Multi-resistant Bacterial Infection Surveillance using a Graph Database with Spatio-temporal Information

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Abstract: Some of epidemiologists' efforts in dealing with multi-resistant bacterial infections acquired in healthcare settings focus on tracing patient's activities, carrying out a contact analysis, and identifying the main risk factors that lead the appearance of these infections. Most contact analysis studies assume information is stored in conventional relational databases. To date, little attention has been paid to other storage paradigms. This paper explores the potential of graph databases to establish the complex relations required to compute contact analysis. We discuss the advances in modelling of the temporal and the spatial information of the Electronic Health Record that has to be introduced in the graph database. In this position paper we propose three points for discussion: advances in formal modelling, specific algorithms for graph analysis, and visualisation tools.

1 INTRODUCTION

We are living in a global pandemic situation this year. We are facing a context where capacity restrictions in any establishment are imperative, especially in hospitals and health care centers, since they may became important sources of contagion. However, the spread of diseases among inpatients is not new, and the appearance of viral or bacterial infection outbreaks is usual in hospitals. These are the nosocomial infections that have become a major health problem today. They are a widespread scourge, which appears in both developed and in-development countries. And its clinical and economic impact are increasingly significant due to increasingly crowded conditions in hospitals, the emergence of new organisms, and increasing bacterial resistance to antibiotics (World Health Organization, 2003).

Infections acquired or associated to healthcare are among the leading causes of death and increased morbidity in hospitalized patients (de Leon, 1991). These

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infections can be caused by a pathogen contracted from another patient in the hospital or by the patient's own flora; and transmitted both through the air, by food or by contact with any inanimate object (World Health Organization, 2003). Given the high level of importance of these infections, together with the wide range of causes they encompass, their detection and prevention has become one of the current challenges in epidemiology (Edwarson and Cairns, 2019).

One important bottleneck of the data analysis of contacts is to extract a clear trace of the activity of patients from the Electronic Health Records (EHRs) stored in the Health Information System (HIS) databases. In general, commercial HIS are supported by relational databases (RDBs) making difficult to manage the complex relations between the different dimensions of study: clinical data and spatialtemporal information.

Specifically, the objective of this preliminary research is to evaluate the use of spatial and temporal data modeling with the language and tools provided by Neo4j¹, a graph-oriented database to carry out a contact analysis among hospitalized patients. This analysis is situated in the context of the appearance of bacterial outbreaks among hospitalized patients, and

¹Neo4j: https://neo4j.com/

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its purpose is to provide support in the detection of the focus of infection through the area of influence of the outbreak. We also compare the results with those of a previous work (Pujante et al., 2020) using the OrientDB database, showing differences between languages and modeling.

2 BACKGROUND

Non-relational databases, among which the graphoriented databases, GDB, arise in response to the limitations that relational databases present to face the new challenges and trends that are emerging in the current world of computing and data management. The GBDs specify their scope of action in scenarios in which it is necessary to work with highly connected data sets, being designed for optimal storage and navigation through the relationships established between them. Thus, in this type of databases, the data are stored as the nodes of a graph, and their relationships as the edges, allowing to apply the theory of graphs to traverse the data stored in the database (Angles and Gutierrez, 2008).

Neo4j is a native graph-oriented database that uses a model of labeled and property graphs. Labeled graphs consist of graphs in which labels can be assigned (generally an integer, although they can also be of another type of data, such as text strings) both to their nodes and to their edges to distinguish them from the rest. As for property graphs, they are weighted graphs (their edges have some kind of numerical evaluation) in which properties can be defined in keyvalue format on both nodes and edges. Neo4j uses its own descriptive language, Cypher, with which the queries are made by describing the nodes, edges and properties to be obtained, having a very different structure from that of SQL.

Regarding the study of infection diseases, researchers of (Lose et al., 2019) focus on Tuberculosis disease research from the biology perspective, representing biological entities in a labelled property graph using Neo4J. From the theoretical point of view, several models recently described the spread of disease (Huang et al., 2016). However, little attention is paid on the use of GDBs for infectious diseases from an epidemiological perspective. There are several studies that explore the advantages that graph modeling can offer for tracing the spread of epidemics. Examples of them are (Grande et al., 2015), where graphs have been used to represent the spread of the hepatitis C virus, distinguishing different types of person nodes according to certain characteristics, such as sex and age; or (Chen et al., 2011), where the authors used social network analysis with a contact network. In (Y. Kai and Jun, 2018) weighted graphs has been theoretically studied to simulate the spread of an epidemic. In (M. Boman and Stenhem, 2006), threedimensional graphs are used to represent the analysis of contacts between individuals in specific geographic areas in which an outbreak has been detected. The work of (Chen et al., 2007) used geographical information to analyse outbreaks for SARS diseases. As far as we know, there is not research on the literature of the use of GDBs for analysing infection spread in hospitals considering spatial and temporal information.

3 MODELING CLINICAL EVENTS AND SPATIO-TEMPORAL RELATIONS

With this modeling we can represent a common case like the following:

A patient arrives at the emergency room with severe stomach pain and is treated by the digestive medicine service, specifically by its emergency unit, and remains in a box for 4 hours. She then goes to the plant where another unit of the same service is responsible for her care for a day. The next day she underwent an operation, which entailed a change of bed for the operating room, although she was still treated by the same unit in the same floor. At the end of the surgery, she returns to the same room and bed where she remains until he is discharged after three days.

It is necessary to model the clinical events, the spatial configuration of the hospital, and the temporal relations between the events and the locations of the patient during the care trajectory. This case is modeled as a graph in Figure 1.

Regarding the locations, it is necessary to establish a physical organization of the hospital that is specific enough to track the care trajectory, but also general enough to adapt to the different architectures that hospital may present. It is also required to have a flexible structure that allows the grouping of *Areas* and *Zones* of the same or different floor. This concept is *LogicalZone*, which can also host other logical zones under the sole condition that no cycles occur. It would also be necessary to create another organization of the space related to the functional distribution of the hospital, with which the units and services that work in it are represented. Thus, spatial modeling can be subdivided into three distributions: physical, logical and functional, which can be seen in a UML domain



Figure 1: Graph for the case shown.

model in Figure 2.

For temporal modeling and clinical events, which can be seen in Figure 3, we represent in a generic way all the events of the patient's medical history, which have a temporal annotation. These events may represent, for example, infections or diagnostic tests. We distinguish events with duration in time (interval) from those without duration (points). The patient stays are special interval events since they are associated with a spatial location.

4 EPIDEMIOLOGY QUERIES

In order to advance from our previous work, we include two new queries of interest for epidemiologists:

- Query (Q1): Given a set of patients, determine what events or locations they have had in common during a time interval.
- Query (Q2): Given a set of patients, determine what other patients have had in common over a period of time.

4.1 Q1: Events or Locations in Common for a Set of Patients

In this query, given a set of patients, we retrieve a subgraph formed by all the spatial elements or events that they have had in common. This query is constrained to a given period of time, that is considered a parameter of the query. The meaning of *in common* should be as broad as possible, since the final objective is that with the resulting graph to be able to analyze which are the facts with the greatest coincidences between the given patients, and thus be able to detect a possible source of infection. Starting from the set of patients given, it will be verified which admissions and other events they have registered in the same location (device, room, corridor, floor, etc.), in which units or department they have been, or if some of these patients the same bacteria have been detected in a microbiology test. To design and solve this query, the admissions, microbiology tests and other events have to be considered. The steps followed in query Q1 are:

- 1. The given *Patients* nodes are retrieved and, from these, we extract all the *Events* associated in the given *Interval* period of time (a parameter) and that are not of the *Admission* or *MicroTest* subclass.
- 2. For each pair of *Events* belonging to different *Pa-tients*, it is checked whether both have been carried out in *Locations* on the same *Floor*.
- 3. If they share the *Location*, the edges that connect each *Patient* nodes with their *Event* nodes, and the edges for the *Locations* in which both *Events* took place, are returned as a result.

Figure 4 depicts part of the Cypher code for the query Q1. In Figure 5 we show the resulting subgraph using as parameters *idPatient*: [1, 2, 3, 11, 22], *dateStart*: "2019-03-13T00:00:00", *dateEnd*: "2019-03-23T23:59:59".

4.2 Q2: Contact Analysis

The query Q2 tries to establish the relation among a set of patients. Given an initial set and all those pa-



Figure 2: UML domain for spatial model: physical, logical and functional elements.



Figure 3: UML domain for temporal model: clinical events and temporal relations.



Figure 4: Code for the query Q1.

tients who within a given time interval have had a spatial relationship with the former will be retrieved, regardless of whether or not they have been diagnosed with a bacterial infection. Instead of helping to find the origin of the outbreak of a certain bacterial infection, the result is a a group of patients among whom the probability of suffering the same infection is high due to their proximity to others who already suffer from it.

The following are the step for the resolution of the query Q1:

1. Given a set of patients identifiers, their corresponding *Patient* nodes are retrieved.

- For each Patient, the Admissions and other Events found in the given Interval of time are retrieved.
- 3. From these *Admissions* and other *Events*, the *Locations* (Devices or Rooms) in which they have been carried out are retrieved.
 - 4. For each *Location*, other *Patients* than those given as an input parameter that have an *Admission* or another type of *Event* that has been carried out in the *Device* or *Room* located on the same *Floor* as the given one.
 - 5. The *Patients* identified in the step 4 will be the outcome of the query.

Note in Figure 6 that query Q2 does not return a complete subgraph, but a set of patients that should be analyzed.

5 DICUSSION

Graph-oriented databases allow the storage of highly connected data such as a patient's medical history. In the problem of surveillance of multidrug-resistant infections, decision support for an epidemiologist can be carried out with a 3-part modeling: clinical events, spatial locations (physical, logical and functional),



Figure 5: Subgraph retrieved for the query Q1.





and temporal relationships between the above. We have focused on the analysis of infections within a hospital, not in the geography or with general population, for which well-established models are known to the scientific community.

Our preliminary evaluation of Neo4j for this purpose has been positive and it presents advantages with respect to OrientDB that we have presented in a previous work. It has been possible to develop all the proposed queries, in a simpler and more readable way than with OrientDB. Furthermore, the more flexible and descriptive structure of the queries has allowed us to be organized the in a way that makes their execution more efficient. There are facilities in functionality such as queries with grouping (OrientDB does not have any grouping mechanism, neither explicit nor implicit) or the passing of parameters. Cypher is a much more powerful and expressive language than OrientDB SQL. We consider its expressiveness one of its main strengths, since a query can be implemented in innumerable ways.

A further efficiency and scalability evaluation of the queries with a simulated dataset or with a real dataset is necessary. Other queries are also possible (e.g. root case search or outbreak detection), but in this preliminary work we have only shown two of the needs of epidemiologists.

As points of discussion and future work after these preliminary results, we propose the following:

- The modeling of graphs with properties and labels is very flexible, but it would be necessary to advance in representing fuzzy relations or probabilities that adapt to the problem of epidemiology. Can we make the relationships more formal and introduce integrity constraints such as those provided by temporal and spatial logics or by spatio-temporal reasoning methods in general? For example, what would happen if only a percentage of patients met a contact criterion in consultation Q1?

- The scalability of GOBs in information storage and retrieval is known, but the resolution of some of the issues in epidemiology requires a more complex graph analysis that is not normally implemented in these GOBs. For example, it should be noted that the analysis of the resulting subgraph to obtain clusters of nodes highly connected to each other does not fall within the objectives of this work. Is it worth abandoning GOBs to go to a strictly graph solution where it is easier to program algorithms? How easy is it to implement algorithms in these databases?

- Graph visualization tools are necessary to help the clinical expert make a decision. The graphs shown in this preliminary work are useful to the data analyst, but the clinician will have serious difficulties in querying and interpreting the resulting graphs. What visualization functionalities are necessary to turn them into a tool for your daily work in decision making?

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REFERENCES

- Angles, R. and Gutierrez, C. (2008). Survey of graph database models. ACM Comput. Surv., 40(1).
- Chen, Y.-D., Chen, H., and King, C.-C. (2011). Social Network Analysis for Contact Tracing, pages 339–358. Springer US.
- Chen, Y.-D., Tseng, C., King, C.-C., Wu, T.-S. J., and Chen, H. (2007). Incorporating geographical contacts into social network analysis for contact tracing in epidemiology: A study on taiwan sars data. In Zeng, D., Gotham, I., Komatsu, K., Lynch, C., Thurmond, M., Madigan, D., Lober, B., Kvach, J., and Chen, H., editors, *Intelligence and Security Informatics: Biosurveillance*, pages 23–36, Berlin, Heidelberg. Springer Berlin Heidelberg.
- de Leon, S. P. (1991). The needs of developing countries. Journal of Hospital Infection, (18):376–381.
- Edwarson, S. and Cairns, C. (2019). Nosocomial infections in the icu. *Anaesthesia and intensive care medicine*, 20(1):14–18.
- Grande, K. M., Stanley, M., Redo, C., Wergin, A., Guilfoyle, S., and Gasiorowicz, M. (2015). Social network diagramming as an applied tool for public health: Lessons learned from an hcv cluster. *American journal of public health*, 105(8):1611–1616.
- Huang, Y., Ding, L., and Feng, Y. (2016). A novel epidemic spreading model with decreasing infection rate based on infection times. *Physica A: Statistical Mechanics* and its Applications, 444:1041 – 1048.
- Lose, T., van Heusden, P., and Christoffels, A. (2019). Combat-tb-neodb: fostering tuberculosis research through integrative analysis using graph database technologies. *Bioinformatics (Oxford, England)*.
- M. Boman, A. Ghaffar, F. L. and Stenhem, M. (2006). Social network visualization as a contact tracing tool. In *Proceedings of WS on Agent Technology for Disaster Management, AAMAS'06*, pages 131–133.
- Pujante, L., Campos, M., Juarez, J. M., Canovas-Segura, B., and Morales, A. (2020). Graph databases for contact analysis in infections using spatial temporal models. In *International Work-Conference on Bioinformatics* and Biomedical Engineering, pages 98–107.
- World Health Organization (2003). Prevention of healthcare associated infections: practice guide, 2nd ed.
- Y. Kai, W. Lei, G. W. and Jun, H. (2018). A transmissionlimit inspired immunization strategy for weighted network epidemiology. *International Journal of Modern Physics B*, 32(23):1850251.