Curriculum vitae

Education/Experience

2010-present: Post-Doc at the Department of Radiology, **Stanford University School of Medicine** under the supervision of Prof. Sylvia Plevritis, Stanford, USA

2009: Post-doc in cancer bioinformatics at the lab of Prof. Dr. Ir. Bart De Moor (ESAT-SCD, Katholieke Universiteit Leuven, Belgium).

2004-2008: PhD in Bioinformatics at ESAT-SCD, Katholieke Universiteit Leuven under the supervision of Prof. Dr. Ir. Bart De Moor. PhD Defence: December 8, 2008, Archived at: http://hdl.handle.net/1979/2018

2003-2004 Katholieke Universiteit Leuven, **Master of Artificial Intelligence** engineering and computer science option, graduated Magna cum laude, project on text genre classification at the faculty of law, in the law and information technology research unit

1999-2003 Katholieke Hogeschool Sint-Lieven, **Master of Science in Industrial Engineering in Electronics** option information and Communication Technology. graduated Magna cum laude, thesis on an intelligent system for electricity load management in Konstanz, Germany

Awards or fellowships

- 2009-2010: Honorary Fulbright Scholar of the Commission for Educational Exchange between the United States of America, Belgium and Luxembourg
- 2009-2010: Henri Benedictus Fellow of the King Baudouin Foundation and the Belgian American Educational Foundation
- 2009-2012: Post-doctoral researcher of the Fund for scientific research Flanders (FWO-Vlaanderen).
- ISCB travel fellowship to attend the 14th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2006) in Fortaleza, Brazil for the amount of $1000
- ASL (Academische Stichting Leuven) travel fellowship to attend the 14th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2006) in Fortaleza, Brazil for the amount of 1000 euro

Research interests

My research interests include the following:

- Bayesian networks and extensions of Bayesian networks for medical decision support systems based on clinical, transcriptomic, genomic or proteomics data or a combination of these with applications in oncology or gynaecologic oncology. This includes the development of methods to integrate the abovementioned data sources.
- Reverse engineering genetic networks using Bayesian network and their extensions. Moreover this includes the use of publicly available data sources as prior information.
- The use of kernel methods in general and Least Squares Support Vector Machines (LS-SVM) more specifically to classify microarray data (e.g. breast cancer, ovarian cancer) or to integrate multiple data sources.

Projects

I was or I'm currently involved in the following projects:

- The International Ovarian Tumour Analysis Consortium: data analysis using mostly Bayesian methods to predict the malignancy of ovarian tumours based on a large multi-centre clinical data set (> 3500 patients).
- FP6 BIOPATTERN: European project where I was involved in creating methods for data fusion based on Bayesian theory.
- SymBioSys: KU Leuven centre of excellence in computational systems biology www.kuleuven.be/symbiosys
- Interuniversity Attraction Pole (IAP) BioMagNet: Bioinformatics and modeling: from genomes to networks, www.kuleuven.be/biomagnet
- MaNet: Mathematical engineering tools for Networks: Data driven mining, identification, control and optimization (GOA KU Leuven)

Participated in writing proposals for several applications for national and international funding:

- KU Leuven funding:
    - Fundamental research project on gathering microarray data on rectal cancer patients.
- Flemish funding:
    - IWT: my own phd-fellowship, biomedical projects in breast and ovarian cancer
    - FWO (phd-fellowship and research projects of max 1 million euro),
- Three projects submitted to the Belgian federal cancer plan
- European funding (FP7):
    - participated in three medium scale European project proposals in the area of biomedical decision support in cancer
    - European funding (FP7): participated in one large scale European project proposal
        - Systems Biology of Inflammation and Cancer: The Role of the Gut Microbiota and Host-Pathogen Interactions
- in Initiating and Promoting Disease Progression
- NIH's Integrative Cancer Biology Program (ICBP)

Courses

- Master class in Partial Least Squares, CQ consultancy, November 2005
- PhD course in Biological Sequence Analysis, Technical University of Denmark April 2005
- Bioinformatics by Robert Gentleman, Ghent University, 2004-2005

Master thesis projects

- Paolo Pilozzi, Modularized Learning of Genetic Networks, Master of Aritifical Intelligence, 2005-06
- Joachim Jacobs, Data mining in health insurance, Master of Electrical Engineering, 2006-07
- Nico Verbeeck, Learning cancer biology: the combination of Bayesian networks and prior information, Master of Artificial Intelligence, 2008-09

Seminars

- At ESAT-SCD:
    - Predictive models in medical decision problems
    - Causality in Graphical models
- At CHU St Pieters Hospital in Brussels:
    - Predicting the outcome of pregnancies of unknown location
- At complex genetics group, UZ Leuven, 18/02/2009
    - Recurrent copy number changes differentiate BRCA1-mutated from sporadic ovarian tumors

Publications

- Book chapters
  - Co-author
    - Daemen A., **Gevaert O.**, Leunen K., Vanspauwen V., Michils G., Legius E., Vergote I., De Moor B. Genome-wide computational study of copy number variations to classify familial ovarian cancer, in Chapter 9, **Investigating Human Cancer with Computational Intelligence Techniques**, (Vellido A., and Lisboa PJG., eds.), Future Technology Press (Shoreham-by-sea, UK), 2009, pp. 107-118
    - Van Calster B., **Gevaert O.**, Van Holsbeke C., De Moor B, Van Huffel S., Timmerman D. Clinical decision support for ovarian tumor diagnosis using Bayesian models: Results from the IOTA study. Computational intelligence in bioengineering, Essays in memory of Antonina Starita. Edited by Masulli F., Micheli A. and Sperduti A. IOS Press, **Frontiers in Artificial Intelligence and Applications,** Volume 196, 2009
- Comments online
  - **Gevaert O**. Model refinement on test data constitutes a dangerous case of overfitting, **BMC Cancer**, 5 August 2009, Comment on Balko et al. BMC Cancer 2009, 9:145
  - **Gevaert O**., De Moor B., Libbrecht L. Suboptimal mRNA expression of CYFIP1, **Cell**, 2009, Comment on Silva et al. Cell 2009, 137, 1047-1061
- Journal papers
  - First author:
    - **Gevaert O**., Daemen A., De Moor B., Libbrecht L. A Taxonomy of Epithelial Human Cancer and their Metastases. **Accepted for publication in BMC Medical Genomics 2009**
    - Leunen K.*, **Gevaert O.***, Daemen A., Vanspauwen V., Michils G., De Moor B., Moerman P., Vergote I. and Legius E. Recurrent copy number changes characterize BRCA1 ovarian tumors by altering specific pathways, *equally contributing first authors. **Human Mutation,** 30:1693–1702, 2009 Cites 1
    - **Gevaert O.**, De Moor B. Prediction of cancer outcome using DNA microarray technology: past, present and future, **Expert Opinion in Medical Diagnostics**, 2009, 3(2):157-165
    - **Gevaert O**., Pochet N., De Smet F., Engelen K., Van Gorp T., Amant F., De Moor B., Timmerman D., Vergote I., Expression profiling to predict the clinical behaviour of ovarian cancer fails independent evaluation, **BMC Cancer**, 8(18),pp1-26, 2008, Cites 4
    - **Gevaert O**., Van Vooren S., De Moor B., A framework for elucidating regulatory networks based on prior information and expression data, **Annals of the New York Academy of Sciences**, 1115, pp.240-248, 2007. Cites 2

- **Gevaert O.**, Pochet N., De Smet F., Van Gorp T., De Moor B., Timmerman D., Amant F., Vergote I., Molecular profiling of platinum resistant ovarian cancer: use of the model in clinical practice, **International Journal of Cancer**, 119(6), pp1511-1512, 2006
- **Gevaert O.**, De Smet F., Timmerman D., Moreau Y., and De Moor B. Predicting the prognosis of breast cancer by integrating clinical and microarray data with Bayesian networks, **Bioinformatics**, 22(14):e184–190, 2006, Cites 13
- **Gevaert O**., De Smet F., Kirk E., Van Calster B., Bourne T., Van Huffel S., Moreau Y., Timmerman D., De Moor B and Condous G., Predicting the outcome of pregnancies of unknown location: Bayesian networks with expert prior information compared to logistic regression, **Human Reproduction**, 21(7), pp1824-1831, 2006, Cites 7

- Co-author:
  - Gravendeel L, Kouwenhoven M, **Gevaert O.**, de Rooi J., Stubbs A., Duijm J., Daemen A., Bleeker F., Bralten L., Kloosterhof N., De Moor B., van der Spek P., Kros J., Sillevis Smitt P., van den Bent M. , French P. Intrinsic gene expression profiles of gliomas are a better predictor of survival than histology. Accepted for publication in **Cancer Research**
  - Mihalyi A., **Gevaert O**., Kyama C., Simsa P., Pochet N., De Smet F., De Moor B., Meuleman C., Billen J., Blanckaert N., Vodolazkaia A., Fulop V., D'Hooghe T. Diagnosis of minimal-mild endometriosis following combined analysis of 6 plasma biomarkers. **Accepted for publication in Human Reproduction,** 2009
  - Van den Bosch T., Daemen A., **Gevaert O.**, De Moor B., Timmerman D., Building decision trees for diagnosing intracavitary uterine pathology. **Accepted for publication in Facts, Views & Vision in ObGyn**
  - Bokor A., Kyama C.M., Vercruysse L., Fassbender A., **Gevaert O.**, Vodolazkaia A., De Moor B., Fulop, V., D'Hooghe T. Density of Small Diameter Sensory Nerve Fibers in Endometrium: a Semi–Invasive Diagnostic Test for Minimal to Mild Endometriosis. **Human Reproduction,** 24:12:3025-32, 2009
  - Debucquoy A., Haustermans K., Daemen A., Aydin S., Libbrecht L., **Gevaert O**., Tejpar S., McBride W.H., Penninckx F., Scalliet P., Stroh C., Vlassak S., Sempoux C., Machiels J-P. Molecular response to cetuximab and efficacy of preoperative cetuximab-based chemoradiation in rectal cancer, **Journal of Clinical Oncology,** 2009 Jun 10;27(17):2751-7, Cites 1

- Daemen A., **Gevaert O.**, Ojeda F., Debucquoy A., Suykens J.A.K., Sempoux C., Machiels J.-P., Haustermans K., De Moor B., ``A kernel-based integration of genome-wide data improving clinical decision support", **Genome Medicine**, 2009, 1:39.
- Condous G., Kirk E., Lu C., Van Huffel S., **Gevaert O**., De Moor B., De Smet F., Timmerman D., Bourne T. Diagnostic accuracy of varying discriminatory zones for the prediction of ectopic pregnancy in women with a pregnancy of unknown location, **Ultrasound in Obstetrics and Gynecology** 26,(7), pp.770-775, 2005. Cites 19
- Van den Bosch T., Verguts J., Daemen A., **Gevaert O.**, Domali E., Claerhout P., Vandenbroucke V., De Moor B., Deprest J., Timmerman D. Experienced pain during vaginal ultrasound, hydrosonography, hysteroscopy and office sampling: a comparative study **Ultrasound in Obstetrics and Gynecology**, 31(3), pp.346-351, 2008. Cites 4
- Van den Bosch T., Verguts J., Daemen A., **Gevaert O.**, Domali E., Claerhout F., Vandenbroucke V., De Moor B., Deprest J., Timmerman D. In reply: Pain experienced during transvaginal ultrasound, saline contrast sonohysterography, hysteroscopy and office sampling: a comparative study, **Ultrasound in Obstetrics and Gynecology**, 32(1), pp.118-119,2008

- Submitted or in preparation
  - Daemen A., Signoretto M., **Gevaert O.**, Suykens J., De Moor B. Improved Microarray-Based Decision Support with Graph Encoded Interactome Data, Internal Report 09-216, ESAT-SISTA, K.U.Leuven (Leuven, Belgium), 2009., Lirias number: 248316.
  - Antal P., Millinghoffer A., Hullam G., Timmerman D., Moreau Y., **Gevaert O.**, De Moor B., ``Structure learning of Bayesian networks with MCMC : extension to incomplete data and decision trees as local models", Internal Report 09-170, ESAT-SISTA, K.U.Leuven (Leuven, Belgium), 2009., Lirias number: 243249.
  - **Gevaert O.,** Daemen A., Debucquoy A., Machiels JP., Haustermans K., De Moor B. Bayesian integration of microarray and proteomics data to predict therapy response in patients with rectal cancer, Internal Report 07-172, ESAT-SISTA, K.U.Leuven (Leuven, Belgium), 2007
  - **Gevaert O.**, Timmerman D., De Moor B., ``Optimizing variable order, selection and cost using a genetic algorithm for modeling ovarian masses with Bayesian networks", Internal Report 08-18, ESAT-SISTA, K.U.Leuven (Leuven, Belgium), 2008.
  - van Malenstein H., **Gevaert O.**, Libbrecht L., Daemen A., Allemeersch J., Nevens F., Van Hummelen P,, Cassiman D., De

Moor B., Verslype C. and van Pelt J. Chronic Hypoxia predicts Poor Prognosis in Hepatocellular Carcinoma.

- Daemen A., Van Holsbeke C., **Gevaert O.**, Fruscio R., Guerriero S., Czekierdowski A., Valentin L., Savelli L., Testa A., Fischerova D., Bourne T., Vergote I., De Moor B., Timmerman D., ``Prospective comparison of one-step and two-step models for the classification of adnexal masses", Internal Report 08-194, ESAT-SISTA, K.U.Leuven (Leuven, Belgium), 2008.
- Kyama CM., Mihalyi A., **Gevaert O**., Waelkens E., Simsa P., Van de Plas R., Meuleman C., De Moor B., D'Hooghe TM. Evaluation of endometrial biomarkers for semi-invasive diagnosis of endometriosis, Internal Report 07-134, ESAT-SISTA, K.U.Leuven (Leuven, Belgium), 2007
- Fassbender A., Simsa P., Kyama C.M., Waelkens E., Mihalyi A., **Gevaert O.**, Van de Plas R., Meuleman C., D'Hooghe T.M.. Combined proteomic and RNA microarray analysis after TRIzol extraction of eutopic endometrium for endometriosis biomarker discovery.

- Conferences
  - Full papers
    - **Gevaert O**., Van Vooren S., De Moor B. Integration of microarray and textual data improves the prognosis prediction of breast, lung and ovarian cancer patients, In Pacific Symposium on Biocomputing (PSB), Kohala Coast, Hawaii, pp. 279-290, 2008.
    - **Gevaert O.**, De Smet F., Timmerman D., Moreau Y., and De Moor B. Integration of clinical and microarray data using Bayesian networks. In Proceedings of the 14th IFAC Symposium on System Identification (SYSID), Newcastle, Australia, March 2006.
    - Daemen A., **Gevaert O.**, Leunen K., Legius E., Vergote I., De Moor B., Supervised classification of array CGH data with HMM-based feature selection. In Pacific Symposium on Biocomputing (PSB), Kohala Coast, Hawaii, 2009
    - Daemen A., **Gevaert O.**, Leunen K., Vanspauwen V., Michils G., Legius E., Vergote I., De Moor B., Classification of sporadic and BRCA1 ovarian cancer based on a genome-wide study of copy number variations, In Proceedings of 12th International Conference on Knowledge-Based and Intelligent Information and Engineering Systems (KES), Zagreb, Croatia, 2008
    - Daemen A., **Gevaert O**., De Bie T., Debucquoy A., Machiels J.-P., De Moor B., Haustermans K., Integrating microarray and proteomics data to predict the response on cetuximab in patients with rectal cancer, In Pacific Symposium on Biocomputing (PSB), Kohala Coast, Hawaii, pp. 166-177, 2008.

- Daemen A., **Gevaert O**., De Moor B. Integration of clinical and microarray data with kernel methods, In 29th Annual International Conference of the IEEE Engineering in Medicine and Biology Society, Lyon, France, Aug. 2007.
- De Moor B., Van Delm W., **Gevaert O**., Engelen K., Coessens B., Systems Biology, Come Forth ! In Foundations of Systems Biology in Engineering (FOSBE), Stuttgart, Germany, 2007.

- Abstracts
  - **Gevaert O**., De Moor B., Timmerman D., Optimizing variable selection and cost using a genetic algorithm for modelling adnexal masses with Bayesian networks, In 17th World Congress on Ultrasond in Obstetrics and Gynecology (ISUOG), Firenze, Italy, Oct 2007
  - **Gevaert O**., Van Holsbeke C., Fruscio R., Guerriero S., Czekierdowski A., Savelli L., Testa A., Fischerova D., Jurkovic D., Bourne T., Neven P., Valentin L., De Moor B., Timmerman D. Multicenter prospective testing to predict malignancy in adnexal masses using Bayesian network models, In 18th World Congress on Ultrasond in Obstetrics and Gynecology (ISUOG), Chicago, Illinois, Aug. 2008
  - **Gevaert O**., Testa A., Daemen A., Van Holsbeke C., Fruscio R., Epstein E., Leone FPG., Czerkierdowski A., Valentin L., Savelli L., Bourne T., Amant F., De Moor B., Timmerman D. Investigation of the performance of mathematical models on small ovarian masses on IOTA phase 1 and 2 data. In 18th World Congress on Ultrasond in Obstetrics and Gynecology (ISUOG), Chicago, Illinois, Aug. 2008
  - **Gevaert O**., Van Vooren S., De Moor B. Integration of expression and textual data enhances the prediction of prognosis in breast cancer. International workshop on Probabilisitc Modelling in Computational Biology: Probabilistic methods for Active Learning and Data Integration in Computational Biology, Vienna, July 2007
  - Kirk E., **Gevaert O**., Haider Z., Condous G., Bourne T. Can the hCG ratio be used to predict the likelihood of success of conservative management of ectopic pregnancies? In 15th World Congress on Ultrasond in Obstetrics and Gynecology (ISUOG), Vancouver, Canada, Sept. 2005
  - Kyama CM., Mihalyi A., **Gevaert O**., Simsa P., Waelkens E., Van de Plas R., Mwenda JM., Meuleman C., De Moor B., D'Hooghe TM. Endometrial biomarkers for semi-invasive diagnosis of endometriosis, In 23rd Annual Meeting of the European Society for Human Reproduction and Embryology (ESHRE), Lyon, France, 2007
  - Kyama CM., Mihalyi A., **Gevaert O**., Simsa P., Waelkens E., Van de Plas R., Mwenda JM., Meuleman C., De Moor B., D'Hooghe TM. Proteomics in translational research: an integrated approach in

the pathogenesis and diagnosis of endometriosis. In The 10th world congress on endometriosis, Melbourne, Australia, March 2008

- Daemen A., Bottomley C., **Gevaert O**., De Moor B., Timmerman D., Bourne T. Predicting early pregnancy loss with Functional Linear Discriminant Analysis (FLDA) In 17th World Congress on Ultrasond in Obstetrics and Gynecology (ISUOG), Firenze, Italy, Oct 2007
- Daemen A., Van Holsbeke C., **Gevaert O**., Fruscio R., Guerriero S., Czekierdowski A., Valentin L., Savelli L., Testa A., Fischerova D., Bourne T., Vergote I., De Moor B., Timmerman D. Prospective comparison of one-step and two-step models for the classification of adnexal masses as benign or malignant, In 18th World Congress on Ultrasond in Obstetrics and Gynecology (ISUOG), Chicago, Illinois, Aug. 2008
- Van den Bosch T., Daemen A., **Gevaert O**., Timmerman D. Mathematical decision trees versus clinician based algorithms in the diagnosis of endometrial disease In 17th World Congress on Ultrasond in Obstetrics and Gynecology (ISUOG), Firenze, Italy, Oct 2007
- Machiels J.H., Debucquoy A., **Gevaert O**., Daemen A., Sempoux C., McBride W., Stroh C., Vlassak S., Haustermans K. Prediction of pathological response to preoperative chemoradiotherapy with cetuximab in rectal cancer. In Annual Meeting of American Society of Clinical Oncology (ASCO), Chicago, Illinois, May-June 2008

Workshops and conferences

I attended the following Workshops and international conferences (Project workshops are in italic):

- 2009
  - Benelux Bioinformatics Conference, Liège, December 2009
    - Oral presentation: Unsupervised microarray analysis of glioma reveals prognostically relevant subgroups
  - BioMagNet workshop: Bioinformatics and modeling, from genomes to networks, October 22nd, Ghent, Belgium
    - Oral presentation: studying the ovarian cancer genome using Array CGH and Hidden Markov models.
  - Translational summit on Bioinformatics, San Francisco, USA,
- 2008

- Benelux Bioinformatics Conference, Maastricht, The Netherlands
- 18th World Congress on Ultrasound in Obstetrics and Gynecology, 24-28 August 2008, Chicago, USA
  - Oral presentation: Multi-center prospective testing to predict malignancy in adnexal masses using Bayesian network models
  - Oral presentation: Investigation of the performance of mathematical models on small ovarian masses on IOTA phase 1 and 2 data.
- 16th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2008), July 2008, Toronto, USA
  - Poster presentation: A Bayesian network framework for integrating high throughput/high dimensional data to model the regulatory networks behind cancer outcomes.
- Microarrays in Medicine 2008, 19-20 May, Boston, USA
- PSB 2008, Big Island of Hawaii, January 2008
  - Oral presentation: Integration of microarray and textual data improves the prognosis prediction of breast, lung and ovarian cancer patients.

- 2007

  - NIPS workshop: Machine learning in computational biology, Dec 7-8 2007, Whistler, Canada

  - 2nd DREAM conference, Dec 3-4 2007, New York, USA.
  - Benelux Bioinformatics Conference, 12-13 Nov, Leuven, Belgium
    - Poster presentation: Integration of microarray and textual data improves prediction of breast, lung and ovarian cancer patients.

  - 5th Annual Cytoscape retreat and symposium, Nov 8th 2007, Amsterdam, The Netherlands

  - 17th World Congress on Ultrasound in Obstetrics and Gynecology, 7-11 Octobre 2007, Florence, Italy.
    - Oral presentation: Optimizing variable selection and cost using a genetic algorithm for modelling adnexal masses with Bayesian networks.

  - International Workshop on Probabilistic modelling in Computational Biology, 26 July, Vienna, Austria
    - Oral presentation: Integration of expression and textual data enhances the prediction of prognosis in breast cancer.

  - 15th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB) and 6th European Conference on Computational Biology (ECCB), 21-25 July, 2007, Vienna, Austria.
    - Poster presentation: A Bayesian network framework for modelling the regulatory mechanisms behind cancer outcomes.

- 8th BioPathways meeting at ISMB-ECCB 2007, July 19-20, 2007, Vienna, Austria.

- 2006
  - RECOMB satellite conference on Systems Biology and Computational Proteomics, San Diego, US, 1-3 December 2006
  - Algorithmic Biology 2006, San Diego, US, 30 November 2006
    - Poster presentation: Integration of expression and textual data enhances the prediction of prognosis in breast cancer.
  - Benelux Bioinformatics Conference (BBC), Wageningen, The Netherlands, 17-18 October 2006
    - Poster presentation: A Bayesian network framework for modelling the regulatory mechanisms behind cancer outcomes.
  - 14th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), Fortaleza, Brazil, 6 Aug - 10 Aug
    - Oral presentation: Predicting the prognosis of breast cancer by integrating clinical and microarray data with Bayesian networks
  - In Silico Analysis of Proteins - Celebrating the 20th Anniversary of Swiss-Prot, Fortaleza, Brazil, 30 Jul - 4 Aug
    - Poster presentation: Integrating proteomics in medical decision support systems using Bayesian networks
  - Probabilistic modelling and Machine Learning in Structural and Systems Biology (PMSB), Tuusula, Finland, 17 Jun - 18 Jun
    - Poster presentation: Prior distributions for learning genetic networks
  - Workshop on Knowledge Discovery and Emergent Complexity in Bioinformatics (KDECB 2006), Ghent, Belgium, 10 May
  - 14th IFAC symposium on System Identification, SYSID, Newcastle, Australia, 29 Mar - 31 Mar
    - Oral presentation: Integration of clinical and microarray data using Bayesian networks
  - *BIOPATTERN(FP6 project) - EWADP workshop, Liverpool, UK, 15 Feb - 17 Feb*
  - *BIOPATTERN(FP6 project) - Bioinformatics workshop, Florence, Italy, 10 Jan - 12 Jan*
    - *Oral presentation: integration of clinical and microarray data with Bayesian networks*
- 2005
  - Integrative Post Genomics Meeting, Lyon, France, 30 Nov - 2 Dec
    - Poster presentation: Combining clinical and microarray data to predict prognosis of breast cancer
  - Microarray uses group meeting, Ghent, Belgium, 18 Nov
  - *ERNSI, Louvain-La-Neuve, Belgium, 19 Sept - 21 Sept*

        - Poster presentation: Bayesian networks with prior knowledge to predict ectopic pregnancies
    - *IUAP study day, Liege, Belgium, 19 May*
        - Poster presentation: Modelling ovarian masses with Bayesian networks
    - Benelux Bioinformatics Conference (BBC), Ghent, Belgium, 14 Apr - 15 Apr
        - Poster presentation: Modelling ovarian masses with Bayesian networks
    - *BIOPATTERN - Cancer data analysis workshop, Leuven, Belgium, 21 Feb - 22 Feb*
- 2004
    - 4th VIB Microarray user group meeting, Brussels, Belgium, 18 Nov - 19 Nov

Referee for

- International Journal of Artificial Intelligence in medicine
- International Journal of Computer Mathematics
- BMC Bioinformatics
- Bioinformatics
- Genome Biology
- Human Reproduction

Membership

- International Society for Computational Biology (ISCB) since August 2006

Computer knowledge

Software

- Windows, MS-Office, Linux (basics)
- Eclipse
- Cytoscape
- Matlab

Programming languages

- Java
- Perl
- C++
- SQL

- R (basics)
- SAS (basics)
- Prolog
- Pascal

Web

- HTML, JavaScript
- XML
- PHP(basics)

Database experience

- Entrez
- Ensembl
- BIND

Other

- LaTeX

Languages

Dutch: Mother tongue
English: very good
French: good
German: basics
Spanish: beginner

Hobbies

- Basketball
- Snowboarding
- Cycling
- Reading (Fiction: Science Fiction and Fantasy, Non-fiction: history, economics, popular science)
- Cooking: Mediterranean and South-American kitchen
- Swimming
- Squash
- Travel