

Reporting Standards for Omics-Based Investigations

An Overview

Susanna-Assunta Sansone, PhD

NET Project Coordinator

EMBL- EBI, Cambridge, UK

Nutrigenomics, Environmental Genomics, Toxicogenomics (NET)

www.ebi.ac.uk/net-project

Outline

- Reporting standards
 - Omics-based investigations

- Standardization initiatives
 - Regulatory-driven
 - Grass-root communities

- Synergistic standards projects
 - Content (MIBBI)
 - Semantic (OBO Foundry and the OBI ontology)
 - Syntax (FuGE)

Omic Investigations - An Example



Carcinogenomics

INVESTIGATION

(hypothesis, design, contact persons etc)

STUDY(1)

ASSAY(s) and DATA

Compound X treatment



Euthanasia

Target organ, tissue

DESIGN

Number of animals, controls, doses, length etc

Conventional assays

- Physical parameters
- Clinical Chemistry
- Histopathology

RNA → **Transcriptomics**

RNA

Fluids, Tissues, Cells

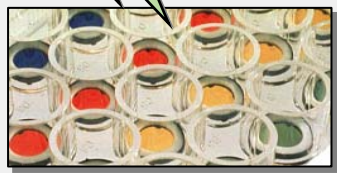
→ **Metabolomics**

Proteins

→ **Proteomics**

Compound X treatment

STUDY(2)



Conventional assays

- Genotoxicity
- Carcinogenicity

Information Intensive Investigations

- Need to understand the resulting *data* in context
 - We need to be able to describe the laboratory workflow (*metadata*)
- The challenges we face
 - Large in volume: lots of data types and metadata!
 - Lots of free text descriptions: hard to mine, subject to mistakes!
 - Babel of terminologies: lack of definitions, hard to map!
 - Heterogeneous file formats: software lock-in!
- Need for reporting standards
 - **Content**: Minimal descriptors
 - Report the same 'core essentials'
 - **Semantics**: Controlled vocabularies or ontology
 - Use the same word and mean the same thing
 - **Syntax**: Common formats
 - Make tools interoperable, allow data exchange and integration

Reporting Standards - The Benefits

- **Unlock the value in the *data***
 - Compare, query and evaluate data
 - Facilitate **scientific validation** of the findings
 - Understand variability within/between different technologies and protocols
 - Facilitate technical validation
 - Enable optimization of the **experimental designs**
 - Identify critical checkpoints and develop **quality metrics**
- **Define exchange, submission and/or publication requirements**
 - Between collaborators, within a consortium or project
 - To journals or repositories
 - To regulatory bodies
- **Ensure data integrity and quality**

Standardization Initiatives - Omics Domains

■ Different driving forces

- Regulatory driven discussion (broader understanding), e.g. FDA, EMEA
- World-wide organizations (agreed recommendations), e.g. OECD
- Measurements and methods validation focus, e.g. NIST
- Grass-root movement, e.g. omics research communities

■ Multi-stakeholders

- Academics, industries, governmental and regulatory bodies
- Manufacturers, software vendors, journal editors and funders

■ Two main, different focus

• Regulatory bodies and industries

- Data review
- Data submission models, focus on the *meta-level*
 - > Transport file, minimal burden on sponsors

• Research communities and database developers

- Data exchange and deposition to databases
- Data annotation tools, both *meta-level* and *object level*
 - > Mandatory fields, use of public terminologies

Regulatory-driven Initiatives, e.g.


- **Pharmacogenomics Standards Group (CDISC, HL7 and I3C)**
 - Pharmacology, Clinical genomics, Pre-clinical/non-clinical genomics
 - Minimal descriptors, data content and format
 - Reuse SEND, CDISC and HL7 RIM, also looking at OMICS standards
 - > *Requirements for pharmacogenomics data submission to FDA*
- **CDISC (Clinical Data Interchange Standards Consortium)**
 - Model to report clinical trials
 - A flat file format with pre-defined categories
 - > *Electronic, clinical data submission to FDA*
- **SEND Consortium (Standard for Exchange of NonClinical Data)**
 - Model to report animal toxicity study
 - SEND model is a flat file format with pre-defined categories
 - SEND + CDISC = Study Data Tabulation Model (SDTM)
 - > *Electronic, pre-clinical data submission to FDA*

Grass-Root Initiatives

- **MGED Society** (Microarray Gene Expression Data) since 1999
 - Minimal requirements (MIAME), data exchange format and ontology
 - > *Data management and data sharing among databases and tools*
 - **HUPO-PSI** (Proteomics Standards Initiative) since 2001
 - Minimal requirements (MIAPE), data exchange format and ontology
 - > *Data management and sharing among databases and tools*
 - **MSI** (Metabolomics Standards Initiative) since 2006
 - Minimal requirements (CIMR), data exchange format and ontology
 - > *Data management, sharing, future regulatory acceptance facilitation*
- ↓
- ✓ Volunteers contributing time and effort to the developments
 - ✓ Thematic Working Groups (WGs), no membership required
 - ✓ Websites, mailing lists, annual meeting and workshops

Grass-Root Initiatives

MGED Society

 © 2001 Nature Publishing Group <http://genetics.nature.com> *commentary*

Minimum information about a microarray experiment (MIAME)—toward standards for microarray data

nature

Alvis Brazma¹,
Chris Stoeckert
Terry Gaasterla
Markowitz^{1,3}, J
Schulze-Kremer

26 September 2002 Volume 419 Issue no 6905

Microarray standards at last

Not a moment too soon, the microarray community has issued guidelines that will make their data much more useful and accessible. *Nature* and the Nature research journals will respond accordingly.

HUPO-PSI

MSI

Papers
in press



nature.com

nature
biotechnology

PUBLICATIONS A-Z INDEX > BROWSE BY SUBJECT > SEARCH

[Journal home](#) > [Community Consultation](#)

COMMUNITY CONSULTATION

The standards papers below are under consideration for publication in *Nature Biotechnology*. We urge you to participate in the development of these standards by sending us your comments, which will be collated and posted on this page each week. New papers will be added as they become ready, so please check back to this page from time to time.

2. [The Minimum Information About a Proteomics Experiment \(MIAPE\) \(PDF 3705K\)](#)

Posted 01/02/07

[Reader comments \(PDF 20K\)](#)

Grass-Root Initiatives

- **MGED Society** (Microarray Gene Expression Data) since 1999
 - Minimal requirements (MIAME), data exchange format and ontology
 - > Data management and data sharing among databases and tools
 - **HUPO-PSI** (Proteomics Standards Initiative) since 2001
 - Minimal requirements (MIAPE), data exchange format and ontology
 - > Data management and sharing among databases and tools
 - **MSI** (Metabolomics Standards Initiative) since 2006
 - Minimal requirements (CIMR), data exchange format and ontology
 - > Data management, sharing, future regulatory acceptance facilitation
- ↓
- ✓ Volunteers contributing time and effort to the developments
 - ✓ Thematic Working Groups (WGs), no membership required
 - ✓ Websites, mailing lists, annual meeting and workshops

Why are Synergies Required?

- Standardization activities operate in a single domain
 - But research is multidisciplinary and multitechnology
- Reporting standards should stand alone *but* also function together
 - Build it in a modular way, maximizing interactions
 - Share common modules, where applicable
- Reusability is crucial
 - Compare with neighbouring domains
 - E.g. Human nutrition study (epidemiological or clinical)
 - Facilitate integration
 - Data producers, miners, reviewers
 - Optimize development of tools (time and costs)
 - Manufactures and vendors covering in multiple technologies
- Capitalize on synergies, where commonality exists
 - Extensive community liaisons is required!

Synergistic Projects - Work in Progress

- Standard content
 - Minimal Information for Biological/Biomedical Investigation (MIBBI)
 - > Modularize the (many) minimum requirements
 - Standard semantics
 - Open Biomedical Ontology (OBO) Foundry and Ontology for Biomedical Investigation (OBI)
 - > Harmonize the (diverse) terminologies
 - Standard syntax
 - Functional Genomics Experiment (FuGE) model
 - > Underpins the (different) XML formats
- ↓
- ✓ Bring together biological-medical communities and MGED, PSI, MSI
 - ✓ Open efforts, no membership required
 - ✓ Websites, mailing lists and papers

MIBBI Project - Standard Content

<http://mibbi.sf.net>

- **New international collaboration**
 - Communities developing a 'minimum information' checklist
 - Define what is the 'core essentials' to be reported
 - Describe *not* prescribe!
- **Phase 1: Portal as a 'one-stop shop' (ONGOING)**
 - For **researchers**, **journal editors** and **reviewers**, and **funders**
 - To discover (whether there are) checklists for a particular domain
 - To raise awareness of the scope and progress of extant efforts
 - To facilitate investigation of overlaps and gaps between checklists
- **Phase 2: Foundry for integration**
 - To **refactor the checklists**
 - Create integrable checklist modules
 - A suite of self-consistent, clearly bounded and orthogonal
 - Biology and technology delineated modules
 - > Link to similar effort in the biomedical domain

MIBBI Project - Standard Content

<http://mibbi.sf.net>

ACRONYM	DOMAIN
CIMR	Meta
MIACA	Cellu
MIAME	Trans
MIAME/Env	Envir
MIAME/Nut	Nutr
MIAME/Plant	Plant
MIAME/Tox	Toxic
MIAO	ORFs
MIAPA	Phyle
MIAPE	Prote
MIARE	RNA
MIFACE	Flow
MIGS	Geno
MIMix	Prote
MIRIAM	Bioc
MISFISHIE	In Si

MIAME — Minimum Information About a Microarray Experiment

1 General features

1.1 Domain	Microarray Technology
1.2 Document Type	Checklist
1.3 Group	MGED
1.4 Main Website	http://www.mged.org/Workgroups/MIAME/miame.html
1.5 MI Checklist's Name	Minimum Information About a Microarray Experiment
1.6 MI Checklist's Acronym	MIAME
1.7 Current Version Designation	MIAME 1.1
1.8 Release Date for Current Version	2003
1.9 General Comments	A shorter version is coming soon.

2 Contact Person

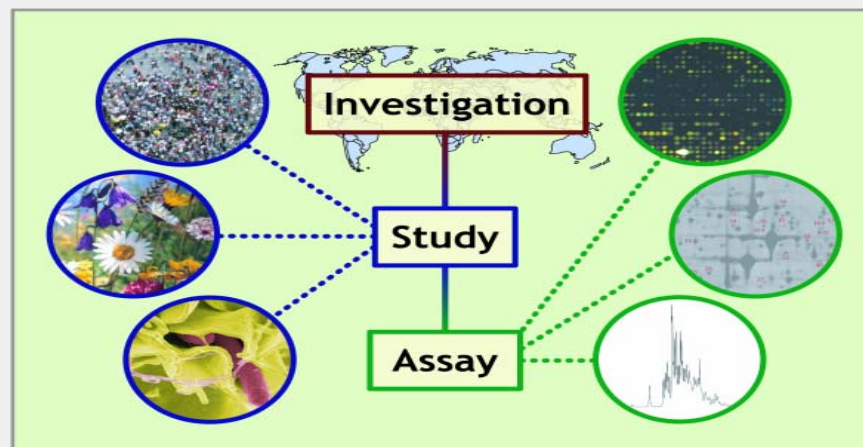
2.1 Full Name	Alvis Brazma
2.2 Email Address	brazma[@]ebi.ac.uk

4 Bibliography

4.1 PubMed Identifier	11726920
4.2 Digital Object Identifier	10.1038/ng1201-365
4.3 URL	http://www.nature.com/ng/journal/v29/n4/abs/ng1201-365.html

MIBBI Project - Standard Content

<http://mibbi.sf.net>



Generalized view of the structure of investigative projects

An **Investigation** (of a particular medical syndrome, environmental effect, *etc.*) consists of one or more linked **Studies** (each in the context of a particular biological domain such as toxicology or environmental science) that themselves consist of one or more **Assays** (analysis of material generated or collected for the study, e.g. by use of an omics techniques such as proteomics).

■ Phase 2: Foundry for integration

- To **refactor the checklists**
- Create integrable checklist modules
 - A suite of self-consistent, clearly bounded and orthogonal
 - Biology and technology delineated modules
 - > Link to similar effort in the biomedical domain

EQUATOR - Enhancing the QUALITY and Transparency Of health Research

The EQUATOR Network seeks to improve the quality of health care by promoting the transparent and accurate reporting of health research

Concerns about the deficiencies of health research publications have led to the creation of the EQUATOR Network. The Network will act as an 'umbrella' organisation, bringing together developers of reporting guidelines, medical journal editors and peer reviewers, research funding bodies and other collaborators with mutual interest in 'improving the quality of research publications and of research itself.

During the last ten years a considerable number of guidelines have been developed for reporting health research. They specify the minimum information necessary for a clear account of research methodology and findings. Examples include the [CONSORT Statement](#) (randomised controlled trials), QUOROM, recently renamed PRISMA (systematic reviews of randomised trials), [STARD](#) (diagnostic accuracy studies), [STROBE](#) (observational studies), and [REMARK](#) (tumour marker prognostic studies).

Use of reporting guidelines can lead to improved accuracy and transparency of publications; it facilitates appraisal for research quality and relevance, and can improve the efficiency of literature searches and ability to find requested information.

For the next five years, the EQUATOR Network has two primary objectives:

1. Provide resources enabling the improvement of health research reporting;
2. Monitor progress in the improvement of health research reporting.

Key deliverables will include:

- Web-based Resource Centre with easy access to reporting guidelines and other relevant information;
- Support for the development of robust reporting guidelines;
- Training courses for authors, editors and peer reviewers, facilitating transparent and accurate reporting and use of reporting guidelines;
- Annual assessment of how journals implement reporting guidelines;
- Annual audit of reporting quality across the health research literature.

The project is being led by Professor Doug Altman, one of the key movers of the CONSORT initiative. Its international steering group includes leading experts in the field of health research methodology, reporting and editorial work:

- Prof Doug Altman, Director, Centre for Statistics in Medicine, Oxford, UK
- Dr John Hoey, Advisor to the Principal on Public Health, Queen's University, Kingston, Canada
- Dr David Moher, Director, Chalmers Research Group, Ottawa, Canada
- Dr Ken Schulz, Vice president, Quantitative Sciences, Family Health International, USA

■ Minimal information guidelines to report health research, e.g.

- CONSORT Statement (randomised controlled trials)
- QUOROM, recently renamed PRISMA (systematic reviews of randomised trials)
- STARD (diagnostic accuracy studies)
- STROBE (observational studies)
- REMARK (tumour marker prognostic studies)

OBO Foundry Project - Standard Semantics

<http://obofoundry.org>

- A prospective standard (since 2006)
 - To guarantee interoperability of the ontologies from the start
 - Opposite to *post hoc* mapping, like UMLS Metathesaurus
 - To ensure division of the labour and avoid duplication
 - Where common terms exists across domains
 - To overcome the different grade of formal rigor
 - Different degree of completeness, variable quality, different update policies
- Provide a framework of rules governing best practices
 - To counteract the current policy of *ad hoc* creation of ontologies
 - To create a complete suite of orthogonal and interoperable ontologies
 - Tight connected to biomedical basic science
- OBO Foundry ontologies a subset of OBO
 - OBO is a shared portal for 60 ontology (managed by NCBO BioPortal)
 - Some OBO Foundry ontology are being constructed *ab initio*
 - Developers have agreed to accept the set of rules

OBO Foundry Project - Standard Semantics

<http://obofoundry.org>

ONTOLOGY	SCOPE
Mature ontologies undergoing incremental reform	
Cell Ontology (CL)	cell types from prokaryotes to mammals
Gene Ontology (GO)	attributes of gene products in all organisms
Foundational Model of Anatomy (FMA)	structure of the mammalian and in particular the human body
Zebrafish Anatomical Ontology (ZAO)	anatomical structures in <i>D. rerio</i>
Mature ontologies still in need of thorough review	
Chemical Entities of Biological Interest (ChEBI)	molecular entities which are products of nature or synthetic products used to intervene in the processes of living organisms
Disease Ontology (DO)	types of human disease
Plant Ontology (PO)	flowering plant structure, growth and development stages
Sequence Ontology (SO)	features and properties of nucleic sequences

Early versions exist	
Clinical Investigation Ontology (CIO)	clinical trials and related clinical studies
Common Anatomy Reference Ontology (CARO)	anatomical structures in all organisms
Ontology for Biomedical Investigations (OBI)	design, protocol, instrumentation, and analysis applied in biomedical investigations
Phenotypic Quality Ontology (PaTO)	qualities of biomedical entities
Protein Ontology (PRO)	protein types and modifications classified on the basis of evolutionary relationships
Relation Ontology (RO)	relations in biomedical ontologies
RNA Ontology (RnaO)	RNA features, interactions and motifs

Table from Smith *et al.*

- Custodians and Foundry coordinators, respectively
 - Individuals or consortia for each ontology
 - M. Ashburner, S. Lewis, C. Mungall and B. Smith

OBO Foundry Project - Standard Semantics

<http://obofoundry.org>

■ Provide a framework of rules governing best practices, including

- Open
- Common format language (OBO, OWL)
- Orthogonal (avoid domain overlap)
- Common architecture (Relation Ontology)
- Update
- Unique identifier space in OBO
- Versioning (backward compatibility)
- Documentation

■ Example

- Body weight
 - PATO:weight that *inheres_in* CARO:whole_organism
- Dead cell
 - CELL TYPE root node: cell *has_quality* PATO:dead

	RELATION TO TIME		CONTINUANT	OCCURRENT	
	←		→		
GRANULARITY	INDEPENDENT		DEPENDENT		
	ORGAN AND ORGANISM	Organism (NCBI Taxonomy?)	Anatomical Entity (FMA, CARO)	Organ Function (FMP, CPRO)	Phenotypic Quality (PaTO)
CELL AND CELLULAR COMPONENT	Cell (CL)	Cellular Component (FMA, GO)	Cellular Function (GO)	Cellular Process (GO)	
MOLECULE	Molecule (ChEBI, SO, RnaO, PrO)		Molecular Function (GO)		Molecular Process (GO)

Credit to B. Smith

OBO Relation Ontology

Foundational	<i>is_a</i> <i>part_of</i>
Spatial	<i>located_in</i> <i>contained_in</i> <i>adjacent_to</i>
Temporal	<i>transformation_of</i> <i>derives_from</i> <i>preceded_by</i>
Participation	<i>has_participant</i> <i>has_agent</i>

OBI - An OBO Foundry Ontology

<http://obi.sf.net>

- **Ontology for Biomedical Investigation (since 2006)**
 - International collaboration, started from the omics- communities
 - MGED (transcriptomics), PSI (proteomics) and MSI (metabolomics)
 - > Consistent annotation, powerful queries and data integration
- **Describe the laboratory workflow**
 - Set of **universal terms**
 - Investigation (organization, intent, design etc)
 - Material (biological and chemical, manipulation and transformation)
 - Protocols and instrumentations
 - Data generated and types of analysis performed on it
 - Set of biological and technological **domain-specific terms**
 - To meet the annotation requirements of any given community
- **'Interoperable by construction**
 - Orthogonality and x-referencing with other OBO Foundry ontologies

OBI - An OBO Foundry Ontology

<http://obi.sf.net>

Ontology for Biomedical Investigations

*Home | [Ontology](#) | [Community](#) | [Resources](#) |

1. Coordination Committee (CC): Representatives of the communities -> Monthly conferences

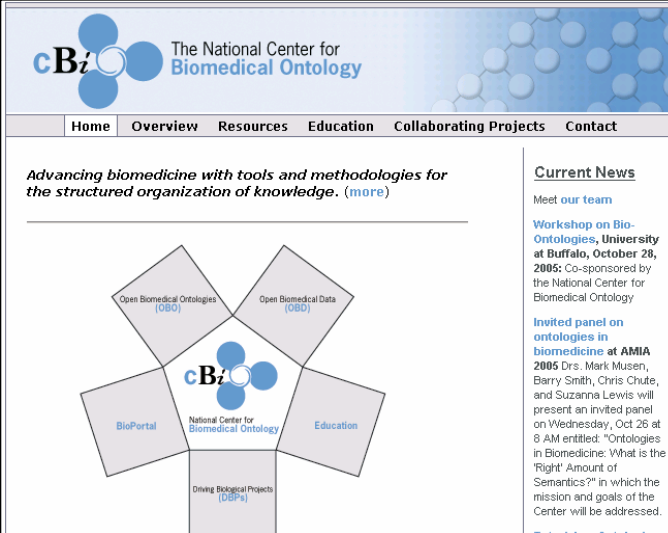
- [Bio-imaging](#), Coordinators: Jeff Grethe, Daniel Rubin
- [Cellular Assays](#), Coordinator: Stefan Wiemann
- [Crop Sciences](#), Coordinator: Richard Bruskiwich
- [Clinical Trials](#), Coordinator: Jennifer Fostel
- [Environmental Biology](#), Coordinator: Norman Morrison
- [Flow Cytometry](#), Coordinator: Ryan Brinkman
- [Genomics/Metagenomics](#), Coordinators: Dawn Field, Tanya Gray
- [ImmPort](#), Coordinator: Richard Scheuermann
- [Immune Epitope Database and Analysis Resource](#), Coordinator: Bjoern Peters
- [In Situ Hybridization and Immunohistochemistry](#), Coordinator: Eric Deutsch
- [Metabol/nomics](#), Coordinators: Susanna Sansone, Daniel Schober
- [Neuroinformatics and Bio-imaging](#), Coordinator: Bill Bug
- [Nutrigenomics](#), Coordinator: Philippe Rocca-Serra
- Polymorphism, Coordinator: Tina Hernandez-Boussard
- [Proteomics](#), Coordinators: Luisa Montecchi, Susanna Sansone, Daniel Schober, Chris Taylor
- [Toxicogenomics](#), Coordinator: Jennifer Fostel
- [Transcriptomics](#), Coordinators: Helen Causton, Liju Fan, Jennifer Fostel, Gilberto Fragoso, M Susanna Sansone, Chris Stoeckert, Trish Whetzel, Joe White

2. Developers WG: CC and other communities' members

↓
Weekly conferences calls

3. Advisors:

- Frank Hartel
- Suzi Lewis
- Mark Musen
- Steve Oliver
- Barry Smith
- Robert Stevens

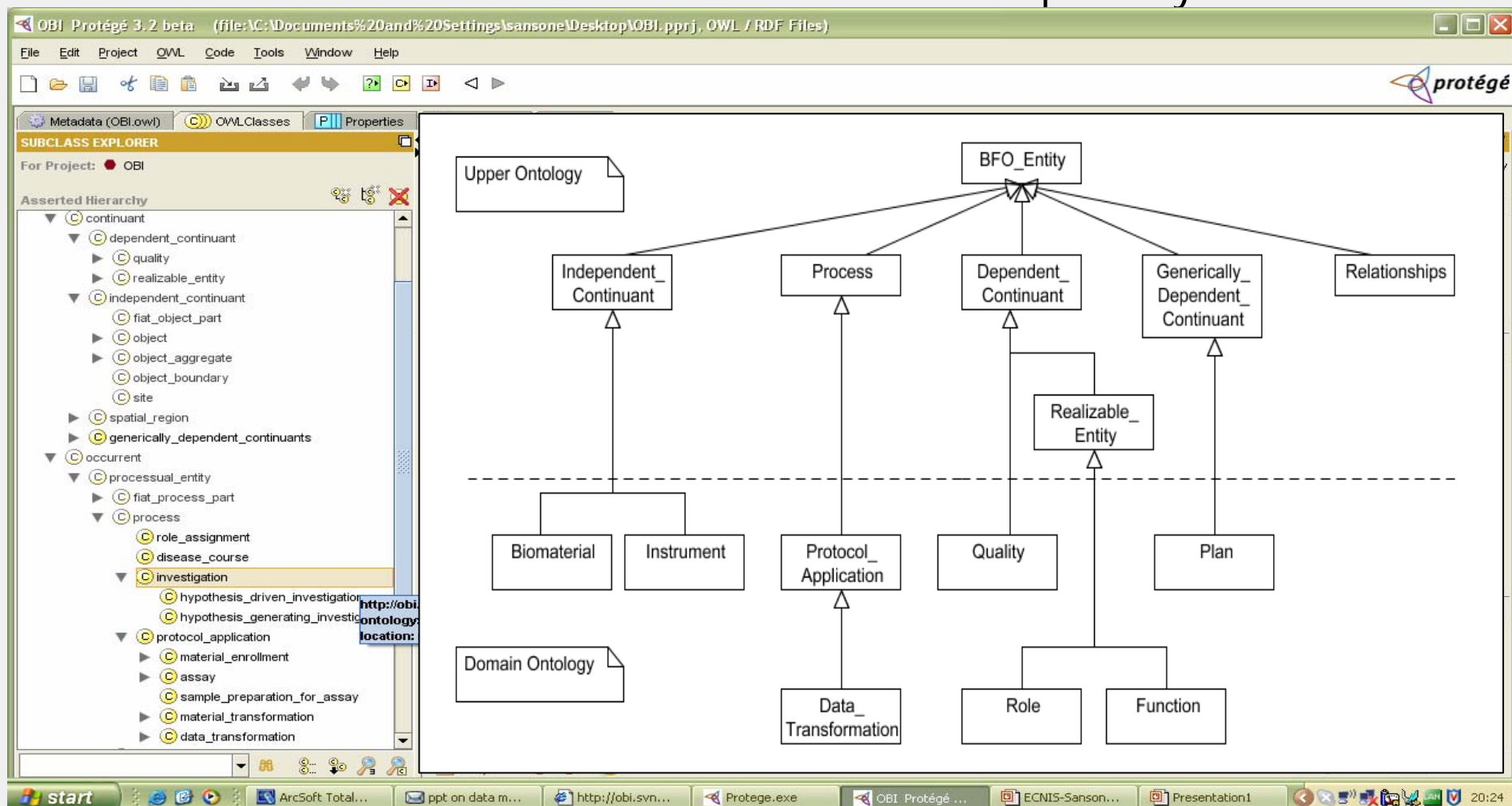
The screenshot shows the website for the National Center for Biomedical Ontology (cBio). The header includes the cBio logo and the text "The National Center for Biomedical Ontology". The navigation menu includes: Home, Overview, Resources, Education, Collaborating Projects, and Contact. The main content area features a central graphic with the cBio logo and five surrounding boxes labeled: "Open Biomedical Ontologies (OBO)", "Open Biomedical Data (OBD)", "BioPortal", "National Center for Biomedical Ontology", and "Driving Biological Projects (DBPs)". To the right, there is a "Current News" section with a link to "Meet our team" and a detailed announcement for a "Workshop on Bio-Ontologies, University at Buffalo, October 28, 2005".

-> cBio will oversee the Open BioMedical Ontology (OBO) initiative

OBI - An OBO Foundry Ontology

<http://obi.sf.net>

- Open source, standards compliant and version management
 - Ontology Web Language (OWL) using Protégé editor
 - OBI.owl files are available from the OBI SVN Repository



FuGE Project - Standard Syntax

<http://fuge.sf.net>

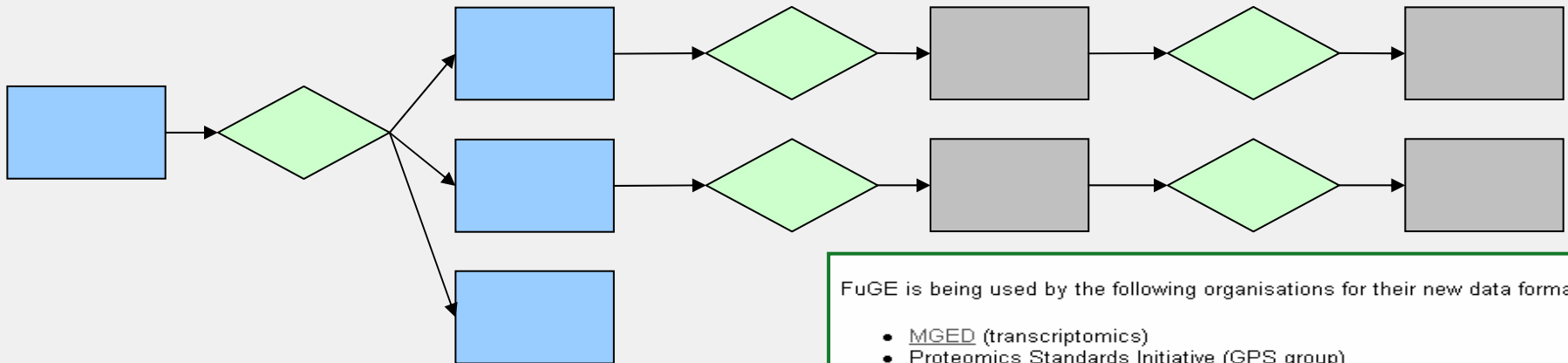
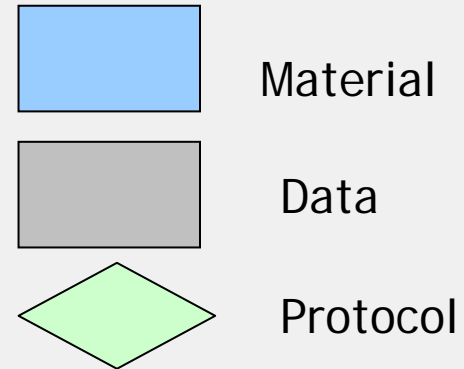
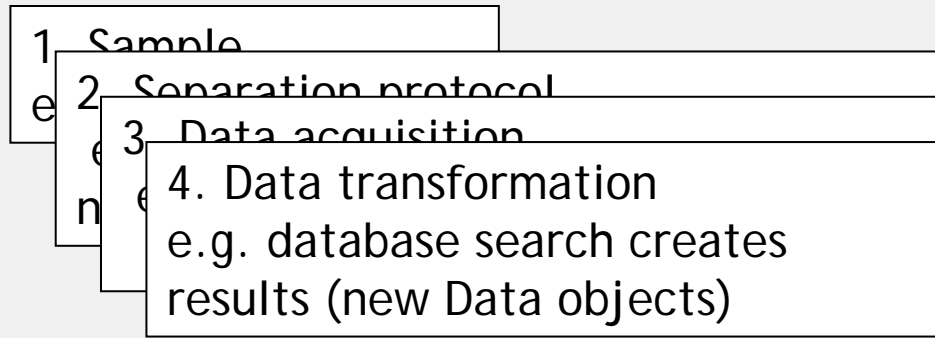
- International collaboration (since 2005)
 - Communities developing XML-based formats for data exchange
- Objective 1: Model of common classes
 - For describing **laboratory workflows** for functional genomics

F U G E	C O M M O N	Audit	Contacts, auditing and security settings for all objects.
		Description	Additional annotations and free-text descriptions for all objects.
		Ontology	A mechanism for referencing external ontologies or terms from a controlled vocabulary.
		Protocol	A model of procedures, software, hardware and parameters. The package can define workflows by relating input and output materials and/or data to the protocols that act on them.
	B I O	Reference	External bibliographic or database references that can be applied to many objects across the FuGE model.
		ConceptualMolecule	Captures database entries of biological molecules such as DNA, RNA or amino acid sequences and an extension point for other molecule types, such as metabolites or lipids.
		Data	Defines the dimensions of data and storage matrices, or references to external data formats.
		Investigation	Defines an overview of the investigation structure by capturing the overall design and the experimental variables and by providing associations to related data.
	Material	Models material types such as organisms, samples or solutions. Materials are characterized by ontology terms or by extension of the Material package.	

- Objective 2: Common framework
 - To develop **modular data format** with consistent structure
 - Does NOT replace, but underpins different XML formats
- Object model in UML and XML schema v1 (**AVAILABLE**)
 - Transmission/interpretation of information between applications

FuGE Project - Standard Syntax

<http://fuge.sf.net>



FuGE is being used by the following organisations for their new data formats:

- [MGED](#) (transcriptomics)
- [Proteomics Standards Initiative \(GPS group\)](#)
- [Metabolomics Standards Initiative \(NMR and sample processing groups\)](#)

Other data formats planned to extend from FuGE:

- [In Situ Hybridization and Immunohistochemistry Experiments](#)
- [Flow cytometry](#)

FuGE implementations in software (in development):

- [CPAS](#) at Fred Hutchinson Cancer Research Centre
- [Genomics](#) in Proteus LIMS software
- [Generation Challenge Program, Article](#)
- [CISBAN data portal](#)

Acknowledgements and Resources

Nature Biotechnology

<http://mibbi.sf.net>

Promoting Coherent Minimum Reporting Requirements for Biological and Biomedical Investigations: The MIBBI Project

Chris F Taylor¹, Dawn Field^{2,3}, Susanna-Assunta Sansone¹, Rolf Apweiler¹, Michael Ashburner⁴, Catherine A Ball⁵, Pierre-Alain Binz^{6,7}, Alvis Brazma¹, Ryan Brinkman⁸, Eric W Deutsch⁹, Oliver Fiehn¹⁰, Jennifer Fostel¹¹, Peter Ghazal¹², Graeme Grimes¹², Nigel W Hardy¹³, Henning Hermjakob¹, Randall K Julian, Jr.¹⁴, Matthew Kane¹⁵, Eugene Kolker¹⁶, Martin Kuiper¹⁷, Nicholas Le Novère¹, Jim Leebens-Mack¹⁸, Suzanna E Lewis¹⁹, Ruth McNally²⁰, Alexander Mehrle²¹, Norman Morrison^{3,22}, John Quackenbush²³, Donald G Robertson²⁴, Philippe Rocca-Serra^{1,25}, Barry Smith²⁶, Jason Snape²⁷, Peter Sterk¹, Stefan Wiemann²⁰

<http://obofoundry.org>

The OBO Foundry: Coordinated Evolution of Ontologies to Support Biomedical Data Integration

Barry Smith,^a Michael Ashburner,^b Cornelius Rosse,^c Jonathan Bard,^d William Bug,^e Werner Ceusters,^f Louis J. Goldberg,^g Karen Eilbeck,^h Amelia Ireland,ⁱ Christopher J Mungall,^j the OBI Consortium,^k Neocles Leontis,^l Philippe Rocca-Serra,ⁱ Alan Ruttenberg^m, Susanna-Assunta Sansone,^j Nigam Shah,ⁿ Patricia L. Whetzel,^o Suzanna Lewisⁱ

<http://fuge.sf.net>

The Functional Genomics Experiment model (FuGE): an extensible framework for standards in functional genomics

Andrew R. Jones^{1,2,16}, Michael Miller³, Ruedi Aebersold⁴, Rolf Apweiler⁵, Catherine A. Ball⁶, Alvis Brazma⁵, James DeGreef⁷, Nigel Hardy⁸, Henning Hermjakob⁵, Simon J. Hubbard², Peter Hussey⁹, Mark Igra^{9,10}, Helen Jenkins⁸, Randall K. Julian Jr.¹¹, Kent Laursen¹¹, Stephen G. Oliver², Norman W. Paton¹, Susanna-Assunta Sansone⁵, Ugis Sarkans⁵, Christian J. Stoeckert Jr.¹², Chris F. Taylor⁵, Patricia L. Whetzel¹², Joseph A. White¹³, Paul Spellman¹⁴ and Angel Pizarro^{15,16}

NET
Funds and
Collaborators



The National Center for Toxicological
Research (NCTR)
[Center for Toxicoinformatics](http://www.nctr.nih.gov)

