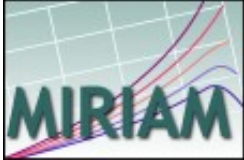
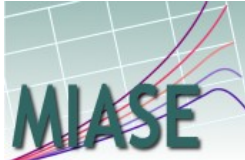







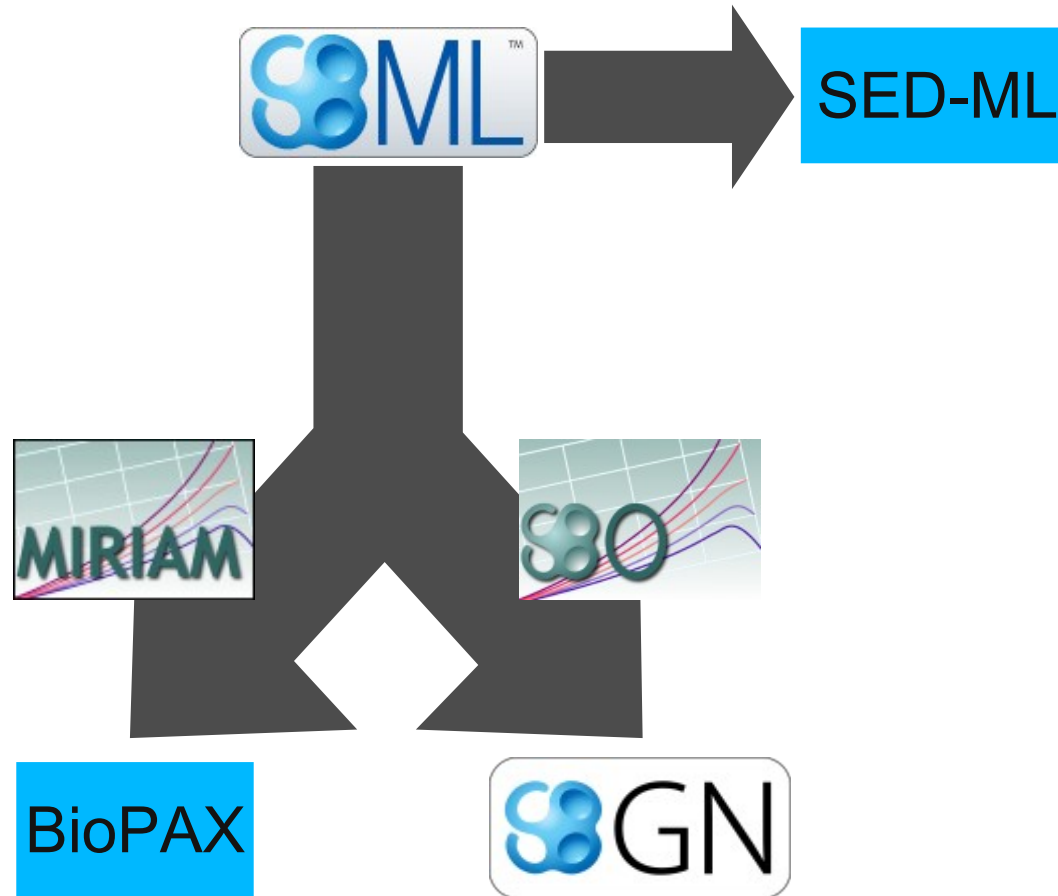
Welcome to the last joint SBML hackathon/
annual BioModels meeting ...

(before the first HARMONY gathering next year)

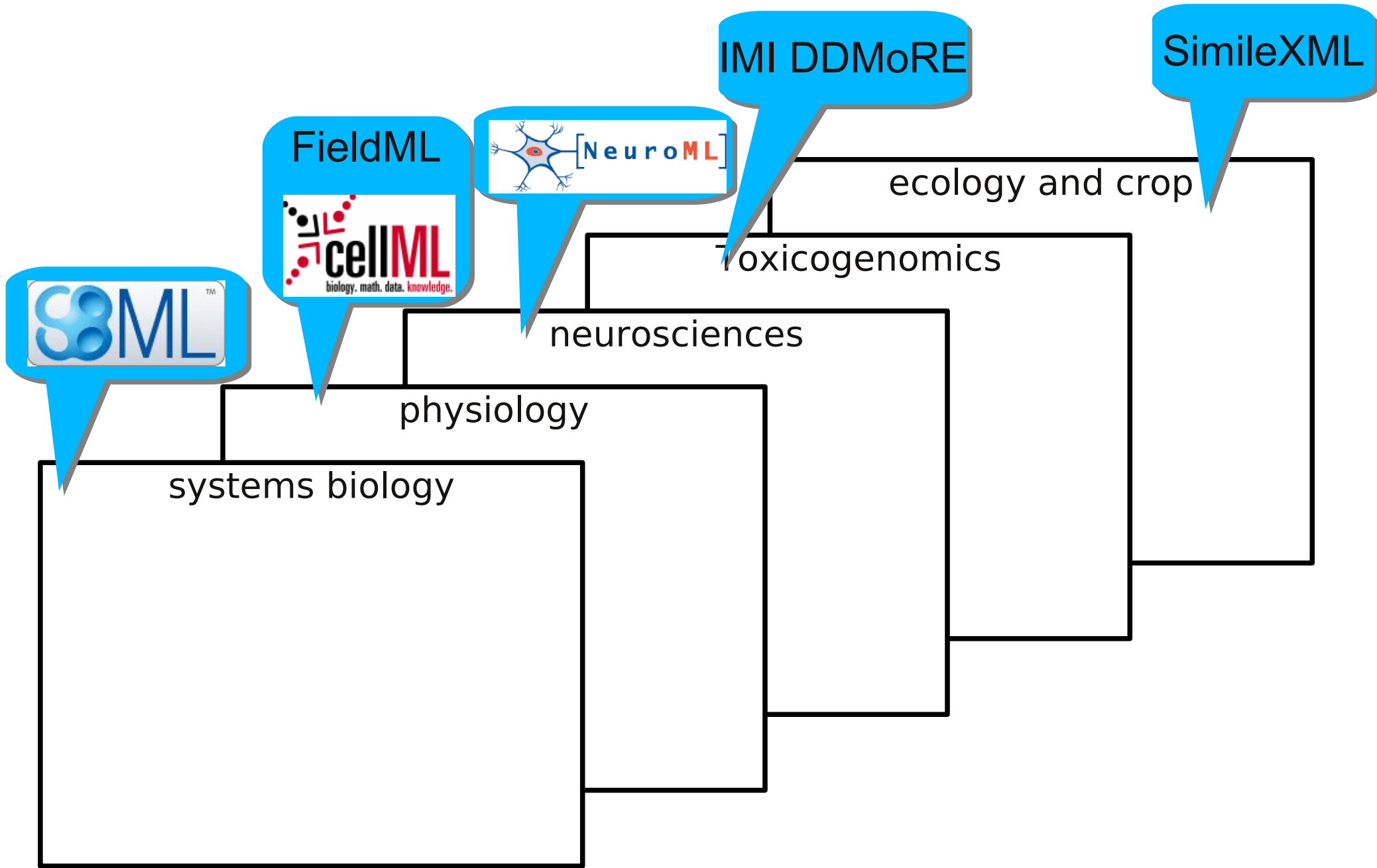
A mosaic of standards in Systems Biology

	Models	Simulation	Results
Minimal requirements			
Data-models	 	SED-ML	SBRML
Ontologies			

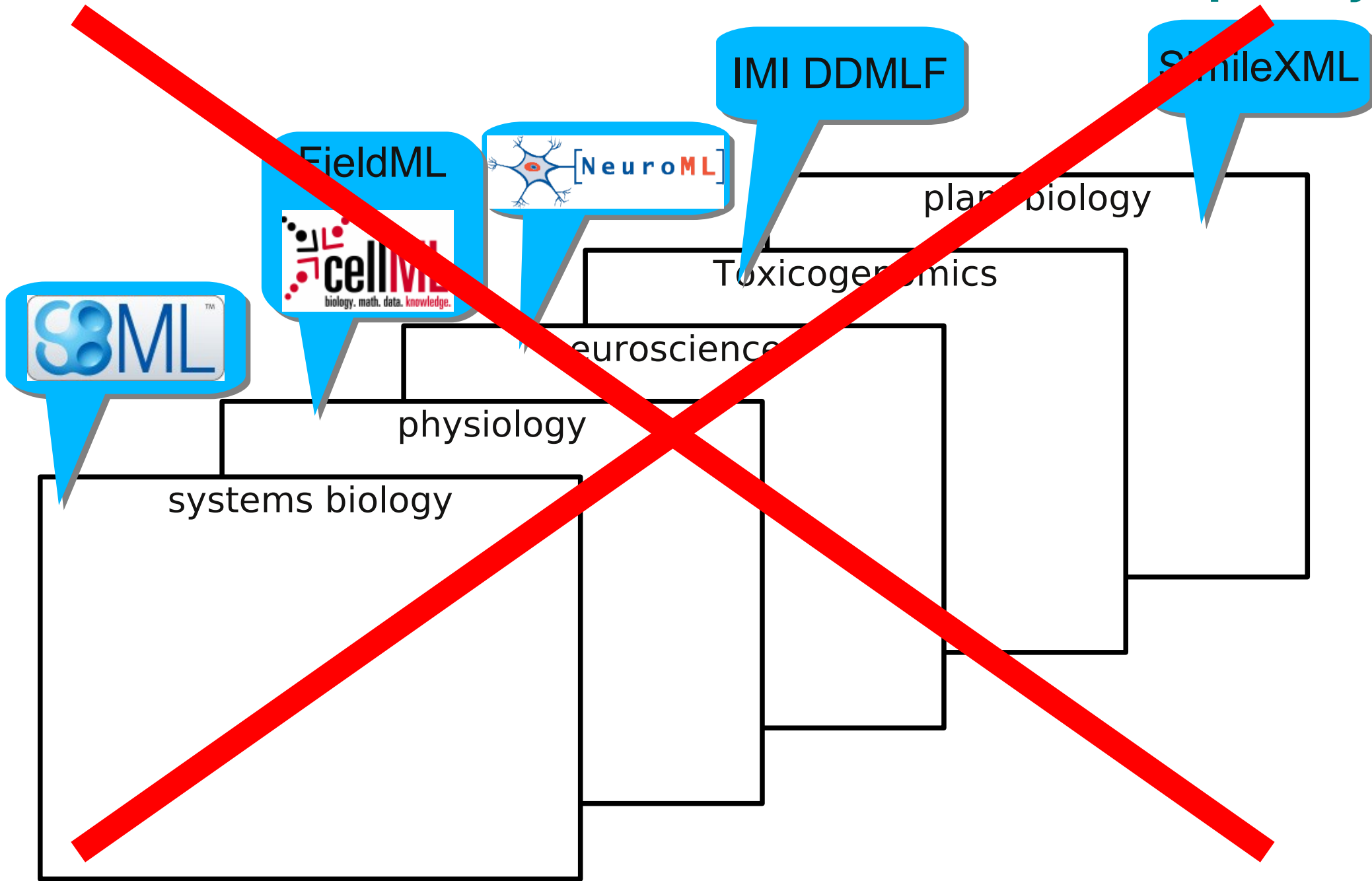
Those standards build up on each others



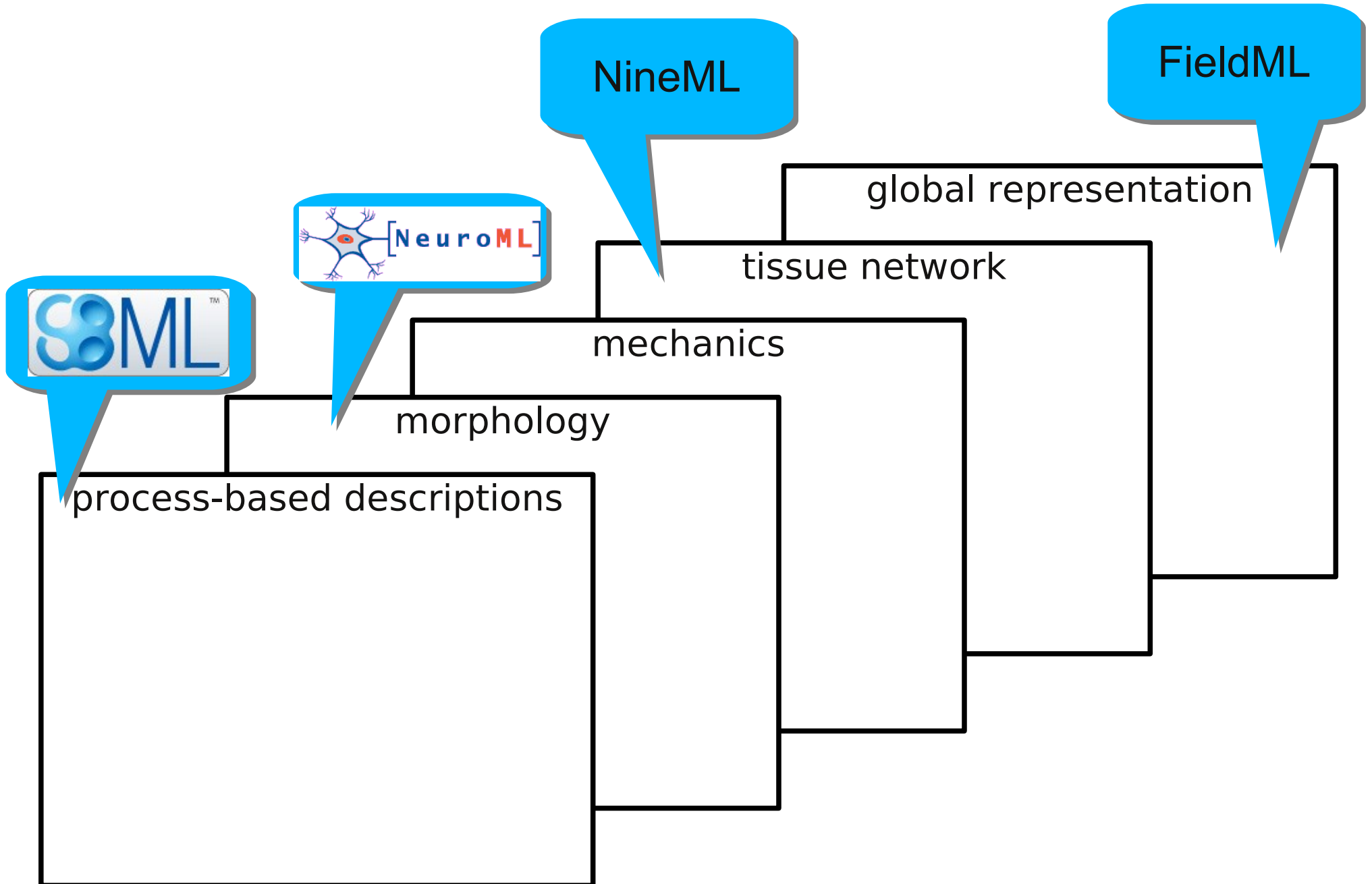
Similar efforts in other disciplines



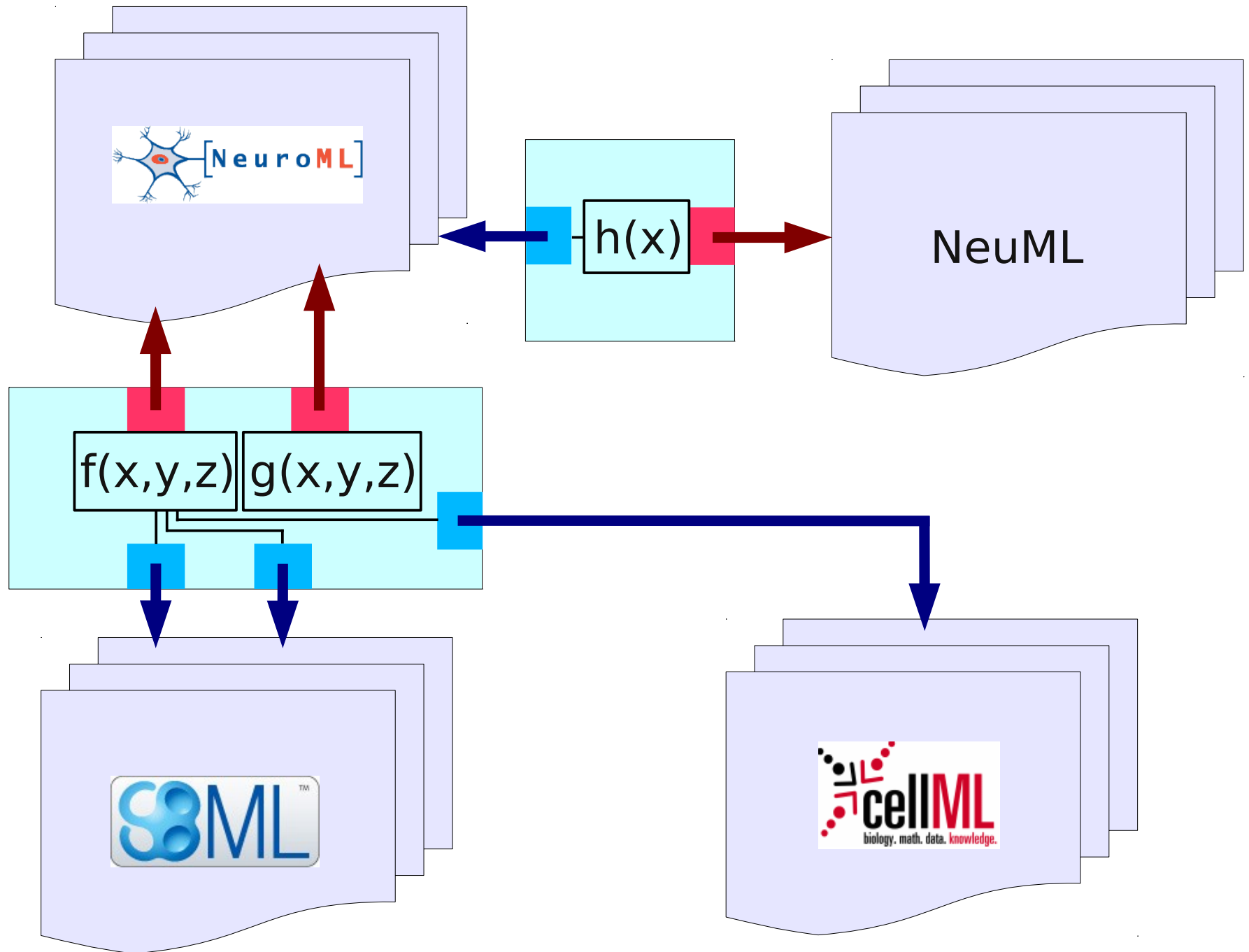
The issues to tackle are trans-disciplinary



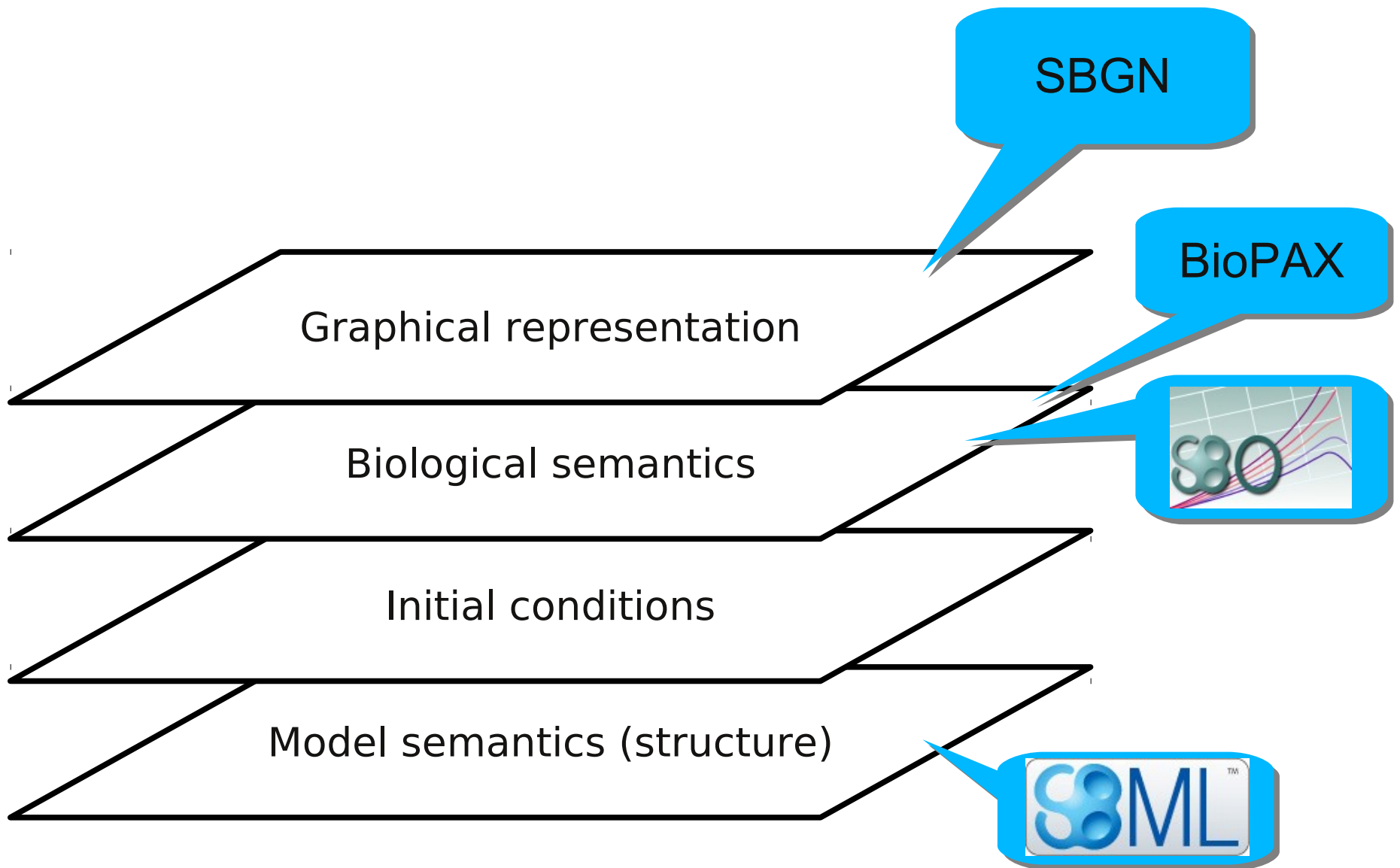
Non-overlapping languages



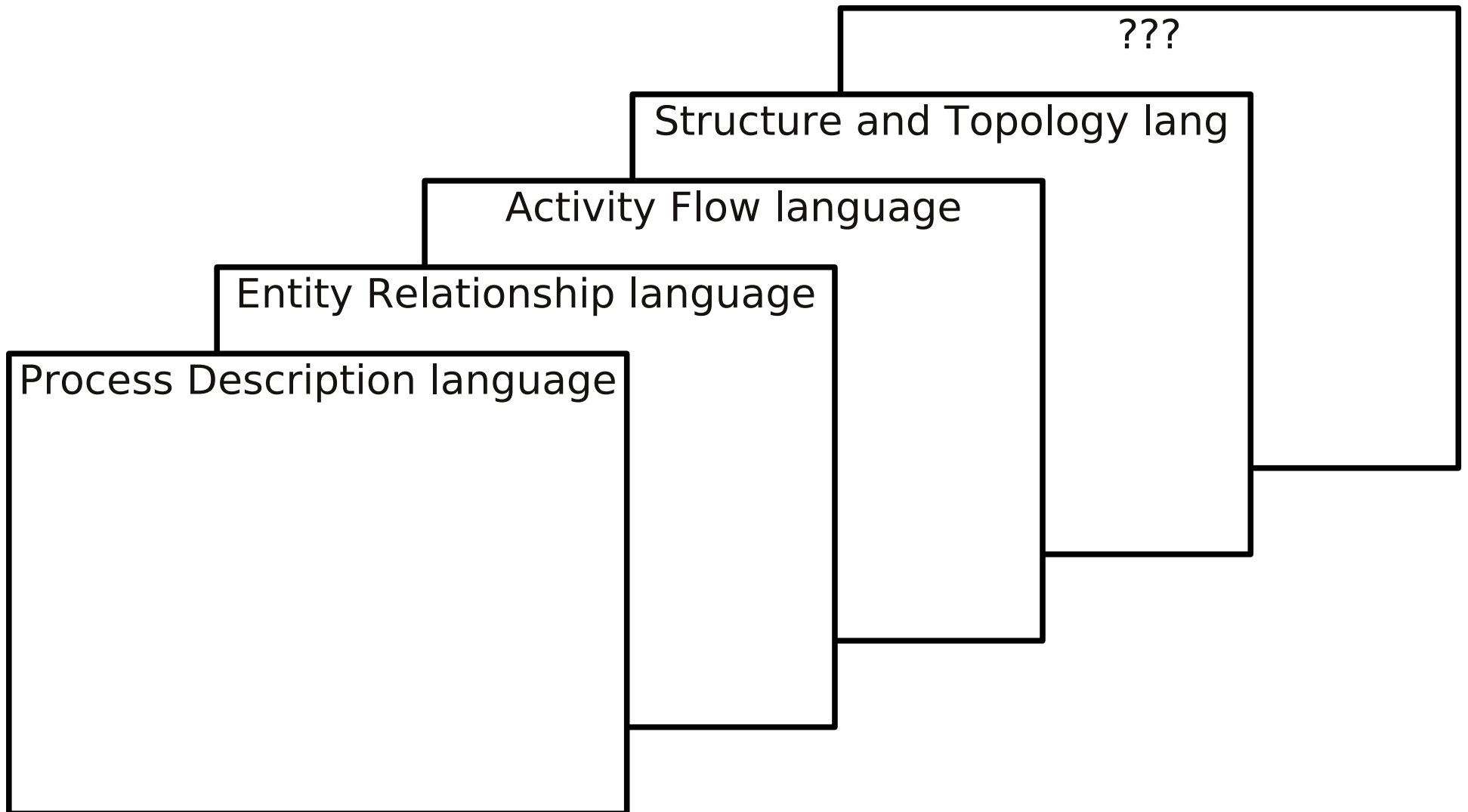
Multi-scale representation using adapters



Disentangling the level of discourse



Non-overlapping representation



Disentangling the model life-cycle

PMML



SED-ML

SBRML

model generation

model description

parameterisation

simulation and analysis

numerical results

[STANDARDS](#) [Web Design and Applications](#)[Web Architecture](#)[Semantic Web](#)[XML Technology](#)[Web of Services](#)[Web of Devices](#)[Browsers and Authoring Tools](#)[All Standards and Drafts](#)[About W3C Standards](#)

WEB DESIGN AND APPLICATIONS

On this page → [technology topics](#) • [news](#) • [upcoming events and talks](#)

Web Design and Applications involve the standards for building and Rendering Web pages, including HTML, CSS, SVG, Ajax, and other technologies for Web Applications ("WebApps"). This section also includes information on how make pages accessible to people with disabilities (WCAG), internationalized, and work on mobile devices.

HTML & CSS

HTML and CSS are the fundamental technologies for building Web pages: HTML (html and xhtml) for structure, CSS for style and layout. Find resources for good Web page design as well as helpful tools.

Scripting and Ajax

Standard APIs for client-side Web Application development include those for Geolocation, XMLHttpRequest (Ajax), and mobile widgets. W3C standards for document models (the "DOM") and technologies such as XBL allow content providers to create interactive documents through scripting.

Graphics

W3C is the home of the widely deployed PNG raster format, SVG vector format, and the Canvas API. WebCGM is a more specialized format used, for example, in the fields of automotive engineering, aeronautics.

Audio and Video

Some of the W3C formats that enable authoring audio and video presentations include HTML, SVG, and SMIL (for synchronization). W3C is also working on a timed text format for captioning and other applications.

Accessibility

W3C's Web Accessibility Initiative (WAI) has published Web Content Accessibility Guidelines (WCAG) to help authors create content that is accessible to people with disabilities. WAI-ARIA gives authors more tools to create accessible Web Applications by providing additional semantics about widgets and behaviors.

Internationalization

W3C has a mission to design technology that works across cultures and languages. W3C standards such as HTML and XML are built on Unicode, for instance. In addition, W3C has published guidance for authors related to language tags bi-directional (bidi) text, and more.

Mobile Web

W3C promotes "One Web" that is available on any device. W3C's Mobile Web Best Practices help authors understand how to

Privacy

The Web is a powerful tool for communications and transactions of all sorts. It is important to consider privacy and security

Math on the Web

Mathematics and formula are used on the Web for business reports, education materials and scientific research. W3C's

BioModels.net

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For computational modeling to become more widely used in biology, researchers must be able to exchange and share their results. The development and broad acceptance of common representation formats such as SBML is a crucial step in that direction, allowing researchers to exchange and build upon each other's work with greater ease and accuracy.

BioModels.net is another step: an international effort to

- 1) define agreed-upon standards for model curation
- 2) define agreed-upon vocabularies for annotating models, and
- 3) provide a free, centralized, publicly-accessible database of annotated models in SBML and other structured formats.

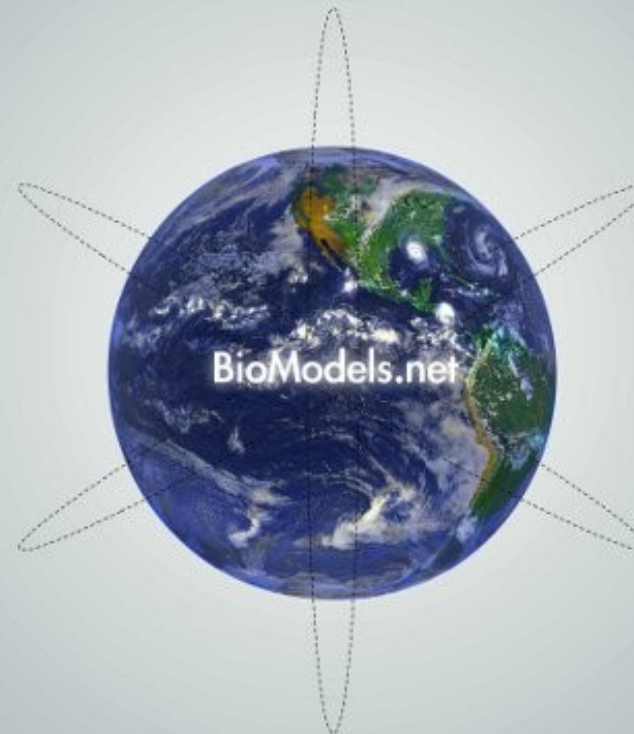
Poster presented
by Mike Hucka
at the 6th ICSB
Boston 2005

SBO

The **Systems Biology Ontologies (SBO)** are a set of interlinked controlled vocabularies tailored to the needs of the systems biology modeling community. The aim is to capture consensus definitions of commonly-used concepts and their relationships. Using SBO terms as a basis for annotating models and performing database searches (e.g., in BioModels Database) can lead to a greater degree of consistency, quality and interoperability.

BioModels Database

BioModels Database is a free, public repository of published quantitative models of biochemical and cellular systems. The models are curated to verify that they correspond to the reference publication and give the proper numerical results. Curators annotate the components of the models with terms from controlled vocabularies and links to external relevant data resources, allowing users to search accurately for the models they need and precisely identify their components.



References

Le Novère N, Bornstein B, Broicher A, Courtot M, Donizelli M, Dharuri H, Li L, Sauro H, Schilstra M, Shapiro B, Snoep JL, Hucka M. BioModels Database: A Free, Centralized Database of Curated, Published, Quantitative Kinetic Models of Biochemical and Cellular Systems. (2006) *Nucleic Acids Res*, in press.

Le Novère N, Finney A, Hucka M, Bhalla U, Campagne F, Collado-Vides J, Crampin EJ, Halstead M, Klipp E, Mendes P, Nielsen P, Sauro H, Shapiro B, Snoep JL, Spence HD, Wanner BL. Minimal Information Requested in the Annotation of biochemical Models (MIRIAM). (2005) *Nature Biotechnology*, in press.

MIRIAM

The **Minimum Information Requested in the Annotation of Models (MIRIAM)** is a proposed set of rules for curating quantitative models of biological systems. The rules define procedures for encoding and annotating models represented in machine-readable form. Their application will enable users to (a) have confidence that curated models are an accurate reflection of their associated reference description; (b) search collections of curated models with precision; (c) quickly identify the biological phenomena that a given curated model or model constituent represents; and (d) facilitate model reuse and composition into large subcellular models.

Acknowledgments

Funding for different aspects of the BioModels.net effort currently comes from the following organizations: the National Institute of General Medical Sciences (USA, grant GM070923-02S1), the International Joint Research Program of NEDO (Japan), DARPA BioComp Bio-SPIRE (USA), the European Molecular Biology Laboratory (EU), the California Institute of Technology (USA), the Systems Biology Institute (Japan), and the University of Hertfordshire (UK).



BioModels.net

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BioModels.net

The Next Step After Standard Formats

For computational modeling to become more widely used in biological research, researchers must be able to exchange and share their results. The development and broad acceptance of common model representation formats such as [SBML](#) is a crucial step in that direction, allowing researchers to exchange and build upon each other's work with greater ease and accuracy.

The BioModels.net project is another step: an international effort to:

1. define agreed-upon standards for model curation
2. define agreed-upon vocabularies for annotating models with connections to biological data resources
3. provide a free, centralized, publicly-accessible database of annotated, computational models in SBML and other structured formats

Helping to Define Community Standards

To facilitate assembling useful collections of quantitative models of biological phenomena, it is crucial to establish standards for the vocabularies used in model annotations as well as criteria for minimum quality levels of those models. The BioModels.net project aims to bring together a community of interested researchers to address these issues. We are working towards defining these standards through white papers and process definitions. All of the products of our efforts are open and freely available through this site.

Standards and Processes Developed Hand-in-Hand with a New Database

The database component of BioModels.net is especially designed for working with *annotated* computational models: each model is carefully reviewed and augmented by human annotators on the BioModels.net team to add metadata linking the model elements to other biological databases and resources. The [BioModels Database](#) at the [EBI](#) system goes far beyond other collections of models by being a *true* database, featuring browsing, cross-referencing, searching, and facilities for visualization, exporting models in different formats, and remote API access.

Projects

The projects we are currently coordinating are:

- [BioModels Database](#)
- [MIRIAM](#) and the associated [set of qualifiers](#) and [MIRIAM Resources](#)
- [SBO](#)

A first step: common meetings

- January 2008: SBGN hackathon; BioModels DB; MIRIAM; SBO
- March 2009: SBML hackathon; BioModels DB; MIRIAM; SBO
- April 2009: CellML; SED-ML; SBGN hackathon
- NOW: SBML hackathon; BioModels DB; MIRIAM; SBO; SED-ML
- October 2010: 1st **COMBINE** MEETING with SBML; SBGN; BioPAX; SBO; MIRIAM
- From now on, two grouped annual meetings
 - **COMBINE** forum: presentation of support, discussion about future developments and collaboration etc.
 - **HARMONY** hackathon: developing support, writing specifications, tinkering with interoperability etc.

THE END

THE **X** END

THE BEGINNING