# On the Use of the Symbolic-Addition Procedure in P1 and Related Space Groups

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The symbolic-addition method is known to break down frequently in  $P\overline{1}$  and related space groups. Analyses of the generation of signs in some known cases have been made in order to find useful modifications of the method. Errors can often be traced back to the acceptance of structure factors whose signs have been directly determined from  $\sum_2$  relations. When incorrect signs have entered into the data more errors may develop very rapidly. As a consequence, E maps based on a very limited number of the structure factors signed in the first stages may be significantly better than maps calculated in the usual way with all E's above some arbitrary limit. Structural information can be used directly as an aid for selecting the most probable sign models from a given starting set.

## Introduction

The power of the symbolic-addition procedure in crystal-structure work is by now well established, and a large number of reports exist on its successful application. It is well known, however, that failures do occur and more frequently in some space groups than in others. This is the case with *e.g.* the triclinic space groups. In general, difficulties are to be expected when the method is applied in space groups without translational symmetry (centring is not considered an element of translation in this context).

We have tried to find useful ways of overcoming such difficulties by a closer examination of the generation of signs in known cases. Since  $P\overline{I}$  is probably the most common of these space groups it will be used as an example in the following.

#### General

It is well known that by choosing the sign + for the origin-defining reflexions in  $P\overline{1}$ , all generated signs and indications for symbols will be +, thus giving the *trivial solution* which is not, as a rule, the correct solution. In general, any sign generated by the  $\sum_2$  relation  $sE_{\mathbf{h}} \simeq s \sum_{\mathbf{k}} E_{\mathbf{k}} E_{\mathbf{h}-\mathbf{k}}$  (Hauptman & Karle, 1953) from the origin-defining set in the  $P\overline{1}$  case is only dependent on the index parity of the structure factor in question. Consequently, indications of sign for a particular symbol p introduced into the starting set must be either

all + or all -, the sign being determined by the choice of origin and the parity of the structure factor signed p. Relations between symbols must also be in agreement with the parity conditions that are set out in matrix form in Table 1. Owing to symmetry in the main diagonal only the upper half of the parity matrix is shown. The sign of the third member in a Sayre triplet,  $E_{\mathbf{h}}E_{\mathbf{k}}E_{\mathbf{h}-\mathbf{k}}$ , can be looked up in this table when the signs of the other two members, in the top row and the left column respectively, are known. An origin set chosen as e.g. ooe = +, eeo = -, eoe = - is found to give the following trivial set of signs for the other parity groups: (eee = +), oee = -, eoo = +, oeo = +and ooo = -. Assume that symbols a, b and c have been assigned to three structure factors of parities ooe, ooo and eeo respectively, in addition to the origindefining reflexions. Possible relations between symbols are then e.g. a=bc, a=-b and b=c, all in keeping with the trivial solution. The problem of structure determination is thus one of extracting the correct solution from the trivial distribution of signs and symbols in the data.

We have studied some aspects of this problem by examining more closely the development of signs in the data for three known structures in space group  $P\overline{1}$ . They are: (A) 4-yne-octadecanoic acid,  $C_{18}H_{32}O_2$ , a long-chain fatty acid with a triple bond at C(4), cell parameters are a=8.71, b=5.475, c=45.13 Å,  $\alpha=$ 92.55,  $\beta=93.15$ ,  $\gamma=123.95^{\circ}$  (Mo, 1971); (B) crocetindialdehyde,  $C_{20}H_{24}O_2$ , a dialdehyde with a polyene chain structure (Hjortås, 1972) and (C)  $\delta$ -pyrazincar-

Table 1. Parity table for space group  $P\overline{1}$ 

			е	е	е	е	е	0	е	0	е	0	е	е	е	о	0	0	е	0	0	0	е	0	0	0
е	е	е	е	е	е	е	е	0	е	0	е	0	е	е	е	0	0	0	е	0	0	0	е	0	0	0
е	е	0				е	е	е	е	0	0	0	е	0	е	0	е	0	е	е	0	0	0	0	0	е
е	0	е							е	е	е	0	0	е	е	е	0	0	0	0	0	е	е	0	е	0
0	е	е										е	е	е	0	0	0	е	е	0	е	0	е	е	0	0
е	0	0													е	е	е	0	0	е	0	е	0	0	е	е
0	е	0																е	е	е	е	0	0	е	0	е
0	0	е																			е	е	е	е	е	0
0	0	0																						е	е	е

boxamide, C5H5N3O, an almost planar structure containing a six-membered ring (Rø & Sørum, 1972).

#### **Experimental and results**

Generation of signs and symbols with the  $\sum_{2}$  formula was carried out by the program SYMBOL (Hjortås, 1969). It permits up to 4 symbols to be used in a starting set in addition to the origin-defining reflexions. Only reflexions with E's greater than some preset value  $E_{\text{start}}$  are considered first. When no more new signs can be found the program lowers the E limit by 0.1 and repeats the search for triplets. SYMBOL thus works in cycles, gradually lowering the E limit until a preset lower limit  $E_{stop}$  is attained. Acceptance of new reflexions is based on the common probability measure P(+) (Cochran & Woolfson, 1955) which is used in a rather cautious manner: when different symbolic indications of the sign for a reflexion are obtained, P(+) is calculated by assuming that all indications other than the dominant one are wrong.

#### Significance of intersymbolic relations

In order to assess the possible value of relations obtained between symbols in  $P\overline{1}$ , signs and symbolic relations were developed from 14 different starting sets for structure A and five sets for structure B. Data sets of 2-300 E's were used in both cases. For each starting set the number  $(N_c)$  of satisfied intersymbolic relations with correct signs being substituted for the symbols was compared with the maximum number of satisfied relations obtained for any sign combination, except the trivial one. The relative number  $N_c$  was found to range from 0 to 100% with an average of 50.9% for the 19 starting sets. The average for 14 sets with 4 or more intersymbolic relations was 44.1%. The results show that a relation like, for example, a=b is not more likely to be true than a=-b.





#### E maps calculated with few terms

Structure factors that come out with a specific indication of sign, + or -, during the symbolic-addition procedure call for special attention. If many of these 'directly determined' signs are wrong the correct structure may never be found with this starting set. Both the stage at which errors show up and the kind of reflexions involved are, of course, decisive for the total number of incorrect signs. Sometimes the acceptance of a few or just one wrong sign may set off a fatal chain of errors in the sign propagation. The work on structure B provides an excellent example of this kind of trouble. One of the starting sets was B6: 111 = -,  $3\overline{7}0 = +, 4\overline{5}4 = +, 222 = + (\text{from } \sum_{1}) \text{ and } 10\overline{1} = a.$ With the correct sign + substituted for *a* there were no errors in the first 50 signs, among these 21 directly determined. The next reflexion to be accepted was 002 but the sign + (directly determined) is wrong for this particular choice of origin. Since 002 enters into a large number of  $\sum_{2}$  relations the error spreads very quickly through the remainder of the data. The development of wrong signs for B6 is illustrated in Fig. 1. This figure also shows the sign development for starting sets A 10 (structure A):  $2,\overline{1},33 = -, 0,3,20 = -,$  $2,\overline{3},14 = +,0,2,\overline{19} = a,4,\overline{2},30 = b,0,1,\overline{18} = c \text{ and } 2,\overline{3},\overline{23} = d,$ where a=b=d=- and c=+\* and C3 (structure C):

\* Because of pseudosymmetry in structure A, only half the cell (halving of a axis) need be considered.

#### Table 2. Listing of strongest maxima in reduced and full E maps

Maxima corresponding to atomic positions have been marked according to the system used in Table 3.

-							
Reduced $E$ map: 50 terms							
Relative	peak						
x y z heigl	ht						
0.564 0.920 0.339 410	) C(13)						
0.645 0.710 0.418 400	C(16)						
0.427 0.733 0.311 390	C(12)						
0.518 0.723 0.364 380	C(14)						
0.673 0.913 0.393 370	C(15)						
0.305 0.753 0.257 350	C(10)						
0.443 0.930 0.286 340	C(11)						
0.327 0.940 0.233 340	) C(9)						
0.766 0.907 0.448 280	C(17)						
0.755 0.700 0.470 28	C(18)						
0.205 0.957 0.181 250	C(7)						
0.205 0.767 0.203 244	$\mathbf{C}(8)$						
Full E map: 191 terms							
0.418 0.727 0.310 87	0 C(12)						
0.441 $0.923$ $0.285$ $810$	$\tilde{\mathbf{C}}$						
0.302 $0.743$ $0.255$ $730$	$\tilde{\mathbf{C}}$						
0.325 $0.940$ $0.233$ $730$	$\tilde{\mathbf{C}(9)}$						
0.541 $0.913$ $0.339$ $670$	$\tilde{\mathbf{C}(13)}$						
0.523 $0.717$ $0.365$ $57$	$\tilde{O} = \tilde{C}(14)$						
0.636 0.707 0.418 47	0 C(16)						
0.659 $0.907$ $0.394$ $410$	$\tilde{C}(15)$						
0.202 $0.757$ $0.203$ 41	$\tilde{\mathbf{C}(8)}$						
0.209 0.953 0.181 36	$\tilde{O}$ $\tilde{C}(7)$						
0.759 0.893 0.448 31	$\tilde{\mathbf{C}(17)}$						
0.736 0.690 0.473 28	0 C(18)						

Table 2 (cont.)

Starting set	<i>B</i> 6
Reduced E map:	50 terms

		F	Relative pea	ak
x	У	Z	height	
0.030	0.445	0.035	530	C(8)
0.090	0.325	0.073	520	C(7)
0.145	0.210	0.123	460	C(6)
0.210	0.093	0.175	430	C(5)
0.265	-0.028	0.222	390	C(4)
0.325	<i>−</i> 0·140	0.268	310	C(3)
0.400	-0.2258	0·318	250	C(2)
0.300	-0.425	0.625	230	
0.620	-0.428	0.318	220	0
0.280	-0.345	0.283	200	C(1)
0.253	-0.340	0.283	200	
0.445	-0.375	0.375	190	
	Full E	map: 352 te	erms	
0.023	0.455	0.043	1880	C(8)
0.135	0.333	0.035	1120	C(7)
0.515	0.493	0.560	630	$\mathbf{C}(i)$
0.215	0.230	0.108	610	C(6)
0.325	-0.258	0.350	590	0(0)
0.215	-0.205	0.505	480	
0.400	-0.405	0.578	480	
0.450	-0.395	0.343	420	
0.210	0.083	0.158	400	C(5)
0.225	-0.025	0.285	400	C(4)
0.130	-0.085	0.463	390	0(1)
0.060	-0.148	0.578	390	
	C to			
	Reduced	F man: 50 t	erme	
	Reduced	L map. 50 t		. 1.
r	V	r 7	height	iĸ
0.020	0.100	0.046	COO	
-0.020	-0.100	0.121	690	$C(\mathbf{r})$
-0.112	-0.280	0.210	630	$C(\eta)$
-0.103	-0.857	0.219	620 580	C(2)
-0.253	-0.200	0.060	570	
0.080	-0.557	0.009	510	$\Gamma(0)$
-0.153	-0.664	0.217	400	C(3)
0.153	-0.103	0.006	490	O(0)
0.120	-0.371	0.196	480	0(9)
-0.337	-0.579	0.250	430	N(1)
0.203	0.000	0.012	430	14(1)
0.033	-0·750	0.369	400	N(4)
		100		- ( - )
	Full E	map: 189 te	rms	
-0.020	-0.079	0.020	1450	
-0.087	-0.450	0.230	1020	C(2)
-0.227	-0.171	0.071	840	N(8)
0.207	-0.886	0.408	780	C(5)
0.1/3	-0.171	0.112	660	O(9)
0.072	-0.086	0.069	610	<b>C</b> (-)
0.0/3	-0.364	0.269	550	C(3)
0.127	-0.786	0.431	540	
0.652	-0.564	0.200	510	
-0.023	- 0.286	0.335	500	
0.320	- 0.393	0.342	500	
0.14/	-0.629	0.300	500	

The features in Fig. 1 suggest that E maps calculated with a smaller number of terms might prove useful. We have calculated E maps from the 50 first signs developed by SYMBOL (reduced E map) for the three cases and compared them with E maps based on all accessible reflexions with  $E \ge E_{stop}$  (full E map); *i.e.* for structure A: 191 E's ( $E_{stop} = 1.20$ ), B: 352 E's ( $E_{stop} =$ 1.10) and C: 189 E's ( $E_{stop} = 1.10$ ). In Table 2 are given the coordinates of the highest peaks in pairs of such maps. Peaks corresponding to atomic positions in Table 3 have been marked appropriately.

## Table 3. Relevant atomic coordinates in structures A, B and C

Coordinates of structure A correspond to the regular part of the hydrocarbon chain and are averaged values for two crystallographically independent molecules at an R index of  $13\cdot8\%$ . Coordinates of B are as given by Hjortås (1972). Coordinates of C are the centrosymmetrical equivalents of those given by Rø & Sørum (1972).

		Α	
	x	У	Z
C(7)	0.224	0.966	0.178
C(8)	0.203	0·748	0.203
C(9)	0.335	0.952	0.232
C(10)	0.309	0.743	0.256
C(11)	0.436	0.937	0.285
C(12)	0.418	0.725	0.310
C(13)	0.543	0.928	0.339
C(14)	0.522	0.716	0.363
C(15)	0.645	0.911	0·392
C(16)	0.631	0.715	0.416
C(17)	0.746	0.906	0.446
C(18)	0.732	0.700	0.471
		В	
	x	У	z
C(1)	0.5763	-0.3527	0.2630
C(2)	0.4320	-0·2476	0.3069
C(3)	0.3671	-0·1443	0.2251
C(4)	0.2400	-0.0223	0.2443
C(5)	0.2033	0.0826	0.1563
C(6)	0.0920	0.2160	0.1656
<b>C</b> (7)	0.0832	0.3123	0.0653
C(8)	-0.0083	0.4535	0.0524
C(9)	0.3714	-0.2609	0.4368
C(10)	-0.0022	0.2439	0.2845
0	0.6683	-0.4438	0.3244
		С	
	x	У	Z
N(1)	-0.3414	<b>−0.</b> 5757	0.2213
C(2)	-0·1116	-0.4882	0.2221
C(3)	0.0742	-0.5810	0.2824
N(4)	0.0375	-0.7570	0.3694
C(5)	-0·1910	-0.8460	0.3962
C(6)	-0.3760	-0.7535	0.3360
<b>C</b> (7)	-0.0638	-0.2885	0.1262
N(8)	-0·2539	-0.2153	0.0719
O(9)	0.1510	-0.1990	0.1006

 $2\overline{3}6 = -$ ,  $32\overline{5} = -$ ,  $5\overline{2}\overline{2} = +$ ,  $5\overline{1}0 = a$ ,  $6\overline{3}\overline{4} = b$  and  $31\overline{1} = c$ , where a = b = c = +. In all three cases the number of wrong signs is reasonably low for the first 50-60 E's. Thereafter an increasing fraction of wrong signs develops, the effect being most pronounced in case C and smallest in case A.

For structure A both full and reduced E maps give the regular part of the chain molecule. Maxima in the full E map are maybe slightly closer to refined values, but the small differences between the two maps have no practical consequences for the structure solution. Structure B is bent in the main molecular plane and also twisted out of this plane (Hjortås, 1972). The irregularities of the chain are manifested by very diffuse maxima both in the Patterson and the E maps. All 9 atoms (C and O) in one half of the centrosymmetric chain [branching methyl groups not included, see Fig. 2(a)] are found among the 10 highest peaks in the reduced E map. Estimated positions of the atomic peaks are at an average distance of 0.29 Å from corresponding refined positions. A least-squares refinement (3 cycles) of coordinates for the 9 peaks forming a zigzag array followed by calculation of a difference map showed very clearly the missing atoms C(9) and C(10).

In the full E map 5 of the 10 strongest peaks are near true atomic sites. The average deviation from refined atomic coordinates is 0.40 Å, atom C(6) being considerably displaced, *ca.* 0.90 Å, from its refined position. A difference map was calculated after some refinement of the coordinates for the 5 peaks conforming to a chain. This map shows, in addition to many spurious peaks, two maxima of medium height somewhat shifted from the final positions of C(3) and C(2). Final positions of the 4 missing atoms are only slightly above background or on negative area. In the original analysis all trials to solve structure *B* from the full *E* map based on starting set *B*6 were unsuccessful.

Case C: in the reduced E map 8 of the strongest maxima correspond to true atomic positions. The only missing heavier atom, C(6), which is needed to close the hexagon of the pyrazine ring [see Fig. 2(b) for atomic numbering] is found as a peak of lower relative height 240.

C(9) C(10) C(2) C(4) 0 C(6) C(8) C(3) C(1) C(5) C(7) (b) N(1) N(8) C(6) C(7) C(2) C(5) 0(9) C(3) N(4) (a)

Fig. 2. (a). Atomic numbering in structure B. (b) Atomic numbering in structure C.

Among the 12 strongest maxima in the full E map only 5 correspond to true atomic positions. This map is inferior to the reduced map for other reasons also. The *true* hexagonal pattern of atoms is not easily recognized here since both N(4) and C(6) fall in minima. [N(1) and C(7) are on low maxima.] However, hexagons in various wrong positions are readily established by using other peaks, and in the work of Rø & Sørum (1972) the structure could not be found from the full E map based on starting set C3. It is also seen from Table 2 that of the true atomic peaks found in both maps, *i.e.* C(2), C(3), C(5), N(8), O(9), those in the reduced map are closer to the refined coordinates.

Among the false peaks, there are two common to both maps: the strongest one and another at approximately -0.150, -0.660, 0.315. Both peaks can be identified as false features when the true position of the hexagon has been established, as it is in the reduced *E* map.

## Aids for selecting most probable models

In many instances the correct structure model is not easily recognized just by comparing different E maps. This is very often found with the kind of highly regular structures considered here. It is also a matter of experience that refinements of structures like hydrocarbon chains often converge very slowly, even when most coordinates are fairly well known at the outset. Therefore, various aids for the exclusion of less probable models are valuable. Large variations in peak heights and the presence of ghost maxima in the E map are known to be indications of wrong models. The correct model of e.g. structure A was found in maps with a fairly even distribution of peak heights and there were only two rows of maxima corresponding to a single zigzag pattern in the hydrocarbon chain. Spurious maxima beyond true chain ends were weak. They are caused mainly by the pronounced translational symmetry within the molecule as noted by e.g. Bürgi & Dunitz (1971). These authors suggest extension of the structure-factor set to include smaller E values as a means of reducing the level of such detail. In the  $P\overline{1}$ case, however, we would like to emphasize the dangers involved in such a procedure. A better way of suppressing 'translational' peaks appears to be the commonly used method of normalizing the structure factors in groups, e.g. according to parity.

Case A also provides an example of the possible use of structural knowledge as an aid to the application of direct methods. There is a sequence of 00/ reflexions in the data with  $34 \le l \le 44$  corresponding to d spacings in the range  $1 \cdot 32 - 1 \cdot 02$  Å. The molecular axis in A is approximately parallel to [201], and the distribution of signs in the 00/ sequence must conform to the repeating pattern of peaks in a hydrocarbon chain. Table 4 gives the 00/ signs for various sign combinations in starting set  $A1: 215 = -, 2, \overline{1}, 32 = +, 20\overline{3} = +, 4, \overline{2}, \overline{10} =$ + (from  $\sum_{1}$ ),  $2, \overline{2}, 33 = a, 2, \overline{3}, \overline{23} = b$  and  $0, 3, \overline{18} = c$ . Combinations VI and VII both give the sign – for the whole set of 00l reflexions and can be ruled out. I and IV give alternating signs for consecutive reflexions in the set and were considered unlikely; moreover, IV corresponds to the trivial solution. Only V and VIII of the four combinations left gave models with a satisfactory distribution of peak heights in the *E* maps and no ghost peaks. The model from VIII proved to be correct.

# Table 4. Signs of some 001 reflexions for various sign combinations in starting set A 1

	I	II	ш	IV	V	VI	VII	VIII
	a = +	<i>a</i> = +	<i>a</i> = +	<i>a</i> = +	a = -	a = -	a = -	a = -
	b = +	b = +	b = -	b = -	b = +	b = +	b = -	b = -
00/	c = +	c = -	c = +	c = -	c = +	c = -	c = +	<i>c</i> = -
l = 34	+	+	+	+	_	_	-	-
35	-	+	+	-	+	-		+
36	+		-	+	+	-		+
37	-	-	_	—	-		—	_
38	+	-	_	+	+		_	+
39	_	+	+	-	+	-	-	+
40	+	+	+	+	-		-	_
41	-	_	_	_	-	-	_	-
42	+	_	-	+	+	_	-	+
43	-	+	+	—	+	-		+
44	+	+	+	+	-	-	_	—

## Conclusions

Intersymbolic relations are of no significance in selecting the correct sign combination in a chosen starting set in  $P\overline{1}$ .

When incorrect signs have been included in the data, they may cause a very rapid propagation of more errors during the symbolic-addition procedure. It may therefore prove advantageous to break off the  $\sum_2$ process at an early stage and calculate E maps with a small number of terms. For three cases examined, Emaps were calculated with the 50 structure factors signed in the first stages by  $\sum_2$ . They were found to contain as much or even significantly more correct information than maps based on all E's above some arbitrary limit, *e.g.* 1·2. It is implied that if incorrect signs enter into the data at a very early stage, even reduced E maps may contain too many erroneous features.

Discrimination between probable and less probable sign models may be aided by the use of structural information. A rather crude application of structural knowledge is shown as an example from the work on a chain structure. More refined methods based on these principles could certainly be of great value, in particular with structures giving heavy overlap in Patterson space.

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# A Complete Catalogue of Polyhedra with Eight or Fewer Vertices

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All non-isomorphic convex polyhedra with 4, 5, 6, 7 and 8 vertices are listed. The relationships within each class are described.

In the course of an attempt to describe in a systematic way the coordination of eight ligand atoms around a central atom with no symmetry restrictions, we encountered the problem of enumerating all possible non-isomorphic convex polyhedra with eight vertices. According to Alexandrow (1958) the number N(n) of polyhedra with *n* vertices is: N(4) = 1, N(5) = 2, N(6) = 7, N(7) = 34, N(8) = 257, but we were unable to find any publication in which these polyhedra are described. Grace (1965) has determined by computer search all polyhedra with up to eleven faces with the restriction that only three edges meet at each vertex. The duals of these polyhedra are the polyhedra with up to eleven vertices with the restriction that all faces are triangular; these, however, are only a small fraction of the

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