Dynamic software infrastructures for the life sciences
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About the author

Curriculum Vitae

Morris Swertz was trained as MSc in information engineering and management with propadeuse in Psychology at the University of Groningen. As a young entrepreneur, his first contact with novel biomolecular tools for microbe research was in a software project for the Department of Molecular Genetics at the University of Groningen. This seeded a strong scientific interest in the dynamic field of bioinformatics and the software infrastructures to support it. As a result he started a Ph.D. in 2002 at the Groningen Bioinformatics Center under the supervision of Ritsert Jansen and Bert de Brock.

Collaborations with various colleagues served to widen his interest to the information management and analysis of biomolecular experiments on humans, livestock and plants. For two years he studied the integration of biological information resources in the international EU-BioGRID project on protein–protein interactions, co-managing a workpackage and resulting in several technical reports. Then he procured funding from the NWO-Biopartner organisation for a one year ‘sabbatical’ from his PhD project to explore alternative business models for MOLGENIS (and to hire business development, legal and software engineering support). In a multi-disciplinary team he led the development of a business plan, marketing materials, legal support documents, and several pilots of MOLGENIS and supervised software engineers assisting in the professionalization of MOLGENIS. The last two years have been spend on developing informatic concepts for building bioinformatics software, testing them in microarrays and genetical genomics and reporting the results in this thesis.

At present, he is developing an independent research line in dynamic software infrastructures for life sciences, improving and applying model-driven/generative strategies to infrastructures for microarrays, sequencing, proteomics, clinical trials, genetical genomics and systems biology.
Journal publications

Nature Reviews Genetics 8: 235-43

Nature Protocols 2: 1-10

Briefings in Bioinformatics 6:135-45.

Bioinformatics 20: 2075-83.


Submitted and draft manuscripts

Swertz MA, Tesson BM, Scheltema RA, Vera G, Jansen RC (Submitted) MGG: A customizable software infrastructure for genetical genomics. 
Submitted to Bioinformatics.

Swertz MA, Matthijssen DI, de Brock EO, Jansen RC (Submitted) How to generate dynamic software infrastructures for systems biology: a practical example. 
Submitted to Bioinformatics.

Swertz MA, Oostergo RJ, de Brock EO (Submitted) A system for uniform treatment of clinical data. 
Submitted to the Journal of the American Medical Informatics Association.

Smedley D, Swertz MA, Wolstencroft K, Proctor G (In preparation) Technical issues concerning data compatibility and interoperability: a case example using the mouse community resources.
Grants and awards

NWO BioRANGE Grant (2005) to develop bioinformatic resources (models, methods, algorithms and software) genetical genomics. Jansen RC & Swertz MA. 175keuro/PhD position.

NWO Biopartner First Stage Grant (2004) to develop business plan for MOLGENIS. Swertz MA, de Brock EO, Jansen RC. 150keuro/1SE + investigator + consultancy support.

1st prize Informatie/NGI thesis award (2002) for MSc thesis on “transactions in federated databases” for Ordina finance Utopics, The Netherlands. 5keuro.

Best first year report "Training" (1997) Rabeling E, Swertz MA, Reinders JJ, Psychology, University of Groningen;

Best first-year report "Informatie Beheer Groep" (1996) Swertz MA & Lubbers LA, Technology management, University of Groningen;


Presentations


Smedley D, Zouberakis M, Mueller W, Rampp M, Swertz MA (2007) CASIMIR WP5: Technical issues concerning database compatibility and interoperability – introduction and summary so far. Co-author on invited presentation at the 1st Annual (public) meeting for the EU Coordination FP6 action CASIMIR - Coordination and Sustainability of International Mouse Informatics Resources, November 28, Rome, Italy.

Swertz MA, Jansen RC (2007) Beyond standardization: dynamic software infrastructures for systems biology. Invited presentation at the 1st Networking (invited only) meeting for the EU Coordination FP6 action CASIMIR - Coordination and Sustainability of International Mouse Informatics Resources, October 4, Corfu, Greece.


Swertz MA (2004) “Information infrastructures for the life sciences by example”.

Selected presentation at the Wageningen Springschool Bioinformatics, March 31-April 2, Wageningen, The Netherlands.


Invited presentation at the Dutch Informatics Society (NGI-Noord) meeting, December 9, Groningen, The Netherlands

Posters


Swertz MA, Scheltema RA, de Brock EO, Jansen RC (2006) “Quick development of bioinformatics infrastructures using generative methods”.

Presented at the Health Grid, January 2004, Clermont Ferrand, France.

Reports

Swertz MA (2006) MOLGENIS – Flexible software life scientists want to have. Contents:
Summary of business model, software product, financial scenarios, and legal organization.

Business plan, 18 pages, appendices and software.

Swertz MA, de Brock EO (2005) “Functional design of the TCC Metabase, a meta database for the controlled distribution of clinical trial databases”.

Technical report for Trial Coordination Center/UMCG, Groningen, The Netherlands. 25 pages.

manual and technical documentation of BioGRID demonstrator and underlying meta model.


Swertz MA (2001) Transacties binnen federated database systems: criteria voor ontwerp en specificatie van FDBSs in staat tot transactieondersteuning (Transactions in federated database systems: criteria for design and specification of FDBSs capable of transactions).

**Award-Winning MSc Thesis**, University of Groningen.
Software prototypes

Data infrastructures:
LIMS-like database for the management of rodent experimental animals in the lab.

Online showcase generative methods
Generating MOLGENIS software infrastructures online, including a simple catalogue of examples. Swertz MA (2007). Published in NatRevGen.

Integration tool for biological databases.
Van der Veen, MJ, Scheltema RA, Swertz MA (2006) ‘Using context information to automatically reduce the cardinality in the schema mapping task’. MSc Artificial Intelligence project, University of Groningen.

Pilot study of LIMS-like database for two-color microarray experiments on plant, human, bacteria and mammals respectively.

Processing infrastructures:
Online tool: design an optimal genetical genomics experiment

Online tool to manage and share statistical scripts in the R language.

R package for the statistical analysis of the genetics of metabolism.

Integrative visualization of microarray, protein-interaction and literature data.