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3.3. CLASSIFICATION AND USE OF POWDER DIFFRACTION DATA

diffraction measurements were made, how the refinement was performed *etc*. While reflection tables for each phase can be placed in each phase block, it is better to include a single reflection table in the block that contains the diffraction data. This block will also contain a phase table that uses the block pointer _pd_block_diffractogram_id to link to the phase blocks. The phase blocks can also be linked to the data block using the block pointer _pd_phase_block_id. For most Rietveld refinements, each phase is allowed to have different profile parameters, so _pd_proc_ls_profile_function should also be included in the phase-table loop.

3.3.9.3. One phase, multiple sets of measurements

It is fairly common to use more than one diffraction data set to determine a model for a single phase. Some examples include: combined refinement using both neutron and X-ray powder diffraction; use of multiple X-ray wavelengths to make use of anomalous dispersion; and the use of single-crystal X-ray and powder neutron diffraction data in a single refinement. For these cases, there will be a CIF block for each data set. Each of these blocks will contain a reflection table and a loop with the observed and calculated diffraction intensities, as described in Section 3.3.9.1.

As explained in Section 3.3.7, the resulting structural parameters could be placed in a block with one of the sets of diffraction data. However, it is better practice to create one additional block for these parameters, as it then becomes clear that the result is from a combined refinement. This is indicated by linking the phase block and the data-set blocks using a loop of _pd_block_diffractogram_id values in the phase block. The data-set blocks can also have a link to the phase information using the block pointer pd phase block id.

3.3.9.4. Multiple sets of measurements and phases

Multiple data sets may be used for mixtures as well as single phases. This is becoming increasingly common as more complex materials are studied using powder diffraction. The treatment of this case follows logically from that of Sections 3.3.9.2 and 3.3.9.3. If there are M diffraction data sets and P phases, there will be P blocks containing the crystallographic parameters for each phase. There will be M blocks with the observed and calculated diffraction intensities, as well as reflection tables. Depending on the Rietveld software, there may be $M \times P$ sets of some parameters, for example phase fractions and profile descriptions. These parameters may be placed in the phase table loop within the dataset block(s).

Ideally, the same specimen, or at least the same sample, will be used for all measurements. Sometimes, however, different samples are used for combined refinements to extend the number of observations, despite the possibility that the samples might have slightly different structures or compositions. If there are *S* samples, there will be an additional *S* blocks that record the sample and specimen preparation and characterization information. Thus, in this case there will be a total of M + P + S blocks.

As before, the phase blocks will use the block pointers <u>pd_block_diffractogram_id</u> to link to the data-set blocks. Likewise, the data-set blocks will have phase tables with <u>pd_phase_block_id</u> values that link to the phase blocks. The sample blocks can use both <u>_pd_block_diffractogram_id</u> values and <u>_pd_phase_block_id</u> values to link to the the diffraction data and the analysis results. This is shown in the CIF in Example

Example 3.3.10.1. Phase identification using a reflection table and a phase table. 100p pd peak 2theta centroid pd peak id 3 A1 4 B1 6 A2 8 B2 9 A3 12 A4 15 A5 16 B3 loop refln index h _refln_index_k refln index 1 pd refln peak id _pd_refln_phase id ? ? ? A1 Phase1 ? ? ? A2 Phase1 ? ? ? A3 Phase1 ? ? ? A4 Phasel ? ? A5 Phasel loop _____pd_phase id _pd_phase_name Phase1 'component 1'

3.3.7.1. The program *GSAS2CIF* (Toby *et al.*, 2003) can create CIFs for multiple sets of measurements and phases.

3.3.10. Other pdCIF applications

As mentioned above, there are other applications for pdCIF than the storage of unprocessed measurements and the reporting of the results of a Rietveld refinement. This section describes the use of data items in other common pdCIF applications.

3.3.10.1. Simulated intensities

It is common to simulate a diffraction pattern from a known or hypothetical structural model. The structural model is recorded in CIF using core data items, such as <u>_atom_site_label</u>, <u>_atom_site_fract_x</u>, <u>_atom_site_fract_y</u>, <u>_atom_site_fract_z</u>, <u>_atom_site_Uiso_or_equiv</u> and <u>_atom_site_occupancy</u>, as well as the unit cell in <u>_cell_length_*</u> and <u>_cell_angle_*</u>. Calculated reflection intensities can be recorded using <u>_refln_index_*</u> and <u>_refln_F_squared_calc</u>, as described in Section 3.3.5.4. The simulated pattern can be recorded using <u>_pd_calc_*</u> data items, as described in Section 3.3.5.2.

The simulated diffraction pattern will be determined not only by the structural parameters, but also by the type of experiment that is being simulated. For example, it is good practice to define data items to specify the type of radiation in _diffrn_radiation_probe, the wavelength in _diffrn_radiation_wavelength and the profile in _pd_proc_1s_ profile_function.

3.3.10.2. Phase identification and indexing

For phase identification, a CIF will include unprocessed measurements, as described in Section 3.3.8. Sample characterization information, for example chemical analysis information, can often aid phase determination. Characterization information is described in Section 3.3.4.1. Similarly, sample preparation information can also be quite valuable (see Section 3.3.4.1). Since preferred orientation or other artifacts of the measurement can make phase Table A3.3.1.1. *Categories in the powder CIF dictionary* Numbers in parentheses refer to the section of this chapter where each category is described in detail.

PD_BLOCK group (§3.3.7)	PD_MEAS group (§3.3.4.4)
PD_BLOCK (§3.3.7)	PD_DATA (part of category) (§3.3.4.4(a))
PD_CALC group (§3.3.5.2)	PD_MEAS_INFO (§3.3.4.4(b))
PD_CALC (§3.3.5.2(b))	PD_MEAS_METHOD (§3.3.4.4(c))
PD_DATA (part of category) (§3.3.5.2(a))	PD_PEAK group (§3.3.5.3)
PD_CALIB group (§3.3.4.3)	PD_PEAK (§3.3.5.3(a))
PD_CALIB (§3.3.4.3(a))	PD_PEAK_METHOD (§3.3.5.3(b))
PD_CALIBRATION (§3.3.4.3(b))	PD_PHASE group (§3.3.6.1)
PD_CHAR group (§3.3.4.1)	PD_PHASE (§3.3.6.1)
PD_CHAR (§3.3.4.1(a))	PD_PREP group (§3.3.4.1)
PD_DATA group	PD_PREP (§3.3.4.1(b))
pd_calc_ * items (§3.3.5.2(<i>a</i>))	PD_PROC group (§3.3.5.1)
pd_instr_var_illum_len	PD_DATA (part of category) (§3.3.5.1(a))
$(\S3.3.4.3(d))$	PD_PROC_INFO (§3.3.5.1(b))
_pd_meas_ * items (§3.3.4.4(<i>a</i>))	PD_PROC_LS (§3.3.5.1(c))
pd_proc_ * items (§3.3.5.1(<i>a</i>))	PD_SPEC group (§3.3.4.2)
PD_INSTR group (§3.3.4.3)	PD_SPEC (§3.3.4.2)
PD_DATA (part of category) (§3.3.4.3(d))	REFLN group (§3.3.5.4)
PD_INSTR (§3.3.4.3(c))	REFLN (§3.3.5.4)

identification more difficult, it is a good idea to include specimen preparation and mounting information, as described in Section 3.3.4.2.

Peaks will be located and documented in the peak table, as discussed in Section 3.3.5.3. In this case, it can be very helpful to specify $pd_peak_wavelength_id$ for peaks that are clearly a $K\alpha_2$ component. Similarly, recording a peak width can also be helpful for some autoindexing programs.

To identify peaks by phase in the case where at least one phase in a material is known but other peaks remain unidentified requires the use of a reflection table and a phase table, as shown in Example 3.3.10.1. This example shows a diffraction pattern with eight peaks, of which five have been identified as arising from a phase where the unit cell has not yet been determined. The peaks labelled B1, B2 and B3 are referenced in the peak table, but are not defined in the reflection loop. This implies that they arise from an unknown phase or phases. The remaining peaks A1 to A5 are referenced in the peak table. Note that the reflection table must include the _refln_index_* data items, even though no reflection indices are assigned. This is because CIF rules require that the _refln_index_* data items be present in this loop, as noted in the pdCIF dictionary definitions for _pd_refln_peak_id and _pd_refln_phase_id. The place holder ? is used to indicate that the reflection indices are not yet known.

Appendix 3.3.1 Category structure of the powder CIF dictionary

Table A3.3.1.1 provides an overview of the structure of the powder CIF dictionary by informal category group.

Many people contributed to the creation of this dictionary, most notably Syd Hall, I. David Brown and Brian McMahon. Ian Langford helped considerably with the evolution of the dictionary. This project also benefited from the efforts of many members of the PDF-3 Database Format Subcommittee of the International Centre for Diffraction Data; I am particularly indebted to Walter Schriener for useful concepts and discussions. My initial involvement with powder diffraction file formats was prompted by the encouragement of Richard Harlow; I may someday forgive him.

References

- Finger, L. W., Cox, D. E. & Jephcoat, A. P. (1994). A correction for powder diffraction peak asymmetry due to axial divergence. J. Appl. Cryst. 27, 892–900.
- HDF (1998). NCSA HDF home page. http://www.hdfgroup.org/.
- International Centre for Diffraction Data (2004). Powder Diffraction File. International Centre for Diffraction Data, 12 Campus Boulevard, Newtown Square, Pennsylvania, USA. http://www.icdd.com.
- Le Bail, A., Duroy, H. & Fourquet, J. L. (1988). Ab initio structure determination of LiSbWO₆ by X-ray powder diffraction. Mater. Res. Bull. 23, 447–452.
- NeXus (1999). NeXus data format. http://www.nexusformat.org.
- Pawley, G. S. (1981). Unit-cell refinement from powder diffraction scans. J. Appl. Cryst. 14, 357–361.
- Rietveld, H. M. (1967). Line profiles of neutron powder-diffraction peaks for structure refinement. Acta Cryst. 22, 151–152.
- Rietveld, H. M. (1969). A profile refinement method for nuclear and magnetic structures. J. Appl. Cryst. 2, 65–71.
- Toby, B. H. (2003). CIF applications. XII. Inspecting Rietveld fits from pdCIF: pdCIFplot. J. Appl. Cryst. 36, 1285–1287.
- Toby, B. H., Von Dreele, R. B. & Larson, A. C. (2003). CIF applications. XIV. Reporting of Rietveld results using pdCIF: GSAS2CIF. J. Appl. Cryst. 36, 1290–1294.