# FullProf School

## Simulated Annealing on powder and single crystal data for determining magnetic structures


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# Outline

1: Le Bail fits for extracting integrated intensities

2: Solving (magnetic) structures in direct space

3: What is Simulated Annealing?

4: How to use Simulated Annealing in FullProf.

A very simple example $KTB_3F_{12}$.

# Le Bail fits for extracting integrated intensities

$$y_{ci} = \sum_{\{\mathbf{h}\}} I_{\mathbf{h}} \Omega(T_i - T_{\mathbf{h}}) + b_i$$

**When the resolution function of the diffractometer and the cell parameters are known approximately, one can try to get the value of the integrated intensities from the powder diffraction pattern.**

**Problem: If one uses least squares to refine the values of $I_{\mathbf{h}}$ (Pawley) one has to introduce strong constraints because the problem is not well defined, sometimes negative intensities can be obtained due to overlap.**

# Le Bail fits for extracting integrated intensities

$$y_{ci} = \sum_{\{\mathbf{h}\}} I_{\mathbf{h}} \Omega(T_i - T_{\mathbf{h}}) + b_i$$

$$'I_{\mathbf{h}}(obs)' = I_{\mathbf{h}} \sum_i \left\{ \frac{\Omega(T_i - T_{\mathbf{h}})(y_{obs,i} - B_i)}{(y_{calc,i} - B_i)} \right\}$$

Provides 'observed' integrates intensities for calculating Bragg R-factor

**Starting from an arbitrary set of values for $I_{\mathbf{h}}$ and using the Rietveld formula for calculating the Bragg R-factor, it is possible to obtain the so called '$I_{\mathbf{h}}$(obs)'.**

**These intensities can be taken as new values for $I_{\mathbf{h}}$ and repeat iteratively the procedure up to no net improvement of the whole profile is reached.**

# Le Bail fits for extracting integrated intensities

$$'I_{\mathbf{h}}(obs)' = I_{\mathbf{h}} \sum_i \left\{ \frac{\Omega(T_i - T_{\mathbf{h}})(y_{obs,i} - B_i)}{(y_{calc,i} - B_i)} \right\}$$

**The values of $I_{\mathbf{h}}$ are of low quality when the overlap of reflections is important. This is the reason one cannot use these integrated intensities directly for solving the structure.**

**Many methods of solving the structure from powders (direct methods) use a special strategy for changing the partitioning of overlapped reflections**

# SOLVING STRUCTURES

**Classically, crystal structure determination is considered as a process to determine the "phases" of the structure factors**

$$\rho(\mathbf{r}) = \sum_{\{\mathbf{h}\}} F_{\mathbf{h}} \; exp\{-2\pi i \mathbf{hr}\}$$

$$\rho(\mathbf{r}) = \sum_{\{\mathbf{h}\}} |F_{\mathbf{h}}| exp\{-2\pi i(\mathbf{hr} + \Phi_{\mathbf{h}})\}$$

**For a centrosymmetric structure $\Phi_{\mathbf{h}}$ is 0 or 1/2**

**The knowledge of all phases for the measured structure factors provides a density map from which the structure is derived (chemically recognised).**

# SOLVING STRUCTURES

**The resolution of the "phase problem" is the goal of the crystal structure determination methods**

**Direct Methods tackle the problem looking for**
**phase relations (tangent formula) between structure factors of different reflections**
**Direct methods need a high number of reflections and good resolution (powders)**

**Direct methods are generally very efficient**

**But …**

sometimes direct methods fail in solving particular structures

**or**

**cannot be applied because poor data quality (low resolution)**

# SOLVING STRUCTURES

$$F(\mathbf{h}) = \sum_{j=1}^{n} O_j \, f_j(\mathbf{h}) T_j \sum_s exp\left\{2\pi i\left[\mathbf{h}\{S|\mathbf{t}\}_s \mathbf{r}_j\right]\right\}$$

**If the chemical composition and the space group are known we have to determine just the 3n variables**

$$F_{obs}(\mathbf{h})_r \approx \left| \sum_{j=1}^{n} O_j \, f_j \, T_j \sum_s exp\left\{2\pi i\left[\mathbf{h}\{S|\mathbf{t}\}_s \mathbf{r}_j\right]\right\} \right|_r$$

$$\mathbf{h}_r = (h,k,l)_r \quad (r = 1,2,\ldots N)$$

$$\mathbf{r}_j = (x_j, y_j, z_j) \quad (j = 1,2,\ldots n)$$

# Solving structures by Direct Space methods

**Look directly for atom positions explaining the experimental data**

**Minimize a reliability factor with respect to the "configuration vector"**

$$\boldsymbol{\omega} = \left| x_1, y_1, z_1, x_2, y_2, z_2, \ldots x_n, y_n, z_n \right\rangle$$

$$R(\boldsymbol{\omega}) = c \sum_{r=1}^{N} \left| F_{obs}^2(\mathbf{h}_r) - F_{calc}^2(\mathbf{h}_r, \boldsymbol{\omega}) \right|$$

# MAGNETIC STRUCTURES

**Look directly for magnetic moments of atoms explaining the experimental data**

**Minimize a reliability factor with respect to the "configuration vector"**

$$\boldsymbol{\omega} = \left| m_{x1}, m_{y1}, m_{z1}, m_{x2}, m_{y2}, m_{z2}, \ldots m_{xn}, m_{yn}, m_{zn} \right\rangle$$

$$\boldsymbol{\omega} = \left| S_{\mathbf{k}x1}, S_{\mathbf{k}y1}, S_{\mathbf{k}z1}, S_{\mathbf{k}x2}, S_{\mathbf{k}y2}, S_{\mathbf{k}z2}, \ldots S_{\mathbf{k}xn}, S_{\mathbf{k}yn}, S_{\mathbf{k}zn} \right\rangle$$

$$\boldsymbol{\omega} = \left| C_1, C_2, \ldots C_n \right\rangle$$

$$R(\boldsymbol{\omega}) = c \sum_{r=1}^{N} \left| \mathbf{M}^2_{\perp obs}(\mathbf{h}_r) - \mathbf{M}^2_{\perp calc}(\mathbf{h}_r, \boldsymbol{\omega}) \right|$$

# Solving structures by Simulated Annealing

The SA method is a general purpose optimisation technique for large combinatorial problems introduced by:

Kirpatrick, Gelatt and Vecchi, *Science* **220**, 671-680 (1983).

**Minimize a cost function, energy E(ω), with respect to the configuration vector ω.**

**Origin: Monte Carlo methods for simulating properties of liquids (Metropolis algorithm)**

Algorithm trying to mimic the process of annealing a sample to obtain a good crystalline state (ground state):

**A temperature schedule (starting high temperature + cooling rate) is needed.**

**Procedure to generate new configurations (Markov chains) and a Boltzmann probability to explore the phase space (importance sampling)**

# THE SIMULATED ANNEALING ALGORITHM

**begin**

**Initialise** (set to zero useful quantities, do preliminary calculations )

$\tau = 1$

**do**

**do**

**Perturb the system**:

$\omega_{old} \rightarrow \omega_{new}$, $\Delta = E(\omega_{new}) - E(\omega_{old})$

**if** $\Delta \leq 0$ **then accept**, **else**

**if** $\exp(-\Delta/T_\tau) >$ **random[0,1] then accept**

**if accept** then **Update** (**replace** $\omega_{old}$ **by** $\omega_{new}$)

**until equilibrium is approached closely enough** (Ncyc)

$T_{\tau+1} = f(T_\tau)$ **(decrease temperature, usually** $T_{\tau+1} = q\, T_\tau$, $q \approx 0.9$)

$\tau = \tau + 1$

**until stop criterion is true** (maximum $\tau$, **convergence, low % accepted...)**

**end**

# Steps for using the Simulated Annealing option in FullProf for Magnetic Structure Determination

**1-** Refine the crystal structure in the paramagnetic state

**1'-** If there is a structural phase transition at $T_N/T_C$, then refine the crystal structure in the ordered state using high-Q reflections without magnetic contribution

**2-** Indexing: determine the propagation vector using the program **K-Search**

**3-** In the ordered state fix all structural parameters and introduce the magnetic contribution as a new phase using the Le Bail fit mode and putting **`More`**=1, **`Irf`**=1 and **`Jvi`**=11

**4-** The above step produces an output file *.int that can be used as input data for Simulated Annealing runs

# $Tb^{3+}/Tb^{4+}$ Charge ordering in $KTb_3F_{12}$: magnetic frustration in the $Tb^{3+}$ sublattice

JOURNAL OF APPLIED PHYSICS VOLUME 91, NUMBER 10 15 MAY 2002

**Magnetic properties of a mixed-valence (III/IV) terbium fluoride $KTb_3F_{12}$**

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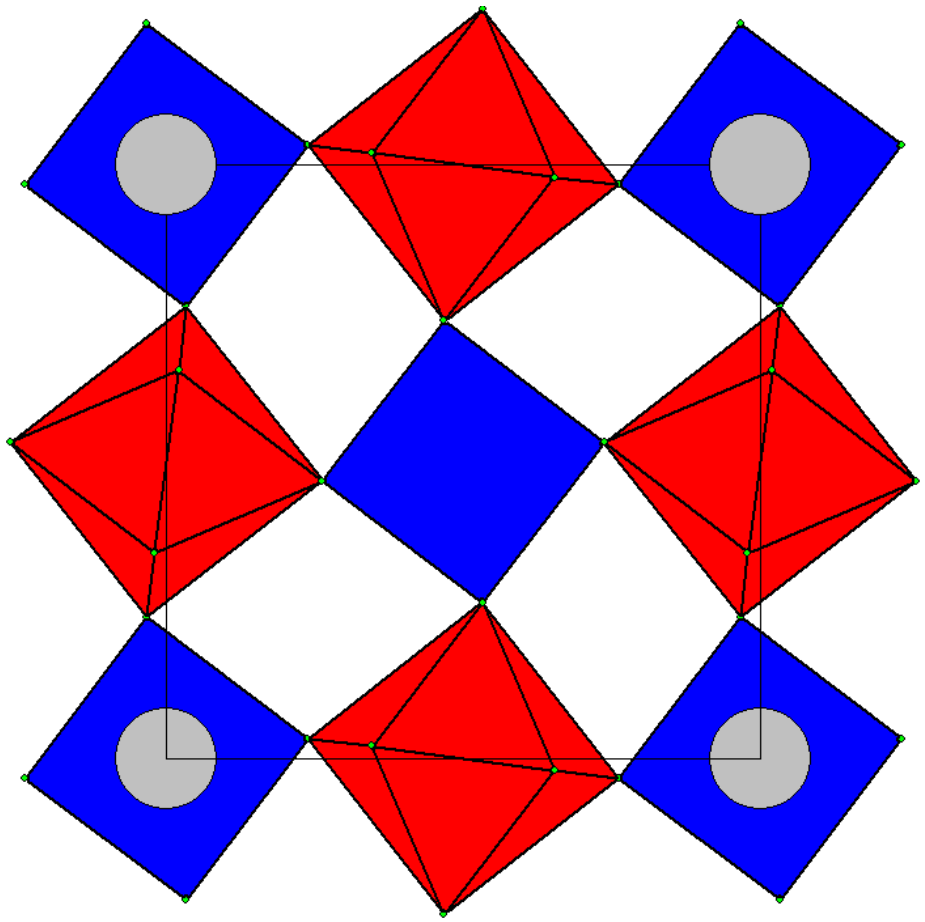
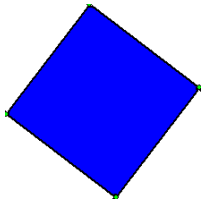
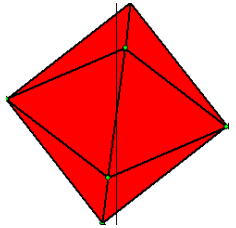
# Simulated Annealing in FullProf with a simple example: $KTb_3F_{12}$

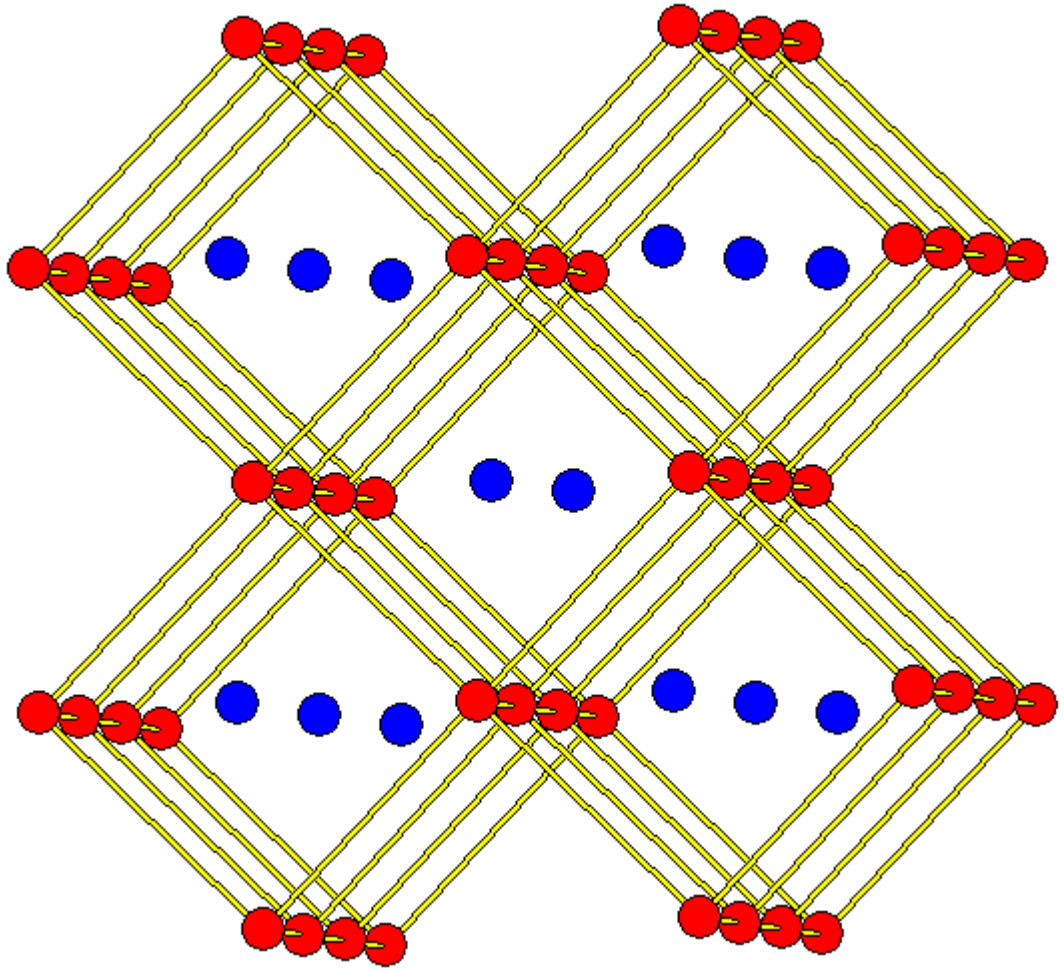


$Tb^{3+}$



$Tb^{4+}$

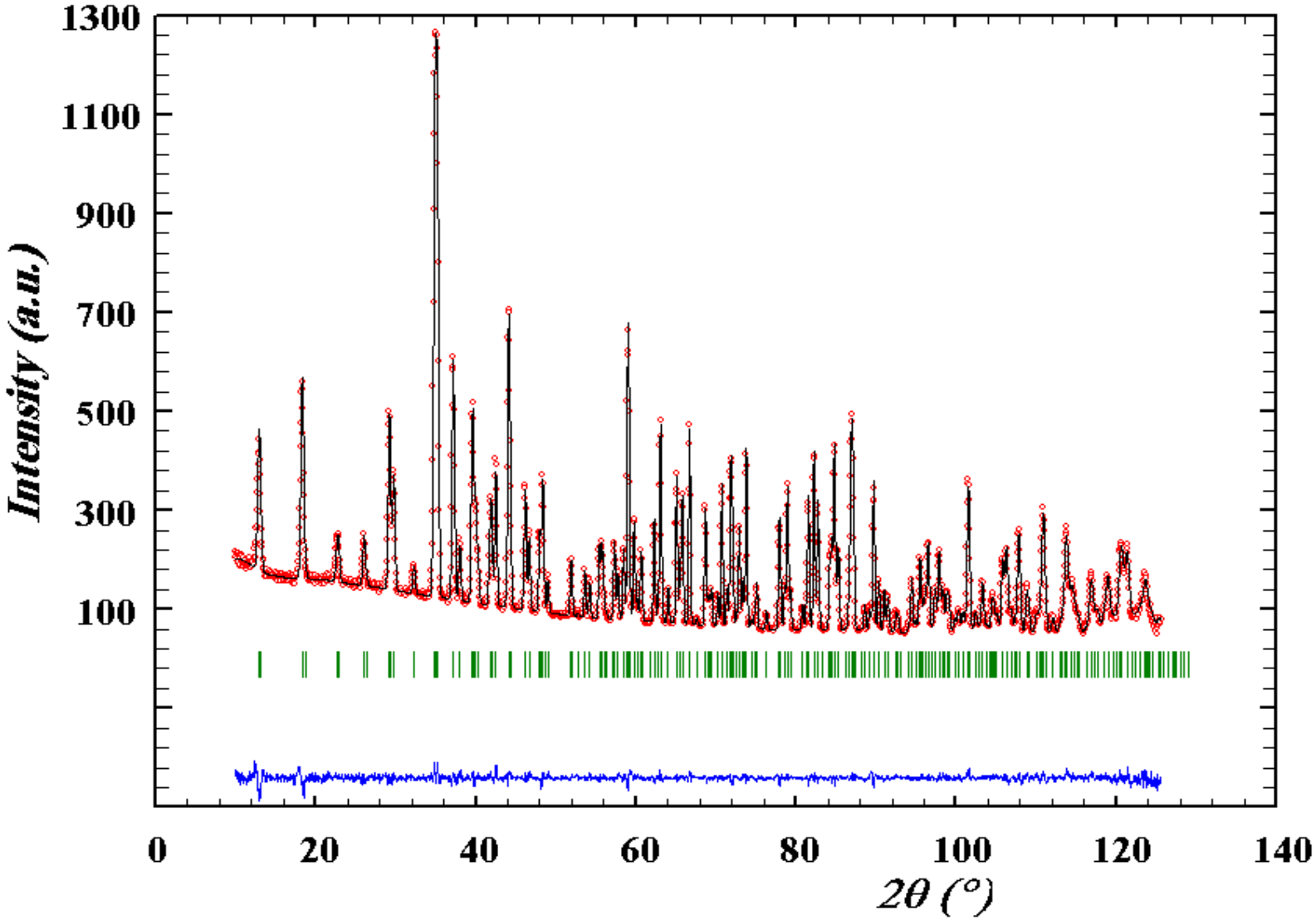




# Simulated Annealing in FullProf with a simple example: $KTb_3F_{12}$

```
I 4/m                          <--Space group symbol
!Atom Typ        X         Y         Z      Biso       Occ     In Fin N_t Spc /Codes
!    beta11    beta22    beta33    beta12    beta13    beta23  /Codes
K    K        0.00000   0.00000   0.00000   0.00000   0.12500   0   0   2    0  # color green
                 0.00      0.00      0.00      0.00      0.00
    0.00264   0.00264  -0.00038   0.00000   0.00000   0.00000
       0.00      0.00      0.00      0.00      0.00      0.00
Tb3+ TB       0.00000   0.00000   0.50000   0.04652   0.12500   0   0   0    0  # color blue
                 0.00      0.00      0.00      0.00      0.00
Tb4+ TB       0.00000   0.50000   0.25000   0.01556   0.25000   0   0   0    0  # color red
                 0.00      0.00      0.00      0.00      0.00
F1   F        0.34606   0.02658   0.00000   0.00000   0.50000   0   0   2    0  # color brown  conn
                 0.00      0.00      0.00      0.00      0.00
    0.00149   0.00259   0.00036   0.00039   0.00000   0.00000
       0.00      0.00      0.00      0.00      0.00      0.00
F2   F        0.23820   0.04363   0.67942   0.00000   1.00000   0   0   2    0  # color brown
                 0.00      0.00      0.00      0.00      0.00
    0.00167   0.00227   0.00082  -0.00006  -0.00032  -0.00012
       0.00      0.00      0.00      0.00      0.00      0.00
```

# Refinement of the crystal structure of: $KTb_3F_{14}$ at 5K in the paramagnetic state




This allows to know all structural parameters near the Néel temperature ($T_N$=3.65K)

# How to prepare a PCR file for generating integrated intensities for SAnn?

```
!-------------------------------------------------------------------------------
!  Data for PHASE number:   2  ==> Current R_Bragg for Pattern#  1:     0.45
!-------------------------------------------------------------------------------
KTb3F12-M
!
!Nat Dis Ang Pr1 Pr2 Pr3 Jbt Irf Isy Str Furth       ATZ    Nvk Npr More
   0   0   0 0.0 0.0 1.0   2  -1   0   0   0          0.000   1   7    1
!
!Jvi Jdi Hel Sol Mom Ter  Brind   RMua    RMub    RMuc   Jtyp  Nsp_Ref
  11   0   0   0   0   0  1.0000  0.0000  0.0000  0.0000   1    0
!
I -1                        <--Space group symbol
!-------> Profile Parameters for Pattern #  1
!  Scale        Shape1      Bov      Str1      Str2      Str3   Strain-Model
  4.3356       0.00000   0.00000   0.00000   0.00000   0.00000       0
     0.00000     0.000     0.000     0.000     0.000     0.000
!       U          V          W          X          Y        GauSiz   LorSiz
   0.794074  -0.280000   0.080000   0.000000   0.045159   0.000000   0.000000
     61.000      0.000      0.000      0.000     71.000      0.000      0.000
!     a          b          c        alpha      beta       gamma
   7.695388   7.695388   7.540170  90.000000  90.000000  90.000000
   31.00000   31.00000   41.00000    0.00000    0.00000    0.00000
!  Pref1    Pref2      Asy1     Asy2     Asy3     Asy4      S_L      D_L
  1.00000  0.00000  0.00000  0.00000  0.00000  0.00000  0.00000  0.00000
     0.00     0.00     0.00     0.00     0.00     0.00     0.00     0.00
! Propagation vectors:
   1.0000000   0.0000000   0.0000000          Propagation Vector  1
    0.000000    0.000000    0.000000
```

# How to prepare a PCR file for generating profile intensities for SAnn?

## From fp2k.inf document (9 October 2019)

Simulated annealing has been extended to work with the full powder diffraction profile, for that it is necessary to make a previous run using a LeBail fit, putting Ipr=-2 and include the name of the *.spr file in the next line of the PCR file. Moreover the creation of a cluster of intensities is needed but it is necessary to make Jvi=13, for the case of superspace description, or Jvi=11 for other cases.

This *.int file is used in the simulated annealing work with the full profile only for reading the indices of reflections. The information contained in the *.spr file is really what is used in the process of minimizing the cost function. The PRF file for visualizing the final profile is identical to that generated using the Rietveld method.

In case of several phases, the calculated profile of the LeBail Fit corresponding to the desired phase is output to the *.spr file instead of the total observed profile. This is very useful in case of known impurities (treated using the Rietveld method with fixed positions) to extract an unknown phase or to extract pure magnetic reflections to solve a magnetic structure. If the use wants to use the calculated profile even in the case of a single phase in the LeBail fit the value of Jvi should be negative: Jvi=-13 or Jvi=-11.

# How to prepare a PCR file for generating profile intensities for SAnn?

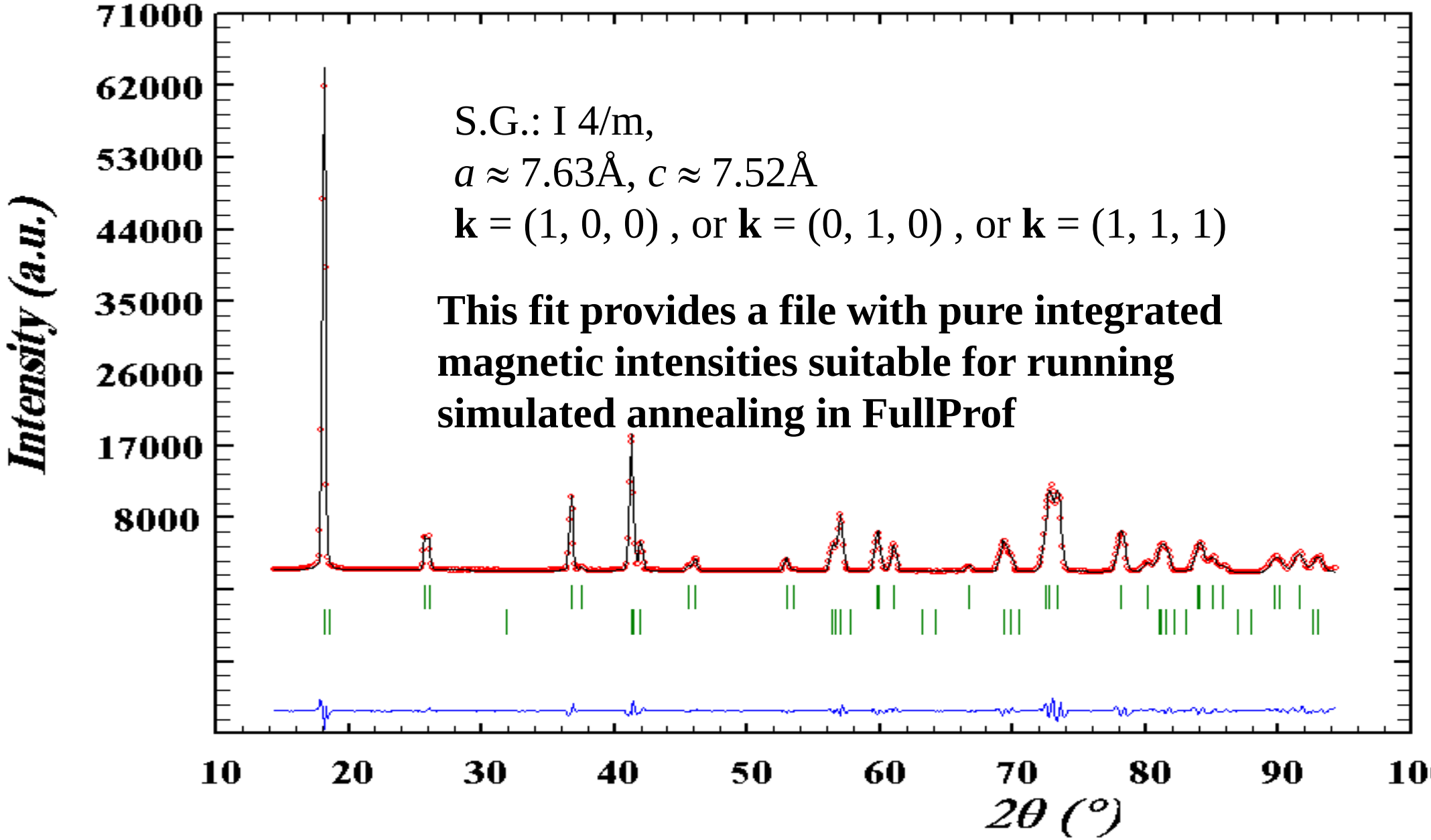
Example of the relevant parts of a PCR file for preparing the simulated annealing work. We have used superspace operators to generate only incommensurate magnetic reflections (keyword "mag_only") because we are treating a difference pattern. Notice that this PCR file generates the profile information in the file test.pcr and the reflection clusters in the file: test-pm1_ctrl.int

```
.......................................Start of the example
COMM My Title: LeBail fit to prepare a SAnn work with the full powder profile
! Current global Chi2 (Bragg contrib.) =    999999
! Files => DAT-file: xxxxx.dat,  PCR-file: test-pm
!Job Npr Nph Nba Nex Nsc Nor Dum Iwg Ilo Ias Res Ste Nre Cry Uni Cor Opt Aut
   1   0   1  25   2   0   1   1   0   0   1   0   0   0   0   0   0   0   1
!
!Ipr Ppl Ioc Mat Pcr Ls1 Ls2 Ls3 NLI Prf Ins Rpa Sym Hkl Fou Sho Ana
  -2   0   1   1   1   0   4   0   0   3   8   0   0   0   0   0   0   !
! File name (or filecode) of the *.spr file containing profile points information
test.spr
. . . . .
```

# How to prepare a PCR file for generating profile intensities for SAnn?

```
!-----------------------------------------------------------------------------
!  Data for PHASE number:   1  ==> Current R_Bragg for Pattern#  1:     0.08
!-----------------------------------------------------------------------------
Magnetic Structure of:  mag_only
!
!Nat Dis Ang Pr1 Pr2 Pr3 Jbt Irf Isy Str Furth        ATZ     Nvk Npr More
   0   0   0 0.0 0.0 1.0   2  -1   2   0    0        956.092   1   7   1
!
!Jvi Jdi Hel Sol Mom Ter  Brind    RMua     RMub     RMuc    Jtyp  Nsp_Ref Ph_Shift N_Dom
  13   0   0   0   0   0  1.0000  0.0000   0.0000   0.0000    1       0       0       0
!
Pmn2_11'(0,0,g)s0ss  31.1.9.2.m124.2   <--Magnetic Super Space group symbol
Parent Setting: Pnm2_11'(0,0,g)ss0s (a1,a2,a3,a4;0000)
! Generators
Genr  -x1+1/2,-x2,x3+1/2,x4,1
Genr  x1,-x2+1/2,x3,x4+1/2,1
Genr  x1,x2,x3,x4+1/2,-1
N_qc   1
Q_coeff
. . . . .
```

# Profile matching (Le Bail) fit: $KTB_3F_{14}$




S.G.: I 4/m,
$a \approx 7.63$Å, $c \approx 7.52$Å
**k** = (1, 0, 0) , or **k** = (0, 1, 0) , or **k** = (1, 1, 1)

**This fit provides a file with pure integrated magnetic intensities suitable for running simulated annealing in FullProf**

# Example of *.int file generated by *FullProf*

## using More=1, Jvi=11

```
  Phase No:    2 KTb3F12-M                    Overlapped reflections re-grouped
(4i4,2f12.2,i4,3f14.4)                      <- Format of h,k,l,iv, Int, sigma, multip.
  2.4260    0    2                          <- Wavelength, type of data, powder ind.
   1                                        <- Number of propagation vectors
  1    1.00000    0.00000    0.00000        <-  Propagation vector
   0    0    0    1        -1.00       47.42    2
  -1    1    0    1     18893.78       67.06    2
  -1    0    1    1         0.00        1.00    2  Negative intensity means that
  -2   -1    1    1        -1.00        0.00    2  the reflection contributes to the
  -2    1    1    1        -1.00        0.00    2  next positive observation
   0   -1    1    1        -1.00        0.00    2
   0    1    1    1         0.00        0.00    2
   0    2    0    1        -1.00        7.41    2
   0   -2    0    1        -1.00        1.00    2
   1   -1    0    1        -1.00        7.41    2
   1    1    0    1        -1.00        7.41    2
  -3    0    1    1        -1.00        0.42    2
  -1   -2    1    1        -1.00        0.42    2
  -1    2    1    1        -1.00        0.42    2
   1    0    1    1      6566.70       14.85    2
  -2    0    2    1        -1.00        2.24    2
  -1   -1    2    1        -1.00        2.24    2
  -1    1    2    1        -1.00        2.24    2
   0    0    2    1      1327.23        4.48    2
. . . . . . . . . . . . . . . . . . . . . . . . .
```

# How to prepare a PCR file for Simulated Annealing?

**Cry=3** tells the program to use the Simulated annealing mode

**Nre=8** number of free parameters with box constraints

```
COMM KTb3F12 - T=1.4K - G4.1
! Files =>
!Job Npr Nph Nba Nex Nsc Nor Dum Iwg Ilo Ias Res Ste Nre Cry Uni Cor Opt Aut
   1   0   1   0   0   0   0   0   0   0   0   0   0   8   3   0   0   0   1
!
!Ipr Ppl Ioc Mat Pcr Ls1 Ls2 Ls3 NLI Prf Ins Rpa Sym Hkl Fou Sho Ana
   0   0   1   0   1   0   0   0   0   3   5   0   0   0   0   0   0
!
!NCY  Eps  R_at  R_an  R_pr  R_gl     Thmin       Step       Thmax    PSD    Sent0
  1  0.10  1.00  1.00  1.00  1.00     15.0000   0.100000    94.9000   0.000   0.000
!
!
       8    !Number of refined parameters
!-----------------------------------------------------------------------------
!  Data for PHASE number:   1  ==> Current R_Bragg for Pattern#  1:     2.03
!-----------------------------------------------------------------------------
KTb3F12-M
!
```

# How to prepare a PCR file for Simulated Annealing?

```
!Nat Dis Mom Pr1 Pr2 Pr3 Jbt Irf Isy Str Furth       ATZ    Nvk Npr More
   3   0   0 0.0 0.0 1.0  -1   4  -1   0   0         0.000   1   0   0
!
I -1                        <--Space group symbol
!Nsym Cen Laue MagMat
   1   1   1   1
!
SYMM  x,y,z
MSYM  u,v,w,0.0
!
!Atom Typ  Mag Vek    X       Y       Z       Biso    Occ      Rm      Rphi  Rtheta
!     Im   Iphi   Itheta  beta11  beta22  beta33   MagPh
T3_1 JTB3  1  0  0.00000 0.00000 0.50000 0.06775 1.00000   0.09    0.976   0.000
                    0.00    0.00    0.00    0.00    0.00   11.00   31.00   41.00
   0.000   0.000   0.000   0.000   0.000   0.000 0.00000
    0.00    0.00    0.00    0.00    0.00    0.00    0.00
T4_1 JTB3  1  0  0.00000 0.50000 0.25000 0.03425 1.00000   1.909   1.927    0.00
                    0.00    0.00    0.00    0.00    0.00   21.00   51.00   61.00
   0.000   0.000   0.000   0.000   0.000   0.000 0.00000
    0.00    0.00    0.00    0.00    0.00    0.00    0.00
T4_2 JTB3  1  0  0.00000 0.50000 0.75000 0.03425 1.00000   1.909   0.561    0.00
                    0.00    0.00    0.00    0.00    0.00   21.00   71.00   81.00
   0.000   0.000   0.000   0.000   0.000   0.000 0.00000
    0.00    0.00    0.00    0.00    0.00    0.00    0.00
```

**No symmetry constraints:**

**Spherical components, m_Tb$^{4+}$(1)= m_Tb$^{4+}$(2)**

# How to prepare a PCR file for Simulated Annealing?

No profile parameters,
part of the file similar to single crystal format

```
!  Scale Factors
!  Sc1        Sc2        Sc3        Sc4        Sc5        Sc6
  4.336      0.000      0.000      0.000      0.000      0.000
      0.00       0.00       0.00       0.00       0.00       0.00
!  Extinction Parameters
! Ext1       Ext2       Ext3       Ext4       Ext5       Ext6      Ext7   Ext-Model
  0.000      0.000      0.000      0.000      0.000      0.000      0.000        0
       0.00       0.00       0.00       0.00       0.00       0.00       0.00
!     a          b          c        alpha      beta       gamma
   7.695388   7.695388   7.540171  90.000000  90.000000  90.000000
    0.00000    0.00000    0.00000    0.00000    0.00000    0.00000
! x-Lambda/2  +          Not yet used parameters
     0.00000    0.00000    0.00000    0.00000    0.00000
        0.00       0.00       0.00       0.00       0.00
! Propagation vectors:
   1.0000000  0.0000000  0.0000000          Propagation Vector  1
    0.000000   0.000000   0.000000
```

# How to prepare a PCR file for Simulated Annealing?

Parameter number

Ranges and steps

boundary conditions

```
! Limits for selected parameters (+ steps & BoundCond for SA):
   1        0.0000       9.0000       0.5831    0   Rmom_T3_1
   2        0.0000       9.0000       0.0582    0   Rmom_T4_1
   3        0.0000     360.0000       2.0000    1   RPhi_T3_1
   4        0.0000     180.0000       2.0000    0   RThet_T3_1
   5        0.0000     360.0000       2.0000    1   RPhi_T4_1
   6        0.0000     180.0000       2.0000    0   RThet_T4_1
   7        0.0000     360.0000       2.0000    1   RPhi_T4_2
   8        0.0000     180.0000       2.0000    0   RThet_T4_2
!
! T_ini    Anneal   Accept NumTemps NumThCyc InitConf
   5.000    0.900    0.050       45     0        0
! NCyclM    Nsolu Num_Ref Nscalef  NAlgor
     150        1    110      0       0
```

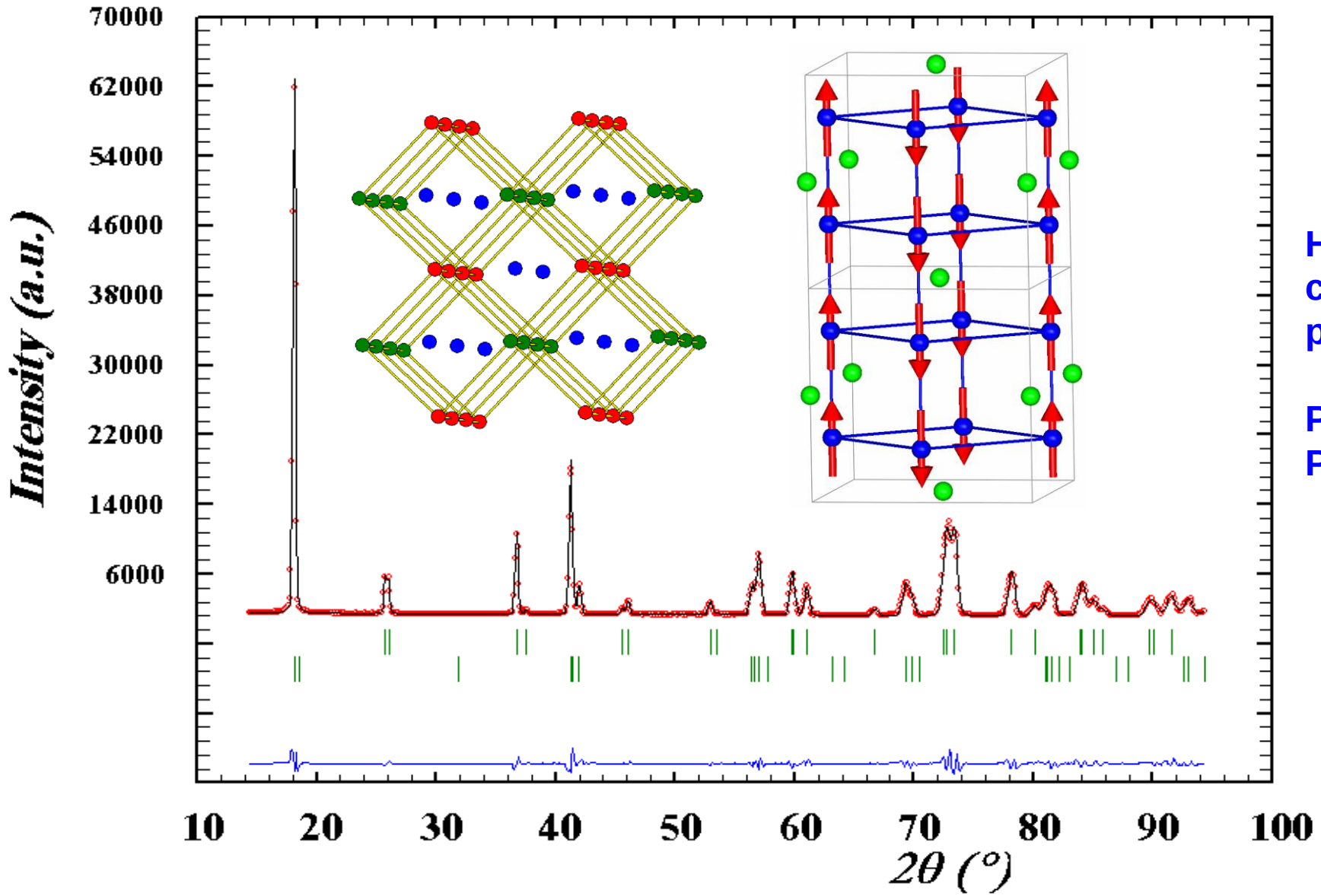
Random initial configuration

Corana algorithm
Initial step = range

Number of reflections to consider

Automatic treatment(1) or fixed(0) scale factor

# Rietveld refinement of the magnetic structure of $KTb_3F_{12}$ on G4.1 (LLB)




Here we have used the conventional way of working putting two phases:

Phase 1: Nuclear contribution
Phase 2: Magnetic contribution

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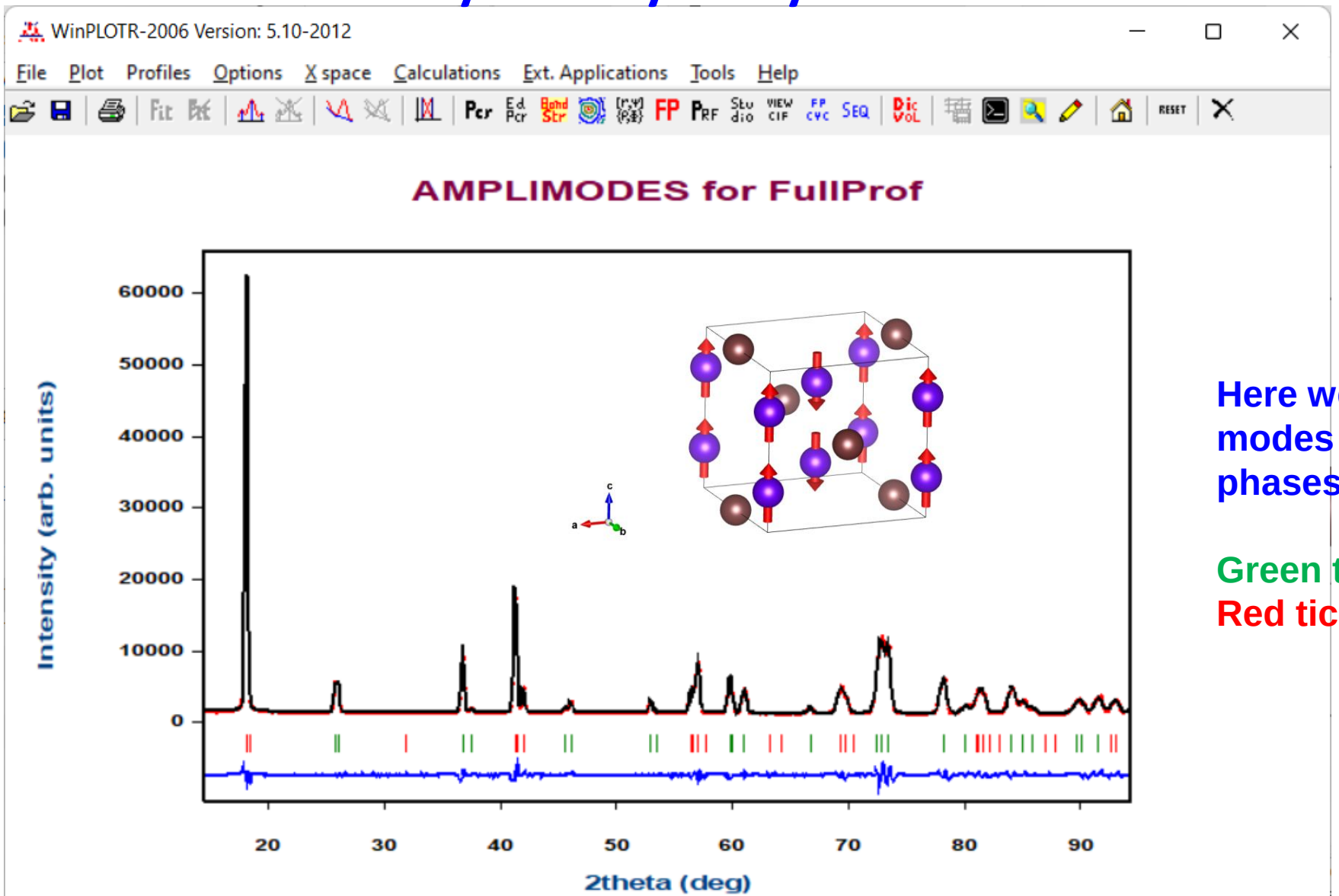
# Symmetry analysis with ISODISTORT

**The results obtained with Simulated Annealing can be straitforwardly corroborated by symmetry analysis using BasIreps or ISODISTORT**

**ISODISTORT generates a PCR file with the proper magnetic group and the basis vectors of the irreducible representations involved in the magnetic phase transition.**

# Symmetry analysis with ISODISTORT




**Here we have used the symmetry modes approach using a single phases**

**Green ticks: Nuclear contribution**
**Red ticks: Magnetic contribution**

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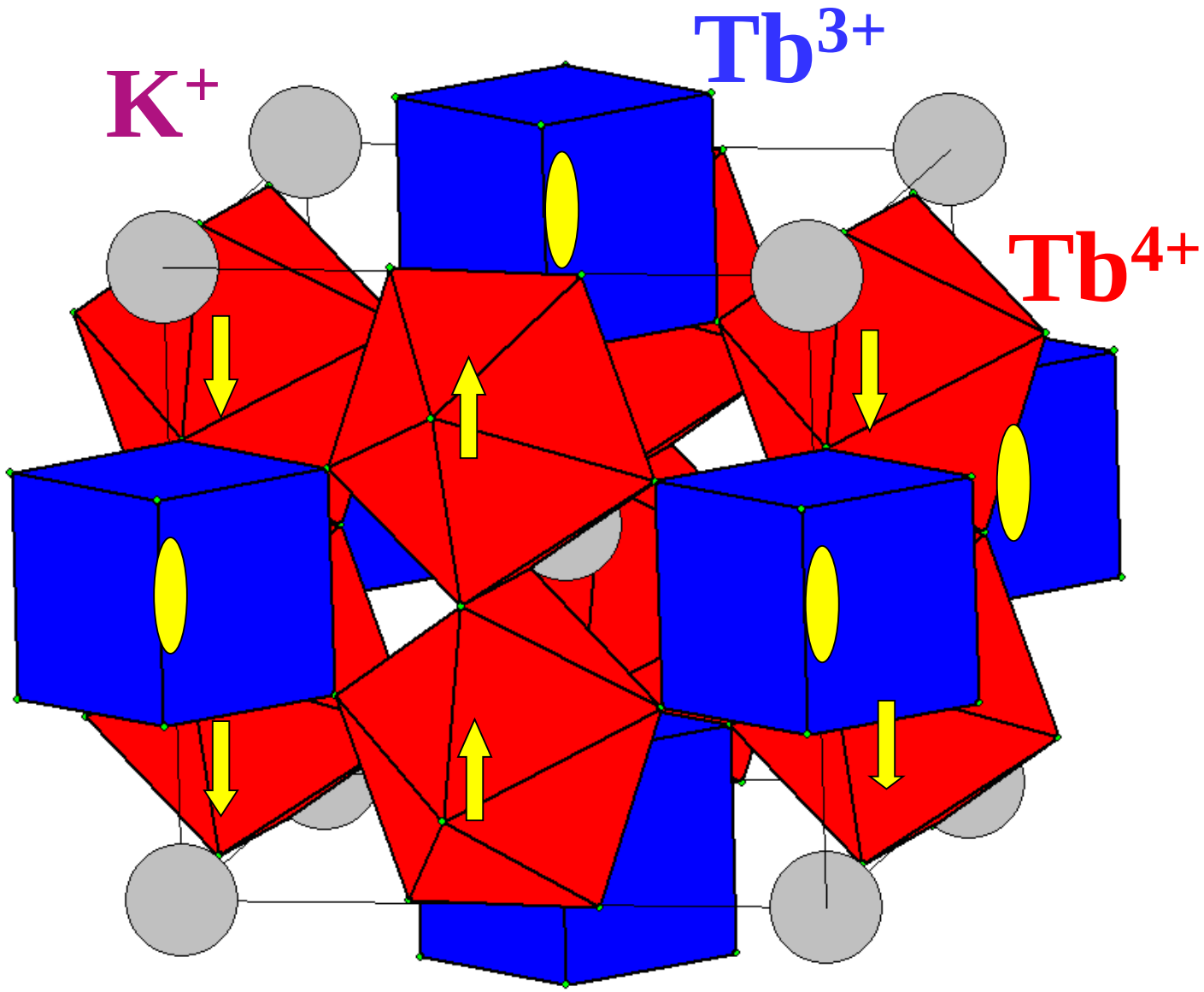
# Magnetic Structure of $KTb^{3+}Tb_2^{4+}F_{12}$

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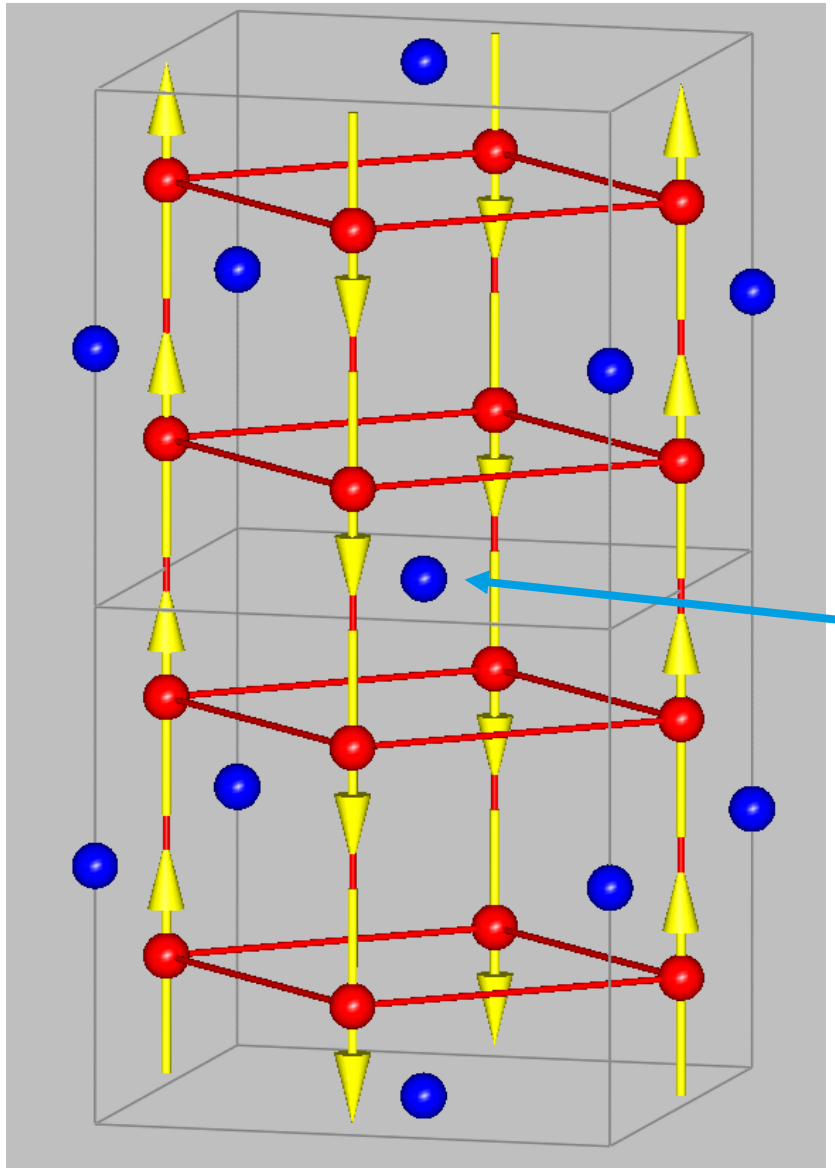
# Magnetic Structure of $KTb^{3+}Tb_2^{4+}F_{12}$



**Only $Tb^{4+}$ is ordered as F chains along c that are AF coupled in the basal plane**

**$Tb^{3+}$ does not have static magnetic moment because the molecular field due to $Tb^{4+}$ is exactly zero at its site. $Tb^{3+}$ remains paramagnetic**

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# Conclusions about the determination of the magnetic structure of $KTb_3F_{12}$

**Simulated Annealing:**

In this case, the information contained in the powder diffraction pattern is enough to obtain the magnetic structure without symmetry constraints.

**Representation Analysis:**

The irreducible representation involved in the magnetic phase transition, $\Gamma_3$, is not allowed for the site of $Tb^{3+}$, so that this ion remains disordered (idle spin, "spin fou"). One can verify that in the Shubnikov group $I_P4'/m$ (OG notation) the magnetic point group of the site $2b(Tb^{3+})$, $4'/m$, is not admissible.

**Full Symmetry Analysis with ISODISTORT**

This combines magnetic space groups together with basis functions of irreducible representations. The obtained magnetic group in BNS setting is $P_I4_2/m$.


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THANK YOU!