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Short paper: Study of synchronous and colocated collaboration for search tasks

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Abstract

Nowadays, Collaborative Virtual Environments offer new working methods allowing for the association of several experts in the same problem-solving process. These new platforms have the potential to improve the processing of complex environments with large dataflow and requiring different skills. This article proposes the investigation of a synchronous and colocated approach for a molecular design task. The aim of this research is to highlight the role and the contribution of Collaborative Virtual Environments for the improvement of complex tasks fulfillment.

Categories and Subject Descriptors (according to ACM CCS): H.5.3 [INFORMATION INTERFACES AND PRESENTATION]: Group and Organization Interfaces—Computer-supported cooperative work

1. Introduction

Collaborative Virtual Environments (CVE) are emerging as a key research interest, at the intersection between Human-Computer Interfaces (HCI), Information and Communication Technologies (ICT), and Computer Supported Cooperative Work approaches (CSCW) [EML07]. These environments have the potential to change the way research teams create, exchange, manipulate, and disseminate information in several collaborative project configurations (e.g., distant/local, synchronous/asynchronous) [RI08].

Among complex environments, molecular design and Docking simulation are suitable applications for the emergence of CVE approaches. This research area arouses an interest within the scientific and industrial community and represents a considerable challenge in the fields of pharmacology and biotechnology. The current molecular manipulation and analysis tools allow the prediction of new molecular complexes and thus the development of new drugs and medicines. However, the manipulation and analysis of relevant molecules constitutes a complex task for Biologists, both from the point of view of the involved physical phenomena and the topological complexity. These tasks require the interpretation and manipulation of a high level of DoF and physical parameters. Furthermore, these tasks are based upon several areas of expertise (e.g., modelling expertise for the structural and flexibility features, biological expertise for the functional features).

Since the emergence of the molecular modelling research field, several works have investigated and developed different platforms (distant/collocated, synchronous/asynchronous, collaboration/cooperation, etc.) to enable Biologists to work together [KFR*03] [CBZ*05]. However, all the existing approaches consist mainly to enable the partners to work and interact in the same virtual space without defined working strategies [GGW*05] [PGH*04]. Nevertheless, as for Virtual Reality Environments, CVE need the investigation of new working methods adapted and taking benefit from the synchronous association of several partners in the same virtual environment. Thus, it's necessary to carry out studies to understand the role and the contribution of these new environments in order to propose suitable working strategies.

Among the several levels of collaboration that can take place in molecular environments (e.g., brainstorming, briefing, review, collaborative manipulation), we propose the investigation of synchronous co-realisation of some critical tasks requiring the combination of several skills and knowledge. This paper focuses on the study of the collaborative

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search of residues (important biologic structures). In fact, before the deformation and assembling of molecules, Biologists must find and select some important targets. However, some of these residues can sometimes be difficult to find or to access. Thus, a collaborative strategy can improve the efficiency of search processes. The presented study proposes to evaluate this new configuration of work and to highlight the main mechanisms that take place.

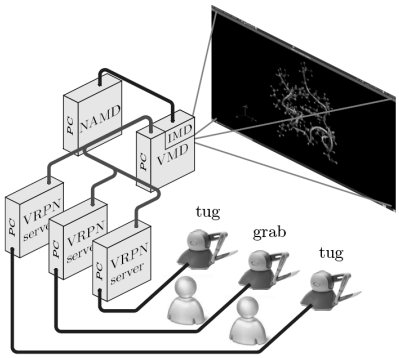

Figure 1: *Collaborative Virtual Environment and corresponding software and hardware deployment and architecture*

2. Experiments

2.1. Hardware setup

The experiment was conducted on a collaborative platform connecting standard desktop workstations, providing individual private views, with a large screen display, for the public and global views (video projector). This solution has the advantage to take into account the existing working procedures of Biologists (Desktop environment) while proposing extension to CVE (public view with a large screen, several haptic arms for bimanual mode, etc.). The visualization and the simulation of molecular environment is conducted with respectively VMD and NAMD packages. The software connection is supported by IMD package. The interaction with the molecular environment is supported by a set of 6 DoF (3 DoF actives) haptic interfaces of type of PHANToM Omni from SensAble. Figure 1 presents the software and hardware set-up of the collaborative platform.

2.2. Methods

The experiment investigates two factors. First, the number of involved participants for the achievement of collaborative tasks. In fact, this study compares the task fulfilment between single participants and groups of two participants. Since the experiment concerns elementary search tasks, we enrolled participants without specific skills (e.g., Biologists, computer scientists, engineer). The second investigated factor concerns the complexity of the task. This factor is

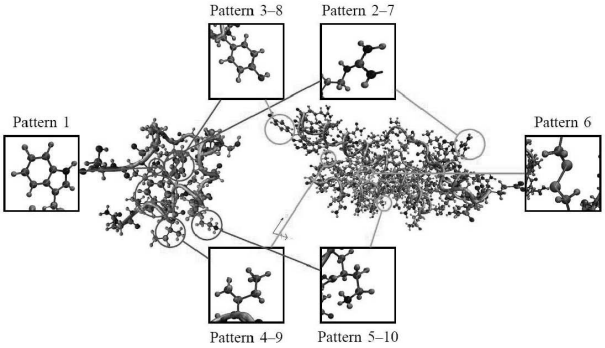

Figure 2: *Repartition of patterns on TRP-CAGE and Prion molecules*

linked to the different features of the manipulated molecules (shape, size, number of atoms, etc.) and defined structures to find. For this experiment, we selected two molecules with different sizes: the TRP-CAGE with 304 atoms and the Prion with 1776 atoms (see Figure 2).

As mentioned above, the aim of this experiment is the search of noticeable biologic structures in molecules (see Figure 2). The participants have ten different structures to find, five on the small TRP-CAGE molecule and five on the big Prion molecule. To validate the task, once the structure is found, the participant have to catch one atom of the structure with the *tug* tool and pull it out the molecule according a defined configuration.

Table 1 summarizes the different features of the experimented structures. Each feature corresponds to a specific factor of the task complexity. The first column indicates the geometrical position of the structures in the molecule. The second column indicates the geometrical structure of the pattern. Three shapes are proposed: circle, chain, and star. The third column indicates the color of the concerned structures. The last column describes the level of presence of similar structures in the molecule (similar number of atoms, similar colors, etc.).

Pattern		Position	Shape	Color	Other pattern
TRP-Cage	1	Intern	Circle	8 C, 1 N	No
	2	Intern	Star	1 C, 3 N	No
	3	Intern	Circle	6 C, 1 O	No
	4	Extern	Chain	4 C	No
	5	Extern	Chain	4 C, 1 N	No
Prion	6	Intern	Chain	2 C, 2 S	No
	7	Extern	Star	1 C, 3 N	No
	8	Extern	Circle	6 C, 1 O	No
	9	Intern	Chain	4 C	Yes
	10	Intern	Chain	4 C, 1 N	Yes

Table 1: *Involved factors in the complexity of molecules(Carbon, Oxygen, Nitrogen and Sulfur)*

Two ways of interacting with the molecular environ-

ment are proposed. The first tool, called *grab* in VMD, allows the positioning and the orientation of the manipulated molecules. The second proposed tool, called *tug*, allows the manipulation and the interaction with atoms. These two interaction tools (*grab* and *tug*) are shared on three haptic interfaces. The *grab* tool is linked to the middle haptic arm in order to be accessible for the two participants. Thus, only one participant can manipulate the point of view of the molecule at any time. The *tug* tool is linked to the two other haptic arms to allow each participant to manipulate simultaneously the molecule (see Figure 1).

24 participants, 4 women and 20 mens aged between 21 and 54 years completed the experiment. The participants have several skills and work in different research fields. In order to compare collaborative work and simple user configuration, the participants completed two times the experiment: in one condition they performed the task alone and in another condition they performed the task in pairs. The task is exactly the same for the two conditions. However, in the pair configuration, only one of the two participants have the ability to manipulate the point of view through the *grab* tool.

The experiment is based on the Bowman navigation process [Bow99]. First, the participants were asked to explore the molecule during 1 minute. Afterward, the searching task begins by displaying the series of ten patterns. No predefined strategies is imposed to the participants. Finally, the task is achieved when the participants find and hold together simultaneously the specified patterns (with the VEE / *tug* tool). The participants were asked to place the patterns outside the molecule according to defined configurations.

Several measures were collected including execution time, position and trajectory of VEE, distance between working space and applied force on haptic arms. In addition to these objective measures, a questionnaire is proposed to participants at the end of the experiment. The questionnaire concerns the subjective evaluation of the different features of collaborative work as compared to single configuration of work (e.g., perceived efficiency, perceived partner contribution, communication) using a 5 points Likert's scale.

3. Results and discussion

An ANOVA was conducted on the execution time for tasks fulfilment with 2 factors: the level of complexity of molecules (small versus large) and the number of participants (single versus pair). The results reveal a significant effect of the molecule factor $[F(1,11) = 71.02, p < 0.00001]$, a significant effect of the group factor $[F(1,11) = 6.10, p < 0.05]$, and no significant interaction between these two factors $[F(1,11) < 1, ns]$.

These results show mainly the average efficiency obtained on a set of tasks presenting different levels of complexity. They reveal that collaborative configuration improves substantially tasks fulfilments as compared to simple users configuration. It should be mentioned that the fulfillment of collaborative tasks includes communication between participants (e.g., oral, gestural), while single user configuration does not include these exchanges. The details of the results is developed in the following sections.

Figure 3 shows the mean execution time for all patterns including collaborative and single participant configurations. First, this result highlights the different levels of difficulty to search the different patterns. Thus, some structures appear more difficult to find than others. In fact, a Duncan post-hoc test carried out on all patterns (10 levels) shows a significant difference (all ps <.01) between the patterns (6;9;10) and the patterns (1;2;3;4;5;7;8). Thus, we can consider patterns 6, 9 and 10 more complex than the others structures. The difficulty to find the different patterns is linked to the complexity factors developed above (Table 1).

The small size of the TRP-Cage molecule presents a limited number of patterns to consider. Thus, the first step of exploration allows a rapid construction of a mental map about the global structure of the molecule. During the search step, participants find rapidly the presented patterns thanks to the geometrical structure and the color features of the patterns. Pattern 4 is little less difficult to find because of its solid color.

The large Prion molecule presents a more complex structure with a high number of residues. The first step of exploration allows the understanding of the global structure of the molecule and the identification of some noticeable patterns (e.g., rare color, particular geometrical structure). Several strategies of search are involved. They begin with a peripheral exploration of the molecule to find external patterns (patterns 7 and 8). If patterns are not found (patterns 6, 9, and 10), a deformation procedure is involved to highlight the internal structure of the molecule. The execution time is more important and is linked to the different features of the patterns (e.g., position, structure, color).

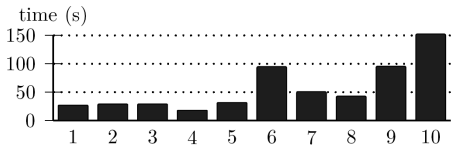

Figure 3: *Total execution time including collaborative and single participants configurations*

Figure 4 compares the execution time of collaborative and single participant configurations. The first five patterns present a low execution time for both collaborative and single participant configurations. In fact, the small size of the TRP-Cage molecule presents patterns rapidly accessible. We observe a small advantage for collaborative configuration. The contribution of the second participant concerns the visual search of patterns (same visual rendering and same point of view).

For the Prion molecule there are two cases. First, patterns 6 and 9. An important improvement of execution time for collaborative configuration is observed. A Duncan post-hoc test performed on the group factor (alone/group) and pattern factors (10 levels) shows a significant difference between single participant and group for pattern 9 ($p < 0.0001$) and pattern 6 ($p < 0.2$). These two patterns are internal structures with low differences with the rest of the molecule (chain structures, carbon atoms, etc.). After a peripheral exploration, the participants deform and manipulate the different structures of the molecule to find patterns.

Several collaboration strategies presenting close coupling between partners are observed. This mutual action enables, on the one hand, a better control of coupled and complex structures, and on the other hand, the assistance of partners when they meet difficulties (gesture guidance).

The three other patterns (patterns 7, 8, and 10) present a very small (although non-significant) difference between collaborative and single participant configurations. In fact, these three configurations present noticeable patterns which are quickly identified. The contribution of the second participant concerns, on the one hand, the visual search of patterns (patterns 7 and 8), and on the other hand, the deformation of the molecule to reach the pattern once identified (pattern 10).

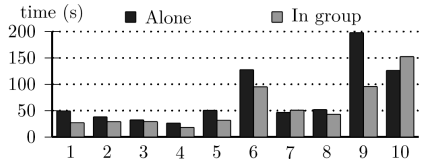

Figure 4: *Mean execution time depending on the biologic structure to search*

Figure 5 shows that usually there is a difference in efficiency between partners of the same pair (during individual experiments). Therefore, there are always a fast partner and a slow partner. However, when participants work together the global execution time converges to the minimum time of the two partners (individual execution time). Thereby, collaborative work tends to improve the global efficiency of the group and smooth performance of ineffective partners.

The questionnaire feedback shows that a large proportion of participants tend to overestimate the role of the partner as compared to their implication. The answers of participants highlight the role and the efficiency of explicit communication (oral, gestural, etc.) for global coordination (task sequence). However, the participants highlight some difficulties to view and understand low amplitude movements of partner during close manipulation. Beyond the complexity of the molecular environment and the limits of 3D perception, this limit of awareness is due to the physical absence of the partner in the virtual environment. In fact, the representation

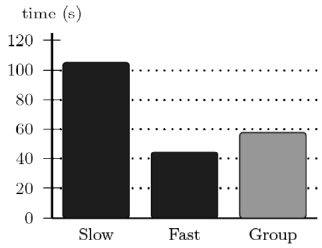

Figure 5: *Pattern 9: Mean execution time for fast and slow participants for single configuration and corresponding mean execution for collaborative configuration*

of the body plays an important role for the understanding of the associated gestures.

4. Conclusions

This study highlights the role of collaboration between several participants for the fulfilment of a complex task. Results show that the efficiency of teamwork is linked to several human and task factors (e.g., complexity of tasks, skill of groups). Moreover, the more the task is difficult the more the contribution of collaboration is important.

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