



The **MOSAIC** Publication Repository:  
*Supplemental Archives/ Structured Research Reporting/Plugins*

## Overview

In recent years — as publishing has become more “digitized” — many online platforms have emerged for scientists to share and publish their research work, including both raw data and scientific papers. These portals generally provide an index/search feature where readers can locate research based on the name of the author, title of the publication, keywords, or subject matter, along with a document viewer where readers can view the abstract of each publication (and sometimes full text of the article) and other publication details (such as co-authors, date of publication, bibliographic references, etc.). However, these portals offer only limited features for interactively exploring publications, particularly when it comes to examining data sets and/or browsing multimedia assets associated with publications, such as audio, video, interactive diagrams, or **3D** graphics.

The “**MOSAIC**” system (“Multi-Paradigm Ontologies for Scientific and Technical Publications”) is a suite of code libraries developed by LTS allowing institutions to host publication repositories free of the limitations of existing scientific document portals. With **MOSAIC**, each publication can be linked to a supplemental archive which contains information about the author’s research methods, data sets, and focal topics. If desired, these archives can include machine-readable representations of full publication text, to support advanced text-mining techniques across the repository.

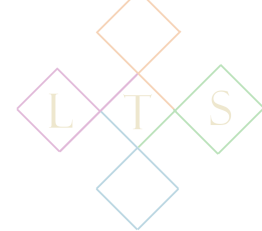
Using **MOSAIC**, developers can implement a hosting platform for this supplemental material, in addition to the publications themselves, where the platform provides software enabling readers to browse and access supplemental archives and their data sets and/or methodological descriptions. A **MOSAIC** publication repository, also called a **MOSAIC** “portal,” is a structured collection of data and documents which can be hosted via web servers (including fully encapsulated and containerizable cloud services) implemented with the help of **MOSAIC** libraries.

**MOSAIC** repositories can serve as general-purpose portals, hosting academic papers covering a broad range of topics. Alternatively, **MOSAIC** repositories can serve as targeted portals hosting papers focused on more narrowly focused subject domains. Organizations can utilize **MOSAIC** internally as the basis of a private document management system (**DMS**), or to provide (public) open access to complete publications, including human-readable and machine-readable full text and all supplemental content, with no restrictions<sup>1</sup>. **MOSAIC** can be customized for different subject areas by incorporating domain-specific ontologies into document-search features as well as machine-readable document-text annotations.

**MOSAIC** is designed so that the software to access publications and publications’ supplemental archives can be embedded in scientific-computing applications via **MOSAIC plugins**. This ensures that publications and data sets can be examined interactively with the same software that scientists employ to conduct research. **MOSAIC** also introduces a *structured reporting system* (**MOSAIC-SR**) for describing research/experimental/lab methods/protocols. Supplemental archives, plugins, and the structured reporting system are outlined below.

---

<sup>1</sup> Excepting sensitive/private information which might be provided via a dedicated component within the portal with specific features for authors, editors, and administrators. Any project which *does* restrict access to some part of any document requires a commercial **MOSAIC** license



### Supplemental Archives

MOSAIC supplemental archives are additional resources paired with MOSAIC publications. In general, supplemental archives may include raw data, descriptions of research methods, or annotated data linked to publication texts. Each supplemental archive could have any of the following resources:

1. Interactive versions of the publication, with annotations indicating important concepts and phrases, perhaps aggregated into a "glossary" defining technical terms;
2. Machine-readable representations of document texts, with special-purpose character encodings designed to facilitate Text and Data Mining (**TDM**);
3. Structured files containing raw data discussed in the publication, along with interactive software allowing scientists to access and reuse the data;
4. Detailed reports of the author's research methods and experimental setup and/or protocols, conforming to the relevant standards with respect to the publication's subject classification — for instance, the "Minimum Information for Biological and Biomedical Investigations" (**MIBBI**) includes about 40 specific standards for different branches of biology and medicine;
5. Representations of analytic methods and algorithms underlying the research findings, which are provided directly via computer code or indirectly via formal descriptions of computational workflows;
6. Self-contained computer software which demonstrates code that the author developed and/or used for analyzing/curating research data;
7. Multi-media assets such as audio or video files, annotated images, **3D** graphics, interactive **2D/3D** plots and diagrams, or other kinds of non-textual content which needs to be viewed with special multi-media software.

The contents of a supplemental archive will be different for different publications, depending on whether the archive contains specific raw data or just a summary of the methods used to obtain the raw data. In the former case, a typical archive will include a *data-set application*, or a semi-autonomous software component allowing researchers to study and visualize the data set, typically provided in turn via data files that are also located in the archive. The data-set application will, in general, provide both a visual interface for raw data and code libraries for computationally manipulating this data; typically raw data files will encode serialized data structures that can be deserialized by code (e.g., **C++** classes) included in the data-set application. MOSAIC includes generic implementations of a data-set explorer ("**MdsX**"), which can be adopted to the specific kind of information that needs to be serialized for a given publication. As a result, data-set application can then be packaged as a plugin to existing scientific software within the relevant scientific discipline.

### MOSAIC Plugins

By design, MOSAIC Portals will provide a suite of plugins for existing scientific software, allowing publications and supplemental archives hosted on the portal to be read and examined within computer software associated with each publication's subject matter. For example, articles about chemistry could be read within **IQMOL**, a molecular visualization program; articles about cellular biology and bioimaging could be read within **CAPTk** (the Cancer Imaging and Phenomics Toolkit), an image-processing application; articles discussing novel computer code could be read within **QT** Creator, an Integrated Development Environment (**IDE**) for programming; etc. The advantage of accessing a publication and a supplemental archive within actual scientific software is that it allows research work to be understood, evaluated, and reused within the computing environments which scientists typically use to conduct professional research. This is different than existing science publication portals, which generally rely on web browsers to access supplemental materials like data sets and multimedia files — in this standard setup the software ecosystem wherein readers examine published research is fundamentally separate from the software platforms where research is actually conducted. This



example demonstrates how existing portals are *limited* in their ability to share research in rigorously reusable and replicable ways — and how **MOSAIC** offers a potential improvement.

Embedding presentations of their research within existing scientific software has the added benefit for authors of making their work more practically and immediately useful for the scientific community. Such presentations establish the computational framework for pragmatically deploying their techniques in real-world scientific contexts, accelerating the pace at which research work can be translated to concrete scientific (and clinical/lab/experimental) practice. As one example, research involving novel image analysis techniques could be packaged so as to target a **MOSAIC** plugin for bioimaging software such as **CAPTK**, so that readers could actually run the author's code as a **CAPTK** module.<sup>2</sup> This is important because such functional assessment and adoption of novel contributions is harder to carry out if a body of research work is described indirectly within article text, as opposed to being concretely implemented within a specific scientific application.

Another benefit of using plugins to access supplemental archives is that the host application will usually provide more sophisticated multimedia and data visualization capabilities, compared to static **PDF** images or even interactive web portals. Publishers have begun to develop online platforms for browsing research papers in conjunction with multimedia content such as interactive diagrams and **3D** graphics — a physical model of a protein or a chemical compound, for instance, can be viewed online via **WEBGL**; such graphics could even be embedded as an "iframe" within an **HTML** version of the publications. Publishers consider this to be cutting-edge technology. However, the same molecular **3D** model, when viewed in **IQMOL**, can be enhanced with many additional visual features, representing bonds, orbitals, torsion angles, etc. The multimedia experience of exploring chemistry data in custom software like **IQMOL** is therefore much greater than the experience of generic web multimedia, which means that the scientific software is a better forum for showcasing novel research.

## MOSAIC Structured Reporting (**MOSAIC-SR**)

The **MOSAIC** structured reporting framework (**MOSAIC-SR**) includes tools to help authors develop interactive presentations supplementing academic documents, and specifically to use supplemental archives to document how their research has been conducted. With **MOSAIC-SR**, authors can implement or reuse code libraries that report on research/experiment methods, workflows, and protocols. The **MOSAIC-SR** information may be structured as a "minimum information checklist" conformant to standards such as those collectively gathered into the **MIBBI** recommendations; in this case **MOSAIC-SR** would be applied by implementing object models instantiating **MIBBI** policies. Alternatively, **MOSAIC-SR** reports can be derived from actual computer programs simulating research workflows, similar to **BIOCORDER**<sup>3</sup> (which is included by LTS, in an updated **C++** version, as one **MOSAIC** library). Finally, **MOSAIC-SR** presentations may be based on annotations applied to research/analytic code. For example, in the context of image analysis, the **PANDORE** project (an image-processing application) provides an "Image Processing Objectives" Ontology as well as a suite of image-processing operations that can be called from computer code. Image-analysis pipelines can therefore be explained by annotating the pertinent function-calls (which **PANDORE** calls "operators") with terms from the **PANDORE** controlled vocabulary, providing annotation targets for **MOSAIC-SR** presentations.

**MOSAIC-SR** can express both computational workflows that are fully encapsulated by published code and real-world protocols concerning laboratory equipment and physical materials or samples under investigation. In the latter guise, **MOSAIC-SR** code can employ or instantiate standardized terminologies and data structures for describing experiments — such as **MIBBI** policies or **BIOCORDER** functions. In this case, the role of **MOSAIC-SR** code is to serve as a serialization/deserialization endpoint for sharing research metadata. Conversely, when workflows are fully implemented within software developed as part of a body of research, **MOSAIC-SR** can provide a functional interface allowing this code to

<sup>2</sup>This toolkit provides a good case-study for research publication because it has an innovative **QT** and Common Workflow Language based extension mechanism; cf. [https://cbica.github.io/CaPTk/tr\\_integration.html](https://cbica.github.io/CaPTk/tr_integration.html).

<sup>3</sup>See <https://jbioleng.biomedcentral.com/articles/10.1186/1754-1611-4-13>.



be embedded in scientific software. For the latter, **MOSAIC-SR** provides a framework for modeling how a software component specific to a given research project exposes its functionality to host and/or networked peer applications. There are also instances where both scenarios are relevant — the **MOSAIC-SR** code would simultaneously document real-world experimental protocols and construct a digital interface as part of a workflow which is part digital ("*in silico*") and part "real-world" ("in the lab").

## MOSAIC Annotations

Included in any **MOSAIC** plugin would be specially-designed **PDF** viewers for interactively reading authors' papers. In particular, these **PDF** applications would recognize cross-references linking between publications and their associated supplemental archives. This would allow authors to identify concepts which are discussed and/or represented both in the research paper and in the archive, annotating their papers accordingly. For example, the concept "**RNA** Extraction" may be discussed in a publication text, and also formally declared as one step in the lab processing as represented via **BIOCODER**, summarized in a **BIOCODER**-generated chart, and included in the supplemental archive (a similar example is used in the documentation for **BIOCODER**). The **PDF** viewer would then ensure that the phrase "**RNA** Extraction" in the text is interactively linked to the concordant step in the experimental process, so that readers would then be able to view the **BIOCODER** summary as a context-menu action associated with the phrase where it appears in the **PDF** file. For a different example, the phrase "Oxygenated Airflow" refers to airflow in assisted-breathing devices, such as ventilators; to ensure that the device is working properly, the equipment must be monitored to check that a steady stream of oxygen reaches the patient. Research into the design and manufacturing of ventilators and similar devices may then include "Oxygenated Airflow" both as a phrase within the article text and as a parameter in data sets evaluating the device's performance. In this situation, the publication-text location of the "Oxygenated Airflow" phrase should once again be annotated with links to the relevant part of the data set (e.g., a table column) where measurements of airflow levels are recorded.

## Part II: Concrete Applications

### MOSAIC in the context of Image Analysis

This section will focus on one specific application of **MOSAIC-SR** in the context of image analysis and bioimaging — specifically, what we term **D-SPIN** ("Data Structure Protocol for Image-Analysis Networking"). **D-SPIN** adds a narrower focus by extending **MOSAIC-SR**. Software that uses the **D-SPIN** protocol is able to provide a description of image processing capabilities which have been utilized and/or are functionally exposed by code and data associated with a research project. This includes "structured reporting" of research objectives as well as a concrete interface for invoking analyses associated with the relevant research (either new algorithms or techniques used to obtain reported findings). **D-SPIN**, in turn, is based on **CAPTK** and **PANDORE** (which includes both data models and interactive software) and the **PANDORE** "Image Processing Objectives" Ontology, mentioned above. **D-SPIN** adopts protocols from **CAPTK** in order to accept information about how different objectives are merged into workflows, particularly with respect to implementing image-analysis capabilities as extensions to a core application, and with respect to **CAPTK**'s implementation of the Common Workflow Language (**CWL**). In effect, **D-SPIN** formalizes the data models and prototypes adopted by **PANDORE** and **CAPTK** so as to concretize **MOSAIC-SR** for the specific domain of image processing and Computer Vision. The sections below will therefore outline **D-SPIN** features in the context of **MOSAIC-SR** design principles and objectives.





## Meta-Procedural Modeling in D-SPIN and MOSAIC-SR

When developed as a systematic outline of computational workflows — not just a digital summary of real-world (e.g. lab) protocols — MOSAIC-SR reports can be formalized using a MOSAIC component which we call “Hypergraph Multi-Application Configuration Language” (HMCL). Most approaches to modeling research workflows involve some concept of “meta-objects”,<sup>4</sup> “tools” (in the terminology of **CWL**), or “transitions” (in the language of Petri Net theory). In HMCL, the equivalent concept is that of *metaprocedures*, which are analogous to ordinary computational procedures but add extra sources of information concerning input and output parameters. In general, rather than simply passing an input value into an executable routine, metaprocedures define steps which can be taken to acquire the proper values when needed. Aside from ordinary runtime values, the most important input sources are methods defined on **GUI** components; command-line parameters; file contents; and not-yet-evaluated expressions (perhaps encapsulated in scripts or function pointers). A metaprocedure formulation abstracts the acquisition of input arguments (or the consumption of values within “channels” via which a procedure sends and receives data) from the concrete procedure or procedures which are eventually executed. Therefore, an HMCL metaprocedure definition has two separate parts: a preamble where input sources are described; and an executive sequence where concrete procedures are indicated. A *meta-evaluator* then operates in accord with these definitions, concretizing the input values and launching the actual procedure(s). For D-SPIN, metaprocedures can be defined using a framework based on **BIOCORDER**, but adopted to the imaging and Computer Vision context.

Image analysis methods are often described in academic literature in terms of mathematical formulae and/or characterizations of computing environments (such as Graphical Processing Units). It requires additional construction to translate these overviews into actual computer code. Once Computer Vision innovations are in fact concretely implemented, there is then an additional stage of development requisite for users to enact in practice the computations described in the research. Although it is theoretically possible to demonstrate novel methods within fully self-contained autonomous applications, it is more convenient for users if research code is integrated with existing imaging software. Along these lines, the D-SPIN interface can help connect new code to existing applications, allowing users to access the new code’s functionality through **GUI** actions, command-line invocations, or inter-application messaging.

In addition to pragmatically enabling application embedding, D-SPIN models represent research methods and theories, contributing to transparency and reusability according to the **MIBBI** and **FAIR** (Findable, Accessible, Interoperable, Reusable) standards.<sup>5</sup> This can be achieved, in part, by implementing data structures conforming to **PANDORE** Image Processing Objectives. However, D-SPIN embeds this logic in an Object-Oriented context which allows imaging-specific workflow notations to be paired with specifications outside of image-processing in the narrowest sense. This allows D-SPIN to be available for hybrid computational-objectives representations which are only partially covered by the imaging domain — analogous to the **MIAPE-GI** (Gel Electrophoresis Informatics) component of **MIAPE** (Minimum Information About a Proteomics Experiment). The following section will discuss several domains where D-SPIN has been explicitly integrated with code libraries codifying **MIBBI**-style research protocols.

## D-SPIN in Contexts Supplemental to Image Processing.

### Image Flow Cytometry

One important use-case for biomedical image processing is to analyze cellular microscopy in conjunction with cytometric experiments which indirectly investigate cells and cellular-scale entities (such as proteins). Conceptually, image analysis and flow cytometry (**FCM**) analysis are mathematically similar, and some commercial cytometry software has been extended with image-processing capabilities.

<sup>4</sup>See the **VISSION** system: <https://pdfs.semanticscholar.org/1ad7/c459dc4f89f87719af1d7a6f30e6f58dff17.pdf>.

<sup>5</sup>See [https://www.researchgate.net/publication/331775411\\_FAIRness\\_in\\_Biomedical\\_Data\\_Discovery](https://www.researchgate.net/publication/331775411_FAIRness_in_Biomedical_Data_Discovery).



The overlap between cytometric and image analysis has also inspired attempts to merge cytometry standards, such as **MIFLOWCYT** (the Minimum Information about a Flow Cytometry Experiment policy within **MIBBI**), with bioimaging standards such as **DICOM** (Digital Imaging and Communications in Medicine). One such proposal is due to Robert Leif, who argues that "The large overlap between imaging and flow cytometry provides strong evidence that both modalities should be covered by the same standard" and has formalized an **XML** language (**CYTOMETRYML**) to serve as that overarching bridge.<sup>6</sup> The **D-SPIN** project builds off this work by introducing its own **FCM/DICOM** hybrid, although in an object-oriented rather than **XML**-based context, although it also incorporates an expanded **XML**-oriented schema (discussed in the next part of this paper). As a reference implementation for this **D-SPIN** extension, the project also provides a pure-**C++** cytometry library based on the **OPENCYTO** (see <https://www.bioconductor.org/packages/release/bioc/html/cytolib.html>) and **FACSANADU** (see <https://www.biorxiv.org/content/biorxiv/early/2017/10/13/201897.full.pdf>) libraries, while eliminating external dependencies such as **R** and **JAVA**.<sup>7</sup> The **FCM/DICOM** bridge is implemented in this context via a **D-SPIN** supplement to **DICOM** based on "Semantic **DICOM**," which is an effort to standardize query processing within **PACS** (Picture Archiving and Communications Service) workstations and to more effectively integrate **DICOM** with clinical data.

## A Semantic **DICOM** Object Model

As a formal representation of imaging workflows, **D-SPIN** would reasonably be paired in many contexts with **DICOM**, insofar as **DICOM** represents the canonical standard for exchanging medical image data. For its applications within the medical-imaging context, **D-SPIN**, therefore, provides object-oriented accessors to **DICOM** data such that image-objectives and **DICOM** object models can interoperate. This object-oriented foundation also provides a basis on which to further integrate clinical data in the form of "Semantic" **PACS** models.<sup>8</sup> The original Semantic **PACS** implementation draws clinical data from **DICOM** headers, and represents this extracted information via **RDF**. In keeping with **MOSAIC**'s more object-oriented focus, the **MOSAIC-Semantic DICOM** (**MOSAIC-SD**) integration is engineered instead as an extension to the **DICOM** Toolkit (**DCMTK**) library, though it imports many constructs within Semantic **DICOM** in the guise of a "Hypergraph Ontology" — one example of a system **MOSAIC** uses to merge Semantic Web schema with Object-Oriented code. In short, **MOSAIC-SD** extends **D-SPIN** by defining a central **DICOM** object model affixed to both clinical and image-processing object models.

The **MOSAIC-SD** object system applies not only to **DICOM** integrated with statements of image-processing objectives, but also to other biomedical contexts where image analysis should be integrated with other analytic modalities as well as with clinical or epidemiological information. For example, Flow Cytometry overlaps with clinical data tracking because one of **FCM**'s essential investigative roles is to examine patients' immunological response to diseases and/or interventions. In the context of Covid-19, say — with respect to achieving a deeper understanding of how and why SARS-CoV-2 symptoms present differently in different patients — "The starting point will likely be a deep characterization of the immune system in patients with different stages of the disease."<sup>9</sup> That is, **FCM** observations need to be matched with clinical data in order to classify (and consider statistical correlations between) immunological findings and clinical facts: risk factors, sociodemographics, disease progression, and so forth. This analysis intrinsically assumes that **FCM** data can be transparently linked with all relevant clinical data, but such integration is difficult even in **DICOM**, where **DICOM** headers are specifically designed for preserving patient data across picture-sharing networks (there is no analogous "header" component in the Flow Cytometry Standard, **FCS**). In brief, **D-SPIN** ex-

<sup>6</sup>See <https://spie.org/Publications/Proceedings/Paper/10.1117/12.2295220?SSO=1>.

<sup>7</sup>Upon request, LTS can provide a detailed summary of this project reconciling **OPENCYTO** and **FACSANADU**. Specifically, although **OPENCYTO** as a whole uses **R** for its visual layer, **OPENCYTO** contains **CYTOLIB**, a **C++** library for cytometric analysis, which LTS employs as the basis for a standalone pure-**C++** flow cytometry application. Meanwhile, **FACSANADU** is a **JAVA** application which uses a **QT** front-end that LTS is migrating to **C++**. The supplemental information supplied by LTS about the **FACSANADU/CYTOLIB** integration identifies the specific data types where **CYTOLIB** code (different kinds of gates, for instances) can be incorporated as alternatives to the **FACSANADU JAVA** equivalents, while still using **FACSANADU GUI** classes.

<sup>8</sup>See <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5119276/>.

<sup>9</sup>See <https://onlinelibrary.wiley.com/doi/full/10.1002/cyto.a.24002>.



tensions to non-imaging domains can promote data integration insofar as **D-SPIN Clinical Object Models**, based on Semantic **DICOM**, provide an affixation point for clinical data in analytic contexts which are operationally related to image analysis, and not just to image analysis by itself.

### Semantic **DICOM** via **DCMTK** Extensions

As a concrete example of how a Semantic **DICOM** Object Model could be implemented, consider the process of developing **DICOM** extensions by modifying existing **DICOM** client libraries, such as **DCMTK**. As a file *standard*, **DICOM** itself is an abstraction; the **DICOM** protocol only becomes a concrete phenomenon insofar as **PACS** workstations, radiology software, and other applications employ **DICOM** client libraries. Therefore, any **DICOM extension** is similarly concretized only by an application which links against modified **DICOM** libraries that recognize the extended syntax and/or semantics. When implementing **DICOM**, accordingly, we can assume that the modified client libraries exist in an ambient context which provides capabilities that can be leveraged by the extension as it becomes formalized. For example, if a **DICOM** extension provides a unified **FCM/DICOM** format, we can assume that the workstation linking against modified **DCMTK** libraries supports **FCM** features, such as the ability to construct geometric gating models (that is, rectangular or ellipsoid segments on **FCM** images) and to consume information about the cytometric equipment used to derive the current **FCM** data.

In the case of Semantic **DICOM**, we can similarly assume that the host application which loads an enhanced "Semantic" version of a **DICOM** client library has the ability to consume more complex clinical data models than are incorporated into conventional **DICOM**. In the case of **DCMTK**, patient information is accessed through a **DcmDataset** object, which in turn contains multiple **DcmObject** values spanning several more specific types. A **DICOM** extension can, accordingly, be concretized by expanding the range of object types subsumed under **DcmObject**, as well as modifying the **DcmDataset** code so that instances of these extended types could be identified and passed off to the appropriate handlers. Developers can then bundle files serializing these extended types within the overall collection of files zipped into a single **DICOM** resource.

The steps outlined above allow an extension object model to be embedded in **DICOM** by hooking extra processing code into the procedures whereby conventional **DcmDatasets** are extracted from **DICOM** files. It is then necessary to ensure that the **DICOM** client application can properly manipulate the extension object data. This could be handled simply by linking all necessary libraries into the **DICOM** client itself, but a more flexible solution is to employ some form of multi-application networking. In the case of non-standard clinical data, a flexible approach would be to pair client libraries for serializations of such data with a standalone application that can parse these serializations and respond to requests about the encoded information. With such an application in place, the **DCMTK** host application would not need to implement all logic related to the extension object model; it would simply need to be able to launch and/or communicate with a secondary application tailored to each individual extension in particular.

As a concrete example, consider a specialized data model and self-contained application specifically devoted to tracking immunological responses and post-recovery symptomology for Covid-19. The goal would be to develop more sophisticated technology for modeling the progression of active Covid-19 infections, as well as the lingering effects of the disease for patients who experience adverse reactions (such as lasting neurological damage or lung impairment) even after their ostensive recovery. Detailed models of Covid-19 affliction could then be matched against epidemiological, treatment, and sociodemographic data to determine whether there are predictors that determine which patients may experience more severe or long-lasting symptoms, and whether these symptoms can be mitigated by different treatment options. The data consumed by such a Covid-specific application might be bundled into **DICOM** files even if **DICOM** clients cannot directly process this data. In such a case, they could, instead, be programmed to launch the Covid-specific application and query that application for select pieces of information that *are* relevant for a **DICOM** workstation (e.g., an immunological profile of the patient adding layers of detail to cytological imaging). In short, a Covid-specific application would potentially be accessed by several different peer applications addressing several



different biomedical domains (bioimaging, cytometry, epidemiology, genomics), and could provide different sorts of information from a Covid-specific data model for different contexts: given an overall information package about a patient's SARS-CoV-2 immunology and symptomology, some categories of data will be relevant for bioimaging, while others will be relevant for genomics and so forth. The file formats employed by these various peer applications (such as **DICOM**, in the bioimaging context) may then be extended only as much as is needed to seed shared data packages with enough information to launch the Covid-specific application and request information specific to the peer application's specific biomedical domain.

## Geo-Imaging and Geographic Information Systems

Another area where **D-SPIN** provides structured object models is that of Geographic Information Systems (**GIS**) annotations. There is a direct link between image processing and **GIS** insofar as identifying geotaggable features is one dimension or application of Computer Vision. Effectively manipulating geoimaging data requires mathematical translations between several different coordinate systems, in both two and three dimensions. These coordinate transforms — as well as semantic interpretations of geoimage segments (buildings, land features, roads, etc.) — can serve as the basis for an object model attaching image-processing objectives to **GIS** workflows.

In conventional **GIS** annotation, data structures are linked to both geospatial coordinates and to visual cues or icons allowing locations of interest to be indicated on maps. The actual geotagged data structures could be derived from any domain; as such any object model may be integrated with **GIS** annotations so long as one can assign spatial interpretations to the phenomena computationally encapsulated by the domain in question. In a medical context, for instance, geotagged data might represent the scope of a vaccination campaign, or the extent of an epidemic, along with relevant geographic or civic features (villages, medical clinics, national borders, and so on). The actual map as a visible digital artifact therefore serves as a virtual glue where clinical, geographical, governmental, and **GUI** data are all sutured together. Insofar as geoimaging involves analysis of photographed land features and/or urban environments, image processing information represents a further object model that can be added to the mix. Even when dealing solely with virtual maps, however — rather than with satellite images or other geospatial photography — the analysis and application-level rendering of map features is sufficiently similar to image processing that a rigorous model of **GIS** integration belongs properly within **D-SPIN**, specifically within a **MOSAIC-GIS** extension.

## Part III: MOSAIC Data Models

### Hypergraph Database Models for Publication Data

At the core of any **MOSAIC** portal is a collection of distinct files, representing individual publications and supplemental archives. However, in a typical case it becomes necessary to ground the system of files in a database that hosts publication information, so that readers could search the portal for specific authors, keywords/phrases, titles, subject areas, and so forth. Searches within publication metadata are the simplest example of this functionality. However, searches within publication texts themselves are more complex, because what seems like a straightforward keyword search from a user's point of view might be more complicated at the processing level by documents' markup structure. That is, technical terms or acronyms which readers simply see as single words/phrases might be defined in a more complicated way within the document, such as by internally structured text segments rather than raw character streams. In addition, keyword searches might also be tripped up by ligatures, footnote interruptions, and other visual features wherein the document in human-readable formats like **PDF** markedly diverges from machine-readable raw text.

To address these potential search complications, **MOSAIC** provides a "Hypergraph Text Encoding Protocol" (**HTXN**) which effectively separates document text into different layers, dividing presentation-related content from textual content and making search capabilities more reliable. Each publication can have an **HTXN** representation, essentially a machine-readable structure encapsulating document text, as part of its supplemental archive. These **HTXN** resources can then be used to support robust





searching among text publication sets.

Apart from metadata and keyword searches within texts, **MOSAIC** allows an additional layer of search functionality: the option to search across supplemental archive contents such as data sets and research protocol descriptions. **MOSAIC** provides a hypergraph-based database engine that can be used, at a minimum, for publication info; in addition, developers have the option of including supplemental content within this central database. Each supplemental archive encompasses raw data and/or methodological descriptions via files internal to the archive; these assets are not necessarily shared with the host **MOSAIC** repository database (except via operations that directly examine archive files). However, those who create or maintain a repository could choose to model some or all archive content within its publication database, either directly storing archives' data sets or importing certain select information (such as object/type schema or representative data samples). In this case, some such data in the supplemental archives will be mirrored in the central database, so that it is accessible for user-facing searches. To accommodate many different kinds of data models (from "**SQL**-like" tables to graphs and hierarchical collections types) **MOSAIC** employs a flexible Hypergraph Database engine. Thus, the publication database within a **MOSAIC** portal would have the flexibility to import most data which is present in supplemental content associated with given publications.

In some contexts, however, authors are giving the option to structure their shared research data in a format that can be exported to a **MOSAIC** publication database. This is possible because **MOSAIC**'s hypergraph data model supplies a rigorous framework for documenting how a data set is organized, which in turn can provide a formal overview of the theoretical or methodological commitments informing the research. The **MOSAIC** database engine — called **ConceptsDB** — represents an expanded hypergraph metamodel built around different paradigms for expressing scientific knowledge, such as Conceptual Space Theory and Conceptual Role Semantics.<sup>10</sup>

## Markup Serialization and "Grounding" in Portals

The data-integration mechanisms discussed up to now have focused on object models and object-oriented programming techniques. It is understood that while composing special-purpose object-based libraries specifically tailored to individual data-integration problems is a powerful tool for solving such problems, data integration initiatives in practice are often organized around standards for sharing or serializing conformant data structures. Therefore, an important aspect of data integration is implementing proper data-serialization technology that is sufficiently rigorous to serve as a *proxy* for formal interface definitions. **XML** formats present a good case-study for such formalizations because most serialization in the biomedical and bioimaging context operates through **XML** languages.

Standardizing a data format by stipulating how **XML** files may encode the data is much simpler than defining an analogous specification in terms of executable computer code: one way to document the shape of any relevant data is simply to explain how an **XML** document will be structured insofar as it encodes data accordingly. Potentially, such specification can be a single **XML DTD** file, or an **XML** sample, providing a convenient reference point for developers to grasp the underlying data model. However, the structure of an **XML** document does not, in and of itself, present a clear picture of how the information which the document represents is semantically organized. Even though **XML** is processed by computer programs, one cannot even determine from an **XML** document or schema which **XML** elements (if any) correspond to data types recognized by applications which read and/or write the corresponding **XML** code. For example, the **XML** portion of **OME-TIFF** (the principal Open Microscopy Environment imaging format) includes an explicit **Image** element (which gathers up all significant image metadata); an application reading **OME-TIFF** files might, therefore, introduce a single datatype — analogous to (and maybe wrapping an) **itk::Image** from the Insight Toolkit imaging libraries — bundling the data in that part of the **OME XML**. In this case, there will be a one-to-one correspondence between **XML** structure and application-level data types, at least for that

<sup>10</sup> Or at least a variation of Conceptual Roles consistent with **AI** tools such as **GRAKEN.AI**, and formalizations of Conceptual Spaces such as those described in <https://arxiv.org/abs/1706.06366>.

one **Image** node. On the other hand, software reading **OME-TIFF** information might not manipulate images directly, but rather pull out other kinds of metadata, such as an experimenter's name or description of the microscopic setup. In this case, the application might not have an explicit "object" representing the image itself, but it may still read information about the image from child nodes of the **XML Image** element.

In short, because applications can read or use data from an **XML** document in different ways, the document's structure does not itself provide a clear picture of how the specific code that reads the **XML** is organized. Such uncertainty becomes significant when one wishes to use **XML** specifications as an indirect strategy for documenting parameters and features of the data structures which are serialized via the relevant **XML** language. In effect, **XML** serialization operates on two levels: on the one hand, the specific **XML** document provides an encoding of data conforming to a given structure; but, at a more abstract level, one can model the relationship between the surface-level **XML** node structure and the application-level data structures thereby serialized. This second level of detail is usually implicit and unstated, but in the **MOSAIC** technology, such "meta-serialization" — a term we are using to suggest the idea of providing meta-data *about* a serialization — is directly formulated through a notion of "grounding," which involves adding supplemental markup clarifying how documents instantiating a serialization format (such as **XML**) relate to the coding protocols and data types of software that reads or creates these documents.

For maximum expressivity, **MOSAIC** introduces a meta-serialization system that can be applied to languages more flexible than **XML** — notably **TAGML** — as well as to **XML** proper.<sup>11</sup> In effect, **MOSAIC** provides parsers for an extended version of **TAGML** which includes an additional "grounding" layer. Grounding, in this context, means describing how elements in the markup — nodes, attributes, and character sequences — are "grounded" in application-level types, data fields, and other programming constructs. **MOSAIC** provides parsers for this "Grounded **TAGML**" (**GTagML**) language as well as converters to output serialized data as conventional **XML**, so that **GTagML** specifications can be used in contexts (**MIFLOWCYT**, for instance) where ordinary **XML** is expected and serves as a basis of standardization. **MOSAIC** also provides code libraries for extracting data from **GTagML** documents.

**GTagML** documents, with certain restrictions enforced, are structurally isomorphic to **XML** and can be rendered as pure **XML**; as such, **GTagML** schemata can be used to define norms for **XML** languages, although the logical role and operations of such requirements is not identical to **XML** schema definitions. By design, **GTagML** schemata operate on two levels: first, they constrain the organization of **GTagML** files themselves; and second, they stipulate how **GTagML** document structure relates to the type systems of code libraries serializing and deserializing **GTagML** files. To model the second level of metadata, **GTagML** introduces a hypergraph-based type model organized around "infosets," which are structured overviews of application-level data types. To fully utilize **GTagML** features, programmers may consequently compose "infoset classes" as wrappers around ordinary data types (e.g., **C++** classes), whose instances are serialized via nodes or character strings within **GTagML** documents. Infoset classes provide hypergraph "views" onto type-instances, and act as a bridge between data types and their associated **GTagML** schema. In particular, infoset classes (rather than the types they encapsulate) are the basis for schematizing the relation between **GTagML** document elements and type instances (and the data they contain).

The hypergraph-based modeling incorporated into **GTagML** reuses much of the code associated with **ConceptsDB**, the new hypergraph database being developed alongside **MOSAIC**. More information about **ConceptsDB** — and on the **HTXN** text encoding protocol for **MOSAIC** portal manuscripts, mentioned earlier — can be found on the github project page for Linguistic Technology Systems (<https://github.com/Mosaic-DigammaDB/LingTechSys>).

*For more information please contact:*  
**Amy Neustein, Ph.D., Founder and CEO**  
**Linguistic Technology Systems**  
[amy.neustein@verizon.net](mailto:amy.neustein@verizon.net) • (917) 817-2184

<sup>11</sup>See <http://www.balisage.net/Proceedings/vol21/print/HaentjensDekker01/BalisageVol21-HaentjensDekker01.html>.



## Appendix: Integration between Different Flow Cytometry Libraries

As discussed above, one use-case for data integration via **D-SPIN** is to merge the features of multiple **FCM** libraries, such as **CYTOLIB** and **FACSANADU** (although the techniques discussed here could be applied to other libraries as well). In the **CYTOLIB/FACSANADU** reconciliation, **FACSANADU** code (translated from **JAVA** to **C++**) provides **GUI** logic whereas **CYTOLIB** provides most of the analytics and **FCS** processing. These two code bases come into contact insofar as **CYTOLIB** data needs to be visualized within **FACSANADU GUI** components. Constructing a bridge between the two systems therefore involves translating **CYTOLIB** data structures to the data types expected by **FACSANADU** when it initializes visual renderings of **FCS** data, such as event plots and gate boundaries.

To facilitate this translation, the **D-SPIN**-based strategy involves isolating certain geometric and data-modeling primitives and implementing them in a separate code base distinct from either of the **FCM** components. These modeling primitives then act as an intermediary between **CYTOLIB** and **FACSANADU**, but they are also designed with an eye toward being applicable in other image-processing contexts. Important data structures involved in this bridge code include the following:

**Vertex Sets** The important feature of geometric vertices in the **FCM** context is that vertices need to be expressed within and mapped between several different coordinate systems. For example, **CYTOLIB** uses a different "coordinate" class when reading data via Protocol Buffers than for internally defining gates. At the **GUI** level, at least three different notions of two-dimensional locations are important (and require transforms such as **mapFcsToScreen** in **FACSANADU**) depending on whether one is tracking visual objects — or events, such as mouse clicks — relative to the entire computer screen, or one **GUI** window, or the top-left corner of the object whose method handles a given user-interaction event. A further complicating factor is that some coordinate systems use integer values, while others use floating-point numbers. In other contexts related to **FCM**, such as **PDF** rendering and image analysis, there are still further coordinate systems; so it is not uncommon for a code base (even just in the **2D** context) to manage spatial positions recorded in at least seven different formats. It is therefore a reasonable practice to factor out different coordinate systems into a common **2D** position/vertex model from which context-specific locations can be derived.

**Ellipses** Different applications represent ellipses in different ways, including via antipodal points, axis radii, or covariance matrices. The matrix form (which entails four values, or  $2 \times 2$ , for a two-dimensional shape) is preferred for **FCM** (as standardized in **GATING-ML**, say), but other representations are more common in other contexts, such as image analysis (, for instance, distinguishes "object space" from "world-space", which has the effect of separating a two-valued description of the elliptical shape as an intrinsic morphological quality, whereas the ellipse's axis angles are a feature of how its intrinsic space relates to a parent space). In **QT**, for its part, ellipses (a kind of **QGraphicsItem**) are defined in terms of a bounding rectangle together with a rotational transform. Given this diversity of representations, **D-SPIN** uses a separate ellipse class (based on eccentricity and major-axis angles) which can be mathematically transformed into these different formats.

**Data/Coordinate Transformations** Only linear and logarithmic transformations are defined in **FACSANADU**, although it is straightforward to further subclass the **Transformation** base type. To be consistent with the **GUI**, modified transformation algorithms need to be registered with a context menu in "**ViewWidget**" (a menu activated by clicking in a boundary area, outside any rendered data). This is an example of where data modeling/analytic features and **GUI** setup needs to be correlated, which **D-SPIN** approaches via structured **GUI** modeling and annotations (see the **MOSAIC Annotations** section above). A wider inventory of transformation strategies are implemented in **CYTOLIB**, such as biexponentials and "logicles," but there are other transformation methods proposed in academic literature which are not implemented for **CYTOLIB**. The **D-SPIN** approach is to prioritize extensibility, with a transformation class structured to facilitate both subclassing and **GUI** integration. This is part of a more general design philosophy for image-processing algorithms where code extensions can be deployed and annotated to demonstrate novel analytic techniques described in scientific literature, with microcitation-based cross-references between code, publications, and **GUIs**.

