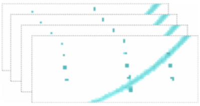

Current Status of the imgCIF dictionary and Related Software - a Work in Progress

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Introduction

What is imgCIF/CBF?

1. A clearly defined set of terms to use in describing raw diffraction images and the way in which they were collected; and
2. A workable and efficient format in which to record, archive and transmit this information; and
3. Support software (e.g. CBFlib)

Status?

Little use, some support (fit2d, mosflm, adxv)

Community uses dozens of distinct formats

Use starting now at SLS and Diamond

Introduction (cont.)

Pending Issues?

1. Integration with SAS
   - Axis definitions without a goniometer
2. miniCBFs
3. Jiffies

Why Does imgCIF/CBF exist?

Issue:

Managing massive amounts of data in structural biology; e.g. in proteomics

Problem:

Many different data formats.

Practical Solution:

Provide a common approach to interchange

Crystallographic Information Framework (CIF)

Crystallographic Information Framework (CIF)

Started in 1990 by the International Union of Crystallography to reduce friction in managing structural data

[Hall, Allen, Brown 1991] [Hall, McMahon 2005]

Great success in handling of structural data for small molecules

Clarified the terms for macromolecules

mmCIF, PDBML

Effort to bring similar organization to synchrotron image data

imgCIF/CBF

Other Important Frameworks

CCP4 [CCP4 1994]

Collaborative Computational Project, No. 4, (CCP4) is a suite for protein crystallography. It “is a set of separate programs which communicate via standard data files”. Many programs have been adapted to CCP4 file formats

XML [Bray, Paoli, Sperberg-McQueen 98]

The eXtensible Markup Language is a text-based approach to marking up documents that has become a standard tool for managing data about data (metadata), e.g. in PDBML and CML.

Other Important Frameworks

NeXus [Klosowski et al. 1998].

"NeXus is a data format for the exchange of neutron and synchrotron scattering data between facilities and user institutions. It has been developed by an international team of scientists and computer programmers from neutron and X-ray facilities around the world. The NeXus format uses the hierarchical data format (HDF) that is portable, binary, extensible and self-describing. The NeXus format defines the structure and contents of these HDF files in order to facilitate the visualization and analysis of neutron and X-ray data. In addition, an application program interface (API) [was] produced in order to simplify the reading and writing of NeXus files. The details of the format are available at http://www.neutron.anl.gov/NeXus/".

What Makes CIF Different

CIF clearly defines its terms in dictionaries

- core CIF, powder CIF , modulated structures CIF, electron density CIF, macromolecular CIF, image CIF, symmetry CIF

The same terms can then be used in multiple formats with no loss of information

- e.g. mmCIF vs PDBML

CIF is very database-friendly

CIF is documented (IT Volume G)

CIF supports arrays, binary and compression well

What Makes CIF Relevant?

"Diamond intends to provide their PX beam lines with imgCIF data, but to work to having a true [NeXus] infrastructure. Soleil intends to produce imgCIF for their PX beam lines and simply to encapsulate the imgCIF data sets as data (headers and all) within a [NeXus] infrastructure. ISIS is working purely in [NeXus]. At the moment, the critical need seems to be for both [NeXus] and imgCIF instrument definitions. [NeXus] seems to be well equipped with neutron instrument tokens and the X-ray tokens are a work soon to be in progress. ..."

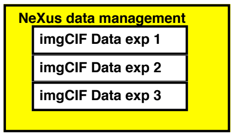
-- from email summary for the group by HJB subsequent to meeting at Diamond, 10 January 2006

Where Should imgCIF, NeXus and mmCIF fit?

imgCIF dictionary extends mmCIF to manage data images

NeXus to provide a data framework within which to manage multiple sets of experimental data for multiple experiments

mmCIF provides the base within which to manage the entire crystallographic experiment



Integration with SAS

1998 -- 2007 -- cif_sas.dic Marc Malfois, Dmitri Svergun, revisions by I. D. Brown

Add categories for description of beam, detector and sample

Needs work to align with imgCIF, mmCIF

Major issue: axis definitions

miniCBFs

Issues

- Not all information available at time of data collection
- Time constraints may limit complexity of what can be written
- Processing programs may need a minimal header

Issues came to a head in setting up for SLS detector

Proposed solution

- Write miniCBF at collection
- Convert to full imgCIF with convert_minicbf program

Jiffies

Small programs to convert to/from imgCIF
Recommended by Hawaii imgCIF workshop in 2007
Conversion to imgCIF from MAR and ADSC working
Work on Bruker-AXS starting
2 year project funded by DOE starting now

Upcoming imgCIF Workshops

See: http://www.medsbio.org/meetings

Diamond, 17 Aug 2007 (H. Bernstein, A. Ashton)

Third imgCIF workshop (new series) at BSR 2007 in Manchester and at Diamond. Sponsored by DOE under grant ER64212-1027708-0011962, NSF under grant DBI-0610407.

bsr_imgcif_aug07@medsbio.org

Software status

CBFlib (http://arcib.dowling.edu/CBF) provides

API (C function library, under GPL or LGPL, your choice)
  more compressions, major speedup, support for maps
Manual and sample files
Utilities (under GPL only)
  convert_image (works for Mar or ADSC)
  convert_miniCBF (e.g. for SLS images)
  cif2cbf
  vcif2

mosflm (http://www.mrc-lmb.cam.ac.uk/harry/mosflm/) supports imgCIF

adxv (http://www.scripps.edu/~arvai/adxv.html) supports imgCIF

Status of CIF in PX

Core CIF (used for ligands):
An effective, working standard, heavily used

mmCIF (macromolecular structures):
Some use, community prefers old PDB format.

imgCIF (synchrotron data images, other images):
Little use, some support (fit2d, mosflm, adxv)
Community uses dozens of distinct formats
Use starting now at SLS and Diamond

Problem

Use of many different data formats causes delay and confusion; may lead to errors

Synchrotron image data formats:

Wladek Minor is “dealing with 197 (!!!!) frame formats” [email Wladek Minor to H. J. Bernstein, 15 May 2006].

2003 Denzo manual lists 107 available detector formats [Gewirth 2003] [Otwinowski, Minor 1997]

An Impractical Solution
(The Esperanto Solution)

Mandate one perfect format for everyone to use for everything (internals and externals)

Not workable:

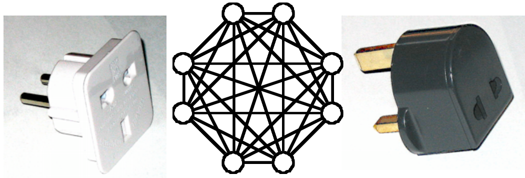
Might suppress new ideas and good science

There is no agreement on the “perfect” format
  What is perfect for the internals of one project might be imperfect for the internals of another project

A Solution: Focus on Interchange

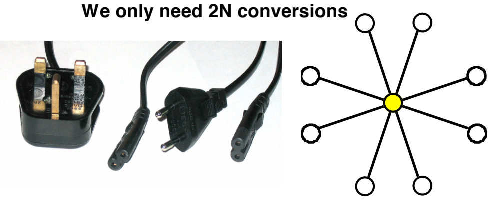
Include adapters with/in each system to handle many formats

For N systems with N-1 foreign formats, need N*(N-1) adapters



A Better Solution

Provide a common format for interchange (e.g. CIF)
- Instead of N*(N-1) conversions
- We only need 2N conversions



The Basics of imgCIF

There are multiple types of CIF

- DDL1 CIFs (e.g. coreCIF, pdCIF)
- DDL2 CIFs (e.g. mmCIF, imgCIF)
- DDL3 is coming

CIF Dictionaries define the terms that can be used and their relationships.

Users can add terms of their own, but you should not use an existing term with a meaning that conflicts with the meaning in a dictionary or in a way that could be confused with terms that have been officially adopted.

For all CIFs:

- Information is organized into blocks of data
- Each block of data is managed essentially in terms of tables
  - Tables are called “categories” or “loops”
  - The column headings are called tags” or “data names”
  - Some tables have only one row of data
    - then each tag can be put with its value
  - Some tables have multiple rows of data

- A given tag can appear only once in a block

- DDL1 CIFs treat all categories similarly
- DDL2 CIFs explicitly state relationships
  - e.g. parent-child relationships

imgCIF is a DDL2 dictionary that extends the macromolecular CIF (mmCIF) dictionary.

imgCIF Categories

- ARRAY_DATA
  - presents the actual numeric data
  - (e.g. the numeric values of the pixels in an image)
- ARRAY_INTENSITIES
  - tells you what you need to do to recover intensities form ARRAY_DATA values
- ARRAY_STRUCTURE
  - how the bits and bytes are organized
  - ARRAY_STRUCTURE_LIST
    - how the array dimensions are organized
    - ARRAY_STRUCTURE_LIST_AXIS
      - how axis settings relate to array indices
- AXIS
  - the physical parameters of each axis

imgCIF Categories (cont.)

- DIFFRN
  - mmCIF category describing diffraction data
  - DIFFRN_DATA_FRAME
    - details about each frame of data
  - DIFFRN_DETECTOR
    - information about each detector
    - DIFFRN_DETECTOR_AXIS
      - information about each detector axis
    - DIFFRN_DETECTOR_ELEMENT
      - layout of detector elements
  - DIFFRN_MEASUREMENT
    - goniometer information
    - DIFFRN_MEASUREMENT_AXIS
      - information about each goniometer axis

imgCIF Categories (cont.)

- DIFFRN_RADIATION
  - incident radiation (crossfire, polarization, etc.)
  - DIFFRN_REFLN
    - reflection-by-reflection parameters for each frame
  - DIFFRN_SCAN
    - relationship of axis settings to scans
    - DIFFRN_SCAN_FRAME
      - relationship of particular frames to scans
      - DIFFRN_SCAN_FRAME_AXIS
        - relationship of axis settings to particular frames

imgCIF Categories (cont.)

Categories under development

- MAP
  - density maps and masks
  - MAP_SEGMENT
    - bricks, slices and other segments of maps

Similar categories for compressed binary arrays are being considered.

CIF Syntax

A collection of data blocks

Each data block contains data names (tags) and their values

White space delimits tokens

Tags start with a leading underscore ("_") to distinguish them from values
- Values that might be confused with data names or keywords or that contain whitespace are quoted

Quoting
- single quote (single line only)
- double quote (single line only)
- semicolon in column 1 (multiple lines OK)

- terminal quote mark must be followed by whitespace

- Characters with special meaning
  - Underscore
  - Quote marks
  - Period (“.”) or question mark (“?”) (null value)
  - Hash mark (“#”) (comment)
- Reserved words
  - "global_", "data_", "loop_", "stop_", and "save_"

In addition to the underscore, and the three quote marks, three other characters have special meaning: the period ("."), the question mark ("?") and the hash mark ("#"). The period is used when no value is specified. The question mark is used when a value is desired but not available. The hash mark indicates that the remaining characters on that line are part of a comment.

There are a small number of reserved words:
"global_", "data_", "loop_", "stop_", and "save_".
The last two reserved words are not used by CIF but are reserved to prevent conflict with the language from which CIF is derived (STAR). "global_" and "data_" mark the start of a data block.

"data_" should be followed immediately with the name of the block, without intervening whitespace.

If "loop_" appears, it is followed by a sequence of tags without intervening data values. Those tags are considered as the column headings of a table. These are followed by rows of data values corresponding to those column headings.

Outside of a table, tags and data values appear in simple alternation. Within a data block a given tag may appear only once.

The meaning of a CIF document is not altered by changing the order of presentation of data blocks nor is it altered by changing the order of presentation of tags within a block.

There are two styles of CIF in use for crystallography: DDL1 and DDL2.

DDL1 CIF (e.g. coreCIF, pdCIF)

Partial example of a small molecule coordinate list [Longridge 98]

```
loop_
_atom_site_label
_atom_site_fract_x
_atom_site_fract_y
_atom_site_fract_z
_atom_site_U_iso_or_equiv
_atom_site_adp_type
_atom_site_calc_flag
_atom_site_refinement_flags
_atom_site_occupancy
_atom_site_disorder_assembly
_atom_site_disorder_group
_atom_site_type_symbol
Fe1 1 0 1 .0084(2) Uani d S 1 . . Fe
Na1 .50907(11) .13980(8) 1.09450(9) .0185(3) Uani d . 1 . . Na
Na2 .89904(10) .37128(8) 1.21657(9) .0171(3) Uani d . 1 . . Na
C1 .7997(2) -.01740(18) 1.0419(2) .0110(4) Uani d . 1 . . C
N1 .6788(2) -.02885(18) 1.0696(2) .0166(4) Uani d . 1 . . N
C2 .9306(3) -.01004(16) .8075(3) .0130(4) Uani d . 1 . . C
```

DDL2 CIF (e.g. mmCIF, imgCIF)

Partial example of a macromolecular CIF (1CRN) as converted to mmCIF by the program pdb2cif [Bernstein et al. 98]

```
loop_
_atom_site.label_seq_id
_atom_site.group_PDB
_atom_site.type_symbol
_atom_site.label_atom_id
_atom_site.label_comp_id
_atom_site.label_asym_id
_atom_site.auth_seq_id
_atom_site.label_alt_id
_atom_site.cartn_x
_atom_site.cartn_y
_atom_site.cartn_z
_atom_site.occupancy
_atom_site.B_iso_or_equiv
_atom_site.footnote_id
_atom_site.label_entity_id
_atom_site.id
1
ATOM N N THR * 1 . 17.047 14.099 3.625 1.00 13.79 . 1 1
1
ATOM C CA THR * 1 . 16.967 12.784 4.338 1.00 10.80 . 1 2
```

ImgCIF Binary Data

```
_array_structure.id ARRAY1
_array_structure.encoding_type "signed 32-bit integer"
_array_structure.compression_type packed
_array_structure.byte_order little_endian
_array_data.array_id ARRAY1
_array_data.binary_id 1
_array_data.data
;
--CIF-BINARY-FORMAT-SECTION--
Content-Type: application/octet-stream;
conversions="x-CBF_PACKED"
Content-Transfer-Encoding: BINARY
X-Binary-Size: 3745758
X-Binary-ID: 1
X-Binary-Element-Type: "signed 32-bit integer"
Content-MD5: 1zsJjWPfol2GYl2V+QSXrw==
’ ∏P«q «q FA• f¡Æ• àR˜u<ˇ›k2˙b |5ß …
```

Background

Imagine trying to do electronics without any agreement as to how to draw schematics.

That is how we have managed massive amounts of data in structural biology.

Some points of coherence in the chaos:

- **BNL Protein Data Bank format**
  - **[Bernstein et al. 1977]**
  - ***de facto* standard for macromolecular studies**
- **CCDC's Cambridge Structural Database**
  - **[Allen et al. 1973]**
  - **de facto standard for small molecules**

Background (cont.)

In general
Each vendor of data collection equipment
Each group maintaining a software package
has their own approach to
representing and storing raw data

This causes delays and confusion -- friction -- in working with data in so many different formats

Is the Problem Real?

Date: Sat, 06 Jan 2007 16:32:12 -0500
From: Arun Malhotra <malhotra@miami.edu>
To: CCP4 Bulletin Board <ccp4bb@dl.ac.uk>

“One common source of errors is changes made in reflection or coordinate files… For example, only recently, someone in my lab just manually edited out a hkl format file to change a few reflections from the exponential format into the standard F format, so that it could be converted into the mtz format. … Format conversions (hkl to mtz or vice-versa) or simple manual edits to coordinate files are very common, and are fertile places for mistakes to creep in. Once such mistakes are made, they are not often easy to catch since there is no easy way to compare files.…”

Is the Problem Real?

Date: Sun, 07 Jan 2007 11:25:26 +0900
From: Charlie Bond <Charles.Bond@uwa.edu.au>
To: ccp4bb@dl.ac.uk

“… Often at the synchrotron one is in a tired hurry to get an image indexed and processed. If the wrong parameters are used (eg the ones from the home lab with a bit of editing), a dataset in the wrong hand can be quickly produced

“Increasingly beamlines automatically prepare the correct parameter files for you, but it is cases where images are difficult to process (low resolution, disorder) that processing may occur later at home and the details of the beamline may be disregarded.

“Correct me if I'm wrong, but even the deposition of images would not help this as the critical information is the geometry of the beamline set up which is probably not recor[d]ed with the images.

…”

Frequently Asked Questions

Can I change it?

Yes, please do. We would appreciate:

- New ideas
- New items for the dictionary
- New support software
- Bug fixes and improvements
- Translations to and from other presentations

Please don't use existing terms in ways that conflict with their meanings; define a new term with a new name instead

Frequently Asked Questions (Cont.)

The BIG Frequently Asked Question Can I make proprietary software using imgCIF and CBFlib?

Yes, the API in CBFlib is available under the LGPL.

If you change CBFlib itself, you must publish the changed source code under the LGPL, but even if you change CBFlib, you do not have to make your program into an open source program.

How to Make Changes to the imgCIF Dictionary

1. Get the best current version of the dictionary from the IUCr

2. Check that what you propose is not already there, or if there is at least an appropriate category

3. To avoid conflicts with others doing the same thing, get a prefix from Brian McMahon (bm@iucr.org)

4. If you are going to be sending files to other people, discuss your new definition with them and, please, on the imgcif-l list

5. If this will remain just a local change, use it in good health

6. If you think this should be added to the main dictionary for community use, please say so on the imgcif-l list, and, if appropriate, on other lists

7. If there is sentiment to add it to the main imgCIF dictionary, we will post a revised dictionary for comments, and then, if the dictionary working group agrees, forward the dictionary to COMCIFS for adoption

How to Use and Make or Propose Changes to CBFlib

Use:

1. Download the package (source or binary)
2. If source, build for your machine
3. If you need help building, contact yaya@dowling.edu
4. If you are using the utilities, install them in your favorite location for binaries and use them
5. If you are building an application against the API, install the library in your favorite location and use it

Changes:

1. Changes in your own programs that just use the API:
   Just do it (LGPL)
2. Changes to the API or Program
   Do it, but follow the GPL/LGPL rules on changes
   (making source available, carrying the license forward)

Credit

We would appreciate a credit and knowing about changes.
Please cite [Bernstein, Ellis 2005] (see below)

Where to Find imgCIF Information

IUCr Crystallographic Information Framework:
  International Tables, Volume G
  http://www.iucr.org/iucr-top/cif/index.html
    official copies of dictionaries and stable releases of software
Image CIF/Crystallographic Binary File (imgCIF/CBF)
  http://arcib.dowling.edu/CBF
  http://www.bernstein-plus-sons.com/software/CBF
    development versions of dictionary and software
  http://www.iucr.org/iucr-top/cif/cbf/imgcif-l
  http://scripts.iucr.org/mailman/listinfo/imgcif-l
    imgCIF discussion list (please join)
Management of Experimental Data in Structural Biology (MEDSBIO)
  http://www.medsbio.org
    A broader perspective (imgCIF, NeXus, …) concentrating on interfaces
  http://www.medsbio.org/meetings
    information on this workshop and future ones of interest
  http://scripts.iucr.org/pipermail/medsbio-l/
  http://scripts.iucr.org/mailman/listinfo/medsbio-l
    MEDSBIO discussion list (please join)
Protein Data Bank
  http://www.pdb.org
    Information on dictionaries and file format, BioSync, etc.

References

[Allen et al. 1973] Allen, F. H., Kennard, O., Motherwell, W. D. S., Town, W. G. & Watson, D. G. (1973), "Cambridge Crystallographic Data Centre. ii. Structural Data File", *J. Chem. Doc.* 13, 119 – 123.

[Berman et al. 2000] Berman, H. M., Westbrook, J., Feng, Z., Gilliland, G., Bhat, T. N., Weissig, H., Shindyalov, I. N. & Bourne, P. E. (2000), 'The Protein Data Bank', Nucleic Acids Research 28, 235 – 242.

[Bernstein et al. 1977] Bernstein, F. C., Koetzle, T. F., Williams, G. J. B., Meyer, Jr., E. F., Brice, M. D., Rodgers, J. R., Kennard, O., Shimanouchi, T. & Tasumi, M. (1977), 'The protein data bank: a computer based archival file for macromolecular structures', *J. Mol. Biol.* 112, 535 – 542.

[Bernstein 2005] Bernstein, H. J. (2005) "The Classification of Image Data", chapter 3.7 in "*International Tables For Crystallography, Volume G: Definition and Exchange of Crystallographic Data,*" S. R. Hall and B. McMahon, eds. International Union of Crystallography, Springer, Dordrecht, NL, pp. 199 – 205.

References (Cont.)

[Bernstein, Bernstein 2005] Bernstein, H. J., Bernstein, F. C. (2005) "Databanks of Macromolecular Structure", chapter 4 in "*Database Annotation in Molecular Biology,*" A. M. Lesk, ed., Wiley, Chichester, UK, pp. 63 –79.

[Bernstein, Ellis 2005] Bernstein, H. J., Ellis, P. J. (2005). "CBFlib: An ANSI C Library for Manipulating Image Data", chapter 5.6 in "*International Tables For Crystallography, Volume G: Definition and Exchange of Crystallographic Data,*" S. R. Hall and B. McMahon, eds., International Union of Crystallography, Springer, Dordrecht, NL, pp. 544 – 556."

[Bernstein, Hammersley 2005] Bernstein, H. J., Hammersley, A. P. (2005) "Specification of the Crystallographic Binary File (CBF/imgCIF)", chapter 2.3 in "*International Tables For Crystallography, Volume G: Definition and Exchange of Crystallographic Data,*" S. R. Hall and B. McMahon, eds., International Union of Crystallography, Springer, Dordrecht, NL, pp. 37 – 43.

References (Cont.)

[Bray, Paoli, Sperberg-McQueen 98] Bray, T., Paoli, J., Sperberg, C. M., eds, "Extensible Markup Language (XML)", W3C Recommendation 10-Feb-98, REC-xml-19980210, http://www.w3.org/TR/1998/REC-xml-19980210

[CCP4 1994] COLLABORATIVE COMPUTATIONAL PROJECT, NUMBER 4. 1994. ``The CCP4 Suite: Programs for Protein Crystallography''. *Acta Cryst.* D50, 760-763.

[Gewirth 2003] Gewirth, D. (2003). "*THE HKL MANUAL, A Description of the Programs Denzo, XDisplayF, Scalepack An Oscillation Data Processing Suite for Macromolecular Crystallography,*" 6th ed. (written with the cooperation of the program authors Zbyszek Otwinowski and Wladek Minor, revised and updated by Wladyslaw Majewski", http://www.hkl-xray.com/hkl_web1/hkl/manual_online.pdf

[Hall, Allen, Brown 1991] Hall, S. R., Allen, F. H. & Brown, I. D. (1991), 'The crystallographic information file (CIF): a new standard archive file. for crystallography', *Acta Cryst.* A47, 655 – 685.

References (Cont.)

[Hall, McMahon 2005] Hall, S. R. & McMahon, B. (2005), *Volume G: Definition and Exchange of Crystallographic Data, International Tables For Crystallography*, Springer: Dordrecht, chapter 1.1. Genesis of the Crystallographic Information File

[Hammersley, Bernstein, Westbrook 2005] Hammersley, A. P., Bernstein, H. J., Westbrook, J. D. (2005). "Image Dictionary (imgCIF)", chapter 4.6 in "*International Tables For Crystallography, Volume G: Definition and Exchange of Crystallographic Data,*" S. R. Hall and B. McMahon, eds., International Union of Crystallography, Springer, Dordrecht, NL, pp. 444 – 458.

[Klosowski et al. 1998] Klosowski, P.; Koennecke, M.; Tischler, J. Z.; Osborn, R. (1998). "NeXus: A common format for the exchange of neutron and synchrotron data", *Physica B: Physics of Condensed Matter*, 241,1-4, pp. 151-153.

[Otwinowski, Minor 1997] Otwinowski, Z., Minor, W. (1997). "Processing of X-ray Diffraction Data Collected in Oscillation Mode", *Methods in Enzymology, 276: Macromolecular Crystallography*, part A, pp. 307 -- 326.

References (Cont.)

[Powell 2001] Powell, H. (2001), "Recent improvements to Mosflm - version 6.11", *CCP4 Newsletter on Protein Crystallography*, 39, 18. See http://www.ccp4.ac.uk/newsletters/newsletter39/18_mosflm.html.

[Westbrook et al. 2003] Westbrook, J., Feng, Z., Chen, L., Yang, H., Berman, H. M.. (2003) "The Protein Data Bank and structural genomics," *Nucleic Acids Research,* Vol. 31, No. 1 489-4

ADDITIONAL READING

[BIOXHIT 2004]. "Bioxhit: biocrystallography (X) on a highly integrated technology platform for European structural genomics," EU Genomics News, No. 3, November 2004. See http://icarus.embl-hamburg.de/bioxhit/index.html

[Fitzgerald et al. 2005] Fitzgerald, P. M. D., Westbrook, J. D., Bourne, P. E., Mcmahon, B., Watenpaugh, K. D. (2005). "Macromolecular dictionary (mmCIF)", chapter 4.5 in "International Tables For Crystallography, Volume G: Definition and exchange of crystallographic data," Vol. G, S. R. Hall and B. McMahon, eds., International Union of Crystallography, Heidelberg: Springer, pp. 444 – 458.

[Szebenyi, Arvai, Ealick, Laluppa, Nielsen, 1997] Szebenyi, D. M. E., Arvai, A., Ealick, S., Laluppa, J. M., Nielsen, C. (1997) "A System for Integrated Collection and Analysis of Crystallographic Diffraction Data", J. Synchrotron Rad. 4, 128-135. For adxv see http://www.scripps.edu/~arvai/adxv.html

People Involved

Frances C. Bernstein

imgCIF Workshops:
- **Dowling: HJB**
- **BNL: Robert M. Sweet**

ARCiB Lab:
- **Dowling College: HJB, Isaac Awuah Asimah, Darina Boycheva, Georgi Darakev, Nikolay Darakev, John Jemilawon, Nan Jia, Georgi Todorov**

SVEVSL Project:
- **Dowling College: ARCiB Lab group**
- **RIT: Paul A. Craig, Jared Carter, Brett Hanson, Scott Mottarella, Charlie Westin**

And many more over the years.