

**MANY PATTERNS AND MANY METHODS:
NEW METHODS UTILISING MULTIPLE ANALYSIS TECHNIQUES IN
POLYMORPH AND SALT SCREENING SYSTEMS**

Gordon Barr, Christopher Gilmore, and Gordon Cunningham,
*WestCHEM, Department of Chemistry, University of Glasgow, Glasgow
G12 8QQ, Scotland, UK. E-mail: snap@chem.gla.ac.uk*

In high throughput crystallisation experiments designed to search for polymorphs, solvates, co-crystals etc., it is usual to consider powder X-ray diffraction (PXRD) data as the primary source of information for classifying the results, and most software used in this environment is designed to use such data [1]. In fact it is often referred to as the 'gold standard'. However, PXRD data can have difficulties with preferred orientation, sample distribution, crystallinity etc., which is not always the case for other complimentary methods that are also available.

Methods developed to work with PXRD as a fingerprinting technique must be flexible to deal with different techniques; for example, although the differences in Raman spectra are often not as pronounced as those in PXRD, we have found that the same techniques we have used to match powder patterns work well with Raman data providing the data have been properly smoothed and the background subtracted.

We have developed a computer program to address these issues [1] that uses techniques of multivariate analysis and classification as well as sophisticated data visualization methods to present and interpret the results. This method uses the full measured spectra not only the peaks, with additional options of using gradient data either by itself or in conjunction with the original spectrum. Additionally, raw numeric data (*e.g.* melting points; sample preparation information) can be incorporated into the analysis. We will present pharmaceutical examples involving data collected using PXRD, Raman, IR and DSC methods, where the spectroscopic data outperforms that of the PXRD data, and where combining the results from multiple data methods can (a) provide better results than any single individual method, and (b) highlight where there are inconsistencies or problems between different techniques.

Additionally, new visualization tools to help interpret results from salt-screening systems will also be introduced, as well as methods to prescreen a new unknown sample against a large (>10,000 patterns) in-house database of identified samples.

[1] Barr, G., Dong, W. & Gilmore, C.J. *J. Appl. Cryst.* (2004). **37**, 658-664