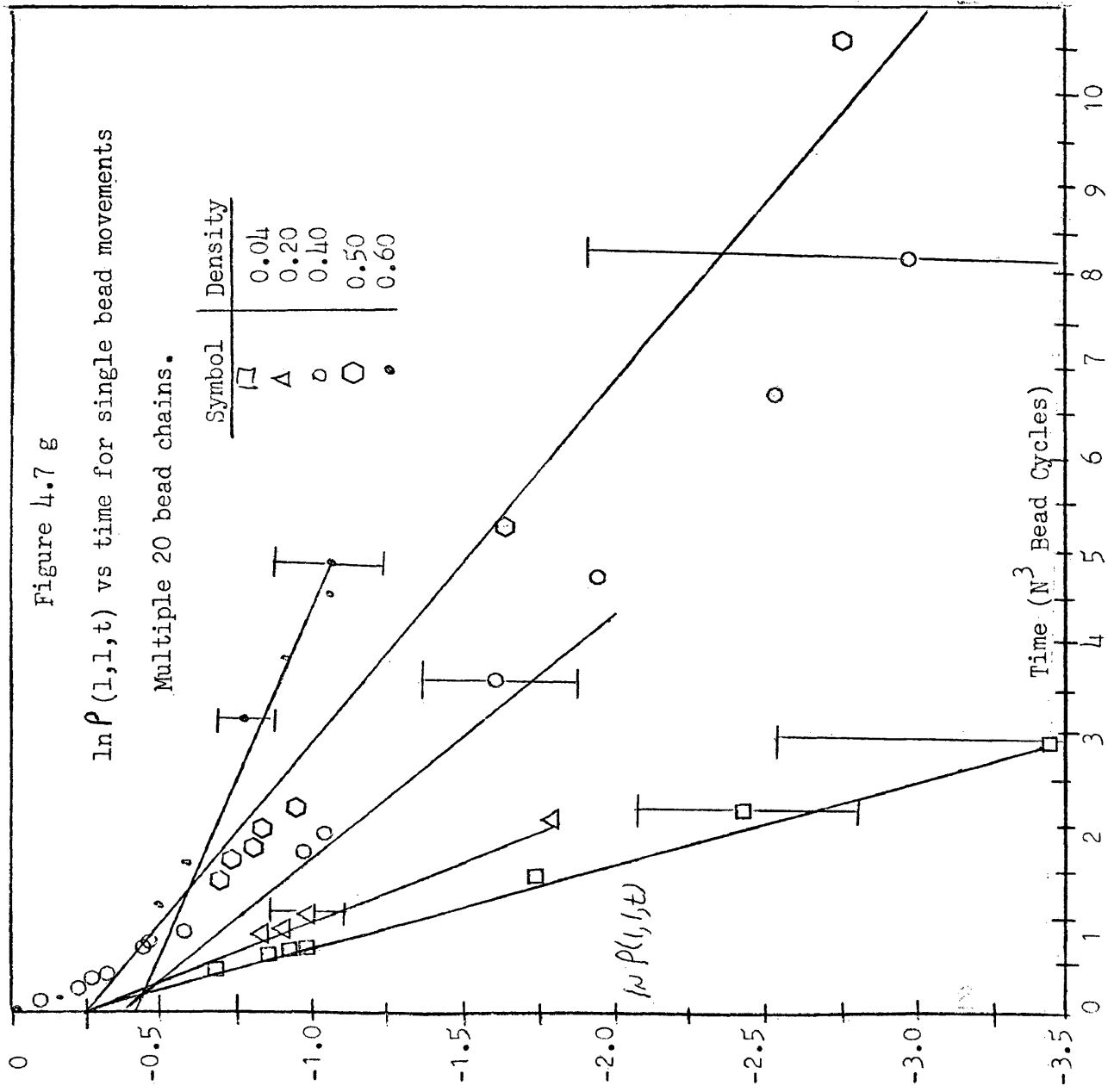












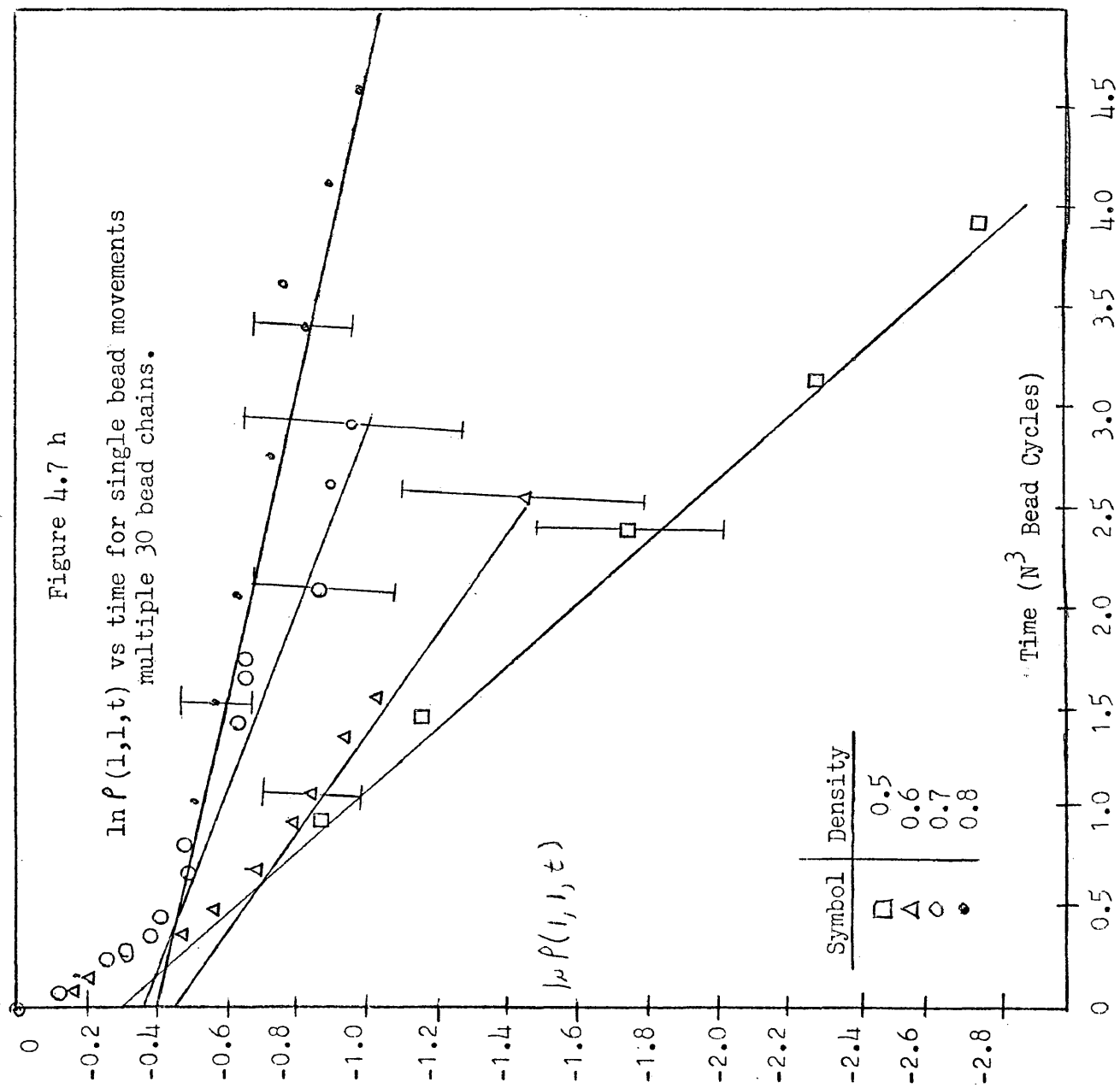
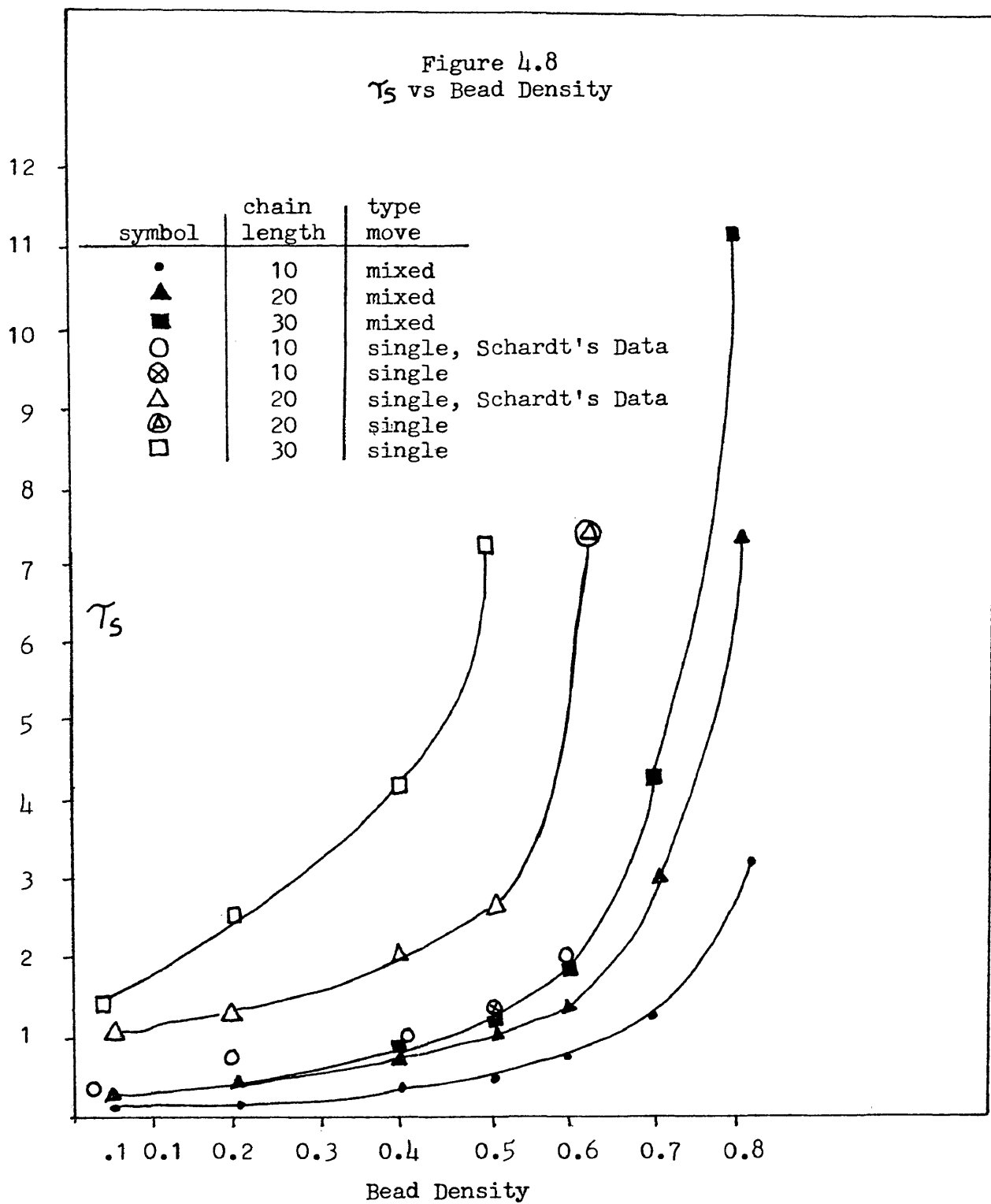
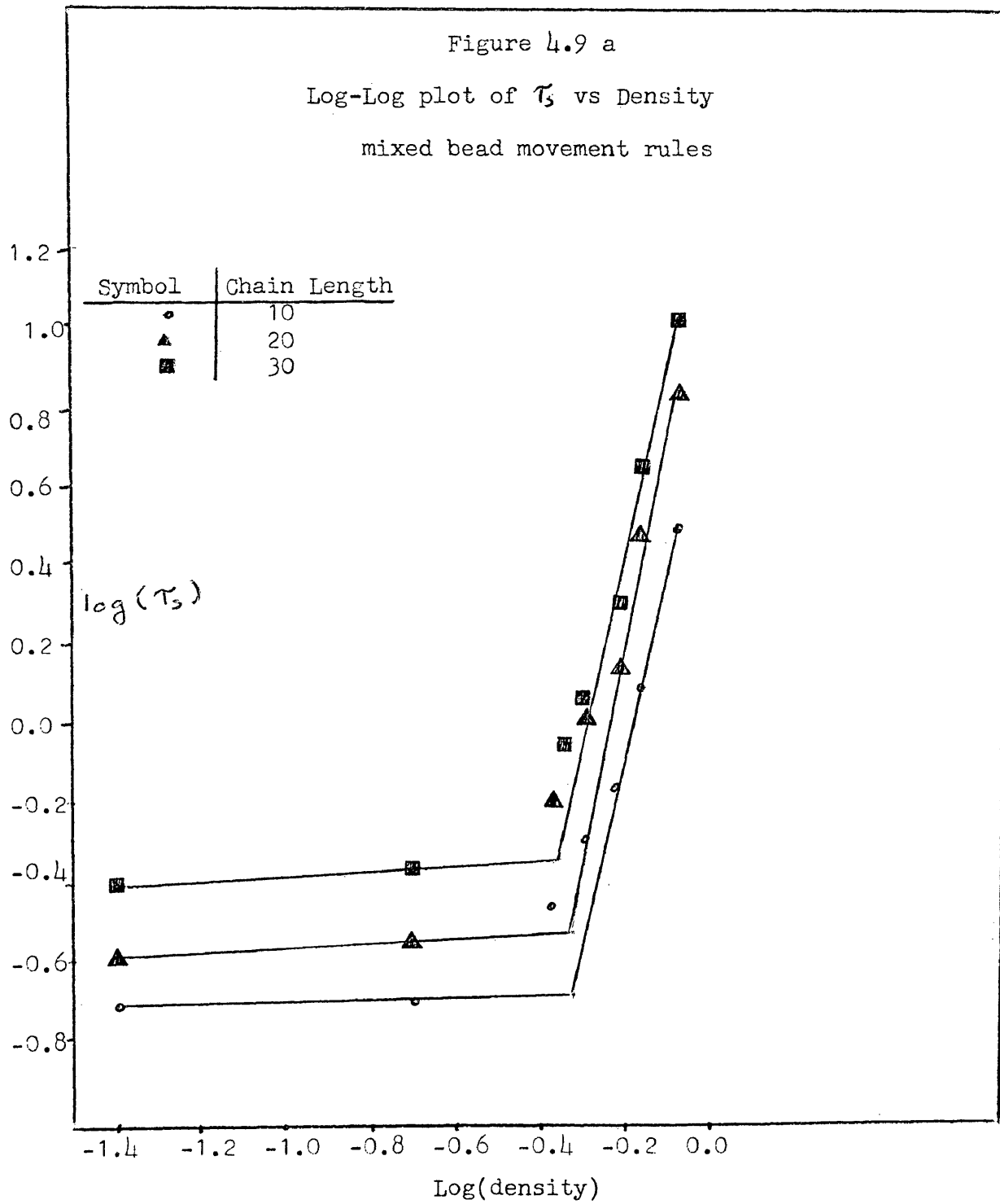
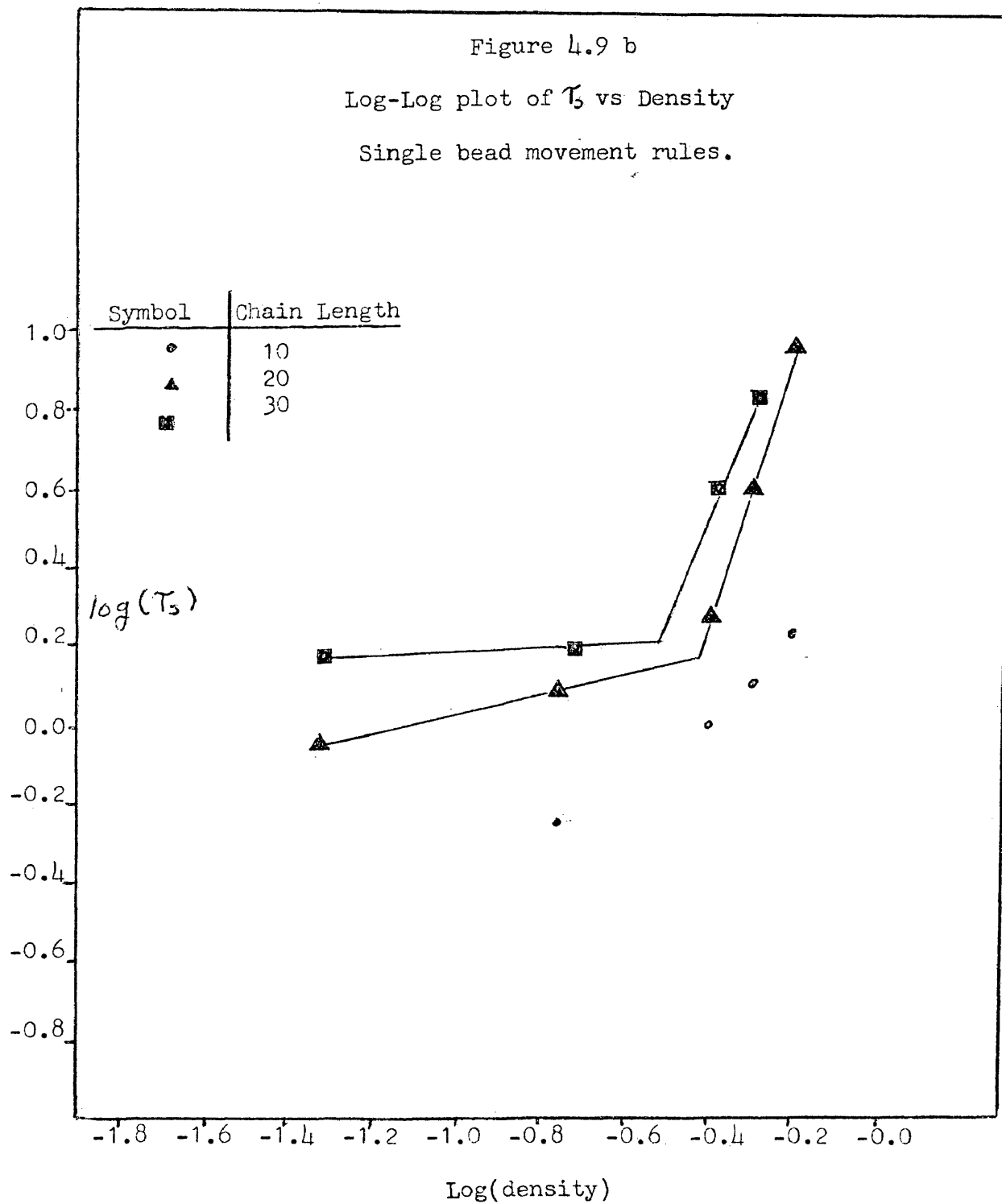
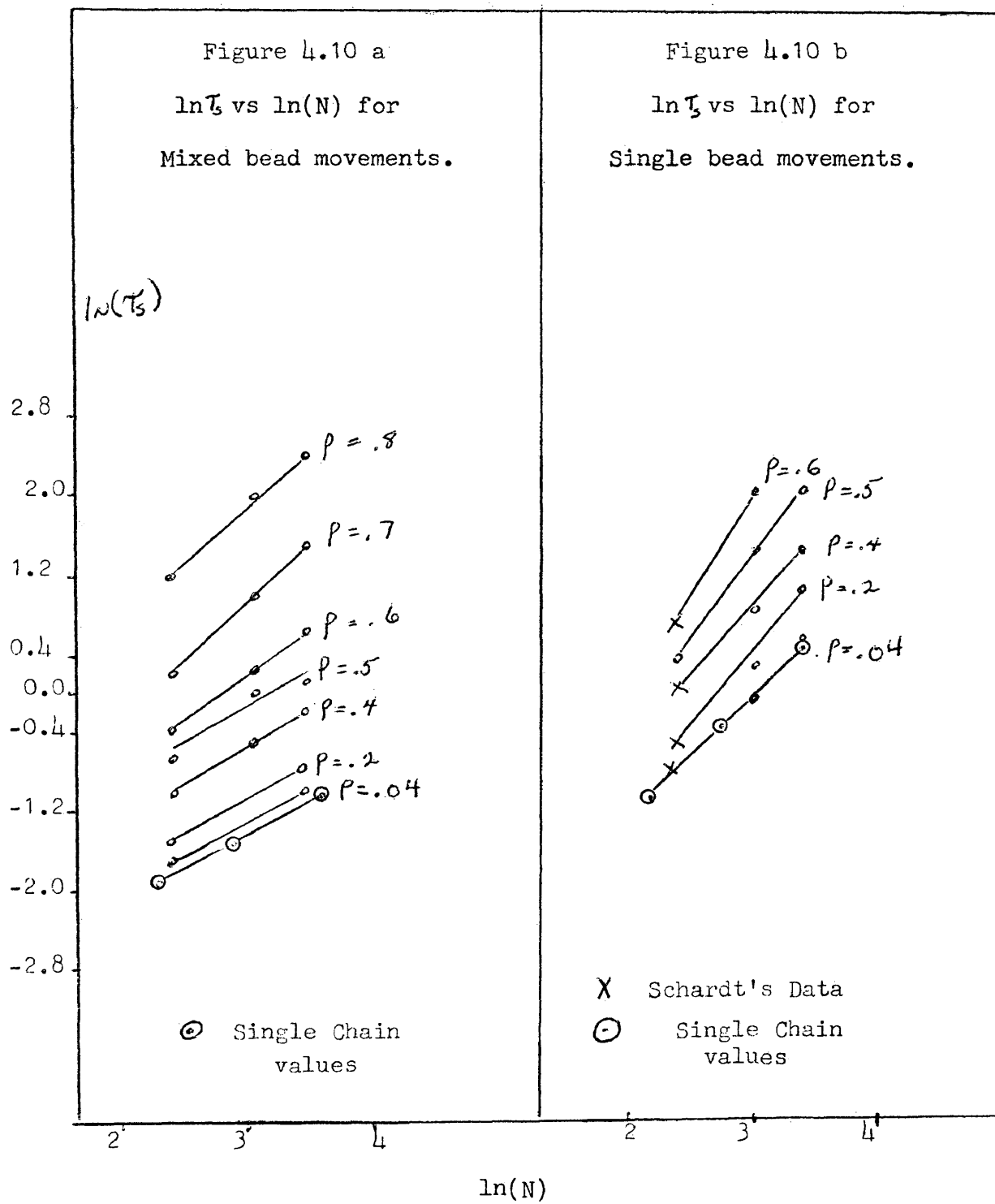


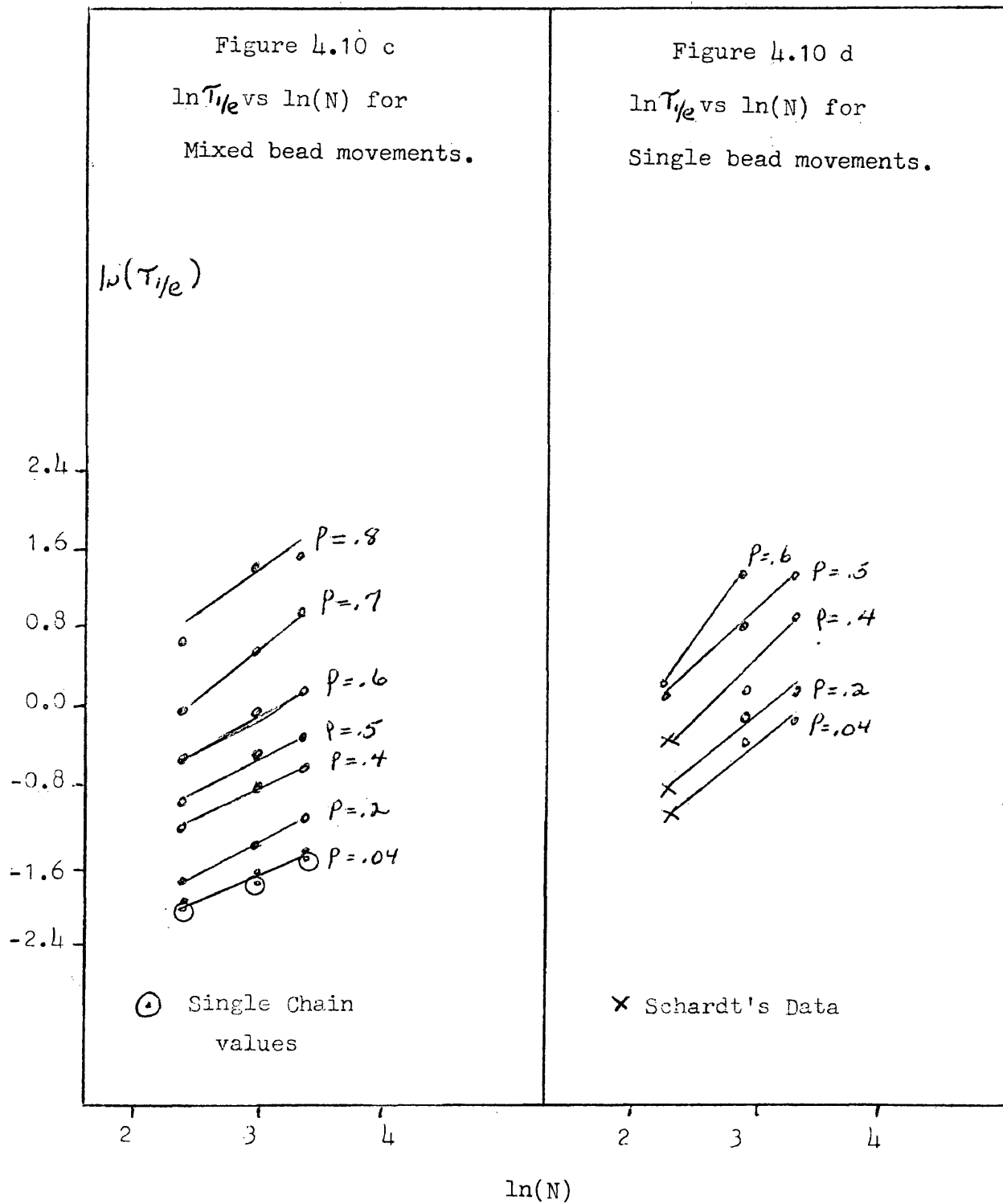
Figure 4.8
 τ_s vs Bead Density

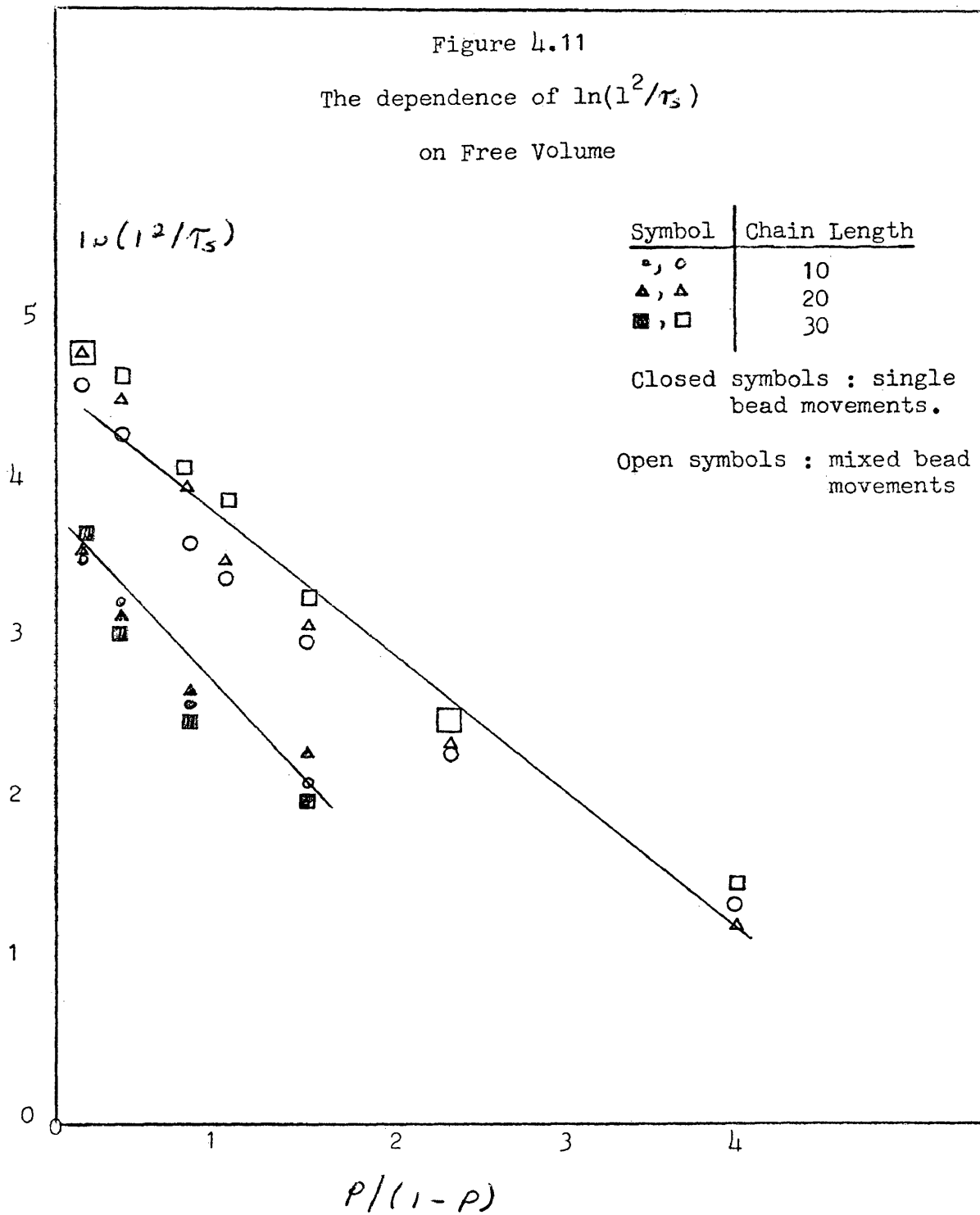


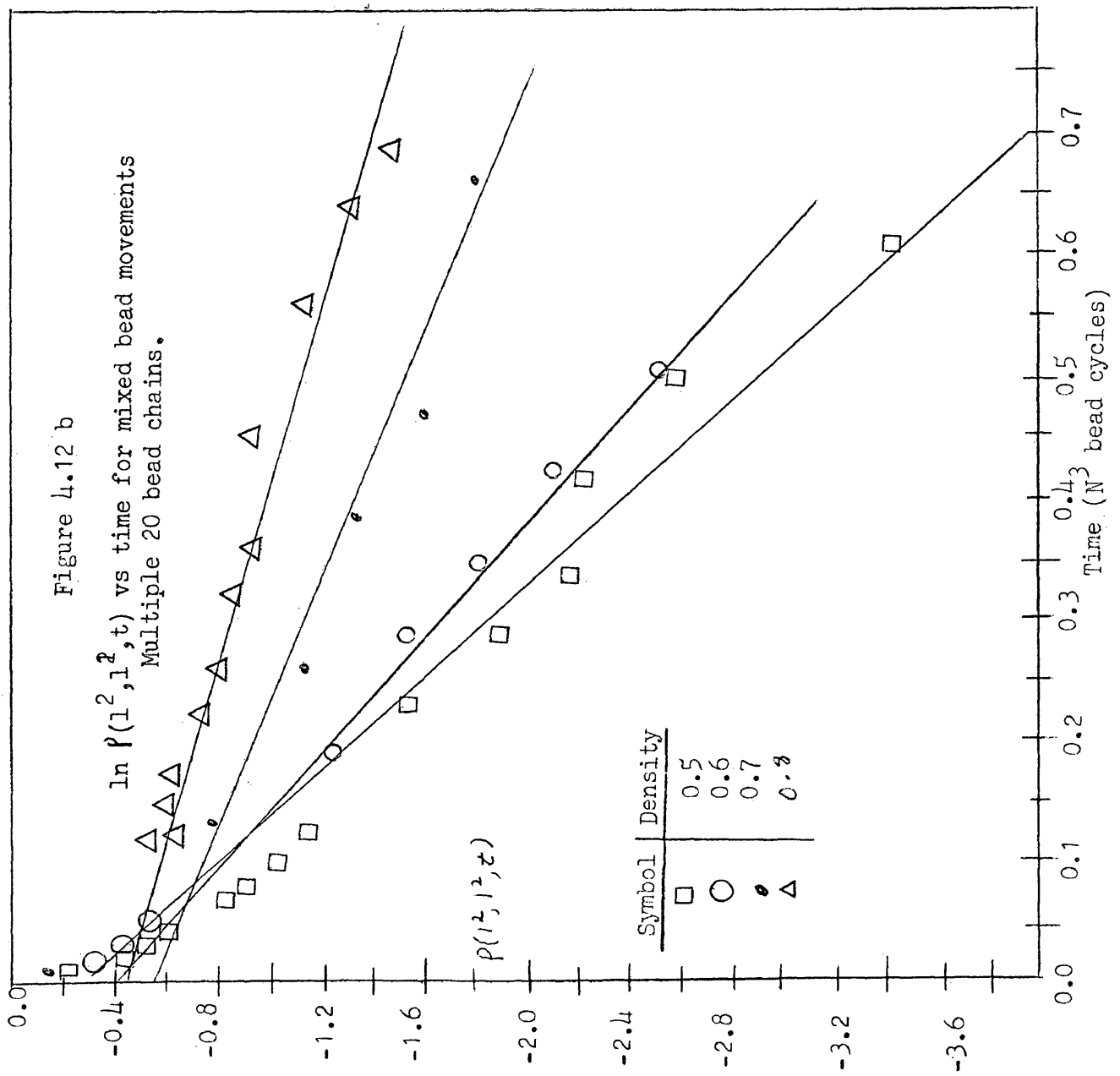


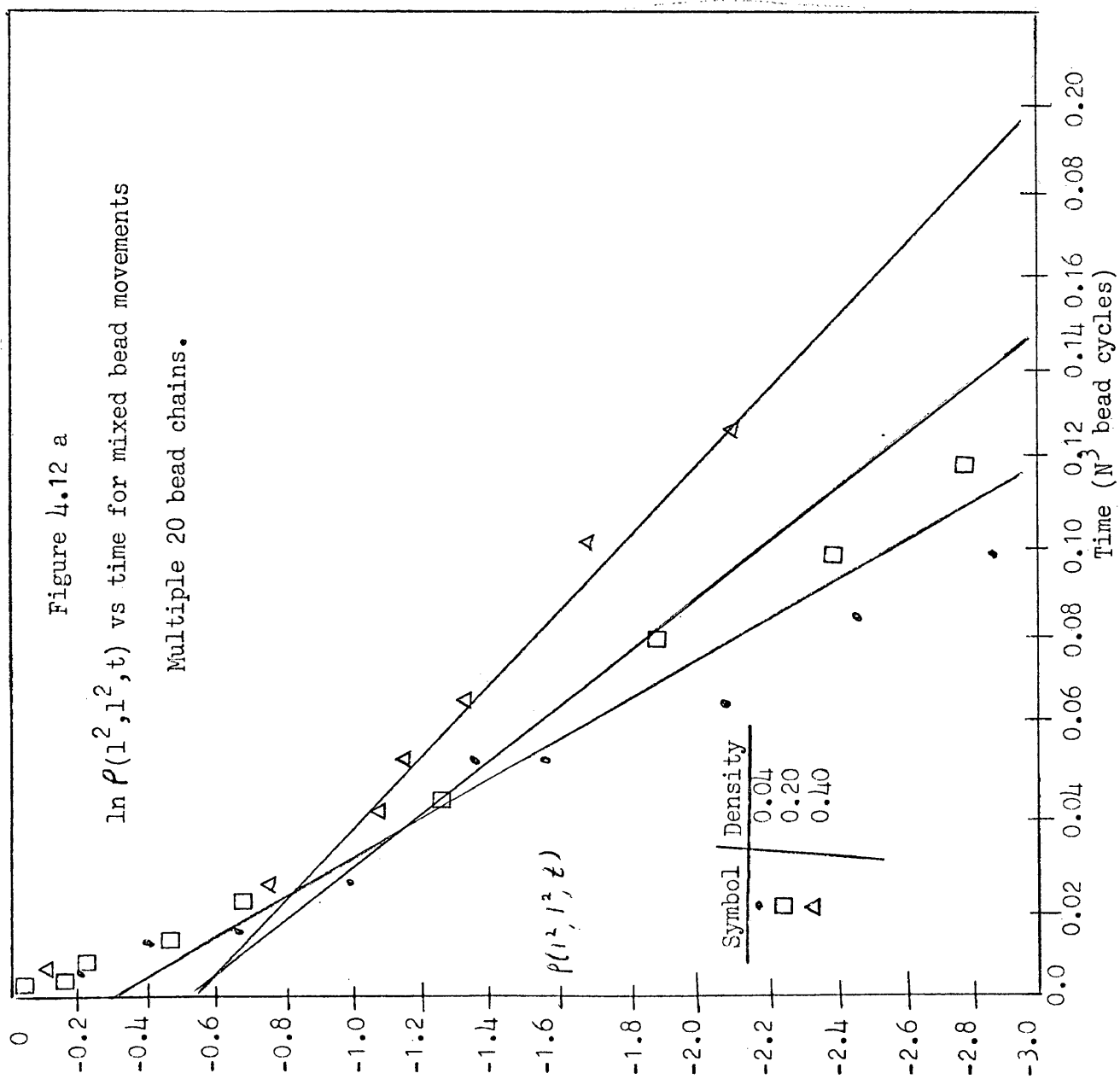


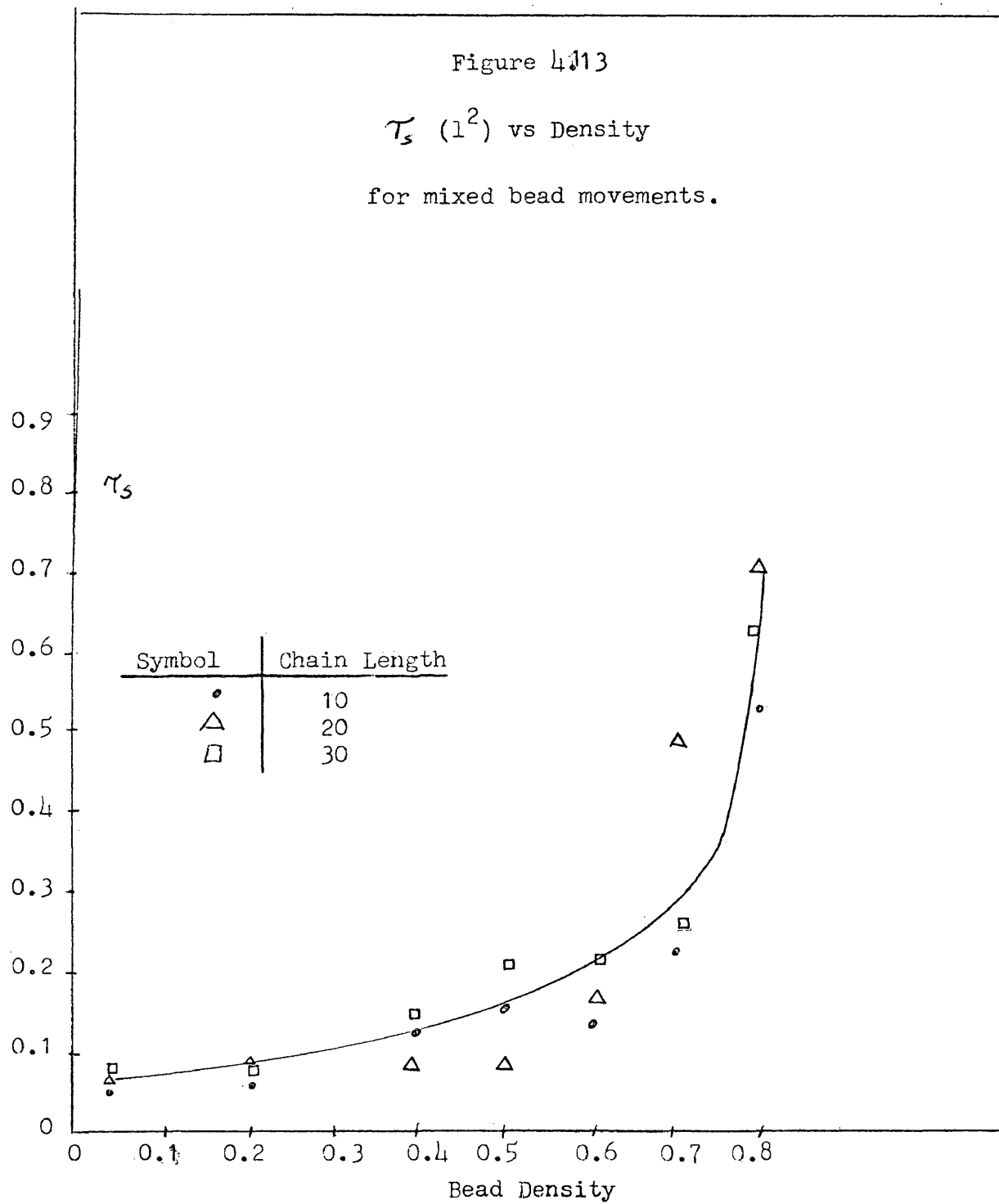


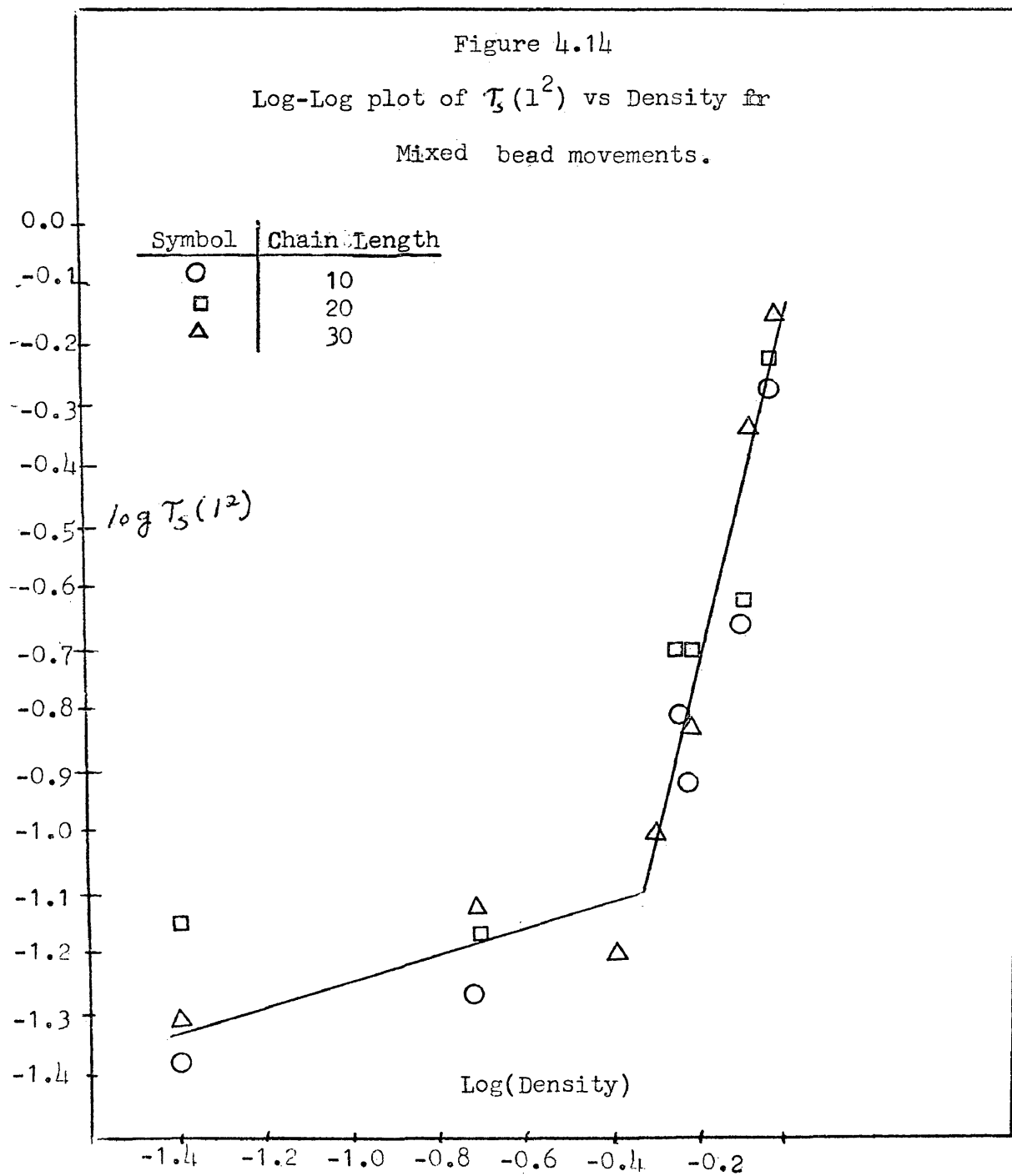












APPENDIX A

A Solution of the Eigenvalue Problem.

The matrix A derived in Chapter 1 may be written as

$$A = \begin{pmatrix} 2 & -1 & 0 & 0 & \cdot & \cdot & \cdot & 0 & 0 & 0 \\ -1 & 2 & -1 & 0 & \cdot & \cdot & \cdot & 0 & 0 & 0 \\ 0 & -1 & 2 & -1 & \cdot & \cdot & \cdot & 0 & 0 & 0 \\ & & & & \cdot & \cdot & \cdot & & & \\ 0 & 0 & 0 & 0 & \cdot & \cdot & \cdot & -1 & 2 & -1 \\ 0 & 0 & 0 & 0 & \cdot & \cdot & \cdot & 0 & -1 & 2 \end{pmatrix}$$

by performing a series of row and column additions on the original matrix. This matrix may be diagonalized by an orthogonal transformation,

$$R^{-1} AR = \Lambda = \lambda_i \delta_{ij}$$

where λ_p is the pth eigenvalue of A, and δ_{ij} is the Kronecker delta.

Writing A as the sum of two matrices, C and D gives

$$A = \begin{pmatrix} 0 & -1 & 0 & 0 & \dots & 0 & 0 & 0 \\ -1 & 0 & -1 & 0 & \dots & 0 & 0 & 0 \\ 0 & -1 & 0 & -1 & \dots & 0 & 0 & 0 \\ & & & & \ddots & & & \\ 0 & 0 & 0 & 0 & \dots & -1 & 0 & -1 \\ 0 & 0 & 0 & 0 & \dots & 0 & -1 & 0 \end{pmatrix} + \begin{pmatrix} 2 & 0 & 0 & \dots & 0 & 0 \\ 0 & 2 & 0 & \dots & 0 & 0 \\ 0 & 0 & 2 & \dots & 0 & 0 \\ & & & \ddots & & \\ 0 & 0 & 0 & \dots & 2 & 0 \\ 0 & 0 & 0 & \dots & 0 & 2 \end{pmatrix}$$

= C + D. The orthogonal matrix, R, which diagonalizes C also diagonalizes D. The eigenvalues of A are related to the eigenvalues, c_i , of C by³⁷

$$\lambda_i = 2 + c_i. \quad (A1)$$

The eigenvalues of C are easily found by considering a more general matrix, π , which is of the same form as C,

$$\pi = \begin{pmatrix} 0 & p & 0 & 0 & \dots & 0 & 0 & 0 \\ q & 0 & p & 0 & \dots & 0 & 0 & 0 \\ 0 & q & 0 & p & \dots & 0 & 0 & 0 \\ & & & & \ddots & & & \\ 0 & 0 & 0 & 0 & \dots & q & 0 & p \\ 0 & 0 & 0 & 0 & \dots & 0 & p & 0 \end{pmatrix}$$

Using the orthogonal transformation $B \pi B^{-1} = \lambda_i \delta_{ij}$, or $B \pi = \lambda B$ with $B = (\beta_1, \beta_2, \dots, \beta_{N-1})$, yields upon multiplication the following set of second order difference equations:

$$p \beta_{k-1} + q \beta_{k+1} = \lambda_k \beta_k \quad (k = 0, 1, 2, \dots, N-1). \quad (A2)$$

The quantities β_0 and β_N are set to zero¹⁵.

This set of equations may be solved by assuming a solution of the form³⁸

$$\beta_k = \alpha r^k. \quad (A3)$$

Substituting A3 into A2 shows that this can be a solution only if r is a root of the quadratic

$$p - \lambda r + q r^2 = 0. \quad (A4)$$

There will, in general, be two distinct, independent roots to this quadratic, r_1 and r_2 . Therefore a solution to the difference equation (A2) will be in the form of a geometric progression

$$\beta_k = \alpha_1 r_1^k + \alpha_2 r_2^k. \quad (\text{A5})$$

Because $\beta_0 = \beta_N = 0$, it is easy to show that $\alpha_1 + \alpha_2 = 0$ and that $r_1^N = r_2^N$. Rewriting this last equation gives

$$r_1^N = r_2^N \exp(2\pi i j), \text{ or}$$

$$r_1 = r_2 \exp(2\pi i j/N) \text{ for } j = 0, 1, 2, \dots, N-1. \quad (\text{A6})$$

where³⁹ $i = \sqrt{-1}$ and $\exp(2\pi i j) = \cos 2j\pi + i \sin 2j\pi = 1 + i \cdot 0 = 1$.

By equation A6, r_1 and r_2 must be complex conjugates of each other. The absolute values of r_1 and r_2 may be found by using this fact as follows, $r^2 - \lambda/q + p/q = (r - r_1)(r - r_2) = 0$. Equating the coefficients of the two equations gives $\lambda = q(r_1 + r_2)$ and $r_1 r_2 = p/q$. The roots of A4 are

$$r = p/q \exp(\pi i j/N) \text{ and}$$

$$r_2 = \sqrt{p/q} \exp(-\pi i j/N) \text{ (} j = 0, 1, 2, \dots, N-1 \text{)}. \quad (\text{A7})$$

The eigenvalues of Π are $\lambda_i = q(r_1 + r_2) = -2\sqrt{pq} \cos(\pi i/N)$ $j = (1, 2, \dots, N-1)$. Substituting $p = q = -1$ gives $c_i = 2 \cos(\pi i/N)$ ($i = 1, \dots, N-1$), and from equation A1

$$\lambda_i = 2 + 2 \cos(\pi i/N) = 4 \sin^2(\pi i/2N) \text{ (} i = 1, \dots, N-1 \text{)} \quad (\text{A8})$$

The corresponding eigenvectors are given by the columns of the matrix R . The elements of R are given by Verdier⁴⁰ as $R_{nj} = \cos((n - 1/2)\pi j/N)$.

APPENDIX B

Procedure used for the calculation of Diffusion Data

The exact number of lattice sites each chain moved during some time interval was calculated by the following method. This method is valid only if the chain length is less than or equal to the box size.

The subroutine performing the bead movements needed two arrays. These are $IMOVE(I,J)$ and $IWALL(I,J)$. The subscript I is 1,2, or 3 if the chain moved in the x,y , or z dimension, respectively. The J subscript is used to denote the chain of interest.

Each time an end bead moves out of the box a one is added to or subtracted from $IMOVE(I,J)$. If the new coordinates of the bead in the I dimension is greater than the box size then a one is added. Otherwise a one is subtracted from $IMOVE(I,J)$. The wall through which the the bead moved is also recorded. The walls are defined as:

Wall Hit	I	IWALL(I,J)
x < 0	1	1
x > Box	1	4
y < 0	2	2
y > Box	2	5
z < 0	3	3
z > Box	3	6

Initially, $IMOVE(I,J)$ is set to zero if the chain is connected. If it is broken then $IMOVE(I,J)$ is set to -1 if $0 < \text{the center of the chain} < \text{Box Size}/2$. If $\text{Box Size}/2 \leq \text{the Center of mass of the chain}$ then $IMOVE(I,J)$ is set to +1. If the chain is broken more than once then the diffusion of the chain is not calculated for that frame. This initialization procedure also occurs before each call to the subroutine which performs bead movements. The center of mass of each chain is calculated by summing over the x, y, or z coordinates and dividing by the number of beads in the chain. These sums always start with the first bead of the chain. If the difference in coordinates between two beads is greater than one then the chain is split and a box dimension is added or subtracted to the bead coordinate before the center of mass is calculated. This is to say that the center of mass is always calculated from a fully connected chain. If the center of mass lies outside the box then a box dimension is added to or subtracted from it to put it inside the box.

The diffusion is then calculated by the procedure outlined in Figure B1. The variables in this flowchart are defined as

CMO(I,J) = the position of the center of mass of the chain the last time its properties were sampled.

CM(I,J) = the current position of the center of mass of the chain

Box = the box dimension and

DCM = the distance the chain has moved in one of the three dimensions since the last time its properties were sampled.

The function INT(A) where A is a floating point number is defined as $\text{INT}(A) = \text{largest integer} \leq |A|$.

There is one exception to this procedure which had to be accounted for. This case is outlined in Figure B2. Diffusion is considered in the x dimension only. The bead represented by the open circle is bead number 1. The arrows mean that some number of bead movements have occurred to cause the chain to reach the new configuration pictured. It was reached in such a way that the variables IMOVE(I,J) and IWALL(I,J) set according to the above rules are as shown.

To calculate DCM by the procedure of Figure B1 the following choices would be made:

- (1) The chain is not connected
- (2) A wall was hit
- (3) The center of mass, CM(I) is nearest wall 1

(4) Wall 1 was hit.

The formula used to calculate DCM is, then

$$DCM = CM(1) - CMO(1,1) + INT(IMOVE(1,1)) + INT(IMOVE(1,1)/2)$$

* BOX. Substituting for these variables from Fig B2 gives

$$DCM = 2.2 - 7.3 + 0 = -5.10.$$

This is clearly wrong. The chain did not move 5.10 lattice sites to the left but $10.2 - 7.3 = 2.9$ lattice sites to the right.

The correction was made to the program by the addition of the subroutine CHAIN. This subroutine checks to see if an end bead moves through a wall, and then through the opposite wall. If this type of movement is detected the IWALL(I,J) is set to zero. In the above example, the choices made in B1 are

- (1) The chain is not connected
- (2) no wall was hit.

Therefore, $DCM = CM(I) - CMO(1,1) = 2.2 - 7.3 = -5.10$

and

- (3) $-5.10 < BOX/2$, so

$$DCM = 8.0 - 5.10 = 2.90 ,$$

which is correct.

FIGURE B1

Algorithm for calculation of diffusion

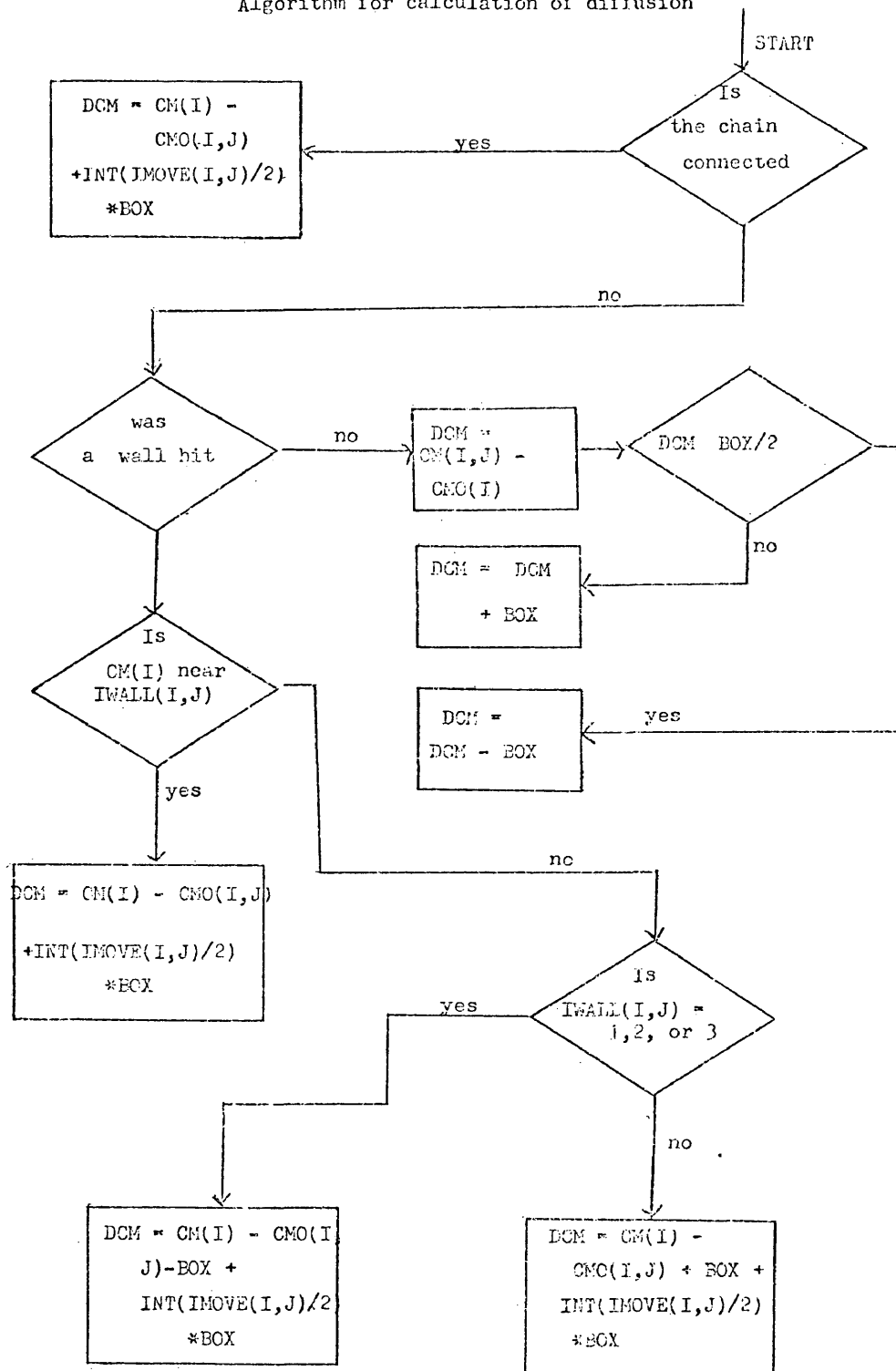
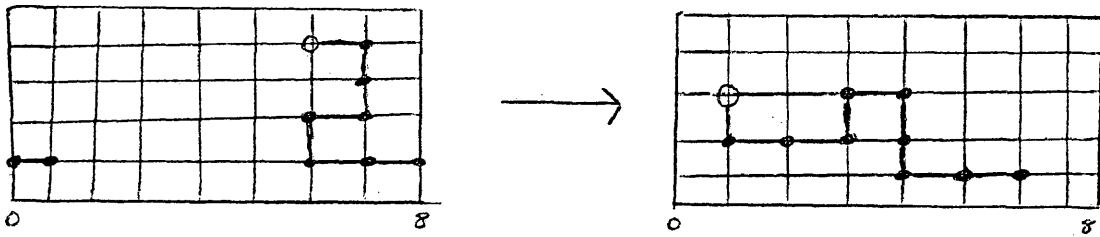


Figure B2

Example of diffusion in the
x dimension for a
1 chain system



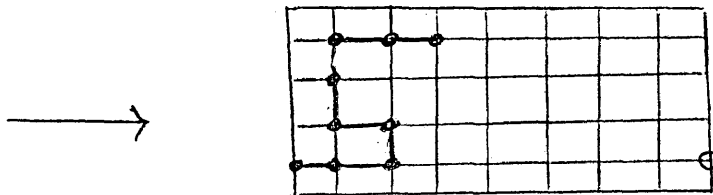
$$\text{CMO}(1,1) = 7.3$$

$$\text{IMOVE}(1,1) = 1$$

$$\text{IWALL}(1,1) = 0$$

$$\text{IMOVE}(1,1) = 2$$

$$\text{IWALL}(1,1) = 4$$



$$\text{CM}(1) = 10.2 - 8 = 2.2$$

$$\text{IMOVE}(1,1) = 1$$

$$\text{IWALL}(1,1) = 1$$

APPENDIX C

The Simulation Program

	Page
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Ctmap	121
Pack	122

MEMBER NAME MAIN

THIS PROGRAM HANDLES ONLY CHAINS THAT ARE ALL
 THE SAME LENGTH, GREATER THAN A READS LCNG
 IT IS FOR EXCLUDED VOLUME CONDITIONS ONLY
 DIFFUSION CALCULATIONS ARE EXACT, BUT THE BOX
 SIZE MUST BE AT LEAST AS LARGE AS THE CHAIN
 LENGTH FOR THE DIFFUSION TO BE CORRECT.

***** MAXIMUM DIMENSIONS *****

NO. CHAINS TO BE SAMPLED = 50

NO. READS = 15000

NO. RENS = 30

NO. FRAMES = 500

NO. SAMPLES = 15

MAXIMUM BOX SIZE = 32X32X32

LOGICAL #1 HEADER(30), SPACE

COMMON N, IR, IRAN, IXS, IYS, IZS, IN, ICHAIN, ISUM(3), IS(3), ISEP(3),

1 IFRAME, NFRAME, KCHAIN, NCHAIN, NRUN,

2 IRUN, NCYCLE, NEV, KYS, IPRINT, KOUNT, TABLE(32), IMOVE(3,50),

3 I WALL(3,50), NTAB(15000), MAP(4096),

4 NSTART(15000), NEND(15000)

COMMON/CORRFN/FLSOR(50), FLFOUR(50), NCYCS(35), TCYCS(35), TCNC(35),

1 CORSM(2,50,35), CORRF(4,50,35), ISAMP, INCR, RCX(3), SDCM(3,50),

2 SVDCM(50), KSB(50), KFRAME(50), D2(50), D4(50), AVGL2(2,50),

3 AVGL4(2,50)

COMMON/CROSS/ALF(4,50,500), CROSS(5,2,50), START(3,50), START2(50),

2 RCROSS(5,2,50), RCROSS2(5,2,50), CCROSS(5,2), CCROSS2(5,2)

COMMON/FREQ/D2FR(30), NFN(50)

DATA SPACE/1H /

DIMENSION AVG(4), CORFC(4)

INTEGER #4 LTAB(3)

READ THE RANDOM NUMBER SEED

READ 10, IRAN

FORMAT(110)

READ 12, IIN, IOUT

FORMAT(2110)

IF IIN=0 READ IN LTAB

IF IOUT=0 WRITE FINAL BEAD CONFIGURATION

ONLY ON PRINTER

IF IOUT=1 WRITE FINAL BEAD CONFIGURATION TO DISK FILE

AS SPECIFIED ON FTCSF001 ON JCL

DC 20 I=1,30

HEADER(1)=SPACE

READ (5,30) HEADER

FORMAT (30A1)

PRINT 40, HEADER

FORMAT(1H1,30A1)

READ 10, NRUN

00000010
 00000020
 00000030
 00000040
 00000050
 00000060
 00000070
 00000080
 00000090
 00000100
 00000110
 00000120
 00000130
 00000140
 00000150
 00000160
 00000170
 00000180
 00000190
 00000200
 00000210
 00000220
 00000230
 00000240
 00000250
 00000260
 00000270
 00000280
 00000290
 00000300
 00000320
 00000330
 00000340
 00000350
 00000360
 00000370
 00000380
 00000390
 00000400
 00000410
 00000420
 00000430
 00000440
 00000450
 00000460
 00000470
 00000480
 00000490
 00000500
 00000510
 00000520
 00000530
 00000540
 00000550
 00000560
 00000570
 00000580
 00000590

```

MEMBER NAME MAIN
50 READ (5,50) N,NFRAME,KCHAIN
   FORMAT(3I10)
60 WRITE (6,60) N,NUN,NFRAME
   FORMAT(1H0,'THE NUMBER OF RUNS= ',I3,5X,'THE
   *NUMBER OF FRAMES PER RUN= ',I3)
70 READ 70,IXS,IYS,IZS
   FORMAT(3I10)
   BOX(1)=IXS
   BOX(2)=IYS
   BOX(3)=IZS
   PRINT 80
80 FORMAT(1H,' ',IXS, IYS, IZS')
   PRINT 90,IXS,IYS,IZS
90 FORMAT(1H,'19,2110)

C
C WHEN MORE THAN ONE CHAIN IS USED, TREAT THEM AS ONE CHAIN
C WITH MORE THAN TWO END HEADS
   NCF=0
100 READ (5,100) NCHAIN,(NSTART(I),NEND(I),I=1,NCHAIN)
   IF (NCHAIN.EQ.1) NCF=1
   IF (NSTART(NCHAIN).LT.9000) GO TO 130
   N=NSTART(NCHAIN)-9000
   NCF=NEND(NCHAIN)
   KS=NCHAIN
   NCH=NCHAIN+NCF-1
   DO 120 I=KS,NCHAIN
   IF (NCF.EQ.1) GO TO C 110
   NSTART(I)=NEND(I-1)+1
   GO TO 120
110 NSTART(I)=1
   NCF=0
120 NEND(I)=NSTART(I)+NB-1
130 CALL NCFC

C
C INITIALIZE THE ARRAYS
   DO 135 I = 1,30
   D2F(I) = 0
   DO 140 I=1,N
   NTAB(I)=0
140 IF (IIN.EQ.1) GO TO 515
   DO 510 J=1,N
   READ 500,(LTAB(I),I=1,3)
   CALL PACK(LTAB,J)
500 FORMAT(3I10)
510 CONTINUE
   GO TO 515
515 READ 520,(NTAB(I),I=1,N)
520 FORMAT(5(Z9,4X))
525 PRINT 520,IRAN,IR
530 FORMAT(11,' INITIAL CONFIGURATION NFRAME',5X,'IRAN= ',
   *,I12,5X,'IR= ',I3)
   DO 540 J=1,NCHAIN
   J1=NSTART(J)
   J2=NEND(J)
   PRINT 540,J,(NTAB(I),I=J1,J2)
540 FORMAT(' ',3X,'CHAIN#',I4,' ',8(Z9,4X))

```

```

00000600
00000610
00000620
00000630
00000640
00000650
00000660
00000670
00000680
00000690
00000700
00000710
00000720
00000730
00000740
00000750
00000760
00000770
00000780
00000790
00000800
00000810
00000820
00000830
00000840
00000850
00000860
00000870
00000880
00000890
00000900
00000910
00000920
00000930
00000940
00000950
00000960
00000970
00000980
00000990
00010000
00010100
00010200
00010300
00010400
00010500
00010600
00010700
00010800
00010900
00011000
00011100
00011200
00011300
00011400
00011500
00011600
00011700

```

```

MEMBER NAME MAIN
550 CONTINUE
IF (NCHAIN.LE.50) ISAMP=NCHAIN
IF (NCHAIN.LE.50) INCR=1
IF (NCHAIN.LE.50) GC TO 560
INCR=NCHAIN/50
ISAMP=NCHAIN/INCR
IF (INCR.EQ.0) INCR=1
IF (ISAMP.GT.50) ISAMP=50
560 DO 570 J=1,ISAMP
IFEN(J) = 0
DO 570 I=1,2
AVGL2(I,J)=0.0
AVGL4(I,J)=0.0
D4(J)=0.0
D2(J)=0.0
IF (NFRAME.LE.5) NTIME=NFRAME
IF (NFRAME.GT.5) NTIME=5
DO 570 KMM=1,NTIME
RCROSS(KMM,I,J)=0.0
570 RCROSS(KMM,I,J)=0.0
IFRAME=1
CALL LDMAP
FRAME=NFRAME
CALL CHMAP
CALL CTMAP
NCYCLE=0
NTEV=0
DO 580 I=1,A
DO 580 J=1,ISAMP
DO 580 K=1,KYS
580 CORFN(I,J,K)=0.0
CALL PRIME
C COMPUTE THE FRACTION OF EXCLUDED VOLUME CONFLICTS
PEVCF=FLOAT(NTEV)/FLOAT(NCYCLE)
C COMPUTE THE BEAD DENSITY
BDEN=FLOAT(N)/(BOX(1)*BOX(2)*BOX(3))
IF (ICUT.EQ.0) GO TO 585
WRITE (9,595) (NTAB(J),J=1,N)
595 FORMAT (8(2R,4X))
C COMPUTE AND PRINT DATA FOR EACH CHAIN
585 DO 600 J=1,ISAMP
PRINT 40,HEADER
PRINT 50,NFRAME,NFRAME,NCYCLE,PEVC
590 FORMAT ('01,4R,13,'NFRAME=',14,'TOTAL BEAD CYCLES=',
*18,'% V CONF=',F6.4)
C COMPUTE THE NUMBER OF BEADS IN JTH CHAIN
NB=END(J)-NSTART(J)+1
PRINT 600,J,IXS,IXS,IXS,N,BDEN
600 FORMAT ('01,4R,12,' BOX ',3I3,'
*,14,' BDENE=',F6.4)

```

```

00001180
00001190
00001200
00001210
00001220
00001230
00001240
00001250
00001260
00001261
00001280
00001290
00001300
00001310
00001320
00001330
00001340
00001350
00001360
00001370
00001380
00001390
00001400
00001410
00001420
00001430
00001440
00001450
00001460
00001470
00001480
00001490
00001500
00001510
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00001530
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00001600
00001610
00001620
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00001650
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00001680
00001690
00001700
00001710
00001720
00001730
00001740
00001750

```


MEMBER NAME MAIN
C

```

IF (ISAMP.LE.2) GO TO 915
PRINT 40,HEADER
PRINT 600,KCHAIN,NRUN,NFRAME
690 FORMAT('AVERAGES OF ',I2,' CHAINS FOR ',I3,' RUNS OF ',I4,
* ' FRAMES EACH. ')
PRINT 700,NCYCLE,PEVC,BDEN
700 FORMAT('H ',TOTAL BEAD CYCLES',I8,' REV/100',F6.4,
* ' BEAD DENSITY ',F6.4)
PRINT 710,IXS,IYS,IZS,N,ISAMP
710 FORMAT('H ',BOX',I2,2('X',I2),TOTAL # OF BEADS ',
* IA,TOTAL # OF CHAINS ',I3)
D1=0.0
D2=0.0
D3=0.0
MCH=0
720 DC 720 I=1,4
AVG(1)=0.0
DC 730 J=1,ISAMP
AVG(1)=AVGL2(1,J)+AVG(1)
AVG(2)=AVGL2(1,J)**2+AVG(2)
AVG(3)=AVGL4(1,J)+AVG(3)
AVG(4)=AVGL4(1,J)**2+AVG(4)
IF(D2(J).NE.0) MCH=MCH+1
D1=D2(J)+D1
D3=D2(J)**2+D3
730 D3=D2(J)**2+D3
AVG(2)=SQRT((AVG(2)-AVG(1)**2/ISAMP)/(ISAMP-1))
AVG(1)=AVG(1)/ISAMP
AVG(4)=SQRT((AVG(4)-AVG(3)**2/ISAMP)/(ISAMP-1))
AVG(3)=AVG(3)/ISAMP
PRINT 510,(AVG(I),I=1,4)
D2=SQRT((D3-D1**2/MCH)/(MCH-1))
D1=D1/MCH
731 PRINT 620,D1,D3
PRINT 630
DC 740 K=1,KOUNT
DC 740 I=1,4
CORFC(1)=0.0
DC 750 J=1,ISAMP
CORFC(1)=CORFN(I,J,K)+CORFC(1)
CORFC(2)=CORFN(1,J,K)**2+CORFC(2)
CORFC(3)=CORFN(1,J,K)+CORFC(3)
CORFC(4)=CORFN(1,J,K)**2+CORFC(4)
CONTINUE
750 CORFC(2)=SQRT((CORFC(2)-CORFC(1)**2/ISAMP)/(ISAMP-1))
CORFC(1)=CORFC(1)/ISAMP
CORFC(4)=SQRT((CORFC(4)-CORFC(3)**2/ISAMP)/(ISAMP-1))
CORFC(3)=CORFC(3)/ISAMP
TEMP=CORFC(1)
IF (TEMP.LE.0.0) TEMP=.0001
ALN1=ALOG(TEMP)
TEMP=CORFC(3)
IF (TEMP.LE.0.0) TEMP=.0001
ALN2=ALOG(TEMP)
IF (K.NE.1) GO TO 755
PRINT 640,K,(CORFC(I),I=1,2),ALN1,(CORFC(I),I=3,4),ALN2
IP = 0
WRITE(8,240) IP,CORFC(1)

```

000J2340
00002350
00002360
00002370
00002380
00002390
00002400
00002410
00002420
00002430
00002440
00002450
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MEMBER NAME MAIN
GO TO 760
755 PRINT #50,K,TCNC(K-1),(CORFC(I),I=1,2),ALN1,(CCRFC(I),I=3,4),
*ALM2,NCYCS(K-1),TCYCS(K-1)
WRITE (#,540) TCNC(K-1),CORFC(I)
940 FORMAT(' ',2F6.3)
760 CONTINUE
IF (NFRAME.LE.5) NTIME=NFRAME
IF (NFRAME.GT.5) NTIME=5
DO 840 KMM=1,NTIME
DP 840 I=1,2
CCROSS(KMM,I)=0.0
CCROSS2(KMM,I)=0.0
DO 770 KMM=1,NTIME
DO 770 KMM=1,NTIME
CCROSS(KMM,1)=CCROSS(KMM,1,J)+CCROSS(KMM,1)
CCROSS(KMM,2)=CCROSS(KMM,1,J)+CCROSS(KMM,2)
CCROSS2(KMM,1)=CCROSS2(KMM,1,J)+CCROSS2(KMM,1)
CCROSS2(KMM,2)=CCROSS2(KMM,2,J)+CCROSS2(KMM,2)
DO 780 KMM=1,NTIME
CCROSS(KMM,2)=SQRT((CCROSS(KMM,2)-CCROSS(KMM,1)**2/ISAMP)/
*(ISAMP-1))
CCROSS(KMM,1)=CCROSS(KMM,1)/ISAMP
CCROSS2(KMM,2)=SQRT((CCROSS2(KMM,2)-CCROSS2(KMM,1)**2/ISAMP)/
*(ISAMP-1))
780 CCROSS2(KMM,1)=CCROSS2(KMM,1)/ISAMP
PRINT #10 CROSS CORRELATION TABLE'
810 FORMAT(' CROSS CORRELATION TABLE')
820 PRINT #20 TIME P(L,L) STD P(L2,L2) STD'
DO 790 KMM=1,NTIME
790 PRINT #30,KMM,(CCROSS(KMM,I),I=1,2),(CCROSS2(KMM,I),I=1,2)
830 FORMAT(' ',1A,4F12.4)
900 PRINT #00
FORMAT(' THE DISTRIBUTION FUNCTION FOR D**2 IS ')
910 PRINT #10
FORMAT('0 D**2 F(D**2)')
DO 920 I=1,30
D2F(I)=D2F(I)/NRUN
L=I**2
920 PRINT #30,L,D2F(I)
930 FORMAT(' ',19,EX,F8.4)
1000 STOP
END
SUBROUTINE NCYC
C NCYC CALCULATES THE NUMBER OF CYCLES THAT WILL ELAPSE BETWEEN SAMPLES.
COMMON N,IR,IRAN,IXS,IYS,IZS,IN,ICHA,IN,ISUM(3),IS(3),ISEP(3),
1 IFRAME,NFRAME,KCHAIN,NCHAIN,NRUN,
2 IWIN,NCYCLE,NEVT,KYS,IPRINT,KOUNT,TABLE(32),IMOVE(3,50),
3 IVAL(5,50),NTAB(15000),M4P(4095),NSTART(15000),
4 NEND(15000)
C
COMMON/CORRFN/FLSOR(50),FLFOUR(50),NCYCS(35),TCYCS(35),TCNC(35),
1 CORSM(2,50,35),COPFN(4,50,35),ISAMP,INCR,BCKX(3),SDCM(3,50),
2 SVDGM(50),KSB(50),KFRAME(50),D2(50),D4(50),AVGL2(2,50),
3 AVGL4(2,50)
C
READ 10, FACTOR, FCUBE, FADD

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MEMBER NAME MAIN
10 FORMAT (F10.4)
IN = NEND(1)-NSTART(1)+1
TOTAL = AINT(FCUBE*FLCAT(IN*IN*N))
TOLD = 0.0
KYS = 0
KOUT = 0
IG=0
DO 50 I=1,50
KYS = KYS + 1
TNEW = INT(TOLD*FACTOR) + FADD
IF(TNEW - TOTAL) 40,30,20
20 TNEW = TOTAL
30 NCYCS(I) = TNEW - TOLD
TCYCS(I) = TNEW
TCNC(I) = FCUBE*TCYCS(I)/TOTAL
GO TO 50
40 NCYCS(I) = TNEW-TOLD
TCYCS(I) = TNEW
TCNC(I) = FCUBE*TCYCS(I)/TOTAL
50 CONTINUE
PRINT 70
70 FORMAT (1H,NCYCS RESPONDING)
WRITE (F,20) KYS,N
80 FORMAT (1H,NUMBER OF SAMPLES PER FRAME = ,I3,5X,
*,NUMBER OF BEADS = ,I5)
PRINT 90, FACTOR, FCUBE, FADD
90 FORMAT (1H0,FACTOR = ,F10.3,5X,FCUBE = ,F10.3,5X,FADD = ,
*,F10.3)
PRINT 200,TOTAL
200 FORMAT (1H0,TOTAL NUMBER OF BEAD CYCLES PER FRAME = ,F7.0)
PRINT 210
210 FORMAT (1H0,TNEW = INT(TOLD*FACTOR) + FADD)
PRINT 220
220 FORMAT (1H0,NO. OF SAMPLE NCYCS TCYCS
PRINT 230,(1,NCYCS(I),TCYCS(I),TCNC(I),I=1,KYS)
230 FORMAT (1H,I8,I12,F12.1,F15.4)
RETURN
END
SUBROUTINE PRIME
C
C
C
COMMON N,IR,IPAN,IXS,IYS,IZS,IN,ICHAIN,ISUM(3),IS(3),ISEP(3),
1 IFRAME,IFRAME,KCHAIN,NCHAIN,NRUN,
2 IWIN,NCYCLE,NEVT,KYS,IPRINT,KOUNT,TABLE(32),IMOVE(3,50),
3 IMA,LL(3,50),NTAB(15000),MAP(4096),NST,PT(15000),
4 NEND(15000)
C
COMMON/CJORSF/ELSOR(50),FLFOUR(50),NCYCS(35),TCYCS(35),TCNC(35),
1 CORFN(2,50,35),CORFN(4,50,35),ISAMP,INCR,BOX(3),SDCM(3,50),
2 SVDCM(50),KSR(50),KFRAME(50),D2(50),D4(50),AVGL2(2,50),
3 AVGL4(2,50)
C
C
C
INTEGER*4 T,NOFF

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MEMBER NAME MAIN
80 FORMAT (0,' FINAL CONFIGURATION OF RUN #',I2,' FRAME #',I3)
WRITE (7,82) (NTAB(J),J=1,N)
82 FORMAT (8(Z8,4X))
DO 90 J=1,KCHAIN
J1=NSTART(J)
J2=NEST(J)
PRINT 85,J,(NTAB(I),I=J1,J2)
90 FORMAT (1,'3X',CHAIN#',I4/',',8(Z8,4X))
CONTINUE
DO 95 J=1,ISAMP
IF (KFRAME(J).EQ.0) GO TO 95
SVDCM(J)=SVDCM(J)/KFRAME(J)
95 CONTINUE
DO 101 I=1,30
IF (NDFR.EQ.0) GO TO 101
IFREQ(II) = IFREQ(II)/NDFR
101 A2FR(II) = D2FR(II)+IFREQ(II)
PRINT 110,IFUN,NFRAME
110 FORMAT (1,'AVERAGE FOR RUN #',I2,' FRAME# ',I4)
DO 250 J=1,ISAMP
PRINT 120,J
120 FORMAT (0,' AVERAGES FOR CHAIN#',I2)
PRINT 130,FLSQ(J),FLFOUR(J)
130 FORMAT (0,'LSQ SUM =',F10.1,10X,'LFQR SUM =',F10.1)
FLSQ(J)=FLSQ(J)/(NFRAME*KYS)
FLFOUR(J)=FLFOUR(J)/(NFRAME*KYS)
AVGL2(1,J)=FLSQ(J)+AVGL2(1,J)
AVGL4(1,J)=FLFOUR(J)+AVGL4(1,J)
AVGL2(2,J)=AVGL2(2,J)+FLSQ(J)**2
AVGL4(2,J)=AVGL4(2,J)+FLFOUR(J)**2
PRINT 140
140 FORMAT (0,' AVG L5QR',26X,'AVGLFCUR1)
PRINT 150,FLSQ(J),FLFOUR(J)
150 FORMAT (1H,F10.4,125X,F10.4)
PRINT 160,SVDCM(J),KFRAME(J)
160 FORMAT (0,'KD**2',FRAME',F10.4,10X,'NUMBER OF FRAMES =',I4)
D2(J)=SVDCM(J)+D2(J)
D4(J)=SVDCM(J)**2+D4(J)
IF (SVDCM(J).NE.0) NFN(J) = NFN(J) + 1
FLG=0.0
IF (FLFOUR(J)-FLSQ(J)**2.EQ.0.0) FLG=1.0
DO 200 I=1,KOUNT
CORSM(1,J,I)=CORSM(1,J,I)/(FLSQ(J)*NFRAME)
IF (FLG.EQ.1.0) GO TO 190
CORSM(2,J,I)=(CORSM(2,J,I)/NFRAME-FLSQ(J)**2)
*/(FLFOUR(J)-FLSQ(J)**2)
GO TO 200
190 CORSM(2,J,I)=1.0
200 CONTINUE
PRINT 210,CORSM(1,J,I)
210 FORMAT (0,'CORSM(1,J,I) =',F13.4)
PRINT 260
260 FORMAT (1H,KOUNT AVCORR(L*L) AVCOR(L2*L2) TCYCS
I=1
PRINT 220,I,(CORSM(K,J,I),K=1,2)
DO 230 I=2,KOUNT

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MEMBER NAME MAIN
PRINT 220,I, (CORSM(K,J,I),KEL,2),TCYCS(I-1),NCYCS(I-1)
FORMAT(1H,13,F12.4,9X,1PF12.4,0PF11.1,I7)
CONTINUE
DO 240 I=1,KOUNT
CORFN(1,J,I)=CORSM(1,J,I)+CORFN(1,J,I)
CORFN(2,J,I)=CORSM(1,J,I)*2+CORFN(2,J,I)
CORFN(3,J,I)=CORSM(2,J,I)+CORFN(3,J,I)
CORFN(4,J,I)=CORSM(2,J,I)*2+CORFN(4,J,I)
IF (NFRAME.LT.5) NTIME=NFRAME
IF (NFRAME.GT.5) NTIME=5
DO 240 KMM=1,NTIME
CROSS(KMM,1,J)=ALF(1,J,KMM)*START(1,J)+ALF(2,J,KMM)*START(2,J)
*+ALF(3,J,KMM)*START(3,J)
CROSS(KMM,2,J)=ALF(4,J,KMM)*START2(J)
NFRAME=NFRAME+KMM
DO 245 TEL=1,NF
IF (NF.LE.1) GO TO 265
CROSS(KMM,1,J)=ALF(1,J,T)+ALF(1,J,T)+KMM)+ALF(2,J,T)*ALF(2,J,T)+KMM)
*+ALF(3,J,T)*ALF(3,J,T)+KMM)+CROSS(KMM,1,J)
CROSS(KMM,2,J)=ALF(4,J,T)+ALF(4,J,T)+KMM)+CROSS(KMM,2,J)
CONTINUE
245 NFRAME=NFRAME+KMM+1
CROSS(KMM,1,J)=CROSS(KMM,1,J)/(NF*FLSQR(J))
CROSS(KMM,2,J)=(CROSS(KMM,2,J)/NF-FLSQR(J)*2)/
*(FLSQR(J)-FLSQR(J)**2)
FCROSS(KMM,1,J)=CROSS(KMM,1,J)+FCROSS(KMM,1,J)
FCROSS2(KMM,1,J)=CROSS(KMM,1,J)**2+FCROSS2(KMM,1,J)
FCROSS(KMM,2,J)=CROSS(KMM,2,J)+FCROSS(KMM,2,J)
FCROSS2(KMM,2,J)=CROSS(KMM,2,J)**2+FCROSS2(KMM,2,J)
CONTINUE
280
PRINT 290
FORMAT(10,'CROSS CORRELATION TABLE')
PRINT 300
FORMAT(1,'TIME(FRAMES), <P(L*2)> ')
DO 320 KM=1,5
PRINT 310,KM,CROSS(KM,1,J),CROSS(KM,2,J)
FORMAT(1,'12,5X,2F12.4)
CONTINUE
PRINT 350
FORMAT(' THE DISTRIBUTION FUNCTION FOR D**2/FRAME IS ')
PRINT 360
FORMAT(10,' D**2 F(D**2) ')
DO 370 I=1,30
L=I**2
PRINT 380,L,IFREQ(I)
FORMAT(1,'18,5X,F8.4)
1000 CONTINUE
RETURN
END
SUBROUTINE SAMPLE
COMMON N,IP,IRAN,IXS,IYS,IZS,IN,ICHAIN,ISUM(3),IS(3),ISEP(3)
1 IFRAME=NFRAME,KCHAIN,NCHAIN,NPUN
2 IFUN,NCYCLENEVT,KYS,IPRINT,KOUNT, TABLE(32),IMOVE(3,50),
3 IW/LL(3,50),NTAB(15000),MAP(4096)

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MEMBER NAME MAIN
4 NSTART(15000),NEND(15000)
C
COMMON/CORP/N/FLSOR(50),FLFOUR(50),MAYCS(35),TCYCS(35),TCNC(35),
1 CRPSSM(2,50,35),CORFN(4,50,35),ISAMP,INCR,BOX(3),SDCM(3,50),
2 SVDCM(50),KSR(50),KFRAME(50),D2(50),D4(50),AVGL2(2,50),
3 AVGL4(2,50)
C
COMMON/CROSS/ALF(4,50,500),CROSS(5,2,50),START(3,50),START2(50),
2 FCROSS(5,2,50),FCROSS2(5,2,50),CCROSS(5,2),CCROSS2(5,2)
C
INTEGER*4 SIDE(3)
REAL*4 LSQR,LSQR1(50),CMN(3),CMD(3,50),DCM
DIMENSION S(3),S1(3,50),B(3)
C
J=0
DO 140 IJ=1,NCHAIN,INCR
J=J+1
N1=NSTART(IJ)
N2=NEND(IJ)
DO 10 I=1,3
CMN(I)=0
B(I)=(BOX(I)-1.)/2.
ISUM(I)=0
ISCP(I)=0
IS(I)=0
10 CONTINUE
CALL UNPACK(N1,N2)
LSQR=0
DO 20 I=1,3
S(I)=FLOAT(IS(I))
LSQR=LSQR+S(I)*S(I)
20 CMN(I)=FLOAT(ISUM(I))/FLOAT(1+N2-N1)
C PUT CENTER OF MASS INSIDE OF THE BOX
DC 30 I=1,3
IF (CMN(I).LT.0) CMN(I)=CMN(I)+BOX(I)
IF (CMN(I).GE.BOX(I)) CMN(I)=CMN(I)-BOX(I)
LSQR1(J)=LSQR
DO 40 I=1,3
IF (ISCP(I).GT.1) KSR(J)=1
S1(I,J)=S(I)
DO 45 I=1,3
IF (IFR&M*.NE.1) GO TO 45
START(I,J)=S1(I,J)
START2(J)=LSQR
45 CONTINUE
GO TO 100
50 FLSQR(J)=FLSOR(J)+LSQR
FLFOUR(J)=FLFOUR(J)+LSQR*LSQR
C CALCULATE DIFFUSION
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MEMBER NAME MAIN
DO 50 I=1,3
SIDE(I)=0
IF (CMN(I).LE.B(I)) SIDE(I)=1
IF (CMN(I).GT.B(I)) SIDE(I)=I+3
IF (ISEP(I).GT.1) KSR(J)=1
IF (KSR(J).EQ.1) GO TO 100
IF (ISEP(I).EQ.1) GO TO 60
C CHAIN IS NOT SPLIT IN THE END
KAT=MOVE(I,J)/2
DCM=CMN(I)-CMO(I,J)*KAT*BOX(I)
MOVE(I,J)=0
GO TO 30
C CHAIN IS SPLIT IN THE END
60 IF (IWALL(I,J).NE.0) GO TO 70
C THE WALL WAS NOT HIT
DCM=CMN(I)-CMO(I,J)
IF (DCM.GT.B(I)) DCM=DCM-BOX(I)
B(I)=B(I)*(-1)
IF (DCM.LT.B(I)) DCM=DCM+BOX(I)
B(I)=B(I)*(-1)
GO TO 80
C A WALL WAS HIT,(CHAIN SPLIT)
70 KAT=MOVE(I,J)/2
IF (IWALL(I,J).EQ.SIDE(I)) DCM=CMN(I)-CMO(I,J)+
*KAT*BOX(I)/2
IF (IWALL(I,J).EQ.SIDE(I)) GO TO 90
C THE CENTER OF MASS IS NOT NEAR THE LAST WALL HIT
IF (IWALL(I,J).EQ.I+3) DCM=CMN(I)-CMO(I,J)+BOX(I)
**BOX(I)*KAT
IF (IWALL(I,J).EQ.I) DCM=CMN(I)-CMO(I,J)-BOX(I)
**BOX(I)*KAT
80 SDCM(I,J)=DCM+SDCM(I,J)
90 CONTINUE
100 CORSM(1,J,KOUNT)=CORSM(1,J,KOUNT)+S(1)*S1(I,J)+
*S(2)*S1(2,J)+S(3)*S1(3,J)
CORSM(2,J,KOUNT)=CORSM(2,J,KOUNT)+LSQR(J)*LSQR
IF (KOUNT.LE.KYS) GO TO 105
ALF(1,J,IFRAME)=S(1)
ALF(2,J,IFRAME)=S(2)
ALF(3,J,IFRAME)=S(3)
ALF(4,J,IFRAME)=LSQR
DO 110 I=1,3
IWALL(I,J)=0
105 MOVE(I,J)=0
110 IF (ISEP(I).EQ.1) GO TO 120
GO TO 130
120 IF (CMN(I).GT.B(I)) MOVE(I,J)=1
130 IF (CMN(I).LE.B(I)) MOVE(I,J)=-1
CMC(I,J)=CMN(I)
IF (J.EQ.50) IJ=NCHAIN
140 CONTINUE
1000 CONTINUE
RETURN
END
SUBROUTINE PRIMAP
PRIMAP PRINTS NON-ZERO LOCATIONS OF MAP IF CTMAP OR CHMAP DETECT
C AN ERROR IN MAP. I IS THE LOCATION IN MAP, THAT IS THE ITH WORD IN MAP00006970

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MEMBER NAME N,IN
C NOTE: THE FIRST WORD OF MAP CORRESPONDS TO Y=0,Z=0
COMMON N,IS,IFAN,IXS,IYS,IZS,IN,ICHAIN,ISUM(3),IS(3),ISEP(3),
1 IFRAME,NFRAME,KCHAIN,NCHAIN,NPUN,
2 IRUN,NCYCLE,NEVT,KYS,IPRINT,KOUNT,TABLE(32),IMOVE(3,50),
3 IWALL(3,50),FNUM&P(15000),MAP(40&6),NSATET(15000),
4 NEND(15000)
C
C
10 WRITE(6,10) IPRINT
FORMAT(1H0,10) THE CTMAP SUBROUTINE FOUND ,15 . BEADS IN MAP,1/
WRITE (6,20)
20 FORMAT(1H0//,***** PRINTOUT OF MAP *****//1H0,
1 LOCATION,3X,Y,3X,Z,18X,MAP//)
DC 50 I=1,40&6
IF (MAP(I).EQ.0) GO TO 50
IDUMEL
IY=IDUM/128
IZ=IDUM-(IY*128)-1
IF(IZ.LE.63) GO TO 30
IZ=IZ-64
30 CONTINUE
WRITE(6,40) I,IY,IZ,MAP(I)
FORMAT(1H ,2X,14,2X,214,12X,Z8)
50 CONTINUE
WRITE(6, 50)
60 FORMAT(1H0,END OF PRTPMAP)
STOP
END
SUBROUTINE PRINT
COMMON N,IR,IRAN,IXS,IYS,IZS,IN,ICHAIN,ISUM(3),IS(3),ISEP(3),
1 IFRAME,NFRAME,KCHAIN,NCHAIN,NPUN,
2 IRUN,NCYCLE,NEVT,KYS,IPRINT,KOUNT,TABLE(32),IMOVE(3,50),
3 IWALL(3,50),NTAB(15000),MAP(40&6),NSTART(15000),NEND(15000)
C
C
COMMON BLOCK MUST BE IN SAME ORDER IN ALL SUBPROGRAMS
C
C
DO 20 J=1,NCHAIN
J1=NSTART(J)
J2=NEND(J)
PRINT 10,J,(NTAB(I),I=J1,J2)
10 FORMAT(' ',3X,'CHAIN#',14,' ',R(Z8,4X))
20 CONTINUE
RETURN
END
SUBROUTINE SKJ
C
C
THIS SUBROUTINE DETERMINES IF A CHAIN IS TO BE SAMPLED OR NOT
UP TO 50 CHAINS MAY BE SAMPLED. IF THE NUMBER OF CHAINS
IS > 50 THEN THE CHAINS TO BE SAMPLED ARE PICKED SO THAT
THEY ARE EQUALLY SPACED.
C
C
COMMON N,IR,IFAN,IXS,IYS,IZS,IN,ICHAIN,ISUM(3),IS(3),ISEP(3),
1 IFRAME,NFRAME,KCHAIN,NCHAIN,NPUN,
2 IRUN,NCYCLE,NEVT,KYS,IPRINT,KOUNT,TABLE(32),IMOVE(3,50),
3 IWALL(3,50),NTAB(1500),MAP(40&6),
4 NSTART(15000),NEND(15000)

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MEMBER NAME MAIN

C

```

COMMON/CORREN/FLSOR(50),FLFOUR(50),NCYCS(35),TCYCS(35),TCNC(35),
1 CERSN(2,50,35),COPEN(4,50,35),ISAMP,INCR,BOX(3),SDCM(3,50),
2 SVDCM(50),DSB(50),DFRAME(50),D2(50),D4(50),AVGL2(2,50),
3 AVGLA(2,50)

```

C

```

IN=0
J=0
DO 10 IJ=1,NCHAIN,INCR
  J=J+1
  IF (ICHAIN.EQ.IJ) IN=1
  IF (ICHAIN.EQ.IJ) ICHAIN=J
  IF (J.EQ.50) IJ=NCHAIN

```

10

```

CONTINUE
RETURN
END

```

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00007560
00007570
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```

MEMBPP NAME LDMAP
LDMAP CSECT
SAVE (14,12) INITIAL LOADING OF MAP FROM NTAR
* LDMAP INITIALIZES MAP TO ZERO AND THEN LOADS MAP ACCORDING TO LTAE
* EVERY POSSIBLE READ LOCATION CORRESPONDS TO A BIT IN MFP.
* A BIT IN MAP IS ONE IF THE CORRESPONDING READ LOCATION CONTAINS
* A READ AND ZERO OTHERWISE.
* EACH WORD IN MAP CORRESPONDS TO A SET OF READ LOCATIONS WITH A
* PARTICULAR PAIR OF Y AND Z COORDINATES AND VARYING VALUES OF X.
* THE 32 BITS IN EACH WORD CORRESPOND TO EITHER THE 32 LOCATIONS WHERE
* X IS LESS THAN OR EQUAL TO 31 OR THE 32 LOCATIONS WHERE X IS GREATER
* THAN OR EQUAL TO 32. TO DIFFERENTIATE BETWEEN THESE TWO CASES, A
* BIT IN THE ADDRESS OF MAP IS EITHER 1 OR 0.
* HENCE THE CORRESPONDENCE BETWEEN WORDS IN MAP AND READ LOCATIONS IS:
* (X,Y,Z) <=> MAP(Y*(2**7) + Z + C*(2**6))
* WHERE C = 0 IF X<32 AND C=1 IF X>31.
* FOR ANY PARTICULAR WORD IN MAP, IF THE NTH BIT IS 1, THEN THERE IS A
* BEAD AT (N-1,Y,Z) OR (N-1+32,Y,Z).
* FOR EXAMPLE, IF MAP(B'00000000 00000000 00000000 00000011' =
* THEN THERE ARE BEADS AT (X,Y,Z) = (12,4,3), (13,4,3), (24,4,3)
* IF MAP(B'00000000 00000000 00000000 01000011' =
* THEN THERE ARE BEADS AT (X,Y,Z) = (44,4,3), (45,4,3), (56,4,3)
*
BALP 9,0
USING *9
L 12,ACOM
USING N,12
ST 13,SAV1+4
LA 13,SAV1
LA 3,4
LA 4,1
LA 5,31
ST 4,TARLE
SLL 4,1
ST 4,TABLE(3)
A 3,FF'4.
ACT 5,L1
* ZERO OUT ALL OF MAP
LA 1,0
LA 2,4
LA 3,FF'16380.
LA 5,0
ST 5,0(1,15)
BXLE 1,2,AGAIN
* LOAD MAP ( MEANS UNUSED BIT, 1 MEANS WORD BOUNDARY)
* SLR 1,1
* 11,N
* 10,FF'31.
HERE SLR 5,5
L 4,NTAB(1)
SRDL 4,6
SFL 4,1
SFPL 4,9
SPL 5,17
CR 4,10
X__Y__Z| IN REG 4 AND REGS
X__Y__Z| IN REG 4 AND REGS
X__Y__Z| IN REG 4 AND REGS
X IN REG 4 AND Y__Z| IN REG 5
COMPARE X WITH 31

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00000010
00000020
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00000100
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MEMBER NAME LDMAP
BNH DONT
S 4,FF,32'
C 5,TW07
LR 3,5 PUT 1 IN UNUSED BIT BETWEEN Y AND Z
M 2,FF,4' INDEX OF MAP
MH 4,FF,4' INDEX OF TABLE
L 7,TABLE(4)
C 7,0(3,15)
ST 7,0(3,15)
A 1,FF,4' INCREMENT NTAB POINTER
PCT 11,HERE
L 13,SAV1+4
LM 14,15,12(13)
LN 1,12,24(13)
MVI 12(13),X,FF,
RP 14
DS 1RF
DC X,0000004,0'
DC A(N)
DC A(MAP)
COM
DS F
DS 27F
DS 32F
DS 300F
DS 150,00F
DS 4096F
END LDMAP

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MEMBER NAME CHAIN
CHAIN CSECT
* THIS SUBPROGRAM DETERMINES IF A WALL HIT SHOULD BE COUNTED
* AS A HIT. FOR EXAMPLE IF A LOW X WALL WAS HIT FOLLOWED BY
* A HIGH X WALL HIT THEN THE NET EFFECT IS THAT NO WALL WAS
* HIT AND IWALL MUST BE SET TO EITHER 0 OR TO THE NUMBER OF
* THE WALL HIT PREVIOUS TO THESE TWO HITS.
      SAVE (14,12)
      BALP 11,0
      USING *11
      L 12,ACOM
      ST 13,SAV+4
      LA 13,SAV
* R7 CONTAINS THE NUMBER OF WALL HIT. THIS IS PASSED IN R7 FROM CYCLE.
* IWALL = 1 IF THE LOW X WALL WAS PENETRATED
* IWALL = 2 IF THE HIGH X WALL WAS PENETRATED
* IWALL = 3 IF THE LOW Y WALL WAS PENETRATED
* IWALL = 4 IF THE HIGH Y WALL WAS PENETRATED
* IWALL = 5 IF THE LOW Z WALL WAS PENETRATED
* IWALL = 6 IF THE HIGH Z WALL WAS PENETRATED
* IF THIS IS THE FIRST TIME THROUGH CYCLE THEN
* ZFPO THE ARRAYS ENDR,BEGIN,AND BOTH, OTHERWISE DON'T
      ST 3,PLACE
      L 4,0(1)
      L 4,0(4)
      C 4,=F'0.
      BNE NO
*
      XR 3,3
      LA 5,150
      XR 9,9
      ST 9,TBL1(3)
      ST 9,COUNT(3)
      ST 9,TBL(3)
      LA 3,4(3)
      BCT 5,SB
      L 3,PLACE
      L 5,COUNT(3)
      C 5,=F'0.
*
      BE ONE
      RE TWO
* SAME WALL HAS BEEN HIT TWO TIMES BEFORE THIS HIT BY THE SAME CHAIN
      L 5,TBL(3)
      CF 5,7
      RE ZIP
      LA 5,1
      ST 5,COUNT(3)
      L 5,TBL1(3)
      ST 5,IWALL(3)
      XR 5,5
      ST 5,TBL(3)
      R RETURN
      LA 5,1
      ST 5,COUNT(3)
      XR 5,5
ZIP
*
      R4 = ADDRESS OF PASSED ARGUMENT
      R4 = TIME
      IF TIME > 0 THEN
      DON'T ZREC ARRAYS
      ZERO ARRAYS
*
      TEST TO SEE IF A WALL IN THIS
      DIMENSION WAS HIT BEFORE BY THIS
      CHAIN
      IF NOT GO TO ONE
      IF THIS WALL HAS BEEN HIT BY THIS
      CHAIN ONCE BEFORE GO TO TWO
      BEFORE THIS HIT BY THE SAME CHAIN
      FS = LAST WALL HIT
      IF SAME WALL WAS HIT
      THIS TIME GO TO ZIP
      CANCEL LAST HIT
      COUNT = 1
      IWALL IS THE WALL HIT 2 TIMES AGO
      TBL = 0
      WALL HIT THIRD TIME
      SAME AS IF WALL HAS BEEN HIT ONCE

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MEMBER NAME CYCLE
CYCLE CSFCT 12(15)
DC X,7,
DC CL7*CYCLE,
SAVE (14,12)
L 2,0(1)
L RALP 12,0
USING *1,2
L 11,ACOM
USING N,11
ST 13,SAV+4
LA 15,SAV
LA 4,0
ST 4,TIME
START XP 3,3
ST 3,ICHAIN
L 5,IRAN
M 4,MULT
N 5,QR
ST 5,IRAN
LA 3,2
SLL 3,1
MR 4,3
C 4,FF,0,
PE STARTC
**
L 5,IRAN
M 4,MULT
N 5,QR
ST 5,IRAN
L 3,N
SLL 3,1
MR 4,3
ST 4,IR
* DECIDE WHICH CHAIN IS MOVING.
* ARRAYS USED IN DIFFUSION CALCULATIONS.
*
XG 7,7
LA 3,1
XG 6,6
L 9,KCHAIN
L 4,IR
LA 4,1(4)
L 10,ACOM+8
L 9,0(6,10)
CP 4,8
PH ROM
*
ST 3,ICHAIN
R FOUND
LA 3,1(3)
LA 6,A(6)
RCT 3,LOOPC
S 3,EF,1,
SLL 3,2
SUBROUTINE TO PERFORM BEAD MOVEMENTS
BRANCH AROUND CONSTANTS
LENGTH OF ENTRY POINT NAME
ENTRY POINT NAME
SAVE ALL REGISTERS EXCEPT 13
R2 = ADDRESS OF THE PASSED ARGUMENT
R2 = THE NUMBER OF TIMES TO CYCLE
LOAD BASE ADDRESS
USE R12 IN LOCAL ADDRESSING
00000010
00000020
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00000060
00000070
00000080
00000090
00000100
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SUBROUTINE TO PERFORM BEAD MOVEMENTS
BRANCH AROUND CONSTANTS
LENGTH OF ENTRY POINT NAME
ENTRY POINT NAME
SAVE ALL REGISTERS EXCEPT 13
R2 = ADDRESS OF THE PASSED ARGUMENT
R2 = THE NUMBER OF TIMES TO CYCLE
LOAD BASE ADDRESS
USE R12 IN LOCAL ADDRESSING
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00000580
SET UP SUBROUTINE SAVE AREA
TIME = 0
FIRST TIME THROUGH CHAIN
ICHAIN = 0
*****
GENERATE A RANDOM NUMBER OF
ZERO OR ONE
IF IT IS 0 DO A CRANKSHAFT
MOVE
IF IT IS 1 DO A SINGLE
BEAD MOVEMENT
00000010
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00000100
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00000580
SINGLE BEAD MOVEMENT SELECTED
*****
GENERATE A
RANDOM NUMBER FROM 0 TO N-1
R3 = R3 * 2
*****
THIS IS NEEDED FOR ADDRESSING
R7 = 0
R3 = 1 INCREMENT BY 1 EACH TIME
THROUGH THE LOOP
R6=0 USE TO INDEX NEND
R9 = NO OF CHAINS TO BE SAMPLED
R4 = NO. OF MOVING BEAD FROM 1 TO N
R10 = ADDRESS OF NEND
R8=NEND(6)
COMPARE IR+1 TO NEND(6)
IR+1 IS NOT LE NEND, SO CHAIN
NUMBER IS NOT ICHAIN
IR+1 <= NEND(6) SO CHAIN NO = R3
JUMP OUT OF LOOP
ICHAIN = ICHAIN + 1
R6 = R6+4
SEE IF CHAIN NO IS ICHAIN
CHAIN NO IS BETWEEN 0 AND N-1
ICHAIN = ICHAIN #4
00000010
00000020
00000030
00000040
00000050
00000060
00000070
00000080
00000090
00000100
00000110
00000120
00000130
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00000150
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```

MEMBER NAME  CYCLE
ST           4,IF1
C           4,EF1,
BNH        TRY0
C           4,EF3,
BNH        TRY1
L          10,FX'00000001,
C           4,EF4,
BE         ADD
B          SURT
L          10,FX'00000100,
C           4,EF3,
RL         ADD
B          SURT
L          10,FX'00010000,
C           4,EF0,
RE         ADD
*
* SUBT
B          8,10
STSTAB    B
AR         8,10
ST         8,STAB
L          4,STAB
SRDL      4,8
SRL       5,24
L          3,IZS
C           5,EF128,
BNL       TEST1
C           5,IZS
BNL       TEST2
SRDL      4,8
SRL       3,IYS
L          3,8
C           5,EF128,
BNL       TEST1
C           5,IYS
BNL       TEST2
SRDL      4,8
SRL       3,IXS
L          3,16
C           5,EF128,
BNL       TEST1
C           5,IXS
BNL       TEST2
EXVOL     X,Y,Z IN BOX
B          5,STAB
L          5,3
AR         HIT
B          5,STAB
SR         5,3
ST         5,STAB
L          4,STAB
SRDL      4,6
SRL       4,1
SRDL      4,9

```

```

*****
IF IRE = 0 OF 1 THEN MOVE IN
Z DIMENSION
IF IRE = 2 OR 3 THEN MOVE IN
Y DIMENSION
IRE = 4 OR 5 SO MOVE IN
X DIMENSION
IF IRE = 4 ADD 1 TO X DIMENSION
IF IRE = 5 SUBTRACT 1 FROM X DIM.
F10 = A 1 IN Y COORD. POSITION
00001170
00001180
00001190
00001200
00001210
00001220
00001230
00001240
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*****
IF IRE = 0 THEN ADD 1 TO Z POSITION
THE Y POSITION
F10 = A 1 IN Z POSITION
IF IRE = 1 THEN SUBTRACT
1 FROM Z DIMENSION
MOVE AN END BEAD
STAB = MOVED BEAD COORDINATES
R4 = STAB = NEW BEAD POSITION
X = Y - IZ IN REG 4 AND REG 5
R5 = Z COORDINATE OF NEW BEAD COORD.
R3 = Z DIMENSION OF THE BOX
COMPARE R5 TO -1
Z IS < 0
COMPARE R5 TO IZS
Z IS > IZS
Y AT TOP OF R5
Y AT BOTTOM OF R5
R3 = IYS
R3 = IYS
COMPARE R5 TO -1
Y IS < 0
COMPARE R5 TO IYS
Y IS > IYS
X AT TOP OF R5
X AT BOTTOM OF R5
R3 = IXS
R3 = IXS
COMPARE R5 TO -1
X IS < 0
COMPARE R5 TO IXS
X IS > IXS
X,Y,Z IN BOX
ADD IXS,IYS, OR IZS
X,Y, OR Z > IXS,IYS, OR IZS
SUBTRACT IXS,IYS, OR IZS
STOPE NEW BEAD COORDINATES IN STAB
R4 = STAB

```

```

MEMBER NAME CYCLE
SPL 5,17
SLL 5,2
SLL 4,2
SLL 7,TARLE(4)
* TEST TO SEE IF BEAD IS THERE *
L 10,ACOM+12
N 7,0(S,10)
BNZ FINISV
* NO BEAD THERE SO PUT 1 IN MAP FOR NEW LOCATION
L 7,TABLE(4)
L 10,FCCM+12
O 7,0(S,10)
ST 7,0(S,10)
* REMOVE 1 IN MAP FOR OLD LOCATION
L 3,PLACE
L 4,NTAB(3)
L 4,CLDC
SPDL 4,6
SPL 4,1
SPDL 4,9
SPL 5,17
SLL 5,2
SLL 4,2
L 7,TARLE(4)
X 7,0(S,10)
ST 7,0(S,10)
* UPD/TE NTAB WITH NEW MOVED READ FROM STAB
L 4,STAB
L 3,PLACE
L 4,NTAB(3)
* TEST TO SEE IF ENDBEAD MOVED THROUGH A WALL
* USE FOR DIFFUSION CALCULATIONS
L 7,BEAD
C 7,FF,1
BNE NEWCYC
L 3,ICHAIN
L 3,FF,1
S 3,H,12
MH 3,R(3)
LA 3,R(3)
B 3,FF,1
L 5,IRAN
L 4,MULT
M 5,QR
ST 5,IPAN
L 3,N,KCHAIN
A 3,1
SLL 4,3
MP 4,3
ST 4,IF
*
XR 7,7
ST 7,BEAD
LA 3,1
*
XR 6,6
S,KCHAIN
L 4,IF

```

```

R3 = INDEX OF MAP
F4 = INDEX OF TABLE
INDEX IN NTAB OF MOVING BEAD
OLDLC = COORDINATES BEFORE MOVE
INDEX IN NTAB OF OLD LOCATION
F5 = INDEX IN MAP OF OLD NTAB(IR)
F4 = INDEX OF TABLE
NO EXCLUDED VOLUME CHECKS NEEDED
STORE NEW BEAD COORDINATES
THROUGH A WALL
IF A MIDBEAD MOVED
THROUGH THE WALL IT DOESN'T
MATTER FOR DIFFUSION PURPOSES
R3 IS USED TO CALCULATE THE ADDRESS
OF CHAIN IN IMOVE AND IWALL
IF CHAIN IS TO BE SAMPLED
ADDRESS OF CHAIN IN Z DIMENSION
*****
GENERATE A
RANDOM NUMBER FROM 0 TO N+
NCHAIN-1
R3 = R3 * 2
*****
DETERMINE WHICH CHAIN IS MOVEING
R7 = 0
R3 = 1 INCREMENT BY 1 EACH TIME
THROUGH THE LOOP
F6 = 0 USE TO INDEX NEND
R9 = NO OF CHAINS TO BE SAMPLED
R4 = NUMBER OF MOVING BEAD

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MEMBER NAME CYCLE
LOOPCC L 10,COM+8
      CR 8,0(10,6)
      RH 4,IR
      ST R2MC
      B FOUNDC
      LA 3,1(3)
      LA 6,4(6)
      S 4,FF'1'
      BCT 0,LOOPCC
      L 4,IR
      A 4,FF'1'
      ST 4,IRCHAIN
      S 4,IRCHAIN
      SLL 4,FF'1'
      L 4,2
      ST 6,ACCM+4
      L 7,0(5,4)
      ST 7,BEGIN
      L 6,ACCM+8
      L 2,0(6,4)
      ST 8,ENDB
      L 4,IR
      L 5,BEGIN
      CR 4,2
      BL READIC
      RE CNEC
      L 4,ENDB
      CR 4,5
      RE READMC
      S 4,FF'1'
      CR 4,5
      RE ENDC
      *MIDBND
      S 4,FF'1'
      SLL 4,2
      L 6,NTAB-4(4)
      A 6,NTAB+R(4)
      ST 6,INBET
      S 6,NTAB+4(4)
      ST 6,STAB
      L 6,INBET
      S 6,NTAB(4)
      ST 6,STAB1
      ST 4,PLACE
      LA 7,1
      ST 7,BEAD
      B TESTCC
      L 4,IR
      SLL 4,2
      L 8,NTAB+4(4)
      LA 5,2
      ST 5,BEAD
      B STPLACEC
      L 4,IR
      SLL 4,2
      B 8,NTAB-8(4)

```

```

F10 = ADDRESS OF NEND
R8 = NEND(6)
COMPARE IF TC NEND(6)
IF IS NOT LESS THAN NEND TRY AGAIN
IR <= NEND ICHAIN = R3
JUMP OUT OF LOOP
ICHAIN = ICHAIN +1
R6 = R6+4
THERE ARE 1 MORE BONDS THAN BEADS

IR = IR+1 - ICHAIN

R4 = CHAIN NO BETWEEN 0 AND N-1
R4 = ADDRESS IN NSTART AND NEND
R6 = ADDRESS OF NSTART
R7 = NSTART OF MOVING CHAIN
R8 = NSTART OF MOVING CHAIN
R6 = ADDRESS OF NEND
R8 = NEND OF MOVING CHAIN

IR < NSTART MOVE FIRST BOND
IR = NSTART MOVE SECOND BOND
R5 = NEND

IR = NEND MOVE BOND

IR = NEND -1 MOVE BOND N-1
THE BOND MOVING IS NOT ON THE END

R6 = NTAB(IR-1)
R6 = NTAB(IR-1) + NTAB(IR+1)
INBET = R6
R6 = INBET - NTAB(IR+1)
STAB = R6

R6 = INBET - NTAB(IP)
STAB1 = R6
PLACE = R4

BEAD = 1
MOVE FIRST BOND IN CHAIN
R8 = NTAB(IR+1)
BEAD = 2
MOVE LAST BOND IN CHAIN
R4 = R4 + 4
R8 = NTAB(IR -2)

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00002350
00002360
00002370
00002380
00002390
00002400
00002410
00002420
00002430
00002440
00002450
00002460
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00002480
00002490
00002500
00002510
00002520
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00002700
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00002720
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00002740
00002750
00002760
00002770
00002780
00002790
00002800
00002810
00002820
00002830
00002840
00002850
00002860
00002870
00002880
00002890
00002900
00002910
00002920

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```

MEMBER NAME CYCLE
LA 5,3
ST 5,READ
B STPLACEC
  BEADIC L 4,IR
  SLL 4,2
  L 6,NTAB(4)
  L 8,NTAB+4(4)
  LA 5,0
  ST 5,READ
  H STPLACEC
  BEADNC L 4,IR
  SLL 4,2
  L 6,NTAB(4)
  L 8,NTAB-4(4)
  LA 5,0
  ST 5,HEAD
  STPLACEC L 4,PLACE
  RANENDC L 5,IRAN
  M 4,MULT
  N 5,00
  ST 5,IRAN
  LA 3,12
  MR 4,3
  ST 4,IRE
  C 4,FF,1,
  RNH TRYOC
  C 4,FF,3,
  RNH TRYIC
  L 10,EX,00000001,
  C 4,FF,4,
  RE ADDC
  B SUBTC
  L 10,EX,00000100,
  C 4,FF,3,
  BL ADDC
  H SUBTC
  TRYOC L 10,EX,00010000,
  C 4,FF,0,
  RE ADDC
  SUBTC SR 8,10
  ADDC STSTAVC
  STSTAVC AP R,10
  XR 8,STAB
  L 4,PLACE
  C 5,BEAD
  RL 5,FF,2,
  BE TESTCC
  L 5,STAB
  L 4,PLACE
  A 5,NTAB(4)
  BEAD = 3
  FIRST BEAD IN A CHAIN SELECTED
  R4 = 4*(IR - 1) INDEX REGISTER
  R6 = ORC OF FIRST BEAD IN CHAIN
  R8 = ORC OF SECOND BEAD IN CHAIN
  THE LAST BEAD IN A CHAIN SELECTED
  R6 = ORC OF LAST BEAD IN CHAIN
  R8 = ORC OF NEXT TO LAST BEAD IN CHAIN
  PLACE=ADDRESS IN NTAB OF MOVING BEAD
  *****
  GENERATE A RANDOM NUMBER FROM 0 TO 5
  *****
  IF IRE = 0 OR 1 THEN MOVE IN
  Z DIMENSION
  IF IRE = 2 OR 3 THEN MOVE IN
  Y DIMENSION
  IPE = 4 OR 5, SC MOVE IN
  X DIMENSION
  IF IRE = 4 ADD 1 TO X DIMENSION
  IF IRE = 5 SUBTRACT 1 FROM X DIM.
  R10 = A 1 IN Y COORD. POSITION
  IF IRE = 3 THEN ADD 1 TO Y POSITION
  IF IRE = 2 THEN SUBTRACT 1 FROM Y
  THE Y POSITION
  R10 = A 1 IN Z POSITION
  IF IRE = 0 THEN ADD 1 TO Z POSITION
  IF IRE = 1 THEN SUBTRACT
  1 FROM Z DIMENSION
  MOVE AN END BEAD
  STAB = MOVED BEAD COORDINATES
  R8 = 0
  R4 = ADDRESS IN NTAB OF MOVING BEAD
  NO MORE MOVES NECESSARY
  R5 = STAB + NTAB(IR)
00002930
00002940
00002950
00002960
00002970
00002980
00002990
00003000
00003010
00003020
00003030
00003040
00003050
00003060
00003070
00003080
00003090
00003100
00003110
00003120
00003130
00003140
00003150
00003160
00003170
00003180
00003190
00003200
00003210
00003220
00003230
00003240
00003250
00003260
00003270
00003280
00003290
00003300
00003310
00003320
00003330
00003340
00003350
00003360
00003370
00003380
00003390
00003400
00003410
00003420
00003430
00003440
00003450
00003460
00003470
00003480
00003490
00003500

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MEMBER NAME	CYCLE		
S	5,NTAB-4(4)	R5 = R5 - NTAB(IR-1)	00003510
ST	4,PLACE	PLACE = PLACE - 1	00003520
ST	5,STAB1	STAB1 = R5	00003530
L	4,STAB1		00003540
L	TESTCC		00003550
L	5,STAB	MOVE FIRST ROND IN CHAIN	00003560
L	4,PLACE		00003570
L	5,NTAB-4(4)	R5 = STAB + NTAB(IR-1)	00003580
S	5,NTAB(4)	R5 = R5 - NTAB(IR)	00003590
L	6,STAB	STAB1 = STAB	00003600
ST	5,STAB	NTAB(4) = R5	00003610
L	5,PLACE		00003620
L	6,PLACE		00003630
ST	5,PLACE	PLACE = PLACE 4	00003640
LA	10,2		00003650
L	4,STAB	RA = STAB = NEW BEAD COORDINATE	00003660
BE	10,FF,2		00003670
AC	4,STAB1		00003680
L	SPDL	TEST STAB1 SECOND TIME THROUGH	00003690
SRL	5,24	X Y IZ IN REG 4 AND REG 5	00003700
L	3,IZS	R5 = Z-COORDINATE OF NEW BEAD COORD.	00003710
L	9,FF,1	R3 = Z DIMENSION OF THE BCX	00003720
L	5,FF,128	R9 = 1 FOR Z DIMENSION	00003730
C	TESTCC1	COMPARE Z TO 128	00003740
BNL		Z IS < 0	00003750
C	5,IZS	COMPARE Z TO IZS	00003760
BNL	TESTCC2	Z IS > IZS	00003770
L	4,STAB	TEST STAB	00003780
C	10,FF,2		00003790
BE	NNC		00003800
L	4,STAB1	TEST STAB1 SECOND TIME THROUGH	00003810
L	4,14	Y AT TOP OF R5	00003820
SPL	5,24	Y AT BOTTOM OF R5	00003830
L	3,IYS	R3 = IYS	00003840
L	3,9	R3 = 2 FOR Y DIMENSION	00003850
L	9,FF,2	COMPARE R5 TO -1	00003860
L	5,FF,128	Y IS < 0	00003870
C	TESTCC1	COMPARE R5 TO IYS	00003880
BNL		Y IS > IYS	00003890
C	5,IYS	TEST STAB FIRST TIME THROUGH	00003900
BNL	TESTCC2		00003910
L	4,STAB		00003920
C	10,FF,2		00003930
BE	NNC		00003940
L	4,STAB1	TEST STAB1 SECOND TIME THROUGH	00003950
L	4,24	X AT TOP OF R5	00003960
SPL	5,24	X AT BOTTOM OF R5	00003970
L	3,IXS	R3 = IXS	00003980
L	3,19	R3 = 3 FOR X DIMENSION	00003990
L	9,FF,3	COMPARE X TO -1	00004000
L	5,FF,128	Y IS < 0	00004010
C	TESTCC1		00004020
BNL			00004030
C	5,IXS		00004040
BNL	TESTCC2		00004050
L	9,BEAD		00004060
C	2,FF,0		00004070
BE	EXVDC	ONLY ONE BEAD MOVED	00004080

MEMBER NAME	CYCLE		
TESTCC1	LOPCC	10,FF'0'	00004090
	TESTCC3	BE	00004100
		L	00004110
		AR	00004120
		ST	00004130
		B	00004140
		HITC	00004150
TESTCC3	AR	S, STAB1	00004160
	ST	S, STAB1	00004170
	B	HITC	00004180
TESTCC2	C	10,FF'0'	00004190
	RE	TESTCC4	00004200
	L	S, STAB	00004210
	SR	S, STAB	00004220
	ST	S, STAB	00004230
	B	HITC	00004240
TESTCC4	L	S, STAB1	00004250
	SR	S, STAB1	00004260
	ST	S, STAB1	00004270
	LA	2, I(S)	00004280
	L	8, BEAD	00004290
	C	8, FF'0'	00004300
	BE	EXVOLC	00004310
	C	9, FF'2'	00004320
	PL	A1C	00004330
	BE	A2C	00004340
LOPCC	BCT	10, STILLC	00004350
EXVOLC	L	4, STAB	00004360
	SRDL	4, 6	00004370
	SRL	4, 1	00004380
	SRDL	4, 9	00004390
	SRL	5, 17	00004400
	SLL	5, 2	00004410
	SLL	4, 2	00004420
	L	7, TABLE(4)	00004430
*	TEST TO	SEE IF READ IS THERE *	00004440
	L	10, ACM+12	00004450
	N	7, 0(S, 10)	00004460
	BNZ	FINISV	00004470
	L	10, BEAD	00004480
	C	10, FF'0'	00004490
	DE	PUT	00004500
*	ST	4, TABLEID	00004510
	ST	5, MAPID	00004520
	L	4, STAB1	00004530
	SRDL	4, 6	00004540
	SRL	4, 1	00004550
	SRDL	4, 9	00004560
	SRL	5, 17	00004570
	SLL	5, 2	00004580
	SLL	4, 2	00004590
	L	7, TABLE(4)	00004600
	L	10, ACM+12	00004610
	N	7, 0(S, 10)	00004620
	BNZ	FINISV	00004630
	ST	4, TABLEID	00004640
	ST	5, MAPID	00004650
	L	4, STAB1	00004660

IF STAB1 IS OUT ADD BOX TO IT
OTHERWISE
STAB = STAB + IXS, IYS OR IZS

X, Y, OR Z IS < 0 FOR STAB1
ADD IXS, IYS OR IZS TO STAB1

IF STAB1 IS OUT SUBT BOX FROM IT

X, Y, OR Z > IXS, IYS, OR IZS
SO SUBTRACT IXS, IYS, OR IZS

STAB1 = STAB1 - IXS, IYS, OR IZS

ONLY ONE MOVED, DON'T CHECK STAB1

TEST X AND Y
TEST X

RS = INDEX OF MAP
P4 = INDEX OF TABLE

EV CONFLICT ENCOUNTERED FOR STAB

IF ONLY ONE BEAD MOVED DON'T
CHECK EVC FOR STAB1
TABLEID=INDEX IN TABLE FOR STAB
MAPID=INDEX IN MAP FOR STAB

RS = INDEX OF MAP FOR STAB1
RA = INDEX OF TABLE FOR STAB1

P10 = ADDRESS OF MAP
IS A 1 THERE? IF SO
EVC ENCOUNTERED FOR STAB1
TABLEID = INDEX IN TABLE FOR STAB1

```

MEMBER NAME CYCLE
ST 5,MAPIDI
L 4,TABLEID
L 3,MAPID
* NO EXCLUDED VOLUME CONFLICT FOR STAB OR STAB1 SO CHANGE MAP AND
* UPDATE NTAB FOR BOTH OF THEM
PUT 7,TABLE(4)
L 10,ACOM+12
R 7,0(5,10)
ST 7,0(5,10)
* REMOVE 1 IN MAP FOR OLD LOCATION FOR STAB
L 10,READ
C 10,EF,3,
BNE
HLS 3,PLACE
L 3,4(3)
L 4,NTAB(3)
ST 3,PLACE
L 4,DLDC
L 4,NTAB(3)
R HLS1
L 3,PLACE
L 4,NTAB(3)
HLS 4,6
SRDL 4,1
SPDL 4,9
SRL 5,17
SLL 5,2
SLL 4,2
L 7,TABLE(4)
L 10,ACOM+12
X 7,0(5,10)
ST 7,0(5,10)
L 10,DEAD
C 10,EF,0,
RE NEXVALC
* PUT 1 IN MAP FOR NEW LOCATION OF STAB1
L 4,TLIDI
L 5,MAPIDI
L 7,TABLE(4)
L 10,ACOM+12
O 7,0(5,10)
ST 7,0(5,10)
L 3,PLACE
L 3,4(3)
L 4,NTAB(3)
* REMOVE 1 IN MAP FOR OLD LOCATION OF STAB1
SRDL 4,6
SRL 4,1
SRDL 4,9
SRL 5,17
SLL 5,2
SLL 4,2
L 7,TABLE(4)
L 10,ACOM+12
L 7,0(5,10)
X 7,0(5,10)

```

MAPIDI=INDEX IN MAP FOR STAB1
R4 = TABLEID
R5 = MAPID
* NO EXCLUDED VOLUME CONFLICT FOR STAB OR STAB1 SO CHANGE MAP AND
* UPDATE NTAB FOR BOTH OF THEM
PUT 7,TABLE(4)
R10 = ADDRESS OF MAP
MAP(5) = 1
* REMOVE 1 IN MAP FOR OLD LOCATION FOR STAB
L 10,READ
C 10,EF,3,
BNE
HLS 3,PLACE
L 3,4(3)
L 4,NTAB(3)
ST 3,PLACE
L 4,DLDC
L 4,NTAB(3)
R HLS1
L 3,PLACE
L 4,NTAB(3)
HLS 4,6
SRDL 4,1
SPDL 4,9
SRL 5,17
SLL 5,2
SLL 4,2
L 7,TABLE(4)
L 10,ACOM+12
X 7,0(5,10)
ST 7,0(5,10)
L 10,DEAD
C 10,EF,0,
RE NEXVALC
* PUT 1 IN MAP FOR NEW LOCATION OF STAB1
L 4,TLIDI
L 5,MAPIDI
L 7,TABLE(4)
L 10,ACOM+12
O 7,0(5,10)
ST 7,0(5,10)
L 3,PLACE
L 3,4(3)
L 4,NTAB(3)
* REMOVE 1 IN MAP FOR OLD LOCATION OF STAB1
SRDL 4,6
SRL 4,1
SRDL 4,9
SRL 5,17
SLL 5,2
SLL 4,2
L 7,TABLE(4)
L 10,ACOM+12
X 7,0(5,10)

IF LAST BOND MOVED
THEIN PLACE=PLACE+4

OLDCENTAR OF LAST BEAD ON CHAIN
R4 = NTAB OF LAST BEAD IN CHIAN

END BOND DID NOT MOVE
R4 = NTAB CF MOVING BEAD
CLDC = NTAB(PLACE)

R5 = INDEX IN MAP OF OLD NTAB(IR)
R4 = INDEX OF TABLE

R10 = ADDRESS OF MAP
MAP(5) = 0

IF ONLY ONE BEAD MOVED
UPDATE NTAB
OF STAB1

F10 = ADDRESS OF MAP
MAP(5) = 1

RA = OLD NTAB OF SECOND BEAD
BEFORE MOVE
OF STAB1

R10 = ADDRESS OF MAP

00004670
00004680
00004690
00004700
00004710
00004720
00004730
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00004980
00004990
0005000
0005010
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0005030
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0005070
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0005110
0005120
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0005240

00005250
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 00005690
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 00005790
 00005800
 00005810
 00005820

MEMBER NAME CYCLE
 * UPDATE NTAB WITH NEW MOVED BEAD FROM STAR MAP(S) = 0
 NOEXVOLC L 4, STAR NO EXCLUDED VOLUME CHECKS NEEDED
 L 3, PLACE STORE NEW BEAD COORDINATES
 L 4, NTAB(3) IF ONLY ONE BEAD MOVED THEN
 C 4, EF, 0, DON'T UPDATE STAB1 IF
 RE CUT IF ONLY ONE BEAD MOVED
 * LA 3, A(3) STORE MOVED BEAD COORDINATES
 L 4, STAB1 IF MIDREAD MOVED NO NEED
 L 4, NTAB(3) TO CALCULATE DIFFUSION
 L 4, BEAD
 C 4, EF, 1, NEWCYC
 RE TEST TO SEE IF ENDREAD MOVED THROUGH A WALL
 * OUT L 1, ADELIST
 L 3, INCHAIN RZ = TOTAL NUMBER OF CHAINS
 C 3, EF, 51, IF MORE THAN 50 CHAINS ALL ARE
 BL FEW, ADDRESS+4 SAMPLED
 L 14, 15, BRANCH TO SKJ R15 = ADDRESS OF SKJ
 L 10, IN CHECK TO SEE IF IN = 0
 C 10, EF, 0, IF IT IS THEN CHAIN IS NOT TO BE
 BE NEWCYC SAMPLED.
 L 3, INCHAIN F3 IS USED TO CALCULATE THE
 S 3, EF, 1, I WALL IF CHAIN IS SAMPLED ADDRESS OF THE CHAIN IN IMOVE ADN
 MH 3, SAMP, 12, ADDRESS OF CHAIN IN Z DIM
 ST 9, OLDC R8 = COORDINATE BEFORE MOVE
 L 6, STAB R6 = COORDINATES AFTER MOVE
 L 10, BEAD
 C 10, EF, 3, IF LAST BEAD MOVED CHECK STAB1
 ONE CW OTHERWISE CHECK STAR
 * L 6, STAB1
 * TEST TO SEE OF OLD COORD. - NEW COORD. IS GREATER THAN |2|. *
 * ALL 3 DIMENSIONS MUST BE CHECKED. IF OBC-NBC > |2| THEN *
 * A BOX WALL WAS PENETRATED. ADD ONE TO IMOVE IF A HIGH WALL WAS *
 * HIT OR SUBTRACT ONE IF A LOW WALL WAS HIT. THEN BRANCH *
 * TO SUBROUTINE CHAIN AND SET I WALL. *
 PW SDDL 8, 8 NTAB(Z) IN R9
 SRDL 6, 8 STAB Z IN R7
 SRL 9, 24 NTAB(Z)-STAB(Z) IN R9
 SPL 7, 24
 SP 9, 7
 C 0, EF, 2, HIGH WALL HIT
 RH Z1 LOW WALL HIT
 C 9, EF, -2, LOW WALL HIT
 BL 20
 SDDL 9, 8 NTAB(Y) IN R9
 SRDL 6, 8 STAB(Y) IN R7
 SRL 5, 24 NTAB(Y)-STAB(Y) IN R9
 SPL 7, 24
 SR 6, 7
 C 5, EF, 2, HIGH WALL HIT
 BH Y1 LOW WALL HIT
 C 9, EF, -2, LOW WALL HIT
 BL Y0

MEMBER NAME	CYCLE		
BAGGINS	5,8		
SFDL	9,24	NTAB(X) IN R9	00005830
SFDL	6,8		00005840
SPL	7,24	STAB(X) IN R7	00005850
SF	9,7	NTAB(X)-STAB(X) IN R9	00005860
C	9,7		00005870
CH	X1	HIGH WALL HIT	00005880
C	9,7		00005890
BL	X0	LOW WALL HIT	00005900
R	NEWCYC	ALL 3 DIMENSIONS HAVE BEEN CHECKED	00005910
		* THE FOLLOWING LINES UP TO FINISFV ARE BRANCHED TO IF A WALL	00005920
		* HAS BEEN PENETRATED. OTHERWISE THEY ARE NOT EXECUTED.	00005930
X0	3, SAMP		00005940
L	7, MOVE(3)	LOW X WALL HIT	00005950
S	7, FF1		00005960
ST	7, MOVE(3)	IMOVE=IMOVE-1	00005970
LA	7,1	R7 = 1, PASS TO CHAIN	00005980
L	15, ADDR SUB	R15 = ADDRESS OF CHAIN	00005990
RALP	14,15	BRANCH TO CHAIN	00006000
ST	14, TIME	R14 > 0	00006010
B	NEWCYC	MOVE NEXT BEAD	00006020
L	3, SAMP		00006030
L	7, MOVE(3)	HIGH X WALL HIT	00006040
A	7, FF1		00006050
ST	7, MOVE(3)	IMOVE=IMOVE+1	00006060
LA	7,4	PASS FT=4 TO CHAIN	00006070
L	15, ADDR SUB	R15 = ADDRESS OF CHAIN	00006080
RALR	14,15	BRANCH TO CHAIN	00006090
ST	14, TIME	TIME > 0	00006100
R	NEWCYC	MOVE NEXT BEAD	00006110
L	3, SAMP		00006120
LA	3,4(3)		00006130
L	7, MOVE(3)	LOW Y WALL HIT	00006140
S	7, FF1		00006150
ST	7, MOVE(3)	IMOVE = IMOVE-1	00006160
LA	7,2	R7 = 2 PASS TO CHAIN	00006170
L	15, ADDR SUB	R15 = ADDRESS OF CHAIN	00006180
RALR	14,15	BRANCH TO CHAIN	00006190
ST	14, TIME	TIME > 0	00006200
R	BAGGINS		00006210
L	3, SAMP		00006220
LA	3,4(3)		00006230
L	7, MOVE(3)	HIGH Y WALL HIT	00006240
A	7, FF1		00006250
ST	7, MOVE(3)	IMOVE = IMOVE+1	00006260
LA	7,5	R7 = R7+1	00006270
L	15, ADDR SUB	R15 = ADDRESS OF CHAIN	00006280
RALR	14,15	BRANCH TO CHAIN	00006290
ST	14, TIME	TIME > 0	00006300
R	BAGGINS	CHECK X	00006310
L	3, SAMP		00006320
LA	3,3(3)		00006330
L	7, MOVE(3)	LOW Z WALL HIT	00006340
S	7, FF1		00006350
ST	7, MOVE(3)	IMOVE = IMOVE -1	00006360
LA	7,3	R7 = 3 PASS TO CHAIN	00006370
L	15, ADDR SUB	R15 = ADDRESS OF CHAIN	00006380
RALR	14,15	BRANCH TO CHAIN	00006390
			00006400

MEMBER NAME	CYCLE	A(MAP)
N	DS	
IR	DS	F
IFAN	DS	F
IXS	DS	F
IYS	DS	F
IYS	DS	F
IN	DS	F
IN	DS	F
ICHAIN	DS	F
ICHAIN	DS	11F
KCHAIN	DS	F
NCHAIN	DS	AF
NEVT	DS	F
TABLE	DS	3F
IMOVE	DS	32F
IMOVE	DS	150F
NTAB	DS	1500F
MAB	DS	15000F
NSTART	DS	4095F
NEND	DS	15000F
END	DS	CYCLE

00006990
00007000
00007010
00007020
00007030
00007040
00007050
00007060
00007070
00007080
00007090
00007100
00007110
00007120
00007130
00007140
00007150
00007160
00007170
00007180
00007190
00007200
00007210

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MEMBER NAME CTMAP
CTMAP CSFCT (14,12)
SAVE #,P
BALR #,P
USING #,P
L 12,ACOM
LA 11,4095(12,0)
LA 11,1(11)
LA 6,4095(11,0)
LA 6,1(5)
USING N,12,11,6
ST 13,SAV+4
LA 13,SAV
* THIS SUBPROGRAM COUNTS THE 1 BITS IN MAP AND STORES THE SUM IN IPRINT
L 4,EF,4
L 5,EF,16380
SLR 8,9
SLR 10,ACOM+4
L 3,0(8,10)
L2 3,EF,0
BZ L1
A 7,EF,1
LR 2,3
S 2,EF,1
MR 3,2
B L2
LI RXLE 3,4,LOOP1
ST 7,IPRINT
C 7,N
BE CK
L 15,V(IPRINT)
BALP 14,15
L 15,V(IPRINT)
L 14,15
OK L 13,SAV+4
LM 14,15,12(13)
LM 1,12,24(13)
L 15,V(IPRINT)
L 12(13),X,FF
MVI 14
BR 14
DS 18F
DC A(N)
DC A(MAP)
COM
DS 25F
IPRINT DS 1533F
MAP DS 4096F
END CTMAP
00000010
00000020
00000030
00000040
00000050
00000060
00000070
00000080
00000090
00000100
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00000340
00000350
00000360
00000370
00000380
00000390
00000400
00000410
00000420
00000430
00000440
00000450
00000460
00000470
00000480
00000490
00000500

```

```

MEMBER NAME CHMAP
CSECT (14,12)
CHMAP SAVF
HALF 9,0
USING *9
L 12,ACOM
LA 8,1(B)
LA 8,4095(B,0)
LA 6,1(E)
USING N,12,R,6
ST 13,SAV+4
LA 13,SAV
L 15,ACOM+4
L 11,N
L 10,FF*31
L 5,5
L 4,NTAB(1)
SPDL 4,6
SPDL 4,1
SPDL 4,9
SRL 5,17
CR 4,10
BNH L2
S 4,FF*32
L 3,5
L 2,FF*4
MH 4,FF*4
L 7,NTAB(4)
N N
BNZ L3
L 15,FF(V(PFINT))
L 14,15
L 15,FF(V(PRTMAP))
L 14,15
R NO
L 1,FF*4
A 11,L1
RCT L 13,SAV+4
LM 14,15,12(13)
LM 1,12,24(13)
MVI 12(13),X*FF
BR 14
DS 14F
DC X'00000040'
DC A(N)
DC A(MAP)
COM
DS F
DS 27F
DS 32F
DS 300F
DS 15000F
MAP DS 4096F
END CHMAP

```

* THIS SURPROGRAM CHECKS TO SEE IF THE MAP CONFIGURATION MATCHES NTAB

```

00000010
00000020
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00000050
00000060
00000070
00000080
00000090
00000100
00000110
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00000550
00000560
00000570

```

MEMBER NAME PACK
PACK CSECT

* THIS SUBPROGRAM PACKS THE X,Y, AND Z COORDINATES OF ONE BEAD
* INTO NTAB.
* NTAB(1) = (L*NTAB(1,1)) + (2**16) + (L*NTAB(2,K)) + (2**8) + (L*NTAB(3,1))

SAVE (14,12)
BALR 3,0
USING *
L 12,ACOM
USING N,12
L 2,4(1)

USE R9 IN LOCAL ADDRESSING
R12 = ADDRESS OF BLANK COMMON

L 3,0(2)
S,FF,1
SLL 3,2
L 2,0(1)

R2 = ADDRESS OF CHAIN NO.
ARGUMENT PASSED FROM MAIN
R3 = CHAIN NO. FROM 1 TO N
OF MOVING BEAD
R2 = ADDRESS OF LTAB
ARGUMENT PASSED FROM MAIN
R4 = LTAB
R5=Y(1)
R6=Z(1)
Z IN TOP OF R7
Y,Z IN TOP OF R7

L 4,0(2)
L 5,4(2)
L 6,R(2)
SEDL 6,R
L 6,5
SEDL 6,R
L 6,4
SEDL 6,R
L 7,8
ST 7,NTAB(3)
LM 14,15,12(13)
LM 1,12,24(13)
MVI 12(13),X,FF,
BR 14

X,Y,Z IN TOP OF R7
X,Y,Z IN TOP OF R7
X,Y,Z IN BOTTOM OF R7

* ENTRY UNPACK
* UNPACK CALCULATES THE SUM OF X,Y, AND Z COORDINATES
* AS WELL AS VECTOR END TO END LENGTH AND THE NUMBER
* OF TIMES THE CHAIN IS SPLIT. THESE ARE USED IN
* SUBROUTINE SAMPLE

UNPACK SAVE (14,12)
USING UNPACK,15
L 12,ACOM
USING N,12
L 2,4(1)

R2 = ADDRESS OF N2
PASSED ARGUMENT FROM SAMPLE
R3 = N2

L 3,0(2)
S,FF,1
SLL 3,2
ST 3,N2
L 2,0(1)
L 2,0(2)
S,FF,1
SLL 2,2
ST 2,N1

N2 = (N2 - 1) * 4
N2 IS THE ADDRESS IN NTAB OF
THE LAST BEAD IN THE CHAIN
R2 = ADDRESS OF N1, PASSED FROM SAMPLE
R2 = N1
N1 = (N1 - 1) * 4

* N1 IS THE ADDRESS IN NTAB OF THE
* FIRST BEAD IN THE CHAIN
* FIND OUT HOW MANY TIMES THE CHAIN IS SPLIT

00000010
00000011
00000012
00000013
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00000060
00000070
00000080
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00000100
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00000950
00000956
00000970
00000980
00000990
00001000
00001010
00001020
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00001060
00001070
00001080
00001090
00001100
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00001120
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00001140
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00001180
00001190
00001200
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00001500
00001510
00001520

```

```

P10 = 3
R4 = -X2Y2Z2
R5 = -X2Y2
P5 = Z2

```

```

F11 = INDEX REGISTER
R7 = XL,YL OR ZL
R7 = XL-X1, YL-Y1 OR ZL-Z1
IF R7 = 1 THEN CHAIN NOT SPLIT
IF R7 = 0 CHAIN IS NOT SPLIT
IF R7 = -1 THEN CHAIN NOT SPLIT

```

```

* SUBTRACT A BOX DIMENSION(PECONNECT THE CHAIN)
X2 = X2 +IXS,Y2=Y+IYS,OR Z2=Z2+IZS
X2=X2-IXS,Y2=Y2-IYS, OR Z2=Z2-IZS
LAST = X2,Y2, OR Z2
ISUM=ISUM+X2,ISUM+4 = ISUM+4+Y2
OR ISUM+8 = ISUM+8+Z2

```

```

** COMPUTE VECTOR END TO END LENGTH

```

```

R4 = XLYLZL OF LAST BEAD
R5 = XFYFZF OF FIRST BEAD
R4 = XLYLZL - XFYFZF
IS = END TO END LENGTH

```

```

ADDRESS IN NTAR OF LAST BEAD IN CHAIN
ADDRESS IN NTAR OF LAST BEAD IN CHAIN
BEAD COORD OF BEAD AFTER PECONNECTION
BEAD COORD OF FIRST BEAD IN CHAIN

```

```

SUM OF RECONNECTED BEAD COORDINATES
END TO END LENGTH

```

```

MEMBER NAME PACK
LOOP1 L 6,N1
LA 6,4(6)
LA 10,3
L 4,NTAB(6)
SRDL 4,8
SRL 5,24
LR 11,10
S 11,FF,1
SLL 11,2
L 7,LAST(11)
SR 7,5
C 7,FF,1
BE WHOLE1
C 7,FF,0
BE WHOLE1
C 7,FF,-1
BE WHOLE1
RL SUBT

```

```

* SUBTRACT A BOX DIMENSION(PECONNECT THE CHAIN)
A 5,IXS(11)
R WHOLE1

```

```

* ADD A BOX DIMENSION
SURT 5,IXS(11)
WHOLE1 S 5,LAST(11)
A 5,ISUM(11)

```

```

* ST 5, ISUM(11)
BCT 10,LLL
C 6,N2
DNE LOOP1

```

```

** COMPUTE VECTOR END TO END LENGTH

```

```

LA 3,3
XR 10,10
L 4,LAST(10)
L 5,FIRST(10)
SP 4,5
ST 4,IS(10)
LA 10,4(10)
BCT 3,LOOP2
LM 14,12,12(13)
MVI 12(13),X,FF,
BR 14
DS F
DS F
DS F
DS 3F
DS 3F
DS 3F
CC A(N)
CCM
N
DS F
DS 2F
DS 3F
DS 2F
DS 3F
DS 3F
DS 3F
DS 3F
DS 343F

```

```

ADDRESS IN NTAR OF LAST BEAD IN CHAIN
ADDRESS IN NTAR OF LAST BEAD IN CHAIN
BEAD COORD OF BEAD AFTER PECONNECTION
BEAD COORD OF FIRST BEAD IN CHAIN

```

```

SUM OF RECONNECTED BEAD COORDINATES
END TO END LENGTH

```

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Vita

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