# NoMoRe web

NoMoRe web (normal mode refinement web server) is a free of charge web server which enable for refinement of frequencies of normal modes evaluated using *ab-initio* periodic computations against single crystal X-ray data. In this approach instead of refining anisotropic displacement parameters (ADPs) as in routine X-ray refinement, we are refining only few frequencies related to low-frequency modes, which corresponds to the external vibrations of molecule.

Schematic workflow of our method is presented in **Scheme 1**. The frequencies, which are obtained after the refinement, enable calculation of thermodynamic properties.
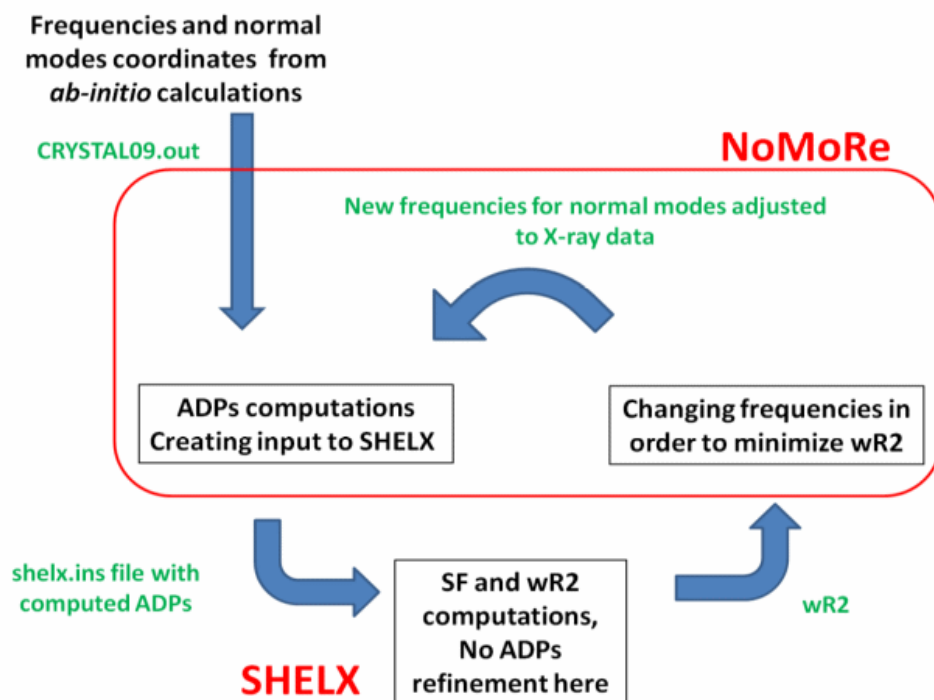
Scheme 1. Schematic workflow with Normal Mode Refinement (*NoMoRe*).

For more details related to *NoMoRe* see:

1. Hoser A. A., Madsen A. Ø., **Acta Cryst A** 2016, A72, 206-214
2. Hoser A. A., Madsen A. Ø., **Acta Cryst A** 2017, A73, 102-114
3. Kofoed, P. M., Hoser, A. A., Diness, F., Capelli, S. C., Madsen, A. Ø., **IUCrJ**, 2019, 558
4. Sovago I, Hoser A. A., Madsen A. Ø., **Acta Cryst A** 2020, A76, 32-44

How to run *NoMoRe*?

Calculations can be time-consuming thus we decided to create an accounts for users. After each calculations user will receive an e-mail and the results will be available from the user account in the dashboard section.

Please create an account and sign in with Login/Sign up section on the top right corner of screen.

After login in the menu two new options will appear

1. Dashboard - hence, you will be able to download the results file
2. Add - form for ordering new calculations

To **start NoMoRe** three files are needed:

1. Results of periodic ab-initio Gamma point frequency calculations - from CRYSTAL09 or CRYSTAL14 or CRYSTAL17 – input for such calculations can be generated by cif2crystal program (http://shade.ki.ku.dk/docs/cif2crystal.html)
2. Structure factors files in shelx format (hkl file)
3. Input file for shelx (.ins file)

In addition, the following fields are available in the form. *(Those with a default value are required.)*

- name and description - for identification purposes
- parameters:

Temperature: single-crystal X-ray diffraction measurement temperature

Number of refined frequencies:

1. **Heat capacity estimation –** the best is to refine only few the lowest frequencies! Refinement of only acoustic modes (0-2) in many cases is enough. With too many refined frequencies heat capacity might be inaccurate!

2. **H-ADPs estimation** - the best would be to try different refinements, and increase number of refined frequencies until wR2 convergence.

The output files:

final.cif – final cif file with ADPs calculated after refinement

NoMoRe.log – final log file, contain number of refined frequencies, final wR2, final frequencies

NoMoRe.frequencies – final frequencies after NoMoRe, can be used for further thermodynamic functions estimation

NoMoRe.debug – contain wR2, scaling factors and frequencies after each refinement step

shelxl_results.p and least_squares_result.data – pickled files which can be used for standard uncertainties estimation by auxiliary program read_results.py

How refinement is conducted?

The normal-mode coordinates and frequencies are derived from the dynamical matrix.

The mean square displacement can be calculated as (Willis & Pryor, 1975; Madsen, 2011):

$$\boldsymbol{B_{atom}}(k) = \frac{1}{Nm_k} \sum_{jq} \frac{E_j(\boldsymbol{q})}{\omega_j^2(\boldsymbol{q})} \; e(k|j\boldsymbol{q})e^*(k|j\boldsymbol{q}))^T .$$

Where $e(k|j\boldsymbol{q})$ represents the kth component of the eigenvector e(jq) and correspond to atom k in normal mode j along the wavevector q. $\omega_j^2(\boldsymbol{q})$ is the frequency of mode j , m_k is the mass of atom k and $E_j(\boldsymbol{q})$ is the energy of the mode, given by

$$E_j(\boldsymbol{q}) = \hbar\omega_j \; (\boldsymbol{q}) \left\{ \frac{1}{2} + \frac{1}{\exp\left[\hbar\frac{\omega_j \; (\boldsymbol{q})}{k_B T}\right] - 1} \right\}$$

where k_B is the Boltzmann constant. These atomic MSD matrices are directly related to the ADP matrix by a transformation of coordinate basis.

In approximation, which we use the atomic Debye-Waller factors are therefore based on mean square displacement matrices where the summation is over all phonon branches, but without the q-dependence,

$$\boldsymbol{B}_{atom}(k) = \frac{1}{Nm_k} \sum_j \frac{E_j}{\omega_j^2}\, e(k|j)e^*(k|j))^T.$$

$$E_j = \hbar\omega_j \left\{ \frac{1}{2} + \frac{1}{\exp\left[\hbar\frac{\omega_j}{k_B T}\right] - 1} \right\}.$$

The variables refined against the observed structure factors are those usually refined in a standard structure refinement, namely scaling parameters, atomic coordinates, occupancies, etc., but the refinement of anisotropic displacement parameters is replaced by the refinement of the frequencies ω_j of the normal mode vibrations. We include all normal modes in the calculations of DW factors, but we only refine a small subset of the modes with lowest frequencies. Notice that the normal mode vectors (e(k|j) or e(k|jq)) are not altered during the refinement, and remain as computed.

Refinement details

Initially all normal mode coordinates and their frequencies are derived from the CRYSTAL17 calculations. Each frequency is assigned a scaling factor of 1.0. For this model the ADPs for all atoms (including hydrogen atoms) are calculated and together with coordinates are submitted to SHELXL (Sheldrick, 2007), which calculates structure factors and all statistics and discrepancy factors (R, wR2). In the next steps of a refinement, the selected frequencies are optimized by refining frequency scaling factors against the diffraction data, in order to minimize wR2. As NoMoRe is written in Python 3, we used the least-squares minimization routine from the SciPy python package. We used a Trust Region Reflective algorithm25. The trust region for the frequency scaling parameters was chosen to be from 0 to 6.

It is important to stress that in current version of NoMoRe positions and ADPs are not refined at any stage of the refinement procedure. ADPs are always computed directly from the normal mode frequencies, which for high frequency modes are obtained from CRYSTAL calculations and for low frequency modes are refined against X-ray diffraction data.