PDB format considerations



- Fixed-format PDB files
 - Advantages
 - Easy & fast parsing, manual editing, visual inspection
 - Problem
 - Does not scale to larger structures
- Alternatives
 - Diverse approaches
 - mmCIF (but no breakthrough after 20+ years)
 - XML (extremely verbose, slow parsing, not human-readable)
 - Wide-PDB (http://biomol.dowling.edu/WPDB/)
 - Problem common to all approaches
 - Incompatible with old format -> huge investment in time
 - Nobody in a position to dictate that everybody spends time+money to quickly move the entire community over to something new

Format evolution adopted in PHENIX



- We need a working format that scales to larger structures
 - Not to be confused with deposition format accepted by wwpdb.org members
- Where are the most pressing problems?
 - More than 100k atoms (27 structures in PDB, Oct 2007)
 - Only 62 "official" chainid characters
 - Automatic model building needs more (George Sheldrick)
 - More than 10k residues in one chain
- Maximally backward compatible extensions
 - Most users will not see a change
 - Visible changes only for
 - very large structures
 - or if researchers intentionally use the extensions
 - e.g. for more meaningful chainids

chainid AB



- Use ATOM columns 21-22 for two-character chainid
 - Suggested by George Sheldrick (many chain fragments)
 - Standard is just column 22
 - Thorough examination of PDB: two-character chainid compatible with all PDB records in which they appear

DBREF SEQADV SEQRES MODRES HET HELIX SHEET TURN SSBOND LINK CISPEP SITE ATOM SIGATM ANISOU SIGUIJ TER HETATM

Backward compatibility

- Writing: chainid right-adjusted, e.g. chainid A written as "A"
- Reading: only strip leading spaces!

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ATOM	369 PEAK PEAK	1	61.114	12.134	8.619	1.00 20.00	PEAK
ATOM	504 SITE SITE	2	67.707	2.505	14.951	1.00 20.00	SITE
	* *						

- Preserving trailing spaces maximizes backward compatibility
 - Reading-writing cycle preserves intended meaning

serial numbers = strings



- Atom serial numbers: 5 columns
 - referenced in CONECT records
- Residue sequence numbers: 4 columns
 - referenced in several other records (e.g. LINK)
- Basic idea for maximum flexibility
 - Simply preserve strings
 - Convert from/to integers "just in time"
 - Conversion only needed for arithmetic
 - resseq 10:20 implies integer ordinal for each string
 - resseq + 1

"hybrid" serial numbers



- Assignment of integer ordinals to strings
- "Hybrid-36" maximizes compatibility
 - Strings that look like integers: no change (base-10)
 - -999 to 9999
 - Only if we run out of colums: switch to upper-case base-36 0123456789ABCDEFGHIJKLMNOPQRSTUVWXYZ
 - First character is an upper-case letter
 - Examples: A000, A001, A002, ..., ZZZZ
 - Only if upper-case exhausted: switch to lower-case base-36
 - First character is a lower-case letter
 - Examples: a000, a001, a002, ..., zzzz
 - Mixed-case symbols intentionally avoided to minimize potential for confusion
 - Atom serial numbers: 87,440,031
 - Residue sequence numbers: 2,436,111

Practical advice



Golden Rule:

Preserve as much as possible, as long as possible.

- Preserve chainid trailing spaces
- Preserve serial number strings
- Convert to/from integers only if necessary
 - Hide base-10 integers from users; convert back to strings for ouput! The PDB format dictates that we show strings. To avoid confusion, show the same symbol in all contexts. Don't confuse users with a mix of base-10 symbols in one context and hybrid-36 symbols in another.

Use our open-source hybrid-36 implementations

- Python
- Java
- C/C++
- Fortran
- Drop-in replacement of built-in string<->integer conversions
- NO dependencies other than compiler or interpreter
- NO strings attached

rrr Resources BERKELEY L **Open-source hybrid-36 implementations:** http://cci.lbl.gov/hybrid 36/ Fast C++ PDB parser with Python interface (iotbx.pdb.input) http://cci.lbl.gov/publications/download/iucrcompcomm nov2006.pdf **Contact: Ralf W. Grosse-Kunstleve** rwgk@cci.lbl.gov September/October 2007