UNIVERSITEIT
GENT

SOLLICITATIEFORMULIER VOOR EEN BEVORDERING IN HET ZELFSTANDIG ACADEMISCH PERSONEEL [*]

SOLLICITATIE voor een bevordering tot (ambt):

tijdens het jaar: 2015

in de faculteit: Wetenschappen

brief decaan dd.:

1. PERSONALIA

Naam:	Marchal
Voornamen:	Kathleen
Geboortedatum:	30/10/1972
Huidige graad (met vermelding voltijds of deeltijds met aanduiding omvang):	Hoofddocent (voltijds)
Vakgroep of dienst:	Plantenbiotechnologie en Bio-informatica
Vakgebied:	Computationele Biologie
Dienstadres:	Technologiepark 927 9052 Zwijnaarde
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[*] Ook te gebruiken voor uitbreidingen van ZAP-ambt. In dat geval dient de vermelding in het eerste tekstvak aangepast

ACADEMISCH (UNIVERSITAIR) ONDERWIJS

1.1 ACADEMISCHE OPLEIDINGEN

Diploma 2de cyclus

naam: Bio IR Scheikunde

behaalde graad: Grote onderscheiding

universiteit: KU Leuven

jaar: 1995

ANDERE ACADEMISCHE OPLEIDINGEN (2de cyclus, met inbegrip van lerarenopleiding):
(met naam van het of de diploma's, behaalde graad, universiteit, jaar)

Naam diploma	Behaalde graad	Universiteit	Jaar
Acad. lerarenopleiding.Bio-ingenieurswet			
Aggregaat Biologie	Voldoening	KU Leuven	**1998**

1.2 VOORTGEZETTE ACADEMISCHE OPLEIDINGEN (3^de^ cyclus) en POSTACADEMISCHE VORMING

Aanvullende opleidingen, specialisatieopleidingen, doctoraatsopleiding, docententraining, …

(met vermelding van behaald diploma of getuigschrift, behaalde graad, universiteit en jaar)

Diploma of getuigschrift	Graad	Universiteit	Jaar
DOCT Bio–ingenieurswetenschappen	Geen graad	KU Leuven	1999

Doctoraat (of Aggregaat Hoger Onderwijs) in de: Bio–ingenieurswetenschappen

Titel van proefschrift:	The O_2 paradox of Azospirillum brasilense under diazotrophic conditions
Promotor:	Prof. J. Vanderleyden
Behaalde graad:	Geen graad
Universiteit:	KU Leuven
Datum:	25/11/1999

2. **BEROEPSLOOPBAAN** (met vermelding van de nevenactiviteiten)

Functie of opdracht	Instelling of werkgever	Van (d/m/j)	Tot (d/m/j)
aspirant f.w.o. (100%)	FWO	01/10/1995	30/09/1999
wetenschappelijk medewerker KU Leuven ESAT (100%)	KU Leuven	01/10/1999	30/11/1999
wetenschappelijk medewerker KU Leuven ESAT (100%)	KU Leuven	01/12/1999	30/09/2001
postdoctoraal onderzoeker f.w.o. (100%)	FWO	01/10/2001	30/09/2004
buitengewoon gastdocent KU Leuven (100%)	KU Leuven	01/10/2002	30/09/2004
docent KU Leuven (100%)	KU Leuven	01/10/2004	30/09/2008
hoofddocent KU Leuven (100%)	KU Leuven	01/10/2008	31/08/2011
hoofddocent KU Leuven (20%)	KU Leuven	01/09/2011	31/08/2014
hoofddocent UGent (100%)	UGent	01/09/2011	heden

3. ONDERWIJS

Beschrijf in maximum één bladzijde:

- het gepresteerde onderwijs (vermelding van instelling, duur en voorwerp van het reeds gegeven onderwijs)
- uw persoonlijke inbreng (opvatting en opbouw van de cursus, koppeling onderwijs-onderzoek, onderwijsvernieuwing, verdere planning ...)

Gepresteerd onderwijs

KU Leuven

Onderwijsactiviteiten aan de KU Leuven als docent:
IF17: Bio-informatica werkcollege, 2e ir bio-ir Cel en Gen Biotechnologie
2002-2003 (formeel toekend voor 50%)
2003-2004 (formeel toekend voor 100%)
2004-2005 (formeel toekend voor 100%)
2005-2006 (formeel toekend voor 100%)

Sinds 2006 werd het master vak een bachelorvak (Bachelor in Bioengineering: Cel en Gen)

I0O15a: Bioinformatica
2006-2007 (formeel toekend voor 100%)

Onderwijsactiviteiten aan de KU Leuven als hoofddocent:

Lesactiviteiten

Vaknr	Titel	Totaal ECTS	Toegewezen/ECTS	Begeleidingsuren	Jaar
Master of Science in Bioinformatics (KU Leuven)					
I0D51a	Bio-informatics: High-Throughput Analysis	5.00	2.33	39.00	2008-2011
I0D52a	Bio-informatics: Structural and Comparative Genomics	4.00	2.00	26.00	2008-2011
I0S08a	Applied Statistical Methods, Part I	2.00	1.00	17.00	2008-2011
I0S09a	Applied Statistical Methods, Part II	1.00	0.50	9.00	2008-2011
I0S11a	Exercises in Applied Statistical Methods, Part I	1.00	0.50	12.00	2008-2011
I0S12a	Exercises in Applied Statistical Methods, Part II	1.00	0.50	12.00	2008-2011
Bachelor in Bioengineering: Cel en Gen					
I0O15a	Bioinformatica	4.00	4.00	39.00	2008-2013
Master in Bioengineering: Cel en Gen					
I0P53a	Seminarie cel- en gentechnologie	4.00	0.29	40.04	2008-2011
I0P49a	Bioinformatica en genoomtechnologie	6.00	1.50	52.00	2008-2011

Masterscripties

In het totaal werden minstens 19 masterscripties/masterprojecten begeleid in zowel de bioingenieurs als de ingenieursfaculteit.

Hieronder enkel een overzicht van de begeleide masterscipties aan de KU Leuven sinds 2011-2012

2011-2012

Sabrina Knapen, Identification of disease molecular subtypes and specific drug responses, master of science in bioinformatics, KU Leuven (2012-2013)
Bram Weytjens, Network based QTL analysis for bacterial trait selection master of science in ingenieurswetenschappen, KU Leuven (2012-2013)
Jimmy Van den Eynde: master of science in bioinformatics, KU Leuven

Nele Cosemans, master of science in bio-ingenieurswetenschappen, KU Leuven (2013-2014)
Ruiyang Jing, master of science in bioinformatics, KU Leuven (2013-2014)
Monica Roxana Ticlla Ccenhua, master of science in bioinformatics, KU Leuven (2013-2014)

UGent

Lesactiviteiten

Academiejaar 2013-2014 (UGent)

Bio-informatica I (C002374, Bachelor of Science in biochemie en biotechnologie), 50% met V. Vermeirssen als colesgever). Totaal eigenaandeel: A uren 12.5 h, B uren 7.5 h (zelf gegeven).

Biostatistiek (C000133, 3ECTS; Master of Science in de biochemie en de biotechnologie), 50% met als colesgever L. Clement). Totaal eigenaandeel: A uren 7.5 h, B uren 3 h (zelf gegeven).

Deze vakken zullen in de volgende jaren behouden blijven

Bachelor- en masterprojecten

Project in de bachelorproef (olv S. Goormachtig) (2012-2013)
Master project Master of science biochemie en bio-technologie, Els Bauwens (203-2014)
Master project Master of science biochemie en bio-technologie, Johannes Lauenstein (203-2014)

Masterscripties

UGent
A human network to interpret high-throughput cancer data Bo Colruyt, Master of science in biochemistry and biotechnology, U Gent (2012-2013)

Andere

a) Universitaire permanente vorming
ICES: Institute for Continuing Education in Science, Universiteit Gent, 2001
Module : Bioinformatics, (3 u)

ICES: Institute for Continuing Education in Science, Universiteit Gent, 2003, 2006
Module : Bioinformatics (6u)
Module: Biostatistics (3u)

b) in het kader van ontwikkelingssamenwerking
Docent bioinformatics in het kader van een VLIR samenwerking tussen Vlaanderen en Cuba (www.uclv.edu.cu). Verblijf van 19/03/05-4/04/05 in Santa Clara, Cuba; Verblijf van 02/12/06-12/11/06 in Santa Clara, Cuba.

Persoonlijke inbreng

1.4.1.B Visie voor de toekomst:

Probleemoplossend denken, interdisciplinariteit, flexibilteit en openheid voor permanente wetenschappelijke kennisontwikkeling zijn onderwijsspecifieke leerresultaten, essentieel voor het domein van de bio-informatica

Deze interdisciplinariteit impliceert dat ten minste een bepaald onderdeel van de leerstof niet in de lijn ligt van het vakgebied waarvoor de student initieel heeft gekozen (bv wiskundige aspecten gedoceerd aan een publiek met biologische achtergrond en vice versa). Om studenten te 'motiveren' voor een vakdomein waarmee ze niet vertrouwd zijn, heb ik via praktijkervaring geleerd dat het zoeken naar aanknopingspunten van de leerstof me de leef- en ervaringswereld van de studenten essentieel is (bv het belang van bio-informatica voor personalized medicine, sustainable agriculture,...). Dit vereist het volgen van prominente vakliteratuur (nature, science, ...) waarin nieuwe trends beschreven worden.
Het aanbrengen van meer wiskundig georiënteerde lesonderdelen aan biologen is gebaseerd op concrete voorbeelden, toepassingen waarmee een wiskundige intuitie kan worden gestimuleerd eerder dan op exacte bewijsvoeringen. Op dit principe zijn mijn cursussen bio-informatica en biostatistiek gebaseerd (een eigen cursus werd hiervoor opgesteld). Omdat bio-informatica een snel evoluerend onderzoeksdomein is moeten de gebruikte voorbeelden steeds aangepast worden. Dit vereist het continue volgen van de literatuur en het introduceren van nieuwe technieken/methoden/concepten van zodra deze voldoende ingeburgerd zijn in het onderzoeksdomein (dus van zodra het standaard analysemethoden geworden zijn in het bio-informatica onderzoek, e.g. next-generation sequencing heeft microarray analyse vervangen). Cursussen moeten dus continue bijgeschaafd en geupdated worden (zeker op het masterniveau).
In een cursus zijn naast kennisontwikkeling het ontwikkelen van cognitieve vaardigheden zoals analytisch en probleemoplossend denken en het ontwikkelen van communicatieve vaardigheden essentieel. Om deze voldoende te ontwikkelen werd gekozen voor een combinatie van verschillende onderwijs en evaluatievormen (hoorcollege, PC werkcollege waar studenten praktische ervaring opdoen in R, begeleide zelfstudie om eigen analytische skills te ontwikkelen, groepswerk ". Naar evaluatie toe probeer ik zo transparant mogelijk te zijn, door studenten reeds bij de eerste les op de hoogte te brengen van de aard van het examen en ze tijdens het jaar ook voorbeeld vragen aan te rijken. Het examen bestaat uit open vragen met o.a. juist/fout vragen waar studenten die een goed doordacht antwoord geven kunnen onderscheiden worden.

Naar de toekomst toe zou ik willen gebruik maken van vernieuwde onderwijsvormen (bv afstandsonderwijs, electronische leeromgeving). Dit laatste ook meer in het kader van internationalisatie en ontwikkelingshulp waarvoor ik in het kader van VLIR samenwerkingen reeds een aantal keren heb lesgegeven. Ook indien de interfacultaire master of Science in de Bio-informatica er zou komen kan internationalisatie en afstandsonderwijs een pluspunt zijn (zeer goede cursussen die via afstandsonderwijs worden aangeboden zijn interessant voor de PR van de organiserende opleiding).

In het kader van het onderwijs heb ik mij actief ingezet voor het oprichten van een interfacultaire master of Science in de Bio-informatica (als voorzitter van de werkgroep) (het opstellen van het programma, het opmaken van het dossier voor de NVAO, het bespreken van de master met de verschillende betrokken faculteiten). Als de master er komt zou ik mij willen blijven inzetten voor deze master o.a. om de master nationaal en internationaal op de kaart te zetten (door de nodige PR te organiseren en deel te nemen aan internationale onderwijscommissies zoals deze georganiseerd door ISCB). Bovendien heb ik in mijn hoedanigheid als voorzitter van de onderwijscommissie van de 'Master of Science in Bioinformatics' aan de KU Leuven inzicht verworven in hoe bestaande onderwijsstructuren en de praktisch-administratieve implementatie van het onderwijs (ISPs, programmawijzigingen) vaak niet aangepast zijn aan de dagelijkse organisatie van een interfacultaire master. Het vlot organiseren van de master, moest deze er komen zal dan ook niet triviaal zijn en de nodige inzet vereisen.

4. WETENSCHAPPELIJK CURRICULUM : (cf. bijlagen 1, 2 en 3)

5. WETENSCHAPPELIJKE ONDERSCHEIDINGEN EN PRIJZEN

Laureaat DSM prijs voor Chemie en Technologie, 2000: The O2 paradox of Azospirillum brasilense.
Toekennende instantie: DSM

Gehanteerde criteria: het werk van de kandidaat onderscheidt zich door zelfstandigheid, originaliteit, nieuwheid en kwaliteit. Uitstraling buiten het vakgebied en toepasbaarheid zullen medebepalend zijn bij de selectie (citaat uit aanvraag formulier DSM prijs). Het merendeel van de geselecteerde onderwerpen situeerden zich in in het domein van onderzoek naar duurzame landbouw en nanotechnologie;
Jaar van toekenning: 2000
Bedrag: 1250 Euro

Tweejaarlijkse Siemens prijs 2002 voor Yves Moreau, Kathleen Marchal en Janick Mathys. Medische bio-informatica: een interdisciplinair kruispunt.
Bedrag: 7000 euro

Ik bevestig dat de bovenstaande gegevens alsook het wetenschappelijk curriculum in eer en geweten werden ingevuld en mogen nagegaan worden.

04/03/2014

Datum en handtekening

Aantal bijlagen: 3

Bijlage 1

PUBLICATIES (GERANGSCHIKT PER CATEGORIE VOLGENS ONDERSTAANDE DEFINITIES EN BINNEN IEDERE CATEGORIE CHRONOLOGISCH)

Boeken

(b_1) auteur of co-auteur van boeken

(b_2) hoofdstukken in boeken (geen proceedings van conferenties)

(b_3) boeken als editor

Artikels

(a_1) artikels opgenomen in ISI Web of Science (Science Citation Index, Social Science Citation Index, Arts and Humanities Citation Index) – beperkt tot artikels van het type: article, review, letter, note, proceedings paper

(a_2) artikels in wetenschappelijke tijdschriften die een ruime verspreiding kennen, een beroep doen op internationale deskundigen voor de beoordeling van de ingezonden manuscripten en niet begrepen zijn in (a_1)

(a_3) artikels in nationale tijdschriften die gebruik maken van een leescomité en niet begrepen zijn in (a_1) en (a_2)

(a_4) artikels in tijdschriften niet begrepen in (a_1), (a_2) en (a_3)

Andere publicaties

(c_1) artikels in proceedings van wetenschappelijke congressen, niet begrepen in vorige rubrieken (volledige artikels met uitsluiting van abstracts)

(c_2) octrooien

(p_1) artikels in proceedings opgenomen in één van de ISI Web of Science databanken 'Conference Proceedings Citation Index – Science' of 'Conference Proceedings Citation Index – Social Science and Humanities' en beperkt tot publicaties van het type: article, review, letter, note, proceedings paper, met uitzondering van de publicaties die reeds onder de rubriek (a_1) zijn opgenomen

Bibliography

For a full list of peer-reviewed publications see also
http://scholar.google.nl/citations?user=MAjGtncAAAAJ&hl=nl
http://www.researcherid.com/rid/B-5001-2013)

Articles

A1 (Articles in internationally reviewed academic journals)

1. Duitama, J., Sanchez-Rodriguez, A., Goovaerts, A., Pulido-Tamayo, S., Hubmann, G., R Foulquié-Moreno, M.R., Thevelein, J.M., Verstrepen K.J., and Marchal K. Improved linkage analysis of Quantitative Trait Loci using bulk segregants unveils a novel determinant of high ethanol tolerance in yeast. BMC Genomics, accepted.

2. Yao Y., Marchal, K. and Van de Peer, Y. Improving the adaptability of simulated swarm evolutionary robots in dynamically changing environments. Plos One, accepted.

3. Fu, Q., Fierro Gutiérrez, A., Meysman, P., Sanchez Rodriguez, A., Vandepoele, K., Marchal, K., Engelen, K. (2014). MAGIC: access portal to a cross-platform gene expression compendium for maize. *Bioinformatics, Ahead of print* (most recent IF: 5.32).

4. Ishchukov, I., Wu, Y., Van Puyvelde, S., Vanderleyden, J., Marchal, K. (2014). Inferring the relation between transcriptional and posttranscriptional regulation from expression compendia. *BMC Microbiology, Ahead of print* (1), 14. (most recent IF: 3.1).

5. Wuyts, V., Mattheus, W., De Laminne de Bex, G., Wildemauwe, C., Roosens, N., Marchal, K., De Keersmaecker, S., Bertrand, S. (2013). MLVA as a tool for public health surveillance of human Salmonella Typhimurium: prospective study in Belgium and evaluation of MLVA loci stability. *PLoS One, 8* (12), art.nr. 10.1371/journal.pone.0084055, e84055. (most recent IF: 3.73).

6. Meyer, P., Siwo, G., Zeevi, D., Sharon, E., Norel, R., DREAM6 Promoter Prediction Consortium, Segal, E., Stolovitzky, G., Marchal, K. (2013). Inferring gene expression from ribosomal promoter sequences, a crowdsourcing approach. *Genome Research, 23* (11), art.nr. 10.1101/gr.157420.113, 1928-37. (most recent IF: 14.4).

7. Venken, L., Marchal, K., Vanderleyden, J. (2013). Synthetic biology and microdevices: a powerful combination. *ACM Journal on Emerging Technologies in Computing Systems, 9* (4), art.nr. 30 (most recent IF: 0.76).

8. Spaepen, S., Bossuyt, S., Engelen, K., Marchal, K., Vanderleyden, J. (2013). Phenotypical and molecular responses of Arabidopsis thaliana roots as a result of inoculation with the auxin-producing bacterium Azospirillum brasilense. *The New Phytologist*, art.nr. doi: 10.1111/nph.12590 (most recent IF: 6.74).

9. De Maeyer, D., Cloots, L., Renkens, J., De Raedt, L., Marchal, K. (2013). PheNetic: Network-based interpretation of unstructured gene lists in E. coli. *Molecular Biosystems, 9* (7), art.nr. Web of Science 000319882200006, 1594 -1603. (citations: 1) (most recent IF: 3.35).

10. Verbeke, L., Cloots, L., Demeester, P., Fostier, J., Marchal, K. (2013). EPSILON: an eQTL prioritization framework using similarity measures derived from local networks. *Bioinformatics, 29* (10), 1308-1316. (most recent IF: 5.32).

11. Sanchez Rodriguez, A., Cloots, L., Marchal, K. (2013). Omics derived networks in bacteria. Current Bioinformatics. *Current Bioinformatics, 8* (4), 489-495. (most recent IF: 2.02).

12. Thilakarathne, P., Verbeke, G., Engelen, K., Marchal, K., Lin, D. (2013). Identifying Differentially Expressed genes in the Absence of Replication. *International Journal of Bioinformatics Research and Applications, 9*

(1), 71-90.

13. Meysman, P., Marchal, K., Engelen, K. (2013). Identifying common structural DNA properties in transcription factor binding site sets of the LacI-GalR family. *Current Bioinformatics, 8* (4), 483-488. (citations: 0) (most recent IF: 2.02).

14. Meysman, P., Sanchez Rodriguez, A., Fu, Q., Marchal, K., Engelen, K. (2013). Expression divergence between Escherichia coli and Salmonella enterica serovar Typhimurium reflects their lifestyles. *Molecular Biology and Evolution, 20*, art.nr. PMID: 23427276, doi: 10.1093/molbev/mst029. (citations: 0) (most recent IF: 10.35).

15. Aslankoohi, E., Zhu, B., Rezaei, M., Voordeckers, K., De Maeyer, D., Marchal, K., Dornez, E., Courtin, C., Verstrepen, K. (2013). Dynamics of the Saccharomyces cerevisiae Transcriptome during Bread Dough Fermentation. *Applied and Environmental Microbiology, 79* (23), art.nr. 10.1128/AEM.02649-13, 7325-33. (citations: 0) (most recent IF: 3.68).

16. Meysman, P., Sonego, P., Bianco, L., Fu, Q., Ledezma, D., Gama-Castro, S., Liebens, V., Michiels, J., Laukens, K., Marchal, K., Collado-Vides, J., Engelen, K. (2013). COLOMBOS v2.0: An ever expanding collection of bacterial expression compendia. *Nucleic Acids Research*, art.nr. 10.1093/nar/gkt1086 (most recent IF: 8.28).

17. Sun, H., Guns, T., Fierro Gutiérrez, A., Thorrez, L., Nijssen, S., Marchal, K. (2012). Unveiling combinatorial regulation through the combination of ChIP information and in silico cis-regulatory module detection. *Nucleic Acids Research, 40* (12), art.nr. e90, 1-16. (citations: 1) (IF publication year: 8.28) (most recent IF: 8.28).

18. Aslankoohi, E., Voordeckers, K., Sun, H., Sanchez Rodriguez, A., van der Zande, E., Marchal, K., Verstrepen, K. (2012). Nucleosomes affect local transformation efficiency. *Nucleic Acids Research, 40* (19), 9506-9512. (citations: 1) (IF publication year: 8.28) (most recent IF: 8.28).

19. Claeys, M., Storms, V., Sun, H., Michoel, T., Marchal, K. (2012). MotifSuite: workflow for probabilistic motif detection and assessment. *Bioinformatics, 28* (14), 1931-1932. (citations: 0) (IF publication year: 5.32) (most recent IF: 5.32).

20. Voordeckers, K., De Maeyer, D., van der Zande, E., Vinces, M., Meert, W., Cloots, L., Ryan, O., Marchal, K., Verstrepen, K. (2012). Identification of a complex genetic network underlying Saccharomyces cerevisiae colony morphology. *Molecular Microbiology, Ahead of print*, art.nr. 10.1111/j.1365-2958.2012.08192.x (citations: 3) (IF publication year: 4.96) (most recent IF: 4.96).

21. Wu, W., Cai, H., Sun, H., Lu, J., Zhao, D., Qin, Y., Han, X., Niu, X., Lu, C., Xia, Y., Wang, S., De Moor, B., Marchal, K., Wang, X. (2012). Follicle stimulating hormone receptor G-29A, 919A>G, 2039A>G polymorphism and the risk of male infertility : a meta-analysis. *Gene, 505* (2), 388-392. (citations: 5) (IF publication year: 2.2) (most recent IF: 2.2).

22. Meysman, P., Marchal, K., Engelen, K. (2012). DNA structural properties in the classification of genomic transcription regulation elements. *Bioinformatics and Biology Insights, 6*, 155-168.

23. Xu, S., Wu, W., Sun, H., Lu, J., Yuan, B., Xia, Y., De Moor, B., Marchal, K., Wang, X., Xu, P., Cheng, W. (2012). Association of the vascular endothelial growth factor gene polymorphisms (-460 C/T, +450G/C and +936T/C) with endometriosis : a meta-analysis. *Annals of Human Genetics, 76*, 464-471. (citations: 1) (IF publication year: 2.22) (most recent IF: 2.22).

24. Meysman, P., Dang, T., Laukens, K., De Smet, R., Wu, Y., Marchal, K., Engelen, K. (2011). Use of structural DNA properties for the prediction of transcription-factor binding sites in Escherichia coli. *Nucleic Acids Research, 39* (2), art.nr. e6 (citations: 5) (IF publication year: 8.03) (most recent IF: 8.28).

25. Van Puyvelde, S., Cloots, L., Engelen, K., Das, F., Marchal, K., Vanderleyden, J., Spaepen, S. (2011). Transcriptome analysis of the rhizosphere bacterium Azospirillum brasilense reveals an extensive auxin response. *Microbial Ecology, 61* (4), 723-728. (citations: 7) (IF publication year: 2.91) (most recent IF: 3.28).

26. Vercruysse, M., Fauvart, M., Jans, A., Beullens, S., Braeken, K., Cloots, L., Engelen, K., Marchal, K., Michiels, J. (2011). Stress response regulators identified through genome-wide transcriptome analysis of the (p)ppGpp-dependent response in Rhizobium etli. *Genome Biology, 12* (2) (citations: 12) (IF publication year: 9.04) (most recent IF: 10.29).

27. Zhao, H., Cloots, L., Van den Bulcke, T., Wu, Y., De Smet, R., Storms, V., Meysman, P., Engelen, K., Marchal, K. (2011). Query-based biclustering of gene expression data using Probabilistic Relational Models. *BMC Bioinformatics, 12,* art.nr. S37 (citations: 3) (IF publication year: 2.75) (most recent IF: 3.02).

28. Cloots, L., Marchal, K. (2011). Network-based functional modeling of genomics, transcriptomics and metabolism in bacteria. *Current Opinion in Microbiology, 14* (5), 599-607. (citations: 4) (IF publication year: 7.93) (most recent IF: 8.23).

29. Fauvart, M., Sanchez-Rodriguez, A., Beullens, S., Marchal, K., Michiels, J. (2011). Genome Sequence of Rhizobium etli CNPAF512, a Nitrogen-Fixing Symbiont Isolated from Bean Root Nodules in Brazil. *Journal of Bacteriology, 193* (12), 3158-3159. (citations: 3) (IF publication year: 3.83) (most recent IF: 3.19).

30. Peyman, Z., Fierro Gutiérrez, A., Sanchez Rodriguez, A., De Moor, B., Engelen, K., Marchal, K. (2011). COMODO: an adaptive coclustering strategy to identify conserved coexpression modules between organisms. *Nucleic Acids Research, 39* (7), E41-U45. (citations: 7) (IF publication year: 8.03) (most recent IF: 8.28).

31. Engelen, K., Fu, Q., Meysman, P., Sánchez-Rodríguez, A., De Smet, R., Lemmens, K., Fierro, A., Marchal, K. (2011). COLOMBOS: access port for cross-platform bacterial expression compendia. *PLoS One, 6* (7), art.nr. e20938 (citations: 6) (IF publication year: 4.09) (most recent IF: 3.73).

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111. Marchal, K., Sun, J., Keijers, V., Haaker, H., Vanderleyden, J. (1998). A cytochrome cbb3-type (cytochrome c) terminal oxidase in Azospirillum brasilense Sp7 supports microaerobic growth. *Journal of Bacteriology, 180*, 5689-5696. (citations: 20) (most recent IF: 3.19).

A3 (Articles in other academic journals)

1. Tytgat, H., Sanchez Rodriguez, A., Schoofs, G., Verhoeven, T., De Keersmaecker, S., Marchal, K., Vanderleyden, J., Lebeer, S. (2012). A combined approach to study the protein glycosylation potential of Lactobacillus rhamnosus GG (LGG). *Communications in Agricultural and Applied Biological Sciences,* 77(1), 15-19.
2. Thijs, I., Marchal, K., Vanderleyden, J. (2010). Synthetische biologie. *Het Ingenieursblad,* 79(4), 59-62.
3. Thijs, I., De Keersmaecker, S., Fadda, A., Engelen, K., Zhao, H., McClelland, M., Marchal, K., Vanderleyden, J. (2007). Combining omics data to unravel the regulatory network controlling Salmonella invasion of epithelial cells. *Communications in Agricultural and Applied Biological Sciences,* 72(1), 55-59.
4. De Smet, F., Marchal, K., Timmerman, D., De Moor, B., Vergote, I., Moreau, Y. (2001). Gebruik van microroosters in de klinische oncologie. *Tijdschrift voor Geneeskunde,* 57(18), 1225-1236.
5. Marchal, K. (2000). De O 2 -paradox. *Chemisch Weekblad,* 14, 29.

Books

B2 (Article in academic book, internationally recognised scientific publisher)

1. Cloots, L., De Maeyer, D., Marchal, K. (2011). Path Finding in Biological Networks to Interpret Functional Data. In: Brown C. (Eds.), *Handbook of Bio- and Neuroinformatics*Springer Verlag.
2. Fu, Q., Lemmens, K., Thijs, I., Meysman, P., Sanchez Rodriguez, A., Sun, H., Fierro, A., Engelen, K., Marchal, K. (2010). Directed module detection in a large-scale expression compendium. In: Van Helden J., Toussaint A., Thieffry D. (Eds.), *Methods in Molecular Biology - Bacterial Molecular Networks (MMB)*.
3. De Smet, R., Lemmens, K., Fierro, A., Marchal, K. (2009). Systems Microbiology: Gaining Insights in Transcriptional Networks. In: Sintchenko V. (Eds.), *Infectious Disease Informatics*. New York: Springer New York, 93-122.
4. Van Hellemont, R., Blomme, T., Van de Peer, Y., Marchal, K. (2007). Divergence of regulatory sequences in duplicated fish genes. In: Folff J. (Eds.), *Genome Dynamics Gene and Protein Evolution*. Basel, Switzerland: Karger, 81-100.
5. Sheng, Q., Moreau, Y., De Smet, F., Marchal, K., De Moor, B. (2005). Advances in cluster analysis of microarray data. In: Azuaje F., Dopazo J. (Eds.), *Data analysis and visualization in genomics and proteomics*, Chapt. 10. Chichester, UK: John Wiley & Sons Ltd., 153-173.
6. Thijs, G., De Smet, F., Moreau, Y., Marchal, K., De Moor, B. (2004). Gene regulation bioinformatics of microarray data. In: Metin A. (Eds.), *Genomics and Proteomics Engineering* 1-41.
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Other publications

P1 (Papers at international scientific conferences and symposia, published in full in proceedings)

1. Le Van, T., Fierro Gutiérrez, A., Guns, T., van Leeuwen, M., Nijssen, S., De Raedt, L., Marchal, K. (2012). *Mining local staircase patterns in noisy data*. International workshop on Co-Clustering and Applications (CoClus'12) in conjunction with IEEE ICDM 2012. Brussels, 10 December 2012 (pp. 1-8).
2. Sun, H., Lemmens, K., Van den Bulcke, T., Engelen, K., De Moor, B., Marchal, K. (2009). *Layout and Post-Processing of Transcriptional Modules*. In : IEEE Computer Society, In the proceedings of IJCBS 2009. the International Joint Conference on Bioinformatics, Systems Biology and Intelligent Computing (IJCBS 2009). Shanghai, China, Aug. 2009 (pp. 116-121). IEEE Computer Society.
3. Agueero-Chapin, Guillermin; Sanchez-Rodriguez, Aminael; Hidalgo-Yanes, Pedro I. (2013) An alignment-free approach for eukaryotic ITS2 annotation and phylogenetic inference PROCEEDINGS IWBBIO 2013: INTERNATIONAL WORK-CONFERENCE ON BIOINFORMATICS AND BIOMEDICAL ENGINEERING, 155-156.
4. Thanh Hai Dang, Engelen, K., Meysman, P., Marchal, K., Verschoren, A., Laukens, K. (2009). Conditional Random Fields feature subset selection based on Genetic Algorithms for phosphorylation site prediction. *International Conference on Knowledge and Systems Engineering (KSE 2009)*. 1st International Conference on Knowledge and Systems Engineering. Hanoi: VIETNAM, OCT 13-17, 2009 (pp. 7-12). NEW YORK: IEEE.
5. De Bie, T., Monsieurs, P., Engelen, K., De Moor, B., Cristianini, N., Marchal, K. (2005). *Discovering transcriptional modules from motif, chip-chip and microarray data*. In : Proceedings of the Pacific Symposium on Biocomputing (PSB 2005). Pacific Symposium on Biocomputing. Hawai, 4-8 january 2005 (pp. 483-494).

C1 (papers in proceedings of international conferences not in previous categories (full articles)

1. Cloots, L., Zhao, H., Van den Bulcke, T., Wu, Y., De Smet, R., Storms, V., Meysman, P., Engelen, K., Marchal, K. (2011). *Query-based biclustering of gene expression data using Probabilistic Relational Models*. In : Proceedings of The Ninth Asia Pacific Bioinformatics Conference (APBC2011). The Ninth Asia Pacific Bioinformatics Conference (APBC2011). Incheon, Korea, 11-14 January 2011.
2. Guns, T., Sun, H., Marchal, K., Nijssen, S. (2010). *Cis-regulatory module detection using constraint programming*. In : Proc. of IEEE International Conference on Bioinformatics & Biomedicine. IEEE International Conference on Bioinformatics & Biomedicine. Hong Kong, 18-21 December 2010 (pp. 363-368). IEEE Computer Society.
3. De Smet, R., Marchal, K. (2010). *An ensemble method for querying gene expression compendia with experimental lists*. In : Proceedings of IEEE International Conference on Bioinformatics & Biomedicine. IEEE International Conference on Bioinformatics & Biomedicine. Hong Kong, 18-21 December 2010 (pp. 363-368).
4. Thilakarathne, P., Verbeke, G., Engelen, K., Marchal, K. (2009). *The Use of Mixed Models to Identify Differentially Expressed Genes when a Single Replicate per Biological Condition is Present*. In : The 2009 International Conference on Bioinformatics & Computational biology, 1, (Arabnia, H., Yang, M. (Eds.)). BIOCOMP09. Las Vegas Nevada, USA, 13-16 July 2009 (pp. 186-190). CSREA press.
5. Sun, H., De Bie, T., Storms, V., Fu, Q., Dhollander, T., Lemmens, K., Verstuyf, A., De Moor, B., Marchal, K. (2009). *ModuleDigger: an itemset mining framework for the detection of cis-regulatory modules*. In : Proceedings of 7th Asia-Pacific Bioinformatics Conference APBC2009, (Zhang, M., Waterman, M., Zhang, X. (Eds.)). 7th Asia-Pacific Bioinformatics Conference APBC2009. Beijing, China, 2009 (pp. 345-369). Tsinghua University Press.
6. Pastor, D., Lemmens, K., Cortés-Calabuig, A., Marchal, K., Denecker, M., De Moor, B. (2007). *GeneReg: Integration of experimental data on the DNA transcription process*. In : Proceedings of the 19th Belgian-Dutch Conference on Artificial Intelligence, (Dastani, M., de Jong, E. (Eds.)). The 19th Belgian-Dutch Conference on Artificial Intelligence. Utrecht, The Netherlands, November 5-6, 2007 (pp. 260-267).
7. De Moor, B., Marchal, K., Mathys, J., Moreau, Y. (2005). *Bioinformatics : Organisms from Venus, Technology from Jupiter, Algorithms from Mars*. In : Mathematics and Genomics(pp. 37-102).
8. Smets, I., Cappuyns, A., Bernaerts, K., van Boxel, N., Sonck, K., De Keersmaecker, S., Monsieurs, P., Van den

Bulcke, T., Marchal, K., Mathys, J., De Moor, B., Vanderleyden, J., Van Impe, J. (2005). *Identifying new drug targets to combat pathogenic infections: An interdisciplinary approach.* In : Proceedings of the 16th IFAC World Congress. 16th IFAC World Congress. Prague (Czech Republic), July 4-8, 2005 (pp. ID 03952).

9. Pochet, N., Janssens, F., De Smet, F., Marchal, K., Vergote, I., Suykens, J., De Moor, B. (2005). *M@CBETH: optimizing clinical microarray classification.* In : Proc. of the 2005 IEEE Computational Systems Bioinformatics Conference (CSB2005). 2005 IEEE Computational Systems Bioinformatics Conference (CSB2005). Stanford, California (US), Aug. 2005 (pp. 89-90).
10. Smets, I., Bernaerts, K., Sun, J., Marchal, K., Vanderleyden, J., Van Impe, J. (2002). *Sensitivity function based model reduction: a bacterial gene expression case study.* In : Preprints of the 15th Triennial World Congress IFAC, International Federation of the Automatic Control (CD-ROM), (Camacho, E., Basañez, L., de la Puente, J. (Eds.)). IFAC World Congress on Automatic Control. Barcelona (Spain), July 21-26, 2002.
11. Moreau, Y., Thijs, G., Marchal, K., De Smet, F., Mathys, J., Lescot, M., Rombauts, S., Rouzé, P., De Moor, B. (2002). *Integrating quality-based clustering of microarray data with Gibbs sampling for the discovery of regulatory motifs.* In : Proceedings JOBIM 2002. JOBIM 2002. St. Malo, France, Jun. 2002 (pp. 75-79).
12. Thijs, G., Marchal, K., Lescot, M., Rombauts, S., De Moor, B., Rouzé, P., Moreau, Y. (2001). *A Gibbs Sampling method to detect over-represented motifs in upstream regions of co-expressed genes.* In : 5th Annual International Conference on Computational Biology (RECOMB 2001). 5th Annual International Conference on Computational Biology (RECOMB 2001). Montreal, Canada, Apr. 2001 (pp. 296-302).
13. Thijs, G., Marchal, K., Lescot, M., Rombauts, S., De Moor, B., Rouzé, P., Moreau, Y. (2001). *A Gibbs Sampling method to detect over-represented motifs in upstream regions of co-expressed genes.* In : Proc. of the 5th Annual International Conference on Computational Biology (RECOMB'2001). 5th Annual International Conference on Computational Biology (RECOMB 2001). Montreal, Canada, Apr. 2001 (pp. 305-312).
14. Thijs, G., Rombauts, S., Lescot, M., Marchal, K., De Moor, B., Moreau, Y., Rouzé, P. (2000). *Detection of cis-acting regulatory elements in plants: a Gibbs sampling approach.* In : Proc. of Bioinformatics of Gene regularisation and structure (BGRS'2000). The second international conference on bioinformatics, genome regulation and structure. Novosibirsk, Russia, Aug. 2000 (pp. 119-123).
15. Marchal, K., Sun, J., Keijers, V., Haaker, H., Vanderleyden, J. (2000). *The cytochrome cbb3 (cytochrome C) terminal oxidase of A. brasilense Sp7.* Nitrogen Fixation: from molecules to crop productivityKluwer Academic Publishers.
16. Marchal, K., Keijers, V., Haaker, H., Vanderleyden, J. (1997). *Evidence for a cbb 3 -type cytochrome c terminal oxidase in Azospirillum brasilense Sp7.* In : Proceedings 11 th International Congress on Nitrogen Fixation(pp. 164).

Bijlage 2

WETENSCHAPPELIJKE ACTIVITEITEN (GERANGSCHIKT PER CATEGORIE VOLGENS ONDERSTAANDE DEFINITIES EN BINNEN IEDERE CATEGORIE CHRONOLOGISCH)

(a) studieverblijven in het buitenland van langere duur (minimum 1 maand)
(met opgave van instelling, periode en aard van de activiteiten)

Aard	Totaal aantal maanden
Verblijf in het kader van doctoraat, Universiteit Wageningen, H. Haaker	4
Verblijf als gastdocent aan de Universiteit van Pretoria, South Africa, Department of Genetics P. Bloomer (Dec 2013)	1

(b) door uzelf georganiseerde internationale of nationale congressen en symposia

Titel	Mijn taak	Aantal deelnemers	Jaar	Duur
IECA: International E. coli Alliance	Member of the organizing committee of IECA	?300	2011	5 days
At the interface between systems and synthetic biology: the conceptualization of modularity" special interest session at ISCB 2011.	Organizing the meeting	20	2011	0.5 day
ECCB (European Conference on Computational Biology)	Member of the organizing committee	+/-500	2010	4 days
DREAM Reverse Engineering Challenges	Member of the Scientific committee		2007, 2009	1 day
special interest session on ISMB (BioRegSig, F. Drablos)	Member of the organizing committee	+/-40	2009, 2010, 2011	1 day
Belgian Bioinformatics Conference	Member of the Scientific committee	+/-200	2003, 2005, 2006	1 day

(c) internationale congressen, symposia en lezingen waarop een actieve bijdrage werd geleverd
(met opgave van plaats, datum, titel van de bijeenkomst en aard van de bijdrage : voordracht, ingestuurde voordracht, postermededeling, sessievoorzitter, rapporteur, enz...) met vermelding in voorkomend geval of de bijdrage is gebeurd op uitnodiging van de organisatoren

1. ***K. Marchal,** J. Vanderleyden, and H. Haaker. Biochemical and genetic evidence for different terminal oxidases in Azospirillum brasilense Sp7. NATO/ESF Workshop: Biological electron-transfer chains: genetics, composition and mode of operation, May 3-7, 1997, Tomar, Portugal, Book of Abstracts, p. 20.*
2. ***K. Marchal,** V. Keijers, H. Haaker, and J. Vanderleyden. Evidence for a cbb$_3$-type cytochrome c terminal oxidase in Azospirillum brasilense Sp7. 1997. In proceedings of the 11th International Congress on Nitrogen Fixation, Paris, Dordrecht, Boston, London p.164. oral presentation*

3. **K. Marchal**, J. Sun, V. Keijers, H. Haaker, and J. Vanderleyden. The cytochrome *cbb*$_3$ (cytochrome *c*) terminal oxidase of *Azospirillum brasilense* Sp7. 2000. In "Nitrogen Fixation: from molecules to crop productivity", eds. F.O. Pedrosa, M. Hungria, M.G. Yales, W.E. Kluwer Academic Publishers, p. 417-418, invited speaker.

4. A. Croonenborghs, S. Dobbelaere, F. Dosselaere, V. Keijers, M. Lambrecht, **K. Marchal**, Y. Okon, D. Ptacek, O. Steenhoudt, E. Somers, J. Sun, A. Thijs, A. Vande Broek, J. Vanderleyden, and A. Van Dommelen. Genetic enhancement of associative microorganisms. 8th international symposium on Nitrogen Fixation with non-legumes, December 3-7, 2000, Sydney, Australia, Book of Abstracts, p. 68.

5. S. De Keersmaecker, G. Thijs, J. Mathys, J. Vanderleyden, B. De Moor, and **K. Marchal.** Extension of the Motif Sampler with a higher order *Salmonella typhimurium* background model. SIM Annual Meeting, July 29-August 2, 2001, St-Louis (Student abstract award, Lecture Abstract), Book of Abstracts, p. 92.

6. **K. Marchal,** J. Sun, I. Smets, K. Bernaerts, J. Van Impe, B. De Moor, and J. Vanderleyden. Quantitative analysis of a bacterial gene expression by using the *gusA* reporter system in a non-steady state continuous culture. ISMB 2001 (9th international conference on intelligent systems for molecular biology), July 21-25, 2001, Kopenhagen, Denmark, Book of Abstracts p. 51.

7. F. De Smet, **K. Marchal,** J. Mathys, G. Thijs, B. de Moor, and Y. Moreau. Adaptive quality-based clustering of gene expression profiles. ISMB 2001 (9th international conference on intelligent systems for molecular biology), July 21-25, 2001, Kopenhagen, Denmark, Book of Abstracts p. 48.

8. G. Thijs, F. De Smet, J. Mathys B. De Moor, and Y. Moreau, and **K. Marchal.** From clustering expression data to motif finding: a multistep online procedure. ISMB 2001 (9th international conference on intelligent systems for molecular biology), July 21-25, 2001, Kopenhagen, Denmark, Book of Abstracts p. 47.

9. *G. Thijs, S. Rombauts, M. Lescot, **K. Marchal**, B. De Moor, Y. Moreau, and P. Rouzé. Detection of cis-acting regulatory elements in plants: a Gibbs sampling approach. 2000. The second international conference on bioinformatics, genome regulation and structure, Novosibirsk, Russia. (BGRS' s 2000) p. 116-119. http://www.bionet.nsc.ru/bgrs2000/index_local.html oral presentation*

10. *G. Thijs, **K. Marchal,** M. Lescot, S. Rombauts, B. De Moor, P. Rouzé, and Y. Moreau. A Gibbs Sampling method to detect over-represented motifs in upstream regions of co-expressed genes. In proceedings of RECOMB 2001. p. 296-302. oral presentation*

11. S. Rombauts, M. Lescot, G. Thijs, **K. Marchal,** C. Simillion, B. De Moor, Y. Moreau, and P. Rouze. *In silico* search for *cis*-acting regulatory sequences in co-expressed gene clusters. ISMB 2001 (9th international conference on intelligent systems for molecular biology), July 21-25, 2001, Kopenhagen, Denmark, Book of Abstracts p. 48.

12. J. Mathys, **K. Marchal,** P. Glenisson, G. Fannes, P. Antal, Y. Moreau, B. De Moor, and P. Van Hummelen. *In silico* search for *cis*-acting regulatory sequences in co-expressed gene clusters. ISMB 2001 (9th international conference on intelligent systems for molecular biology), July 21-25, Kopenhagen, Denmark, 2001, Book of Abstracts p. 51.

13. **K. Marchal**, S. De Keersmaecker, P. Monsieurs, G. Thijs, J. Vanderleyden, and B. De Moor. Analysis of the regulatory elements involved in the *Salmonella typhimurium* invasion pathway using a combination of motif finding and phylogenetic footprinting. PSB2002 (7th Pacific symposium on biocomputing), Januari 2-5, 2002, Kauai, Hawai, Book of Abstracts p. 116.

14. S. Rombauts, M. Lescot, G. Thijs, **K. Marchal,** C. Simillion, Y. Moreau, P. Déhais, Y. Van de Peer, and P. Rouzé. The PlantCARE database and tools for *in silico* search of plant *cis*-acting regulatory elements. PSB2002 (7th Pacific symposium on biocomputing), Januari 2-5, 2002, Kauai, Hawai, Book of Abstracts p. 136.

15. ***K. Marchal,*** *G. Thijs, P. Monsieurs, S. De Keersmaecker, F. De Smet, J. Mathys, Y. Moreau, J. Vanderleyden, and B. De Moor. Studying regulatory pathways using a combination of motif finding and phylogenetic footprinting. 9th International Symposium on Nitrogen Fixation with Non-Legumes, September 1-5, 2002, Leuven, Belgium, selected for oral presentation.*

16. **K. Marchal,** G. Thijs, P. Monsieurs, S. De Keersmaecker, F. De Smet, J. Mathys, Y. Moreau, J. Vanderleyden, and B. De Moor. Studying regulatory pathways using a combination of motif finding and phylogenetic footprinting. 8th Annual Conference and Exhibition of the Society for Biomolecular Screening, September 23-26, 2002, The Hague, The Netherlands, selected for oral presentation.

17. K. Engelen, B. Coessens, P. Van Hummelen, J. De Brabanter, B. De Moor, and **K. Marchal.** Implementation of a generic ANOVA model for the analysis of gene expression data. European conference on computational biology, October 6-9, 2002, Saarbrucken, Germany, Book of Abstracts p 54.

18. G. Thijs, S. Aerts, Y. Moreau, **K. Marchal**, and B. De Moor. Motif Scanner: a novel probabilistic aproach to screen DNA sequences for predefined regulatory elements. European conference on computational biology, October 6-9, 2002, Saarbrucken, Germany, Book of Abstracts p 244.

19. **K. Marchal,** S. De Keersmaecker, P. Monsieurs, N. van Boxel, K. Lemmens, G. Thijs, J. Vanderleyden, and Bart De Moor. *In silico* identification and experimental validation of novel PmrAB targets in *Salmonella typhimurium* by regulatory motif detection. ASM conference on *Salmonella*, September 20-24, 2003, Sardinia, Italy, Book of Abstracts p 70.

20. S. De Keersmaecker, **K. Marchal,** T. L. Verhoeven, C.S. Detweiler, S. Falkow, and J. Vanderleyden. Cluster analysis and motif detection reveal possible new targets of the HilA regulatory protein in *Salmonella typhimurium*. ASM conference on *Salmonella*, September 20-24, 2003, Sardinia, Italy, Book of Abstracts p 83.

21. R. Van Hellemont, **K. Marchal,** P. Monsieurs, G. Thijs, Y. Van de Peer, and B. De Moor. Development of a strategy to identify regulatory elements in eukaryotic promoters based on phylogenetic footprinting. SMBE conference (Society for Molecular Biology and Evolution), June 26-29, 2003, Newport Beach, California.

22. K. Engelen, **K. Marchal,** J. De Brabanter, T. Ayoubi, P. Van Hummelen, and B. De Moor. Comparison of different methodologies to identify differentially expressed genes in two-sample cDNA microarrays European conference on computational biology, September 27-30, 2003, Paris, France, Book of Abstracts p 359.
23. **K. Marchal**, P. Monsieurs, K. Lemmens, N. van Boxel, S. De Keersmaecker, G. Thijs, and J. Vanderleyden, B. De Moor. *In silico* identification and experimental validation of novel PmrAB targets in *Salmonella typhimurium* by regulatory motif detection. European conference on computational biology, September 27-30, 2003, Paris, France, Book of Abstracts p. 425.

24. P. Monsieurs, **K. Marchal,** G. Thijs, S. De Keersmaecker, J. Vanderleyden, and B. De Moor. Characterization of the PhoPQ-regulon by *in silico* motif detection. European conference on computational biology, September 27-30, 2003, Paris, France, Book of Abstracts p. 443.

25. ***K. Marchal,*** *S. De Keersmaecker, P. Monsieurs, N. van Boxel, K. Lemmens, G. Thijs, B. De Moor1, and J. Vanderleyden. Reconstruction of the PmrAB dependent transcriptional network of Salmonella typhimurium by in silico regulatory motif detection, ESF: Bacterial Neural Networks: EuroConference on Inter- and Intracellular Signalling, and Global Regulation in Bacteria, May 8-13, 2004, San Feliu de Guixols, Spain (selected for oral presentation).*

26. P. Monsieurs, **K. Marchal,** S. De Keersmaecker, G. Thijs, B. De Moor, J. Vanderleyden. Comparison of the PhoPQ regulon in *Escherichia coli* and *Salmonella typhimurium,* ESF: Bacterial Neural Networks:

EuroConference on Inter- and Intracellular Signalling, and Global Regulation in Bacteria, May 8-13, 2004, San Feliu de Guixols, Spain.

27. **K. Marchal**, B. Naudts, K. Van Leemput, K. Engelen, A. Verschoren and B. De Moor. Is it realistic to infer a gene network from a small set of microarray experiments? 5th international conference on systems biology, 9-13 oktober 2004.

28. K. Engelen, **K. Marchal,** J. De Brabanter and B. De Moor. Comparison of different methodologies to identify differentially expressed genes in two-sample cDNA microarrays. 5th international conference on systems biology, 9-13 oktober 2004.

29. K. Lemmens, T. Debie, P. Monsieurs, K. Engelen, B. De Moor, N. Christianini and **K. Marchal.** Discovering regulatory modules from heterogeneous information sources. ESF workshop on transcription networks: a global view, 26-28 May, Madrid 2005, Book of Abstracts p. .37.

30. P. Monsieurs, S. De Keersmaecker, W. W. Navarre, M. W. Bader, F. De Smet, M. McClelland, F. C. Fang, B. De Moor, J. Vanderleyden, and **K. Marchal**. Comparison of the PhoPQ regulon in *Escherichia coli* and *Salmonella typhimurium*. International conference on Bacterial Genomes. April 12-16, 2005, Halifax, Canada. Book of abstracts p.54

31. *T. Van den Bulcke, K. Van Leemput, B. Naudts, P. van Remortel, A. Verschoren, B. De Moor and* ***K. Marchal.*** *A generator of biologically plausible synthetic gene expression data for design and analysis of structure learning algorithms, ECAL Systems biology workshop, 5-9 September, 2005, oral presentation.*

32. K. Engelen, B. Naudts, K. Van Leemput, B. De Moor and **K. Marchal.** Normalization of cDNA microarrays using external control spikes. ECCB, 2005. Madrid, 28 september-1 October.

33. *K. Lemmens, T. De Bie, P. Monsieurs, K. Engelen, B. De Moor, N. Cristianini , and* ***K. Marchal.*** *Discovering regulatory modules from heterogeneous information sources. ECCB, 2005. 28 september-1 October. Oral presentation student symposium.*

34. T. Van den Bulcke, K. Van Leemput, **K. Marchal,** P. van Remortel, A. Verschoren, B. Naudts, and B. De Moor A synthetic gene expression data generator for validation of reverse engineering methods. ECCB, 2005. 28 september-1 October.

35. P. Monsieurs, G. Thijs, B. De Moor, **K. Marchal.** Motif Detection combining Gibbs Sampling and Comparative Genomics . September 28 – October 1, 2005, Madrid, Spain. Book of abstracts p.94.

36. *K. Engelen, B. De Moor,* ***K. Marchal.*** *A calibration method for estimating abolute expression levels from microarray data. 29-31 May, 2006, Amsterdam, International Symposium on networks in bioinformatics. Oral presentation.*

37. *K. Lemmens, T. Dhollander, T. De Bie, P. Monsieurs, K. Engelen, B. Smets, J. Winderickx, B. De Moor, and* ***K. Marchal.*** *Inferring transcriptional module networks from ChIP-chip-, motif- and microarray data, 29-31 May, 2006, Amsterdam, International Symposium on networks in bioinformatics. Oral presentation.*

38. *T. Van den Bulcke, K. Van Leemput, P. van Remortel, B. De Moor,* ***K. Marchal****. SynTreN: a synthetic gene expression data generator for validation of reverse engineering methods. 29-31 May, 2006, Amsterdam, International Symposium on networks in bioinformatics. Oral presentation.*

39. *T. Van den Bulcke, K. Van Leemput, P. van Remortel, B. Naudts, B. De Moor, and* ***K. Marchal.*** *Benchmarking gene network inference algorithms using synthetic gene expression data. Benelearn-Workshop on bioinformatics & nature inspired computing, May 10 - Ghent – Belgium. Oral presentation.*

40. T. Van den Bulcke, K. Van Leemput, T. Dhollander, B. De Moor, P. van Remortel and **K. Marchal**. Assessing characteristics of gene network inference algorithms using synthetic gene expression data. Workshop: Probabilistic Modeling and Machine Learning in Structural and Systems Biology June 17-18. Finland.

41. K. Lemmens, T. Dhollander, T. De Bie, P. Monsieurs, K. Engelen, B. De Moor, **K. Marchal.** Inferring transcriptional modules from ChIP-chip-, motif- and microarray data. ISMB 2006, Aug 6-10, Fortaleza, Brasil.

42. K. Engelen, B. De Moor, **K. Marchal.** A calibration method for estimating absolute expression levels from microarray data. ISMB 2006, Aug 6-10, Fortaleza, Brasil.

43. T. Van den Bulcke, K. Van Leemput, T. Dhollander, B. De Moor, P. van Remortel, **K. Marchal**. Using synthetic gene expression data to assess characteristics of gene network inference algorithms. ISMB 2006, Aug 6-10, Fortaleza, Brasil.

44. S. De Keersmaecker, D. De Coster, N. van Boxel, K. Sonck, I. Thijs, H. Zhao, K. Engelen, P. Monsieurs, **K. Marchal** and J. Vanderleyden. In search for the role of LuxS in *Salmonella enterica* sv. Typhimurium biofilm formation. ASM 2006, Sept 9-13, Victoria, Canada.

45. P. Monsieurs, G. Thijs, A. A Fadda, S. C. J. De Keersmaecker, J. Vanderleyden. B. De Moor, **K. Marchal**. More robust detection of motifs in coexpressed genes by using phylogenetic information. ASM 2006, Sept 9-13, Victoria, Canada.

46. I. M. Thijs, S. C. J. De Keersmaecker, **K. Marchal**, K. Engelen, M. McClelland, S. Porwollik, J. Vanderleyden. Genomewide location analysis in Salmonella enterica SV. Typhimurium: expanding the hilA regulon, ASM 2006, Sept 9-13, Victoria, Canada.

47. A. Fadda, P. Monsieurs, **K. Marchal.** A compendium of predicted motifs for Bacillus subtilis. ESF 2006, San Feliu, Spain.

48. *P. Monsieurs, K. Engelen, K. Lemmens, A.A. Fadda, J. Vanderleyden,* ***K. Marchal.*** *A genome-wide compendium of regulatory motifs using a comparative genomics approach. Bacterial Genomes 2007, April 12-16, Hinxton-Cambridge, UK. Oral presentation.*

49. A. Fadda, P. Monsieurs, **K. Marchal.** A compendium of predicted motifs for *Bacillus subtilis* Microbial Genomes 11-14 April, 2007, Hinxton, UK

50. *D. Pastor, A. Cortes-Calabuig, K. Lemmens, B. De Moor, K. Marchal, M. Denecker. GeneReg: Integration of Experimental Data on the DNA Transcription Process. BNAIC 2007. oral presentation*

51. K. Lemmens, T. De Bie, T. Dhollander, K. Engelen, B. De Moor, **K. Marchal**. Unveiling combinatorial transcriptional regulation using microarray and motif compendia. ISMB/ECCB 2007, 21-25 July 2007, Vienna, Austria.

52. T. Van den Bulcke, H. Zhao, K. Engelen, B. De Moor, **K. Marchal.** Identification of overlapping biclusters using probabilistic relational models, applied to simulated gene expression data. ISMB/ECCB 2007, 21-25 July 2007, Vienna, Austria.

53. M. Claeys , V. Storms, **K. Marchal** De novo detection and evolution rate of regulatory motifs based on conservation in a dual space. ISMB/ECCB 2007, 21-25 July 2007, Vienna, Austria.

54. H. Zhao, K. Engelen, B. De Moor, and **K. Marchal.** CALIB: a Bioconductor package for estimating absolute expression levels from two-color microarray data. ISMB/ECCB 2007, 21-25 July 2007, Vienna, Austria.

55. T. Dhollander, Q. Sheng, K. Lemmens, B. De Moor, **K. Marchal** and Y. Moreau. Query-Driven Module Discovery in Microarray Data. ISMB/ECCB 2007, 21-25 July 2007, Vienna, Austria.

56. A. Sánchez, P. Monsieurs, V. Storms, O. Portal, E. Jiménez and **K. Marchal.** Detection of pathogenicity related regulatory motifs in *Ascomycete* fungi. ISMB/ECCB 2007, 21-25 July 2007, Vienna, Austria.

57. *T. Van den Bulcke, H. Zhao, K. Engelen and* ***K. Marchal.*** *Identification of overlapping biclusters using Probabilistic Relational Models. International Workshop on Machine Learning in System Biology, 24-25 Sep 2007, Evry, France. Oral presentation.*

58. K. Lemmens, T. De Bie, T. Dhollander, K. Engelen, R. De Smet, B. De Moor, K. Marchal. Unveiling combinatorial transcriptional regulation using microarray and motif compendia. Functional genomics & systems biology, 10-13 October 2007, Hinxton-Cambridge, UK. Book of abstracts p.39.

59. SCJ. De Keersmaecker, K. Sonck, A. Cappuyns, D. De Coster, I. Thijs, N. van Boxel, H. Zhao, K. Bernaerts, K. Engelen, K. Marchal and J. Vanderleyden. Omics approach of AI-2 mediated quorum sensing in Salmonella Typhimurium. CSHL/WT Meeting on Functional Genomics & Systems Biology, Hinxton, UK. October 10-13, 2007.

60. IMV. Thijs, SCJ. De Keersmaecker, D. De Coster, A. De Weerdt, K. Engelen, H. Zhao, M. McClelland, **K. Marchal** and J. Vanderleyden. Mapping the Salmonella Typhimurium LsrR regulon through ChIP-chip and transcriptomic analyses. CSHL/WT Meeting on Functional Genomics & Systems Biology. Hinxton, UK. October 10-13, 2007.

61. *K. Lemmens, T. De Bie, T. Dhollander, K. Engelen, B. De Moor,* ***K. Marchal.*** *Unveiling combinatorial transcriptional regulation using microarray and motif compendia. Benelux Bioinformatics Conference 2007, Leuven, Belgium. Oral presentation.*

62. T. Van den Bulcke, H. Zhao, K. Engelen, B. De Moor, **K. Marchal.** Identification of overlapping biclusters using Probabilistic Relational Models. Benelux Bioinformatics Conference 2007, Leuven, Belgium.

63. ***K. Marchal,*** *K. Lemmens, T. De Bie, T. Dhollander, K. Engelen, R. De Smet, B. De Moor. Condition dependent regulation in Escherichia coli. DREAM conference, Second dialogue on reverse engineering assessment and methods , NY, 3-4 December, 2007. Oral presentation.*

64. T. Michoel, R. De Smet, A. Joshi, **K. Marchal,** Y. Van de Peer. Reverse engineering transcriptional modules from gene expression data. DREAM conference, Second dialogue on reverse engineering assessment and methods , NY, 3-4 December, 2007. Poster.

65. SCJ. De Keersmaecker, K. Sonck, A. Cappuyns, D. De Coster, N. van Boxel, H. Zhao, K. Bernaerts, K. Engelen, **K. Marchal** and J. Vanderleyden J. High-throughput analyses of AI-2 signaling in Salmonella Typhimurium. 3rd ASM Conference on Cell-Cell Communication in Bacteria (CCCB). October 7 -10, 2007. Austin, Texas.

66. **K. Marchal,** K. Lemmens, T. De Bie, T. Dhollander, K. Engelen, R. De Smet, B. De Moor, Kathleen Marchal. "Condition-dependent Combinatorial control in *E. coli*". 2nd International Workshop on Bioinformatics (Cuba-Flanders) 2008, Santa-Clara February 5-7.

67. K. Engelen, Q. Fu, **K. Marchal**. Exploiting public microarray databases. IWOBI 2008, Santa Clara, Cuba. Oral presentation.

68. *S.C.J. De Keersmaecker, K. Sonck, I. Thijs, D. De Coster, G. Kint, N. van Boxel, H. Zhao, K. Engelen,* ***K. Marchal,*** *J. Vanderleyden. Towards systems biology, the Salmonella Typhimurium LuxS/AI-2 related pathway as a case study. Genomes 2008. Paris. April 8-11, 2008. Selected for oral presentation.*

69. I.M.V. Thijs, R. De Smet, K. Engelen, S.C.J. De Keersmaecker, J. Vanderleyden, **K. Marchal.** Facilitating ChIP-chip-based reconstruction of regulatory networks by combining omics data. Genomes 2008. Paris. April 8-11, 2008. Poster.

70. K. Lemmens, T. De Bie, T. Dhollander, P. Monsieurs, S. De Keersmaecker, I. Thijs, B. De Moor, J. Vanderleyden, J. Collado-Vides, K. Engelen, **K. Marchal.** Condition-dependent combinatorial regulation in Escherichia coli. ESF Systems Biology 2008. Sant Feliu de Guixols, Spain, April 12-17. poster presentation

71. K. Engelen, Q. Fu, K. Lemmens, R. Desmet, **K. Marchal**. A cross-platform microarray compendium of Escherichia coli. ESF Systems Biology 2008. Sant Feliu de Guixols, Spain, April 12-17.

72. T. Van den Bulcke, H. Zhao, K. Engelen, T. Michoel, B. De Moor**, K. Marchal.** ProBic: identification of overlapping biclusters using Probabilistic Relational Models, applied to simulated gene expression data. ENFIN-DREAM Conference. Madrid. April 28 - 29, 2008.

73. **K. Marchal,** In silico search for new potential typing targets. 8th International meeting on microbial epidemicological markers, Zakopane Poland, May 14-17, 2008. Invited speaker.

74. K. Lemmens, T. De Bie, T. Dhollander, P. Monsieurs, I. Thijs, S. De Keersmaecker, B. De Moor, K. Engelen, **K. Marchal.** Transcriptional Programs in Escherichia coli. ASM 108 general meeting, Boston, June 1-5, 2008, poster.

75. T. Van den Bulcke, H. Zhao, K. Engelen, **K. Marchal.** Identification of overlapping biclusters using Probabilistic Relational Models, applied to gene expression data. Oral presentation. Data Integration in the Life Science. 25-27 June, 2008, Evry, France.

76. R. De Smet, A. Joshi, Y. Van de Peer, **K. Marchal**, T. Michoel. Reverse-eningeering transcriptional modules from gene expression data. ISMB 2008. Toronto. July 18-24, 2008. Selected for poster presentation.

77. **K. Marchal,** 4th IECA meeting, Wellcome Trust Hinxton Genome Campus, Cambridge, UK, September 24-17, 2008. Invited speaker.

78. A.C. Fierro, P. Zarrineh, K. Engelen, L. Verlinden, G. Eelen, E. Vanoirbeek, A. Verstuyf, **K. Marchal.** Comparative analysis of gene expression across species. Second International Workshop on Machine Learning in Systems Biology. Brussels. September 13-14, 2008.

79. K. Lemmens, T. De Bie, T. Dhollander, P. Monsieurs, S. De Keersmaecker, I. Thijs, B. De Moor, J. Vanderleyden, J. Collado-Vides, K. Engelen, **K. Marchal**. Condition-dependent combinatorial regulation in Escherichia coli. ESF Bacterial networks, 14-18 September, 2008. Sant Feliu de Guixols, Spain, poster presentation.

80. K. Engelen, Q. Fu, T. Van Den Bulcke, K. Lemmens, R. De Smet, C. Fierro, I. Thijs, and **K. Marchal**. Generation of expression compendia from cross-platform microarray data. ECCB 2008. Cagliari. September 22-26, 2008.

81. A.C. Fierro, P. Zarrineh, K. Engelen, L. Verlinden, G. Eelen, E. Vanoirbeek, A. Verstuyf, **K. Marchal**. Comparative analysis of gene expression across species. European conference on Computational Biology. Cagliari. September 22-26, 2008.

82. V. Storms, M. Claeys, A. Sanchez, B. De Moor, **K. Marchal.** Evaluation of existing motif detection tools on their ability to retrieve regulatory motifs in sequence data. ECCB 2008. Cagliari. September 22-28, 2008.

83. I.M.V. Thijs, R. De Smet, K. Engelen, S.C.J. De Keersmaecker, J. Vanderleyden, **K. Marchal.** Facilitating ChIP-chip-based reconstruction of regulatory networks by combining omics data. ECCB 2008. Cagliari. September 22-26, 2008. Poster.

84. A. Fadda, A. Joshi, P. Monsieurs, K. Engelen, K. Lemmens, A. C. Fierro, Y. Van de Peer, **K. Marchal.** An integrative approach to infer the transcriptional regulatory network of Bacillus subtilis. ECCB 2008. Cagliari. September 22-26, 2008.

85. H. Sun, T. Van den Bulcke, K. Lemmens, K. Engelen, B. De Moor and **K. Marchal.** ModuleVisualization: a tool for visualizing gene module network. ECCB. Italy. September 22-26, 2008.

86. T. Van den Bulcke, H. Zhao, K. Engelen, T. Michoel, B. De Moor, **K. Marchal.** Efficient Query-Driven and Global Biclustering of Gene Expression Data Using Probabilistic Relational Models. DREAM3 Reverse Engineering Challenges. Boston. October 29 - November 2, 2008.

87. *R. De Smet, A. Joshi, Y. Van de Peer, **K. Marchal,** T. Michoel. Characterization of transcriptional modules in Escherichia coli. BBC 2008. Maastricht. December 15-16, 2008. Selected for oral presentation.*

88. *I. Thijs*, **K. Marchal,** iGEM teams K.U.Leuven, TUDelft en Groningen. *iGEM student competition for synthetic biology - Introduction. Benelux Bioinformatics Conference, 15-16 Dec 2008, Maastricht, Nederland. Oral presentation.*

89. T. Van den Bulcke, H. Zhao, K. Engelen, T. Michoel, B. De Moor, **K. Marchal.** Query-driven and global biclustering of gene expression data using probabilistic relational models. Benelux Bioinformatics Conference, 15-16 Dec, Maastricht, Netherlands. Poster.

90. I.M. Thijs*, M. Breckpot, N. Busschaert, J. Demeulemeester, A. Doldurucu, J. Mertens, B. Moeyaert, S. Roberfroid, H. Tytgat, E. Van Assche, N. Van Damme, A. Vandermeersch, D. Vercruysse, S.C. De Keersmaecker, J. Vanderleyden, B. De Moor and **K. Marchal.** *Modeling for Dr. Coli: a synthetic biology approach to intelligent bacterial drug delivery. European Conference on Synthetic Biology, 29 Mar - 3 Apr 2009, San Feliu de Guixols, Spain. Oral presentation.

91. I.M. Thijs*, R. De Smet, K. Engelen, C. Fierro, F. Qiang, K. Lemmens, S.C. De Keersmaecker, J. Vanderleyden and **K. Marchal**. *Facilitating ChIP-chip-based reconstruction of regulatory networks by combining omics data. IET BioSysBio Conference 2009, 23-25 Mar 2009, Cambridge, UK. Poster presentation.

92. I.M. Thijs*, M. Breckpot, N. Busschaert, J. Demeulemeester, A. Doldurucu, J. Mertens, B. Moeyaert, S. Roberfroid, H. Tytgat, E. Van Assche, N. Van Damme, A. Vandermeersch, D. Vercruysse, S.C. De Keersmaecker, J. Vanderleyden, B. De Moor and **K. Marchal.** *Dr. Coli, a synthetic biology approach to intelligent bacterial drug delivery. IET BioSysBio Conference 2009, 23-25 Mar 2009, Cambridge, UK. Poster presentation.

93. R. De Smet, L. Venken, I.M. Thijs, K. Engelen, C. Fierro, F. Qiang, K. Lemmens, S.C. De Keersmaecker, J. Vanderleyden, **K. Marchal.** Facilitating ChIP-chip-based reconstruction of regulatory networks by combining omics data. European Conference on Synthetic Biology 2009, San Feliu de Guixols, Spain, March 29 – April 3 2009. Poster.

94. *H. Sun, T. De Bie, V. Storms, Q. Fu, T. Dholllander, K. Lemmens, M. Verstuyf, G. Eelen, L. Verlinden, B. De Moor, and* ***K. Marchal.*** *ModuleDigger: an itemset mining framework for the detection of cis-regulatory modules. Accepted for APBC2009. Oral presentation.*

95. *H. Sun, K. Lemmens, T. Van den Buckle, K. Engelen, B. De Moor,* ***K. Marchal.*** *Layout and Post-Processing of Transcriptional Modules. Accepted for publication in IEEE Computer Society, 2009 (proceeding of IJCBS09, Shanghai, China, 2009. oral presentation*

96. A. Fadda, A.C. Fierro, A. Joshi, K. Lemmens, P. Monsieurs, K. Engelen, Y. Van de Peer, **K. Marchal.** Inference of the transcriptional regulatory network of *Bacillus subtilis.* Systems Biology: Networks, 18-22 March 2009, Cold Spring Harbor, NY, USA. Poster presentation.

97. H. Zhao, T. Van den Bulcke, L.Cloots, K. Engelen, T.Michoel, B.De Moor and **K. Marchal***. Efficient query-driven and global biclustering of gene expression data using probabilistic relational models. ISMB 2009, June 27 - July 2 2009. Poster

98. R. De Smet, A. Joshi, Y. Van de Peer, **K. Marchal** and T. Michoel. Characterizing transcriptional modules in Escherichia coli inferred from gene expression data. BioSysBio Conference, 23-25 March 2009, Cambridge, United Kingdom. Poster presentation.

99. R. De Smet, A. Joshi, Y. Van de Peer, **K. Marchal,** T. Michoel. Characterizing transcriptional modules in Escherichia coli inferred from gene expression data. BioSysBio Conference. Cambridge, United Kingdom. Poster presentation. 23-25 March 2009

100. R. De Smet, T. Dhollander, I. Thijs, K. Engelen, **K. Marchal.** Validation of ChIP-chip targets by query-driven biclustering. ISMB 2009. Stockholm, Sweden. Jun 27 - July 2 , 2009. Poster presentation.

101. P. Zarrineh, A.C. Fierro, B. De Moor, **K. Marchal**. Fusion of sequence data and microarray data, a systematic approach toward cross-species comparison. ISMB/ECCB 2009. Stockholm. June 27-July 2, 2009. Poster presentation.

102. Q. Fu, K. Engelen, P. Meysman, K. Lemmens, R. De Smet, C. Fierro, I. Thijs, **K. Marchal.** Cross-platform microarray compendium and a corresponding web interface, ISMB ECCB 2009, 27th June – 2nd July 2009, Stockholm, Sweden, Poster.

103. M. Claeys, V. Storms, **K. Marchal.** De novo detection and evolution rate of regulatory motifs based on conservation in a dual space. ISMB/ECCB. Stockholm. June 27 -July 2, 2009. Poster.

104. T. Van den Bulcke, H. Zhao, L. Cloots, K. Engelen, T. Michoel, B. De Moor, **K. Marchal.** Efficient query-driven and global biclustering of gene expression data using Probabilistic Relational Models. ISMB/ECCB. Stockholm. June 27 - July 2, 2009. Poster.

105. K. Engelen, K. Lemmens, C. Fierro, R. De Smet, Q. Fu, I. Thijs, L. Cloots, H. Zhao, A. Sanchez[1], P. Meysman, P.Zarrineh K. Marchal. Reconstructing transcriptional networks in micro-organisms Workshop on "bacterial regulatory networks: Baeza (Spain), 12-14 November 2009. Oral presentation.

106.R. De Smet, H. Sun, K. Lemmens, I. Thijs, **K. Marchal.** A query-based framework to validate ChIP-chip targets. Benelux Bioinformatics Conference 2009. Liege, Belgium. December 14 - 15. 2009.

107.V. Storms, M. Claeys, A. Sanchez, B. De Moor, ***K. Marchal****. The effect of orthology and coregulation on detecting regulatory motifs. BBC 2009. Luik. December 14-15, 2009. Selected for oral presentation.*

108.I. Ishchukov, I. Thijs, **K. Marchal. In** silico study of the regulation of sRNAs in *Escherichia coli*. BBC09, the fifth Benelux Bioinformatics Conference, December 14-15 2009, Liege, Belgium, Book of Abstracts p 75.

109.V. Storms, M. Claeys, A. Sanchez, B. De Moor, K. Marchal. The effect of orthology and coregulation on detecting regulatory motifs. RECOMB 2009. Boston (USA). December 02-06, 2009. Selected for poster presentation.

110. P. Meysman, K. Engelen, K. Laukens, T.H. Dang, ***K. Marchal.*** *Use of structural DNA properties for the prediction of regulator binding sites with conditional random fields. RECOMB Regulatory Genomics. Boston. December 2-6, 2009. Oral presentation.*

111.K. Engelen, K. Lemmens, A. Fadda, C. Fierro, R. De Smet, Q. Fu, I. Thijs, L. Cloots, H. Zhao, A. Sanchez, P. Meysman, P. Zarrineh, **K. Marchal.** Reconstructing transcriptional networks in micro-organisms", Systems Biology of Microorganisms Conference in Paris, March 2010.

112.R. De Smet, H. Sun, K. Lemmens' **K. Marchal**. A validation strategy for ChIP-chip analysis using a genome-wide expression compendium. Reconstructing transcriptional networks in micro-organisms", Systems Biology of Microorganisms Conference in Paris, March 2010.

113.De Smet, R., ***Marchal K*** *(2010). An ensemble method for querying gene expression compendia with experimental lists. In : Proc. of IEEE International Conference on Bioinformatics & Biomedicine. IEEE International Conference on Bioinformatics & Biomedicine. Hong Kong, 18-21 December 2010 (pp. 363-368). IEEE Computer Society. oral presentation*

114. H. Sun, T. De Bie, V. Storms, Q. Fu, T. Dhollander, K. Lemmens, K., A. Verstuyf, B. De Moor, and **K. Marchal** ModuleDigger: an itemset mining framework for the detection of cis-regulatory modules.' Poster presentation at ISMB 2010 in Boston, USA, July 11-13.

115. Storms V, Claeys M, Sanchez A, **Marchal K.** The effect of orthology and coregulation on detecting regulatory motifs. Invited oral presentation at the Special Interest Group on Bioinformatics for Regulatory Genomics (BioRegSIG) ISMB 2010 in Boston, USA, July 11-13.

116.L. Cloots, H. Zhao, T. Van den Bulcke, Y. Wu, R. De Smet, V. Storms, P. Meysman, K. Engelen, **K. Marchal.** Query-based biclustering of gene expression data using Probabilistic Relational Models. Fourth International Workshop on Machine Learning in Systems Biology, 15-16 October, 2010, Edinburgh, United Kingdom, Proceedings of the Fourth International Workshop p 119.

117. H. Zhao, T. Van den Bulcke, R. De Smet, L. Cloots, K. Engelen, B. De Moor, **K. Marchal.** Efficient query-driven biclustering of gene expression data using Probabilistic Relational Models. International Conference on Intelligent Systems for Molecular Biology, 11-13 July, 2010, Boston, United States of America, Poster presentation X016

118. L. Cloots, H. Zhao, T. Van den Bulcke, R. De Smet, Y. Wu, K. Engelen, B. De Moor, **K. Marchal.** Efficient query-driven biclustering of gene expression data using probabilistic relational models. Systems Biology and New Sequencing Technologies, 16-18 June, 2010, Barcelona, Spain, Book of Abstracts p 47

119. A. Sanchez-Rodriguez, C. Martens, K. Engelen, Y. Van de Peer, **K. Marchal.** The potential for pathogenicity was present in the Ascomycete ancestor. The EMBO meeting 2010, September 4-7, 2010, Barcelona, Spain.

120. R. De Smet, H. Sun, K. Hermans, K. Lemmens, S. De Keersmaecker & **K. Marchal**¨ Cross-checking experimental results with publicly available gene expression data: a query-driven approach. Systems Biology and New Sequencing Technologies, 16-18 June, 2010, Barcelona, Spain, Book of Abstracts p

121. Ivan Ishchukov, Peyman Zarrineh, Lore Cloots, Inge Thijs, Kristof Engelen and **Kathleen Marchal.** Studying sRNA regulation in Escherichia coli. BGRS\SB-2010 (Bioinformatics of Genome Regulation and Structure\Systems Biology June 2011, Novosibirsk). Poster presentation.

122. L. Cloots, H. Zhao, T. Van den Bulcke, Y. Wu, R. De Smet, V. Storms, P. Meysman, K. Engelen, **K. Marchal.** Query-based biclustering of gene expression data using Probabilistic Relational Models. 15-16 October, 2010, Edinburgh, United Kingdom, Proceedings of the Fourth International Workshop p 119

123. P. Meysman, K. Engelen, K. Laukens, T.H. Dang, **K. Marchal.** Use of structural DNA properties for the prediction of regulator binding sites with conditional random fields. ECCB 2010, September 26-29, 2010, Ghent, Belgium.

124. T. Guns, H. Sun, S. Nijssen, L. De Raedt, **K. Marchal.** Proximity-based cis-regulatory module detection using constraint programming for itemset mining. European Conference on Computational Biology 2010. September 26, Ghent, Belgium.

125. P. Zarrineh, A.C. Fierro, A. Sánchez-Rodríguez, B.D. Moor, **K. Marchal.** Module-based comparative gene expression analysis: evolutionary conserved coexpression in Bacillus subtilis and Escherichia coli. European conference on Computational Biology. Ghent. September 26-29, 2010.

126. H. Sun, T. Guns, S. Nijssen, A. Sanchez Rodriguez, L. De Raedt, **K. Marchal.** Cis-regulatory module detection using constraint programming. 3rd Annual Joint Conference on System Biology, Regulatory Genomics, and Reverse Engineering Challenges (RECOMB 2010), November 16, 2010, New York, USA.

127. *T. Guns, H. Sun, S. Nijssen,* ***K. Marchal.*** *Cis-regulatory module detection using constraint programming. IEEE International Conference on Bioinformatics & Biomedicine. December 18, 2010, Hong Kong, China. Oral presentation.*

128. *L. Cloots, H. Zhao, T. Van den Bulcke, Y. Wu, R. De Smet, V. Storms, P. Meysman, K. Engelen,* ***K. Marchal.*** *Query-based biclustering of gene expression data using Probabilistic Relational Models. Asia Pacific Bioinformatics Conference, 11-14 January, 2011, Incheon, South Korea, Oral Presentation*

129. *P. Zarrineh, A.C. Fierro, A. Sánchez-Rodríguez, B.D. Moor,* ***K. Marchal.*** *Module-based comparative gene expression analysis: evolutionary conserved coexpression in Bacillus subtilis and Escherichia coli. VOG meeting (Dutch/Flemish Classification Society (called VOC: http://www.voc.ac). November 26, Leiden, The Netherlands.*

130. *P. Meysman, K. Engelen, K. Laukens, T.H. Dang, **K. Marchal**. Use of structural DNA properties for the prediction of regulator binding sites with conditional random fields. BioRegSig (ISMB special interest meeting July 2011, Vienna). Selected for oral presentation.*

131. *Hong Sun, Tias Guns, Siegfried Nijssen and **Kathleen Marchal**. Unveiling combinatorial regulation through the combination of ChIP information and in silico cis-regulatory module detection. BioRegSig (ISMB special interest meeting July 2011, Vienna). Selected for oral presentation.*

132. Carolina Fierro, R. De Smet, Y. Wu, L. Cloots, D. De Maeyer, P. Zarrineh, A. Sanchez, I. Ischukov1, P. Meysman, Q. Fu, K. Engelen, K. Marchal. Network-based approaches for mode of action determination. IECA 2011, Cancun, December 2011, invited talk.

133. Van Assche, E, Van Puyvelde, S, Monsieurs, P, **Marchal, K**, Vanderleyden, J, De Keersmaecker, SC. Possible alternative targets of the sRNA MicA in Salmonella Typhimurium. ASM Conference on Regulating with RNA in Bacteria. March 7-11, 2011. San Juan, Puerto Rico. Poster presentation.

134. Ishchukov, I, Ryan, D, Van Puyvelde, S, Cloots, L, Sonawane, A, Vanderleyden, J, **Marchal, K.** Prediction of sRNA targets in Escherichia coli. ASM Conference on Regulating with RNA in Bacteria. March 7-11, 2011. San Juan, Puerto Rico. Poster presentation.

135. *Van Puyvelde, S, De Keersmaecker, S, **Marchal, K,** Vanderleyden, J, Busby, S, Lee, D. DNA sampling tool implemented for in vivo identification of regulatory proteins in Salmonella Typhimurium. 5th IECA Conference 2011. December 5-9, 2011. Cancun, Mexico. Oral presentation.*

136. *Y. Wu, L. Verbeke, **K. Marchal**. Probic: Simultaneously detecting coexpression modules and their regulatory patternsOral presentation, BBC, Luxemburg, December 2011.*

137. *A. Sanchez, R. De Smet, K. Engelen, Q. Fu, Y. Wu, **K. Marchal**. Evolutionary events involved in pathogenic trait acquisition in Ascomycetes. ISCB Latin America 2012, March 17-21,Santiago di Chili, oral presentation.*

138. ***K. Marchal,** H. Sun, T. Guns, A.C. Fierro, L. Thorrez, S. Nijssen. Unveiling combinatorial regulation through the combination of ChIP information and in silico cis-regulatory module detection. ISCB Latin America 2012, Santiago di Chili, March 17-21, oral presentation.*

139. K. Marchal. International Conference on Microbiology (VAAM 2013), March 10-13, 2013, Bremen, keynote lecture

140. *D. De Maeyer, International Conference on Microbiology (VAAM 2013), March 10-13, 2013, Bremen, Interaction networks to analyze gene lists from omics data, selected for oral presentation.*

141. *Carolina Fierro, L. Verbeke, R. De Smet, Y. Wu, L. Cloots, D. De Maeyer, J. Renkens, A. Sanchez, Q. Fu, K. Engelen, J. Vanderleyden, H. Steenackers, J. Fostier, L De Raedt, **K. Marchal** Network-based dataintegration for microbial systems biology. ESF-EMBO Conference on Bacterial Networks (bacnet13). Warsaw, PL, Poland, 16 - 21 March 2013. Selected for oral presentation.*

142. *L. Verbeke, J, Fostier and **K. Marchal**. EPSILON: localized networks for eQTL prioritization, RegGen SIG meeting, Satellite meeting on ISMB 2012, July 20, 2013, Berlin, selected for oral presentation*

143. *Y. Yao, K. Marchal and Y. Van de Peer. Using novel bio-inspired principles to improve adaptability of evolutionary robots in dynamically changing environment. ECAL 2013, selected for oral presentation.*

144. L. Verbeke, J. Fostier, J. Van den Eynde, C. Fierro and **K. Marchal.** Identifying relevant pathways for different breast cancer subtypes using network based data integration. ISMB 2013, Toronto, poster presentation

145. D. De Maeyer, **K. Marchal**. Discerning passenger from driver mutations in artificial evolution experiments by interaction network analysis, ISMB 2013, poster presentation.

146. Y. Wu and K. **Marchal.** PROBIC-II: simultabeiyly detecting coexpression modules and their regulatory patterns, BBC 2013, Luxemburg, poster presentation..

147. D. De Maeyer, J. Renkens, L. De Raedt and **K. Marchal.** Mechanistic interpretation of gene lists using interaction networks, BBC 2013, Luxemburg, poster presentation..

148. T. Le Van, A.Fierro, T. Guns, M van Leeuwen,S. Nijssen, L.De Raedt**, K. Marchal.** Bi-clustering gene expression data under constraints, BBC 2013, Luxemburg, poster presentation.

149. K. Marchal. 2014 Microbial Stress Response Gordon Research Conference. Keynote lecture

Blue keynote or invited
Italics selected presentation
Underlined : presenting author

(d) idem voor nationale congressen en symposia

I. Ishchukov, I. Thijs, K. Marchal. In silico study of the regulation of sRNAs in *Escherichia coli*. BioMaGNet's Annual Meeting, October 22, 2009, Ghent, Belgium, Book of Abstracts p 25.

Q. Fu, K. Engelen, P.Meysman, A. Sanchez-Rodriguez, R. De Smet, K. Lemmens, A.C. Fierro, K. Marchal. COLOMBOS: access port for bacterial cross-platform microarray compendia. K.U.Leuven PhD Interaction Day. April 23, 2010, Leuven, Belgium. Oral talk.

(e) lezingen aan universiteiten en wetenschappelijke instellingen

K Marchal. Network-based dataintegration. Institut Pasteur, June 14 2011 (invited by B. Schwikowski)
K. Marchal. Network-based dataintegration. Universiteit van Groningen, Nov 2013 (invited by M. Heinemann)

(f) verworven kredieten, toelagen en schenkingen (met opgave van het organisme, de aard en het bedrag)

Opsomming van kredieten bekomen voor wetenschappelijk onderzoek waar K. Marchal optreedt als woordvoerder/hoofdpromotor

Sponsor (FWO, IWT, BOF,…)	Woordvoerder / Promotor	Aard van het krediet (aspirant, BOF 2-jarig, GOA, BILA,…)	Apparatuur (€)	Werking (€)	Personeel (FTEmaanden)			Periode (van-tot)
					ATP	PhD stud.	Post doc	
BOF KU Leuven	K. Marchal	*BIL10/07 (bilaterale samenwerking)*		*11.328,00*				*01.10.2010* *30.09.2012*
BOF KU Leuven	K. Marchal	*VES/09/030 SYNCELLS (verkennende internationale samenwerking)*		*1.436,31*				*01.10.2009* *31.03.2011*
BOF KU Leuven	K. Marchal	*DBOF*				48		*01.01.201131* *.12.2015*
FWO	K. Marchal	*G.0329.09 (totaal **305.577,54 EUR)*** *Organisatie en evolutie van prokaryote transcriptionele netwerken.*				48		*01.01.2009* *31.12.2014*
FWO	K. Marchal	*WO.020.11N SYSTEEM* *Systeem- en synthetische biologie: synthetische cellulaire systemen.*		*62.500,00 EUR*				*01.01.2011* *31.12.2017*
FWO	K. Marchal	3G042813 Netwerk-gebaseerde analyse van genotype-expressie fenotype data		*? EUR*		48		*01.01.2013* *31.12.2017*
IWT	K. Marchal	*3H070549* *ZL362801* *IWT/060045/SBO* *Bioframe: an algorithmic framework for integrative modeling in systems biology. **(898.591,57** EUR totaal voor mijn groep)*				96	48	*01.04.2007* *31.03.2011*
VLIR	K. Marchal	*ZEIN2012Z108 ECUADO (South initiative)*		*66.480,93 EUR*				*01.12.2012* *30.11.2014*

Opsomming van projecten waarbij ik als copromotor betrokken ben (geweest)

Sponsor (FWO, IWT, BOF,…)	Woordvoerder / Promotor	Aard van het krediet (aspirant, BOF 2-jarig, GOA, BILA,…)	Totaal apparatuur (€)	Totaal werking (€)	Totaal personeel (FTEmaanden)			Periode (van-tot)
					ATP	PhD stud.	Post doc	
BOF KU Leuven	K. Engelen	*3E080340 (CREA,* ***160.000,00*** *EUR)* *ZKB8933* *CREA/08/023*						*01.10.2008* *30.09.2012*
BOF KU Leuven	J. Vanderleyden	*GOA/2008/11*				48		*01.10.2007* *30.09.2014*
BOF KU Leuven	K. Verstrepen	*3E100477* *ZKC1895* *PF/10/010 (excellentiefinanciëring)*		10000/ yr			84	*01.11.2010* *31.10.2017*
FWO	M. Verstuyf	*3M100551* *ZKC2666* *G.0859.11* *Moleculair werkingsmechanisme van 1,25-dihydroxyvitamine D3: van chromatine tot eiwit.*	0	0	0	0	0	*01.01.2011* *31.12.2016*
HFSPO OZ	K. Verstrepen	*Totaal bedrag voor mijn onderzoeksgroep* ***198.122,49 EUR***						*01.12.2007* *31.05.2011*
BOF UGent	Y. Van de Peer	*MRP N2N*		40000 euro (eenmalig)				*01.01.2013* *1.12.2016*
IWT	Hoofdpromotor J. Vanderleyden K. Marchal woordvoerder UGent	*SBO NEMOA* ***(993,000.00 euro*** *voor mijn onderzoeksgroep in samenwerking met Y. Van de Peer en J. Fostier)*		331,000.00 euro totaal		96	48	*01.01.2013* *31.12.2017*

Doctorale en of postdoctorale beurzen waarbij K. Marchal promotor was

BOF KU Leuven	K. Marchal	*Postdoc mandaat Monsieurs Pieter (KU Leuven)*					12	*01.01.2007* *31.12.2007*
BOF KU Leuven	K. Marchal	*Postdoc mandaat Lemmens Karen (KU Leuven)*					1	*01.10.2009* *19.10.2009*
BOF KU Leuven	K. Marchal	*Postdoc mandaat Alejandro Herrada (KU Leuven)*					12	*01.10.2011* *30.09.2012*
IWT	K. Marchal	*PhD mandaat De Smet, Riet (KU Leuven)*				48		*01.01.2007* *31.12.2010*
IWT	K. Marchal	*PhD mandaat Venken, Lyn (KU Leuven)*				48		*01.01.2009* *31.12.2009*
IMEC	K. Marchal	*3E080625* *ZKB9481* *SLT-DOCTORAAT*				48		*01.01.2009* *31.12.2013*
IWT	K. Marchal	*PhD mandaat Meysman, Pieter (KU Leuven)*				48		*01.01.2009* *31.12.2012*
IWT	K. Marchal	*PhD mandaat De Maeyer, Dries (KU Leuven)*				48		*01.01.2012* *31.12.2015*

(g) promotorschap of dagelijkse leiding van scripties en doctoraatsproefschriften
(opgave van de universitaire instelling)

Afgelegde doctoraten

Naam doctorandus	Instelling(en)	Startjaar	Jaar van verdediging	Bijdrage in de begeleiding (in %)
Kristof Engelen	KU Leuven, *Faculteit Ingenieurswetenschappen*	2001	*23.12.2005*	90
Ruth Van Hellemont	KU Leuven, *Faculteit Ingenieurswetenschappen*	2003	*23.03.2007*	90
Pieter Monsieurs	KU Leuven, *Faculteit Ingenieurswetenschappen*	2002	*20.12.2006*	90
Tim Van den Bulcke	KU Leuven, *Faculteit Ingenieurswetenschappen*	2004	*18.05.2009*	90
Karen Lemmens	KU Leuven, *Faculteit Ingenieurswetenschappen*	2004	*29.09.2008*	90
Abeer Fadda	KU Leuven, *Faculteit Bio−ingenieurswetenschappen*	2005	*27.04.2009*	100
Hui Zhao	KU Leuven, *Faculteit Bio−ingenieurswetenschappen*	1/02/06	*03.03.2010*	100
Riet De Smet	KU Leuven, *Faculteit Bio−ingenieurswetenschappen*	1/01/07	*15.12.2010*	100
Hong Sun	KU Leuven, *Faculteit Ingenieurswetenschappen*	1/07/07	*07.07.2011*	90
Valerie Storms	KU Leuven, *Faculteit Bio−ingenieurswetenschappen*	1/10/06	*29.03.2011*	90
Peyman Zarrineh	KU Leuven, *Faculteit Ingenieurswetenschappen*	1/09/07	*09.11.2011*	90
Lore Cloots	KU Leuven, *Faculteit Bio−ingenieurswetenschappen*	13/10/08	*16.10.2012*	90
Pieter Meysman	KU Leuven, *Faculteit Bio−ingenieurswetenschappen*	13/10/2008	*18.12.2012*	90
Aminael Sanchez Rodriguez	KU Leuven, *Faculteit Bio−ingenieurswetenschappen*	1/06/08	14/10/2013	100
Inge Thijs	KU Leuven, *Faculteit Bio−ingenieurswetenschappen*		*18.12.2007*	10
Pushpike Jayantha Thilakarathne	*Faculteit Geneeskunde*		*21.09.2011*	10
Bart Smets	KU Leuven, *Faculteit Wetenschappen*		*20.11.2009*	10

Lopende doctoraten

Naam doctorandus	Instelling(en)	Startjaar	Bijdrage in de begeleiding (in %)
Qiang Fu	KU Leuven, *Faculteit Bio−ingenieurswetenschappen*	1/09/07	90
Yan Wu	KU Leuven, *Faculteit Bio−ingenieurswetenschappen*	01.09.2009	100
Marleen Claeys	KU Leuven, *Faculteit*	2/06/07	100

	Bio–ingenieurswetenschappen		
Dries De Maeyer	KU Leuven, *Faculteit Bio–ingenieurswetenschappen*	25.10.2010	100
Sergio Pullido	KU Leuven, *Faculteit Bio–ingenieurswetenschappen/UGent Faculteit Wetenschappen*	2012	100
Bram Weytjens	KU Leuven, *Faculteit Bio–ingenieurswetenschappen/UGent Faculteit Wetenschappen*	2013	100
Mushthofa Mushthofa	*UGent Faculteit Wetenschappen*	2013	50
Than Levan	KU Leuven, *Faculteit Ingenieurswetenschappen*	2010	50
Lieven Verbeke	U Gent, *Faculteit Ingenieurswetenschappen*	2011	50
Yao Yao	U Gent, *Faculteit Ingenieurswetenschappen*	2010	50
Joris Renkens	KU Leuven, *Faculteit Ingenieurswetenschappen*	2010	30
*Sam Crauwels**	KU Leuven, *Faculteit Bio–ingenieurswetenschappen/UGent Faculteit Wetenschappen*		5
*Véronique Wuyts**	KU Leuven, *Faculteit Bio–ingenieurswetenschappen/UGent Faculteit Wetenschappen*		5
Anyiawung Forcheh Chiara	*Faculteit Geneeskunde*		5
Akanksha Dubey	KU Leuven, *Faculteit Bio–ingenieurswetenschappen/*		10
Seppe Dierckx	KU Leuven, *Faculteit Bio–ingenieurswetenschappen/*		5
Pieter Albers	KU Leuven, *Faculteit Bio–ingenieurswetenschappen/*		5

* zijn copromotorschappen met hoge scholen en onderzoeksinstituten die zelf geen promotor kunnen zijn. De bijdrage van de universitaire promotor is beperkt tot het controleren van de kwaliteit van het onderzoek. Dagelijkse begeleiding gebeurt in het instituut zelf.

Alle andere copromotorschappen zijn het resultaat van samenwerkingen met onderzoekers uit een andere discipline. PS de percentages met copromotorschap kunnen veranderen in de toekomst afhankelijk van het stadium van het onderzoek waarin de onderzoeker zich bevindt. De aangegeven percentages reflecteren de huidige situatie.

DIENSTVERLENING MET BETREKKING TOT UW FUNCTIE (GERANGSCHIKT PER CATEGORIE VOLGENS ONDERSTAANDE DEFINITIES EN BINNEN IEDERE CATEGORIE CHRONOLOGISCH)

(met uitsluiting van bezoldigde cumulatieactiviteiten waarvoor toestemming werd bekomen)

(a) intern: voorzitter opleidingscommissie, functies decaan, onderwijsdirecteur, commissies, raden, ..., uitstralingsactiviteiten, organisatie stages, bezoeken, ... interne adviesverlening, leiding centrale diensten, ...

Aan de KU Leuven

- Actieve rol bij het oprichten van de master of Science in Bioinformatics (KU Leuven)
- Voorzitter van de onderwijscommissie van de Master of Science in Bioinformatics (2009-2011)
- Lid van de examencommissie van de Master of Science in Bioinformatics (2009-2011)
- Lid van de departements en faculteitsraad
- Regelmatig aanwezig op SID in dagen

Aan de UGent

- Lid van de vakgroepraad
- Actieve rol bij het opmaken van het dossier van de master in Science in Bioinformatics (voorzitter van de werkgroep die verantwoordelijk was met het uittekenen van de master en het opstellen van het dossier voor de NVAO).

(b) extern:

(b_1) wetenschappelijke dienstverlening : wetenschappelijke adviesverlening, lidmaatschap van wetenschappelijke commissies, editoriaat wetenschappelijke tijdschriften, e.d.m. ...

Editorial werk
Associate editor of
BMC Bioinformatics (2011-)
BMC Release Notes (2008-)
Peer Journal (2012-)
Microorganisms (2012-)
Journal of Integrated Omics (2012-)
Current Plant Biology (2014-)

Refereewerk en beoordelingscommissies:

- Member of the evaluation committee of the research outputs of Professor VB Bajic (The South African National Bioinformatics Institute, University of the Western Cape)
- Lid van de IWT beoordelingscommissie voor een postdoctoraal mandaat 2006

- Lid van de IWT beoordelingscommissie voor predoc beurzen 2006, 2010
- Reviewer for ISF, FIRST Program, 2008
- Reviewer for BBSCR 2010 research grant (UK)
- Inserm, ATIP Avenir grants, 2011, 2012
- Review van ERACAPs projecten 2013
- Review voor ZAP profiel van de ULiege 2013
- Review van een industrieel project IWT (2013)
- Lid van de FWO-Expertpanel Bio1: Moleculaire en Cellulaire Biologie (2014-)

- Reviewer NAR, Bioinformatics, BMC series, Genome biology, Plos Computational biology, Nature communications, Nature Methods...

Examencommissiedoctoraten:

Als lid van de begeleidingscommissie (lopende doctoraten)

- Anna Yssel, promotor Prof. J. Vanderleyden, Center for Microbial and Plant Genetics, KU Leuven
- Stefanie Roberfroid, promotor Prof. J. Vanderleyden, Center for Microbial and Plant Genetics, KU Leuven
- Raf Winand, Promotor Jan Aerts, ESAT, KULeuven
- Bram Van den Bergh, promotor Prof. J. Michiels, Center for Microbial and Plant Genetics, KU Leuven
- Stijn Bossuyt, promotor Prof. J. Vanderleyden, Center for Microbial and Plant Genetics, KU Leuven
- Stijn Vanderzande, Prof. W. Keulemans, Afdeling Plantenbiotechniek KU Leuven
- Aaron New, promotor Prof. K. Verstrepen, Center for Microbial and Plant Genetics, KU Leuven
- Tim Snoek, promotor Prof. K. Verstrepen, Center for Microbial and Plant Genetics, KU Leuven
- Elke Van Assche, promotor Prof. J. Vanderleyden, Center for Microbial and Plant Genetics, KU Leuven
- Marijn Schouteden, promotor Prof. I. Van Mechelen, Kwantitatieve Psychologie en Individuele Verschillen (OE), KU Leuven
- Tom Wilderjans, promotor Prof. I. Van Mechelen, Kwantitatieve Psychologie en Individuele Verschillen (OE), KU Leuven
- Marina Naval Sanchez, Prof. S. Aerts, Departement Menselijke Erfelijkheid, KU Leuven
- Thanh Hai, Dang, promotor Prof. K. Laukens, Intelligent Systems Laboratory, U. Antwerpen
- Frederik Gwinner, promotor Prof. B. Schwikowski, Systems Biology, Institut Pasteur
- Lucia Pannnier, promotor Prof. J. Collado Vides, Laboratory of Computational Biology, UNAM, Mexico

Als assessor (en geen lid van de begeleidingscommissie werd niet vermeld)

Als assessor buiten eigen departement

- Sara Movahedi, Promotor: Y. Van de Peer Ghent University, January 12, 2012,
- Hossein Rahmani, Promotors: Prof. Dr. J.N. Kok Leiden University, Hendrik Blockeel, KULeuven, September 2012.

(b$_2$) maatschappelijke dienstverlening : voordrachten, informatiesessies, lidmaatschap van beroepsorganisaties

Ontwikkelingssamenwerking:

In het verleden actief heb ik actief deelgenomen aan het VLIR netwerk met Cuba, Santa Clara. In 2012 werd een South initiatief goedgekeurd tussen mijn groep en de groep Centro de Biotecnología, Universidad Nacional de Loja, Ecuador (Study of pathogen-pathogen interactions established during wilt disease development in Babaco (Vasconcellea helbornii)). Naast het onderzoeksluik vind ik het maatschappelijke luik van deze projecten belangrijk (bv concreet voor de samenwerking met Equador en vroeger Cuba zorgen dat de locale onderzoekers zich bewust zijn van hun mogelijkheden.

Voordracht voor:

- Universiteit Derde Leeftijd Leuven (UDLL). "From Systems to Synthetic Biology" 2009-2010.
- Reeks DNA60 (C. Waelkens, KU Leuven, http://wet.kuleuven.be/wetenschapinbreedbeeld/DNA60) on "computerwetenschappen en moleculaire biologie" 15/10/2013.