



Dissertation Project

A Comparison of NoSQL and Indexing Solutions for Big Data

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Declaration

I, Callum George William Guthrie confirm that this work submitted for assessment is my own and is expressed in my own words. Any uses made within it of the works of other authors in any form (e.g., ideas, equations, figures, text, tables, programs) are properly acknowledged at any point of their use. A list of the references employed is included.

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Abstract

The era of Big Data is upon us bringing with it a range of new challenges, and encouraging the formulation of new approaches for cleaning, processing and using these enormous amounts of data. These new methods have led to the development of a range of technologies designed to meet the needs of Big Data.

This project focuses on a subset of the new technologies, in particular those products designed to deliver high performance querying of large data sets. It shall compare leading NOSQL solutions (e.g., MongoDB [1], and Neo4j [2]) against modern search and analytics engines (e.g., Elasticsearch [3], and SOLR [4]). The overall goal is to compare and contrast the functionally, performance and analytical capabilities of the different solutions. With the ultimate aim of gaining an understanding of, and insight into, these technologies and their application to Big Data.

The student will produce several versions of a prototype application; with each version employing a different technology (or approach). This work will be undertaken using a real world dataset from the biological environment.

[1] <http://www.mongodb.org/about/introduction/>

[2] <http://www.neo4j.org/>

[3] <http://www.elasticsearch.org/webinars/introduction-elk-stack/>

[4] <http://lucene.apache.org/solr/>

Contents

Declaration	i
Abstract	ii
Contents	1
1 Dataset Origins	2
1.1 EMAP	2
1.1.1 Data	3
1.1.2 Purpose	3
1.2 EMAPA	3
1.2.1 Data	3
1.2.2 Purpose	3
2 Data Sources	4
2.1 EMA Database	4
2.2 OBO	4
2.3 OWL	4

Chapter 1

Dataset Origins

The dataset used in the prototype applications is a real world dataset taken from the biological environment. The data is constructed by an ontology derived from the combined research projects undertaken on the e-Mouse Atlas Project (EMAP) by Dr Duncan Davidson and Professor Richard Baldock.

The name EMAP carries a certain amount of ambiguity as it is the name of the project that developed the anatomy, and is also the name of the anatomy itself. Therefore with the motivation of clarity, I will refer to the project that developed the anatomy as e-Mouse Atlas (EMA) and the name of the anatomy as EMAP. Inspired by the findings of Theiler (1989) and Kaufman (1992), EMA uses embryological mouse models to provide a detailed map of mouse



development. The EMAP has a developed collection of three dimensional computer models of mouse embryos at the consecutive stages of growth generation with anatomical domains joined by an ontology of anatomical names. The main deliverable of the EMA resource is to provide a comprehensive visualisation of the postimplantation of mouse development and to induct an investigation of the gene expression in the postimplantation mouse embryo.

The EMA ontology has several different branches of deliverables, each providing an alternative aspect of the evolution of a mouse embryo. The branches which will be utilised for this research project are the timed stage specific structures which are EMAP and the aggregated non stage specific e-mouse Atlas Project Abstract (EMAPA) which are respectively discussed below. The EMA dataset's were chosen as the source of data for this research as it is a freely available, rich and substantial data source.

1.1 EMAP

The devised EMAP ontology was originally developed to deliver a structured and controlled vocabulary of stage-specific anatomical structures for the developing laboratory mouse. As the

EMA research has progressed, the ontology has followed suit, continually under development and the current ontology is in scope for a forthcoming release.

1.1.1 Data**1.1.2 Purpose****1.2 EMAPA****1.2.1 Data****1.2.2 Purpose**

Chapter 2

Data Sources

2.1 EMA Database

2.2 OBO

2.3 OWL

Bibliography

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- [3] Stuart Russell and Peter Norvig. Artificial intelligence: a modern approach. 1995.