



Evaluating user interaction with a web-based group decision support system: A comparison between two clustering methods



Martin Swobodzinski^{a,*}, Piotr Jankowski^{b,c}

^a Department of Geography, Portland State University, Portland, OR, United States

^b Department of Geography, San Diego State University, San Diego, CA, United States

^c Institute of Geoeology and Geoinformation, Adam Mickiewicz University, Poznań, Poland

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ABSTRACT

Task-Technology Fit theory and the Technology Acceptance Model identify system utilization as an important indicator for the performance of complex software systems. Yet, empirical evaluations of user interaction with group decision support systems are scarce and often methodologically underdeveloped. For this study we employed an exploratory evaluation of user interaction in the context of web-based group decision support systems. Specifically, we used information-rich server logs captured through a web-based platform for participatory transportation planning to identify groups of users with similar use patterns. The groups were derived through multiple sequence alignment and hierarchical cluster analysis based on varying user activity measures. Subsequently, we assessed the reliability of the classifications obtained from the two clustering methods. Our results indicate limited reliability of classifications of activity sequences through multiple sequence alignment analysis and robust groupings from hierarchical cluster analysis for user activity initiations and durations. The presented work contributes a novel methodological framework for the evaluation of complex software systems that extends beyond the common approach of soliciting user satisfaction.

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1. Introduction

Ideally, the evaluation of complex group decision support systems (GDSS) would be part of an iterative process that aims at improving such systems with close involvement of the users [1]. User-centered evaluations of GDSS, however, require considerable resources to be committed in order to provide insight related to the suitability of GDSS for a given task [2]. Furthermore, evaluations of GDSS based on solicited user satisfaction are complicated by the potential conflation of individual satisfaction related to the decision-making process, the decision-making outcomes, and the decision support technology [3,4]. Specifically, one can stipulate that a non-favorable decision-making outcome would lead to lower satisfaction related to the decision support tools that were employed in the process.

Task-Technology Fit (TTF) theory [5–8,4] and the *Technology Acceptance Model* [9–11] state that perceived usefulness informs engagement with and utilization of decision support technologies [10,5,12]. As such, system utilization constitutes an important observation by which to evaluate the performance of a decision support

system for a given user base and task. Clearly, decision support tools need to be homogenized with the decision-making process in order for users to perceive the tools as useful [13].

Whereas user satisfaction can be elicited through survey methods, empirical evaluations of GDSS based on user interaction often defy prescriptive approaches of analysis [14,15]. In this paper, we report on an exploratory empirical analysis of user interaction with a web-based GDSS for participatory transportation planning. The interaction of individuals with the GDSS was captured in information-rich server log files. Based on the server log files, we derived groups of individuals with similar user interaction using multiple sequence alignment and hierarchical cluster analysis. Subsequently, we assessed the reliability of the classifications from the two clustering approaches.

In the next section, we describe the project in which the data for the presented analysis was collected. In addition, we provide a description on sequence alignment analysis and hierarchical cluster analysis and give a brief overview of evaluation approaches for web-based GDSS. In Section 3, we outline our methodology for the collection and analysis of human–computer interactions within the context of the web-based GDSS at hand. In Section 4, we discuss the results of our analysis as well as its limitations. Finally, in section 5, we state our conclusions and give suggestions for future work.

* Corresponding author. Tel.: +1 503 725 3164; fax: +1 503 725 3166.
E-mail address: swobod@pdx.edu (M. Swobodzinski).

2. Related work

2.1. Participatory Geographic Information System for Transportation

The web-based GDSS analyzed in this paper was designed and implemented as part of the Participatory Geographic Information System for Transportation (PGIST) project, a basic-science research project funded by the Division of Information and Intelligent Systems of the National Science Foundation (EIA-0325916). The objective of the PGIST project was the development of an internet platform for public participation in regional transportation improvement programming [16,17]. The PGIST project culminated in the deployment of the *Let's Improve Transportation* (LIT) website within the *LIT Challenge*, a structured, 4-week-long participatory planning process on the web.

Guided by a small team of moderators, the LIT participants were tasked with deliberating, analyzing, and selecting transportation projects and funding mechanisms that would pay for the implementation of the projects. To facilitate this process, the LIT website provided a host of analytical and deliberative decision support tools. Contextualized in participatory transportation planning, the LIT website exemplifies a web-based, communications-driven GDSS [18].

2.2. Multiple sequence alignment and hierarchical cluster analysis

Multiple sequence alignment analysis originated in molecular biology as a technique for the computational analysis of DNA and protein sequences [19,20], with non-computational approaches going as far back as the 1960s [21]. The primary purpose of sequence alignment analysis is the detection of conserved patterns that reflect evolutionary relationships among sets of sequences [22]. Its output is commonly an arrangement of sequences in a tree structure, with the leaves of the tree representing individual sequences.¹ The shorter the distance between individual leaves along the branches of the tree, the greater the computed similarity between sequences. The topological structure of the tree can be used to derive clusters of similar sequences by grouping sequences that are located in the same vicinity of the tree.

Sequence alignment procedures are computationally demanding, with a running time in the order of $O(n^k)$, with k being the number of sequences and n their average length. As such, the simultaneous alignment of sequences can burden computational resources, even when processing a small number of sequences [23–25]. To mitigate such limitations, many multiple sequence alignment algorithms rely on an iterative approach that is based on a progression of pairwise alignments.

Similar to multiple sequence analysis, hierarchical cluster analysis also produces a classification tree. Rather than using the alignment of sequences as the basis for the calculation of a similarity measure, however, hierarchical cluster analysis derives similarity scores from numeric distances of ratio-level variables. As an agglomerative clustering algorithm, the cluster formation starts out with as many clusters as there are observations, with one observation per cluster. The algorithm iteratively computes distances between pairs of clusters and combines the clusters with the smallest distance (i.e., the most similar clusters). As to derive the final classification tree, various clustering strategies (e.g., nearest neighbor and average linkage between groups) and similarity measures (e.g., Euclidean distance) can be employed.

2.3. Sequence alignment analysis in the social sciences

Sequence alignment analysis found entry into the social sciences through the work of Abbott [27,28,26]. Specifically, researchers aimed at extending existing implementations of sequence alignment algorithms to allow for the coding of observations beyond DNA and proteins. Such efforts led to the creation of the sequence alignment analysis

software ClustalG [29] and ClustalTXY [30], both derivatives of Clustal, a prominent multiple sequence alignment algorithm in the bioinformatics community [31–35]. In addition to the work of Wilson 1998 on daily activity routines [36,37] and activity–space trajectories [30], extended multiple sequence alignment algorithms have been applied to the scheduling of vacations [38], sightseeing behavior [39], and eye movement patterns in the context of static small multiple map displays [40].

2.4. Evaluation of web-based group decision support systems

Among a few examples of empirical evaluations of web-based GDSS, Chen et al. [41] reported on TeamSpirit, a web-based GDSS for problem solving by distributed teams. TeamSpirit was designed to support the Creative Problem Solving (CPS) process. The CPS process entails the exploration and definition of problems, the generation and evaluation of alternatives, and the planning for and evaluation of solutions. The evaluation of TeamSpirit focused on its use by different subjects in relation to the subjects' performance on varying problem-solving tasks, the amount of CPS training, and the amount of TeamSpirit training. Central to the evaluation of TeamSpirit were not individual human–computer interaction patterns, as is the case in our approach, but the effect of the usage of TeamSpirit on tasks external to the system. The results by Chen et al. [41] showed that the quality and quantity of generated ideas increased significantly for groups that received training.

In the context of the PGIST project, our colleagues reported on a spatiotemporal evaluation of discussion contributions within the LIT Challenge [42,43]. In particular, the authors analyzed a subset of deliberation-related data on the creation of discussion posts and the expression of agreement and disagreement with such posts. Focusing on the visual analysis of online discussion in the LIT Challenge, the authors developed a visualization tool which overlaid a map of the study area with a graphical plot of the frequency of discussion contributions during the LIT Challenge. The visualization tool showed the physical locations of contributors as well as categories of responses. Analytical activities were only considered as temporal reference points for deliberation-related activities. The evaluation that we present in this paper, on the other hand, forgoes a particular emphasis on deliberation-related activities in favor of a holistic evaluation of all activities (i.e., deliberation, analysis, and information retrieval) that were captured within the LIT Challenge. Given the lack of prescriptive approaches to the empirical analysis of web-based GDSS, we embarked on an exploratory analysis of the data generated within the LIT Challenge. We opted for multiple sequence alignment analysis and hierarchical cluster analysis as these techniques were most suitable for the analysis of the LIT data.

3. Methods

3.1. Participants and collection of server logs

The pool of participants in the LIT Challenge was comprised of 246 individuals that were recruited proportionally from King, Pierce, and Snohomish County in the central Puget Sound region of the State of Washington. Of these, 179 were eligible for a small stipend as compensation for their participation. The amount of the stipend was cumulative and depended on the number of completed steps in the LIT Challenge, as well as the participation in data-gathering activities that were part of the research design (e.g., online questionnaires and user interviews). A subset of 47 individuals completed all steps in the LIT Challenge, that is, they interacted with LIT from the beginning to the end of the participatory planning process. These 47 individuals constitute the sample for the evaluation of the LIT GDSS that we present in this paper.

The participatory process was structured into five main steps which were divided into one to three sub-steps. The progression through the steps was subject to a set time schedule (Table 1). Within the constraints of the time schedule, the participants were interacting

¹ In the following, we will use the term sequence and leaf interchangeably.

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