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Crystal structure resolution of organic compound from powder diffraction using Monte Carlo approach: FOX and EXPO programs

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Abstract: *The crystal structure of cimetidine has been determined using ab-initio method from X-ray powder diffraction data by Cernik and Vincent Favre-Nicolin with' parallel tempering' Monte-Carlo algorithm.We have re-employ this work by using two programs that work in direct space with different Monte Carlo algorithms: Respectively EXPO program works with 'simulated annealing' (SA) and FOX program works with 'parallel tempering'(PT). In the first, the obtained spectra were decomposed and indexed to obtain the unit cell with DICVOL program. The research of the best space group is undertaken in CHEKCELL program. In the following step, the geometry of a molecule described using AVOGADRO program to obtained a Fenske -Hall z-matrix. After we use the two softwares EXPO and FOX to resolve the crystal structure of cimetidine. We compare the results obtained by the two programs.*

Keywords: *Ab-initio, DICVOL program, CHEKCELL program, EXPO program, FOX program , Monte-Carlo algorithm, Simulated annealing algorithm , parallel tempering algorithm .*

I. Introduction

Determining a crystal structure is generally to determine for a crystal of unknown structure the parameters of cell, a space group and the positions of the atoms in the unit cell usually relies on powder x-ray diffraction (XRD) or neutron diffraction Most often, the crystal structures were determined from single crystal, but this is also possible using powders. The structure determination from powder diffraction (SDPD) (1) is more difficult than structure determination on single crystals, because of the projection of the three –dimensional diffraction pattern on a single dimension. Two methods of SDPD can be used:

A -Reciprocal Space method: they imply, the direct methods, Patterson synthesis, charge flipping, they use the extraction of structure factors amplitudes from the powder pattern.

B -Direct space method: they use global optimization algorithm such as Monte Carlo, simulated annealing, or genetic algorithms, the different algorithms are used to locate the global minimum to find the best structure solution.

Then several computer programs using direct space approach have appeared: ESPOIR(2), ZEFSAII (3), FOCUS(4) , FOX(5),POWDER SOLVE(6) , TOPAS (7), EXPO(8) ,..

The main goal of this work consists in the research about the capabilities of two programs (FOX and EXPO) to solve organic structure from powder diffraction using Monte Carlo approach. At this respect, we consider here organic compound: cimetidine, is well known as a medicin for the treatment of gastric ulcers. The crystal structure of this organic molecule has been determined by using FOX program ; we have re–employ this work by using the two programs that work in direct space with different Monte –Carlo algorithms: the first EXPO works with SA Monte Carlo algorithm and the second FOX works with PT Monte –Carlo.

II. The Monte Carlo process: algorithms and cost function (CF)

The Monte Carlo algorithm applied in SDPD is based on the variation of free parameters in the structure, on starting from a random configuration, the comparison between configuration are based on a CF, which is characteristic for the best structure and is defined using either a knowledge about the compound (energy model , bond distance , ..) , and / or from experimental data. Smaller values of CF represent better configurations. Thus, in the Monte Carlo process, which ensures the sampling of the parameter space, the CF of the new generated structure is kept according to Metropolis algorithm if the CF is smaller than the preceding cost and with probability if the new configuration has a higher cost.

So that to converging the Monte Carlo process, this can be make with simulated annealing, in which the temperature is slowly decreased after each trial configuration. Thus the drawbak of simulated annealing is that if the temperature decreases prematurely, the algorithm can be trapped in a local minimum. To overcome this problem, another closely related algorithm available is parallel tempering, a small number of parallel optimizations are made, each with a different temperature.

III. Modelization of the crystal structure: case of organic molecule

This is the most crucial step: any direct space search requires the definition of the degree of freedom (DOF) which describes the structure. The system of N atoms defined 3N-6 internal degres of freedom; they will 3N-6 deformation parameters, the remaining 6 parameters defining the position of the center of gravity and orientation of the system in space.

The crystal structure can be described as any combination of scatteres objects this can be independent atoms, molecules or polyhedral. The molecule is naturally described using internal coordinates in general using a z-matrix approach, in which the atoms are listed in a matrix, with the position of each atom determined from the bond distance, a bond angle and dihedral angle with respect to their preceding atoms in the matrix.

IV. Application

We will consider a typical flow chart, in Fig1, representing an application of Monte Carlo process to solve the structure solution from powder data

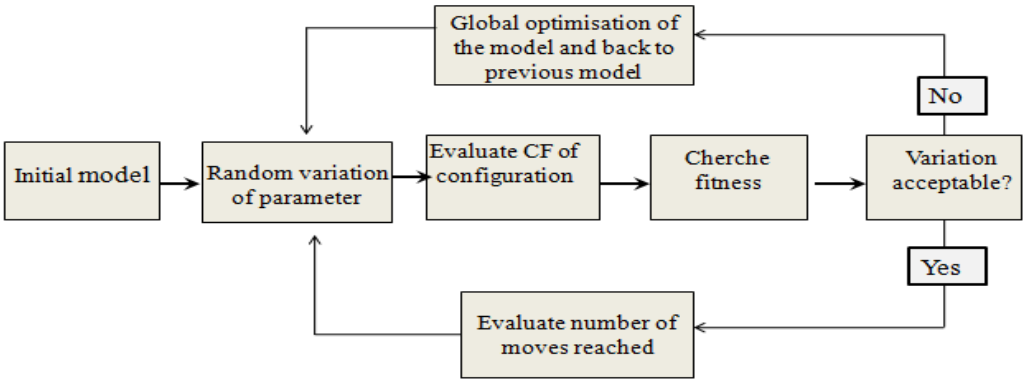


Fig.1. Representation of a direct space method as applied to SDPD.

V. Results and Discussion

The ab initio structural determination was carried out by the following steps:

Indexation: to solve crystal structure of cimetidine compound from powder diffraction, we used x-ray data based on website of FOX program, in which we determined, the unit cell parameters by indexing the powder patterns with the use of DICVOL(9) program, then by examining the data with CHEKCELL(10) program the space group was found .

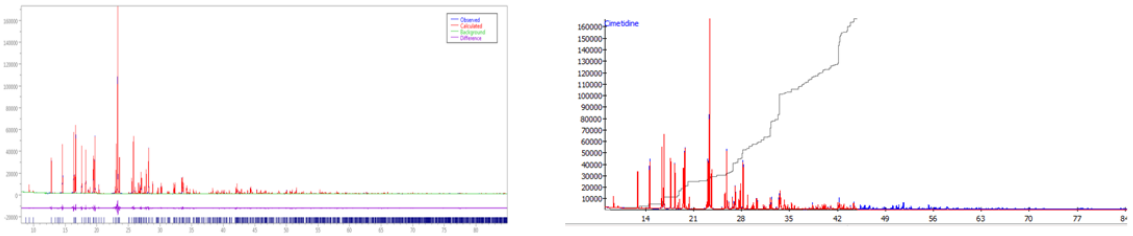
Molecular modelling: when dealing with organic molecules, we used the z-matrix representation to solve crystal structure, in the context of this approach, we have used AVOGADRO program from the obtained the Fenske-Hall z- matrix, which is our main in put in FOX and EXPO programs .

Monte Carlo methods: the structure solution is achieved by Monte Carlo method with two software FOX and EXPO, in which to evaluate the best structure model, we show the results of agreement between the simulated and experimental x-ray diffraction patterns. (table 1 outlines the results of crystallographics parameters) .

Table 1: Crystallographic, parameters of cimetidine and details of x-ray structure determination.

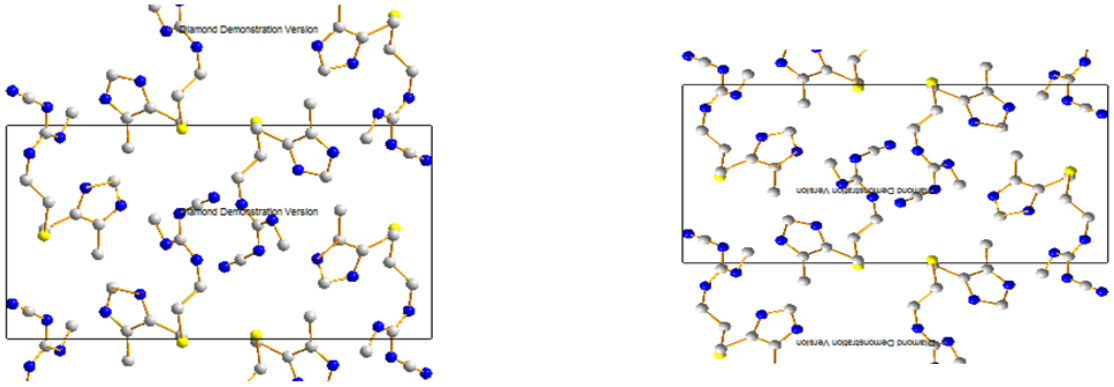
Chemical composition	$C_{10}N_6H_{16}S$
Space group	$P2_1/a$
a. A°	10.3942
b. A°	18.8190
c. A°	6.8250
β. (°)	106.437
V (unit cell A^3)	1280
M(20)	114.00
F(20)	359.00
Z	4
Radiation	CuKα
Maximum Resolution	(sin Θ/λ) = 0.2500 max
Radiation	X-Ray
Spectrum	Monochromatic
λ .A°	1,54056
Scan range, 2Θ (°)	8 -84
Number of real space parameter DOF	14
R_{wp} % of solution with FOX	11%
R_{wp} % of solution with EXPO	14%

The correct solution was found with the FOX program (after 1.5 million trial configuration) and using EXPO program (million trial configuration) , in which we obtained weighted residuals R_{wp} of 0.11 and 0.14 , respectively . figs (a and b).



a) b)

Figs 2: The difference between the simulated and refined x-ray diffraction patterns, to obtained solution with EXPO (fig.2a) and with FOX (fig.2b).



a) b)

Figs 3: Representation of the crystal structure of cimetidine **,** location of the molecule within the unit cell in projection along (001) (view along c.ascis) with EXPO (Fig .3a) and with FOX (fig.3b).

The results obtained with the two software FOX and EXPO show a statistically significant difference between simulated and calculated x-ray powder diffraction patterns .This conclusion is confirmed by final crystal structure of cimetidine in which the bond lengths and bond angles must be chemically correct . Tables 2 and 3 collect the atomic positions of the asymmetric unit for cimetidine (hydrogen atoms excluded).

Table.2.Atomic coordinates of cimetidine with EXPO program.

Atom	X	y	Z	occ	Multiplicit and Wyckoff letter
C1	0.433	0.345	0.663	100%	4e
N2	0.555	0.371	0.607	100%	4e
C3	0.535	0.408	0.430	100%	4e
N4	0.411	0.406	0.308	100%	4e
C5	0.375	0.451	0.135	100%	4e
N6	0.341	0.485	- 0.011	100%	4e
N7	0.640	0.450	0.380	100%	4e
C8	0.761	0.459	0.550	100%	4e
C9	0.867	0.394	0.506	100%	4e
S10	1.014	0.413	0.716	100%	4e
C11	0.973	0.407	0.978	100%	4e
C12	0.913	0.339	0.994	100%	4e
N13	0.797	0.316	0.870	100%	4e
C14	0.767	0.252	0.928	100%	4e
N15	0.867	0.233	1.106	100%	4e
C16	0.966	0.281	1.138	100%	4e
C17	1.099	0.282	1.309	100%	4e

The following results profess the atomic positions of the asymmetric unit for molecules obtained with FOX (table 3) and EXPO (table 2) programs , and show that all atoms in general Wyckoff positions .

Table.3. Atomic coordinates of cimetidine with FOX program.

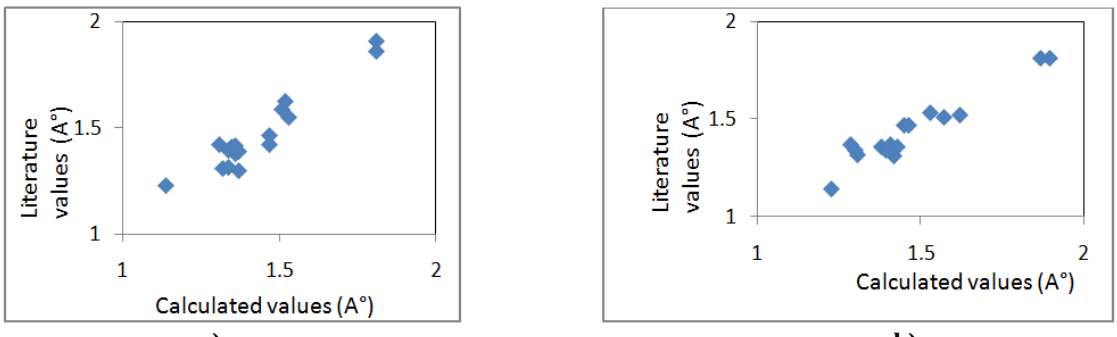
Atom	X	y	Z	occ	Multiplicity and Wyckoff letter
C1	0.561	0.657	0.333	100%	4e
N2	0.443	0.624	0.384	100%	4e
C3	0.461	0.593	0.569	100%	4e
N4	0.584	0.595	0.689	100%	4e
C5	0.622	0.549	0.863	100%	4e
N6	0.661	0.513	1.006	100%	4e
N7	0.358	0.551.	0.623	100%	4e
C8	0.238	0.540	0.454	100%	4e
C9	0.133	0.605	0.495	100%	4e
S10	-0.014	0.585	0.280	100%	4e
C11	0.027	0.593	0.020	100%	4e
C12	0.084	0.660	0.005	100%	4e
N13	0.200	0.683	0.134	100%	4e
C14	0.228	0.748	0.076	100%	4e
N15	0.133	0.765	-0.103	100%	4e
C16	0.033	0.718	-0.140	100%	4e
C17	-0.100	0.717	-0.312	100%	4e

To test the capabilities of the two programs of finding the absolutely best set of structural parameters in order to find global minimum in the parameters space , we measures the relationship between the values of bond length calculation with the two programs and literature values of bond length for cimetidine.

Table .4. Calculated values of bond obtained with the two programs FOX, EXPO and literature values (11).

Bond with EXPO program		**Calculated values(A°)**	**Bond with FOX program**		**Calculated values (A°)**	**Literature values (A°)**
C1	N2	1,50	C1	N2	1,49	1,47
N2	C3	1,35	N2	C3	1,35	1,37
C3	N4	1,32	C3	N4	1,31	1,32
N4	C5	1,41	N4	C5	1,43	1,36
C5	N6	1,15	C5	N6	1,16	1,14
C3	N7	1,47	C3	N7	1,46	1,37
N7	C8	1,46	N7	C8	1,45	1,47
C8	C9	1,72	C8	C9	1,71	1,72
C9	S10	1,80	C9	S10	1,83	1,81
S10	C11	1,95	S10	C11	1,94	1,81
C11	C12	1,44	C11	C12	1,42	1,51
C12	N13	1,33	C12	N13	1,35	1,34
N13	C14	1,34	N13	C14	1,34	1,31
C14	N15	1,39	C14	N15	1,38	1,35
N15	C16	1,34	N15	C16	1,33	1,34
C16	C17	1,53	C16	C17	1,55	1,52
C12	C16	1,45	C12	C16	1,46	1,36

The following plots of data a show specific correlation to illustrate different patterns in strength of the relationships between variables.



a) **b)**

Figs 4. A graphs reveals a relationship between calculated values of bond by two programs EXPO (Fig.4a); FOX (Fig.4b) and literature values.

In these results, the correlation between calculated values of bond length with the two programs and literature values of bond of cimetidine indicates that there is strong positive relationship between the variables, calculation and literature values .

Table . 5 .The value of angles between bonds in cimetidine by EXPO program

Angle			Bond Angles	Torsion				Bond torsion
C1	N2	C3	117.41	C1	N2	C3	N4	- 11.88
N2	C3	N4	115.55	C1	N2	C3	N7	165.27
N2	C3	N7	122.86	N2	C3	N4	C5	170.81
N4	C3	N7	121.53	N7	C3	N4	C5	- 6.38
C3	N4	C5	119.67	N2	C3	N7	C8	-10.08
C3	N7	C8	113.88	N4	C3	N7	C8	166.90
N4	C5	N6	176.60	C3	N4	C5	N6	147.04
N7	C8	C9	103.33	C3	N7	C8	C9	98.05
C8	C9	S10	99.13	N7	C8	C9	S10	177.01
C9	S10	C11	111.21	C8	C9	S10	C11	58.16
S10	C11	C12	109.58	C9	S10	C11	C12	53.15
C11	C12	N13	124.97	S10	C11	C12	N13	-62.07
C11	C12	C16	128.03	S10	C11	C12	C16	115.48
N13	C12	C16	106.96	C11	C12	N13	C14	-178.21
C12	N13	C14	110.27	C16	C12	N13	C14	3.80
C12	C16	N15	105.15	C11	C12	C16	N15	173.22
C12	C16	C17	126.36	C11	C12	C16	C17	1.75
N13	C14	N15	107.61	N13	C12	C16	N15	-8.88
C14	N15	C16	108.95	N13	C12	C16	C17	179.65
N15	C16	C17	127.87	C12	N13	C14	N15	2.57

Table 6. The value of angles between bonds in cimetidine by FOX program

Angle			Bond Angles	Torsion				Bond torsion
C1	N2	C3	119.24	C1	N2	C3	N4	- 1.58
N2	C3	N4	115.49	C1	N2	C3	N7	-171.64
N2	C3	N7	123.18	N2	C3	N4	C5	-163.74
N4	C3	N7	120.57	N7	C3	N4	C5	6.60
C3	N4	C5	119.86	N2	C3	N7	C8	5.10
C3	N7	C8	114.09	N4	C3	N7	C8	-164.47
N4	C5	N6	175.51	C3	N4	C5	N6	162.80
N7	C8	C9	101.94	C3	N7	C8	C9	-97.36
C8	C9	S10	98.63	N7	C8	C9	S10	-178.94
C9	S10	C11	111.10	C8	C9	S10	C11	-60.07
S10	C11	C12	110.00	C9	S10	C11	C12	-53.50
C11	C12	N13	123.78	S10	C11	C12	N13	61.39
C11	C12	C16	129.10	S10	C11	C12	C16	-116.97
N13	C12	C16	107.11	C11	C12	N13	C14	178.34
C12	N13	C14	109.16	C16	C12	N13	C14	-2.99
C12	C16	N15	104.48	C11	C12	C16	N15	-172.46
C12	C16	C17	126.18	C11	C12	C16	C17	1.41
N13	C14	N15	108.23	N13	C12	C16	N15	8.96
C14	N15	C16	109.74	N13	C12	C16	C17	-177.16
N15	C16	C17	129.00	C12	N13	C14	N15	-4.02

V. Conclusion

Powder diffraction data of cimetidine, have been used for solving crystal structure of cimetidine by Monte Carlo method. The structural model was handled by a 'simulated Annealing' Monte –Carlo algorithm implemented in EXPO , and by (PT) Monte Carlo algorithm implemented in FOX , with the aid of the Fenske – Hall z-matrix representation. This work shows that the organic crystal structure can be afforded by means of powder diffraction with the two programs FOX and EXPO.

References

[1] Akito Sa Saki , Akihir himeda , Hisashi Konaka and Norihiro Muroyana , Ab initio crystal structure analysis Based on powder diffraction data using pDxL.
[2] Espoir , Le Bail ,2001,www.cristal.org
[3] Falcioni and Deem,199,www.mwdeem.rice.edu/zefsaII
[4] Grosse –Kunstleve et al,1997,www.crystal.mat.ethz.ch.
[5] FOX. Favre –Nicolin and R.Cerny : fox program for ab initio structure solution from powder diffraction data .
[6] Engel et al,1999,www.accelrys.com
[7] Coelho,2000,pws.prserv.net/Alan.Coelho
[8] EXPO , Instituté of crystallography Bari
[9] Dicvold by D.louer .
[10] CHECHCELL Program , Ed 2004 , Jean Laugier et Bernard Bochu.
[11] Pulver _SA und GA , pulverdiffraktometrie, Kristallchemie und kristallstrukturdatenbanken .