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A. Morawiec

J. Appl. Cryst. (2017). **50**, 647–650



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Ind_X: program for indexing single-crystal diffraction patterns

A. Morawiec*

Polish Academy of Sciences, Institute of Metallurgy and Materials Science, Reymonta 25, 30-059 Kraków, Poland.

*Correspondence e-mail: nmmorawi@cyf-kr.edu.pl

Received 14 November 2016

Accepted 10 January 2017

Edited by Th. Proffen, Oak Ridge National Laboratory, USA

Keywords: crystal diffraction; lattice nodes; indexing; periodograms.

Supporting information: this article has supporting information at journals.iucr.org/j

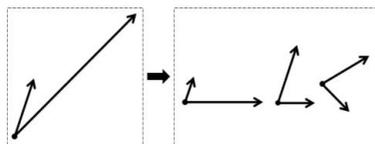
Indexing is an essential step in analysis of diffraction patterns. Diffraction of monochromatic radiation by a single crystal provides approximate positions of some nodes of the reciprocal lattice of the crystal, and the indexing problem lies in determining a lattice matching these positions. *Ind_X* is a program for indexing diffraction data given in the form of several approximate reciprocal lattice nodes. The applied method relies on testing potential volumes of the primitive cell of the reciprocal lattice. A subset of reciprocal lattice vectors supporting a given test volume is used to obtain tentative lattice bases. These are bases of low-index superlattices of lattices based on triplets of supporting vectors. The *Ind_X* solution of the indexing problem consists of a list of best bases. The method turns out to be quite robust to data inaccuracies and spurious reflections. The program is relatively versatile, easily operated and freely accessible.

1. Introduction

The process of ascribing Miller indices to reflections on diffraction patterns is referred to as indexing. Indexing appears in most diffraction-based crystallographic studies. In particular, it is an important element of structure determination by single-crystal diffraction of monochromatic X-rays. In this case, recorded data can be converted to vectors approximating the crystal reciprocal lattice, and the indexing is reduced to determination of the true lattice from several approximate positions of lattice nodes.

It must be noted at the outset that indexing of accurate reciprocal lattice vectors is straightforward. Complications arise when the diffraction data are inaccurate. Consistent and reliable indexing of error-affected input or cases with multiple lattices contributing to a pattern can be difficult. Robustness of indexing procedures to both random errors in locations of diffraction peaks and gross errors (inaccurate instrument settings, spurious reflections) is crucial for correctness of results.

Most indexing programs are just intrinsic parts of structure-determination packages (e.g. Pflugrath, 1999; Otwinowski & Minor, 2001; Leslie *et al.*, 2002; Kabsch, 2010), but also a number of standalone indexing tools have been reported (e.g. Klein, 1975; Duisenberg, 1992; Pilz *et al.*, 2002; Sauter *et al.*, 2004). *Ind_X* is a program for indexing diffraction data given in the form of reciprocal lattice nodes. It was written to extend the capabilities of a software package for analysis of Kossel diffraction patterns (Morawiec, 2016). The intended application was lattice parameter determination, and it concerned relatively simple crystal structures. However, additional tests on simulated diffraction data showed that the program is also applicable to more complicated indexing problems. *Ind_X* can



be compared to *DirAx* (Duisenberg, 1992), which is considered to be most suitable for solving difficult cases. Our tests indicate that *Ind_X* has a similar effectiveness in this regard. For illustration, see the supporting information with solutions for the example data of Duisenberg (1992).

Each indexing program has specific built-in mechanisms for controlling the extent of search for solutions. In some cases, the choice of the control parameters and criteria is essential for getting the right result, and it is important to have diverse instruments for solving such patterns. *Ind_X* adds to the diversity of available indexing tools. Since the program is compact and easily operated, it can be conveniently used for solving small-cell problems. An important feature of *Ind_X* is the simplicity of the applied method.

2. Method

Numerous indexing schemes have been considered in the past (see *e.g.* Jacobson, 1976; Vriend & Rossmann, 1987; Kabsch, 1988; Kim, 1989; Higashi, 1990; Duisenberg, 1992; Steller *et al.*, 1997; Jacobson, 1997; Campbell, 1998; Powell, 1999; Gildea *et al.*, 2014). The procedure implemented in *Ind_X* relies on the volume of the primitive cell of the reciprocal lattice. The initial test volumes can be either automatically determined by the program or provided by the user.

The first approach (automatic determination) is based on period-detection methods. In the error-free case, the volume of the primitive cell would be a submultiple of volumes of parallelepipeds spanned by reciprocal lattice vectors, *i.e.* the latter volumes would be distributed periodically. In practice, the volumes of such parallelepipeds are affected by experimental errors, and the volume distributions show some periodicities but are not exactly periodic. The point is to find the period of the distribution obtained from experimental reciprocal lattice vectors. The volumes calculated by *Ind_X* from triplets of experimental vectors constitute a data series, and to get the period the program uses a periodogram – the primary tool for identification of periodicities in data series (Anderson, 1971). In the considered case, the periodogram can be seen as the frequency of occurrence of particular periods among volumes of parallelepipeds spanned by triplets of the experimental reciprocal lattice vectors. For accurate diffraction data, such periodograms have simple structures, and it is easy to determine the period. For many experimental data sets, however, periodograms tend to be noisy (Fig. 1). Therefore, *Ind_X* extracts a number of test volumes corresponding to the highest peaks of a given periodogram.

Alternatively, the test volumes can be indicated by the user based on visual inspection of a periodogram. If the periodogram is noisy, one may provide a list of (up to 350) properly distributed volumes. On the other hand, the list may contain a single volume if, after getting an indexing solution, one decides to check whether there are any twin-related solutions; the latter correspond to the same volume as the initial solution, so the check is done by running *Ind_X* for this particular test volume. The test volumes do not need to be accurate as the initial set of test volumes is extended by volumes in the

vicinity of those in the initial set; this applies to both user-provided and automatically determined volumes.

For each test volume, the program selects a subset of reciprocal lattice vectors supporting it. Roughly, a vector supports a test volume if it is comprised in numerous triplets spanning parallelepipeds with volumes close to integer multiples of the test volume. The program estimates the quality of support by an individual vector by checking all triplets in which the vector is comprised. The larger the number of parallelepipeds with

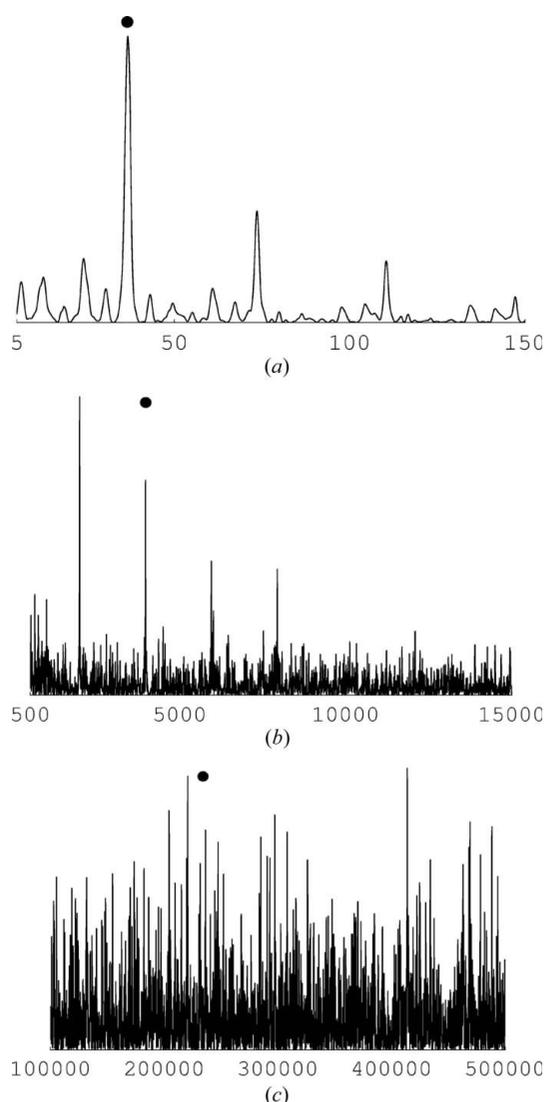


Figure 1 Example Lomb–Scargle periodograms in arbitrary units *versus* volume in direct space (\AA^3). Plots are shown in ranges which one may select on the basis of the type of crystal or the density of reflections. Discs mark volumes of parallelepipeds spanned on primitive bases of best lattices. (a) Periodogram obtained from 16 vectors corresponding to conics in a Kossel diffraction pattern of the martensite phase of Cu–Al–Be alloy (Bouscaud *et al.*, 2014). The smallest primitive cell volume allowing for indexing of the pattern was about $3.7 \times 10^1 \text{\AA}^3$. (b) Periodogram for 30 reflections from a simulated diffraction data set of a crystal with a cell of medium size, $4.0 \times 10^3 \text{\AA}^3$. (c) Periodogram based on 26 reflections from ‘Example 2’ of Duisenberg (1992), representing a small protein with a cell volume of about $2.3 \times 10^5 \text{\AA}^3$.

volumes close to integer multiples of the test volume, the larger the support.¹ The vectors are then ranked, and the best vectors constitute the needed subset. The reasons for using the subset of supporting vectors are twofold: first, the subsequent confinement to this subset eliminates potential spurious reflections, and second, it speeds up the program.

The supporting vectors are used to construct tentative solutions. Briefly, the tentative bases of the reciprocal lattice are bases of low-index superlattices of the lattices based on triplets of the supporting vectors. The scheme is illustrated two dimensionally in Fig. 2. A triplet of legitimate vectors [like the vectors in Fig. 2(a)] determines a certain lattice (Fig. 2b). Trivial but crucial for what follows is the observation that this lattice is a sublattice of the actual reciprocal lattice of the crystal [Fig. 2(b) shows a sublattice of the lattices shown in Fig. 2(c)]. Thus the indexing problem is reduced to checking all bases of small-index superlattices of the lattice based on the triplet. [This corresponds to checking the bases shown in Fig. 2(d).] For details on generation of superlattices in the three-dimensional space see, for example, Santoro & Mighell (1973) and Billiet & Coz (1980). Since the number of superlattices grows fast with the index,² the program checks the bases of superlattices up to index 3 in the quickest case, up to 7 by default and up to 16 in the most extensive calculations. The construction of the solutions also includes two standard steps: fitting integer combinations of basis vectors to the supporting vectors (Kim, 1989) and Buerger reduction of the basis (Buerger, 1957, 1960). Having a tentative basis, indexing of all experimental reflections is attempted. The result of the attempt is used to quantify the quality of the basis. The bases of highest quality are saved. The number of saved bases is controlled by the user (but it cannot exceed 128). These steps are repeated for all tentative bases constructed from a given triplet of supporting vectors, for all triplets of vectors supporting a given test volume and for all test volumes.

As for the important parameter representing the quality of a basis, a number of different quantities have been tested to find a balance between effectiveness, simplicity and flexibility. The implemented approach is based on a user-controlled limit on the allowed deviation of Miller indices from integers. With the number of reflections within this limit denoted by N_h and the number of reflections within half of the limit denoted by N_H , the quality of the basis is proportional to $w_H N_H + w_h N_h$, where w_H and w_h are user-controlled weights.

Ind_X can only process data sets containing a relatively small number of reflections N because the number of reflection triplets grows with N as N^3 , and this has an impact on the execution time. Typically, N is expected to be about 20–50. With a small number of reflections and suitably chosen *Ind_X* parameters (see below), the execution time can be a fraction of a second. However, one must be aware that speed comes at a price of quality. For higher reliability of results, one

can perform an extended search, and this can be a lengthy process.

3. Software and hardware environment

Ind_X is written in Fortran 90. It can be run from a command prompt in a console window on personal computers under

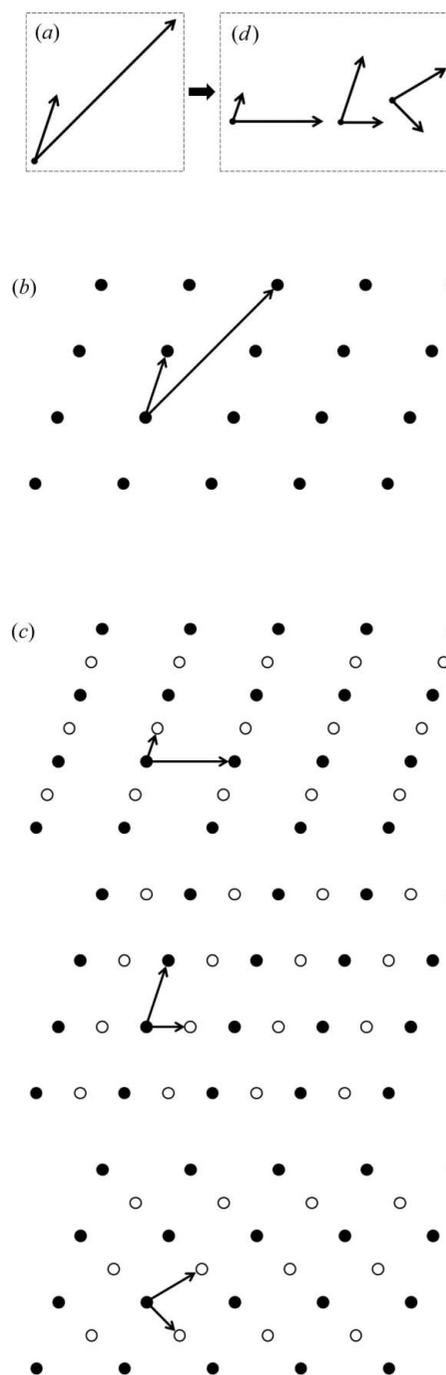


Figure 2 Schematic two-dimensional illustration of the construction of tentative bases from the two ‘experimental’ reciprocal lattice vectors drawn in (a). The lattice based on the two vectors is represented by discs in (b). Its three superlattices (discs + circles) of index 2 are shown in (c). The three bases of the superlattices are used as tentative bases (d).

¹ In other words, if the test volume corresponds to a peak in the periodogram, the support is large if the vector contributed numerous times (*i.e.* as a member of numerous triplets) to the peak.

² For example, for the indices 3, 5, 7, 10 and 16, the number of superlattices is 13, 31, 57, 217 and 651, respectively (*cf.* Santoro & Mighell, 1973).

Microsoft Windows operating systems. The program uses a single input file with keywords followed by appropriate data. The file must contain a set of reflections specified by Cartesian coordinates of reciprocal lattice vectors. There are also a number of optional input parameters, like the above-mentioned limit on the allowed deviation of a Miller index from an integer or the largest allowed absolute value of Miller indices. Besides the number of reflections, three optional parameters have an impact on the execution time. These are (1) limits on the allowed volume of the primitive cell, (2) an upper limit on the number of supporting reflections and (3) a single entity controlling (through a number of secondary parameters) the extent of the search for the solution. In particular, the latter entity determines the density of arguments of the periodogram, the number of automatically detected test volumes and the upper limit on the index of inspected superlattices.

A typical output file contains a list of proposed solutions. The choice of the ultimate solution from the list is left to the user. For each solution, one gets a matrix of basis vectors of the direct lattice.³ Then, there is a table of Miller indices corresponding to particular reflections, the parameters a , b , c , α , β and γ , and the volume of the primitive cell. The program delivers the Buerger-reduced cell, and additional processing is needed to obtain the lattice symmetry. The task can be performed using *LEPAGE* (Spek, 1988) or other procedures of this kind (see *e.g.* Clegg, 1981; Le Page, 1982; Zimmermann & Burzlaff, 1985; Higgins *et al.*, 1990; Macíček & Yordanov, 1992).

4. Availability

A 0.22 MB compressed file with the executable *Ind_X.exe* for Windows can be downloaded from <http://imim.pl/personal/adam.morawiec/>. Program documentation is limited to PDF-formatted instructions. Alternatively, one can download a 0.52 MB package which, besides *Ind_X.exe*, contains a .NET-based graphical user interface written by M. F. Morawiec. The interface facilitates changes of *Ind_X* parameters and analysis of periodograms.

Acknowledgements

The author is grateful to M. F. Morawiec for writing the graphical user interface, and to Professor A. L. Spek of

Utrecht University for permission to include *LEPAGE* in the download package.

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³ This matrix is inverse to the **UB** matrix of Busing & Levy (1967); the product of the saved (**UB**)⁻¹ with an experimental reciprocal lattice vector gives approximate Miller indices of the corresponding reflection.

Supplementary material

(to '*Ind_X*: program for indexing single crystal diffraction patterns' by A. Morawiec)

Tables below show high quality solutions (parts of output files) obtained by running *Ind_X* for data of Duisenberg (1992). In response to a recommendation by an anonymous reviewer, also results for unpublished "examples 6 and 7" are listed. In all cases, the limit on the allowed deviation of Miller indices from integers was the *Ind_X* default of 0.12; reflections within this limit are denoted by **-h** and reflections within half of the limit are denoted by **H-**. The unit of length is Ångström, and angles are in degrees.

Example 1:

Solution nr 2 out of 16.

Direct basis vectors (in rows) = inverse of UB matrix;
transforms RL vectors to Miller indices :

-0.41624538	0.04542523	5.05672819
-2.24425594	-7.88469324	-0.11196100
-11.93485938	1.08178703	-0.99071084

		h	k	l		Real (hkl)				Error
1	H-	2	0	-8		2.01	0.00	-8.03		0.032
2	H-	2	-5	-7		2.00	-5.00	-6.96		0.037
3						1.97	-0.01	-9.20		0.205
4										
5	H-	1	-1	-7		0.99	-1.00	-6.94		0.058
6										
7	H-	1	0	-7		1.00	0.00	-7.03		0.032
8	H-	1	-2	-7		1.00	-2.00	-7.00		0.004
9	-h	2	-3	3		1.93	-3.00	2.93		0.093
10	H-	3	-4	0		3.01	-4.00	0.04		0.039
11	H-	1	-4	1		1.01	-4.00	0.95		0.055
12	H-	1	-4	0		0.99	-4.00	0.04		0.044
13	-h	1	-4	0		1.01	-4.00	-0.07		0.074
14	H-	2	-1	4		2.01	-1.00	4.02		0.026
15						1.93	0.00	4.22		0.232
16	H-	2	-3	-2		2.01	-3.00	-1.98		0.025
17	H-	3	1	6		3.02	1.00	5.99		0.021
18	-h	2	0	8		2.01	0.01	8.07		0.073
19										
20	H-	1	1	6		1.00	1.00	6.00		0.004
21	H-	1	4	-1		0.98	4.01	-0.99		0.026
22						1.97	1.99	2.22		0.226
23	H-	2	1	1		1.99	0.99	0.94		0.061
24	H-	3	2	1		3.00	2.00	0.99		0.011
25						3.04	1.99	-2.16		0.166

18h and 15H vectors out of 25. Quality : 0.684

Primitive cell :

5.074	8.199	12.025
79.26	89.99	89.99

Volume of the cell : 491.47

Example 2:

Solution nr 1 out of 16.

Direct basis vectors (in rows) = inverse of UB matrix;
transforms RL vectors to Miller indices :

22.39827411	23.67373447	19.86433441
-55.72013365	53.74568735	2.85453230
27.36701652	32.99645419	-66.67913680

	h	k	l	Real (hkl)			Error	
1	-h	0	4	7	-0.02	3.92	6.89	0.134
2	H-	3	15	11	3.01	15.01	10.99	0.017
3	H-	4	24	14	4.01	24.03	14.01	0.031
4	-h	1	6	7	0.99	5.94	6.91	0.105
5	H-	6	15	0	6.00	14.95	-0.04	0.059
6	-h	5	22	10	4.99	22.05	10.09	0.100
7	H-	4	27	15	4.01	27.00	14.97	0.037
8	-h	7	26	5	7.00	26.05	5.07	0.090
9	-h	9	27	-6	9.00	26.91	-6.10	0.131
10	-h	6	29	10	6.01	29.11	10.03	0.116
11	-h	5	24	11	4.99	24.03	11.08	0.090
12	-h	1	26	21	0.98	25.90	20.92	0.126
13	-h	6	13	-3	6.01	12.98	-3.08	0.079
14	H-	4	15	8	4.00	15.02	8.03	0.030
15	-h	3	5	-2	3.00	4.98	-2.06	0.066
16	H-	4	7	-3	4.00	6.99	-3.05	0.054
17	H-	4	8	-1	4.00	8.00	-1.02	0.020
18	H-	7	23	3	7.00	22.98	3.03	0.040
19	H-	6	10	-11	5.98	9.96	-11.02	0.051
20	H-	5	13	2	5.00	12.98	1.99	0.021
21	H-	6	20	5	6.00	20.00	5.05	0.049
22	-h	2	26	19	2.00	25.93	18.93	0.101
23	H-	8	28	1	8.01	28.01	1.02	0.023
24	-h	8	30	2	8.00	30.09	2.08	0.118
25	H-	3	13	9	3.00	13.00	9.01	0.008
26	H-	7	16	-5	7.00	15.95	-5.05	0.074

26h and 14H vectors out of 26. Quality : 0.862

Primitive cell :

38.167	77.469	79.271
89.46	88.68	88.43

Volume of the cell : 234225.58

Example 3, solution a:

Solution nr 1 out of 16.

Direct basis vectors (in rows) = inverse of UB matrix;
transforms RL vectors to Miller indices :

```
-0.08757438  2.89242892  -3.33163710
18.02074562  -1.42129210  1.17612284
-3.89689517 -16.76216719 -11.52746836
```

	h	k	l	Real (hkl)			Error
1 H-	1	3	-7	1.00	3.02	-6.99	0.023
2 H-	1	-3	-4	1.00	-2.99	-4.00	0.008
3 H-	0	5	-5	0.00	5.00	-5.00	0.004
4 H-	1	-3	-8	1.00	-3.00	-8.00	0.007
5 H-	0	0	-8	0.00	0.00	-8.00	0.003
6 H-	0	-5	-7	0.00	-5.00	-7.00	0.003
7 H-	0	-5	-3	0.00	-5.00	-3.00	0.005
8 H-	0	0	-12	0.00	0.00	-11.99	0.006
9 H-	-1	4	-6	-1.00	4.02	-6.00	0.016
10 H-	-1	-6	-8	-1.00	-5.99	-8.00	0.012
11 H-	-1	-7	-6	-1.00	-7.01	-6.00	0.012
12 H-	0	0	-12	0.00	-0.01	-12.01	0.016
13 H-	0	5	-13	0.00	5.00	-13.00	0.007
14 H-	1	2	-13	1.00	2.00	-13.00	0.003
15 H-	1	0	-13	1.00	-0.04	-13.01	0.036
16 H-	1	-3	-12	1.00	-3.00	-11.99	0.005
17 H-	1	1	-11	1.00	0.98	-11.01	0.019
18 H-	-1	3	-8	-1.00	3.00	-8.00	0.007
19 H-	-1	4	-10	-1.00	4.01	-9.99	0.014
20 H-	0	10	-10	0.00	10.00	-10.00	0.003
21 H-	1	-7	-9	1.00	-6.98	-9.00	0.023
22 H-	1	3	-11	1.00	3.02	-11.00	0.025
23 H-	1	-3	-8	1.00	-3.00	-8.00	0.003
24 H-	1	2	-9	1.00	2.01	-9.00	0.006
25 H-	1	1	-7	1.00	0.98	-7.00	0.016

25h and 25H vectors out of 25. Quality : 1.000

Primitive cell :

```
4.413  18.115  20.713
99.20  96.11  96.90
```

Volume of the cell : 1609.27

Example 4:

Solution nr 1 out of 16.

Direct basis vectors (in rows) = inverse of UB matrix;
transforms RL vectors to Miller indices :

```
1.20056709  1.71918935 -10.94962184
-0.92071771 -22.25549176 -3.59537022
97.65751543 -5.77590232  9.77179118
```

		h	k	l		Real (hkl)		Error
1	H-	0	-3	-21		0.00 -3.02 -21.06		0.059
2	H-	0	-3	-24		0.00 -3.01 -23.99		0.011
3						0.00 -3.04 -22.14		0.143
4	H-	0	-3	-23		0.00 -3.00 -22.98		0.023
5	H-	0	-5	-16		0.00 -5.00 -15.99		0.009
6	H-	0	-4	-26		0.00 -4.00 -25.95		0.050
7	H-	0	-1	-29		0.00 -1.01 -28.97		0.031
8	-h	0	-1	-31		-0.01 -0.89 -31.03		0.112
9	H-	0	0	-22		0.00 -0.01 -21.97		0.035
10	H-	-1	-4	18		-1.00 -3.99 17.98		0.022
11	H-	-1	-4	17		-1.00 -3.99 16.99		0.014
12	H-	-1	-5	11		-1.00 -4.99 11.00		0.007
13	H-	-1	-5	10		-1.00 -5.01 10.02		0.025
14	H-	-2	1	-19		-2.00 1.00 -18.97		0.025
15	H-	-2	0	-21		-2.00 0.00 -20.99		0.010
16	H-	-2	1	-23		-2.00 1.00 -22.96		0.037
17	H-	-2	0	-23		-2.00 0.00 -22.98		0.020
18	H-	-1	-3	27		-1.00 -2.99 27.00		0.015
19	H-	2	-2	19		2.00 -2.00 19.00		0.004
20	H-	2	-3	16		2.00 -3.00 16.01		0.011
21	H-	2	-4	11		2.00 -4.00 11.05		0.047
22	H-	2	-3	17		2.00 -3.00 17.01		0.013
23	H-	2	-4	9		2.00 -4.00 9.01		0.010
24	H-	2	-5	0		2.00 -5.01 0.01		0.014
25	H-	2	-4	15		2.00 -3.99 15.00		0.007

24h and 23H vectors out of 25. Quality : 0.948

Primitive cell :

```
11.149  22.563  98.315
89.91   89.98   90.00
```

Volume of the cell : 24730.50

The diffraction data of Example 3 were known to originate from an incommensurate structure. According to (Duisenberg 1992), a "supercell" fitting all reflections has the "volume $3942.00 = 49 \times 80.44$ ". The quite accurate *Ind_X* solution (*a*) shown above gives a smaller volume ($1609.27 \approx 20 \times 80.46$). If 100 is the upper limit on the cell volume, *Ind_X* gives the solution (*b*) with the volume of 80.43; see below. The relationship between the two solutions is $\mathbf{M}_a \approx \mathbf{T} \times \mathbf{M}_b$, where \mathbf{M}_a and \mathbf{M}_b are the matrices of direct lattice vectors (in rows) for each of the solutions, and

$$\mathbf{T} = \begin{bmatrix} 1 & -1 & 0 \\ -3 & -2 & 0 \\ 0 & 1 & 4 \end{bmatrix} ;$$

Miller indices of the solution (*a*) can be obtained by multiplying \mathbf{T} and the column of indices of the solution (*b*). The smallest-volume solution accepting all reflections with the default *Ind_X* parameters is listed below as (*c*).

Example 3, solution *b*:

Solution nr 1 out of 16.

Direct basis vectors (in rows) = inverse of UB matrix;
transforms RL vectors to Miller indices :

-3.63857749	1.44382309	-1.57287407
-3.55149346	-1.44846389	1.75859322
-0.08637420	-3.83006631	-3.31877056

		h	k	l		Real (hkl)		Error
1								
2	H-	1	0	-1		1.00 0.00 -1.00		0.001
3	H-	-1	-1	-1		-1.00 -1.00 -1.00		0.001
4	H-	1	0	-2		1.00 0.00 -2.00		0.001
5	H-	0	0	-2		0.00 0.00 -2.00		0.001
6	H-	1	1	-2		1.00 1.00 -2.00		0.001
7	H-	1	1	-1		1.00 1.00 -1.00		0.002
8	H-	0	0	-3		0.00 0.00 -3.00		0.002
9								
10								
11	H-	1	2	-2		1.00 2.00 -2.00		0.001
12	H-	0	0	-3		0.00 0.00 -3.00		0.003
13	H-	-1	-1	-3		-1.00 -1.00 -3.00		0.001
14	H-	0	-1	-3		0.00 -1.00 -3.00		0.000
15								
16	H-	1	0	-3		1.00 0.00 -3.00		0.001
17								
18	H-	-1	0	-2		-1.00 0.00 -2.00		0.001
19								
20	H-	-2	-2	-2		-2.00 -2.00 -2.00		0.001
21								
22								
23	H-	1	0	-2		1.00 0.00 -2.00		0.001
24	H-	0	-1	-2		0.00 -1.00 -2.00		0.000
25								

16h and 16H vectors out of 25. Quality : 0.640

Primitive cell :

4.219	4.219	5.069
89.95	89.99	63.06

Volume of the cell : 80.43

Example 3, solution c:

Solution nr 9 out of 16.

Direct basis vectors (in rows) = inverse of UB matrix;
transforms RL vectors to Miller indices :

0.08764924	-2.89243836	3.33158017
-7.09574696	3.84139431	3.45898860
10.99137244	12.92062820	8.06968392

		h	k	l		Real (hkl)				Error
1	H-	-1	0	7		-1.00	0.05	6.94		0.076
2	H-	-1	2	2		-1.00	2.00	2.00		0.007
3	H-	0	-1	6		0.00	-1.00	6.00		0.003
4	H-	-1	3	5		-1.00	3.00	4.99		0.005
5	H-	0	2	6		0.00	1.99	6.01		0.010
6	H-	0	4	3		0.00	3.99	3.01		0.016
7	H-	0	3	0		0.00	2.99	0.01		0.010
8	H-	0	3	9		0.00	2.99	9.01		0.015
9	H-	1	0	6		1.00	0.02	5.97		0.037
10	H-	1	5	3		1.00	5.02	2.98		0.025
11	H-	1	5	1		1.00	4.98	1.02		0.032
12	H-	0	3	9		0.00	2.99	9.02		0.019
13	H-	0	1	12		0.00	0.99	12.01		0.013
14	H-	-1	2	11		-1.00	2.00	11.00		0.003
15	-h	-1	3	10		-1.00	2.92	10.09		0.121
16	H-	-1	4	8		-1.00	4.00	8.00		0.003
17	H-	-1	2	9		-1.00	1.96	9.04		0.057
18	H-	1	1	7		1.00	0.98	7.02		0.028
19	H-	1	1	9		1.00	1.02	8.97		0.036
20	H-	0	-2	12		0.00	-2.00	12.00		0.003
21	H-	-1	5	4		-1.00	5.04	3.96		0.058
22	H-	-1	1	10		-1.00	1.04	9.96		0.062
23	H-	-1	3	5		-1.00	3.00	5.00		0.004
24	H-	-1	1	8		-1.00	1.00	7.99		0.008
25	H-	-1	1	6		-1.00	0.97	6.04		0.049

25h and 24H vectors out of 25. Quality : 0.988

Primitive cell :

4.413	8.779	18.785
90.15	96.60	90.31

Volume of the cell : 722.90

Examples 6 and 7 are described at <http://www.crystal.chem.uu.nl/distr/dirax/examples.html> as "inaccurate data" and "not very accurate data", respectively. *DirAx* solutions to these examples are available at the same web page. The first solution given by *Ind_X* to example 6 is similar to that given by *DirAx*; in both cases, one reflection is not indexed. Example 7 is fully indexable (solution no 1). However, solutions 2 and 3 of *Ind_X* indicate that the data originate from a twinned crystal. Only solutions similar to 1 and 2 are listed at <http://www.crystal.chem.uu.nl/distr/dirax/examples.html> and, in consequence, the possibility of twinning is overlooked.

Example 6:

Solution nr 1 out of 16.

Direct basis vectors (in rows) = inverse of UB matrix;
transforms RL vectors to Miller indices :

-0.22772791	0.41128973	3.87525272
-0.28186242	-5.94601285	1.00932446
16.69620088	-2.75388915	1.71750269

		h	k	l		Real (hkl)				Error
1	H-	2	0	10		2.00	0.00	10.00		0.007
2	H-	2	2	9		2.00	2.00	9.01		0.011
3	H-	1	-1	13		1.00	-1.01	13.00		0.007
4	H-	0	2	6		-0.03	2.00	5.98		0.033
5	H-	0	3	4		-0.03	3.00	3.96		0.049
6	H-	0	1	9		-0.02	1.00	9.01		0.022
7	H-	1	1	5		0.99	1.00	4.98		0.021
8	H-	1	0	5		0.99	0.01	5.00		0.016
9	H-	2	-2	-2		2.02	-2.00	-2.02		0.028
10										
11	H-	1	-2	2		0.99	-2.00	2.01		0.012
12	H-	0	-2	-6		-0.02	-2.00	-6.00		0.022
13	H-	0	-1	-3		-0.02	-1.01	-2.99		0.026
14	H-	1	-1	-1		1.01	-1.00	-1.01		0.013
15	H-	0	-3	5		-0.01	-3.00	5.02		0.022
16	H-	0	-3	-4		-0.02	-3.00	-3.99		0.020
17	H-	2	1	-7		2.00	1.00	-7.00		0.005
18	H-	1	4	-1		0.98	4.00	-0.99		0.019
19	H-	2	3	-2		2.00	3.00	-1.99		0.013
20	H-	1	5	4		0.98	5.00	4.05		0.052
21	-h	1	4	-4		0.99	4.01	-4.12		0.120
22	H-	1	0	-8		0.99	0.00	-8.00		0.012
23	-h	1	2	-5		0.98	2.01	-5.12		0.117
24	H-	1	4	-7		0.98	4.02	-6.97		0.041
25	H-	0	-1	-6		-0.03	-1.01	-6.02		0.035

24h and 22H vectors out of 25. Quality : 0.936

Primitive cell :

3.904	6.038	17.009
82.50	88.51	86.28

Volume of the cell : 396.55

Example 7:

Solution nr 1 out of 16.

Direct basis vectors (in rows) = inverse of UB matrix;
transforms RL vectors to Miller indices :

1.84344954	3.25703922	8.82866263
22.22374211	1.60108683	-5.22574341
16.66747588	-35.84753215	9.80100707

		h	k	l		Real (hkl)		Error
1	H-	4	10	24		4.01 9.99 23.98		0.024
2	H-	6	12	16		6.00 12.00 16.02		0.018
3	H-	4	12	22		4.01 11.99 21.97		0.034
4	H-	4	8	20		4.00 8.00 19.99		0.015
5	H-	6	7	1		6.00 7.02 1.04		0.049
6	H-	7	10	6		6.99 10.02 6.00		0.021
7	H-	5	15	15		5.00 14.99 14.98		0.017
8	H-	5	15	16		4.99 14.99 15.96		0.041
9	H-	4	-14	-16		4.00 -14.00 -16.03		0.033
10	H-	5	-11	-17		5.00 -11.00 -17.01		0.014
11	H-	5	-13	-21		5.00 -13.00 -21.02		0.023
12	H-	7	4	-14		7.00 4.00 -14.00		0.005
13	H-	6	2	-12		6.01 2.00 -11.97		0.029
14	H-	4	-13	-9		4.00 -13.00 -9.06		0.055
15	H-	5	-9	-14		5.00 -9.00 -13.96		0.041
16	H-	7	-4	-18		7.00 -4.01 -17.96		0.044
17	H-	2	-4	30		2.00 -4.00 30.02		0.020
18	H-	2	-5	29		2.00 -5.00 29.03		0.027
19	H-	2	-16	8		1.99 -16.01 8.00		0.010
20	H-	2	-16	10		1.99 -16.00 9.96		0.038
21	H-	1	-10	20		1.00 -9.99 19.99		0.013
22	H-	1	-12	16		1.00 -11.99 16.03		0.034
23	H-	2	-17	-5		2.01 -17.01 -5.04		0.039
24	H-	1	-13	8		1.00 -13.00 8.06		0.058
25	H-	1	-12	10		1.00 -11.99 10.01		0.012

25h and 25H vectors out of 25. Quality : 1.000

Primitive cell :

9.589	22.886	40.730
73.69	89.93	89.99

Volume of the cell : 8578.63

Example 7:

Solution nr 2 out of 16.

Direct basis vectors (in rows) = inverse of UB matrix;
transforms RL vectors to Miller indices :

```
-1.84244579  -3.25710729  -8.82838295
-2.78455888  -18.72373301  7.51579641
22.22271405   1.60042838  -5.22626771
```

		h	k	l		Real (hkl)				Error
1	H-	-4	7	10		-4.01	6.99	9.99		0.015
2	H-	-6	2	12		-5.99	2.01	12.00		0.010
3	H-	-4	5	12		-4.01	4.98	11.99		0.019
4	H-	-4	6	8		-4.00	5.99	8.00		0.012
5	H-	-6	-3	7		-6.00	-2.99	7.02		0.022
6	H-	-7	-2	10		-6.99	-2.01	10.02		0.024
7	H-	-5	0	15		-5.00	-0.01	14.99		0.011
8										
9	H-	-4	-1	-14		-4.00	-1.01	-13.99		0.015
10	H-	-5	-3	-11		-5.00	-3.00	-11.00		0.003
11	H-	-5	-4	-13		-5.00	-4.00	-13.00		0.006
12	H-	-7	-9	4		-7.00	-9.00	4.00		0.003
13	H-	-6	-7	2		-6.01	-6.99	2.00		0.014
14	H-	-4	2	-13		-4.00	1.98	-13.00		0.023
15										
16	H-	-7	-7	-4		-7.00	-6.97	-4.01		0.030
17	H-	-2	17	-4		-2.00	17.01	-4.00		0.013
18	H-	-2	17	-5		-2.00	17.02	-5.00		0.018
19	H-	-2	12	-16		-2.00	12.01	-16.01		0.012
20	H-	-2	13	-16		-1.99	12.99	-16.00		0.015
21	H-	-1	15	-10		-1.00	14.99	-9.99		0.012
22	H-	-1	14	-12		-1.00	14.01	-11.99		0.019
23	H-	-2	6	-17		-2.01	5.99	-17.01		0.015
24										
25	H-	-1	11	-12		-1.00	11.00	-11.99		0.009

22h and 22H vectors out of 25. Quality : 0.880

Primitive cell :

```
9.589  20.367  22.885
106.34  90.00  90.07
```

Volume of the cell : 4288.81

Example 7:

Solution nr 3 out of 16.

Direct basis vectors (in rows) = inverse of UB matrix;
transforms RL vectors to Miller indices :

```
1.84235217  3.25747591  8.82920015
8.34452110 -17.93160379  4.89513606
22.22639387  1.60217130 -5.22661136
```

		h	k	l		Real (hkl)				Error
1	H-	4	12	10		4.01	12.00	9.99		0.012
2	H-	6	8	12		6.00	8.01	12.00		0.014
3	H-	4	11	12		4.01	10.99	11.99		0.014
4	H-	4	10	8		4.00	10.00	8.00		0.006
5										
6	H-	7	3	10		6.99	3.00	10.02		0.022
7										
8	H-	5	8	15		4.99	7.99	15.00		0.016
9	H-	4	-8	-14		4.00	-8.03	-14.00		0.028
10										
11										
12	H-	7	-7	4		7.00	-7.00	4.00		0.003
13	H-	6	-6	2		6.01	-5.99	2.00		0.012
14										
15	H-	5	-7	-9		5.00	-6.99	-9.00		0.012
16	H-	7	-9	-4		7.00	-8.99	-4.01		0.016
17	H-	2	15	-4		2.00	15.01	-4.01		0.014
18										
19	H-	2	4	-16		2.00	3.99	-16.01		0.013
20	H-	2	5	-16		1.99	4.98	-16.00		0.026
21	H-	1	10	-10		1.00	9.99	-9.99		0.010
22	H-	1	8	-12		1.00	8.01	-11.99		0.018
23										
24	H-	1	4	-13		1.00	4.02	-13.00		0.025
25	H-	1	5	-12		1.00	5.00	-12.00		0.005

18h and 18H vectors out of 25. Quality : 0.720

Primitive cell :

```
9.590  20.375  22.889
73.67  89.99  89.95
```

Volume of the cell : 4291.67

Output of LePage.exe for solution no. 3 of example 7 (cf. solution no 2):

	LATO	LATT	A	B	C	ALFA	BET	GAM	VOL
INPUT CELL		P	9.590	20.375	22.889	73.67	89.99	89.95	4292.00
REDUC CELL		P	9.590	20.375	22.889	73.67	89.99	89.95	4292.00
CONV. CELL	M	P	20.375	9.590	22.889	90.01	106.33	89.95	4292.00