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***SnB* version 2.3: triplet sieve phasing for centrosymmetric structures**

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Abstract

A new version of the direct-methods program *SnB* has been developed. This version incorporates the triplet sieve method for phasing centrosymmetric structures in a way that is transparent to users. The triplet sieve procedure may decrease significantly the time required to achieve a solution for such structures.

1. Introduction

SnB is a computer program (Miller *et al.*, 1994; Weeks & Miller, 1999; Weeks *et al.*, 2002) that implements the direct-methods phasing algorithm known as *Shake-and-Bake* (DeTitta *et al.*, 1994; Weeks *et al.*, 1994). *Shake-and-Bake* is an example of a ‘multi-solution’ or ‘multi-trial’ procedure (Germain & Woolfson, 1968). First, multiple trial structures are created by a random-number generator that is used to assign initial atomic coordinates. Then, these trial structures are subjected to a dual-space refinement procedure that automatically and repetitively alternates reciprocal-space phase refinement, either by using the tangent formula (Karle & Hauptman, 1956) or by reducing the value of the minimal function (Debaerdemaecker & Woolfson, 1983), with complementary peak picking in real-space to impose physical constraints. Potential solutions are identified on the basis of figures of merit such as the minimal function (R_{\min}) itself or a crystallographic R factor (R_{cryst}) calculated at the end of *SnB* refinement.

The time required to achieve a solution depends on (1) the computational time of an individual *SnB* refinement cycle and (2) the success rate or percentage of trial structures that refine to solutions. Success rate can be increased by providing a better-than-random set of starting atoms or phases. For example, the phasing program *SHELXD* (Schneider & Sheldrick, 2002), which is also based on the *Shake-and-Bake* algorithm, uses Patterson minimum functions (Buerger, 1959; Nordman, 1966) to derive sets of starting atoms that are, in some way, consistent with the Patterson function. Alternatively, the triplet sieve method (Smith *et al.*, 2007) uses an integer minimal principle to provide a subset of perfect, or nearly perfect, initial phases that can be expanded using standard *Shake-and-Bake* refinement.

Direct methods rely on the fact that the structure invariants or triplet phases,

$$\phi_{HK} = \phi_H + \phi_K + \phi_{-H-K}, \quad (1)$$

are approximately equal to 0 if the corresponding values of $A_{HK} = 2N^{-1/2}|E_H E_K E_{-H-K}|$ are large. (N is the number of non-H atoms in the unit cell, and the $|E|$ s are normalized structure

factors.) In the centrosymmetric case, φ_{HK} equals 0 or 180 degrees only, and, given a subset of φ_{HK} which are all equal to 0, it is possible to solve the system of homogeneous equations (eqn. 1) with the triplet sieve technique and to obtain the desired subset of perfectly correct phases. However, two complications exist. First, the number of phases (NSP) appearing in the triplets involved in the sieving process must be limited to a small number with the very largest $|E|$ values in order to avoid inclusion of φ_{HK} with values of 180 in the set used for sieving. If such triplets are included, it cannot be guaranteed that the correct set of phases can be found. Consequently, NSP is significantly smaller than the total number of reflections that need to be phased in an *SnB* job. In some cases, it will be necessary to iteratively reduce NSP in order to find a solution, but there is also a minimum value of NSP below which solutions will never be found. To avoid inclusion of triplets with values of 180 degrees, use of the sieving technique should also be limited to structures with fewer than ~ 100 atoms in the asymmetric unit. The second complication to the sieving process is that, depending on the number of phases required to fix the origin in the particular space group as well as the nature of the triplet interactions among the NSP phases, the homogeneous system of equations will have a variable number of degrees of freedom leading to the generation of a variable number of sieve phase sets or trial structures.

2. Materials and Methods

The sieving process can be incorporated into the *Shake-and-Bake* procedure, as illustrated in Figure 1, with the addition of three new operational parameters. These parameters are the number of sieve phases (NSP), the reduction in number of phases (SPR) considered in each successive sieving step, and the minimum number of phases to be used for sieving (NSPmin). A subroutine implementing the procedure described by Smith *et al.* (2007) was added to the *SnB* program, and the additional steps introduced by triplet sieving are indicated by a gray background in the flow chart. If the structure is centrosymmetric and the number of atoms in the asymmetric unit is less than 100, the variable 'UseSieve' is set to TRUE, and the phases of the trial structures are generated by the new subroutine. If the degrees of freedom (DF) are too large, the number of phases used for sieving is reduced, and the trial phase sets are regenerated. If satisfactory trial structures can not be generated, the variable 'UseSieve' is set to FALSE, and the program reverts to standard *SnB* operation using trial structures with randomly positioned atoms.

The modified *SnB* program was applied to the 15 centrosymmetric test data sets listed in Table 1. First, using the deposited CIF file, basic crystallographic information including space group, cell parameters, and chemical formula was input to *SnB*. Then, using the DREAR package (Blessing & Smith, 1999) in *SnB*, E-values were generated from the observed intensity data. As a final initialization step, reflection and invariant files were generated containing $10N$ reflections and $100N$ triplets, respectively. Next, the sieving procedure was carried out, and the three sieve parameters were varied in order to find a combination of values that would optimize the efficiency of the *Shake-and-Bake* procedure for these structures. In all cases, a small number ($0.1N$) of conventional *SnB* refinement cycles was added to expand the set of phased reflections and to improve the quality of the phases. Finally, the best values of the sieve parameters were chosen, and a final *SnB* job was run for each data set in order to measure the time required to obtain a solution. Solutions were identified on the basis of mean phase errors when compared to correct phase sets computed using the known atomic coordinates.

3. Results

As a result of the test jobs, the parameter values (all a function of the size of the structure) given in Table 2 were chosen as default values. The results of the final jobs showing a comparison of the time required to yield *SnB* solutions with and without the sieve procedure

is presented in Table 1. This comparison shows that the computing time required for 14 of the 15 test structures is reduced by a factor of 4.1 to 98.5 when sieving is included. The average reduction factor is 29.5.

The modified version of the *SnB* program with the sieve procedure included with the default parameter values determined in this study is now available as version 2.3 from the *SnB* website, <http://www.hwi.buffalo.edu/SnB/>. Unlike earlier versions of *SnB*, version 2.3 also contains a tool for automatic solution detection that permits calculations to be terminated as soon as a solution is found. Thus, full advantage can be taken of the new sieving feature.

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References

- Alfonso M, Stoeckli-Evans H. *Acta Cryst* 2001;E57:o242–o244.
- Arnold PL, Blake AJ. *Acta Cryst* 2001;E57:o131–o133.
- Blessing RH, Smith GD. *J. Appl. Cryst* 1999;32:664–670.
- Bragg S, Johnson JEB, Graziano GM, alach GJ, Heimer NE. *Acta Cryst* 2002;E58:o1010–o1012.
- Bryan JC, Levitskaia TG. *Acta Cryst* 2002;E58:o240–o242.
- Buerger, MJ. *Vector Space*. John Wiley & Sons; New York: 1959.
- Camiolo S, Coles SJ, Gale PA, Hursthouse MB, Paver MA. *Acta Cryst* 2001;E57:o258–o260.
- Debaerdemaeker T, Woolfson MM. *Acta Cryst* 1983;A39:193–196.
- DeTitta GT, Weeks CM, Thuman P, Miller R, Hauptman HA. *Acta Cryst* 1994;A50:203–210.
- Germain G, Woolfson MM. *Acta Cryst* 1968;B24:91–96.
- Howie RA, Skakle JMS, Wardell SMSV. *Acta Cryst* 2001;E57:o72–o74.
- Karle J, Hauptman HA. *Acta Cryst* 1956;9:635–651.
- Kliegel W, Amt H, Patrick BO, Rettig SJ, Trotter J. *Acta Cryst* 2002a;E58:o473–o475.
- Kliegel W, Drückler K, Patrick BO, Rettig SJ, Trotter J. *Acta Cryst* 2002b;E58:o393–o395.
- Krishnakumar RV, Nandhini MS, Renuga S, Natarajan S, Selvaraj S, Perumal S. *Acta Cryst* 2002;E58:o1174–o1176.
- Lynch DE. *Acta Cryst* 2002;E58:o1025–o1027.
- Miller R, Gallo SM, Khalak HG, Weeks CM. *J. Appl. Cryst* 1994;27:613–621.
- Nordman CE. *Trans. Am. Crystallogr. Assoc* 1966;2:29–38.
- Ohba S, Hiratsuka T, Tanaka K. *Acta Cryst* 2002;E58:o1013–o1015.
- Pletnev VZ, Galitskii NM, Smith GD, eeks CM, Duax WL. *Biopolymers* 1980;19:1517–1534.
- Schneider TR, Sheldrick GM. *Acta Cryst* 2002;D58:1772–1779.
- Smith AB, Xu H, Sahinidis NV. *Acta Cryst* 2007;A63:164–171.
- Sun G-C, Li Y-Z, He Z-H, Li Z-J, Qu J-Q, Liu C-R, Wang L-F. *Acta Cryst* 2002;E58:o417–o418.
- Vande Velde CML, Hoefnagels R, Geise HJ. *Acta Cryst* 2002;E58:o454–o455.
- Weeks CM, DeTitta GT, Hauptman HA, Thuman P, Miller R. *Acta Cryst* 1994;A50:210–220.
- Weeks CM, Miller R. *J. Appl. Cryst* 1999;32:120–124.
- Weeks CM, Blessing RH, Miller R, Mungee R, Potter SA, Rappleye J, Smith GD, Xu H, Furey W. Z. *Kristallogr* 2002;217:686–693.
- Zhuang J-P, Zheng Y, Zhang W-Q. *Acta Cryst* 2002;E58:o720–o722.

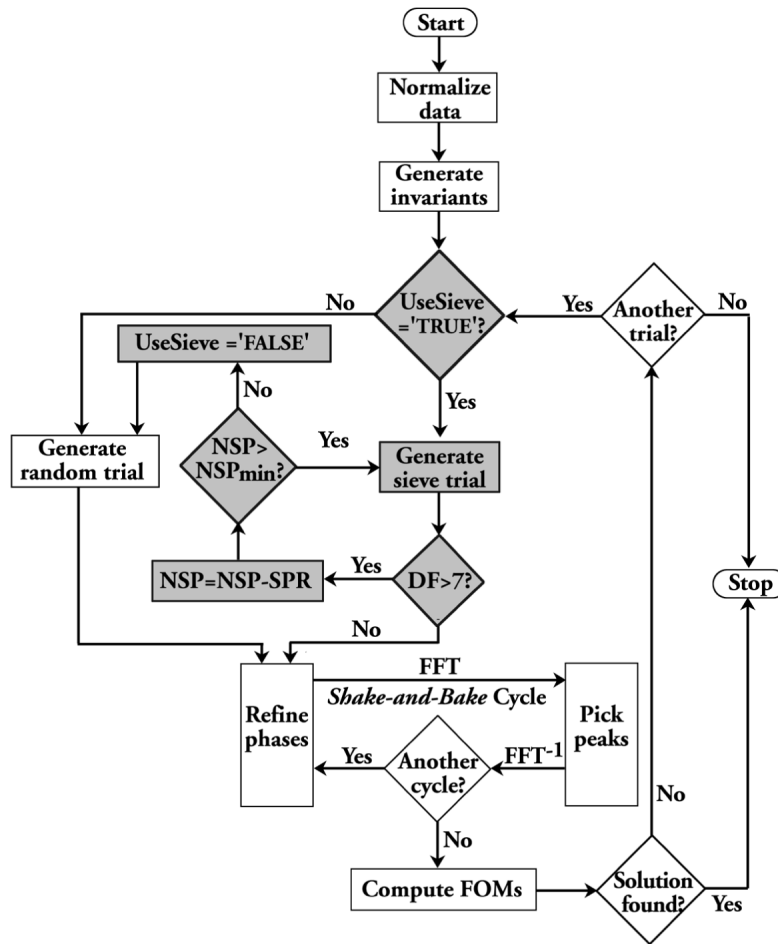


Fig. 1. A flow chart illustrating the *SnB* algorithm after incorporation of the triplet sieving method.

Test structures and crystallographic information. 'Ratio' is the time required to achieve a solution without sieving divided by the time required with sieving.

Table 1

ID	Chemical Formula	Atoms (ASU)	Space Group	Ratio	Reference
1	$C_{12}H_{10}O_3$	15	$P2_1/n$	5.4	Howie <i>et al.</i> (2001)
2	$C_{30}H_{32}N_2O_6$	19*	$P2_1/c$	14.4	Sun <i>et al.</i> (2002)
3	$C_{34}H_{42}B_2N_2O_4$	21*	$P2_1/n$	25.6	Kriegel <i>et al.</i> (2002a)
4	$C_{32}H_{38}N_2O_2$	23*	$P2_1/n$	12.4	Lynch (2002)
5	$C_{44}H_{38}O_4$	24*	$P 1$	20.8	Vande Velde <i>et al.</i> (2002)
6	$C_{44}H_{52}N_4 \cdot C_3H_5OH$	26*	$C2/c$	98.5	Camiolo <i>et al.</i> (2001)
7	$C_{36}H_{62}$	36	$P2_1/c$	0.47	Bragg <i>et al.</i> (2002)
8	$C_{30}H_{22}O_5S$	37	$P2_1/c$	4.1	Krishnakumar <i>et al.</i> (2002)
9	$C_{34}H_{50}N_2O$	37	$P2_1/c$	81.8	Zhuang <i>et al.</i> (2002)
10	$C_{24}H_{12}N_6 \cdot 4CHCl_3$	46	$P2_1/c$	16.0	Alfonso & Stoeckli-Evans (2001)
11	$C_{33}H_{40}B_6N_3O_{11} \cdot 0.5C_4H_{10}O$	57.5	$P 1$	7.9	Kriegel <i>et al.</i> (2002b)
12	$C_{41}H_{78}O_{11}Si_8$	60	$P 1$	70.0	Arnold & Blake (2001)
13	$C_{50}H_{66}O_6 \cdot C_3H_7NO$	61	$P2_1/c$	6.4	Bryan & Levitskaia (2002)
14	$3C_{40}H_{32}O_2 \cdot 4C_6H_6$	75*	$P 1$	44.5	Ohba <i>et al.</i> (2002)
15	$C_{60}H_{102}N_6O_{18}$	84	$P 1$	5.6	Pletnev <i>et al.</i> (1980)

* : Structures which crystallize with a crystallographic center of symmetry in the middle of the molecule. In such cases, the number of atoms in the asymmetric unit is half of the molecule.

Table 2

Parameters for the combined SnB/sieve procedure.

Parameter	<i>SnB</i> alone	<i>SnB</i> with sieving
Total reflections (phases)	$10N$	$10N$
Triplets	$100N$	$100N$
Peaks to select	N	N
<i>SnB</i> cycles	$0.5N$	$0.1N$
No. sieve phases (NSP)	NA	$1.5N-4N^{\ddagger}$
Sieve phase reduction (SPR)	NA	$0.15N$
Min. sieve phases (NSPmin)	NA	$0.5N$

\ddagger : The initial set of sieve reflections is chosen utilizing a binary search for the first instance of non-origin degrees of freedom as described in section 5 of Smith *et al.* (2007).