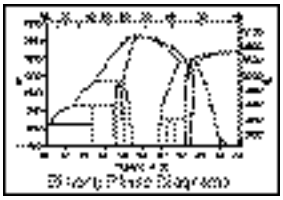
Desktop Microscopist

Desktop Microscopist has been written to supply a broad range of computational and representational methods for the electron/x-ray microscopist and material scientist with the highest degree of flexibility, ease of use and user/program interactivity possible given current technology. Starting from a set of simple programs written on a PDP-11, it evolved to its present state through a direct link to Diffract, a program which was written by Eric Schlienger, Jim Stanley and Hamish Fraser on a MacPlus and a couple of MacIIs. The current version, DM2.0 has been written to solve the day to day questions of working crystallographers. Now you can extract information, postulate models, compare your models with previous workers and simulate experimental results all from the same program.

With Desktop Microscopist 2.0, you get all of DM 1.0's capabilities,and in addition, full dynamic simulations of CBED and SAD patterns, dislocation image simulations, a Monte Carlo modeling package, experimental data reduction for calculating primitive lattices, graphical determination of crystal orientation, point and click orientation relationships, the ability to search four different types of data sets (DM crystals, JCPDF Powder File, the EDD and the NBS Crystal Database (200,000+ crystals), linking, picture distortion correction, speed enhancements (as much as 10x faster calculating diffraction patterns)



Furthemore, every section has dozens of functions added to make your task easier and the data you need accessible and controllable. For example, the SAD section allows the user to simulate diffraction patterns from up to four different crystals and any number of orientations. In addition, DM 2.0 gives control over the exact beam orientation and the ability to control the beam using a double tilt stage simulation that can be tied to your own stage. The user can also elect to create a table of diffracted values, explore the effects of crystal shape and size, and search and overlay patterns generated from crystals found in four separate database sets. Then, the user can import images from actual experiments and use DM 2.0 to extract primitive cell volumes, full primitive cells, orientation relationships which can be plotted to a linked stereogram etc..

A new feature with Desktop Microscopist 2.0, is the ability to link windows. When windows are linked they maintain the same crystals, the same orientation relationships, the same stage orientation, and the same beam orientation. If, dynamic linking is active, all linked windows are immediately updated when any of the linked objects are altered with respect to crystal definition, orientation relationship, stage orientation or beam orientation. This allows the user to quickly update various representations of the experimental situation efficiently, and to gain some insight into the relationship between reciprocal space and the corresponding real space representation.

Please refer to the following URL for additional information: http://easystreet01.easystreet.com/~lacuna/

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