



WHITE PAPER

**New Database Engineering and Archive Construction
Technology to Accelerate Bio-Imaging, Biomedical
Engineering, and Covid-19 Research**

LTS (Linguistic Technology Systems) is founded by Amy Neustein, Ph.D., Series Editor of **Speech Technology and Text Mining in Medicine and Health Care** (de Gruyter); Editor of **Advances in Ubiquitous Computing: Cyber-Physical Systems, Smart Cities, and Ecological Monitoring** (Elsevier, 2020); co-author (with Nathaniel Christen) of **Cross-Disciplinary Data Integration and Conceptual Space Models for Covid-19** (Elsevier, 2021); and co-editor of **Medical Image Processing and Machine Learning** (Institution of Engineering and Technology, forthcoming).

Team

Principal Investigator: Dr. James A. Rodger, Professor of Management Information Systems and Decision Sciences at Indiana University of Pennsylvania

Administrative Officer: Dr. Amy Neustein, founder of Linguistic Technology Systems (LTS)

Contributors

- Nathaniel Christen, Lead Software Architect, LTS
- Professor Amita Nandal, Department of Department of Computer and Communication Engineering at Manipal University, Jaipur
- Professor Arvind Dhaka, Department of Department of Computer and Communication Engineering at Manipal University, Jaipur; recently visiting scholar at University of Varna, Bulgaria
- Professor Todor Ganchev, Vice Rector of Research at University of Varna, Bulgaria

The “MOSAIC Data-Set Explorer” (**MdsX**) and “MOSAIC Structured Reporting” (**MOSAIC-SR**) are tools to help authors develop interactive presentations supplementing academic documents (**MOSAIC** is an acronym for “Multi-Paradigm Ontologies for Scientific and Technical Publications”). With **MdsX**, interactive presentations take the form of software applications that provide access to data sets, analytic techniques, or other digitally representable artifacts to document or encapsulate research work. With **MOSAIC-SR**, authors can implement or reuse code libraries that report on research/experiment methods, workflows, and protocols. Conceptually, **MOSAIC-SR** is functionally similar to the various domain-specific recommendations collectively gathered into the “Minimum Information for Biological and Biomedical Investigations” (**MIBBI**) specifications, and indeed one use-case for **MOSAIC-SR** is that of implementing object models instantiating **MIBBI** policies. In some contexts, **MOSAIC-SR** and **MIBBI** overlap, because elements of scientific workflows are sometimes algorithms implemented within a code package concretizing authors’ research.

MOSAIC-SR can express both computational workflows that are fully encapsulated by published code as well as 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 **BIOCODER** 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 be embedded in scientific software. For these cases, **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 scenarios 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 and part “real-world.”

This paper will focus on one specific application of **MOSAIC-SR** in the context of image analysis and bioimaging — specifically, a “Data Structure Protocol for Image-Analysis Networking” (**D-SPIN**), which both extends and adds a narrower focus to **MOSAIC-SR**. Software using the **D-SPIN** protocol provides 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 research (either new algorithms or techniques used to obtain reported findings). **D-SPIN**, in turn, is based on **CAPTK** (the Cancer Imaging and Phenomics Toolkit) and **PANDORE** (an image-processing environment which includes both data models and interactive software). The **PANDORE** project encompasses an ontology of “Image Processing Objectives” that provides a structural basis for **D-SPIN**. For information about how different objectives are merged into workflows, **D-SPIN** adopts protocols from **CAPTK**, particularly with respect to implementing image-analysis capabilities as extensions to a core application, and **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 following sections 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

Most approaches to modeling research workflows involve some concept of “meta-objects”,¹, “tools” (in the terminology of **CWL**), and “transitions” (in the language of Petri Net theory). In , the analogous concept is that of *meta-procedures*, 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 meta-procedure formulation abstracts the acquisition of inputs (or “channels”) from the concrete procedure or procedures which are eventually executed. Therefore, a **MOSAIC** meta-procedure 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**, meta-procedures can be defined using a framework based on **BioCODER**,² 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 computational 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 actually enact 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. The **D-SPIN** interface can then help connect new code to existing applications, allowing users to access new code’s functionaloty through **GUI** actions, command-line

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

²See <https://jbioleng.biomedcentral.com/articles/10.1186/1754-1611-4-13>



invocations, or inter-application messaging protocols.

In addition to practically 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.³ This can be achieved, in part, by implementing data structures conforming to 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 imaging 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 investigate cells and cellular-scale entities (such as proteins) indirectly. Conceptually, image analysis and flow cytometry (**FCM**) analysis are mathematically similar, and some commercial cytometry software has been extended with image-processing capabilities. 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.⁴ 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 (discussed further in the next section). As a reference implementation for this **D-SPIN** extension, the project also provides a pure-**C++** cytometry library based on the **OPENCYTO** and libraries, but eliminating external dependencies such as **R** and **JAVA**. 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, therefore, **D-SPIN** 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.⁵ In general, Semantic **PACS** applications draw clinical data from **DICOM** headers, though it would be consistent with the Semantic **DICOM** paradigm to expose this information via sufficiently well-structured supplemental information packages as well. This arrangement then forms the basis of a **MOSAIC-Semantic DICOM** () framework which integrates Semantic **DICOM** with **D-SPIN** — specifically, which defines a central **DICOM** object model affixed to both clinical and image-processing object models.

The object system applies not only to **DICOM** integrated with statements of image-processing

³See https://www.researchgate.net/publication/331775411_FAIRness_in_Biomedical_Data_Discovery.

⁴See <https://spie.org/Publications/Proceedings/Paper/10.1117/12.2295220?SSO=1>.

⁵See <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5119276/>.



objectives, but also to other biomedical contexts where image analysis should be integrated with other analytic modalities and also 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 stage of the disease".⁶ That is, **FCM** observations need to be matched with clinical data in order to classify (and consider statistical correlations between) immunology 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 for preserving patient data across picture-sharing networks (there is no analogous "header" component in **FCS**, the Flow Cytometry Standard). In short, **D-SPIN** extensions 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, not just to image analysis per se.

Geo-Imaging and Geographic Information Systems

Another area where **D-SPIN** provides structured object models is that of Geographic Information Systems (**GIS**), and specifically **GIS** annotations.

⁶See <https://onlinelibrary.wiley.com/doi/full/10.1002/cyto.a.24002>.

