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# Federated Data Analytics for Genomics Data

MASTER CANDIDATE

**Mirco Cazzaro**

Student ID 2076745

SUPERVISOR

**Prof. Gianmaria Silvello**

University of Padova

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*To my parents  
and friends  
not to alberto*



## **Abstract**

Biomedical data management is increasingly complex due to the variety of storage systems and evolving data models. This heterogeneity presents obstacles to data integration and querying, crucial for advancing biomedical research and healthcare. The project will involve designing a system architecture that supports the integration of heterogeneous data stores under a unified federated system. The system will also utilize principles from the Ontology-Based Data Access (OBDA) paradigm to facilitate semantic querying capabilities. By developing a federated data analytics system for genomics data, this thesis will contribute to reducing the complexities involved in biomedical data management. The system will enable more effective data integration and querying processes, thereby supporting faster and more accurate genomics research. The completion of this project will result in a prototype of a federated data analytics system capable of handling the specific needs of genomics data.



## **Sommario**





# Contents

<b>List of Figures</b>	<b>xi</b>
<b>List of Tables</b>	<b>xiii</b>
<b>List of Algorithms</b>	<b>xvii</b>
<b>List of Code Snippets</b>	<b>xvii</b>
<b>List of Acronyms</b>	<b>xix</b>
<b>1 Introduction</b>	<b>1</b>
<b>2 Background</b>	<b>3</b>
2.1 Methodological Background . . . . .	3
2.1.1 Resource Description Framework . . . . .	3
2.1.2 Knowledge Graphs . . . . .	4
2.1.3 Ontologies . . . . .	4
2.1.4 Data Federation . . . . .	5
2.1.5 Semantic Data Integration . . . . .	6
2.2 Technical Background . . . . .	7
2.2.1 SPARQL Query Language . . . . .	7
2.2.2 Data Federation Systems . . . . .	8
2.2.3 OBDA Systems . . . . .	11
2.2.4 Triple Stores . . . . .	13
<b>3 Related Works</b>	<b>15</b>
3.1 BigDAWG . . . . .	16
3.2 Optique . . . . .	17

## CONTENTS

<b>4</b>	<b>Context of the Work</b>	<b>19</b>
<b>5</b>	<b>System Architecture</b>	<b>21</b>
5.1	System Architecture Design . . . . .	21
5.2	Data Sources . . . . .	23
5.2.1	MySQL . . . . .	23
5.2.2	PostgreSQL . . . . .	23
5.2.3	Polypheny . . . . .	24
5.3	NAS Folders . . . . .	27
<b>6</b>	<b>Use Cases</b>	<b>29</b>
<b>7</b>	<b>Evaluation Results</b>	<b>31</b>
<b>8</b>	<b>Conclusions and Future Works</b>	<b>33</b>
	<b>References</b>	<b>35</b>
	<b>Acknowledgments</b>	<b>39</b>

## List of Figures

2.1	The OBDA framework . . . . .	7
2.2	The OBDA framework . . . . .	12
3.1	OBDF approach . . . . .	16
5.1	Proposed System Architecture . . . . .	22



# List of Tables

2.1	Comparative among Data Federation Systems . . . . .	11
2.2	Comparative among OBDA Systems . . . . .	11



# List of Algorithms





# List of Code Snippets

2.1	Example of a SPARQL query for genetic markers data. . . . .	8
5.1	The storage plugin configuration file . . . . .	25



# List of Acronyms

**RDF** Resource Description Framework

**URI** Uniform Resource Identifier

**KG** Knowledge Graph

**OWL** Ontology Web Language

**DBMS** Database Management System

**SQL** Structured Query Language

**OBDA** Ontology-Based Data Access

**API** Application Program Interface

**JDBC** Java Database Connectivity

**ODBC** Open Database Connectivity

**FOSS** Free and Open Source

**ARP** Advanced Relational Pushdown

**SPARQL** SPARQL Protocol and RDF Query Language

**OBDF** Ontology-Based Data Federation

**W3C** World Wide Web Consortium

**STARQL** Streaming and Temporal ontology Access with a Reasoning-based  
Query Language

**DL** Description Logic

**CSV** Comma Separated Values

## LIST OF CODE SNIPPETS

**JAR** Java Archive

**JSON** JavaScript Object Notation

**VCF** Virtual Contact File

**NAS** Network Attached Storage

**LAN** Local Area Network

**SMB** Server Message Block



# Introduction





# Background

## 2.1 METHODOLOGICAL BACKGROUND

### 2.1.1 RESOURCE DESCRIPTION FRAMEWORK

The Resource Description Framework (RDF) is a standard<sup>1</sup> by the World Wide Web Consortium (W3C) designed for data interchange on the web. Its definitive syntax was lastly defined on 2003 [1].

RDF is based on the idea of making statements about resources, expressed as triples: for example, a triple might consist of "Gene123" (subject) "hasFunction" (predicate) "DNA Repair" (object). These triples are stored in a graph, making RDF uniquely suited for modern data analytics where relationships and linkages are crucial: this structure is by design flexible, and it is used to represent information in a way that makes it easier to aggregate, integrate, and manage diverse data from various sources.

The standard utilizes Uniform Resource Identifier (URI) to ensure that each element in the triple is uniquely identifiable, allowing to link data across different datasets seamlessly. RDF also supports literal values and datatypes, enabling detailed descriptions of properties and values.

In summary, RDF provides a robust and flexible framework for describing and interlinking data on the web, which is crucial for any federated data system

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<sup>1</sup><https://www.w3.org/RDF/>

## 2.1. METHODOLOGICAL BACKGROUND

that aims to integrate diverse data sources effectively.

### 2.1.2 KNOWLEDGE GRAPHS

Knowledge Graphs represent an innovative way of structuring and querying interconnected data. A Knowledge Graph (KG) organizes data in a graph format, where entities (nodes) and their interrelations (edges) are defined according to a schema that encapsulates both the entities and the possible links between them. This structure allows not only to better visualize data, but is also very well suited for data exploration and analysis.

Central to the concept of KG is the idea of enhancing search and data discovery capabilities beyond simple data retrieval. By semantically linking data entities, KG allow for more intuitive and sophisticated queries that are closer to natural language questions. This capability makes them useful in complex domains like biomedical research, where users may need to uncover hidden relationships and patterns among vast datasets.

Furthermore, KG well suits in scenarios requiring data integration from disparate sources. They support the combination of structured and unstructured data and they can scale well as new data need to be integrated. This flexibility is crucial in fields such as genomics, where new data attributes and relationships are continuously being discovered and need to be rapidly integrated into existing datasets.

In practice, KG are usually powered by technologies such as RDF and other standards discussed earlier, leveraging the strengths of these frameworks to ensure robust data handling and scalability.

### 2.1.3 ONTOLOGIES

Ontologies are a shared vocabulary for a particular domain. They serve as a crucial tool in structuring data by defining classes where data entities can be categorized. This classification system not only standardizes data representation but also simplifies the communication between different systems and users by providing a common understanding of the domain.

Ontologies involve the use of first-order logic to define rules about the relationships between different classes. These rules allow for the logical inference of new information from the data that is already known, which can significantly



deepen data analysis and querying capabilities. This set of first-order logic rules used to model ontologies composes the Ontology Web Language (OWL) [2].

With ontologies integrated within a KG, it is possible to employ inferential algorithms either at query time or at preprocessing time. This capability enables the derivation of new knowledge that isn't explicitly stated in the data but can be inferred based on the ontological representations.

The use of ontologies in a KG is crucial in complex domains like genomics. Here, the ability to infer new relationships and properties can lead to understanding intricate biological connections and processes.

In summary, ontologies provide the foundational structure for managing complex information systems. They not only facilitate a standardized approach to data handling and integration but also enhance the capability of systems to derive and utilize new knowledge effectively.

#### **2.1.4** DATA FEDERATION

Data Federation is a technology that organizes data from multiple different and autonomous data sources and makes it accessible under a uniform data model, allowing for real-time data retrieval from various sources without requiring data deduplication. This approach creates a unified data access layer that abstracts the underlying technical details of each Database Management System (DBMS). Users can query this virtual layer using standard data querying languages, like Structured Query Language (SQL), without needing to know where the data is physically stored or in what format.

A key strength of Data Federation lies in its capacity to harmonize heterogeneous data sources, ranging from traditional relational databases to modern big data solutions and cloud services. This integration is seamless and dynamic, scaling well as soon as new sources come in, without requiring significant reconfiguration. Such agility is crucial in fields like genomics, where data formats and sources evolve rapidly alongside scientific advancements. Moreover, it minimizes the risks associated with data duplication and movement, such as data loss or corruption. It also ensures that data remains current, reflecting real-time changes without delay. This is particularly valuable for decision-making processes where up-to-date information is critical.

Different existing Data Federation systems may have different characteristics, and the choice of which system suits better certain requirements may depend on

## 2.1. METHODOLOGICAL BACKGROUND

many different factors. A recent comparative study on Data Virtualization Systems [3] highlights and evaluates diverse features of many systems coming both from the academia as well as enterprise solutions, such as supported query languages, supported data sources, data security, exposed interfaces and software support.

### 2.1.5 SEMANTIC DATA INTEGRATION

Semantic Data Integration is an approach that aims to integrate data from a single relational source to an ontology that models a specific domain. This integration is achieved by defining mappings that establish semantic relationships among data entities.

The core idea behind semantic data integration involves establishing a global schema, represented by the ontology, which acts as a blueprint for how data from various sources is viewed and accessed. This ontology defines not just the entities and their attributes but also the relationships and constraints between these entities. The mapping between the ontology (global schema) and the relational data source is critical as it dictates how data is interpreted in a meaningful way.

The concept of Data Integration, firstly introduced without a semantic focus [4], has evolved with research advancements in this field. These advancements have led to the development of tools and mapping languages specifically designed for semantic data integration, laying the groundwork for a paradigm known as Ontology-Based Data Access (OBDA) [5].

The OBDA framework, that has been precisely formalized [6], is composed of a chain of procedures that can be summarized as follows:

1. input query  $q(\vec{x})$  is rewritten [7] into  $q'$  over the virtual ABox  $A'$  (i.e. the first-order logic specification of the ontology);
2. the rewritten query  $q'$  is unfolded using the *mappings* into an SQL query  $q^*$ ;
3. the optimised SQL query  $q^*$  is evaluated over the data instance  $D$  (e.g. a relational DBMS).

Figure 2.1 outlines the aforementioned algorithm within a flowchart.

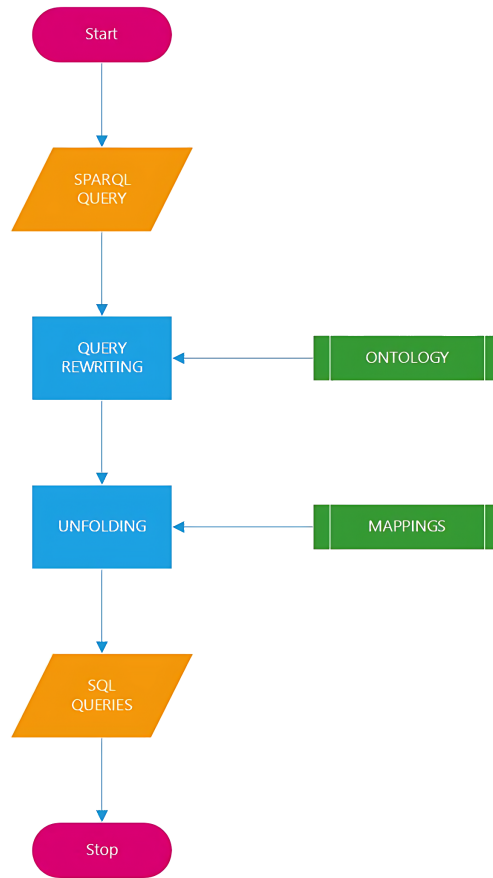


Figure 2.1: The OBDA framework

## 2.2 TECHNICAL BACKGROUND

### 2.2.1 SPARQL QUERY LANGUAGE

SPARQL Protocol and RDF Query Language (SPARQL), developed by the W3C, is the definitive standard for querying and managing data stored in RDF format.

As a key technology in semantic web applications, SPARQL enables sophisticated querying of KG, offering a query syntax that often resembles natural language. This user-friendly syntax facilitates intuitive data exploration and manipulation, differently from traditional relational databases that require joining tables to establish relationships.

For instance, as shown in Code 2.1, if a researcher wishes to find all genetic

## 2.2. TECHNICAL BACKGROUND

markers associated with a particular trait, a SPARQL query might directly reflect the question, “Which patients are associated with genetic markers X?” This parallels natural language questioning closely, making SPARQL particularly suited for domains where complex relationships must be understood and explored, such as genomics and biomedical research.

```
PREFIX bto: <https://w3id.org/brainteser/ontology/schema/>
PREFIX BTO_resource: <https://w3id.org/brainteser/ontology/resource/>

SELECT ?patient ?FUS ?FUS_mutation
WHERE {
  ?p a bto:Patient;
    bto:enrolledIn ?ctp.

  ?ctp bto:inClinicalTrial BTO_resource:BrainteserALSTurin.

  OPTIONAL{
    ?p bto:tested ?FUS_test.
    ?FUS_test bto:hasMutation ?FUS;
              bto:onGene NCIT:C91852.
    OPTIONAL{
      ?FUS_test bto:mutationType ?FUS_mutation.
    }
  }

  BIND(SUBSTR((STR(?p)), 48) AS ?patient)
}
```

Code 2.1: Example of a SPARQL query for genetic markers data.

### 2.2.2 DATA FEDERATION SYSTEMS

As discussed in section 2.1.4, Data Federation Systems are sophisticated softwares and thus evaluable under many aspects. In this background analysis we will focus on four main aspects, considering their importance as the Data Federation System will be part of a broader framework. In particular, by the aforementioned comparison, we will present three most prominent systems considering:

- software support & documentation;
- scalability;

- logging capabilities;
- performances.

These features are also briefly summarized in Tab. 2.1.

## DENODO

Denodo<sup>2</sup> is an enterprise virtualization platform that serves as a data federation system, integrating data from diverse sources to provide a unified view without requiring physical data deduplication. It allows for real-time access to structured and unstructured data from various sources including relational, column and No-SQL databases, web (! (!)API), and flat files.

Denodo provides robust security features, including hashing, encrypting functions and user privileges, ensuring that sensitive data is protected according to compliance standards.

Moreover, it utilizes advanced query optimization techniques, such as caching and query rewriting, to enhance performance. These optimizations ensure efficient data retrieval, reducing latency and improving the overall speed of data access across the federated sources.

Although it is highly scalable, capable of accommodating new data sources, and it is provided also with a custom source wrapper template for unsupported data sources, being it an enterprise solution allows for maximum five connections, unless a premium plan is signed.

## TEIID

Teiid<sup>3</sup> is an open-source Java component developed by Red Hat<sup>4</sup> that provides integrated access to multiple data sources through a single uniform API. Rather than a DBMS, Teiid is more a query engine for integrating data from multiple sources, accessible both through Application Program Interface (API) and Java Database Connectivity (JDBC)/Open Database Connectivity (ODBC) interfaces.

It comes in different shapes: there are Teiid implementations as an Eclipse plugin as well as deployable packages on web containers such as Wildfly and

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<sup>2</sup><https://denodo.com/en>

<sup>3</sup><https://teiid.io/>

<sup>4</sup><https://www.redhat.com/>

## 2.2. TECHNICAL BACKGROUND

OpenShift.

One of the main issues with Teiid is poor documentation when it is not deployed alongside enterprise solutions (like OpenShift). Moreover, no major releases have been published since four years, and many open issues on the official GitHub repository<sup>5</sup> are not being addressed.

### **DREMIO**

Similarly to Denodo, Dremio<sup>6</sup> is a virtualization platform that serves as a data federation system. Although it is developed within an enterprise context, the standard version, comprehensive of most of the Dremio features, it is Free and Open Source (FOSS) under the Apache 2.0 license, combining typical enterprise software robustness with a strong community active on continuous maintenance.

Even if it is possible to use Dremio as a standalone instance (e.g. on a server), it is by design a distributed system and thus it can run on clusters up to more than 1000 nodes. In case of standalone configurations, in linux server environments it is possible to install it using packet managers, but the easiest way is to use the Docker image it comes with.

Dremio makes use of Apache Arrow to enhance processing speeds and reduce latency. Moreover, it optimizes query performance through its advanced query planner and execution engine, which can push down operations to the data source level, minimizing data movement and speeding up response times.

It provides comprehensive security features that include encryption, access controls, and data masking to ensure privacy. It also maintains detailed logs of all queries, which are crucial for compliance purposes in many fields such as the clinical domain, where patient medical data is managed alongside their personal information.

As in Denodo, but under an open-source perspective, it is possible to build custom connectors for unsupported data sources and Dremio. This is realizable through Advanced Relational Pushdown (ARP) connectors: a public repository<sup>7</sup> provides a Maven template, that is customizable for each data source for which a JDBC driver is available.

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<sup>5</sup><https://github.com/teiid/teiid>

<sup>6</sup><https://www.dremio.com/>

<sup>7</sup><https://github.com/dremio-hub/dremio-sqlite-connector>

In conclusion, Dremio offers an open-source virtualization system with the typical robustness of enterprise softwares; it is highly scalable both in the sense of computation distribution over clusters and in the types of supported sources, and it has a comprehensive logging system that suits well for tracking data flow.




	Support	Free and Open Source	Well Documented	Scalability	Solid Logging Capabilities
 Denodo	✓		✓	✓	✓
 Teiid		✓			
 Dremio	✓	✓	✓	✓	✓

Table 2.1: Comparative among Data Federation Systems

### 2.2.3 OBDA SYSTEMS

OBDA, as shown in Fig. 2.2, allows to seamlessly integrate a relational source within an ontology, so to add a semantic layer. Research on this specific topic has been performed not only by the academy, but also from Research & Development branches of big companies, considering the impact on the industry: a preliminary analysis [8] by Siemens<sup>8</sup> that lead subsequently to a custom platform, analyzed existing systems. Table 2.2 summarizes the content of this analysis.

System	Characteristics
Optique (Siemens)	Supports ontology reasoning; supports both static and streaming relational DBMS
Ontop	Supports ontology reasoning
Mastro	Supports ontology reasoning
morph-RDB	Supports ontology reasoning
D2RQ	Does not support ontology reasoning
OntoQF	Does not support ontology reasoning
Virtuoso	Does not support ontology reasoning
Spyder	Does not support ontology reasoning
Ultrawrap	Does not support ontology reasoning

Table 2.2: Comparative among OBDA Systems

<sup>8</sup><https://www.siemens.com/>

## 2.2. TECHNICAL BACKGROUND

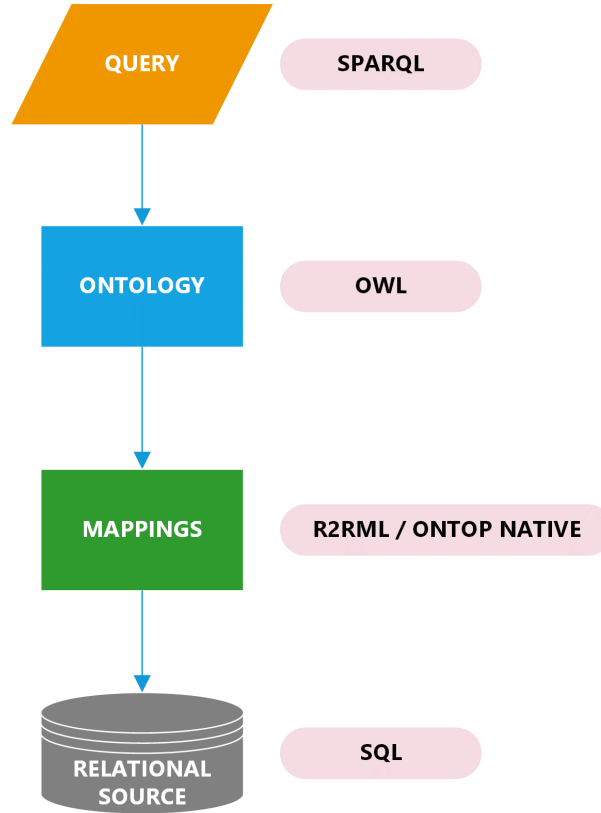


Figure 2.2: The OBDA framework

Given that ontology reasoning is one of the most important requirements in the OBDA approach (without this, using this paradigm would allow just to run queries in SPARQL language, without any other real advantage), and considering that the Optique system is an enterprise, on-premise and closed source solution, more in-depth comparisons [9] studied Ontop and Mastro. Their comparison can be summarized as follows.

### MASTRO

By our knowledge, Mastro [10] was the first OBDA tool, developed at La Sapienza University of Rome. It supports a subset of SPARQL queries and integrates a custom XML-based mapping syntax. Mastro’s mappings were not initially compliant with R2RML standards, which was a strong limitation in standard OBDA environments. The tool used a complex system of view predicate mappings, which may affect its adaptability to standardized environments. Although recent updates have integrated R2RML support, the system’s architecture still lacks certain optimizations due to its design constraints. For instance,



Mastro cannot perform advanced semantic query optimizations because it does not support detailed data constraints in its mappings. This limitation could lead to less efficient query processing and increased execution times, especially with complex queries involving multiple joins or extensive data operations. Moreover, Mastro is less efficient handling of datatype operations and IRI constructions within SQL, leading to potential slowdowns in query processing.

## ONTOP

Ontop [11] is an open-source and well maintained OBDA framework developed at the Free University of Bolzano. It is compliant with W3C standards, including R2RML for ontology mapping, OWL for ontology representation, and SPARQL for querying. Ontop is designed for high-performance query answering over virtualized RDF graphs. Ontop provides an efficient query answering system that leverages R2RML mappings and supports comprehensive optimizations. The system uses advanced query rewriting techniques, which are highly effective in reducing query complexity and execution time. Ontop's strengths are particularly evident in its handling of complex SPARQL queries, where it efficiently translates these into SQL, utilizing T-mappings and database integrity constraints for optimization. Regardless of its adherence to standards, Ontop comprises also a custom mapping language (Ontop Native Language).

The comparison between the two systems has been performed in two different scenarios. In general, Mastro shown faster responses in scenarios requiring extensive in terms of timings, while Ontop performs better in scenarios where a considerable number of mappings is involved for unfolding a certain query. This means that a choice on which system fits better depends on how constraining are timings in the query processing phase and on how many mappings have to be unfolded on average, that strictly depends on the heterogeneity of the underlying relational source.

### 2.2.4 TRIPLE STORES

Triple stores are database management systems specifically designed to store and retrieve triples through semantic queries. Triple stores typically ingests RDF files that contains IRI's in the usual format of subject, predicate, object. These systems are optimized for storing vast amounts of triples and efficiently handling complex queries that involve traversing relationships across a network of

## 2.2. TECHNICAL BACKGROUND

data. Triple stores support SPARQL, enabling semantic queries that are essential for applications in data integration, knowledge management, and semantic web projects. Many comparisons, especially in the biomedical field [12], among different triple stores systems analyze their performances under different point of view such as the volume of ingested data, the implementation of an ontology within the KG, and the language used to represent it (RDF, RDFS, OWL, etc.). For the purposes of this project, where materialized triples are not used, GraphDB has been selected due to its integration with Ontop. This integration allows GraphDB to support virtual graph functionalities, meaning it can perform SPARQL queries over non-RDF relational data by translating these queries into SQL through Ontop's engine. This scenario eliminates any particular requirements from the triple store system regarding the query processing phase, considering that the task will be accomplished by the underlying OBDA system.

### **GRAPHDB**

GraphDB is a robust, enterprise-ready triple store that excels in handling large volumes of data and complex queries. Developed by Ontotext<sup>9</sup>, GraphDB is designed to facilitate efficient data integration, knowledge discovery, and semantic analytics. It uses RDF for data representation and SPARQL for querying, supporting seamless transitions between different data formats and query languages. GraphDB's integration with Ontop for virtual RDF stores and its robust performance metrics make it an ideal choice for projects that require dynamic semantic data integration without the overhead of materialized triples. Its capabilities ensure that it is not only a powerful tool for RDF data management but also a flexible solution for broader data integration challenges in semantic environments.

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<sup>9</sup><https://www.ontotext.com/>



## Related Works

Performing federated analytics tasks over genomics data requires a robust architecture composed by different layers: a federation layer that allows for multiple streaming connections with diverse and heterogeneous sources (relational, no-SQL and columnar DBMSs); a virtualization layer that exposes “virtual” relational views of non-materialized data; an integration, ontology-based layer, so to add a semantic layer to the virtualized relational views, given the importance of exploring complex relationships among genomics data.

This approach has been formalized under the concept of Ontology-Based Data Federation (OBDF) [13], and it is represented in Fig. 3.1. As far as we know, no existing off-the-shelf system implementing this framework has ever been released: who intends to apply this architecture design have to manually install different components choosing among diverse competitors, and combining them together, dealing with possible underlying platform incompatibilities. Moreover, having no off-the-shelf solutions implies no solutions specifically tailored and optimized for dealing with genomics data.

Nonetheless, similar design proposal have been implemented in order to address both research questions as well as enterprise requirements. In this section, we will briefly discuss two solutions, one for each environment, analyzing them in details highlighting strengths and weaknesses.

### 3.1. BIGDAWG



Figure 3.1: OBDF approach

## 3.1 BigDAWG

As an example addressing research questions about managing heterogeneous data we have BigDAWG [14], developed under the Intel Science and Technology Center on Big Data. BigDAWG's architecture is composed of four layers: the base layer, the island layer, the main BigDAWG layer, and the application layer. Each layer serves a distinct purpose, from managing diverse physical data stores to facilitating user interaction through applications. This multi-layered approach allows BigDAWG to support various data models and query languages, thus offering a robust solution for cross-database queries and operations. While traditional systems such as Garlic and IBM DB2 have demonstrated the capability to handle data across different storage systems using a unified interface, BigDAWG distinguishes itself by its comprehensive support for "islands" of different data

models. This island approach not only supports operations across various data types but also enhances performance by optimizing queries based on the data model and the underlying database engine. This feature is critical in environments where performance and response times are crucial, such as in medical or real-time analytics applications. Despite its advanced architecture and capabilities, BigDAWG is not without challenges. It is not available as an off-the-shelf solution; rather, it requires certain levels of expertise if someone intends to install it or develop new islands modules. This means that significant effort would be required to adapt it to specific operational needs. Additionally, there is limited literature and empirical studies on its deployment in real-world scenarios, which poses doubts about considering its implementation. In summary, while BigDAWG represents a significant advancement in the field of database management systems, its practical application is limited by the prototype nature of its current implementation and the lack of extensive real-world testing. Future research could focus on reducing the barrier to its adoption, refining its architecture based on operational feedback, and expanding its use cases across different scenarios to fully realize its potential.

## 3.2 OPTIQUE

Optique [15], developed by Siemens, exemplifies an implementation of OBDA tailored to the industrial applications. Unlike conventional OBDA systems which typically focus on static data, Optique is designed specifically to handle both streaming and static data. This dual capability is crucial for environments like Siemens, where real-time data from sensors needs to be integrated with historical data for comprehensive analysis and monitoring. Optique comprises many technologies: Streaming and Temporal ontology Access with a Reasoning-based Query Language (STARQL), A language that supports complex queries over streaming and static data at the same time; ExaStream, A backend system optimized for low-latency queries on high-velocity streams; OptiqueVQS (Visual Query System), a component that improves usability by enabling users to formulate queries without prior knowledge of query languages. Although it has advanced capabilities, Optique remains a proprietary system not available for public use, which limits its adoption outside Siemens. This exclusivity may impede broader validation and benchmarking against other OBDA systems in real-world settings.





## Context of the Work





# 5

## System Architecture

As discussed in Chapter 3, there exist no off-the-shelf solution implementing the OBDF paradigm. This implies that for the specific task of dealing with clinical and genomics data, it is necessary to design a system architecture, choosing components in such a way that the whole architecture results in being solid, privacy-oriented (with strong logging capabilities), and being capable to manage genomics data. This chapter will firstly discuss the overall proposed architecture, that retraces the one presented in previous chapters. Subsequently, each layer will be presented in details, outlining how each components have been configured, reporting eventual code snippets. In order to better describe the source heterogeneity of data that may occur in contexts such as clinical and genomics, available relational data have been distributed among different sources.

### 5.1 SYSTEM ARCHITECTURE DESIGN

The proposed architecture described in Fig. 5.1 implements the OBDF framework. It adopts Ontop as its semantic data integration layer and Dremio as its data federation layer.

Briefly, Ontop have been chosen because it natively supports two high level mapping languages, that gives more freedom on their optimization, without the need to appeal to low level Description Logic (DL) languages, it is open-source and well maintained by the Free University of Bolzano data integration team, it comes embedded in GraphDB that offers solid APIs, and it comes even with an embedded web endpoint.

## 5.1. SYSTEM ARCHITECTURE DESIGN

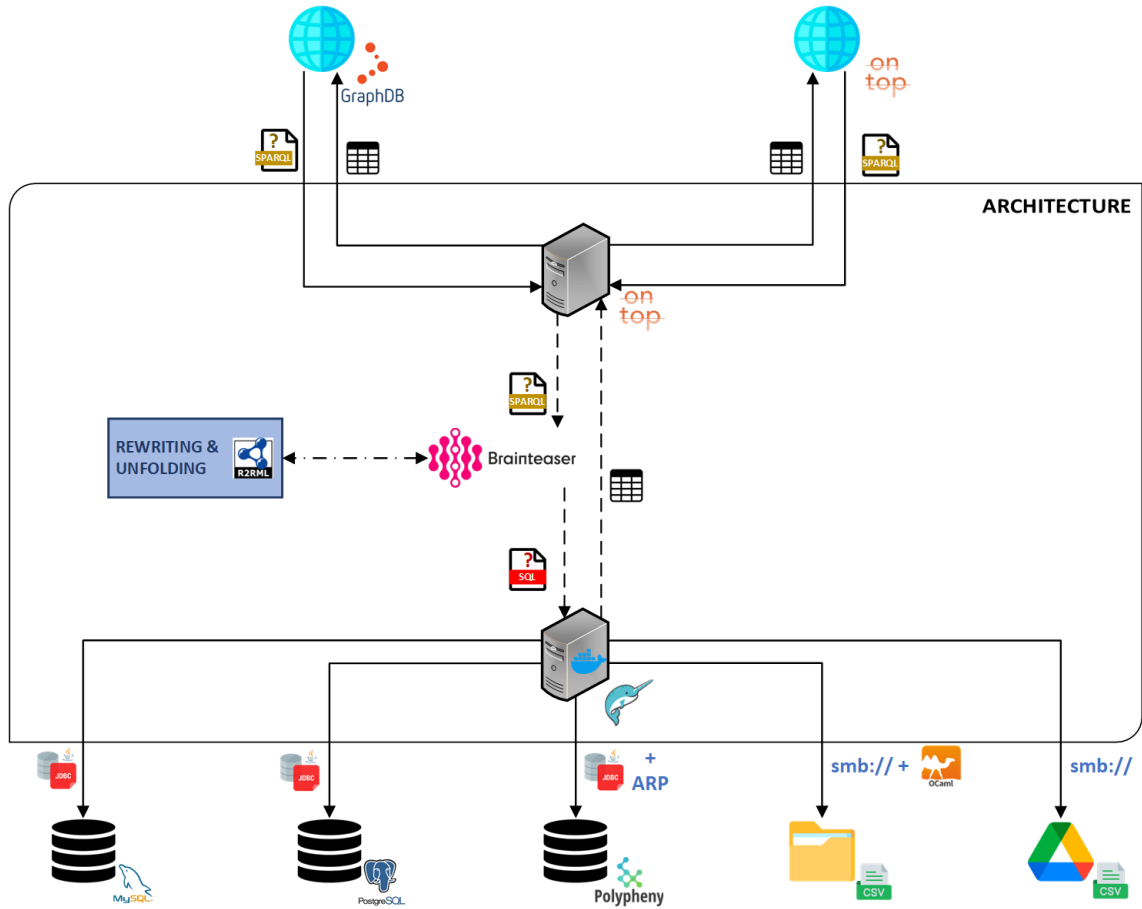


Figure 5.1: Proposed System Architecture

Dremio have been chosen as the virtualization and federation layer because, as discussed in the Chapter 2, it is an open-source, robust and scalable software influenced both from its enterprise nature and from a consistent community providing contributions. Moreover, within its installation methods, it is possible to set it up through a Docker image: this may set the basis for the architecture packaging, expanding the image to other software components.

The semantic integration requires an ontology well describing the domain of clinical and genomics data. Considering the reusability principle that stands at the basis of the semantic web, we identified the Brainteaser ontology<sup>1</sup> as suitable for accomplishing this task.

<sup>1</sup><https://brainteaser.dei.unipd.it/ontology/>

## 5.2 DATA SOURCES

Given the relational nature of available data, we distributed it among five different platforms, so to exploit the federation capabilities of the data federation layer. The choice of the sources has been guided also by surveying commonly used ones in the biomedicine field in contexts like research and hospital diagnostic. As we will discuss, they encompass more structured DBMSs as well as simple Comma Separated Values (CSV) files. We also included a novel DBMS system, so to investigate how new, unknown data sources can be federated as soon as they figure out.

### 5.2.1 MySQL

MySQL<sup>2</sup> is one of the most widely used relational DBMS (DBMS) in the world. It is a FOSS solution now distributed by Oracle<sup>3</sup>. It is extensively employed across a variety of applications, from small personal projects to critical enterprise environments. In our system architecture, we've chosen MySQL considering its extensive adoption, possibly also in application softwares used in clinics and hospitals to collect patients data. In our environment, MySQL's role is to store part of the structured clinical data presented in Chapter 4. The interfacing between MySQL and our data federation layer, Dremio, is performed through MySQL's JDBC connector. This setup allows Dremio to access and query MySQL data seamlessly. No special modifications or configurations were required to integrate MySQL with Dremio, thanks to Dremio's native support for MySQL. We simply established a new data source within Dremio by specifying the connection parameters.

### 5.2.2 POSTGRESQL

PostgreSQL<sup>4</sup> stands out as a widely adopted open-source relational DBMS. It is particularly adopted within the research community due to its robustness, advanced features, and strong compliance with SQL standards. Many research institutions and academics prefer PostgreSQL for its extensive capabilities in

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<sup>2</sup><https://www.mysql.com/it/>

<sup>3</sup><https://www.oracle.com/it/>

<sup>4</sup><https://www.postgresql.org/>

## 5.2. DATA SOURCES

managing complex data types and its support for sophisticated data manipulation operations. We considered PostgreSQL eligible to be a data source due to its common adoption in research contexts as a data collector. Again, PostgreSQL's role in our environment is to store another portion of the structured clinical data presented in Chapter 4. Just like with MySQL, integrating PostgreSQL with Dremio did not require any specific modifications or additional configurations.

### 5.2.3 POLYPHENY

Polypheny [16] is an open-source polystore system designed to support diverse data models including relational, document, and graph data. It is engineered to handle mixed workloads and various query languages, making it a versatile platform suitable for dynamic data environments. In our architecture, we consider Polypheny not just as a standalone polystore but as a potential low-level federator under our main data federation layer managed by Dremio. This perspective is particularly useful because it allows us to leverage Polypheny's ability to handle multiple data models, thus enriching the flexibility and capability of our overall data management system.

#### CUSTOM ARP CONNECTOR DEVELOPMENT

Unlike the straightforward integrations with MySQL and PostgreSQL, incorporating Polypheny required a more sophisticated approach. We performed this task not only to include Polypheny as one of our data sources but also as a proof of concept about the actual possibility of developing custom ARP connectors. Dremio's Advanced Relational Pushdown (ARP) framework offers a powerful mechanism to extend Dremio's capability to interact with various data sources by interfacing Dremio's internal query representations into the native query language of the target data source. For Polypheny, we developed a custom ARP connector to ensure interaction between Dremio and Polypheny. The connector we developed is open-source and available for the community, which can be found at our GitHub repository<sup>5</sup>. These connectors rely on the target source having a JDBC driver and accepting SQL as a query language, so to have an interface to dialog with.

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<sup>5</sup><https://github.com/mircocazzaro/dremio-polypheny-arp>

## CONNECTOR IMPLEMENTATION DETAILS

The custom ARP connector was implemented to translate SQL queries from Dremio into the query formats that Polypheny can execute directly. The ARP plugin template<sup>6</sup> consists of a Java Maven project, that has to be compiled, packed within a Java Archive (JAR) file and injected, together with the target source JDBC driver, into the running Dremio instance. To customize the template, two files need to be customized: the storage plugin configuration, which is a Java class 5.1, and the plugin ARP file, which is a YAML<sup>7</sup> file. The storage plugin configuration file tells Dremio what the name of the plugin should be, what connection options should be displayed in the source UI, what the name of the ARP file is, which JDBC driver to use and how to make a connection to the JDBC driver. The ARP YAML file is what is used to modify the SQL queries that are sent to the JDBC driver, allowing you to specify support for different data types and functions, as well as rewrite them if tweaks need to be made for your specific data source.

```

1  /* ... */
2
3  @SourceType(value = "POLYPHENY", label = "POLYPHENY")
4  public class PolyphenyConf extends AbstractArpConf<PolyphenyConf> {
5      private static final String ARP_FILENAME = "arp/implementation/
        polypheny-arp.yaml";
6      private static final ArpDialect ARP_DIALECT =
7          AbstractArpConf.loadArpFile(ARP_FILENAME, (ArpDialect::new));
8      private static final String DRIVER = "org.polypheny.jdbc.Driver";
9
10     @NotBlank
11     @Tag(1)
12     @DisplayMetadata(label = "Polypheny host <HOST:PORT>")
13     public String database;
14
15     /* ... */
16
17     @Tag(2)
18     @DisplayMetadata(label = "Record fetch size")
19     @NotMetadataImpacting
20     public int fetchSize = 200;

```

<sup>6</sup><https://github.com/dremio-hub/dremio-sqlite-connector>

<sup>7</sup><https://yaml.org/>

## 5.2. DATA SOURCES

```
21
22 @Tag(6)
23 @DisplayMetadata(label = "Polypheny User Name")
24 public String username = "pa";
25
26 @Tag(7)
27 @DisplayMetadata(label = "Polypheny Password")
28 public String password = "";
29
30 @Tag(4)
31 @DisplayMetadata(label = "Maximum idle connections")
32 @NotMetadataImpacting
33 public int maxIdleConns = 8;
34
35 @Tag(5)
36 @DisplayMetadata(label = "Connection idle time (s)")
37 @NotMetadataImpacting
38 public int idleTimeSec = 60;
39
40 @VisibleForTesting
41 public String toJdbcConnectionString() {
42     final String database = checkNotNull(this.database, "Missing
43     database.");
44     return String.format("jdbc:polypheny://%s", database);
45 }
46
47
48 private CloseableDataSource newDataSource() {
49     return DataSources.newGenericConnectionPoolDataSource(DRIVER,
50         toJdbcConnectionString(), username, password, null, DataSources
51         .CommitMode.DRIVER_SPECIFIED_COMMIT_MODE,
52         maxIdleConns, idleTimeSec);
53 }
```

Code 5.1: The storage plugin configuration file

With respect to the storage plugin configuration Java class 5.1, being Polypheny still an embryonic project not allowing for user management, but rather having a default user "pa" with empty password, fields are pre-filled with default values. The class specification is then interpreted at run time from Dremio, setting up a form with input fields corresponding to each `@DisplayMetadata` annota-

tion. The DRIVER static and immutable variable contains the class path of the Polypheny JDBC driver. The `newDataSource()` method is invoked at form submission, setting up the connection to the Polypheny instance.

### 5.3 NAS FOLDERS

Dremio offers native support for a variety of "relational" file types such as CSV, Excel, JavaScript Object Notation (JSON), and Virtual Contact File (VCF). These files may be physically moved within the Dremio instance, but losing any streaming capability, or by attaching a Network Attached Storage (NAS) source to it. In fact, Dremio integrates a connector to local folders, reading supported files within them. The name NAS on this typology of data source is ambiguous: the term refers to storage units usually located within the same Local Area Network (LAN) of one or more hosts accessing it, while in Dremio is used to generically refer to a folder to which it can access. This in practice means Dremio can browse local folders: thus, if NAS shared folders are mounted within the Dremio server through the Server Message Block (SMB) protocol, they can be browsed as well. In Linux environments where the standalone version of Dremio is used, its daemon must have permission to read these folders; in environments where the Docker image is employed, where a clear separation between the host file system and the Docker context occurs, folders and NAS shares must be mapped. This is obtained with Docker Volumes<sup>8</sup>, and in particular the "Host Volume" paradigm.

```
1 $ docker run -v NAS_PATH/folder:/opt/dremio/folder -p 9047:9047 -p
    31010:31010 -p 45678:45678 -p 32010:32010 --name hereditary_dremio
    dremio/dremio-oss
```

For the purposes of our project, we have utilized the NAS data source to store a portion of our genomics data. Specifically, we have chosen to include data in VCF files. VCF is a text file format generally used in bioinformatics for storing gene sequence variations.

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<sup>8</sup><https://docs.docker.com/storage/volumes/>







## Use Cases





## Evaluation Results





## Conclusions and Future Works



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