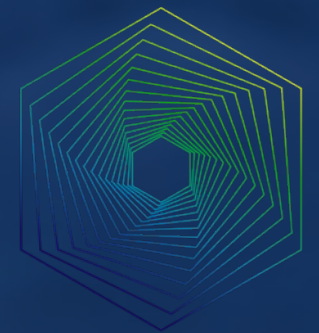


Use case

LENS^{ai}™ Integrated Intelligence Technology
powered by HYFTs®

Solving the Information Integration Dilemma (IID) in life sciences



Disclosures

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In our increasingly data-driven world, integrating and harnessing vast amounts of information effectively is a challenge.

The complexity of biological information is that it relates to multiple dimensions such as functions of proteins, 3D structures of molecules, genetic information involving the whole process of translating DNA code into RNA and proteins, and much more.

Collectively these dimensions need to be captured to understand biological systems and create meaningful predictions and insights.

Information Integration Dilemma (IID) refers to the complex task of integrating, consolidating, analyzing, and utilizing these diverse data, data sources, and formats.

The IID challenges in omics data analysis

- **Data Silos:**
Data that are biologically interconnected are stored and accumulated as isolated data sources, hindering collaboration, data sharing and the development of accurate and reliable analytical insights.
- **Data Inconsistency:**
Diverse data formats, structures, and quality levels make it challenging to reconcile and merge information accurately.
- **Integration Complexity:**
Merging data from disparate sources with varying schemas, standards, and semantics requires substantial effort.
- **Security and Privacy:**
Protecting sensitive information while ensuring data integration introduces additional complexities.
- **Scalability:**
As data volumes grow, integration solutions must handle the increasing load without sacrificing performance or reliability.

Our solution

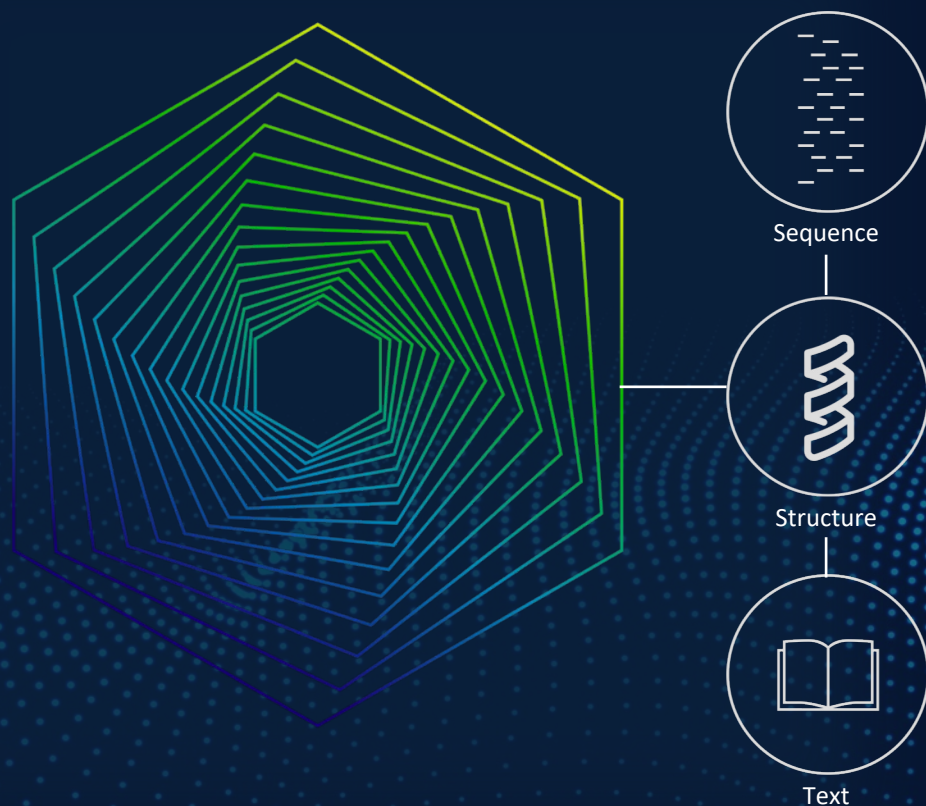
Introducing LENS^{ai}[™] integrated intelligence platform powered by HYFT[®] technology:

Step into the future of biotherapeutic discovery with LENS^{ai}. Our powerful technology is at the forefront of healthcare innovation, accelerating drug discovery through scalable data analysis and insights.

- Patented technology
- Unprecedented data integration and fusion
- Seamless integration through one AI framework
- Create actionable data through infinite scalability
- Understand the specific context and connections in biology
- Make valuable predictions and uncover new information and insights

The differentiator for life science discovery

One revolutionary framework seamlessly integrates mass amounts of multi-omics data



LENS^{ai} powered by HYFTs[™] technology

Unparalleled technology to connect the biosphere's fundamental pillars into one framework: sequence, structure and function.

- Sequence: DNA-RNA-Protein
- Structure: Alpha Fold, ESM-2, Rosetta Fold, Cryo-EM, Crystallography
- Text: Peer-Reviewed Literature, Patents, Clinical Trials

Solving the IID by utilizing the power of LENS^{ai} HYFTs

Reducing noise to make data meaningful

What are HYFTs?

Universal Fingerprint™ patterns found across the entire biosphere.

How do HYFTs serve us?

1. HYFTs function as encapsulated tokens “words” carrying information and knowledge, to provide context and meaning
2. HYFTs are foundational anchor points. They eliminate the background noise inherent in all data (structured and unstructured)
3. HYFTs capture cross data relationships to deduce meaningful and actionable insights

How are HYFTs used?

Process Data

- 1000x more efficient

Analyze data

- Discovery, development and translational strategies
 - Integration of all data set types
 - Hypothesis generation

Act on data

- Improve wet-lab drug discovery

The IID challenge in a researcher's daily life today

Use case:

Biotherapeutic analysis currently requires multiple search queries from several sources and involves heterogeneous AI models.

What it takes today:

- Consulting back and forth on numerous databases, data types and AI models
- Knowledge gathering is a scattered and time-consuming process
- Ultimately, a limited amount of information can be gathered and consumed

The collage illustrates the fragmented nature of biological data. It includes screenshots from the National Library of Medicine (BLAST), the Protein Data Bank (PDB), PubMed, and ImmPort. Each screenshot represents a different type of data and a different search interface, highlighting the complexity and time-consuming nature of gathering information for biotherapeutic analysis.



From a disconnected IID experience to fully integrated biotherapeutic intelligence

LENS^{ai} seamlessly integrates sequence, structure, and text

1.

One comprehensive integrated view:

Explore sequence, structure and textual information concurrently and swiftly

2.

A layered view into insight foundations:

The HYFTs encapsulate the sequential and structural context to guide AI understanding of the biological sequence function

3.

Access deeper analysis through additional AI algorithms:

Explore further meaningful insight and hidden relationships

1. Comprehensive integrated views

• Sequence-structure-text in one graph

One framework connecting information on (sub)sequence-structure-text: full comprehensive insight, easily accessible, ready for in-depth exploration and AI analysis

Data below represented in graph

Antibodies **Antibody (18)** and hotspots **Hotspot (44)** have syntactical representations via

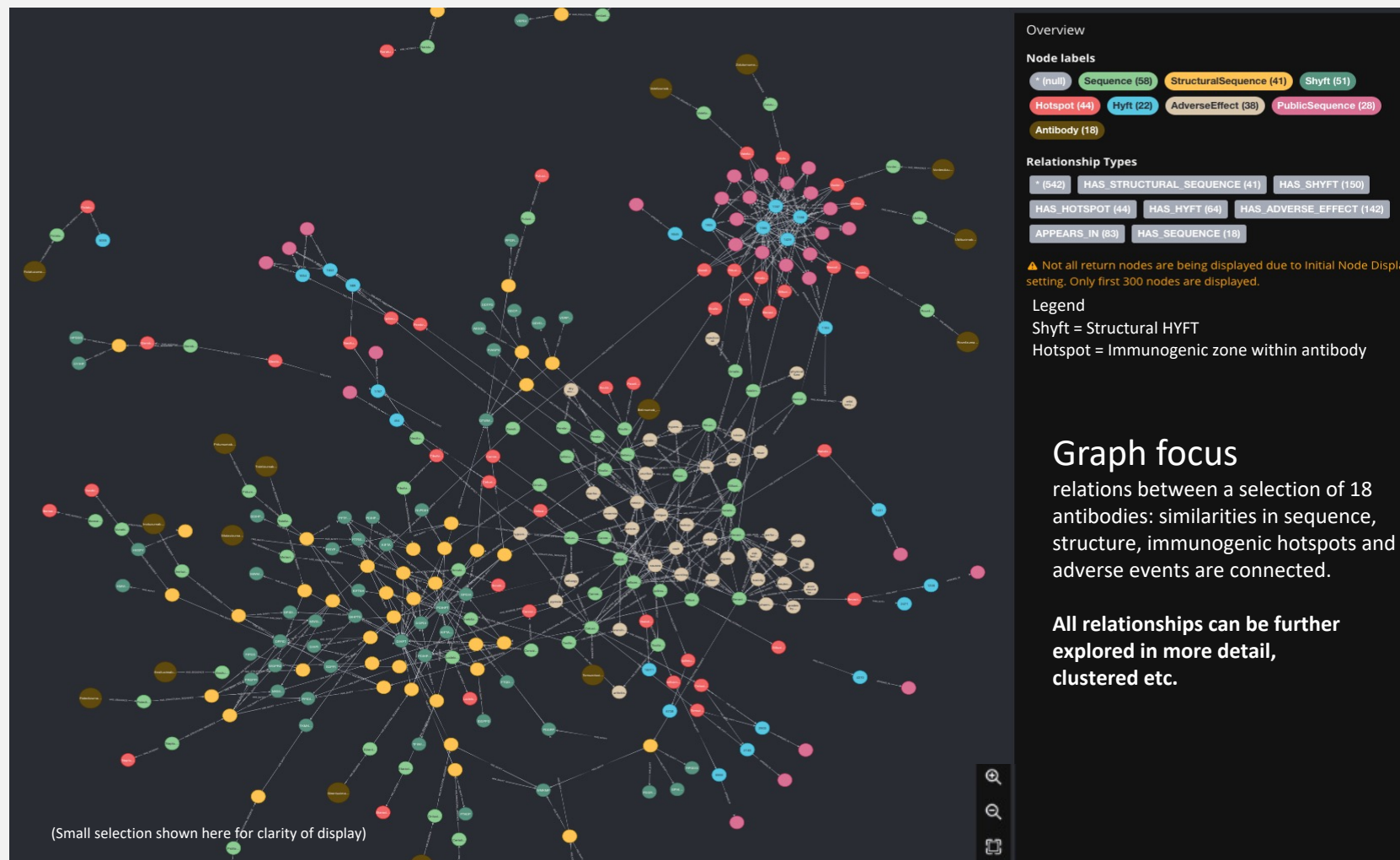
Sequence (58) **Hyft (22)**

and a structural representation via

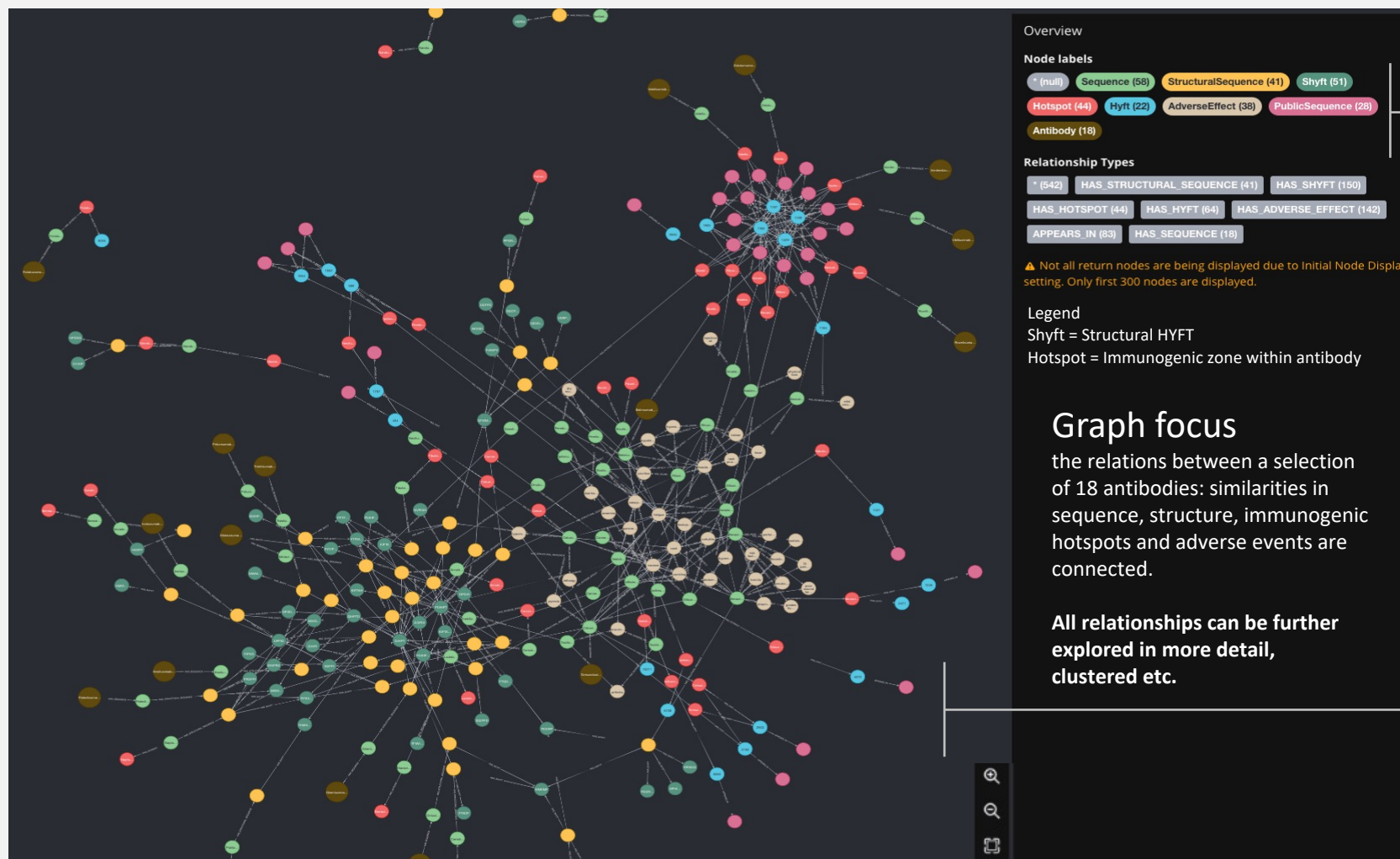
StructuralSequence (41) **Shyft (51)**

Textual information derived through our proprietary NLP technology is represented in **AdverseEffect (38)**

Adverse effect node is a higher order symptomatology clustering used to give a first broader overview of the information gathered out of all Pubmed abstracts



1. Comprehensive integrated views — key features



White box AI approach:

Concepts and relations are traceable

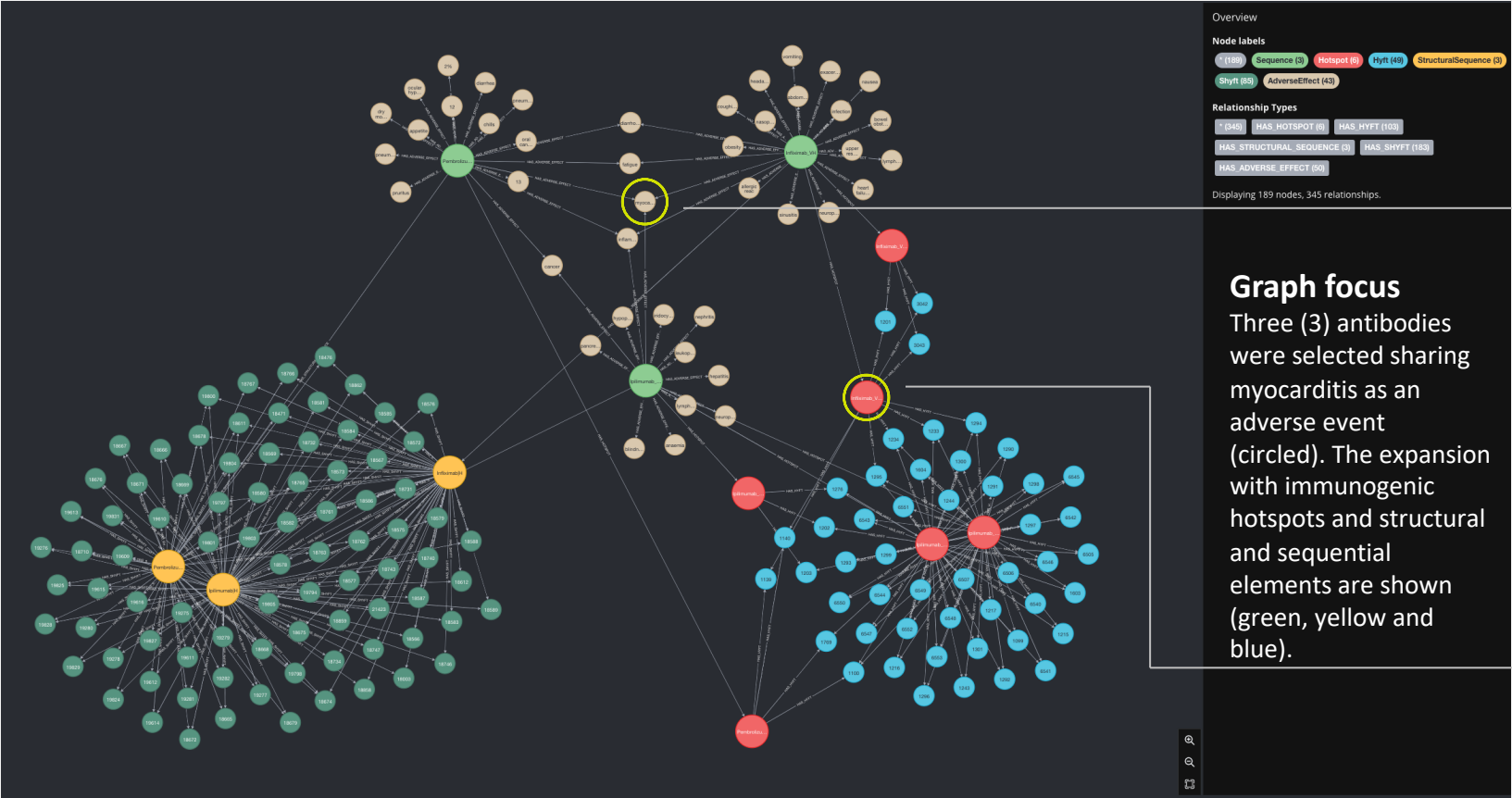
All information that is displayed can be traced back to the original source it came from.

Relation first approach:

By providing an integrated view, the focus is on detecting biologically and functionally relevant relations to understand systems biology and biological complexity.

2. A layered view into insight foundations

Select the items relevant for your query and start exploring the interconnected world of sequence-structure-text



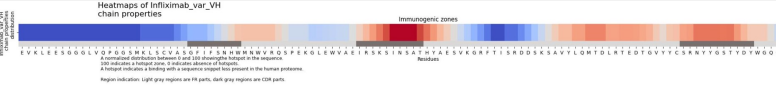
Text-based insight

The myocarditis node is a higher-level symptom representation of all Pubmed abstracts containing findings on myocarditis. This node can be further expanded to the exact sentences mentioning myocarditis. The Pubmed ID is indicated to find the original abstract and paper.

PMID	Title	Sentence
PMID:31439303	Case Series of Ventricular Tachycardia and Myocarditis From Programmed Cell-Death Protein-1 Inhibitor Treated With Infiximab.	Case Series of Ventricular Tachycardia and Myocarditis From Programmed Cell-Death Protein-1 Inhibitor Treated With Infiximab.
PMID:21674722	Myocarditis associated with infiximab: a case report and review of the literature.	Myocarditis associated with infiximab: a case report and review of the literature. ...

Subsequence-based insight

This node represents immunogenicity hotspot data of the heavy chain of Infiximab obtained via the LENS^{ai} *in silico* immunogenicity screening: hotspots represent a higher risk for immunogenicity and are indicated in red

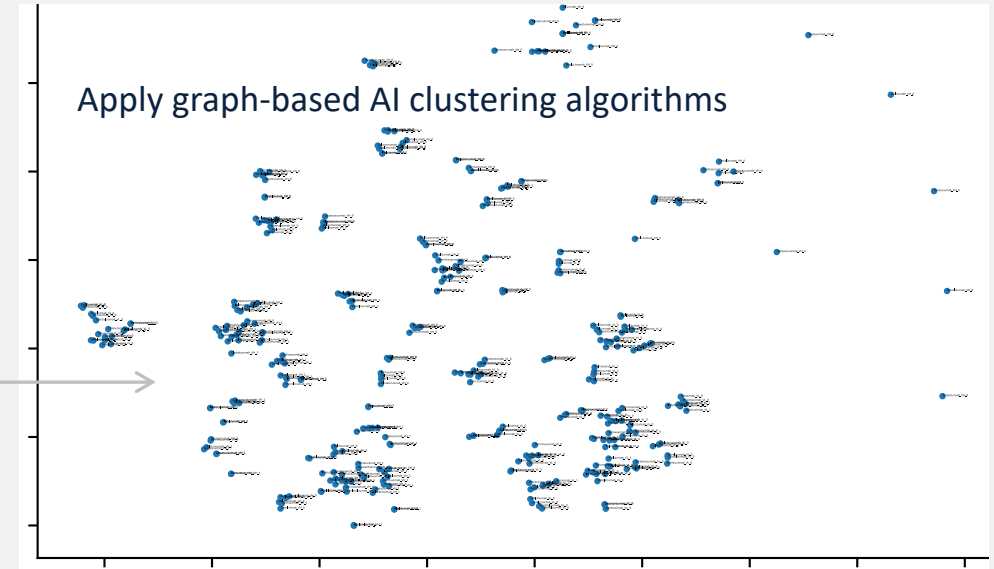
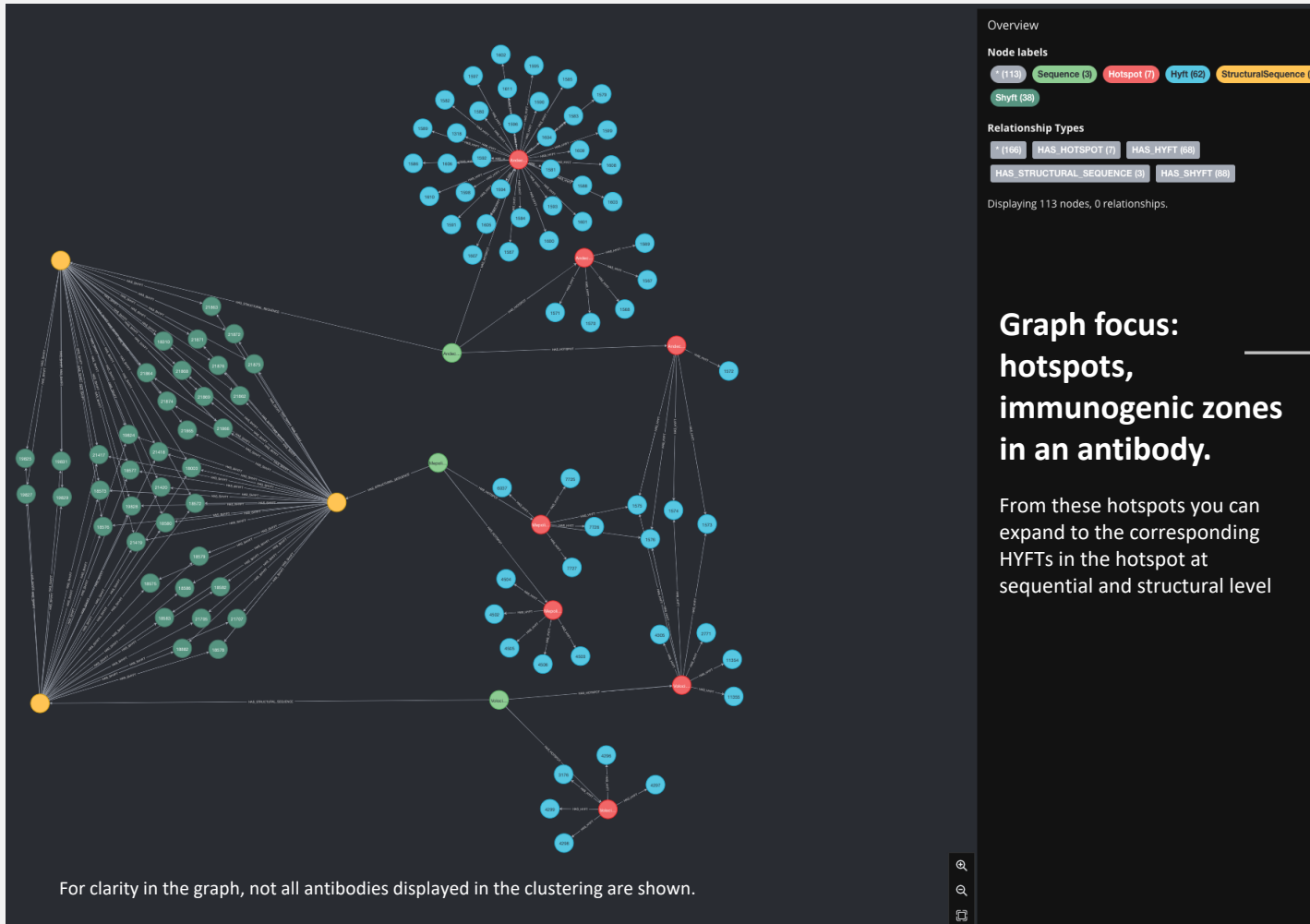


Structural-based insight

Integrated overall into insight and embedded in SHYFT and structural sequence

3. Access deeper analysis through additional AI algorithms

Create predictions and in-depth various subanalysis



Examples:

Predictive modeling
Generative algorithms

From the graph a clustering is performed, the sequential and the structural dimensions related to the immunogenic hotspots of the antibodies are combined in one feature to detect groups that share syntactical and structural 'closeness'. This can be used to do high-throughput screening in early-stage discovery and improve antibody characteristics. Demonstrating value through accelerating the quality and quantity of leads.

LENS^{ai} Integrated Intelligence Technology powered by HYFTs

Empowering actionable data with integrated intelligence

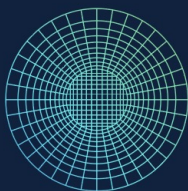
Discover the vast biotherapeutic horizon — from detailed data to expansive insight

- Data integration at subsequence level
- One seamless framework
- Infinitely scalable insights, supported by AI algorithms

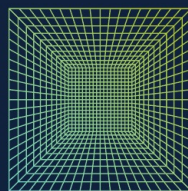
Revolutionary data silo integration and optimization

Public and proprietary databases

Unstructured data



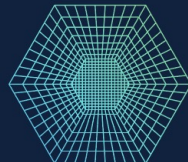
Structured data



Sequence data



Protein structure data

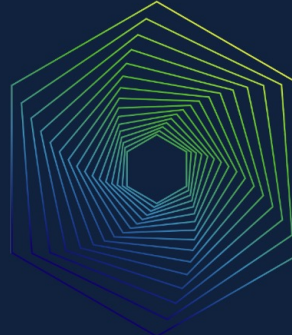


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Unparalleled LENS^{ai} technology

Analyze | Integrate | Learn | Generate

Sequence | Structure | Text

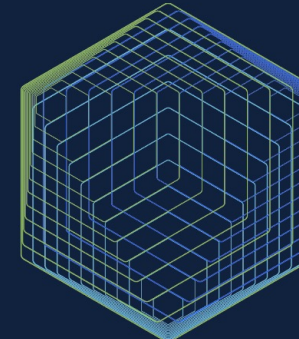


Powered by HYFT Technology

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Powerful real-time infinite scalable data insight

Program design | Target identification | Lead discovery
Biosimilars | Immunogenicity



We look forward to connecting on
how LENS^{ai} can be game-changing
for your discovery.

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