

# A NOTE ON STERIODIAGRAMS OF MOLECULES\*

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## ABSTRACT

*The paper elucidates a simple way of deriving the coordinates for drawing stereodiagrams of molecules. This method is an alternative, but not a substitute, to the ORTEP (suggested by C. K. Johnson) which is extensively used in the literature. Illustrations are given using a program which was written based on the method mentioned here. The program is also given in an appendix for practical help.*

**Keywords:** Stereodiagrams; perspective vision.

## 1. INTRODUCTION

The chemical activity of a molecule depends, apart from other factors such as charge distribution on various atoms, upon its three-dimensional structure. Knowledge of this spatial distribution of atoms in a molecule is obtained by certain physico-chemical methods, one of the accurate approaches being the x-ray crystallographic technique. Together with the three-dimensional structure so obtained, it would be of added interest and an aid to the imagination of a stereochemist to get a perspective vision of the molecule in two dimensions. Though the thermal ellipsoid program of Johnson [1] is widely used by crystallographers, for want of sufficient computer memory, and for reasons of the enormous amount of time a plotter would take, we had written a simpler program (see appendix), to draw perspective, but skeletal diagrams of molecules. This is achieved by obtaining the appropriate coordinates of the atoms from the input data using the imagination of an architectural engineer [2]. The input data could be the atomic coordinates in a Cartesian frame of reference or in a cylindrical polar reference system or fractions of the unit cell as generally reported in crystallographic studies. They could also be the internal parameters of the molecule such as the bond lengths, bond angles and dihedral angles from which the Cartesian coordinates of the atoms could be generated.

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## 2. THEORY

Due to the finite distance of separation between the eyes, the details of a 3-dimensional object seen by the right eye are different from those seen by the left. If two pictures as seen by the two eyes are printed with proper separation between them (corresponding to the separation of the eyes) and if the viewer focusses his attention at infinity, each eye sees its corresponding picture and these get "superimposed" in imagination to give a three-dimensional feeling of the object. The method adopted by Johnson to achieve this result is different from what the present author has used.

According to Johnson's program [3], a model of the molecule of suitable size is imagined at a convenient distance of say 28" from the imaginary viewer. However this distance is adjustable. Then the model is given an additional rotation of about  $2.5^\circ$  to  $3^\circ$ , about a vertical axis, to simulate the difference between a central view and a left-eye view. The projection of the model is drawn by an incremental plotter. After completing this drawing the paper is advanced on the plotter and, after another appropriate rotation of the model, the right-eye view is drawn. It might be then reduced photographically.

The principle of the method used by the author is given below. Consider a picture plane (Fig. 1) at a distance  $\xi$  from the on-looker P (station point). Let this plane be the XY-plane of a right handed Cartesian coordinate system, the z-direction pointing towards the on-looker, and the x-axis being parallel to the line joining the two eyes. The molecular model of suitable size is

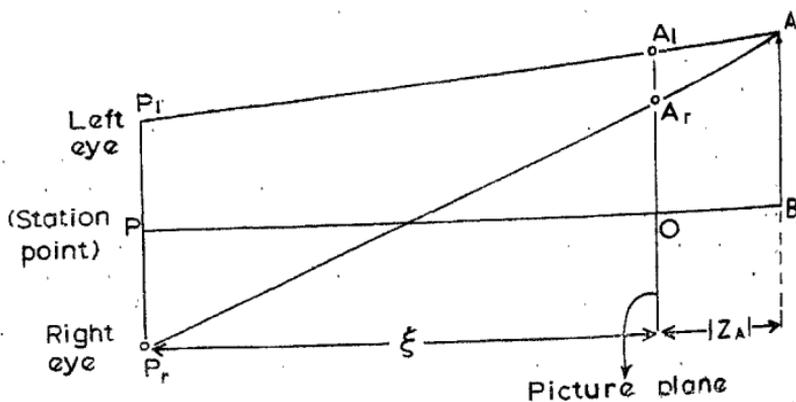


FIG. 1. Principle of getting the coordinates for stereodiagrams of molecules (using the imagination of an architectural engineer).

imagined to be behind the picture plane. Consider an Atom A. The coordinates of this atom for perspective drawing, as seen by the left and the right eye, correspond to those of  $A_1$  and  $A_r$  respectively. The lines  $P_1P_r$ ,  $A_1O$  and  $AB$  are parallel to each other. Hence

$$\frac{P_1A_1}{A_1A} = \frac{P_rA_r}{A_rA} = \frac{PO}{OB} = \frac{\xi}{|z_A|}$$

Let  $PP_1 = PP_r = \epsilon$ . Since we know the coordinates for  $P_1$ ,  $P_r$  and  $A$ , we can calculate the coordinates of  $A_1$  and  $A_r$ . Thus,

$$x = \frac{\xi x_A \pm |z_A| \cdot \epsilon}{\xi \mp |z_A|} \quad (i)$$

$$y = \frac{\xi y_A}{\xi \mp |z_A|} \quad (ii)$$

$$z = 0 \quad (iii)$$

where the positive sign in the numerator of (i) is applicable for the right eye picture. A value of 72.0 cm and 3.5 cm for  $\xi$  and  $\epsilon$  respectively have been found convenient. In case the diagrams are huge and overlap, they could be drawn at suitable separation and then photographically reduced to a convenient separation of about 6 to 7 cm between corresponding atoms. Alternatively, the images corresponding to the left and the right eye could be drawn with different colours (say red and blue) with a common origin. When this pair is viewed by a pair of transparent papers of the corresponding colours, the diagrams again seem to superpose in the imagination to give the stereoview [4].

### 3. RESULTS

By way of example, we have shown in Fig. 2, the  $\alpha$ -helical conformation of the backbone of a polypeptide chain [5]. The input data for this diagram were the cylindrical polar coordinates of the atoms. While it may be difficult to see from the individual diagrams of the couple, whether the chain is in the right-handed or left-handed conformation, the stereovision clearly shows that this representation is in the right-handed helical conformation. Figure 3 gives the perspective view of a cyclic dipeptide, cyclo (L-pro-D-phe) [6]. The input data for this diagram were the fractional coordinates of the atoms taken from the literature cited. It might be seen from this stereodiagram that the phenyl ring of the side chain is stacking over the 2, 5-

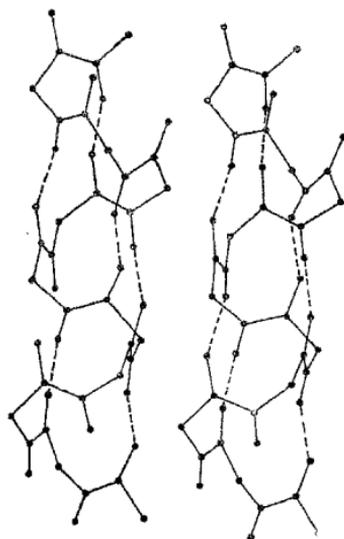


FIG. 2. Stereo pair of a fragment of polypeptide (back-bone) in the  $\alpha$ -helical conformation.

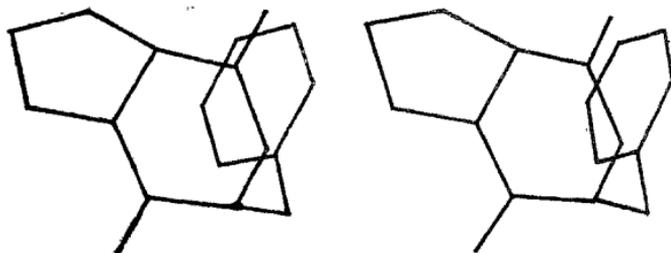


FIG. 3. Stereo pair of the molecule cyclo (D-Phe-L-Pro), showing the folded conformation.

diketopiperazine ring, which seems to be a common feature in many cyclic dipeptides [7].

#### 4. ACKNOWLEDGEMENTS

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C	ORGP IS FOR ORTHOGRAPHIC AND PERSPECTIVE DRAWING	0004
	DIMENSION ANAME (100), XR (3, 100)	0001
	DIMENSION ATOM (3), DC (3), AMAT (3, 3), X1 (3, 1), P (3), NROT (3), PHI (3)	0002
	COMMON A, B, C, ALFA, BETA, GAMMA, NMAX, X (3, 100)	0003
	CONFA = 0.01745329	0005
	READ (5, 2) NSET	0006
	WRITE (6, 2) NSET	0007
2	FORMAT (20F4)	0008
	DO 999 NRAM = 1, NSET	0009
	READ (5, 1)	0010
	WRITE (6, 332)	0011
	WRITE (6, 1)	0012
	WRITE (6, 332)	0013
1	FORMAT (55 H.)	0014
332	FORMAT (//)	0015
	READ (5, 2) NMAX, NRDCN, NTYPE, NVIEW	0016
	WRITE (6, 2) NMAX, NRDCN, NTYPE, NVIEW	0017
C	NMAX = MAXIMUM NO. OF ATOMS, NVIEW = NO. OF VIEW OF THE MOLECULE	0018
C	NRDCN = 1 FOR FRACTIONAL, = 2 FOR CARTECIAN, = 3 FOR CYLINDRICAL POLAR	0019
C	NTYPE = 1 FOR ORTHOGRAPHIC AND = 2 FOR PERSPECTIVE PROJECTION	0020
	READ (5, 4) ZSP, EYE	0021
	WRITE (6, 4) ZSP, EYE	0022
C	ZSP = 72.0 CM, EYE = 3.5 CM.	0023
4	FORMAT (10F8.3)	0024
	READ (5, 3) (ANAME (I), (X (J, I), J = 1, 3), I = 1, NMAX)	0025
3	FORMAT (A4, 3F8.4)	0026
	WRITE (6, 332)	0027
	WRITE (6, 333)	0028
333	FORMAT (2X, ' COORDINATES ORIGINALLY GIVEN')	0029
	WRITE (6, 332)	0030
	WRITE (6, 31) (ANAME (I), (X (J, I), (J = 1, 3), I = 1, NMAX)	0031
31	FORMAT (1X, A4, 3F8.4)	0032
C	FRACTIONAL TO CARTECIAN COORDINATES	0033
	GO TO (40, 41, 42), NRDCN	0034
40	READ (5, 4) A, B, C, ALFA, BETA, GAMMA	0035
	CALL RDCONS (NRDCN)	0036
	GO TO 41	0037
42	CALL RDCONS (NRDCN)	0038
41	CONTINUE	0039
	DO 998 NN = 1, NVIEW	0040
	READ (5, 2) NZERO, NAXIS, NATOM, (NROT (I), I = 1, 3)	0041
	WRITE (6, 2) NZERO, NAXIS, NATOM, (NROT (I), I = 1, 3)	0042
	READ (5, 4) (PHI (I), I = 1, 3)	0043
	WRITE (6, 4) (PHI (I), I = 1, 3)	0044
C	ONE OF THE ATOMS IS KEPT AT THE ORIGIN	0047
	IF (NZERO) 43, 43, 44	0045
44	CONTINUE	0046
	DO 424 J = 1, 3	0048
	ATOM (J) = X (J, NZERO)	0049
	DO 424 I = 1, NMAX	0050
424	X (J, I) = X (J, I) - ATOM (J)	0051
C	ONE VECTOR IS PUT ALONG THE DESIRED AXIS	0052

43	IF (NAXIS) 45, 45, 46	0053
46	DO 451 I = 1, 3	0054
451	P (I) = X (I, NATOM)	0055
	DENOM = P (I) * P (1) + P (2) * P (2) + P (3) * P (3)	0056
	DENOM = SQRT (DENOM)	0057
	GO TO (452, 453, 454), NAXIS	0058
452	IJ = 2	0059
	IK = 3	0060
	GO TO 455	0061
453	IJ = 3	0062
	IK = 1	0063
	GO TO 455	0064
454	IJ = 1	0065
	IK = 2	0066
455	CONTINUE	0067
	DENO = SQRT (P (IJ) * P (IJ) + P (IK) * P (IK))	0068
	TANW = DENO / P (NAXIS)	0069
	TETA = ATAN (TANW)	0070
	TETA = TETA / CONFA	0071
	DC (NAXIS) = 0.0	0072
	DC (IJ) = P (IK) / DENOM	0073
	DC (IK) = - P (IJ) / DENOM	0074
	CALL ROMAX (DC, TETA, AMAT)	0075
	DO 466 I = 1, NMAX	0076
	DO 47 J = 1, 3	0077
47	X1 (J, I) = X (J, I)	0078
	CALL RMM (AMAT, 3, 3, X1, 1, X1)	0079
	DO 48 J = 1, 3	0080
48	X (J, I) = X1 (J, I)	0081
466	CONTINUE	0082
45	CONTINUE	0083
	ROTATION OF THE MOLECULE ABOUT ANY AXIS SUCCESSIVELY	0084
	DO 101 I = 1, 3	0085
	DO 100 II = 1, 3	0086
100	DC (II) = 0.0	0087
	IJK = IABS (NROT (I))	0088
	IF (NROT (I) 102, 101, 103	0089
102	DC (IJK) = - 1.0	0090
	GO TO 104	0091
103	DC (IJK) = 1.0	0092
104	CONTINUE	0093
	ANG = PHI (I)	0094
	CALL ROMAX (DC, ANG, AMAT)	0095
	DO 105 J = 1, NMAX	0096
	DO 106 K = 1, 3	0097
106	X1 (K, J) X = (K, J)	0098
	CALL RMM (AMAT, 3, 3, X1, 1, X1)	0099
	DO 107 K = 1, 3	0100
107	X (K, J) = X1 (K, J)	0101
105	CONTINUE	0102
101	CONTINUE	0103
1052	FORMAT (3 (2X, A4, 3E10.4))	0104

	GO TO (1050, 1060), NTYPE	
1050	CONTINUE	0105
	WRITE (6, 1053)	0106
1053	FORMAT (10X, 'COORDINATES FOR ORTHOGRAPHIC PROJECTION '/')	0107
	WRITE (6, 1052) (ANAME (J), (X (I, J), I = 1, 3), J = 1, NMAX)	0108
	GO TO 998	0109
1060	CONTINUE	0110
	WRITE (6, 1054)	0111
1054	FORMAT (10X, 'COORDINATES FOR PERSPECTIVE PROJECTION '/')	0112
C	MOLECULE IS SHIFTED TO—Z BY ZMAX. . .	0113
	JJ = 1	0114
1012	ZCOR = X (3, JJ)	0115
	IF (ZCOR) 1010, 1011, 1011	0116
1010	JJ = JJ + 1	0117
	GO TO 1012	0118
1011	CONTINUE	0119
	J2 = JJ + 1	0120
	DO 1013 JJ = J2, NMAX	0121
	ZCORI = X (3, JJ)	0122
	IF (ZCORI) 1013, 1014, 1014	0123
1014	CONTINUE	0124
	IF (ZCOR—ZCORI) 1015, 1013, 1013	0125
1015	ZCOR = ZCORI	0126
1013	CONTINUE	0127
	DO 2010 JJ = 1, NMAX	0128
2010	X (3, JJ) = X (3, JJ)—ZCOR	0129
C	CALCULATE THE PERSPECTIVE COORDINATES	0130
1044	CONTINUE	0131
	DO 1030 JJ = 1, NMAX	0132
	ZA = ABS (X (3, JJ))	0133
	DENO = ZSP + ZA	0134
	XR (1, JJ) = (EYE*ZA + X (1, JJ)* ZSP)/DENO	0135
	XR (2, JJ) = X (2, JJ) * ZSP/DENO	0136
1030	XR (3, JJ) = X (3, JJ)	0137
	IF (EYE) 1040, 1041, 1042	0138
1042	EYE = - EYE	0139
	WRITE (6, 332)	0140
	WRITE (6, 1066)	0141
1066	FORMAT (10X, 'COORDINATES AS VIEWED BY THE RIGHT EYE '/')	0142
	WRITE (6, 332)	0143
	WRITE (6, 1052) (ANAME (J), (XR (I, J), I = 1, 3), J = 1, NMAX)	0144
	GO TO 1044	0145
1040	WRITE (6, 332)	0146
	WRITE (6, 1067)	0147
1067	FORMAT (10X, 'COORDINATES AS VIEWED BY THE LEFT EYE '/')	0148
	WRITE (6, 332)	0149
	WRITE (6, 1052) (ANAME (J), (XR (I, J), I = 1, 3), J = 1, NMAX)	0150
	GO TO 998	0151
1041	WRITE (6, 332)	0152
	WRITE (6, 1068)	0153
1068	FORMAT (10X, 'COORDINATES FOR SINGLE PERSPECTIVE DIAGRAM '/')	0154
	WRITE (6, 332)	0155
		0156

	WRITE (6, 1052) (ANAME (J), (XR (J, J), I= 1, 3), J= 1, NMAX)	0157
998	CONTINUE	0158
999	CONTINUE	0159
	STOP	0160
	END	0161
	SUBROUTINE RDCONS (NRDCN)	0162
	DIMENSION ATOM (3)	0163
	COMMON A, B, C, ALFA, BETA, GAMMA, NMAX, x (3, 100)	0164
	CONFA = 0.01745329	0165
	GO TO (13, 11, 16), NRDCN	0166
13	CONTINUE	0167
	PALFA = ALFA*CONFA	0168
	PBETA = BETA*CONFA	0169
	PGAMMA = GAMMA*CONFA	0170
	CA = COS (PALFA)	0171
	CB = COS (PBETA)	0172
	CG = COS (PGAMMA)	0173
	SG = SIN (PGAMMA)	0174
	CPSI = (CB - (CA*CG))/SG	0175
	CRO = SQRT (1.0 - (CA*CA + CPSI*CPSI))	0176
	DO 14 I = 1, NMAX	0177
	ATOM (1) = x (1, I)* SG*A + x (3, I)* CPSI*C	0178
	ATOM (2) = x (1, I)* CG*A + x (2, I)* B + x (3, I)* CA*C	0179
	ATOM (3) = x (3, I)* CRO*C	0180
	DO 14 J = 1, 3	0181
14	x (J, I) = ATOM (J)	0182
	GO TO 11	0183
16	CONTINUE	0184
	DO 17 I = 1, NMAX	0185
	OMEGA = x (2, I)	0186
	OMEGA = OMEGA*CONFA	0187
	ATOM (1) = x (1, I)*COS (OMEGA)	0188
	ATOM (2) = x (1, I)*SIN (OMEGA)	0189
	DO 17 J = 1, 2	0190
17	x (J, I) = ATOM (J)	0191
11	CONTINUE	0192
	RETURN	0193
	END	0194
	SUBROUTINE ROMAX (DC, ANG, AMAT)	0195
	DIMENSION DC (3), AMAT (3, 3)	0196
	CONFA = 0.01745329	0197
	ANG = ANG*CONFA	0198
	C = COS (ANG)	0199
	S = SIN (ANG)	0200
	CC = (1.0 - C)	0201
	AMAT (1, 1) = C + DC (1)*DC (1)*CC	0202
	AMAT (1, 2) = DC (1)*DC (2)*CC - DC (3)*S	0203
	AMAT (1, 3) = DC (1)*DC (3)*CC + DC (2)*S	0204
	AMAT (2, 1) = DC (1)*DC (2)*CC + DC (3)*S	0205
	AMAT (2, 2) = C + DC (2)*DC (2)*CC	0206
	AMAT (2, 3) = DC (2)*DC (3)*CC - DC (1)*S	0207
	AMAT (3, 1) = DC (1)*DC (3)*CC - DC (2)*S	0208

```
AMAT (3, 2) = DC (2) * DC (3) * CC + DC (1) * S      0209
AMAT (3, 3) = C + DC (3) * DC (3) * CC              0210
RETURN                                               0211
END                                                 0212
SUBROUTINE RMM (A, K, L, B, N, C)                   0213
DIMENSION A (3, 3), B (3, 1), C (3, 1), X1 (3)     0214
DO 10 I = 1, N                                     0215
DO 20 J = 1, K                                     0216
X1 (J) = 0.0                                       0217
DO 20 KK = 1, L                                    0218
20 X1 (J) = X1 (J) + A (J, KK) * B (KK, 1)         0219
DO 10 J = 1, K                                     0220
10 C (J, 1) = X1 (J)                               0221
RETURN                                             0222
END                                               0223
```