Recently implemented modules and features in the PROTEIN program system will be in focus that provide high flexibility in the area of density modification and manipulation in real space.

Real space techniques have been an important issue in PROTEIN from its very beginning. Original goals of the "search methods" in the field of molecular replacement have been the correlation of maps for the exploration of non-crystallographic symmetry (Patterson self-rotation), positioning of known molecular models in unknown structures (cross rotation, translation) both in Patterson and Fourier map, location and refinement of local axes in Fourier map, calculation of "mean Fourier maps", and rotated density maps.

The widely used density modification techniques like molecular averaging and solvent flattening aiming at phase improvement and interpretability of density maps have required further extension and flexibility of these capabilities. Following the principles of PROTEIN, this has been achieved by implementing additional modules and features (e.g. simple map algebra incl. rotation and superposition, unit-cell generation from an asymmetric unit, mask calculation by convolution techniques). In this way tools are provided to the user he can combine with the already present elements to powerful procedures on the level of PROTEIN'S flexible command language.

PROTEIN itself has been ported to a variety of platforms and is available for the most prominent Unix systems incl. DEC Alpha, Silicon Graphics, IBM RS/6000, Sun and Hewlett Packard, as well as OpenVMS on VAX and AXP, on particular request.

The Web page http://www.biochem.mpg.de/PROTEIN/ home.html provides detailed information about the package's capabilities, availability, new features, examples, a mailing list for the user community, etc.

A function has been derived through which it is possible to calculate from an atomic model, the appearance of an electron density map at any arbitrary experimental resolution [Chapman (1995) Acta Crystallogr. A51: 69-80]. This serves as the basis of a stereochemically restrained refinement protocol that is very fast when applied to local regions and overcomes many of the problems with previous implementations of real-space refinement. This method has been used in the refinement of 3 virus structures [Chapman & Rossmann (1996), Acta Crystallogr. in press; Balaji & Caspar, in prep.; Blanc et al., IUCR abstract]. The method shows promise for protein crystallography in bridging between model building and reciprocal space refinement, to help bring an initial model within the convergence radius of conventional refinement. The results of ongoing systematic tests with maps of various qualities will be presented. The same mathematical models of electron density are being used for the improvement of indices that measure the quality of a model on a residue-by-residue basis. They are also being used at low (~20 Å) resolution in the development of methods to orient and position domains of known structure within electron micrograph images of large assemblies. The authors will summarize the theoretical foundation common to all of these applications, and present some of the recent results that demonstrate the success of this approach.