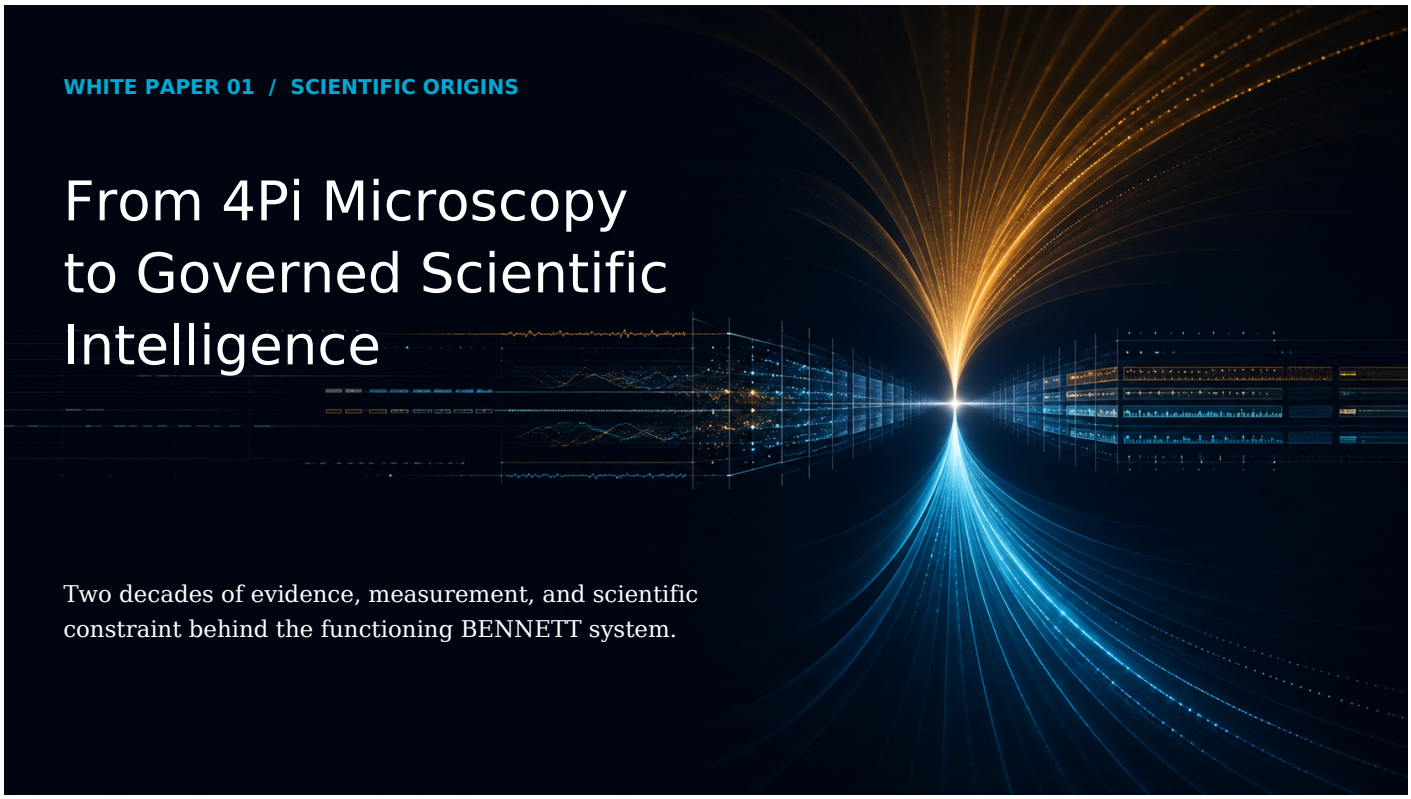

WHITE PAPER 01 / SCIENTIFIC ORIGINS

From 4Pi Microscopy to Governed Scientific Intelligence

Two decades of evidence, measurement, and scientific constraint behind the functioning BENNETT system.

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PAPER 01 OF 10
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NATIVE EVIDENCE / DETERMINISTIC MEASUREMENT / GOVERNED INTERPRETATION / DEFENSIBLE PUBLICATION

CONTENTS

Paper structure

A documented progression from the scientific demands of 4Pi microscopy to a functioning, governed scientific-intelligence system.

All numbered citations in the paper link to the corresponding reference. Linked titles in the reference list open the cited source.

ABSTRACT

BENNETT did not begin as an attempt to place a conversational model in front of image-analysis software. Its scientific logic emerged from a problem that became increasingly visible as microscopy resolution improved: a more precise image does not automatically produce a more defensible biological conclusion. Beginning in 2004, DNA-repair research and the preparation of samples for 4Pi microscopy required control of the complete path from specimen and fluorescence labeling to three-dimensional measurement and interpretation. The 2006 PNAS study of H2AX chromatin structures became a decisive demonstration.[3] Higher axial resolution revealed biological distinctions that conventional imaging could not resolve, while simultaneously making preparation, calibration, spatial analysis, and claim boundaries more consequential. As microscopy became more aggressive in resolution, dimensionality, speed, and multiplexing, it also produced a mountain of heterogeneous data that could be processed and interpreted differently by different users. Subsequent work in fluorescence chemistry, immunolabeling, biplane single-molecule localization, instrumentation, cellular-assay design, and vertically integrated experiment design extended the same principle across the scientific workflow. Identifyn connected that workflow. BENNETT now converts it into governed scientific intelligence: native-data ingestion, file-aware routing, deterministic engines, bounded micro-engines, persistent scientific state, scientist-controlled intervention, validation, and defensible publication. The system is functioning across the supported multi-vendor native-data formats in its current validation set.[17] Independent academic and industry testing is planned to begin in September 2026, followed by a targeted public launch in mid-fall 2026. This paper documents that lineage and establishes the premise for the nine papers that follow: scientific AI must govern the route from experimental intent to claim, not merely generate an answer from an image.

> Central thesis: Higher resolution exposed a larger systems problem. Scientific meaning depends on preserving the complete route from biological question, material, and method to native data, measurement, human judgment, validation, and bounded claim.

How to read this history

This paper does not claim that the BENNETT architecture already existed in 2004, nor that its development was inevitable. It identifies a series of recurring scientific constraints that were first encountered experimentally and later formalized into an engineering system.

This paper separates biological evidence, microscopy methods, patent chronology, founder chronology, internal validation, planned work, and targeted milestones so that each claim can be evaluated at the appropriate evidentiary level.

Different sources support different parts of that history. Peer-reviewed publications establish scientific findings and reported methods. Patent records establish dated disclosures, inventorship, and claimed subject matter, but do not independently prove product performance. Institutional and contemporary reporting documents design and organizational history. Founder chronology identifies continuity where no single publication captures the full development path. Public patent filings document disclosed elements of the later architecture without exposing nonpublic implementation details.

Applying these distinctions to the history is itself part of the BENNETT principle: evidence should be used only for the kind of claim it can support.

Each paper that follows extends the same chronology, vocabulary, evidence hierarchy, and capability-status model.

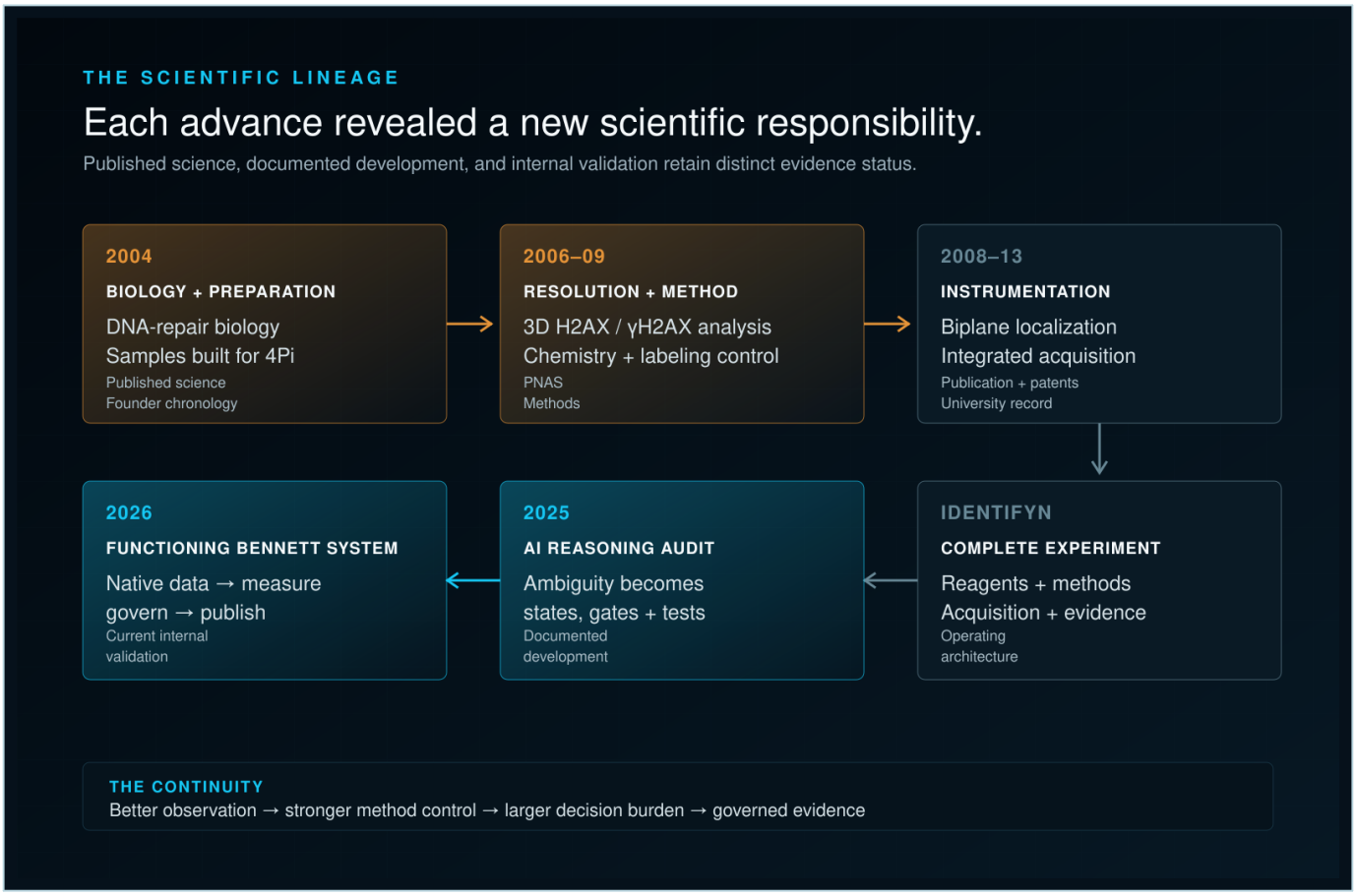

Figure 1. The scientific lineage: increasingly demanding observation exposed successive responsibilities for preparation, measurement, interpretation, and evidence governance.

1. The work began with the biology

The published scientific record begins with questions about the organization and behavior of DNA-repair proteins. In 2004, work on XRCC3 showed that the protein was recruited rapidly to DNA double-strand breaks and that this localization could occur independently of RAD51. Subsequent work detected endogenous RAD51C and XRCC3 in human cells and connected RAD51C to regulation of RAD51 proteolysis during recombinational repair.[1,2]

The project chronology also begins in 2004, when I started adapting DNA-repair samples for the unusual optical and labeling demands of 4Pi microscopy. The immediate objective was not automation. It was to prepare a biological specimen that could withstand a more rigorous form of observation without allowing the method to distort the biology being interpreted.

That objective expanded the meaning of an imaging experiment. Coverslip thickness, refractive conditions, fixation, antibody quality, fluorophore stability, background suppression, antigen preservation, three-dimensional geometry, and positional stability were no longer peripheral details. They were components of the measurement system.

A fluorescence image is a spatially sampled record of detector signal generated by emitted photons after they have passed through the microscope's optical system. The intensity recorded in each pixel or voxel is shaped by fluorophore emission, labeling and specimen conditions, the microscope's point-spread function, background, detector response, exposure, and acquisition settings.[14] A localized region of higher recorded intensity therefore shows where greater fluorescence-derived signal was detected under those experimental conditions. It does not, by itself, establish the identity of a discrete biological structure, direct molecular binding, physical contact, biochemical causation, or the physical size of a protein.

That boundary, between the signal recorded by the imaging system and the biological conclusion drawn from it, is the original evidence problem behind BENNETT.

2. 4Pi microscopy made the hidden system visible

The 2006 PNAS paper, H2AX chromatin structures and their response to DNA damage revealed by 4Pi microscopy, is the scientific center of this history.[3] The study used 4Pi microscopy to examine endogenous H2AX and γH2AX structures in three dimensions. It did not rely only on projections or merged-color impressions. Improved axial resolution was combined with object measurement, three-dimensional spatial analysis, and calibrated compartment-relative reasoning.

4Pi microscopy used two opposing objective lenses in a coherent optical arrangement. In the Type C configuration described in the later methodological review, the approach improved axial resolution approximately five- to sevenfold over standard confocal microscopy. The

central intensity maximum of the 4Pi point-spread function was approximately 100 nanometers wide in the axial dimension; accompanying side maxima were removed computationally during image restoration.[5]

That improvement was scientifically consequential because it allowed neighboring structures that could appear merged at lower resolution to be separated in three-dimensional space. The study also treated the nucleus as a measured spatial environment. Nonoverlapping erosion shells were constructed from the nuclear boundary, allowing H2AX structures to be evaluated according to calibrated position within the nuclear volume. Because different shells contained different amounts of volume, normalization was required. The boundary, shell construction, physical scale, object definition, and normalization method all affected the result.

Most importantly, the work resisted a familiar interpretive shortcut. Apparent color overlap was not accepted as proof of colocalization. Three-dimensional data and quantitative analysis showed that H2AX and γH2AX structures could be adjacent without being coincident. The later Methods paper reported that the diameters of H2AX clusters were 100-600 nanometers smaller than the larger γH2AX clusters observed after ionizing radiation and emphasized that visual judgment alone could conceal important spatial distinctions.[5]

The lasting lesson was not simply that 4Pi produced a sharper image. It was that higher resolution changed the conditions under which an observation became defensible:

1. Resolution changed which biological distinctions could be observed.
2. Improved observation created new requirements for preparation and calibration.
3. Three-dimensional structures required three-dimensional analysis.
4. Visual similarity and measured spatial association were not equivalent.
5. The language of the conclusion had to remain within the limits of the optical and analytical evidence.

These are now recognizable as principles of evidence governance. In 2006, they were first encountered as the practical requirements of doing the biology correctly.

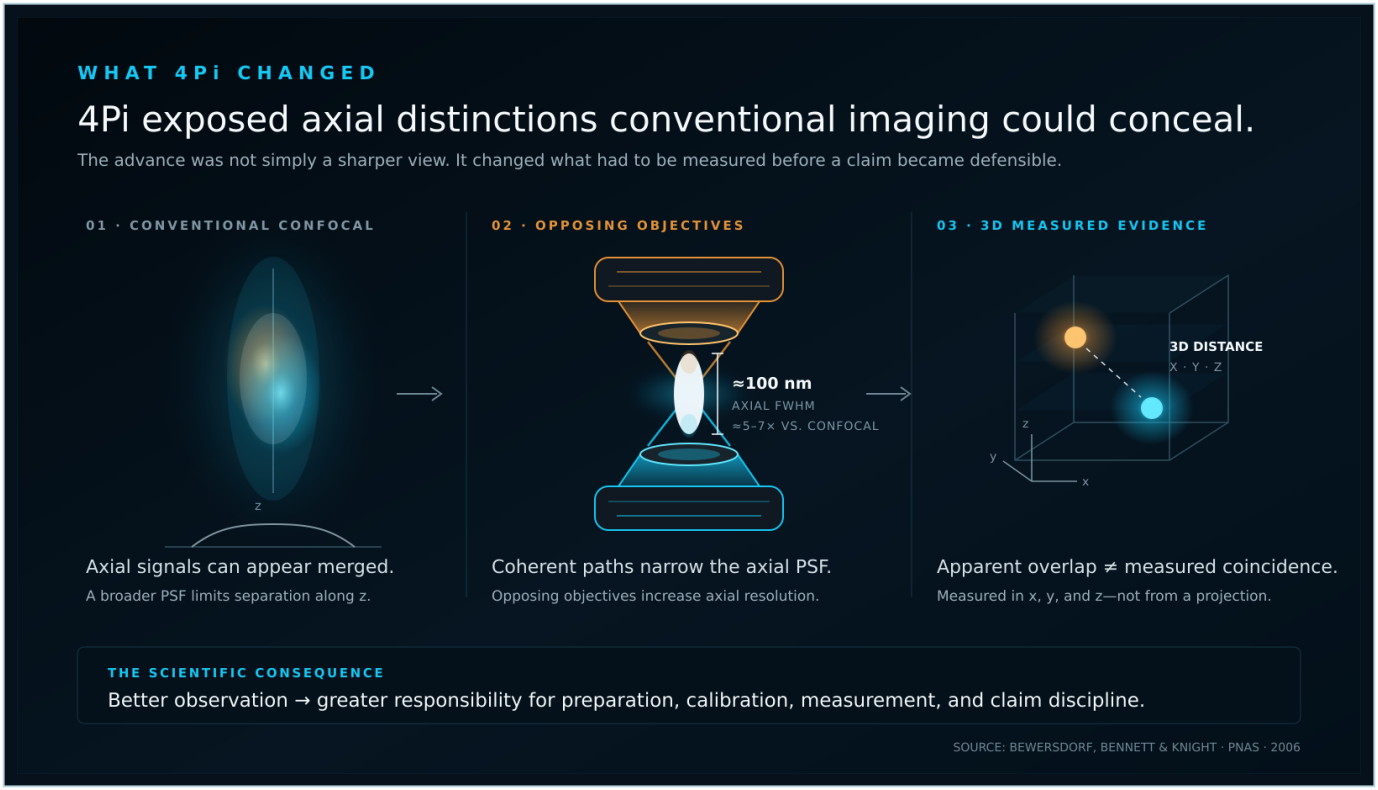

Figure 2. In Type C 4Pi microscopy, coherent opposing optical paths produced an approximately five- to sevenfold axial-resolution improvement; the cited Methods review reported an axial central PSF maximum of approximately 100 nm.

3. Higher resolution moved responsibility upstream

As resolution increased, sample preparation and labeling became more, not less, important. A high-performance microscope could expose positional fluctuation of fluorophore conjugates, refractive-index mismatch, nonspecific staining, antibody competition, and structural changes introduced by fixation. It could therefore produce a more precise representation of an artifact when the upstream method was not equally rigorous.

This problem shaped work at Lake Placid Biologicals during 2006 and 2007. Advanced confocal and 4Pi imaging required fluorescence that remained stable through demanding acquisition. As STED and related super-resolution methods entered practical biological imaging during this period, fluorophore performance and conjugation chemistry became still more consequential.[5] Contemporary reporting documented work on fluorescent stains, microscopy kits, and spectral-imaging applications intended to make advanced microscopy more reliable for the end user.[6]

The 2009 Methods paper made the upstream logic explicit.[5] It examined antibody purification and specificity, fixation, coverslip thickness, blocking, fluorophore behavior,

staining sequence, and the risk of misleading colocalization. It showed, for example, that an antibody-cocktail procedure could create an appearance of Rad51-γH2AX coincidence that changed substantially when the targets were stained sequentially. It also described an additional fixation step used for 4Pi imaging to stabilize antigen-antibody complexes and reduce positional fluctuation visible at the achieved resolution.

The point was not that every experiment required one universal protocol. The point was that upstream conditions had to remain connected to downstream interpretation.

Biological material → reagent quality → conjugation and fluorescence → preparation → acquisition

The image does not begin at the detector. The detector records the consequences of every upstream decision that made the fluorescence visible.

4. Instrument integration moved the bottleneck downstream

In 2008, biplane FPALM demonstrated three-dimensional sub-100-nanometer fluorescence microscopy across several micrometers of sample depth, with reported translationally invariant resolution of 30 × 30 × 75 nanometers.[4] The approach simultaneously recorded fluorescence from axially separated object planes, allowing the axial position of localized emitters to be estimated while retaining cellular-scale imaging depth.

My work at the University of Utah, beginning in 2008, developed this scientific and optical lineage toward integrated instrumentation and practical acquisition. The public patent record includes a 2009-priority microscopy-system family covering three-dimensional probe-molecule imaging with multiple optical paths, a non-coherent-light microscopy family, and a beam-splitter module developed with Jörg Bewersdorf.[7-9] A separate cellular-assay application described individual-cell measurements in relation to markers, treatment, time, dose, and classification.[10]

These records require precise attribution. The foundational 2008 biplane publication and its predecessor patent provide technical context; they do not list me as an inventor on that predecessor family. My documented inventorship is established by the later Utah-related families cited here. The University of Utah’s 2013 Technology & Venture Commercialization report separately states that the Vutara SR-200 was designed by Brian Bennett and describes its use of two axially separated object planes for three-dimensional localization.[11]

The combination of acquisition, localization, rendering, and analysis in an integrated instrument solved important problems. It also exposed the next bottleneck. Scientists still had to decide which data series was relevant, what each channel represented, whether acquisition and reconstruction were valid, which structures should be measured, whether an object persisted through Z or time, which upstream controls applied, which downstream analysis was

eligible, and what the final result could legitimately claim.

Improved instrumentation moved the bottleneck from seeing the evidence to governing it.

5. More capable microscopy created a mountain of data and decisions

Microscopy did not advance along only one axis. Higher spatial resolution was accompanied by larger fields of view, more channels, deeper Z-stacks, time series, tiling, higher detector bit depth, faster acquisition, localization tables, reconstructed volumes, and multiple derived representations. As the technologies became more aggressive, a single experiment could expand from a small set of images into hundreds or thousands of planes, frames, objects, localizations, and analytical choices.

The resulting “data mountain” was not simply a storage problem. It was a problem of heterogeneity and interpretation. Different vendors encoded data and metadata differently. Different modalities required different reconstruction and quality-control assumptions. Native files, exported TIFFs, projections, rendered volumes, segmentation masks, localization tables, and publication figures could all represent different stages of the same experiment without preserving a clear relationship among them.

Microscopy is not devoid of standards. The Open Microscopy Environment provides a common data model and exchange formats; REMBI defines recommended metadata for biological images; and QUAREP-LiMi advances shared quality-control and reproducibility practices.[13,15,16] These efforts are essential. But no single standard makes every instrument, modality, file structure, reconstruction, analytical workflow, and biological interpretation scientifically equivalent.

The remaining variation is often expressed through user decisions: which series to open, which channel corresponds to which target, how axes are interpreted, whether calibration is preserved, which reconstruction is accepted, where a threshold is set, how objects are segmented, which projection is displayed, how regions of interest are drawn, what is excluded, how populations are normalized, and which result is selected for reporting. Two skilled users can make different defensible choices, or different unrecorded choices, and produce different measurements and conclusions from the same source data.

This is why the mountain is composed of both data and decisions. Increasing instrument capability amplified the amount of evidence while fragmenting the context required to interpret it consistently. The scientific need was no longer only for better analysis software. It was for a system capable of preserving how a biological question, acquisition, file, analytical choice, human intervention, and final claim remained connected.

That need is the direct bridge from advanced microscopy into Identifyn and BENNETT.

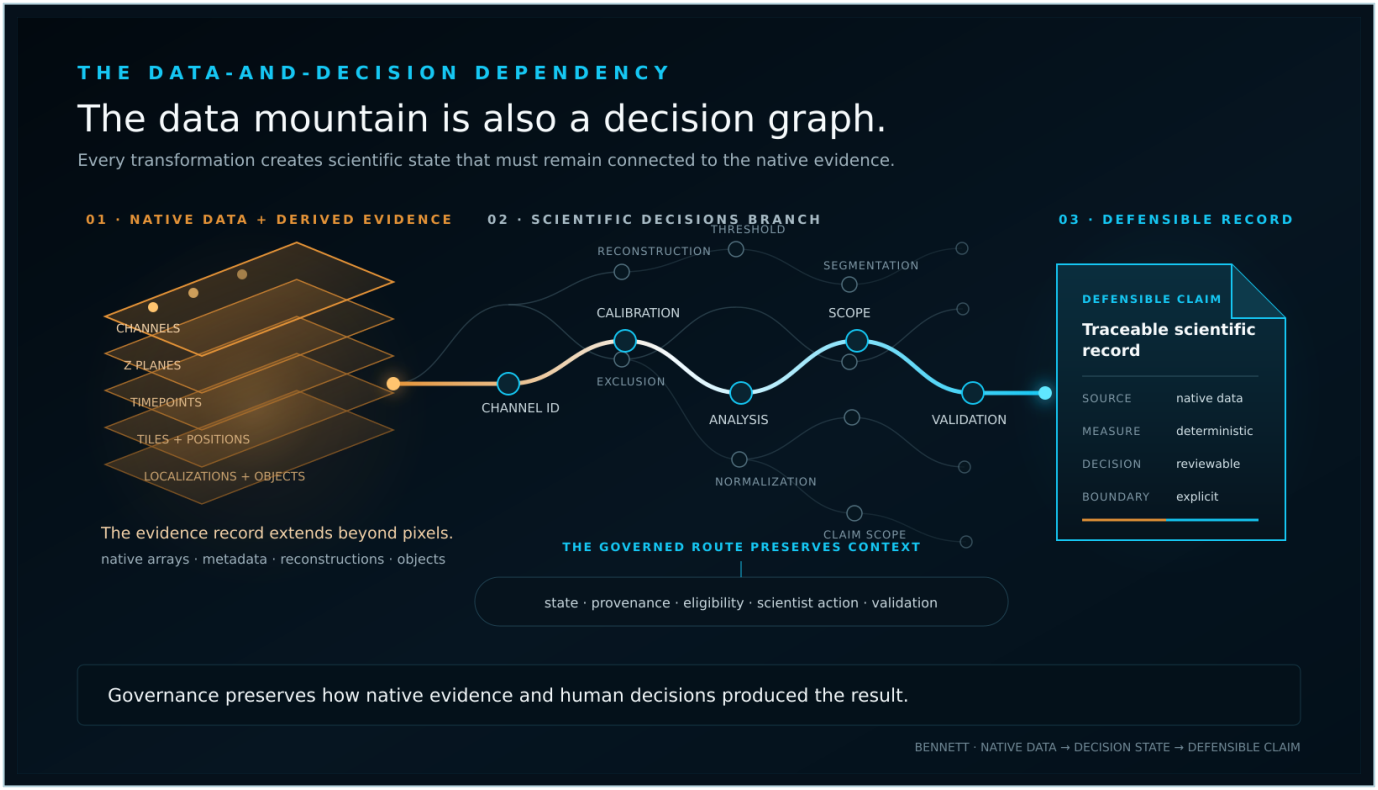

Figure 3. As native evidence expands, scientific decisions multiply. Governance preserves the state, provenance, eligibility, scientist actions, and validation connecting acquisition to claim.

6. Identifyn connected the complete experiment

Identifyn was planned around this accumulated systems view. It did not treat the image as an isolated endpoint. Products and reagents were connected to declared methods; methods to preparation and controls; experiments to instruments and modalities; acquisitions to native files and metadata; and measurements to reports and conclusions.

The objective was vertical scientific integration: preserve the relationships required to understand why a result exists and whether it can be compared, reproduced, extended, or trusted. Widefield, confocal, Airyscan, structured illumination, lattice SIM, SIM², single-molecule localization, and other modalities were not treated as interchangeable picture sources. Each created a different evidence environment with distinct resolution behavior, metadata, failure modes, analytical opportunities, and claim limits.

LEAN operating practice contributed a second principle: undefined work should not be automated. A scientific process must first expose its inputs, decisions, exceptions, failure states, review gates, and measures of success. Standardization is valuable when it preserves those decisions; it is destructive when it forces unlike experiments into the same template.

Beginning in early 2025, the microscopy and analytical work became a deliberate audit of AI reasoning. The objective was not merely to provide examples to a model. It was to determine

how the system interpreted modalities, file structures, channel identities, preparation context, measurement scope, spatial relationships, and claim boundaries. Incorrect assumptions, ambiguous mappings, unsupported inferences, and template carryover were converted into explicit rules and tests.

The public application Systems for Cellular Experiment Design reflects part of this direction. It describes an environment in which natural-language intent can be connected to biological pathways, functional proteins, antibodies, fluorophores, spectral compatibility, imaging systems, settings, protocols, and confidence-scored recommendations.[12] As with the earlier patent record, the application documents a disclosed architecture; it is not a substitute for evidence of implemented performance.

Identifyn therefore remains the scientific and operational foundation of BENNETT. It established that the experiment, not the isolated image, is the correct unit of scientific intelligence.

7. BENNETT turns the lineage into an operating architecture

BENNETT formalizes this accumulated scientific discipline by separating kinds of authority that are often blurred in AI systems.

- Native-data authority: Native numeric arrays, axes, physical calibration, channel structure, acquisition metadata, and provenance remain the source for measurement. A screenshot, adjusted display, projection, or generated illustration is not silently promoted into quantitative evidence.
- Deterministic analytical authority: Engines and micro-engines perform bounded operations under explicit contracts. The component that measures intensity, distance, object burden, apparent fluorescence-defined volume, shell localization, or temporal behavior remains distinct from the language model that explains the result.
- Eligibility authority: File evidence and workflow state determine which analyses are available. Dimensions, axes, scale, channels, temporal content, modality evidence, accepted masks, and required upstream results constrain the route.
- Scientist authority: The user can choose among applicable analyses, inspect intermediate results, modify permitted controls, accept or reject analytical objects or masks, and take over embedded scientific software when direct manipulation is preferable.
- Scientific authority: Interpretation is tested against modality, calibration, measurement scope, validation state, uncertainty, and explicit claim boundaries.
- Publication authority: The BENNETT Scientific Publisher assembles measurements, methods, figures, interventions, warnings, provenance, validation, and blocked claims into a defensible record.

The language model remains important, but its role is intentionally bounded. It supports conversation, intent clarification, explanation, and synthesis. It does not become the source of numeric measurement, rewrite file eligibility, bypass required upstream work, or convert a visually persuasive result into a mechanistic claim.

This division of authority is the architectural expression of the original microscopy lesson: what is observed, what is measured, what is inferred, and what is claimed must remain distinguishable.

8. Routing preserves both efficiency and scientific control

As the number of engines and micro-engines grows, asking a language model to consider every use case on every turn becomes inefficient and scientifically fragile. BENNETT instead moves stable logic into machine-readable capabilities, dependencies, states, and validation rules.

The system first examines the uploaded file. Dimensions, axes, channels, physical scale, temporal content, modality evidence, metadata, and workflow state determine what the file can support. The interface can then present the scientist with applicable tools organized into understandable families such as 2D, 3D, time, spatial relationships, object analysis, or SMLM. Conditional tools can explain their missing prerequisites. Inapplicable routes remain blocked.

The scientist may select a tool directly or describe an objective conversationally. The LLM helps translate that intent into the available route, but it does not invent the route. Deterministic engines execute in a dependency-aware order. Validated upstream outputs become the controlled inputs to downstream analyses.

Crucially, the scientist can take over. Embedded analytical software allows direct inspection and manipulation when expert judgment is needed. Accepted thresholds, masks, objects, exclusions, and review decisions become part of the persistent scientific state. When control returns to the governed workflow, the system knows what changed, who changed it, what evidence was affected, and what downstream work must be rerun or revalidated.

Human intervention is therefore not treated as a failure of automation. It is a first-class operating mode within the evidence architecture.

The complete route is:

1. Ingest: preserve native arrays, metadata, scale, channels, acquisition context, and provenance.
2. Recognize: determine file capabilities, modality evidence, missing prerequisites, and constraints.
3. Present: show applicable analytical routes and explain conditional or blocked options.
4. Select: allow direct scientist choice or conversational expression of intent.
5. Execute: run deterministic engines and micro-engines in governed order.

6 Intervene: permit recorded scientist takeover through embedded tools.

7 Validate: test outputs, state transitions, uncertainty, and claim eligibility, including negative paths.

8 Publish: assemble a reproducible evidence package with methods, provenance, boundaries, and human decisions.

The route is not administrative scaffolding around the analysis. It is the mechanism that prevents the biological question from becoming detached from the material, the image from becoming detached from the native file, the measurement from becoming detached from its assumptions, and the claim from becoming detached from the evidence.

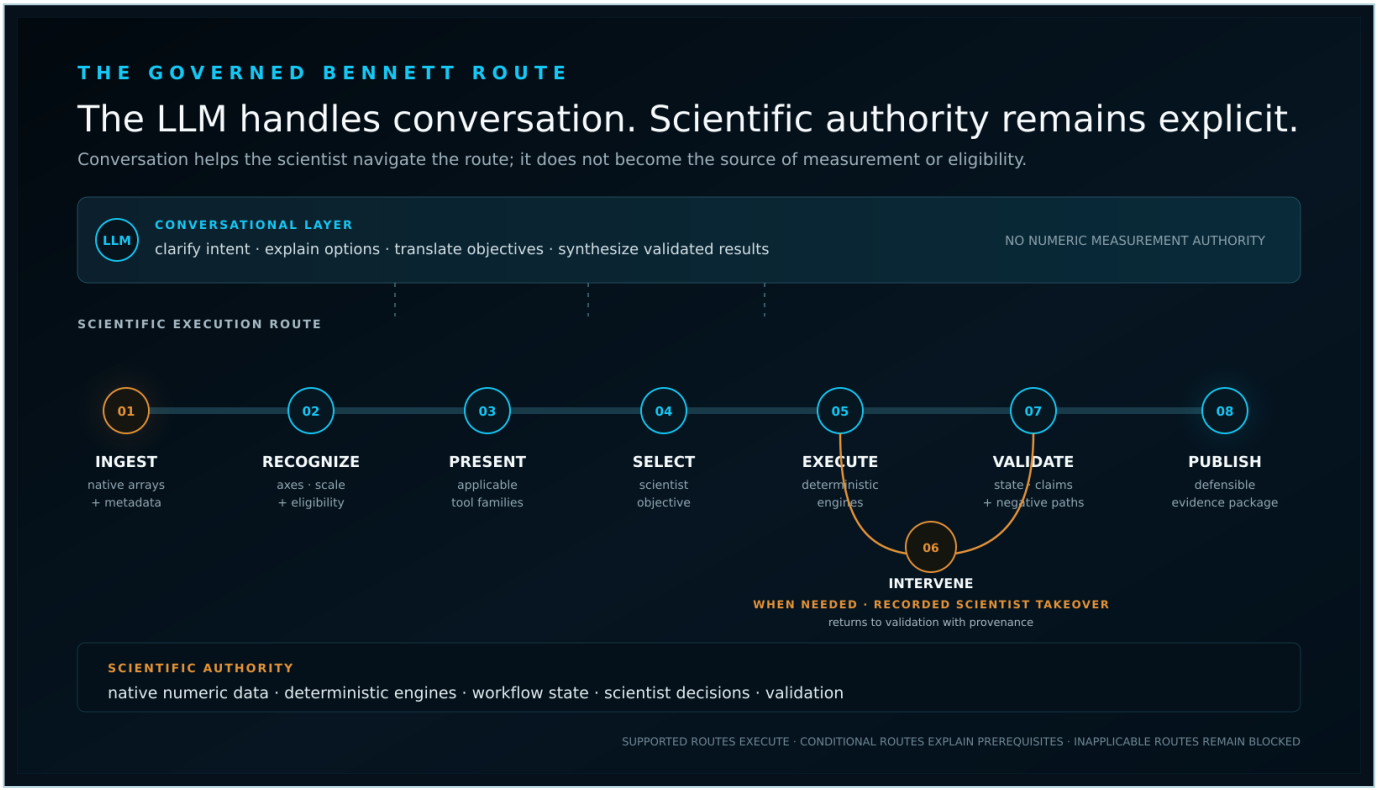

Figure 4. The governed BENNETT route. The language model supports conversation and explanation; native data, deterministic engines, workflow state, scientist decisions, and validation retain scientific authority.

9. One scientific progression

The history can be summarized as a sequence in which each stage exposed the next unresolved responsibility.

Stage	Scientific advance	Responsibility revealed
2004-2006	DNA-repair localization and preparation for 4Pi	The specimen and label are part of the measurement system.

Stage	Scientific advance	Responsibility revealed
2006	Three-dimensional 4Pi analysis of H2AX structures	Resolution, segmentation, calibration, spatial analysis, and claim language must agree.
2006-2009	Fluorescence chemistry and immunolabeling control	The recorded signal carries the consequences of upstream materials and methods.
2008-2013	Biplane localization and integrated instrumentation	Better acquisition moves the bottleneck into data selection, analysis, and interpretation.
Multimodal expansion	Larger, faster, multidimensional, and increasingly heterogeneous datasets	The data mountain is also a decision mountain; interpretation varies when choices and context are not preserved.
Identifyn	Vertical integration of products, methods, experiments, modalities, data, and reports	The complete experiment is the correct unit of scientific intelligence.
BENNETT	Functioning multi-vendor native-data workflow, governed routing, deterministic engines, scientist control, validation, and publication	Scientific meaning must be preserved across the complete evidence route while implemented and planned capabilities remain distinguishable.

This is the through-line of the paper. BENNETT is not an AI layer added after microscopy. It is the formalization of responsibilities revealed by increasingly demanding scientific observation.

10. From architecture to a functioning system

The progression now reaches a functioning system. BENNETT is operating as an AI-guided scientific-intelligence workflow, not merely as an architectural proposal. Across the supported vendor brands and native file types in the current validation set, the system can ingest native numeric data and metadata, resolve dimensions and physical calibration, route eligible analysis, execute bounded measurements, preserve run state and provenance, and produce Publisher outputs.[17]

The current operating chain gives each layer a distinct responsibility. BES-110 performs multi-vendor native-file ingestion and normalization. BES-111 performs fluorescence intensity and distance measurement. BES-112 performs site-of-interest, object, puncta, and apparent fluorescence-defined volume analyses where the data support them. The Publisher then separates measurement evidence, review visualizations, interpretation constraints, blocked claims, and export provenance. A documented end-to-end validation run of this chain returned pass status at each stage within its tested scope.[17]

This distinction matters. Successful operation across the tested multi-vendor data set does not mean that every possible proprietary file variant, modality, experiment, or biological claim has been universally validated. Nor does it mean that every engine in the larger roadmap is already implemented. It means that the core model has crossed from design into execution:

native data can move through a governed analytical route to a reviewable scientific output without making the language model the measurement authority.

The principal remaining product work is the user experience. The UX must make the functioning system legible: recognize the uploaded file, display applicable tools in scientific families, disclose conditional or blocked routes, allow the scientist to select an objective or work conversationally, support direct takeover of embedded analysis software, and return results without obscuring provenance or claim boundaries. In other words, the remaining challenge is not whether BENNETT can operate on supported multi-vendor native data. It is how elegantly and transparently the scientist can operate BENNETT across screens, workflows, and levels of expertise.

Independent testing and review by academic and industry scientists is planned to begin in September 2026. This is practical external peer review of the system's operation and outputs, not journal-editorial peer review. Public launch is targeted for mid-fall 2026. These are prospective milestones, not completed validations, and the public record should continue to distinguish tested performance from review in progress and roadmap capability.

That present state also determines how the rest of this collection should be read. Papers 2-5 explain the evidence chain that the operating system preserves. Papers 6-9 explain how expert practice, routing, micro-engines, scientist control, and publication make that chain executable and governable. Paper 10 describes the research-use path from those controlled measurements toward higher-order biological and disease intelligence. The series therefore moves from origin, to operating principles, to implementation, and toward governed research use, not through ten disconnected claims.

11. Why the architecture matters

For scientists, BENNETT offers a way to preserve expert control while reducing the burden of assembling fragmented tools, files, metadata, and reports. It does not replace experimental judgment. It makes that judgment visible, persistent, and reviewable.

For AI companies, the architecture offers a pattern for high-consequence domains: use a probabilistic model where language and flexible interaction are valuable, while deterministic systems retain responsibility for measurement, eligibility, state transitions, and validation. Human intervention remains governed evidence rather than hidden exception handling.

For instrument and software companies, file-aware routing creates a harmonized layer across heterogeneous tools without pretending that every modality supports the same analysis or claim.

For pharmaceutical, biotechnology, and translational customers, the value is continuity. Treatment, dose, time, marker, acquisition, structure, measurement, population response, and conclusion can remain connected. This creates a credible route from image analysis toward comparative biological and disease intelligence without inflating an image-derived observation

into an unsupported mechanism.

12. The next nine papers

This paper establishes the origin, governing thesis, and present operating state. The remainder of the collection follows the same evidence route in greater depth; each paper develops one responsibility introduced here and hands a controlled output to the next.

Paper	Title	Question developed next
02	The Complete Experiment	How does Identifyn's vertical integration preserve the evidence created before acquisition?
03	Resolution Stepdown	Which observations and claims remain stable when the same biology is examined across resolution scales?
04	Antibodies You Can Trust. Data You Can Defend.	How should reagent identity, specificity, conjugation, and performance remain connected to image evidence?
05	The Native File as the Acquisition GroundTruth™	Why must arrays, axes, physical calibration, metadata, and provenance anchor downstream measurement?
06	From Expert Practice to Governed Scientific Intelligence	How can expert judgment, use cases, states, and negative paths become executable scientific governance?
07	Scientist-in-Control AI	How can file-aware routing and embedded tools transfer analytical control without losing provenance?
08	Micro-Engines, Not a Monolith	How can bounded analytical components be composed without allowing implementation or scientific drift?
09	The BENNETT Scientific Publisher	How do measurements, figures, interventions, validation, provenance, and boundaries become a defensible report?
10	From Image Analysis to Disease Intelligence	How can governed outputs from the functioning platform support a research-use path across perturbation, dose, time, and populations without inflating mechanism?

The sequence is deliberate. It moves from scientific origin, through the complete experiment and native evidence, into governed reasoning, human control, implementation, publication, and finally higher-order biological interpretation.

Conclusion

BENNETT's origin is not a single algorithm, model, or product launch. It is a progression of scientific responsibilities documented across biology, microscopy, method development, fluorescence chemistry, instrumentation, patents, operating systems, and engineering architecture.

DNA-repair biology required reliable localization. Preparing samples for 4Pi microscopy required control of the specimen before acquisition. The 2006 PNAS work required three-dimensional measurement and disciplined interpretation of spatial relationships. Fluorescence and conjugation work required stable, application-aware labeling. Biplane single-molecule localization required optical routing, calibration, and uncertainty awareness. Integrated instrumentation revealed the need to govern data selection and downstream analysis. As microscopy became larger, faster, more multidimensional, and more heterogeneous, the resulting data-and-decision mountain made interpretation increasingly dependent on user choices that were rarely preserved as a complete scientific record. Cellular-assay design required structured relationships among treatment, marker, time, dose, and response. Identifyn connected the complete experiment. BENNETT converts that accumulated discipline into an extensible evidence system in which conversation, computation, scientist intervention, validation, and publication have distinct and reviewable roles. Today, that system is functioning across the supported multi-vendor native-data formats in its current validation set. The work now centers on independent review, UX completion, and launch preparation so scientists can see, select, control, and review the governed route without weakening the evidence model beneath it.

Scientific instruments produce data. BENNETT preserves and governs the route by which those data become understanding.

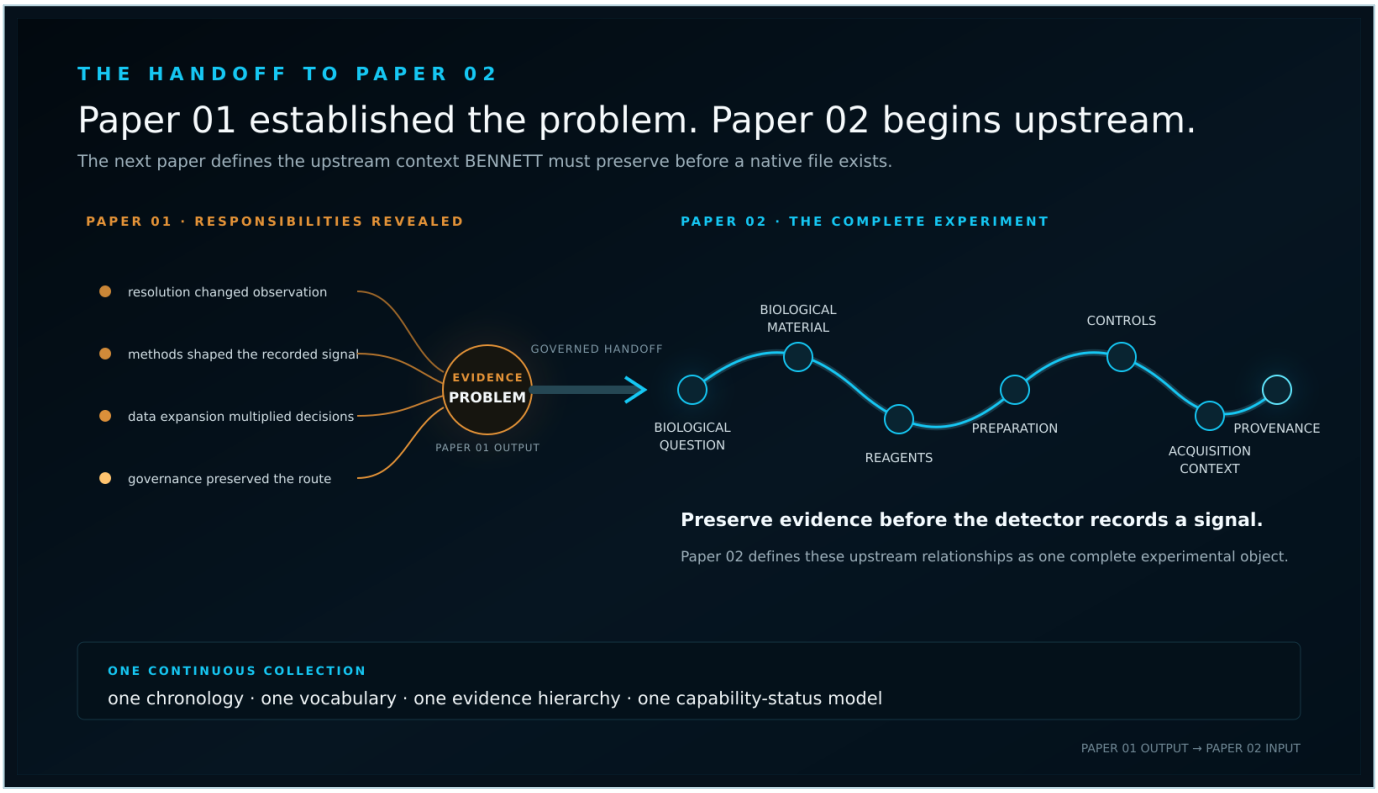

Figure 5. Paper 1 establishes the evidence problem; Paper 2 inherits that problem and defines the complete experiment that preserves context before acquisition.

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