Broken symmetries in macromolecular crystallography

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The space-group symmetry of a crystal structure imposes a point-group symmetry on its diffraction spectrum, giving rise to so-called symmetry-equivalent reflections. This introduces a certain redundancy in diffraction data recorded with area detectors and is exploited in macromolecular X-ray crystallography to increase the accuracy of the data by averaging over the symmetry-equivalent measurements (data merging).

We will discuss two instances where the symmetry in reciprocal space is broken, *i.e.* where symmetry-related reflections are no longer equivalent. One such situation occurs in the presence of resonant (anomalous) scattering, when the resonant sites display anisotropy in their local atomic environment. The second example of a broken symmetry is when the sample suffers from site-specific radiation damage during the X-ray measurement. Both situations commonly occur in macromolecular crystallography. In such cases, the genuine intensity differences between symmetry-related reflections can actually be exploited to yield useful phase information in the structure solution process. In this approach, the usual separation of the data merging and phasing steps is abandoned. At the phasing stage, structural (*i.e.* real-space) models are refined which can account for the observed intensity differences between symmetry-related reflections, thus yielding phase information.

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