Smart Environments for Collaborative Design, Implementation, and Interpretation of Scientific Experiments

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Abstract

Ambient intelligence promises to enable humans to smoothly interact with their environment, mediated by computer technology. In the literature on ambient intelligence, empirical scientists are not often mentioned. Yet they form an interesting target group for this technology. In this position paper, we describe a project aimed at realising an ambient intelligence environment for face-to-face meetings of researchers with different academic backgrounds involved in molecular biology "omics" experiments. In particular, microarray experiments are a focus of attention because these experiments require multidisciplinary collaboration for their design, analysis, and interpretation. Such an environment is characterised by a high degree of complexity that has to be mitigated by ambient intelligence technology. By experimenting in a real-life setting, we will learn more about life scientists as a user group.

1 Introduction

In visions of future computing, humans are surrounded and supported by smart environments and smart objects that are attentive and pro-active. The environments use their sensors to observe and their intelligence to interpret the activities of their inhabitants and provide support. Ubiquitous computing, ambient intelligence, and pervasive computing are among the names that are used in the literature to refer to this vision. Depending on the domain and the users or inhabitants of these environments we can also speak of smart offices, smart home environments, smart meeting rooms, or smart public environments. Some of the environments are task-oriented, e.g., they aim at providing technology that support efficient meetings or problem-solving sessions, while others aim at supporting home or leisure activities. While currently, due to the possibility of commercial home applications, much emphasis is on sensor-equipped physical environments, we also see interest in virtual environments made up from distributed and connected physical environments. Clearly, one impetus for research in this latter direction came from the development of teleconferencing systems. Another impetus came from developments in the area of computer supported collaborative work (CSCW). Originally this work assumed a rather restricted way of communication between users. For example, the 'Coordinator' system introduced by Winograd [Medina-Mora *et al.*, 1992; Winograd, 1987] to coordinate the communication between collaborators has been called "fascist software" [Spinoza *et al.*, 1995]. This qualification is given because 'Coordinator' is some kind of management surveillance software rather than a system that stimulates cooperation and joint problem solving. However, in more recent years these CSCW environments have developed into so-called Future Workspaces [Fernando *et al.*, 2003]. This development is due to the ability to capture more aspects of human verbal and nonverbal communication behaviour and due to advancements in artificial intelligence, allowing us not only to represent and use domain knowledge, but also to reason about domain knowledge. Apart from supporting, in a global way, issues such as workflow systems, design practices and brain storming sessions, these 'spaces' or environments are meant to provide users with mixed reality cooperation and support. That is, virtual environments are created in which scientists, designers, and technology advisers cooperate while not necessarily being present in the same physical environment and manipulate objects and tools that are both virtual and physical. Joint virtual workspaces allowing access from remote places and offering tools for designers and scientists to design and experiment are the future workspaces.

They may be the future, but when we look at current research practices, there still is a rather large distance be-

tween, on the one hand, research on ambient intelligence and smart environments, and, on the other hand, research on future workspaces. Rather independent from these points of view there is the development of ambient intelligence and smart environment technology that can be used in all kinds of smart environments, whether they are inhabited by family members or by collaborating scientists. This includes the development of sensor technology, computer vision, multimodal interaction systems, artificial intelligence, and multimedia presentation technologies. Maybe more interesting are the views expressed in [Pantic *et al.*, 2006] on 'human computing'. As mentioned in this paper, "The key to human computing and anticipatory interfaces is the ease of use, in this case the ability to unobtrusively sense certain behavioural cues of the users and to adapt automatically to his or her typical behavioural patterns and the context in which he or she acts." That is, we need to focus on human behaviour and (joint) activities in smart environments, rather than focussing on intelligent devices (isolated gadgets) and we need to change from a function-oriented view of an environment to a user's goal oriented view [Hellenschmidt and Wichert, 2005].

We are interested in human computing for (life) scientists based on the behaviour of individual scientists and group processes of co-operating scientists. In this paper, we aim to discuss some of the key issues involved in adapting developments in human computing for use in the context of empirical science. Empirical scientists are not often mentioned in the literature on smart environments and ambient intelligence. Yet they form an interesting target group because preliminary studies suggest they differ in certain respects from better studied groups like gamers, patients, and home residents. In particular, scientists seem to prefer to remain in full control.

This paper is organised as follows. We first introduce the habitat of empirical scientists. We then turn to scientific collaborative environments and discuss how workflows may support collaboration within a multidisciplinary team. Part of our work is concerned with the e-BioLab, an environment developed at the University of Amsterdam. We further discuss ways of interacting in the e-BioLab. We round off with a discussion.

2 Ambient Intelligence for Science

We will take molecular biology as an example here. Molecular biology has been the subject of a famous ethnographic study by Latour and Woolgar [1979]. Molecular biologists study the chemistry of life or, more precisely, chemical interactions in and of living cells. They experiment with living organisms (*in-vivo*) and with living cells or material that has been extracted from cells or synthesised (*in-vitro*). Since the time of Latour and Woolgar, the explosion of digital resources (databases and programs) has made a third type of experiment possible, nicknamed *in-silico* or dry-lab. For contrast, the *in-vivo* and *in-vitro* experiments are now also collectively known as wet-lab experiments. A large part of the molecular biologist's work consists of designing experiments and interpreting their results, in both cases heavily aided by the published literature. Living cells are incredibly complex [Papin *et al.*, 2005]. They are studied with the help of modern "omics" technologies that allow large-scale, high-throughput experiments to generate data at a massive scale. The biologist's task of making sense of these data would be infeasible without appropriate software tools.

Roughly, scientific activity of molecular biologists takes place in three different contexts: in the lab, at the desk, and in meetings. All three contexts may profit from ambient intelligence techniques, making scientific research more efficient, effective, and pleasant. In all three contexts, situation awareness implies at least some awareness of the scientific task at hand. This is a challenge because the steps involved in scientific discovery are only to some extent repetitive. It may turn out that a scenario evolves as the discovery process unfolds. We briefly elaborate on the potential benefits of ambient intelligence for each of these contexts.

Lab apparatus is increasingly equipped with sensors and actuators. Many of these devices can communicate with each other and with a base station because they are derived from designs for hard-to-reach or dangerous situations. The tasks such devices can perform are often fixed and they can only obey a few simple commands from the base station. Situation awareness can be achieved by making these devices responsive, enabling two-way communication, and by allowing interaction with lab personnel.

The typical scientist's desktop has a computer with high-speed connections to local servers and the Internet. These systems are still very much classical PCs with some scientific software installed that, however, still falls short of the scientific discovery environment proposed by De Jong and Rip [1997] some ten years ago. The current desktop machine is ill-equipped for high-definition visualisations, interaction with visualisations, and similar multimedia tasks. It requires near-prohibitive overhead to operate it. A desktop PC is, in fact, the wrong tool for much scientific work. Recently, progress has been achieved in packaging recurring task sequences in a single environment. For example, in bioinformatics the Taverna workflow tool [Oinn *et al.*, 2004; Oinn *et al.*, 2002] can in principle perform all computer tasks involved in an *in-silico* experiment. In a similar vein, the Problem Solving Environment (PSE) of the VL-e project [Zhao *et al.*, 2005] packages calls to programs, possibly over a Grid, and information exchange between heterogeneous, distributed computers. Taverna workflows and PSEs resemble scenarios in Crowley's sense, "a description of possible actions or events in the future [...]" [Crowley, 2006]. At the same time, they are also autistic in Crowley's sense: once started, they run to completion. Turning a desktop PC into a scientist's assistant will take a major redesign of both aspects of interaction: the ways the user operates the system and the ways in which the system can convey information to the user.

Meetings, the third context, have been the subject of a lot of research [Rienks *et al.*, 2006]. For example, the AMI project [Nijholt *et al.*, 2006] and its successor project AMIDA investigate fundamental and practical issues one

encounters in situation-aware meeting support tools. Even though current proposals do not address the practices and needs of scientists, they form a good starting point for situation-aware support for scientific meetings. AMI, for example, investigated meetings of a multidisciplinary team involved in a creative activity, the design of a remote control. Distributed participants can meet in a virtual meeting room in which the design can sit on the (virtual) table. It is easily imagined that instead of a remote control, a representation of an experiment sits on the table for all participants to see and manipulate.

Our own research is conducted in the framework of the BioRange[1] project, a large, national project aimed at strengthening the bioinformatics infrastructure of The Netherlands. We concentrate on enhancing the exploration of bioinformatics resources through user-centred design, resulting in enriched interactions.

In a part of our project, we focus on face-to-face meetings that serve the purpose of interpreting the results of a particular class of molecular biology experiment, namely microarray experiments. Microarray experiments are high-tech experiments aimed at finding out the expression levels of typically a large number of genes, either absolutely or relative to expression under different circumstances. The experiments involve many sources of noise and the interpretation of the results is far from straightforward [Stekel, 2003]. Nevertheless, there are stakes involved. For example, breast cancer treatment can currently be based on the result of a microarray experiment [Van 't Veer *et al.*, 2002]. In the experiment itself and its interpretation, practitioners from various disciplines are involved: microarray experts, biologists, bioinformaticians, and statisticians. The MAD/IBU group of the University of Amsterdam is building the e-BioLab, a meeting room equipped with a large display, electronic, interactive whiteboards, and other devices [Rauwerda *et al.*, 2006], see Figure 1. Its aim is to facilitate meetings of the various professions involved in experiments that require multidisciplinary collaboration for their design and interpretation, such as a microarray experiment.
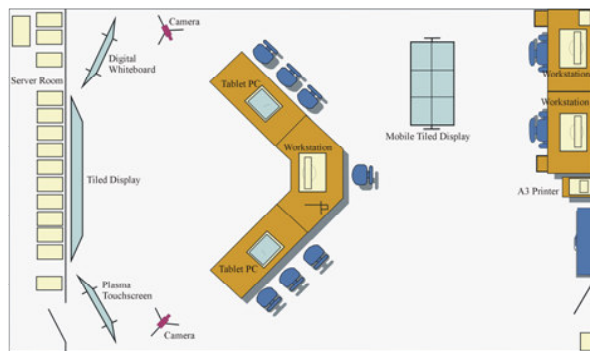

Figure 1. A first design overview of the e-BioLab.

The e-BioLab environment is characterised by a high degree of complexity. This complexity derives from four fac-

tors. First, the meeting participants come from different disciplines and they attempt to understand each other. Second, a microarray experiment itself is complex, as are the procedures to clean the data and to validate the results. Third, to molecular biologists it is a new task to find biological meaning in the diverse, multidimensional and huge (whole-genome) datasets. Methodology for inference of biological models from "omics" data is still in its infancy. Fourth, the devices in the meeting room have to be operated. A smart e-BioLab needs attentive and proactive interfaces to mitigate the complexity of the meeting environment.

Put briefly, we want to contribute to the design of the e-BioLab, and in particular to the interactions of the users and the devices. We are not only interested in the meeting aspect, although it is an important focus of our research. But we imagine that, as prices of large, high-resolution displays drop, these displays and the associated interactions will also find their way into the lab and the scientists' workrooms.

3 Scientific collaborative environments and workflows

Work on smart, supportive environments has been reported in the literature. The environment itself is called by different names, depending on the aspect one wants to emphasise: for example, war room (enabling extreme collaboration [Gloria, 2002] or for managing crisis situations [Sharma *et al.*, 2003]), collaborative interactive environment [Borchers, 2006], ubiquitous computing room [Brad *et al.*, 2002], multi-sensor meeting room [McCowan *et al.*, 2003], among many others. The use of large displays to support meeting participants has itself been the subject of a strand in the literature [Borchers, 2006; Fitzmaurice *et al.*, 2005; Huang, 2006; Rogers and Lindley, 2004]. Much of this work is relevant but has to be adapted to the specific needs of the users of the e-BioLab: molecular biologists, microarray experts, bioinformaticians, and statisticians. As was found for scientists in general by Dunbar [1995], the practitioners of the various disciplines involved in our research bring with them a rich and often implicit background knowledge.

As in any user-centred approach, user studies and task analysis are a core activity [Bartlett and Toms, 2005; Homa *et al.*, 2004; Kulyk *et al.*, 2006; Van Welie and Van der Veer, 2003]. Recently, we conducted an empirical user study to explore working practices and experiences of users from different bioinformatics sub-domains and with different levels of expertise [Kulyk and Wassink, 2006]. We aim to identify, among other things, the key aspects and user requirements for a scientific collaborative environment. Our respondents mention the advantages of large displays for multiple visualisations but at the same time stress the danger of overwhelming the viewer. They strongly prefer to meet face-to-face, and they tend to forget discussion points and decisions of previous meetings. This is corroborated in other research for general users [McCowan *et al.*, 2003; Nijholt *et al.*, 2006; Rienks *et al.*, 2006] and for scientific teams [Dunbar, 1995, 1997]. Our results are preliminary and more work has to be done to obtain a comprehensive picture. In

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[1] http://www.nbic.nl/biorange/

particular, we aim to build a fairly detailed and complete task model of a microarray experiment.

Molecular biology is a highly visual discipline, as any textbook will testify [Alberts *et al.*, 2002; Campbell and Heyer, 2006; Lewin, 2006; Lodish *et al.*, 2004]. In interpreting a microarray experiment in the e-BioLab, results of the experiment itself and of statistical operations on the data can be displayed in the form of visualisations on the large display, as in the example on Figure 2. Moreover, in a multi-disciplinary set-up a large display connected to high-performance computing facilities could be used to construct models of biological mechanisms, perform *in-silico* experimentation with these and adapt the models after interpretation of the results. The large display will frequently be split in a number of separate displays. Additionally, other devices in the room can be allocated display tasks. The visualisations on the various displays are obviously related in the sense that they refer to the same experiment, but it will not always be evident what the precise relation is. To prevent users from getting lost, visual aids will have to identify the relations between the various sub-screens.
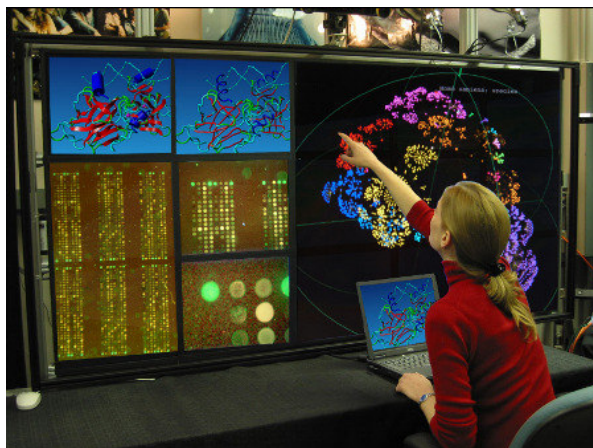

Figure 2. A scenario in which a scientist is interacting with multiple visualizations.

The visualisations may be so closely related that a change in a visualisation on one display will have to be propagated to related visualisations on other displays in a manner pioneered by the Spotfire system[2]. In our case, however, the propagation is far more complex. For example, one display may reveal a number of distinct clusters of gene expression profiles. These clusters then are analyzed on their enrichment with regard to certain pathways. These pathways are visualized on another area of the large display while the up and down regulation and the occurrence of the genes in other clusters is marked in these visualisations. Another example is the design of microarray experimentation. It may take a statistician to establish confidence intervals and statistical power of an analysis. However, only molecular biologists and microarray experts can assess whether it is experimentally possible in the wet-lab to increase statistical

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[2] www.spotfire.com

power or to avoid confounding by choosing a different experimental setup.

The complexity of multiple displays showing often complex material can, as we stated earlier, be mitigated by employing attentive and proactive interfaces. Such interfaces need to have intelligence built in. At the very least, they need to know a scenario [Crowley, 2006]; in fact, a visualisation of the scenario would be very helpful for the users in any case. Workflow tools have proved useful in modelling business processes [Van der Aalst, 1998]; in our view, they can also be of use for building scenarios. In molecular biology, workflow tools have been proposed for modelling signal pathways in cells [Peleg *et al.*, 2001], for scheduling and supporting tasks in a distributed genomics project [Kochut *et al.*, 2003], and for performing *in-silico* experiments on the Grid [Oinn *et al.*, 2004; Oinn *et al.*, 2002]. As Taverna makes clear, among molecular biologists the data perspective on workflow is dominant. The two other perspectives distinguished by Van der Aalst [1998], the process perspective and the actor perspective, receive less attention. In the task analysis we are performing, all three perspectives receive equal attention.

When using a workflow tool for representing a scenario, we come close to using this tool for designing the experiment and its interpretation. In this sense, an experiment's workflow representation may also support ambient intelligence in the other situations mentioned in the introduction. Different stages in the use of a workflow are distinguished:

- **The design stage**, in which the experiment is designed. This is probably the most difficult stage. There is a close relationship between the design stage and task analysis. The difference between the two is that currently molecular biologists are the actors in the design stage while software designers are the actors in the task analysis. Interaction design can be speeded up if we succeed in bringing these two worlds closer together.
- **The execution stage**, in which the experiment is performed. Part of the experiment can be *in-silico*, in which case the workflow tool can also control the execution of that part. For real-life molecular biology experiments, this stage will have to be subdivided further: there are several steps in the wet-lab, followed by a number of interpretation steps including validation.
- **The archive stage**, in which the conditions of the experiment, the raw results, the settings in the post-processing steps, and the final results are archived. In molecular biology parlance, this is called *provenance* [Goble et al., 2003]. Provenance is important; reproducibility is a major quality control in empirical science. In addition, government bodies want to be able to see such information in medical applications and in drug design. Obviously, the work necessary for this stage has to be done at execution time.

Concerning workflow tool requirements, the BioRange programme has a strong preference for open-source freeware. Further requirements a workflow tool has to fulfil are:

- For **the design stage**, the tool has to enable all three perspectives (data, processes, resources). Hierarchical

modelling is preferred. As workflows become more complicated, validation becomes a concern. The tool therefore has to be based on a formal model and has to incorporate automated validation. Petri nets are a *de facto* standard for formal model of workflows [Van der Aalst, 1998]. YAWL is an example of an open-source freeware workflow tool based on Petri nets [Van der Aalst and Ter Hofstede, 2005]. Finally, the users have to be able to interact naturally with the tool as the design takes shape.

- For **the execution stage**, the *in-silico* parts should run (semi-)automatically. In a large display, such a tool can propagate the results of one part of the display to other parts. Interaction with other programs and remote resources should be automatic and can be configured easily. This kind of technology is researched in Grid projects. For example the Taverna workflow tool [Oinn *et al.*, 2004; Oinn *et al.*, 2002] interoperates smoothly with web resources, using BioMoby or WSDL/SOAP. Interaction with users during execution goes beyond the Grid paradigm, yet is important in many situations. For example, in validating a microarray result, different parameter settings are tried out until the users are satisfied. The number of iterations is not determined beforehand and there has to be a possibility to fiat the result, enabling the workflow tool to move to the next process step. In the wet-lab and at the biologist's desk, interaction with sensors and actuators, and human intervention are mandatory. In the wet-lab this tool will eventually coincide with Laboratory Information Management Systems (LIMS) software and will offer a tight integration with the desktop and meeting context. This approach may also facilitate easier implementation of LIMS software in research labs. In the execution stage, it is also important to be able to use the tool for navigation: in which step are we now, what is to follow, and what are the consequences of particular outcomes of the former step. Also it must be possible to capture remarks made in discussions, notions, ideas and hunches and to retrieve these at another time. In other words, the tool must offer the possibility to annotate analyses and biological models. This annotation can be in different forms, for example as text entries in a database or as remarks or sketches drawn on an electronic whiteboard on top of a drawing of a biological model.

- For **the archive stage**, designs, settings, intermediate and final results of the former two stages should be stored. The organisation of this storage is a cause for concern because the amount of data can easily grow enormously. Choices may be necessary about what to keep and what to delete. Such choices are best made at the design stage and the tool has to cater for that. Also, archiving makes no sense if the archived material cannot be retrieved quickly and effectively later. This means that the archive has to conform to standards if they are there. For microarray experiments, for example, the *Minimum Information About a Microarray Experiment*

(MIAME) standard[3], even if still under development, is accepted by most institutes and is mandatory upon submission to a large number of scientific journals.

As far as we are aware, no open-source freeware workflow tool meets all these requirements. For example, YAWL aids design by allowing validation of (complex) workflows, but it does not support execution and archiving of the kind required for molecular biology experiments. Taverna does not smoothly interoperate with resources other than BioMoby and WSDL/SOAP web resources. For instance, microarray experts prefer to use the R statistical package[4] for the interpretation and validation of microarray results. Interaction between Taverna and R proved to be cumbersome. No workflow tool we know allows interaction with human users during execution, for example in iterative parameter fitting exercises. For these reasons, it seems we will have to build our own workflow tool, reusing components from YAWL, Taverna and similar tools.

4 Interaction in the scientific environments

There are three modes of interaction in the e-BioLab, human-human interaction, human-display interaction, and inter-system interaction. We briefly discussed the last category implicitly in the former section. Our focus in this paper is on how users may interact with the scientific collaborative environment, and in particular with the large display in the e-BioLab. Due to the size and high resolution of the large display, classical interaction devices will not suffice [Fikkert *et al.*, 2006]. The lab will have to have characteristics of an ambient intelligence environment [Bowman *et al.*, 2004; Fikkert *et al.*, 2006; Jaimes and Sebe, 2005; Oviatt, 1999; Oviatt *et al.*, 2003; Pantic *et al.*, 2006; Tao *et al.*, 2006], making complex systems accessible for a large variety of users, without the need for explicit, tedious, or extensive training. There is no research on ubiquitous computing environments for empirical scientists or, even more specific, our target group composed of microarray experts, bioinformaticians, molecular biologists, and statisticians. We will provide a short overview of issues we think are important, and point out aspects we believe are particularly relevant for our user group.

In conversations, humans can express themselves through numerous modalities that are held to be associated with the human senses [Fikkert *et al.*, 2006]. For example, speech intonation and gestures accompanying an uttered sentence can change the message completely. Multimodal research has focused on systems that combine speech and pointing gestures as input modalities [Oviatt, 1999]. Other modalities such as facial expressions, gaze direction, and body gestures are thought to be mandatory for automatic human behaviour analysis [Ambady and Rosenthal, 1992; Oviatt, 1999; Oviatt *et al.*, 2003; Pantic *et al.*, 2006]. Ambient intelligence derives its knowledge of the current situation from observational clues. In particular, it has to be able to assess the so-called W5+ questions [Pantic *et al.*, 2006] (what is commu-

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[3] http://www.mged.org/Workgroups/MIAME/miame.html
[4] http://www.r-project.org/

nicated when, where, why, by/to whom, and how) from observed behaviour. Only multimodal observation can provide the necessary information. Issues to be solved include the following. Which modalities have to be used and when? What is the optimal combination of modalities given the current context? At which level should observed information be fused, at feature or semantic level? It is important to determine how these communicative modalities can be observed in a scene; the interpretation of observed behavioural cues is highly context-based. Understanding behaviour enables a system to fully support and anticipate on its users.

In the e-BioLab, scientists with different scientific backgrounds will use large displays to show their preferred types of visualization in order to discuss progress and results of experiments. Visualisations will be 2D and 3D; for example, protein sequence alignment produces a 2D image but the function of a protein may be better illustrated by its 3D shape. Of the many ways to interact with these visualisations, manual gestures are natural way of expression for many researchers [Buxton and Myers, 1986; Balakrishnan and Hinckley, 2000; Tao *et al.*, 2006; Czwerwinski *et al.*, 2006; Guiard, 1987]. We therefore want to further explore gesture interaction. As users become familiar with gesture interaction, a repertoire of gestures will develop that is in principle new. However, as with most new technology, the repertoire will be rooted in the way life scientists currently use gestures in communication.

Many questions are to be solved for natural gesture interaction to be possible. For example, does the size of the display influence gestures? Are there cultural differences in gesture language, in our case possibly along disciplinary boundaries? In the e-BioLab setup, scientists gesture at each other and at the display; can the two kinds of gesture be distinguished? How can gesture information be fused with other information users may provide, for example through hand-held devices? The detection of gestures is a problem in itself. There are many and diverse techniques for gesture detection [Bowman *et al.*, 2004; Fikkert *et al.*, 2006]; in recent years research has focused on unobtrusive detection, for example using computer vision techniques. Other approaches make use of special devices such as coloured gloves, tethered data gloves, and full-body tracking suits. A current point of research in unobtrusive detection of user gestures when several users are present is how to attribute gestures to the user who made them. The next step, gesture recognition, is an active research topic [Aggarwal and Cai, 1999; Jaimes and Sebe, 2005; Moeslund and Granum, 2001]. Techniques are mostly model-based, using skeletons or geometric shapes, or appearance-based, using motion, texture, or colour information in a scene. The current state of the art does not allow detection and tracking of human hands in multi-party unconstrained environments with dynamic illumination and backgrounds; the e-BioLab is an example of such an environment. Automated gesture recognition is not mature. A representation of the gesture repertoire expressed in a technology-neutral language allows us to quickly adapt to another method of gesture recognition.

Natural interaction will not only be found in dry-lab data analysis settings, but will in all likelihood also be found in wet-lab environments in which media, e.g., augmented reality, can support a laboratory technician in performing her tasks. Recall the three contexts mentioned in Chapter 2 here.

5 Discussion

One of the most fascinating questions in this kind of endeavour is: will it help? Expensive equipment and complex software are brought together in the e-BioLab expecting that molecular biology will profit. User studies and iterative design are employed to improve the initial set-up, but that does not validate the design in the sense that it does not answer the question whether molecular biology has changed or, even better, has improved through this technology. The question immediately raises another question: how do we measure this? It is obvious that the problem space is highly multidimensional. Data can be gathered during meetings of which there are only so many in a year. But that leaves more indirect effects like swifter publication or better molecular biology experiments out of view. Statistical significance is out of reach. We could revert to anecdotal evidence, but we think the point can be strengthened somewhat by performing an analysis in the tradition of sociology of science.

Contemporary science is driven by groups having members of different levels of expertise and various scientific backgrounds [Dunbar, 1995]. Scientist's meetings, if recorded, provide a far more complete record of the evolution of their ideas than other sources of information. That is why our target group, a multidisciplinary scientific team working on microarray experiments, is so interesting. We believe that by experimenting in a real-life setting, the e-BioLab and its users, we can learn more about scientists as a user group. Ambient intelligence for science will profit from this; we expect ambient intelligence in general, too. A natural interface able to decipher and anticipate user activities and desires truly immerses our scientists in their cognitive task and thus truly supports them [Butz *et al.*, 2003]. Human-centred design or, in our case, scientist-centred design is a necessary condition to achieve this.

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