## Multidisciplinary collaboration in VL-e

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

The exceptional increase in computing power, storage capacity and network bandwidth of the past decades forms the basis of a digital revolution, which has only just started. Increases in detector resolution also invokes a changing scale and scope of experimental science. Both ongoing developments lead to an immense data explosion and the experimental sciences require a new research paradigm: *(digitally) enhanced science or e-Science.*

Due to recent breakthroughs in optical wide-area bandworking, network bandwidth does not limit distribution of large amounts of data and information generated by modern networked R&D experiments. A new generation of applications for the Internet is now about to be introduced, unleashed by the availability of ample bandwidth. Parallel to this, another technology is emerging that has the potential to enable users share compute power, storage and other resources such as expensive experimental facilities (e.g. a mass spectrometer or a large telescope). In analogy with the electricity power grid, this technology has been called the Grid.

While focusing on the life sciences, the 'Virtual Laboratory for e-Science' project aims to bridge the gap between the technology push of the high performance networking and the Grid and the application pull of a wide range of scientific experimental applications. It will provide generic functionalities that support a wide class of specific e-Science application environments and set up an experimental infrastructure for the evaluation of the ideas.
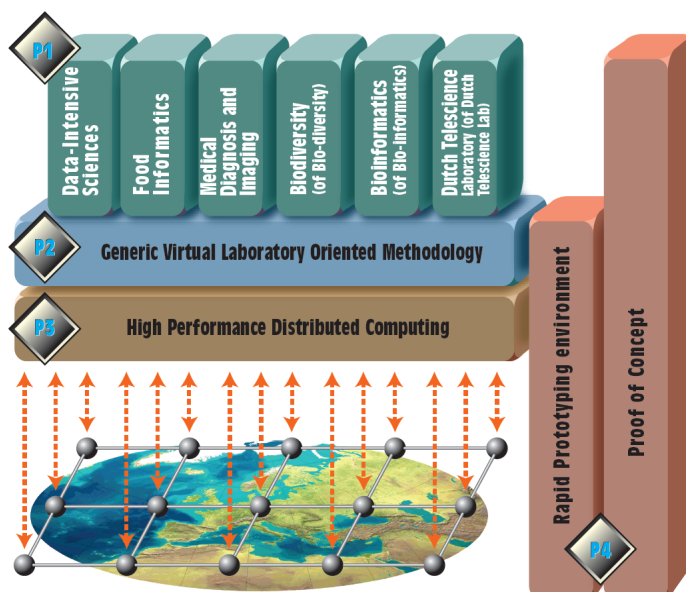
Dutch Telescience –
Remote collaboration, Molecular imaging and proteomics

DUTELLA

The facilitation of inter-institutionary collaborations in the field of integrated high resolution biomolecular imaging in proteomics requires an infrastructure capable of acquiring, storing, processing, combining and sharing information from various resources. In an era where we are experiencing a data explosion in the analytical sciences a need for an innovative e-science infrastructure for bioanalytical studies is evident. In the Dutch Telescience Laboratory DUTELLA this infrastructure is developed and deployed as an integral part of a mass spectrometry based molecular imaging facility.
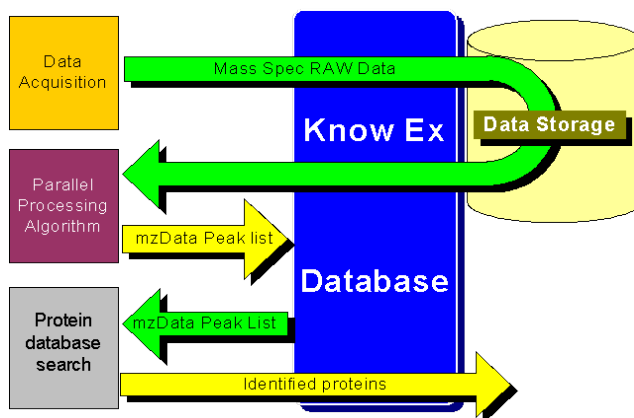
Massively parallel processing of raw mass spectral data with the Knowledge Exchange database.

Biomarker discovery

A new approach for automatic parallel processing of large mass spectral datasets in a distributed computing environment is developed in DUTELLA to significantly decrease the total processing time.
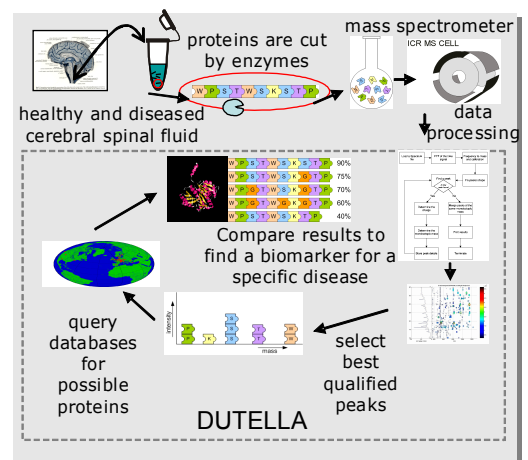
Proteomics workflow in biomarker discovery.

The storage of all raw data is combined with a massively parallel processing approach controlled directly from the Knowledge Exchange (KnowEx) database. This approach of workflow based parallel processing allows access to users outside the ICT research community such as implemented in the proteomics workflow depicted above. As such, this strategy can be applied to all types of serially acquired large mass spectral datasets such as LC-MS, LC-MS/MS and high resolution imaging MS results.

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

VL-e Program line: e-Science in applications

Subprogram: SP1.6 Dutch Telescience

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