Efficient Representation of Very Large Linked Datasets as Graphs

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Abstract: Large linked datasets are nowadays available on many scientific topics of interest and offer invaluable knowledge. These datasets are of interest to a wide audience, people with limited or no knowledge about the Semantic Web, that want to explore and analyse this information in a user-friendly way. Aiming to support such usage, systems have been developed that support such exploration they impose however many limitations as they provide to users access to a limited part of the input dataset either by aggregating information or by exploiting data formats, such as hierarchies. As more linked datasets are becoming available and more people are interested to explore them, it is imperative to provide an user-friendly way to access and explore diverse and very large datasets in an intuitive way, as graphs. We present here an off-line pre-processing technique, divided in three phases, that can transform any linked dataset, independently of size and characteristics to one continuous graph in the two-dimensional space. We store the spatial information of the graph, add the needed indices and provide the graphical information through a dedicated API to support the exploration of the information. Finally, we conduct an experimental analysis to show that our technique can process and represent as one continuous graph large and diverse datasets.

1 INTRODUCTION

The establishment of the RDF data model has made available many large and diverse linked datasets from a wide range of scientific areas[1]. Exploring and querying these datasets as published, though, requires extensive knowledge of the semantic web and expensive infrastructure. As a result these datasets are inaccessible to a wider audience.

In order to alleviate this barrier, linked datasets should be represented using a graph model, where each entity is presented as a distinct object, and the information is explorable through multiple filtering criteria. In order to implement a user-friendly system, a technique should be developed that will meet some important challenges. To begin with, the technique should be able to handle a wide range of datasets that differ in characteristics[2]. Available datasets may have from a few thousands to millions of elements, they may also be incomplete, have no semantic annotations or not follow any data model or hierarchy[3].

In addition, the technique should provide an easy and user-friendly way to support the exploration of the information. As an example, entities should be distinct object and connections between them clearly defined, the complete dataset should be available and the graph topology should be consistent to allow the user to understand where the information is located. The relevant but also the absolute position in the two-dimensional space of the data objects should remain the same regardless of the user actions. Furthermore, plenty of functionalities should be available for the exploration of the information. Keyword search, path exploration, neighbour information, filtering and aggregation, should be available in a user-friendly way without requiring knowledge of querying or programming languages from the user. Last but not least, the information should be available for multiple users simultaneously through commodity hardware such as laptops and tablets. Processing that requires expensive infrastructure should be handled by the server side of the system and not by the devices of the users.

An overview of the techniques and systems that have been developed to address some of these challenges is presented here.

An initial approach to the problem of the exploration of large linked datasets focused on generic visualization systems. These systems aim to extract the information of linked, semantically annotated,

[1]https://lod-cloud.net/

[2]https://www.w3.org/wiki/TaskForces/Community Projects/LinkingOpenData/DataSets/Statistics

[3]https://datahub.io/collections/linked-open-data

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datasets and present it through generic visualization options. These visualization options are limited to charts, such as column, line, pie, bar, scatter and radar, that present the information in a summarized way. Some systems (Voigt et al., 2012; Schlegel et al., 2014) allow the dynamic choice of such visualization types based on the user selection. The user can select what information is of interest and the visualization type to present it. Other systems (Brunetti et al., 2012; Klímek et al., 2013; Atemezing and Troncy, 2014) utilize strict semantic rules and restrict the users to predefined types of visualizations.

These systems handle data fitting specific criteria regarding their structure and semantic information, and present the information summarized in restrictive forms. These approaches can give a general overview of the information but cannot support the graphical representation of the information. In addition, such systems cannot handle datasets that are incomplete or lack semantic annotations.

A large number of systems visualize linked datasets adopting a graph-based approach (Mazumdar et al., 2015). Some of these techniques (Abello et al., 2006; Auber, 2004; Jr. et al., 2006) present small filtered or aggregated graphs of the input dataset based on hierarchical data models. These systems use aggregation and filtering techniques to limit the size of the represented graph and allow navigation only along the hierarchy, making information inaccessible from nodes at the same hierarchy level. While the navigation of highly aggregated data might help initially the user to better understand the structure of the information, at a deeper exploration of the dataset the loss of information might be proven hindering to the usefulness of the representation.

The techniques discussed above meet only a subset of the challenges. However, for many use cases, such as road maps, communication networks and blockchain transactions, it is of utmost importance to meet all the challenges and not a subset of them.

Motivating Example. One of the most characteristic examples of scientific data analysis that requires a system that conforms to all the identified challenges, is the study and analysis of biological structures. Structural biology is a branch of molecular biology concerned with the molecular structure of biological macromolecules such as proteins, made up of amino acids, how they acquire the structures they have, and how alterations in their structures affect their function. This subject is of great interest to biologists because macromolecules carry out most of the functions of cells, and it is only by coiling into specific structures that they are able to perform these functions. The Protein Data Bank[4] is an archive with information about the shapes of proteins, nucleic acids, and complex assemblies. Most of the datasets published there follow the Systems Biology Markup Language[5] aiming to ensure model interoperability and semantically correct information. As an example we take the human cap-dependent 48S pre-initiation complex[6] which represents 47 unique protein chains with 116774 atom count.

Access to the Complete Information. Scientist aiming to study and analyse this protein complex need to have access to the complete information in a way that will respect the initial spatial relations, without causing any alterations to connections between molecules. Systems that use aggregation or summarization techniques cannot be used for this analysis as they alter the initial connections between atoms. Techniques that exclude part of the input dataset if it does not follow pre-defined data formats cannot be used either, as protein chains are not expected to fully comply with specific data formats and atoms that deviate from them contain important information which should be available to the user. Systems that filter the input dataset based on specific characteristics cannot support the exploration of protein complexes as their analysis is mostly based on low level connections.

Combination of Multiple Datasets. In addition, scientists need to study the complete biological structures, so the system should be able to combine multiple protein chains and complexes. As an example, the human cap-dependent 48S pre-initiation protein complex has a relatively small number of atoms as it contains only 47 protein chains. Such complexes, however, are combined or expanded with additional protein chains for analysis purposes. The system should be able to incorporate any additional information and offer to the user exploration and filtering services without any limit to the size of the input dataset. Such dynamic changes in the volume and content of the input dataset is a challenge for all of the available systems. These systems are based on complex pre-processing techniques that aim to identify specific data models that conform with the input dataset or perform a semantic analysis and categorization. Due to their complexity, such techniques fail to combine more than one dataset or adapt to a large and complex one.

Multiple Filtering Criteria. Users interested in such complex datasets also have high demands regarding different and customizable filtering functions that can be used simultaneously. Popular queries during such data analysis include: “isolate specific molecules” ,

[4]https://www.rcsb.org/
[5]http://semanticsbml.org/semanticSBML/simple/index
[6]http://www.rcsb.org/structure/6FEC

"isolate one or more types of connections based on their semantic annotations" , "identify the most/least connected molecules" , "locate connections between two molecules" , "find if two or more molecules are independent to one other" and "identify specific connections in parts of the biological structure that is responsible for a specific function".

The system should offer such exploration queries though a user-friendly interface, without asking the user to write queries over the data. Depending on the way the information is processed, however, systems may not be able to offer such exploration queries. Systems that aggregate the input dataset cannot offer details for one molecule. Systems that present data based on hierarchy levels or through semantic criteria cannot present the connections between two or more molecules or isolate types of connections that are of interest.

Path Exploration. Finally, given the importance of the connections between molecules it is crucial to identify all the neighbors of a molecule or follow paths of interest. All of the available systems, allow either the exploration of the outgoing neighbors of a node or the exploration of nodes along the hierarchy levels of the data model. Therefore, the system does not allow the user to intuitively explore the information associated with a node. For datasets such as the human cap-dependent 48S pre-initiation protein complex, users are very interested in locating all the neighbors of a molecule, either incoming or outgoing, as these connections are valuable to the protein structure analysis.

Contribution. We present here an off-line pre-processing technique that enables the Efficient Representation of Very Large Linked Datasets as Graphs. Our technique has been carefully designed to alleviate the restrictions of the above-mentioned approaches on the input datasets, regarding accompanying metadata related to the model, full or partial semantic annotation, hierarchical structure, data completeness and size limitation. It also meets the challenges of scalability, consistent visualization and data exploration through different filtering functions. The proposed technique is split into three phases, designed to transform any input dataset, such as highly connected, incomplete or lacking semantic annotations, into one continuous graph on the two-dimensional space.

- Pre-processing Technique. Initially, the input dataset is split into smaller parts, the number and size of which is determined by the dataset size and connectivity degree. Next, each part of the input dataset is graphically represented as an independent sub-graph. Finally, the sub-graphs are merged into one continuous graph, using a suitable cost function that ensures small navigation paths and consistent exploration for millions of nodes. Any information omitted during the creation of the sub-graphs is re-introduced to the graph during this merging. The pre-processing result is the representation as a graph of the complete input dataset. We refer to the representation of a dataset as one continuous graph in the two-dimensional space as *graphical representation*.

  Given that no part of the pre-processing phase is based on specific data formats we can handle any dataset including incomplete datasets, datasets that are not annotated with respect to semantic categories or datasets that do not comply with the hierarchical model. Also, the modular design of our technique allows us to handle real datasets, with variable volume and connectivity degrees.
- Dedicated API. The graphical representation of the input dataset is stored, in a distributed database to ensure high performance and query optimization, and indexed to facilitate the accessibility and retrieval of the information. In order to showcase the usability of our technique we have implemented a dedicated API over the storage schema that allows the exploration of the information. The API allows the retrieval of the information using different spatial boundaries including geometrical shapes, multiple filtering criteria and keyword search.
- Experimental Analysis. We performed a thorough experimental study on our technique. We employed our technique for the representation of many real and synthetic datasets with as many as 150 million elements and an average node degree as high as 20, in order to show that we can handle large and diverse datasets without any limitations to their characteristics.

The structure of the paper is as follows: In Section 2, we present the proposed technique for the graphical representation of the input datasets. In Section 3, we present the review of the related work. Finally, in Section 4, we present the experimental evaluation of the proposed technique.

2 PROCESSING METHODOLOGY

We present here the three phases of the off-line, pre-processing technique that allow us to efficiently represent large linked dataset as one continuous graph.

The first phase of the technique ensures that we are able to handle very large datasets. For this reason, the input dataset is split in smaller parts. The number and the size of these parts are decided based on the size, number of entities and relationships, and characteristics, connectivity degree and average label length, of the input dataset.

The second phase of the technique is dedicated to the proper representation of the parts of the input dataset. Each part is transformed into an independent graph, using the Scalable Force Directed Placement algorithm (Kamada and Kawai, 1989). We chose this algorithm due to its flexibility and robustness. We carefully initialize the parameters of the algorithm based on the characteristics of the parts. Our aim is to achieve the right degree of compactness, avoid any overlapping and ensure that each sub-graph has approximately the same horizontal and vertical span.

In the third phase of the technique, the sub-graphs are merged into one continuous graph. It is important to arrange the sub-graphs in a way that the connections between the sub-graphs, as identified and stored at the first phase of the technique, are introduced here as edges between the nodes in a way that minimizes their total length. For this reason, we have implemented a heuristic algorithm, which uses a cost function based on the length of the edges, to arrange the sub-graphs.

Finally, the graphical information is translated to a spatial storage schema and made accessible through a flexible, complete and efficient API.

2.1 Phase A: Dataset Partitioning

This phase of the proposed technique is responsible for receiving as input the linked dataset, model the information with respect to the graph model and partition the graph into smaller sub-graphs. Linked datasets can be mapped to a graph $G = (\mathcal{V}, \mathcal{E})$ where $\mathcal{V}$ is a set of nodes (v) that represent the entities of the input dataset and $\mathcal{E}$ is a set of edges (e) that represent the connections between the entities.

Formally, given a graph $G = (\mathcal{V}, \mathcal{E})$ with $|\mathcal{V}| = n$, the k-way graph partitioning is defined as the partitioning of $\mathcal{V}$ into k subsets, $\mathcal{V}_1, \mathcal{V}_2, ..., \mathcal{V}_k$ where $\mathcal{V}_i \cap \mathcal{V}_j = \emptyset$ for $i \neq j$, $|\mathcal{V}_i| \approx n/k$, and $\cup_i \mathcal{V}_i = \mathcal{V}$.

The k-way graph partitioning aims to minimize the number of edges of $\mathcal{E}$, the vertices of which belong to different subsets. Given a graph $G = (\mathcal{V}, \mathcal{E})$ and a k-way graph partitioning, the edges of the graph G, the vertices of which belong to different subsets, are called *external edges*. $\mathcal{X}_{ij} \subset \mathcal{E}$ is the set of external edges between two subsets $\mathcal{V}_i$ and $\mathcal{V}_j$ where $i \neq j$ and $\mathcal{X}$ is the set of all external edges between all possible pairs of $\mathcal{V}_i \in \mathcal{V}$.

In order to ensure that all datasets, no matter their specific characteristics or volume, are partitioned properly, we chose a robust algorithm with the capability of handling datasets ranging from a few thousands to millions, and from sparse to dense. We use the k-way graph partitioning algorithm of G. Karypis and V. Kumar (Karypis and Kumar, 1998) as implemented in Metis [7], as it meets the requirements of handling any input dataset without any restrictions on its size and properties.

Example 1. *For the 48S pre-initiation protein complex, the k-way partitioning divides the dataset into nine sub-graphs, as shown in Figure 1. Given the 116774 atoms of the dataset each partition has 13.000 atoms. The number of the partitions is selected to support the second phase of the technique as presented in 2.2 and create a continuous graph with similar horizontal and vertical dimensions. Based on the small size of the input dataset here, the possible options are 4, 9 or 16 partitions. While with 4 partitions the sub-graphs have too many elements for the second phase, with 16 they have unnecessary few.*

2.2 Phase B: Graphical Representation of the Sub-graphs

This phase of our technique is dedicated to the transformation of each part of the input dataset to an independent sub-graph. The main requirements of this phase are two, both related with the spatial distribution of the nodes. To begin with, we need to achieve a uniform density of the nodes in the two- dimensional space for each sub-graph. This means that the nodes of the sub-graph should be spaced out enough not to have any overlaps between them while at the same time as close as possible in order not to have a lot of empty space. Moreover, we should have sub-graphs requiring approximately the same horizontal and vertical space. This is very important for the next phase of the proposed technique, which connects all the sub-graphs into one continuous graph by arranging them in a two-dimensional grid. Given that the dimensions of each grid cell are based on the width and height of the included sub-graph, having sub-graphs with similar sizes ensures the lack of empty spaces.

Both requirements should be achieved independently of the specific characteristics of the sub-graphs. For this reason, we choose the Scalable Force Directed Placement algorithm (Kamada and Kawai, 1989) for the graphical representation of the sub-

[7]http://glaros.dtc.umn.edu/gkhome/metis/metis/overview

graphs. The algorithm is based on a physics approach, balancing a system where nodes are considered charged particles and edges are modeled as springs. This allows for the parameterization of many attributes for the output graph including the allowed overlapping percentage, the size of the nodes and the size of the graph.

2.3 Phase C: Merging the Sub-graphs Into One Continuous Graph

In this section, the third phase of the technique that connects the sub-graphs in one continuous graph is described. Given that at we dynamically choose the number of sub-graphs based on the input dataset, we need a solution for the sub-graph arrangement that accepts as input any number of partitions and any set of external edges between them and results to an arrangement of the sub-graphs in the two-dimensional space in a way that the length of long edges connecting different sub-graphs is minimized.

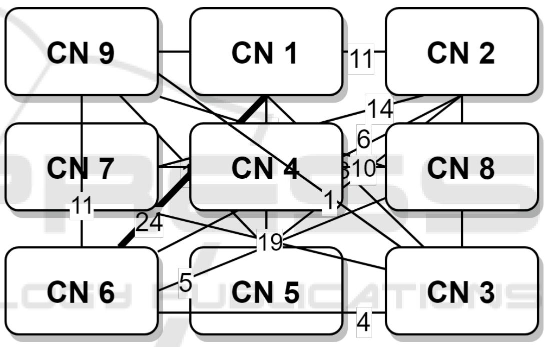
Problem Definition. Let $\mathcal{P} = \{\mathcal{P}_1, \mathcal{P}_2, ..., \mathcal{P}_k\}$ where each $\mathcal{P}_i$ for $i = 1, 2, ..., k$ corresponds to the i-th partition and includes the vertices of the $\mathcal{V}_i$ sub-graph with their coordinates and the edges between them. For each partition $\mathcal{P}_i$ a CN_i, a *Complex Node* (CN) is defined. A *Complex Node* CN_i refers to the two-dimensional area with dimensions the width and height of the $\mathcal{P}_i$ and content all the graph elements, nodes and edges, of the partition. The position of each graph element in the continuous graph is relevant to the position of the *Complex Node* that contains it to the two-dimensional space.

Problem Transformation. Let CN denote the set of all *Complex Nodes* for the partitions, with $|\mathcal{CN}| = k$ and $\mathcal{W}$ the set containing the weights between the *Complex Nodes* as defined by the number of *external edges* between them, $W(i,j) = X_{i,j}$. The process of placing each $CN_i \in \mathcal{CN}$ into the two-dimensional Cartesian integer grid by assigning grid positions to each CN_i, such that it minimizes the weights is defined as *Grid Arrangement Problem (GAP)*. The problem is proven (Oswald et al., 2012) to be NP-hard for every dimension of the grid.

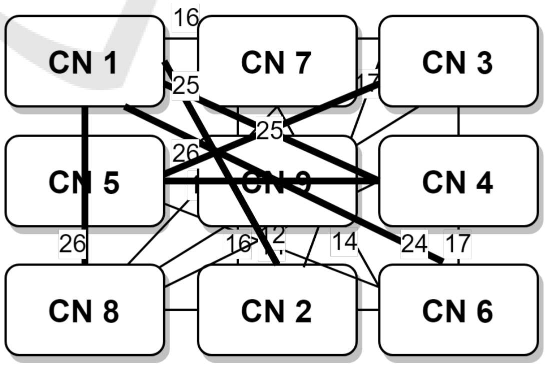
Problem Solution. We present here a greedy heuristic algorithm, as a solution for the *Grid Arrangement Problem* that can be applies with large number of nodes. The algorithm uses a weight-cost function to calculate the cost of adding a CN to a specific position given a grid arrangement. The algorithm, incrementally creates the grid arrangement by selecting, in each iteration, the CN which is going to be to placed in the grid. The CN, with the highest cost as provided by the weight-cost function, is selected on each iteration. The weight-cost function is calculating the sum of the weights between each examined CN to the ones already placed on the grid.

Example 2. *We present the weights between the CNs, of the human cap-dependent 48S pre-initiation complex, in Table 1. To simplify the example the numbers provided in the table have been scaled down, keeping the initial ratio. First, we merge the sub-graphs into one continuous graph, by following the steps of the proposed algorithm. We present the steps followed as well as the intermediate results of the cost function in 2. Then, we merge the sub-graphs into one continuous graph in a random way. The results of the two placements is presented in Figure 1. There is a 40% decrease to the overall weight cost.*

The merged information is stored in a distributed, scalable Accumulo[8] key/value datastore where the GeoMesa[9] XZ-ordering index is used for the spatial information of the graph.



(a) Placement based on the proposed algorithm



(b) Random placement

Figure 1: CN Placement in the Two-Dimensional Cartesian Integer Grid.

[8]https://accumulo.apache.org/

[9]https://www.geomesa.org/documentation/current/index.html

Table 1: Number of External Edges between the Nine CNs.

	CN 1	**CN 2**	**CN 3**	**CN 4**	**CN 5**	**CN 6**	**CN 7**	**CN 8**	**CN 9**
CN 1	0	25	16	27	3	24	1	26	6
CN 2	25	0	17	24	4	6	14	25	11
CN 3	16	17	0	10	25	17	19	4	1
CN 4	27	24	10	0	26	18	13	12	7
CN 5	3	4	25	26	0	14	27	21	11
CN 6	24	6	17	18	14	0	14	5	11
CN 7	1	14	19	13	27	14	0	10	16
CN 8	26	25	4	12	21	5	10	0	9
CN 9	6	11	1	7	11	11	16	9	0

Table 2: Steps of Executing the Proposed Algorithm for the Nine CNs.

Step 1 CN 4 is set at the center of the grid
Step 2 CNs are ranked based on the weight [1,5,2,6,7,8,3,9]
Step 3 CN 1 is placed next in the grid
Step 4 CNs are ranked based on the weight [2,6,8,5,3,7,9]
Step 5 CN 2 is placed next in the grid
Step 6 CNs are ranked based on the weight [8,6,3,5,7,9]
Step 7 CN 8 is placed next in the grid
Step 8 CNs are ranked based on the weight [3,6,5,7,9]
Step 9 CN 3 is placed next in the grid
Step 10 CNs are ranked based on the weight [5,6,7,9]
Step 11 CN 5 is placed next in the grid
Step 12 CNs are ranked based on the weight [6,7,9]
Step 13 CN 6 is placed next in the grid
Step 14 CNs are ranked based on the weight [7,9]
Step 15 CN 7 is placed next in the grid
Step 16 CN 9 is placed next in the grid

2.4 Use Cases

In order to provide access to the graph of the input dataset in an efficient and user-friendly way, we have implemented a dedicated API that allows the retrieval of the information in different ways, including spatial and filtering queries and keyword search. We have implemented a standalone Tomcat application, written using Java servlets,that receives user requests along with multiple parameters and returns the result as an XML file, that follows the GraphML format and includes the proper geometry parameters that specify the position of the nodes in the two-dimensional space. The API is designed to receive any Common Query Language function, including all the spatial functions and geometries. We are going to showcase the usability of the API through a series of use cases as identified in the presented motivating example.

Example 3. *Keyword Search. The initial exploration of the dataset begins when the user wants to locate information of interest. The intuitive way for this is to use a keyword and search among the entities of the dataset. For a protein complex the user may search the identifier of an atom or a group of atoms. The API will return a list containing all the entities containing the given keyword along with their spatial information.*

Example 4. *Spatial Queries. After locating an entity of interest, the user can use its spatial information and query the API over the two-dimensional space, using any Common Query Language spatial function and geometry. As an example, a user interested in identifying specific connections in parts of the biological structure, responsible for a specific function, can perform spatial queries and retrieve this information.*

Example 5. *Filtering based on Connection Types. The API enables the retrieval of the information using one or multiple filtering criteria at the same time. The user can easily select to isolate one or more types of connections between atoms based on their semantic annotations, and can combine this filtering with a spatial query for a specific area of the graph.*

Example 6. *Path Exploration. After locating an entity that is of interest, the user is able to retrieve all the paths of the graph that include this node, up to a customisable length. In contrast to most approaches in which a path can be traversed only with respect to the edge direction, in our API when a node is selected, all neighbors, either incoming or outgoing are retrieved.*

3 RELATED WORK

In this section we describe with further details related work. To begin with, systems that aim to overcome the restriction of the size limitation based on the extraction of the included information and its representation through generic visualization options will be presented.

Facet Graphs (Heim et al., 2010a) allows humans to access information contained in the Semantic Web according to its semantics and thus to leverage the specific characteristic of this Web. To avoid the ambiguity of natural language queries, users only select already defined attributes organized in facets to build their search queries. The facets are represented as nodes in a graph visualization and can be interactively added and removed by the users in order to produce individual search interfaces. This provides the possibility to generate interfaces in arbitrary complexities and access arbitrary domains.

SemLens (Heim et al., 2011) is a visual tool that arranges objects on scatter plots and them using user-defined semantic lenses, offering visual discovery of correlations and patterns in data. Haystack (Huynh et al., 2002) is a platform for creating, organizing and visualizing information using RDF. It is based on the idea that aggregating various types of users' data together in a homogeneous representation, agents can make more informed deductions in automating tasks for users. *LODeX* (Benedetti et al., 2014) is a tool that generates a representative summary of a linked data source. The tool takes as input a SPARQL endpoint and generates a visual summary of the linked data source, accompanied by statistical and structural information of the source. *Polaris* (Stolte and Hanrahan, 2000) is a visual query language for describing table-based graphical presentations of data which compiles into both the queries and the visualization,enabling users to integrate analysis and visualization.

A large number of systems visualize linked datasets adopting a graph-based approach (Mazumdar et al., 2015). Most systems, limit the displayed information by enforcing a path-based navigation of the data to the user. Such examples include the *RelFinder* (Heim et al., 2010b) which is a web-based tool that offers interactive discovery and visualization of relationships between selected linked data resources. Similary, *Fenfire* (Hastrup et al., 2008) and *Lodlive* (Camarda et al., 2012) are exploratory tools that allow users to browse linked data using interactive graph navigation. Starting from a given URI, the user can explore linked data by following the links. *Zoom-RDF* (Zhang et al., 2010) employs a space-optimized visualization algorithm in order to display additional resources with respect to the user navigation choises while *Trisolda* (Dokulil and Katreniaková, 2009) proposes a clustered RDF graph visualization in which input information is merged to graph nodes. *FlexViz* (Falconer et al., 2010) offers node and edge specific filters that are based on search and navigation criteria aiming to reduce the amount of handled data and provide to a meaningful subset to the user.

The *Tabulator* (Berners-Lee et al., 2006) project is an attempt to demonstrate and utilize the power of linked RDF data with a user-friendly Semantic Web browser that is able to recognize and follow RDF links to other RDF resources based on the user's exploration and analysis. It is a generic browser for linked data on the web without the expectation of providing as intuitive an interface as a domain-specific application but aiming to provide the sort of common user interface tools used in such applications, and to allow domain-specific functionality to be loaded transparently from the web and be instantly applicable to any new domain of information. *Explorator* (De Araujo and Schwabe, 2009) is an open-source exploratory search tool for RDF graphs, implemented in a direct manipulation interface metaphor. It implements a custom model of operations, and also provides a Query-by-example interface. Additionally, it provides faceted navigation over any set obtained during the operations in the model that are exposed in the interface. It can be used to explore both a SPARQL endpoint as well as an RDF graph in the same way as "traditional" RDF browsers.

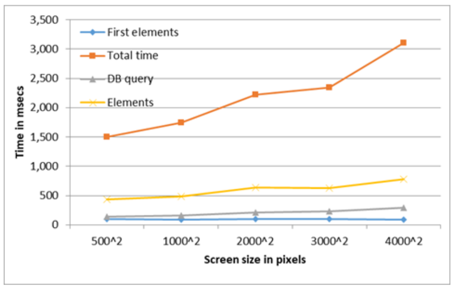
Another approach to the problem of linked data visualization is the visualization of the information based on hierarchical models. GrouseFlocks (Archambault et al., 2007) works only on datasets structured over well-defined hierarchies. It requires complete data and can handle up to 220K elements when the hierarchy is predefined. Tulip (Auber, 2004) develops a technique to solve the problem of presenting to the users the data in only one predetermined way, regardless of the features of the input dataset. This tool stores the input data once and extracts the information with different techniques providing the user with multiple views/clusters over the data. GMine (Jr. et al., 2006) uses the state-of-the-art partitioning algorithm METIS (Karypis and Kumar, 1998) to split the input dataset in reasonable partitions. Each partition is visualized as one node, resulting in the loss of the information included in each partition.

Table 3: Synthetic Datasets.

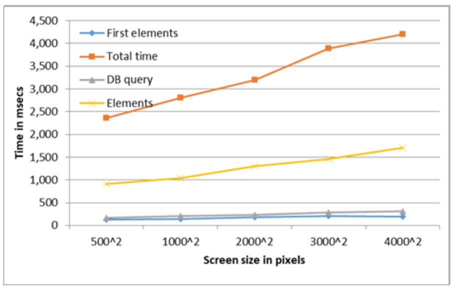
Dataset	#Edges	#Nodes	Degree
1M D5	5.1M	1M	5.09
10M D5	50.2M	10M	5.02
10M D10	103M	10M	10.3
10M D15	157M	10M	15.7
50M D5	259M	50M	5.18

4 EXPERIMENTAL ANALYSIS

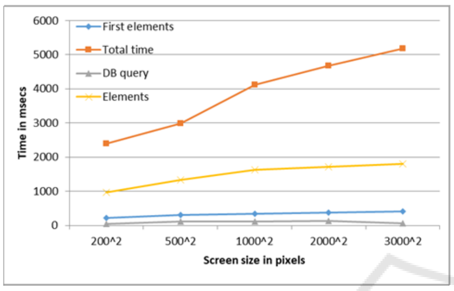
In order to evaluate the proposed technique and carry out an experimental analysis on the efficiency of the information retrieval through the API we developed a web tool. We used the tool to spatially query the API and evaluate the response time. The experiments were conducted using a laptop with an Intel(R) Core(TM)



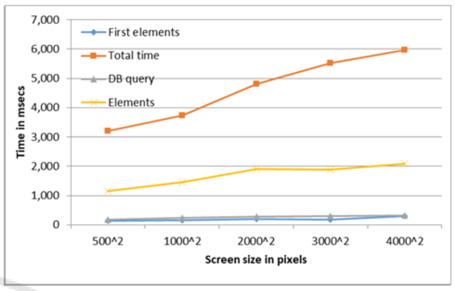
(a) 1M nodes, degree 5



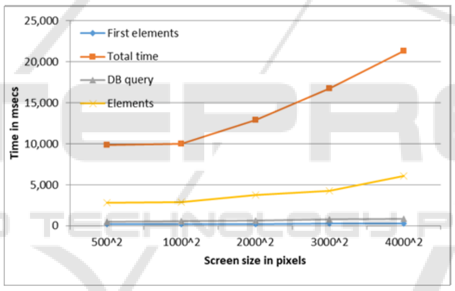
(b) 10M nodes, degree 5



(c) 10M nodes, degree 10

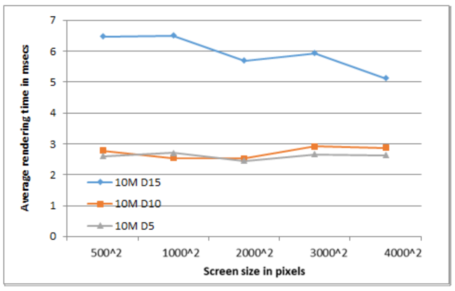


(d) 10M nodes, degree 15

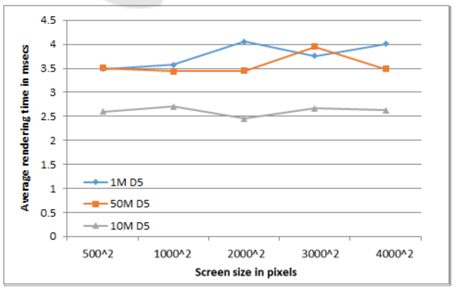


(e) 50M nodes, degree 5

Figure 2: Response Time for Synthetic Datasets.



(a) 10M nodes, all degrees



(b) degree 5, synthetic datasets

Figure 3: Comparison of Average Response Time per Graph Element.

i7-4500U CPU at 1.80GHz, 4GB RAM memory over a 12Mbps network connection.

Datasets. In order to test our system with many diverse datasets with a wide range of characteristics we used synthetic datasets. The synthetic datasets, presented in Table 3, were created to comply with specific requirements for number of nodes and node degree to showcase the scalability of the technique to the size and density as well as the adaptation to any dataset regardless of its characteristics.

Web Tool Over the Dedicated API. We have implemented a basic web tool for the experimental analysis of the presented technique. The web tool is based on the client-server architecture. The server side of the system is the implementation of the pre-processing technique as described above, where the input dataset is transformed into one continuous graph, stored, indexed and made available through the API. The client side consists of simple user interface that directly utilize the *API*, and depicts the user navigation actions, such as panning and scrolling, into spatial queries with respect to the two-dimensional space before sending the request to the server.

4.1 API Efficiency

Metrics. We evaluate the efficiency of the technique based on the time needed to retrieve the nodes from the API and present them at the web tool after a spatial query, measured in msecs. The time presented is the figures is the time needed for the query execution, the rendering time for the first elements to appear on the screen and the total response time of the system when all the elements are rendered.

Methodology. We render randomly selected parts of the datasets using spatial queries with rectangular bounding boxes ranging from 500*x*500 px to 4000*x*4000 px. As the size of the area increases the spatial queries on the dataset match larger number of graph elements, allowing us to examine the response time over a variation of total rendered graph elements. The experiments present the average results of a series of one hundred repetitions of the graph rendering for each rectangle size.

Results. In Figure 2 we present the results for the synthetic datasets. In all cases the total time is closely connected to the number of rendered elements. The system renders more than 500 graph elements in less than two seconds and up to 5200 graph elements without causing lagging, performance issues or hindering the user experience, as shown in 2 (e). The fact that so many graph elements can be rendered smoothly, is of high importance, as similar systems have limits to the number of presented elements. In Figure 3 we examine the average time needed for the rendering of one graph element. In Figure 3 (a) we show that the average rendering time is not dependent on the density of the input dataset, while in Figure 3 (b) we show that it is not dependent on the size of the input dataset. These experiments prove that our technique scales efficiently for any size or density of the input dataset and supports the exploration of the information for datasets with millions of nodes without any performance issues.

5 CONCLUSIONS

In this paper, we present a novel technique for the preprocessing very large datasets with hundreds of millions of elements and their representation as graphs in the two-dimensional space. Our technique has been designed in a way to meet all the identified challenges regarding exploration needs and user experience. The presented technique process large real datasets with millions of elements as well as dense graphs with high node degree. The technique does not impose any restrictions on the dataset while the information is offered through a dedicated API that supports many functionalities, including keyword search, path exploration and neighbor information.

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