

# Steven Maere

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## Personal data



Name	<a href="#">Steven Maere</a>
Date of Birth	Nov 20, 1976
Place of Birth	Ghent, Belgium
Nationality	Belgian
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## Education

- **MSc in Engineering Physics**      **Ghent University, Belgium (1994-1999)**

Specialized in Radiation and Particle Physics and Optoelectronics.

Graduated magna cum laude on July 9, 1999.

Master's thesis: 'Energy minimization of model proteins using the Honeycutt-Thirumalai model and the Effective Diffused Potential method' (in Dutch). Examined the protein-folding problem using a diffusion method derived from theoretical quantum mechanics (advisor: Prof. Dr. H Verschelde).

- **MSc in Biotechnology**      **Ghent University, Belgium (1999-2001)**

Graduated summa cum laude on September 21, 2001.

Master's thesis: 'Structure-activity relationships of Virginiamycin S analogues' (in Dutch). NMR study of several VS analogues, relating chemical and structural differences to antibiotic activity (advisor: Prof. Dr. F Borremans).

- **PhD in Biotechnology**      **Ghent University, Belgium (2001-2006)**  
**(Computational Biology)**

Obtained PhD on May 19, 2006 with 'congratulations of the jury' (~summa cum laude). Title: 'Development of mathematical methods for modeling biological systems'. I developed various analysis methods for functional genomics data. An important part of my PhD work was devoted to the study of gene and genome duplications in *A. thaliana*, in particular the generation, retention and loss of duplicate genes during evolution, their expression divergence and their potential impact on the evolution of complexity in angiosperms. (advisors: Prof. Dr. Marc Zabeau, Prof. Dr. Martin Kuiper and Prof. Dr. Ir. Dirk Aeyels).

## Postdoc experience

- since October 2006: FWO Postdoctoral Fellow in the [Bioinformatics & Evolutionary Genomics lab](#) of Prof. Dr. Yves Van de Peer, Plant Systems Biology dept., VIB/Ghent University, Belgium. Research interests: see below.
- Sept 2008 – Sept 2009: visiting postdoc in the [lab of Prof. Dr. Michael Eisen](#), UC Berkeley, CA, modeling the transcriptional regulation of embryonal development in *D. melanogaster*.

## Research interests

### Modeling Biological Systems

With the availability of fully sequenced genomes and the development of high-throughput functional genomics technologies, we now have the tools to look at the molecular biology of an organism from a systemic viewpoint. Systems biology is a dynamic and highly interdisciplinary field, requiring input from biology as well as engineering, physics and mathematics. My main interest is the development of methods to analyze functional genomics data and integrate them in models that reflect the regulatory wiring and modularity of biological systems, and ultimately predict their behavior. I'm especially interested in figuring out how biological systems evolved.

### Impact of gen(om)e duplications on plant evolution

Expansion of gene families by duplication and subsequent functional diversification is considered to be of major importance for the development of biological novelties during evolution. However, we have only begun to elucidate the mechanisms underlying evolutionary innovation through gen(om)e duplication. Particularly, expansion and functional diversification of regulatory gene families is considered necessary to bring about an increase in morphological complexity. Recent studies in *A. thaliana* have indeed found that transcription factors, signal transducers and developmental genes have been retained in excess after genome duplications. More importantly, it seems that the majority of these genes could have been retained only because they were created through genome duplication, suggesting a key role for large-scale gene duplication events in plant evolution.

I'm currently studying the impact of small- and large-scale gene duplications in the evolution of plant complexity and developmental processes (evo-devo) from a systems biology perspective. In recent years, it has become widely acknowledged that one needs to study the evolution of genetic networks in order to comprehend the evolution of organisms. Such network-level analyses have recently become feasible thanks to the increased availability of relevant functional genomics data.

## A1 Publications

- (10) \* Fawcett J, \* **Maere S**, Van de Peer, Y. (2008) Polyploidization may have contributed to the survival/propagation of many plants during or following the Cretaceous–Tertiary (KT) extinction event. (submitted)
- (9) **Maere S**, Van Dijck P, Kuiper M (2008) Extracting expression modules from perturbational gene expression compendia. *BMC Systems Biology* 2:33.  
IF: - C: 0
- (8) Cline MS, Smoot M, Cerami E, Kuchinsky A, Landys N, Workman C, Christmas R, Avila-Campilo I, Creech M, Gross B, Hanspers K, Isserlin R, Kelley R, Killcoyne S, Lotia S, **Maere S**, Morris J, Ono K, Pavlovic V, Pico AR, Vailaya A, Wang P-L, Adler A, Conklin BR, Hood L, Kuiper M, Sander C, Schmulevich I, Schwikowski B, Warner GJ, Ideker T, Bader GD (2007) Integration of biological networks and gene expression data using Cytoscape. *Nature Protocols* 2, 2366-2382.  
IF: 1.671 C: 17
- (7) Fleury D, Himanen K, Cnops G, Nelissen B, Boccardi TM, **Maere S**, Beemster GTS, Neyt P, Anami S, Robles P, Micol JS, Inzé D, Van Lijsebettens M (2007) The *Arabidopsis thaliana* homolog of yeast BRE1 has a function in cell cycle regulation during early leaf and root growth. *Plant Cell* 19, 417-32.  
IF: 9.868 C: 11
- (6) \* Michoel T, \* **Maere S**, Bonnet E, Joshi A, Saeys Y, Van den Bulcke T, Van Leemput K, van Remortel P, Kuiper M, Marchal K, Van de Peer Y (2007) Validating module networks learning algorithms using simulated data. *BMC Bioinformatics* 8, S5.  
IF: 3.617 C: 2
- (5) Blomme T, Vandepoele K, De Bodt S, Simillion C, **Maere S**, Van de Peer Y (2006) The gain and loss of genes during 600 million years of vertebrate evolution. *Genome Biology* 7, R43.  
IF: 7.172 C: 48
- (4) Casneuf T, De Bodt S, Raes J, **Maere S**, Van de Peer Y (2006) Nonrandom divergence of gene expression following gene and genome duplications in the flowering plant *Arabidopsis thaliana*. *Genome Biology* 7, R13.  
IF: 7.172 C: 23
- (3) **Maere S**, Heymans K, Kuiper M (2005) BiNGO: a Cytoscape plugin to assess overrepresentation of Gene Ontology categories in biological networks. *Bioinformatics* 21, 3448-9.  
IF: 6.019 C: 90
- (2) \* De Bodt S, \* **Maere S**, Van de Peer Y (2005) Genome duplication and the origin of angiosperms. *Trends Ecol Evol* 20, 591-7.  
IF: 14.864 C: 51
- (1) \* **Maere S**, \* De Bodt S, Raes J, Casneuf T, Van Montagu M, Kuiper M, Van de Peer Y (2005) Modeling gene and genome duplications in eukaryotes. *Proc Natl Acad Sci USA* 102, 5454-9.  
IF: 10.231 C: 104

\*contributed equally

IF: Impact Factor

C: Citations

## Conference papers

(1) Baele G, Bredeche N, Haasdijk E, **Maere S**, Schmickl T, Schwartz C, Thenius R, Van de Peer Y (2009) Open-ended on-board evolutionary robotics in the context of a swarm of robots. IEEE Congress on Evolutionary Computation (CEC) 2009 (authors in alphabetical order, submitted)

## Book chapters

(1) **Maere S**, Wischnitzki E, Van de Peer Y (2008) Biased retention of duplicated genes. In: Evolution after Gene Duplication, K Dittmar and D Liberles (eds), Wiley (New York). (in preparation)

## Software

- [BiNGO](#): a Cytoscape plugin for GO enrichment analysis
- [LeMoNe](#): a software tool to learn module networks from gene expression data
- [ENIGMA](#): a tool for inference of expression modules from perturbational gene expression data

## Seminars

- Systems and integrative biology: an overview, keynote, March 2008, Blankenberge (Belgium)
- Combinatorial analysis of perturbational gene expression compendia, Third Benelux Bioinformatics Conference (BBC2007), November 2007, Leuven (Belgium)
- BiNGO, a Cytoscape plugin to assess enrichment of GO categories in biological networks, invited speaker, 5<sup>th</sup> Annual Cytoscape Retreat, November 2007, Amsterdam (Netherlands)
- Combinatorial analysis of perturbational gene expression compendia, invited speaker, VIBE2007 conference (Irish Bioinformatics Conference), September 2007, Dublin (Ireland)
- Reconstructing gene expression networks by combinatorial analysis of perturbed expression profiles, Gent-Lille Workshop on Computational Biology, June 2006, Lille (France)
- Investigating the impact of gene and genome duplications on the evolution of development in angiosperms, invited speaker, Workshop on Biological Networks III: Modularity and Genome Evolution, June 2006, Bertinoro (Italy)
- BiNGO, a Cytoscape plugin to assess overrepresentation of GO categories in biological networks, invited speaker, 5th VIB MicroArray User Group Meeting, November 2005, Gent (Belgium)
- BiNGO, a Cytoscape plugin to assess overrepresentation of GO categories in biological networks, invited speaker, GO Users Meeting, September 2005, Bergen (Norway)

- Modeling the birth and death of genes in *Arabidopsis thaliana* to explain plant evolution and complexity, keynote, First Benelux Bioinformatics Conference (BBC2005), April 2005, Gent (Belgium)
- BiNGO, a Cytoscape plugin for functional annotation of biological networks, invited speaker, 2<sup>nd</sup> Annual Cytoscape Retreat, September 2004, New York (USA)
- Modularity and crosstalk in the transcriptional behaviour of *S. cerevisiae*, VIB seminar, March 2004, Blankenberge (Belgium)

### Teaching

- Institute for Continuing Education in Science (ICES), Ghent University: (Introductory Course in) Bio-informatics (October 2006)
- Marine Genomics Europe (MGE) short training course, Ghent University: Bioinformatics III – Advanced bioinformatics for analyzing eukaryotic genomes (May 2007)
- Computational biology and modeling of biological systems, course in the second Master Biochemistry-Biotechnology, Ghent University (starting 2009-2010)

### Undergraduate thesis guidance

- Karel Heymans, MSc Informatics, Ghent University, 2003-2004: BiNGO: a Cytoscape plugin for functional annotation of gene clusters.
- Ana Belenguer Piles, MSc Informatics, Ghent University, 2004-2005: BiNGO: a Cytoscape plugin to assess enrichment of Gene Ontology categories in biological networks.
- Frederick Depuydt, MSc Computer Science Engineering, Ghent University, 2007-2008: Development of a graph-theoretical method for combining clustering ensembles.

### Organizing committees

- Member of organizing committee Benelux Bioinformatics Conference 2005, April 11-12 2005, Gent.
- Member of organizing committee Marine Genomics Workshop, May 7-11 2007, Gent.

### Scholarships and Awards

- 2008-2009: FWO travel grant
- 2008-2009: Fulbright-Hays Award
- 2008-2009: Belgian-American Educational Foundation (BAEF) Research Fellowship
- 2006-2009: Flanders Fund for Scientific Research (FWO) Postdoctoral Fellowship
- 2002-2006: Flanders Fund for Scientific Research (FWO) Predoctoral Fellowship
- Special Prize for Latin in high school

## Reviewer services

Nature, Science, PNAS, PLoS One, PLoS Computational Biology, Genome Biology, BMC Systems Biology, BMC Bioinformatics, Bioinformatics, Nucleic Acids Research, Molecular Biology and Evolution, Journal of Molecular Evolution, Plant Physiology, ISMB, RECOMB.

## Membership of scientific associations

- Member of the International Society for Computational Biology (ISCB)
- Member of the European Plant Science Organization (EPSO)
- Member of the National Geographic Society

## Languages

- Dutch native
- English, French excellent
- German, Spanish basic

## Computers

- OS Linux, MacOS, Windows
- Languages Java, C, C++, Perl
- Other Matlab, R, LaTeX, ...

## Selected other Activities and Interests

- Built a computer-controlled model of a linear accelerator used in cancer treatment (University Hospital Ghent, Radiotherapy dept., summer 1994).
- Student representative in 1<sup>st</sup> and 2<sup>nd</sup> year of civil engineering studies (1994-1996).
- Active member of student radio URGent, reviewing films and comic books in the cultural program 'Café civilisé' (1994-2001)
- Vice-chair (1997-1998) and culture chair (1998-1999) of the VVN, an association of physics students at the University of Ghent organizing lectures and other activities.
- Analysis, Algebra and Physics Tutor. Tutored students toward successful completion of their undergrad exams (Docentes NV, Ghent, 2000-2001)
  
- Adventurous traveling, backpacking
- Sailing, diving
- Piano
- Classical, jazz and blues concerts, world music festivals
- Collecting European comic books

## References

- Prof. Yves Van de Peer, Dept. of Plant Systems Biology, VIB, Dept. Molecular Genetics, Ghent University, Technologiepark 927, 9052 Gent (Zwijnaarde), Belgium  
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- Prof. Kenneth H Wolfe, Smurfit Institute of Genetics, University of Dublin, Trinity College, Dublin 2, Ireland  
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- Prof. Michael Eisen, Eisen Lab, QB3 Institute, 387 Stanley Hall #3220, University of California, Berkeley, CA 94720-3220, USA  
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