



CCP4 NEWSLETTER ON PROTEIN CRYSTALLOGRAPHY

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Maximum-Likelihood Refinement of Atomic Models using Least-Squares Criterion

by

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1. Notation

$F_{obs}(\mathbf{s})$ - observed structure factors magnitudes

$F^*(\mathbf{s})$ - modified structure factors magnitudes

$F_{mod}(\mathbf{s})$ - magnitudes of structure factors calculated from the model

$w(\mathbf{s})$ - weights for least-squares terms

LS - least-squares criterion calculated with F_{obs}

LS^* - least-squares criterion calculated with F^*

ML - maximum likelihood criterion (logarithm of likelihood gain)

α, β - parameters of the joint probability distribution of structure factors considered as a function of random atomic models

ε - reflection multiplicity

$I_0(x)$, $I_1(x)$, $I_2(x)$ - modified Bessel functions of 0, 1 and 2 order of argument x

$\cosh(x)$, $\tanh(x)$ - hyperbolic cosine and tangent of argument x

2. Least-squares and maximum likelihood criteria

The basic goal of a crystallographic refinement is to find an atomic model such that it minimises the functional

$$R = R_X + R_O.$$

where the crystallographic criterion R_X describes the quality of fit of structure factor magnitudes, F_{mod} calculated from the model, to the experimental data, F_{obs} , and the R_O embodies other terms such as stereochemical criteria, a phasing criterion etc. In order to analyse the dependence of the refinement results on the choice of the crystallographic criterion R_X , in the current work the term R_O was excluded from all calculations.

$$LS = \sum_{\mathbf{s}} w(\mathbf{s}) (F_{mod}(\mathbf{s}) - F_{obs}(\mathbf{s}))^2.$$

In practice, the basic statistical hypotheses for this criterion break when the atomic model is incomplete and the errors in experimental data F_{obs} are not independent, and the LS criterion becomes inadequate to the situation.

Recently, the maximum likelihood criterion started to be used (Bricogne & Irwin, 1996; Pannu & Read, 1996; Murshudov *et al.*, 1997) as R_X . The maximisation of likelihood is equivalent to minimisation of negative logarithm likelihood gain, which may be calculated as (Lunin & Skovoroda, 1995)

$$ML = \begin{cases} \sum_{\mathbf{s}} \left(\frac{\alpha^2 F_{mod}^2}{\varepsilon\beta} - \ln \left(I_0 \left(\frac{2\alpha F_{obs} F_{mod}}{\varepsilon\beta} \right) \right) \right), & \text{for acentric reflections} \\ \sum_{\mathbf{s}} \left(\frac{\alpha^2 F_{mod}^2}{2\varepsilon\beta} - \ln \left(\cosh \left(\frac{\alpha F_{obs} F_{mod}}{\varepsilon\beta} \right) \right) \right), & \text{for centric reflections.} \end{cases}$$

One of its major advantages is that it takes into account the contribution of atoms missed in an available atomic model (Lunin & Urzhumtsev, 1999).

However, an implementation of the ML criterion in existing programs needs their essential modification. An alternative solution would be to approximate this criterion near its minimum by a functional quadratic with respect to structure factor magnitudes, calculated from the atomic model (Lunin & Urzhumtsev, 1999). In this case, such approximation can be written again in the form of the usual LS criterion:

$$LS^* = \sum_{\mathbf{s}} w^*(\mathbf{s}) (F_{mod}(\mathbf{s}) - F^*(\mathbf{s}))^2.$$

The values F^* can be considered as modified magnitudes F_{obs} and can be obtained as the solution of the following equation with respect to F^* :

$$F^* = \begin{cases} \frac{F_{obs}}{\alpha} \frac{I_1(2hF_{obs})}{I_0(2hF_{obs})}, & \text{for acentric reflections} \\ \frac{F_{obs}}{\alpha} \tanh(hF_{obs}), & \text{for centric reflections} \end{cases}$$

with α and β estimated as in (Lunin & Skovoroda, 1995) and

$$h = \frac{\alpha F^*}{\varepsilon \beta}$$

The weights w^* are calculated as

$$w^* = \begin{cases} \frac{2\alpha^2}{\varepsilon\beta} - 4h^2 \left(\frac{I_2(2hF_{obs})}{I_0(2hF_{obs})} - \left(\frac{I_1(2hF_{obs})}{I_0(2hF_{obs})} \right)^2 \right), & \text{for acentric reflections} \\ \frac{2\alpha^2}{\varepsilon\beta} - \left(\frac{h}{\cosh(hF_{obs})} \right)^2, & \text{for centric reflections.} \end{cases}$$

The tests below show the comparison of the refinement with different criteria: LS , ML and LS^* . Complete tests results and their analysis will be published elsewhere.

3. Numerical tests on comparative analysis of different criteria

The refinement tests were carried out with CNS complex (Brünger *et al.*, 1998) using the structure of Fab fragment of monoclonal antibody (Fokine *et al.*, 2000). This model includes 439 amino acid residues and 213 water molecules. The molecule crystallises in the space group $P2_12_12_1$ with the unit cell parameters $a = 72.24$ E, $b = 72.01$ E, $c = 86.99$ E, one molecule per asymmetric unit.

For test purposes the experimental data F_{obs} at 2.2 E resolution were simulated by the corresponding values calculated from the complete exact model (Fig. 1). In all tests described below the starting atomic parameters were exact. Due to the absence of some atoms, removed randomly, the minimisation of the crystallographic criterion shifted the atomic parameters from their exact values showing that the minimum of all these criteria does not correspond to the

correct model any longer. Smaller resulting errors indicate better quality of the criterion.

3.1. *Test1: Random deletion of atoms in the crystal*

In this test the atoms were removed randomly, the percentage of removed atoms varied from 0 to 20%. For each incomplete models the minimisation procedure was carried out using three different crystallographic criteria: *LS*, *ML* and *LS** (we remind that all stereochemical criteria were excluded from this refinement).

Figure 2a shows, for every criterion, the mean error in atomic positions for the models after refinement as a function of the size of a deletion. The errors grow with the percent of a deleted structure. The errors obtained with the *LS** minimisation are systematically less than those for the *LS* minimisation and are almost equal to the errors obtained with the *ML* minimisation. It can be noted that the weights w^* are crucial in order to obtain such results.

3.2. *Test2: Random deletion of water molecules only*

This test is similar to the previous one with the difference that only water molecules were allowed to be deleted from the model. The behaviour of errors (see Fig. 2b) is similar to that in the previous case. However, these errors are significantly larger and they grow faster with the percentage of the deleted structure (compare Fig. 2a and Fig. 2b). The reason for this may be the following: the water molecules are situated at the surface of the protein and not in its volume, and when the same amount of atoms is randomly excluded in both tests, in the case of water molecules they are distributed less uniformly in the space making stronger influence on the structure factors.

4. Conclusions

The tests discussed above show that the incompleteness of the model can seriously affect to the refinement. The more atoms are deleted, the larger are the errors in the model which fits best to the experimental data. Removal of water molecules has a stronger effect than a removal of a similar quantity of atoms randomly in the whole unit cell.

The tests show that the *ML* criterion is less sensible to the absence of a part of a model than the traditional *LS* criterion. In the case when an insertion of the *ML* criterion into an existing program is complicated, it can be replaced by its quadratic approximation. This approximation corresponds to the *LS* criterion calculated with F_{obs} substituted by F^* values and weighted by w^* (expression for both is given in the text). In all tests the least-squares minimisation against modified structure factors F^* gave the models of a significantly higher quality than those obtained by the minimisation against simulated F_{obs} and practically coinciding with the models obtained by maximum likelihood minimisation.

This shows that any crystallographic refinement program based on the minimisation of the least-squares criterion can give the results of the same superior quality as using maximum likelihood criterion without modifying the program itself when proper magnitudes and weights are used.

In this article we presented the results of first tests with an incomplete model without errors. An influence of other sources of imperfection of the model and data on refinement with various criteria will be discussed elsewhere.

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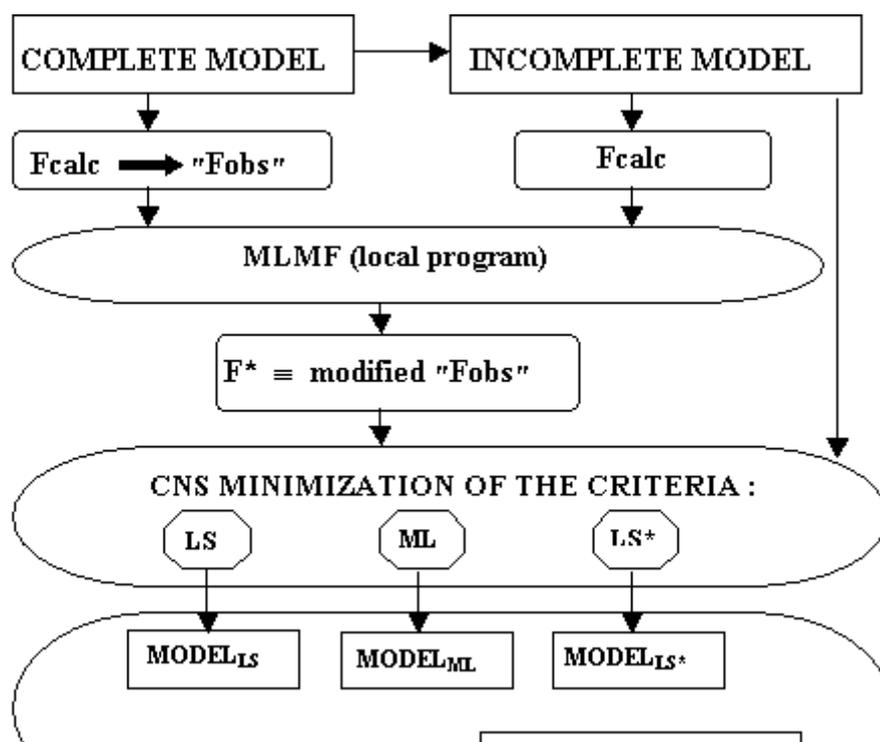
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COMPARISON WITH THE COMPLETE MODEL

Figure 1. A scheme of the numerical tests.

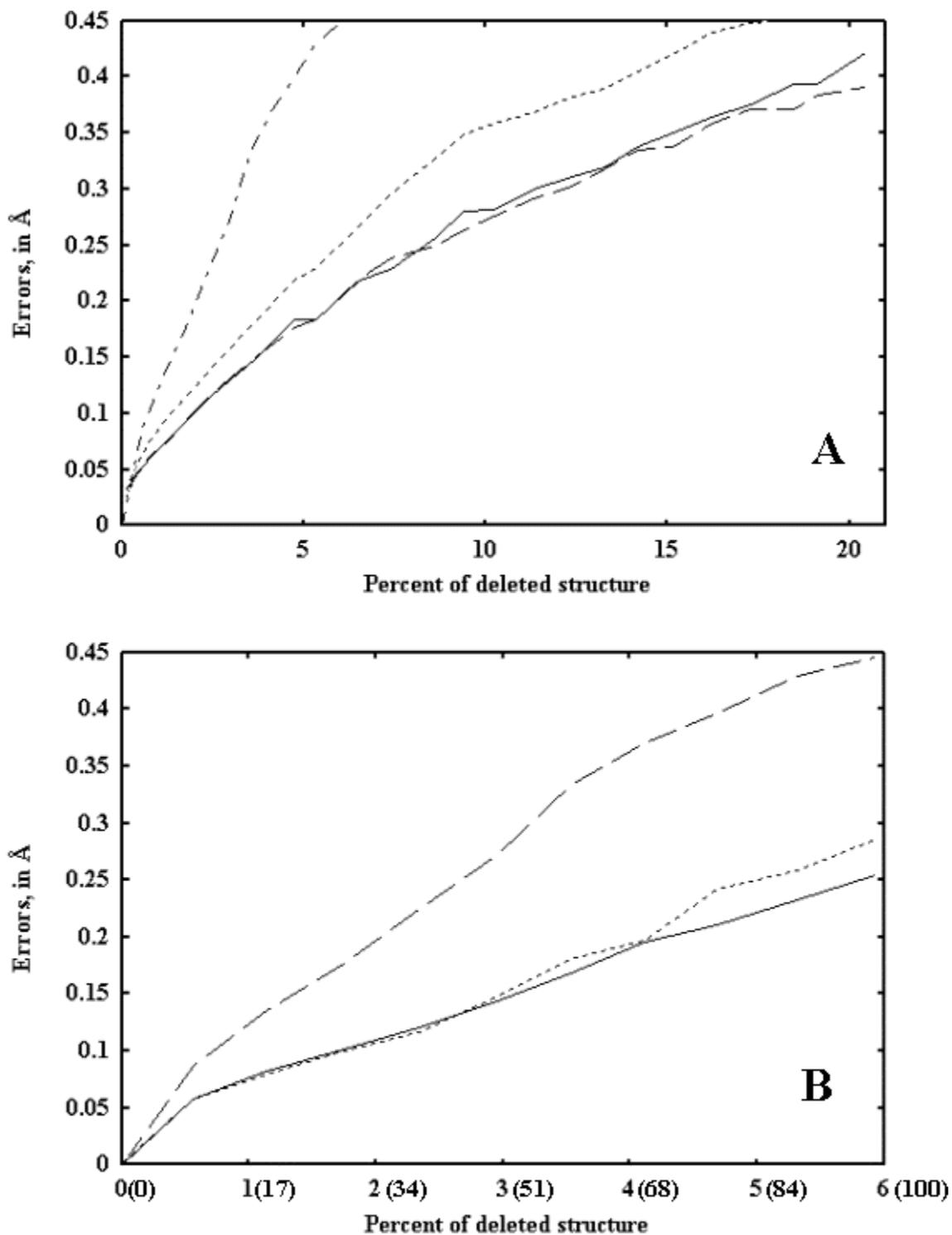


Figure 2. Dependence of mean coordinate error for the models after refinement as a function of the percent of deleted atoms. The dashed, solid and dotted lines show the behaviour of errors after minimisation using *LS*, *ML* and *LS** criteria, respectively.

(A) Deletion of atoms of the whole model. The short line (dashed-and-dotted) is the same as the upper line (dashed) in picture (B) and is shown for comparison.

(B) Deletion of water molecules. Numbers in parentheses specify the percent of deleted water molecules.

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