Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop


Structures of biomolecular systems are increasingly computed by integrative modeling that relies on varied types of experimental data and theoretical information. We describe here the proceedings and conclusions from the first wwPDB Hybrid/Integrative Methods Task Force Workshop held at the European Bioinformatics Institute, UK, on October 6 and 7, 2014. At the workshop, experts in various experimental fields of structural biology, experts in integrative modeling and visualization, and experts in data archiving addressed a series of questions central to the future of structural biology. How should integrative models be represented? How should the data and integrative models be validated? What data should be archived? How should the data and models be archived? What information should accompany the publication of integrative models?

Background

Historical Rationale for the Workshop

The PDB (http://wwpdb.org) was founded in 1971 with seven protein structures as its first holdings (Protein Data Bank, 1971). The global PDB archive now holds more than 100,000 atomic structures of biological macromolecules and their complexes, all of which are freely accessible. Most structures in the PDB archive (~90%) have been determined by X-ray crystallography, with the remainder contributed by two newer 3D structure determination methods, nuclear magnetic resonance (NMR) spectroscopy and 3D electron microscopy (3DEM).

Considerable effort has gone into understanding how to best curate the structural models and experimental data produced with these methods. Over the past several years, the Worldwide PDB (wwPDB; the global organization responsible for maintaining the PDB archive) (Berman et al., 2003) has established expert, method-specific task forces to advise on which experimental data and metadata from each method should be archived and how these data and the resulting structure models should be validated. The wwPDB X-ray Validation Task Force (VTF) made detailed recommendations on how to best validate structures determined by X-ray crystallography (Read et al., 2011). These

(Affiliations continued on next page)
recommendations have been implemented as a software pipeline used within the wwPDB Deposition and Annotation (D&A) system. Initial recommendations of the wwPDB NMR (Montelione et al., 2013) and Electron Microscopy (Henderson et al., 2012) VTFs have also been implemented. In addition, the wwPDB and, in later years, the Structural Biology Knowledgebase (SBKB), spearheaded three workshops focused on validation, archiving, and dissemination of comparative protein structure models (Berman et al., 2006; Schwede et al., 2009). It is anticipated that as new validation methods are developed and as more experience is gained with existing ones, additional validation procedures will be implemented in the wwPDB D&A system.

Increasingly, structures of very large macromolecular machines are being determined by combining observations from complementary experimental methods, including X-ray crystallography, NMR spectroscopy, 3DEM, small-angle scattering (SAS), crosslinking, and many others (Figure 1; Table 1). Data from these complementary methods are used to compute integrative or hybrid models (Ward et al., 2013). Atomic models produced in this fashion have been deposited in the PDB, but there is currently no mechanism within the PDB framework for archiving the experimental data generated by methods other than X-ray crystallography, NMR spectroscopy, and 3DEM. The most recently established task force, the wwPDB SAS Task Force (Trewharga et al., 2013), recommended creation of a SAS data and model repository that would interoperate with the PDB. The SAS Task Force also recommended that an international meeting be held to consider how best to deal with the archiving of data and models derived from integrative structure determination approaches.

In response, a Hybrid/Integrative Methods Task Force was assembled by the wwPDB organization. Its inaugural meeting was held at the EMBL European Bioinformatics Institute (EBI) on October 6 and 7, 2014 (http://wwpdb.org/task/hybrid.php).

In all, 38 participants from 37 academic and government institutions worldwide attended the workshop, which was co-chaired by Andrej Sali (University of California, San Francisco, USA), Torsten Schwede (Swiss Institute of Bioinformatics [SIB] and University of Basel, Switzerland), and Jill Trewharga (University of Sydney, Australia). Attendees included experts in relevant experimental techniques, integrative modeling, visualization, and data and model archiving.

The workshop began with plenary talks followed by focused discussions. Gerard Kleywegt introduced the workshop objectives. Andrej Sali outlined the current state of integrative modeling. Helen Berman gave an overview of the history and status of the wwPDB organization. Jill Trewharga described the increasing role of SAS in integrative structural modeling, the need for the development of community standards and validation tools for biomolecular modeling using SAS data, and how SAS data and modeling resources could interoperate with the PDB. Claus Seidel outlined state-of-the-art single-molecule and ensemble Förster resonance energy transfer (FRET) spectroscopy (Kalinin et al., 2012) and live cell imaging, as well as related label-based spectroscopic methods for measuring select interatomic distances in macromolecular systems. Torsten Schwede presented the Protein Model Portal (Haas et al., 2013), including its linking of large databases of comparative models with experimental structure information in the PDB, and the Model Archive repository for all categories of in silico structural models.

Current Archives for Models and/or Supporting Data

In this section, we review the PDB and management of data derived from crystallography, NMR spectroscopy, 3DEM, and...
Figure 1. Examples of Recently Determined Integrative Structures

The molecular architecture of INO80 was determined with a 17-Å resolution cryo-electron microscopy (EM) map and 212 intra-protein and 116 inter-protein crosslinks (Russel et al., 2009). The molecular architecture of Polycomb Repressive Complex 2 (PRC2) was determined with a 21-Å resolution negative-stain EM map and 60 intra-protein and inter-protein crosslinks (Shi et al., 2014). The molecular architecture of the large subunit of the mammalian mitochondrial ribosome (39S) was determined with a 4.9-Å resolution cryo-EM map and 70 inter-protein crosslinks (Ward et al., 2013). The molecular architecture of the RNA polymerase II transcription pre-initiation complex was determined with a 16-Å resolution cryo-EM map plus 157 intra-protein and 109 inter-protein crosslinks (Alber et al., 2008). The atomic model of type III secretion system needle was determined with a 19.5-Å resolution cryo-EM map and solid-state nuclear magnetic resonance (NMR) data (Loquet et al., 2012). Molecular architecture of the productive HIV-1 reverse transcriptase:DNA primer-template complex in the open educt.
SAS, plus archives for models derived exclusively on the basis of theoretical approaches.

PDB. For more than four decades, the PDB has served as the single global archive for atomic models of biological macromolecules; first for those derived from crystallography, and subsequently for models from NMR spectroscopy and 3DEM. The PDB also archives experimental data necessary to validate the structural models determined using these three methods. In addition, descriptions of the chemistry of polymers and ligands are collected, as are metadata describing sample preparation, experimental methods, model building, refinement statistics, literature references, and so forth. For all structural models in the PDB, geometric features are assessed with respect to standard valence geometry and intermolecular interactions, as recommended by the three wwPDB VTFs mentioned above.

Crystallography: Models and Data. For structures derived using X-ray, neutron, and combined X-ray/neutron crystallography, it has been mandatory to deposit structure factor amplitudes into the PDB since 2008 (http://www.wwpdb.org/news/news?year=2007#29-November-2007); until then, the submission of these primary data was optional. Additional validation against deposited structure factor amplitudes is carried out using procedures recommended by the X-ray VTF (Read et al., 2011). The resulting validation report includes graphical summaries of the quality of the overall model plus residue-specific features. Detailed assessments of various aspects of the model and its agreement with experimental and stereochemical data are also provided. In the near future, unmerged intensities will also be collected, enabling further validation activities.

Example methods that are informative about a variety of structural aspects of biomolecular systems are listed. 3DEM, 3D electron microscopy; DEER, double electron-electron resonance; EPR, electron paramagnetic resonance; FRET, Förster resonance energy transfer; H/D, hydrogen/deuterium; NMR, nuclear magnetic resonance; SAS, small-angle scattering.

Table 1. Types of Structural Data Used in Integrative Modeling

<table>
<thead>
<tr>
<th>Structural Information</th>
<th>Method</th>
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<tbody>
<tr>
<td>Atomic structures of parts of the studied system</td>
<td>X-Ray and neutron crystallography, NMR spectroscopy, 3DEM, comparative</td>
</tr>
<tr>
<td>3D maps and 2D images</td>
<td>modeling, and molecular docking</td>
</tr>
<tr>
<td>Atomic and protein distances</td>
<td>NMR, FRET, and other fluorescence techniques, DEER, EPR, and other</td>
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<tr>
<td>Binding site mapping</td>
<td>spectroscopic techniques; chemical crosslinks detected by mass</td>
</tr>
<tr>
<td>Size, shape, and pairwise atomic distance distributions</td>
<td>spectrometry, and disulfide bonds detected by gel electrophoresis</td>
</tr>
<tr>
<td>Component positions</td>
<td>Super-resolution optical microscopy, FRET imaging</td>
</tr>
<tr>
<td>Physical proximity</td>
<td>Co-purification, native mass spectrometry, genetic methods, and gene/</td>
</tr>
<tr>
<td>Solvent accessibility</td>
<td>protein sequence covariance</td>
</tr>
<tr>
<td>Proximity between different genome segments</td>
<td>Footprinting methods, including H/D exchange assessed by mass</td>
</tr>
<tr>
<td>Propensities for different interaction modes</td>
<td>spectrometry or NMR, and even functional consequences of point</td>
</tr>
<tr>
<td>Shape and size</td>
<td>mutations, such as point mutations, misfolding, and aggregation</td>
</tr>
<tr>
<td>Atomic structures of parts of the studied system</td>
<td>X-Ray and neutron crystallography, NMR spectroscopy, 3DEM, comparative</td>
</tr>
<tr>
<td>Structural models determined using these three methods</td>
<td>modeling, and molecular docking</td>
</tr>
<tr>
<td>The structural model of the ESCRT-I complex was determined</td>
<td>with SAXS, double electron-electron transfer, and FRET (Boura et al.,</td>
</tr>
<tr>
<td>The molecular architecture of the proteosomal lid was</td>
<td>2011). Integrative model of actin and the cardiac myosin binding</td>
</tr>
<tr>
<td>The ensemble of [¹⁵N]NMR structures were fitted into the</td>
<td>protein C was developed from a combination of crystallographic and</td>
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<tr>
<td>The resulting validation report includes graphical</td>
<td>NMR structures of subunits and domains, with positions and</td>
</tr>
<tr>
<td>The structure of HIV-1 capsid protein was determined</td>
<td>orientations optimized against SAXS and small-angle neutron scattering</td>
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<tr>
<td>The human genome architecture was determined based on</td>
<td>to reveal information about the quaternary interactions (Whitten et al.,</td>
</tr>
<tr>
<td>The structural model of the ESCRT-I complex was determined</td>
<td>2008). The ensemble of [¹⁵N]NMR structures were fitted into the</td>
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<tr>
<td>The cargo complex of the ESCRT-I complex was determined</td>
<td>averaged cryo-electron tomography map (Miyazaki et al., 2010).</td>
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<tr>
<td>The molecular architecture of the proteosomal lid was</td>
<td>Integrative model of the cyanobacterial circadian timing KaiB-KaiC</td>
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<tr>
<td>The pre-pore and pore conformations of the pore-forming</td>
<td>complex was obtained based on hydrogen/deuterium exchange and collision</td>
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<tr>
<td>The molecular architecture of the ESCRT-I complex was</td>
<td>cross-section data from mass spectrometry (Snijder et al., 2014). The</td>
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<tr>
<td>The pre-pore and pore conformations of the pore-forming</td>
<td>pre-pore and pore conformations of the pore-forming toxin a-eosin</td>
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<tr>
<td>The molecular architecture of the proteosomal lid was</td>
<td>were obtained combining cryo-EM data and molecular dynamics simu-</td>
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<tr>
<td>The ensemble of [¹⁵N]NMR structures were fitted into the</td>
<td>lations (Degiacomi and Dal Peraro, 2013; Degiacomi et al., 2013).</td>
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<tr>
<td>The pre-pore and pore conformations of the pore-forming</td>
<td>Fragment of a pleurotolysin pore map (~11 Å resolution) with an</td>
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<tr>
<td>The molecular architecture of the proteosomal lid was</td>
<td>ensemble of conformations shows the trajectory of if sheet opening</td>
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<tr>
<td>The molecular architecture of the ESCRT-I complex was</td>
<td>during pore formation (Lukoyanova et al., 2015). A SAXS-based rigid-</td>
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<tr>
<td>The structural model of the ESCRT-I complex was determined</td>
<td>body model of a ternary complex of the iron-sulfur cluster assembly</td>
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<tr>
<td>The cargo complex of the ESCRT-I complex was determined</td>
<td>proteins desulfurase (orange) and scaffold protein Isu (blue) with</td>
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<tr>
<td>The molecular architecture of the ESCRT-I complex was</td>
<td>bacterial ortholog of frataxin (yellow) was validated by NMR chemical</td>
</tr>
<tr>
<td>The pre-pore and pore conformations of the pore-forming</td>
<td>shifts and mutagenesis (Prisch et al., 2010). The molecular architecture</td>
</tr>
<tr>
<td>The molecular architecture of the ESCRT-I complex was</td>
<td>of the complex between RNA polymerase II and transcription factor IIF</td>
</tr>
<tr>
<td>The pre-pore and pore conformations of the pore-forming</td>
<td>was determined using a deposited crystal structure of RNA polymerase</td>
</tr>
<tr>
<td>The molecular architecture of the ESCRT-I complex was</td>
<td>II homology models of some domains in transcription factor IIF, and</td>
</tr>
<tr>
<td>The cargo complex of the ESCRT-I complex was determined</td>
<td>95 intra-protein and 129 inter-protein crosslinks (Chen et al., 2010).</td>
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</tbody>
</table>
NMR Spectroscopy: Models and Data. The Biological Magnetic Resonance DataBank (BioMagResBank or BMRB; http://www.bmrbr.wisc.edu) is a repository for experimental and derived data gathered from NMR spectroscopic studies of biological molecules. The BMRB archive contains quantitative NMR spectral parameters, including assigned chemical shifts, coupling constants, and peak lists together with derived data, including relaxation parameters, residual dipolar couplings, and NMR spectral parameters, including assigned chemical shifts, derived data gathered from NMR spectroscopic studies of biological macromolecules; chemical shift and structure validation reports; and a database of 1D and 2D 1H- and 13C-NMR spectra for more than 1,200 metabolites. The BMRB website also provides tools for querying and retrieving data.

Since 2006, BMRB has been a member of the wwPDB organization (Markley et al., 2008). Chemical shift and restraint data that accompany model data are housed in both the BMRB and PDB archives. Deposited NMR data without model coordinates reside exclusively in the BMRB archive. The wwPDB D&A system provides for deposition, annotation, and validation of NMR models and related experimental data. Depositors of chemical shift and other data sets without accompanying models are automatically redirected to BMRB to deposit their data. Data exchange between the BRMB and PDB archives is facilitated by software tools utilizing correspondences maintained between the PDB Exchange Dictionary (PDBx) and the BMRB NMR-STAR Dictionary. Validation methods for NMR-derived models, measured chemical shifts, and restraint data are currently under development, in response to recommendations of the NMR VTF (Montelione et al., 2013). A working group composed of the major biocentral NMR software developers has created a common NMR exchange format (NEF) for structural restraints, similar to NMR-STAR. The adoption of this NEF by NMR software developers will simplify data exchange and the archiving of NMR structural restraints by the wwPDB.

Electron Microscopy: Models and Maps. Atomistic structural models determined using 3DEM methods were first archived in the PDB in the 1990s. In 2002, the EM Data Bank (EMDB) was created by the Macromolecular Database (now PDB) at the EBI. In 2006, the EMDatabank (http://www.EMDataBank.org) was established as the unified global portal for one-stop deposition and retrieval of 3DEM density maps, atomic models, and associated metadata (Lawson et al., 2011). EMDatabank is a joint effort among PDB, the Research Collaboratory for Structural Bioinformatics (RCSB) at Rutgers, and the National Center for Macromolecular Imaging (NCMI) at Baylor College of Medicine. EMDatabank also serves as a resource for news, events, software tools, data standards, raw data, and validation methods for the 3DEM community. 3DEM model and map data are now stored in separate branches of the wwPDB ftp archive site.

As for NMR-based models, the wwPDB D&A system supports processing of atomistic models and map data from 3DEM structure determinations. 3DEM map data deposited without atomistic models are stored exclusively in EMDB. Again, as for NMR, a mapping is maintained between the PDBx data dictionary and the EMDB XML-based data model. Validation methods for 3DEM maps and atomistic models are currently under development in response to recommendations from the EM VTF (Henderson et al., 2012).

SAS: Data and Model Archiving. The report from the first meeting of the wwPDB SAS Task Force (Trewella et al., 2013) made the case for establishing “a global repository that holds standard format X-ray and neutron SAS data that is searchable and freely accessible for download” and that “options should be provided for including in the repository SAS-derived shape and atomistic models based on rigid-body refinement against SAS data along with specific information regarding the uniqueness and uncertainty of the model, and the protocol used to obtain it.”

At present, there are two databases available for storing SAS data and models with associated metadata and analyses, both of which are freely accessible without limitations on data utilization via the Internet. As of March 2015, BIOISIS (http://www.biosis.net) contained 99 structures and is supported by teams at the Advanced Light Source and Diamond, while SASBDB (http://www.sasbdb.org) (Valentini et al., 2015) contained 195 models and 114 experimental datasets and is supported by a team at EMBL-Hamburg.

Having evolved separately, these databases are distinctive in character. There was in principle agreement within the wwPDB SAS Task Force that BIOISIS and SASBDB will exchange data sets. Such exchange would be a step toward developing a federated approach to SAS data and model archiving, which in turn could ultimately be federated with the PDB, BMRB, and EMDB.

Further development of the sasCIF dictionary is required to permit full data exchange between the two SAS data repositories. sasCIF is a core crystallographic information file (CIF) developed to facilitate the SAS data exchange (Malfois and Svergun, 2000). As its name implies, sasCIF was implemented as an extension of the core CIF dictionary and has recently been extended to include new elements related to models, model fitting, validation tools, sample preparation, and experimental conditions (M.K., J.D.W., and D.S., unpublished data). sasCIFTools were developed as a documented set of publicly available programs for sasCIF data processing and format conversion; currently, SASBDB supports both import and export of sasCIF files.

Protein Model Portal. Comparative or homology modeling is routinely used to generate structural models of proteins for which experimentally determined structural models are not yet available (Marti-Renom et al., 2000; Schwede et al., 2009). Until 2006, such in silico models could be archived in the PDB, albeit in the absence of clear policies and procedures for their validation. Following recommendations from a stakeholder workshop convened in November 2005 (Berman et al., 2006), depositions to the PDB archive are limited to structural models substantially determined by experimental measurements from a defined physical sample (effective date October 15, 2006). The workshop also recommended that a central, publicly available archive or portal should be established for exclusively in silico models, and that methodology for estimating the accuracy of such computational models should be developed.

The Protein Model Portal (PMP) (Arnold et al., 2009; Haas et al., 2013) was developed at the SIB at the University of Basel.
as a component of the SBKB (Berman et al., 2009; Gabanyi et al., 2011). Today, the SBKB integrates experimental information provided by the PDB with in silico models computed by automated modeling resources. In addition, the PMP provides access to several state-of-the-art model quality assessment services (Schwede et al., 2009). Since 2013, the Model Archive (http://modelarchive.org) resource has also served as a repository for individually generated in silico models of macromolecular structures, primarily those described in peer-reviewed publications. Finally, the Model Archive hosts all legacy models that were available from the PDB archive prior to 2006.

Each model in the PMP is assigned a stable, unique accession code (and digital object identifier or DOI) to ensure accurate cross-referencing in publications and other data repositories. Unlike experimentally determined structural models, in silico models are not the product of experimental measurements of a physical sample. They are generated computationally using various molecular modeling methods and underlying assumptions. Examples include comparative modeling, virtual docking of ligand molecules to protein targets, virtual docking of one protein to another, simulations of molecular dynamics and motions, and de novo (ab initio) protein modeling.

Effective archival storage of such models depends critically on capturing sufficient detail regarding underlying assumptions, parameters, methodology, and modeling constraints, to allow for assessment and faithful re-computation of the model. It is also essential that these models be accompanied by reliable estimates of uncertainty. In October 2013, a workshop on “Theoretical Model Archiving, Validation and PDBx/mmCIF Data Exchange Format” (http://www.proteinmodelportal.org/workshop-2013/) was hosted at Rutgers University to launch development of community standards for theoretical model archiving.

**Integrative/Hybrid Structure Modeling**

**Motivation**

Samples of many biological macromolecules prove recalcitrant to mainstream structural biology methods (i.e., crystallography, NMR, and 3DEM), because they are not crystalizable, are insoluble, are not of adequate purity, are conformationally heterogeneous, are too large or small, or do not remain intact during the course of the experiment. In such cases, integrative modeling is increasingly being used to compute structural models based on complementary experimental data and theoretical information (Figures 1 and 2; Table 1) (Alber et al., 2007, 2008; Robinson et al., 2007; Russel et al., 2012; Sali et al., 2003, 1990; Schneiderman-Duhovny et al., 2014; Ward et al., 2013). Structural biology is no stranger to integrative models. Insights into the molecular details of the β-DNA double helix (Watson and Crick, 1953), the α helix, and the β sheet (Pauling et al., 1951) all depended on constructing structural models based on data derived from multiple sources (albeit without the benefit of digital computation). Integrative structure modeling of today has its origins in attempts to fit X-ray derived substructures into an EM density map of a larger assembly (Rayment et al., 1993). Other early examples include the model of the Gla-EGF domains from coagulation Factor X based on NMR and SAS data (Sunnerhagen et al., 1996), and the superhelical assembly of the bacteriophage fd gene 5 protein with single-stranded DNA based on neutron and X-ray SAS data, EM data, and the crystal structure of G5P (Olah et al., 1995); the latter study was inspired in part by molecular dynamics simulations guided by contacts from an NMR structure of the G5P dimer and EM data (Folmer et al., 1994).

Beyond overcoming sample limitations, the integrative approach has several additional advantages (Alber et al., 2007). First, synergy among the input data minimizes the drawbacks of sparse, noisy, and ambiguous data obtained from compositionally and structurally heterogeneous samples. Each individual piece of data may contain relatively little structural information, but by simultaneously fitting a model to all data derived from independent experiments, the uncertainty of the structures that fit the data can be markedly reduced. Second, the integrative approach can be used to produce all structural models consistent with available data, instead of myopically focusing on just one model. Third, comparison of an ensemble of structural models permits estimation of precision and, sometimes, the accuracy of both the experimental data and the model. Fourth, the integrative approach can make structural biologists more efficient by identifying which additional measurements are likely to have the greatest impact on integrative model precision and accuracy. Finally, integrative modeling provides a framework for considering perturbations of the system that are often required to collect the data; for example, spin labels are required for electron paramagnetic resonance experiments, membrane proteins are often reconstituted in micelles for NMR spectroscopy, and point mutations or even entire domains are introduced to stabilize preferred conformations for crystallization.

While such perturbations complicate structural analysis, integrative modeling may allow us to distinguish biologically relevant states from artifacts of any individual approach. In summary, integrative structure determination maximizes the accuracy, precision, completeness, and efficiency of the structural coverage of biomolecular systems.

**Experimental and Computational Methods for Generating Structural Information**

Input information for integrative modeling can come from various experimental methods, physical theories, and statistical analyses of databases of known structures, biopolymer sequences, and interactions. These methods probe different structural aspects of the system (Table 1). In addition to information about average structures, numerous methods provide insights into dynamics of the system, which can also be incorporated into integrative modeling procedures (Russel et al., 2009). For example, both NMR spectroscopy and X-ray crystallography provide access to various measures of conformational dynamics; FRET, time-dependent double electron-electron resonance (DEER) spectroscopies, and even quantitative crosslinking/mass spectrometry (Fischer et al., 2013) can map distance changes in time; small-angle X-ray scattering (SAXS) can provide time-resolved information on the structures and processes with the temporal resolution of a millisecond; molecular dynamics simulations can map the dynamics of an atomic structure up to the millisecond timescale; and high-speed atomic force microscopy imaging can provide the dynamic live images of single molecules (Ando, 2014).

**Approach**

All structural characterization approaches correspond to finding models that best fit input information, as judged by use of
a scoring function quantifying the difference between the observed data and the data computed from the model. Thus, any information about a structure determination target must always be converted to an explicit structural model through computation. Integrative approaches explicitly combine diverse experimental and theoretical information, with the goal of increasing accuracy, precision, coverage, and efficiency of structure determination. Input information can vary greatly in terms of resolution (i.e., precision, noise, uncertainty), accuracy, and quantity. All structure determination methods are integrative, albeit with differences in degree. At one end of the spectrum, even structure determination using predominantly crystallographic, NMR, or high-resolution single-particle EM data also generally requires a molecular mechanics force field description of atomic structure. At the other end of the spectrum, integrative methods rely more evenly on different types of information, often resulting in coarser models with higher uncertainty (Figure 1). Examples of such integrative methods include docking of comparative models of subunits into a 3DEM density map of the macromolecular assembly (Lasker et al., 2009); rigid-body fitting of multi-domain structures and complexes determined by crystallography or NMR to SAS data (Petoukhov and Svergun, 2005); and use of conformational sampling methods with sparse NMR data (Lange et al., 2012; Mueller et al., 2000), chemical crosslinks (Young et al., 2000), or even chemical shift data alone (Shen et al., 2008). It is not difficult to appreciate how integrative methods blur distinctions between models based primarily on theoretical considerations and those based primarily on experimental measurements from a physical sample.

The practice of integrative structure determination is iterative, consisting of four stages (Figure 2): gathering of data; choosing the representation and encoding of all data within a numerical scoring function consisting of spatial restraints; configurational sampling to identify structural models with good scores; and analyzing the models, including quantifying agreement with input spatial restraints and estimating model uncertainty. Input information about the system can be used to (1) select the set of variables that best represent the system (system representation), (2) rank the different configurations (scoring function), (3) search for good-scoring solutions (sampling); and (4) further filter good-scoring solutions produced by sampling.

**Types of Integrative Models**

A structural model of a macromolecular assembly is defined by the relative positions and orientations of its components...
four respects. First, a model can be multi-scale (Grime and
structural biology methods usually produce a single atomistic
ments, domains, subunits, and subcomplexes). While traditional
(e.g., atoms, pseudo-atoms, residues, secondary structure ele-
ments). While traditional biological analysis (Schneidman-Duhovny et al.,
2014). Second, a model can be multi-state, specifying multiple
discrete states of the system required to explain the input infor-
mation (each state may differ in structure, composition, or both)
(Molnar et al., 2014; Pelikan et al., 2009). Third, a model can also
specify the order of states in time and/or transitions between the
states. This feature allows representation of a multi-step biolog-
ical process, a functional cycle (Diez et al., 2004), a kinetic
network (Pirchi et al., 2011), time evolution of a system (e.g.,
a molecular dynamics trajectory) (Bock et al., 2013), or FRET
trajectories; for a comprehensive description of biomolecular
function, it is essential to register state lifetimes, characteristic
relaxation times, and direct rate constants. Finally, an ensemble
of models may be provided to underscore the uncertainty in the
input information, with each individual model satisfying the input
information within an acceptable threshold (e.g., NMR-derived
ensembles currently available in the PDB [Clare and Gronen-
bom, 1991; Snyder et al., 2005, 2014] and the ensembles gener-
ated from SANS [Tria et al., 2015]). This aspect of the represen-
tation allows us to describe model uncertainty and to assess the
completeness of input information; such ensembles are distinct
from multiple states that represent actual variations in the
structure, as implied by experimental information that cannot
be accounted for by a single representative structure (Schneid-
man-Duhovny et al., 2014; Schroder, 2015).

Task Force Deliberations and Recommendations
Charge to the Task Force
A healthy debate is under way about how to classify structural
models. A major motivation for this discussion is the lack of ac-
curate general methods to assess the precision and accuracy
of any model. As a result, models are often classified based on
the predominant type of information used to compute them,
which in turn tends to reflect the data-to-parameter ratio and
thus model accuracy. However, as previously discussed, all
structures are in fact integrative models that have been derived
both from experimental measurements involving a physical
sample of a biological macromolecule and prior knowledge
of the underlying stereochemistry. It is therefore difficult, if
not impossible, to draw definitive lines on the spectrum rang-
ing from very well-determined ultra-high-resolution crys-
tallographic structures (>40 experimental observations per
non-hydrogen atom in the crystallographic asymmetric unit)
and structural models based on a single or even no experi-
mental observation.

Reflecting this debate about model classification, there are in
principle several possibilities for archiving the models and asso-
ciated data among distinct, publicly accessible model/data re-
positories, including: (1) a single mega-archive that serves as
the repository for every type of structural model and data; (2) in-
dependent, free-standing repositories that house distinct types
of models and data; and (3) a federated system of inter-operating
repositories that archive models and data, with “spheres of influ-
ence” based on community consensus.

To address some of the challenges ahead and make recom-
mendations about how best to proceed, the community stake-
holders who assembled at the October 2014 meeting of the
wwPDB Hybrid/Integrative Methods Task Force were divided
into three discussion groups, each tasked with considering a se-
ries of related questions. What experimental data (beyond crys-
tallography, NMR, and 3DEM) should be archived? Where and
how should it be validated? What kinds of non-atomistic models
can we expect and how should they be validated? What are
the criteria for deciding where models should be archived?

How should non-atomistic and mixed atomistic/non-atomistic
models be archived? Should there be a separate archive for inte-
grative (mixed) models (and data)? Should we establish a feder-
ated system of data and model archives to support integrative
structural biology? The three breakout groups were asked to
address these questions, report back with their findings, and
make recommendations for the future. Each group indepen-
dently approached the same set of questions. At the close of
the meeting, the teams converged to compare notes, identify
areas of commonality and diversity, and determine how best
to move forward. The resulting consensus is reflected in this
document.

Recommendations
Recommendation 1. In addition to archiving the models them-

selves, all relevant experimental data and metadata as well as
experimental and computational protocols should be archived;
inclusivity is key.

Ideally, structural models of any kind, derived by any method,
should be archived.

Models are of greatest value when they are independently
tested, potentially improved, and serve to further our under-
standing of how the function of a biological system is determined
by its 3D structure(s). Therefore, models and necessary annota-
tions must be freely available to the research community. The
modeling process should be reproducible. Information concern-
ing all aspects of a model should be deposited, including input
data, corresponding spatial restraints, output models, and pro-
tocols used to convert input data into models. In addition to
the input experimental data, the archival deposition should
specify or include theoretically derived restraints used to
compute the model (e.g., a statistical potential and a molecular
mechanics force field). In practice, frequently used data types
(e.g., distance information) should be prioritized for early com-
plete implementation. Uncertainty in the input data needs to be
well documented; some data uncertainty estimates may require
modeling (e.g., Bayesian error estimates [Rieping et al., 2005]).
Consistency between input data and the structural model should
be documented as part of model validation.

Each expert community should drive decisions as to how
much raw data, processed data, and metadata to deposit,
subject to the minimal requirement that the spatial restraints used for modeling must be derivable from the deposited information. Attention needs to be paid to annotating measurement conditions, such as temperature (Fenwick et al., 2014), sample concentration, environmental conditions (e.g., buffer), construct definition, and identification of all assembly components, all of which can significantly influence the experimental outcome. Cost-benefit analyses should be used to help guide which data should be archived. As much data as practical should be deposited, to facilitate model validation, future improvements of the model, and methods development (e.g., benchmarking sets). Of particular importance will be availability of some raw data to help drive improvement of data processing methods and for use by methods developers, who are often not generating the experimental data themselves.

**Recommendation 2.** A flexible model representation needs to be developed, allowing for multi-scale models, multi-state models, ensembles of models, and models related by time or other order.

Model representation should allow for as many types of “structural” models as possible, thereby encouraging collaboration among developers of integrative modeling software (Russel et al., 2012). At a minimum, the model representation should allow encoding of an ensemble of multi-scale, multi-state, time-ordered models (see the section on Types of Integrative Models). Uncertainty of the model coordinates should be tightly associated with the model coordinates in the model representation. Any model resident within an archive should be “self-contained” to facilitate utilization (e.g., for visualization). A common representation and format for models are useful for reasons of software interoperability. Particle-based representations/primitives need to be prioritized; non-particle-based model representations (e.g., continuum representations) merit further consideration by appropriate community stakeholders.

**Recommendation 3.** Procedures for estimating the uncertainty of integrative models should be developed, validated, and adopted.

Assessment of both an integrative model and the information on which it is based is of critical importance for guiding subsequent use of the model. For atomistic models, extant standard validation criteria from X-ray crystallography should be used. Beyond this test, validation of integrative models and data is a major research challenge that must be addressed and overcome. The following represent promising considerations (Alber et al., 2007; Schniedman-Duhovny et al., 2014): convergence of conformational sampling, fit of the model to the input information, test for clashes between geometrical primitives comprising the model, precision of the ensemble of solutions (visualized with, e.g., ribbon plots), cross-validation and statistical bootstrapping based on available data, tests based on data determined after the model was computed, and sensitivity analysis of the model to input data. Bayesian approaches may be particularly well suited to describe model uncertainty by computing posterior model densities from a forward model, noise model, and priors (Musielok et al., 2008; Rieping et al., 2005). Tools for visualizing model validation should be developed.

Communities generating data used in integrative modeling should agree on the standard set of descriptors for data quality, as has been done for crystallography, NMR, and 3DEM.

**Recommendation 4.** A federated system of model and data archives should be created.

Integrative models can be based on a broad array of different experimental and computational techniques. While the specific spatial restraints implied by the data and used to construct an integrative model should be deposited with the model itself, the underlying experimental data often contain much richer information. This information should be captured in a federated system of domain-specific model and data archives. These individual member archives should be developed by community experts, based on method-specific standards for data archiving and validation. A federated system of model and data archives implies the need for a seamless exchange of information between independent archives. This seamless exchange requires a common dictionary of terms, agreed data formats, persistent and stable data object identifiers, and close synchronization of policies and procedures. Federated model and data archives need to develop efficient methods for data exchange to allow for transparent data access across the enterprise.

A single interface for the deposition of all data and models into the federated system is highly desirable. Such an interface would greatly facilitate the task of the depositor and, thereby, maximize compliance with deposition standards and requirements. In addition, reliance on a single entry point will help to ensure consistency across the federation at the time of deposition. Following successful deposition, individual datasets can be transferred to member databases for data curation and archiving if domain-specific databases exist. There should also be provision for collecting unstructured information in a “data commons,” as proposed by the data science initiative at the NIH (Margolis et al., 2014).

Access to the contents of the federated database through a single portal is also most desirable, to facilitate dissemination of data, models, and experimental/computational protocols.

Of particular importance for integrative modeling will be the option to modify or update any aspect of the modeling procedure, for example, by adding new data. The federated archive should allow versioning for each deposited model. Such capabilities will facilitate the cycle of experiment and modeling, and accelerate production of more accurate, precise, and complete models (Russel et al., 2012).

**Recommendation 5.** Publication standards for integrative models should be established.

Over the past decade, the wwPDB organization has worked with relevant scientific journals to help establish publication standards for structural models coming from crystallography, NMR spectroscopy, and 3DEM. Community standards now include requiring authors to make their validation reports available to reviewers and editors. Through the International Union of Crystallography Small Angle Scattering and Journals Commissions, the SAS community developed and agreed upon publication guidelines for structural modeling of biomolecules therefrom (Jacques et al., 2012). A set of standards for publishing integrative models should be developed along similar lines.

**Implementation**

Implementation of Recommendation 1 poses a host of cultural and technical challenges. Experimentalists and modelers need to provide the data, models, and protocols, thus at least partly addressing increasing concerns regarding reproducibility of
scientific results. From a technical perspective, inter-operating data dictionaries for all methods need to be created. In addition, potential storage bottlenecks need to be addressed.

Implementation of Recommendations 2 and 3 will require significant research as to how best to represent and validate the many different kinds of integrative models. In addition, the community will need to agree on a common set of standards that are sufficiently mutable to allow for future innovation. Efforts such as the “Cryo-EM Modeling Challenge” may facilitate this process (http://www.emdatabank.org/modeling_chllnge).

Implementation of Recommendation 4 will require agreement on a common data exchange system among member repositories. Based on past accomplishments, the wwPDB is well positioned to play a leadership role in establishing the proposed federated system, including provision of common deposition and access interfaces. The wwPDB should begin this process by providing training and advice on data archiving and curation to contributing domain-specific member repositories.

Implementation of Recommendation 5 will require continued work with the journals that publish structural models of biological macromolecules.

Significant resources will be required to implement these recommendations, including grants for research, infrastructure, and workshops. These efforts are international by their very nature and will require funding from multiple public and private sources, including in North America, Europe, and Asia.

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