



information

VL-e enables new approaches to traditional sciences

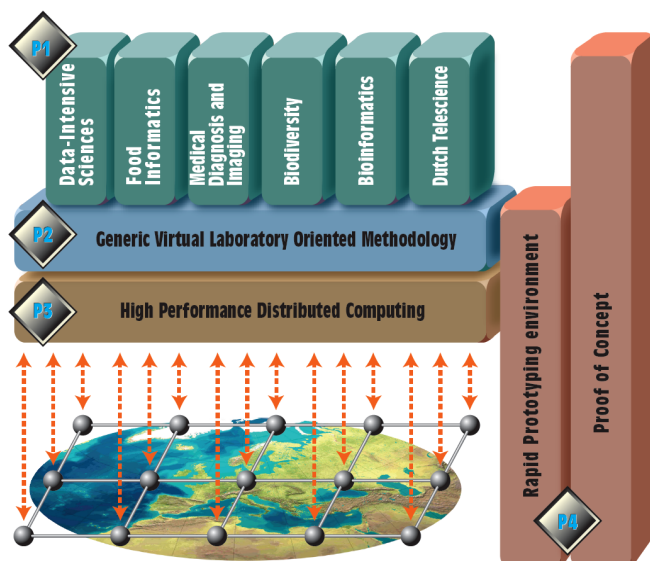
Information has become the fuel of our knowledge society, and our ability to digest, understand and share it will determine our scientific, economic and social progress.

The exceptional increase in computing power, storage capacity and network bandwidth over the past decades forms the basis of a digital revolution which has only just started. Also the changing scale and scope of experimental sciences require a new research paradigm: (digitally) enhanced science or e-Science. The aim of the 'Virtual Laboratory for e-Science' (VL-e) project is to bridge the gap between the technology push of the high performance networking plus the Grid and the application pull of a wide range of scientific experimental application domains. A typical example of this is the life sciences, where VL-e offers solutions for combining laboratory

research with computational experiments and simulations, making use of the knowledge and experience gained from dealing with large data sets in high energy physics. At the same time, however, it is recognised that data sets in the life sciences are far more complex than in high energy physics.

More specifically, VL-e is developing a Proof-of-Concept (PoC) infrastructure (both hard- and software) to enhance location-independent access to scientific information and stimulate global and multidisciplinary collaboration, thereby enabling new approaches to traditional sciences. The VL-e software (both for rapid prototyping and in the PoC) provides generic functionalities that support a wide range of e-Science applications. This PoC infrastructure will boost the knowledge economy of the Netherlands.

Currently, six application domains are involved: Data-Intensive Sciences, Food Informatics, Medical Diagnosis & Imaging, Biodiversity, Bioinformatics and Telescience. Several Dutch universities, academic hospitals and industries in the life sciences and ICT domain participate in this project. There is also strong collaboration with NBIC (Netherlands Bioinformatics Centre). The recently started Dutch BIG GRID project will build a nationwide production grid, making use of methodology still being developed within VL-e.





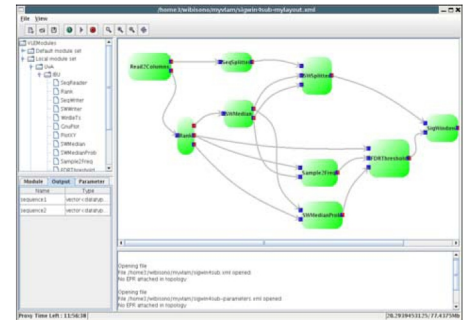
Bioinformatics: towards an e-BioScience Problem-Solving Environment

The near unlimited availability of genomics data has reshaped life sciences research forever. Our ability to translate this data into genomics information and biological knowledge will determine scientific, economic and social progress in the agriculture, food and healthcare domains.

Life scientists today must cope with huge amounts of experimental genomics data that can only be fully dealt with by multi-disciplinary teams of experts carrying out complex and computationally intensive bioinformatics-based analyses and experimentation.

This e-Science based approach is named: e-BioScience.

We meet this e-BioScience challenge with VL-e methodology and by using its resources and tools. We are developing an *e-BioScience Problem Solving Environment* (eBioPSE) for biology in the omics-era.



Reusable SigWindetector workflow can detect regions of increased gene expression

Our e-Bioscience Problem Solving Environment (eBioPSE) focuses on:

- Reusable workflow-based tooling for genomics and transcriptomics. We developed SigWindetector to identify regions of increased gene expression.
- Easy Grid submission of bioinformatics computations. We developed this for the R statistical language to assess gene expression.
- Interaction with the biology domain. We developed an e-BioLab, a physical space for scientists to analyze and visualize large biological data sets, discuss results and biological research questions in an interactive and multi-disciplinary setting. The e-BioLab is equipped with advanced visualization endpoints and uses the eBioPSE.



The e-BioLab: an interactive environment to support collaboration of multi-disciplinary research teams.

This eBioPSE aims to assist life scientists with their transcriptomics experimentation and data handling. It allows for manipulation and use of life sciences data from genome-wide experiments, relevant to the analysis of transcriptomics data. Hence, the eBioPSE enables in-silico experiments such as data analysis and integration.

VL-e Program line: e-Science in Applications

Subprogram: SP1.5 Bioinformatics

Leader: Dr. Timo M. Breit
breit@science.uva.nl

Organization: MicroArray Department & Integrative Bioinformatics Unit, Swammerdam Institute for Life Sciences, University of Amsterdam

vl-e facts

budget 40 M, period 2004-2008
more than 20 consortium partners from industry and academia
director: prof. dr. L.O. Hertzberger
website: <http://www.vl-e.nl>

consortiumpartners

A&F Wageningen, AMC, CWI, DSM, Friesland Foods, FEI, FOM AMOLF, NBIC, Nikhef, IBM, LogicaCMG, Philips Research, Philips Medical, SARA, Top Institute Food and Nutrition, TNO Kwaliteit van Leven, TU Delft, Unilever, UvA-IBED, UvA-ivi, UvA-SILS, VU, VUmc, WTCW