

Facilitating and Augmenting Collaboration in the Biomedical Domain

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ABSTRACT

This paper reports on a Web 2.0 tool that aims to facilitate and augment collaboration and decision making in data-intensive and cognitively-complex biomedical settings. The proposed tool exploits prominent high-performance computing paradigms and large data processing technologies to meaningfully search, analyze and aggregate data existing in diverse, extremely large and rapidly evolving sources. It can be viewed as an innovative workbench incorporating and orchestrating a set of interoperable services that reduce the data-intensiveness and complexity overload at critical decision points to a manageable level, thus permitting stakeholders to be more productive and concentrate on creative activities. Through a particular collaboration scenario, we explore various possibilities and challenges of managing biomedical collaboration with the use of the proposed tool. Much attention is given at the increase of volume, rate of production and complexity of the associated data types.

Keywords: Collaboration, Data Integration, Decision Making, Gene-Expression Data, Gene Ontology, Sense Making, Systems Biology

INTRODUCTION

The field of biomedical research has recently seen a vast growth in publicly available biomedical resources. An enormous amount of content already exists in the digital universe (i.e.,

information that is created, captured, or replicated in digital form), which is characterized by high rates of new information that is being distributed and demands attention. This enables biomedical researchers to have instant access to a great wealth of resources that are critical for supporting their research. As the amount of available resources increases and becomes more specialized, biomedical researchers form

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teams and seek collaboration with their peers to address complex research questions. Within this context, biomedical research has become increasingly interdisciplinary and collaborative in nature (Lee, 2007; Hara, Solomon, Kim, & Sonnenwald, 2003; Schur et al., 1998).

In any case, this collaboration is not without troubles: challenges arise from various problems such as how to store, access, analyze and integrate multiple types of data; or, how to work with multiple databases simultaneously; or even, how to make data accessible and usable to life sciences researchers (Sullivan, Gabbard, Shukla, & Sobral, 2010). At the same time, tools facilitating sense- and decision-making by appropriately capturing the collective intelligence that emerges during such collaboration are lacking. Biomedical researchers need such tools to efficiently and effectively collaborate and make decisions by appropriately assembling and analyzing enormous volumes of complex multi-faceted data residing in different sources. Supporting team collaboration under such circumstances is still considered as a challenging task (Finholt, 2003).

In this paper, we present a Web based tool to support and enhance collaboration of interdisciplinary teams in the field of biomedical research, with the aim of facilitating sense and decision making in data-intensive situations. As an example, the tool aims to support communities of clinical researchers and bioscientists, during their scientific collaboration allowing them to easily examine, reuse and interpret heterogeneous clinico-genomic data and information sources, as well as to reach decisions for the production of new insightful conclusions (or the formation of reliable biomedical knowledge), without having to worry about the method of locating and assembling these huge quantities of data (such as genetic, transcriptomic, proteomic or clinical data, gene ontology, etc.). The tool is able to support the entire life cycle of biomedical collaboration. To achieve this flexibility, it adopts an incremental formalization approach, whereby a set of loosely coupled resources are gradually transformed into argumentative discourse out

of which decisions emerge. The overall idea of the proposed tool is to function as a collective electronic logbook (serving all members of the collaborating group), which captures important discussions about the evaluation and assessment of related resources, the design rationale of the associated experiments and the justification of the decisions made.

The proposed tool is being developed in the context of an FP7 EU project, namely. Dicode (<http://dicode-project.eu/>), which aims at facilitating and augmenting collaboration and decision making in diverse data-intensive and cognitively-complex settings Dicode follows a hybrid approach, in that it will exploit and build on prominent high-performance computing paradigms and large data processing technologies - such as cloud computing, MapReduce (<http://labs.google.com/papers/mapreduce.html>), Hadoop (<http://hadoop.apache.org>), and Mahout (<http://lucene.apache.org/mahout>)—to meaningfully search, analyze and aggregate data existing in diverse, extremely large, and rapidly evolving sources. The services to be developed in the context of Dicode will be tested in real problems from three application areas; one of them concerns clinico-genomic research.

The remainder of this paper is organized as follows. First, we provide a brief overview of how collaboration is supported in the biomedical domain and discuss the shortcomings of existing tools. Next, we present a typical collaboration scenario in the domain under consideration, which motivates our approach. We then outline contemporary problems and requirements of collaboration tools in the biomedical domain and discuss how these can be addressed through the Dicode Workbench. Finally, we further exploit the abovementioned scenario to illustrate the functionalities of the Dicode Workbench. The last section concludes the paper.

SUPPORTING COLLABORATION IN THE BIOMEDICAL DOMAIN

In the domain of biomedical research, the notion of collaboration mainly concerns the

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