s3.m2.p7.la **Automatic model correction by the wARP/ARP method.** I.M.L. Billas, L. Moulinier, A. Podjarny and D. Moras. *Laboratoire de Biologie Structurale, Institut de Génétique et de Biologie Moléculaire et Cellulaire, CNRS/INSERM/Université Louis Pasteur/ College de France, 1, rue Laurent Fries, 67404 Illkirch, C.U. de Strasbourg, France.*
Keywords: macromolecular crystallography, crystallographic computing, methodology.

The weighted automated refinement procedure (wARP) is nowadays well established as a powerful method which allows automatic model building provided high resolution data (beyond about 2.4 Å) is available. This produces improved crystallographic phases. However, even in cases where wARP does not lead to a complete model, it can be utilised as a tool for checking the correctness of partially built structures. This method can be an alternative to more conventional methods which use unbiased R_{free} maps for correcting errors in the structural model. Here, we report the results of a systematic study of model corrections based on the wARP procedure. In particular we describe as an example the case of a recently solved structure of an orphan nuclear receptor ligand binding domain. The efficiency of the wARP method to correct tracing errors is compared to the more classical scheme based on a combination of simulated annealing and omit map calculations. Our model test case consists of the final protein structure in which a small helical part has been replaced by a loop, mimicking an actual tracing error. We show that wARP is able to detect and rebuild this small region of the protein, therefore drastically improving the quality of the phases and allowing further structure building. Furthermore we investigate the power of wARP for correcting this wrongly traced region for different levels of completeness of the structural model, and we show that more conventional methods are not able to correct this type of errors.

s7.m6.p4.la **The challenge of anomalous diffraction experiments at the M_V edge (3.5 Å) of uranium.** M.-L. Chesne[a], E. Fanchon[a], R. Kahn[a], H. Stuhrmann[a,b] and J. Vicat[a]. [a)]*Institut de Biologie Structurale J.-P. Ebel CEA/CNRS, F 38027 Grenoble France,* [b)]*GKSS Geesthacht Germany.*
Keywords: anomalous diffraction, uranium M_V edge, soft X-rays.

Uranium exhibits a huge resonance in its M_V absorption edge ($\lambda = 3.5$ Å) with an imaginary scattering factor, f'', greater than 110 electron units[1,2], which makes it very attractive for MAD experiments in macromolecular crystallography. X-ray diffraction at wavelengths beyond 3 Å opens new perspective for determination of large macromolecular structure : the large anomalous factor of uranium at M_V edge is likely to extend by an order of magnitude the range of molecular weights which can be handled by MAD method with synchrotron radiation. But the use of soft X-ray diffraction is still a technical challenge because of the large attenuation of X-rays by air: experiments are either conducted in a helium atmosphere or in vacuum. Most of biological samples require an aqueous environment and a nitrogen gaz flow for cryo-cooling. First feasibility studies of soft X-ray diffraction have been done at the beam line ID1 of ESRF, Grenoble. The MAD method was used to study an uranium derivative of asp-tRNA synthetase at 4 wavelengths in the U M_V edge. Reflections have been observed up to 4 Å resolution. Most of observed reflections were weak: on the 2200 expected reflections 750 could be observed at 3 wavelengths at least (310 reflections at 4 wavelengths). Dispersion effects due to uranium are clearly visible in these data. Progress in anomalous diffraction at M_V edge of uranium is expected from:
- new uranium derivatives. Uranyl salts often lead to numerous sites with low occupancy (<0.5). In order to get higher site occupancy and thus to increase the anomalous effect per site, some new neutral or charged uranyl complexes have been tested with lysozyme. Results with these uranyl derivatives will be presented.
-the adaptation of a CCD camera to an evacuated environment. Without beryllium window the camera has to be kept in the dark and in the absence of humidity. The CCD camera will cover a solid angle of typically 28% of the unit sphere. An on-line cylindrical image plate scanner would be more appropriate for the simultaneous measurement of the diffraction accessible with the sample cell described hereafter.
-the use of a vacuum-tight cold gas flow cell reasonably transparent for low energy X-ray photons. As diffraction of 3.5 Å photons extends to relatively larger angles, the cylindric cell is open from $-120° \le 2\theta \le +120°$ and from –60° to +60° in the vertical direction, resulting in an open solid angle of 57% of the unit sphere. Such a sample cell is presently under construction and will be presented.

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