

In future computing environments you will be surrounded and supported by all kinds of technologies. You will be able to interact with them in a natural way: you can speak to, point at, or even frown at some piece of presented information: the environment will understand your intent. Natural interaction approaches will improve the way we work. However, this is still in the future. True automated understanding can only come from



Human Media Interaction

context. The BioRange project at the Human Media Interaction (HMI) group addresses such natural interfaces from the viewpoint of scientific experiments in the molecular biology domain.

Human Computing in the Life Sciences

What does the future hold?

Where Molecular Biology and HCI meet

Bio-informatics is a new research domain. Like biochemistry and biophysics, bio-informatics has its roots in the biology domain. Increasing amounts of data are gathered by biologists, mainly as a result of new technological developments in molecular biology. Such vast data sets need to be interpreted and managed, generating even more data in the process. New tools are needed that allow us to perform data analysis, management and annotation. Such tools are rooted in computer science (CS) [1]; hence the name bio-informatics.

A key role in molecular biology is played by bio-informatics. Molecular biology teams are highly multidisciplinary, and include biologists, statisticians, bio-informaticians, computer scientists and microarray experts. Diverse types of expertise contribute to tackling the complex biological challenges of both the present and

the future, such as curing Multiple Sclerosis and Huntington's Disease. These teams need some way to work with these vast data sets in a single location. Understanding one another in the team is as important as a joint understanding and interpretation of the acquired data. More clarity in the relationships between data and the current working progress can help. A picture can say more than a thousand words.

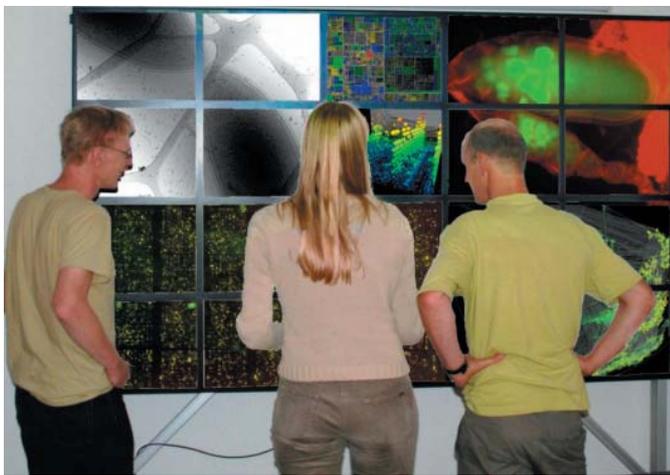
Bio-informaticians use their knowledge of both biology and computer science to develop tools that allow biologists access to data acquired in their complex experiments. Opposite to the current standard in CS, user-centred design is something to be scared of in bio-informatics. Tools are not based on their users' needs and so biologists are lost in a forest of functionality that they do not understand. They simply let it be and pass it by [3]. Biologists should not be struggling to operate sophisti-

cated tools and devices. They should work, in teams, with their data in intuitive ways. It is here that HCI, human-computer interaction, and molecular biology meet.

Smart Surroundings

With the BioRange project, the Netherlands has positioned itself at the forefront of the rapid developments in bio-informatics. HMI's BioRange group develops interaction tools for molecular biology teams [5]. We develop these tools for the *e-BioLab* [4]. The *e-BioLab* is a future computing environment which is under continuous development. Its facilities include large, high-resolution displays and portable PCs. However, state-of-the-art technologies add nothing of themselves. Our aim is to support the molecular biology team with the possibilities that the *e-BioLab's* facilities can offer. In the *e-BioLab*, team members will better understand each other, the team will be more creative due to both new insights and new





functionality, and the surroundings will understand and anticipate users' behavior. It will be a truly smart environment.

The following sections describe how we are addressing this vision. More specifically, they describe our main research questions.

Mutual Understanding

An initial study of current working practices in molecular biology indicates that work is done in a semi-structured way, research is explorative. It is difficult to explicitly define team members' responsibilities for parts of the experiment at hand and to validate and reproduce results, therefore experiments need to be modelled.

Currently, we are investigating the uses of workflows to describe dynamic molecular biology experiments. These are already in wide use today in, for example, business and commerce. Workflows describe which resources are required for each process that is started, in progress and completed. For example, what happens after you have taken an exam at the UT is defined by a workflow system: the relevant teachers and staff will be notified in turn so you can, after some weeks, find your grade in TOST. We ask ourselves how a workflow system can be adopted to describe the dynamic nature of an experiment in molecular biology. A fine line needs to be walked concerning our design's rigidity: too rigid will prevent our team thinking "out of the box" and too generalized will result in meaningless models.

After modelling an experiment, it is vital to assess how such a model can guide an experiment and how a model can provide a focus for discussion. During a meeting, the structure and current progress of an experiment can be displayed. Our research addresses the question of when, where and how to depict an experiment's progress, datasets, user roles and processes. We aim to guide the team members in their work by increasing their mutual understanding of these topics.

Group Creativity

The multidisciplinary nature of molecular biology teams itself stimulates complex thinking and reasoning. In the *e*-BioLab, scientists will work together to interpret very large

We are currently observing teams in the *e*-BioLab, in a series of meetings. By describing the processes that take place and the way in which team members interact with each other and their environment, we work towards an evaluation framework for collaborative, scientific environments. This framework includes requirements and design concepts for such future smart rooms.

Understanding Behavior

A smart room understands its inhabitants. Users can act naturally: the environment will understand their intentions, and react to them. In essence, the traditional computer interface disappears. The ideal natural interface can recognize speech, facial gestures, hand gestures, body

"A smart room understands its inhabitants"

and complex datasets. To visualize a large quantity of data you simply need a lot of physical space to depict them. Large displays immerse their users more than widespread and small displays. But how do the large displays and other technologies in the *e*-BioLab affect the way the team works together? In order to answer this question, we describe the influence of mutual situational awareness: the environment's awareness of its users and their work, and the team's awareness of the opportunities that their new environment offers. To assess this influence, we need to describe the tasks and users we find in molecular biology experiments.

postures and so on: it can deal with all modalities that humans use to communicate. Humans express significant parts of their messages using non-verbal signals. We are exploring intuitive two-handed gesture-based interaction with large displays. Users will be able to navigate, select and manipulate complex experimental data using their hands. They will do so both individually and in groups. However, the current state-of-the-art in gesture-based interaction [6] does not yet allow us to do this out-of-the-box, especially in multi-party unconstrained environments.

So what are the challenges we face? First, we must detect two-handed

gestures from multiple users simultaneously. Specialized gloves, touch screens or computer vision can be used here. Then, we must be able to identify a hand gesture and the person who is making it. Was it Billy or Bob? And did he want to see graph A or did he simply want another coffee? The same pointing gesture can mean both things. So, to resolve this ambiguity, we need a language of hand gestures. User intent needs to be understood: was it the coffee or the graph? Such understanding can

More information

Are you interested in any of the topics we have addressed here? Please contact us to participate in or carry out projects and Capita Selecta assignments! Look for more information at: <http://hmi.ewi.utwente.nl/project/BioRange> or mail us: biorange@ewi.utwente.nl.

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“User intent needs to be understood: was it the coffee or the graph?”

only flow from context and it is context that we model using our workflows. We thus explore how context can help us understand behavior. Also, context helps us to define appropriate feedback.

Looking at the Future

Clearly, our work does not provide solutions for all open topics in creating future “smart” environments. We focus on a narrow use case: supporting life science experiments. However, our findings will be applicable in a broad domain. They contribute to the future vision of human computing: see, hear and feel you in there! ■

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References

- [1] Jacques Cohen. Bio-informatics - an introduction for computer scientists. *ACM Computing Surveys*, 36(2):122–158, 2004.
- [2] Wim Fikkert, Marco D'Ambros, Torsten Bierz, and TJ Jankun-Kelly. Interacting with visualizations. In Andreas Kerren, Achim Ebert, and Joerg Meyer, editors, *Human-Centered Visualization Environments*, LNCS Tutorial. Springer, August 2006. GI-Dagstuhl Seminar.
- [3] Olga Kulyk and Ingo Wassink. Getting to know bio-informaticians: Results of an exploratory user study. In *Workshop on Combining Visualisation and Interaction to Facilitate Scientific Exploration and Discovery* in conjunction with *British HCI 2006*, pages 30–38. ACM Press, 2006.
- [4] Han Rauwerda, Marco Roos, Bob Hertzberger, and Timo Breit. The promise of a virtual lab in drug discovery. *Drug Discovery Today*, 11:228–236, March 2006.
- [5] Paul van der Vet, Olga Kulyk, Ingo Wassink, Wim Fikkert, Han Rauwerda, Betsy van Dijk, Gerrit van der Veer, Timo Breit, and Anton Nijholt. Smart environments for collaborative design, implementation, and interpretation of scientific experiments. In *Workshop on AI for Human Computing* in conjunction with the *International Joint Conference on Artificial Intelligence*, volume 20. AAAI Press, January 2007.

