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Date and Place of Birth

May 6, 1977; Concarneau(29), France

Research Interest

My research interests fall into two major areas: bioinformatics and computational biology.

In computational biology, I develop and analyze models of cellular interactions to better understand their role in determining phenotype. My first contribution in that field has been to investigating the role of cellular organizational units in determining phenotype, using high throughput proteomic data and graph theoretic approaches. I now focus on modeling signaling pathways at the system level to better understand the regulatory mechanisms.

My work in bioinformatics has mainly been on data quality assessment. My first contribution has been on microarray experiment embodied in the MADTOOLS project (<http://www.madtools.org>). My second is on flow cytometry data quality assessment and standardization (<http://www.bioconductor.org>). Lately, I have been involved in the data quality assessment and processing of cell-based assays (siRNA high throughput screen).

Education

- 2001-2005 Ph.D. in Bioinformatics, INSERMU533, Supervisor Jean Léger, University of Loire Atlantique, Nantes, France.
- 2000-2001 Master in Genomics and Bioinformatics, University of Bretagne Occidentale, Rennes, France.
- 1997-2000 Engineering School of Microbiology and Food Safety, University of Bretagne Occidentale, Brest, France.
- 1996-1997 Biology Diploma, University of Bretagne Occidentale, Brest, France.
- 1995-1996 School of Chemistry, University of Bretagne Occidentale, Rennes, France.

Research

INSERM Rennes, FR
Post-Doctoral Research Associate Feb. 2008 – present
Dr N. Théret, EA 4427.

Dynamic modeling of EGF and TGF-beta signaling pathways in the control of cell proliferation.

Fred Hutchinson Cancer Center Research Seattle, USA
Post-Doctoral Research Associate Jul. 2005–Jan. 2008

Dr R. Gentleman, Computational Biology Group, Public Health Department.

The role of multiprotein complexes in determining phenotype in Yeast.
Quality assessment of flow cytometry data.

Teaching Experience

Introductory courses: R and Bioconductor - Formation Continue - Université de Rennes I, 2008

cDNA microarrays - Advance R and Bioconductor Mini Course, Fred Hutchinson Cancer Center Research, 2007. (<http://www.bioconductor.org>)

Analysis of cDNA microarrays - Introductory R and Bioconductor Mini Course, Fred Hutchinson Cancer Center Research, 2006. (<http://www.bioconductor.org>)

Initiation au langage R. Groupe de travail "bioinformatique biopuces". IRISA, Rennes, 2004. (http://www.ogepucesadnantes.org/animations_fr.php)

Traitements numériques des données issues de puces ADN. DEA Génomique et Informatiques, module Génération de données en masse. Rennes, 2002-2003.

Employment

Predictive Microbiology : Research on the minimal concentration of fatty acid to inhibit *Listeria monocytigenes* in food. Genomic characterization of *Listeria* spp. ADRIA, Quimper, France, 2000

Jackson County Health Department, Member of the EDB program, Marianna, FL, 1999.

Internet Database in microbiology and bacteriology, 1999.

Market study on Seafood by-products valorization, Mane, Queven, France, 1999.

Publications

A. Bankhead III, I. Sach, C. Ni, **N. LeMeur**, M. Kruger, M. Ferrer, R. Gentleman, Carol R. Knowledge based identification of essential signaling from genome-scale siRNA experiments. [Accepted in BMC Systems Biology]

F. Hahne*, **N. LeMeur***, R.R. Brinkman, B. Ellis, P. Haaland, D. Sarkar, J. Spidlen, E. Strain and R. Gentleman. *owCore: a Bioconductor package for high throughput ow cytometry*. BMC Bioinformatics 2009, 10:106 (* Equal contributors).

N. Le Meur and R. Gentleman. *Modeling synthetic lethality*. Genome Biology 2008, 9:R135.

D. Sarkar, **N. Le Meur**, R. Gentleman. *FlowViz: Visualization tool for high throughput flow cytometry data*. Bioinformatics. 2008 Mar 15;24(6):878-9.

A. Le Béhec, P. Zindy, T. Sierocinski, D. Petritis, A. Bihoue, **N. Le Meur**, J. Léger, N. Théret. *M@IA: A modular open-source application for microarray workflow and integrative datamining*. In Silico Biology.2008 ;8(1):63-9.

N. Le Meur, A. Rossini, M. Gasparetto, C. Smith, R.R. Brinkman, R. Gentleman. *Quality*

Assessment of Ungated Flow Cytometry data in High Throughput experiments, Cytometry A. 2007 Jun;71(6):393-403.

S. Cardin, E. Libby, P. Pelletier, S. Le Bouter, A. Shiroshita-Takeshita, **N. Le Meur**, J.J Léger, S. Demolombe, A. Ponton, L. Glass, S. Nattel. *Contrasting Gene Expression Profiles in Two Canine Models of Atrial Fibrillation*. Circulation Research. Circ Res. 2007 Feb 16;100(3):425-33.

N. Le Meur and F. Hahne. *Analyzing Flow Cytometry Data with Bioconductor*, Rnews. 2006 Dec;6(5):27-32.

J. Spidlen, R.C Gentleman, P.D Haaland, M. Langille, **N. Le Meur**, M.F Ochs, C. Schmitt, C.A Smith, A.S Treister AS, R.R Brinkman. *Data standards for flow cytometry.*, OMICS. 2006 Summer;10(2):209-214.

J. Buitink, J.J Léger, I. Guisle, B. Ly Vu, S. Wuillème, G. Lamirault, A. Le Bars, **N. Le Meur**, A. Becker, H. Kster. *Transcriptome profiling uncovers metabolic and regulatory processes occurring during the transition from desiccation sensitive to -tolerant stages in Medicago truncatula seeds*, Plant J. 2006 Sep;47(5):735-50.

Y. Blanchard , **N. Le Meur**, M. Le Cunff , P. Blanchard , J.J. Léger, A. Jestin. *Cellular Gene Expression Survey of Pseudo Rabies Virus (PRV) Infection of Human Embryonic Kidney Cells (HEK-293)*, Veterinary Research. 2006 Sep-Oct;37(5):705-723.

S. Le Jan, **N. Le Meur**, A. Cazes, P. Josette, M. Le Cunff, J.J. Léger, P. Corvol, S. Germain. *Characterization of the expression of the Hypoxia-induced genes neuritin, TXNIP and IGFBP3 in cancer*. FEBS Lett. 2006 Jun 12;580(14):3395-400.

G. Lamirault , N. Gaborit , **N. Le Meur**, C. Chevalier, G. Lande , S. Demolombe, D. Escande, S. Nattel, J.J. Léger, M. Steenman *Gene expression profile associated with chronic atrial fibrillation and underlying valvular heart disease in man*. J Mol Cell Cardiol. 2006 Jan;40(1):173-84.

M.B. Troadec, D. Glaise, G. Lamirault, M. Le Cunff, É. Guérin, **N. Le Meur**, P.J. Zindy, P. Leroyer, I. Guisle, H. Duval, P. Gripon, N. Théret, C. Guillouzo, P. Brissot , J.J. Lger *Hepatocyte iron loading capacity is associated with differentiation and repression of motility in the HepaRG cell line*. Genomics. 2006 Jan;87(1):93-103.

N. Gaborit, M. Steenman, G. Lamirault, **N. Le Meur**, S. Le Bouter, G. Lande, J.J. Leger, F. Charpentier, T. Christ, D. Dobrev, D. Escande, S. Nattel and S. Demolombe. *Human Atrial Ion Channel and Transporter Subunit Gene-Expression Remodeling Associated With Valvular Heart Disease and Atrial Fibrillation*. Circulation. 2005;112 : 471 - 481.

D. McIlroy , S. Tanguy-Royer , **N. Le Meur**, I. Guisle , P.J. Royer , J.J. Léger, K. Meflah. *Profiling dendritic cell maturation with dedicated micro-arrays*. Journal of Leukocyte biology. 2005;78(3):794-803.

M. Steenman , G. Lamirault , **N. Le Meur**, J.J. Léger. *Gene expression profiling in human*

cardiovascular disease. Clin Chem Lab Med. 2005;43(7):696-701. Review.

M. Steenman , G. Lamirault , **N. Le Meur**, M. Le Cunff , D. Escande , J.J. Léger. *Distinct molecular portraits of human failing hearts identified by dedicated cDNA microarrays*. European Journal of Heart Failure. 2005;7(2) : 157-65.

G. Lamirault, M. Steenman,**N. Le Meur**, S. Demolombe , J-N. Trochu , J.J. Léger. *DNA chip technology in cardiovascular research*. Archives des Maladies du Coeur et des Vaisseaux. 2004; 97(12) : 1251

N. Le Meur, G. Lamirault, A. Bihouée, M. Steenman, H. Bédrine-Ferran, R. Teusan, G. Ramstein, J.J. Léger. *A dynamic, web-accessible resource to process raw microarray scan data into consolidated gene expression values. Importance of replication*. Nucleic Acids Research. 2004; 32(18) : 5349-5358.

H. Bédrine-Ferran , **N. Le Meur** , I. Gicquel, M. Le Cunff, N. Soriano, I. Guisle , S. Mottier , A. Monnier , R. Teusan, P. Fergelot , J.Y. Le Gall, J.J. Léger, J. Mosser. *Transcriptome variations in human CaCo-2 cells: a model for enterocyte differentiation and its link to iron absorption*. Genomics. 2004; 83(5):772-89.

Book chapter

N. Le Meur, M. Lawrence, M. Tewari R. Gentleman. R and Bioconductor packages in Bioinformatics: toward systems biology. *In* Statistical Bioinformatics: A Guide for Life and Biomedical Science researchers. John Wiley & Sons.[To appear Summer 2009]

N. Le Meur and R. Gentleman. Analyzing statistical properties of networks with R. *In* Bacterial Molecular Networks. Series: Methods in Molecular Biology. Springer. [In preparation]

Technical Report and Master thesis

N. Le Meur, R. Gentleman. Assessing The Role Of Multi-protein Complexes In Determining Phenotype. Bioconductor Project Working Papers, 2008 (<http://www.bepress.com/bioconductor/paper13>)

MADSCAN online, Tutorial for MicroArrays Data Suite of Computed Analysis-Accessible, 2004. (http://www.madtools.org/madscan/MadScan_online_Tutorial.pdf)

De l'acquisition des données de puces ADN vers leur interprétation : importance du traitement des données primaires. Master thesis, 2005. University of Loire Atlantique, Nantes, France. (French version http://www.ogepucesadnant.es.org/publis_fr.php)

Submitted Papers

J. Gruel, M LeBorgne, **N. Le Meur** , N. Théret. *In silico investigation of ADAM12 effect on TGF-beta receptors trafficking*.

Manuscript In Preparation

N. Le Meur, RC. Gentleman. *The role of multiprotein complexes in determining phenotype*.

Selected Presentations

N. Le Meur, M Le Borgne, J Gruel and N Théret. *Discrete multi-clock modeling of biological systems*, ECCS 2009, Warwick, 21-25 September 2009.

N. Le Meur, F. Hahne, D. Sarkar and R. Gentleman. High throughput flow cytometry analysis with Bioconductor. UseR 2009, Rennes, 8-10 July 2009.

N. Le Meur, M Le Borgne, J Gruel and N Théret. Multiclock Discrete Models of the Eukaryotic Cell Cycle. JOBIM 2009 satellite meeting : Dynamical modelling and simulation of biological networks, Nantes, 12 Jun 2009.

N. Le Meur, M Le Borgne, J Gruel and N Théret. Modeling the influence of EGF and TGF- β pathways in tumor progression of hepatocellular carcinoma. Asian Pacific Association for the Study of the Liver (APASL), Hong Kong, 13-16 Feb 2009

J. Gruel, Le Borgne M, **N. Le Meur**, and Théret N. In silico investigation of ADAM12 effect on TGF- β receptors trafficking. Lyon's International Multidisciplinary Meeting on Integrative Post-Genomics (IPG), Lyon, 19-21 Nov., 2008.

N. Le Meur, F. Hahne, D. Sarkar and R. Gentleman. The flowCore package. Tutorial, ISAC XXIV International Congress, Budapest, Mai 2008.

N. Le Meur and R. Gentleman. Multi-protein complexes and synthetic lethality. Symbiose seminars, IRISA, Rennes, April 2008.

N. Le Meur, D.Sarkar and R. Gentleman. Flow cytometry data analysis with R: the flowCore package, BioC2007 conference, FHCRC, Seattle, August 2007.

N. Le Meur and R. Gentleman. Data quality assessment in flow cytometry experiment. Genetics and Genomics Group seminars, FHCRC, Seattle, March 2006.

N. Le Meur, A. Bihoue and J. Lger. Outils pour l'analyse et la gestion des données de puces AND (R, Base), Journée Réseau National des Génopoles, Toulouse, 2005.

N. Le Meur and J. Lger. MADSCAN: a microarray data processing tool to get consolidated gene expression data matrix, Séminaire du Laboratoire de Neurobiologie de l'ESPCI, Paris, 2004.

N. Le Meur and J. Lger. The challenges of Bioinformatics for Microarray Data Analysis, Le Croisic, 2004.

N. Le Meur. Beyond Microarrays Data Acquisition, OuestChips, 2003.

N. Le Meur, A. Bihoue and L. Lger. MicroArray Data Analysis: Numerical treatment and knowledge Extraction, Université Paris XI-Hôpital Marie Lannelongue, 2003.

N. Le Meur and L. Lger. Développement d'une procédure dynamique de traitement des images de puces ADN : Filtration et normalisation. Action Informatique Mathématique

Physique pour la Génomique, Groupe Analyse Statistique du Transcriptome, Montpellier, 2002.

N. Le Meur and L. Lger. Numerical Analysis of MicroArray Data - Physical and theoretical bases Automation under Excel. Journées bioinformatiques génopole ouest, Nantes, 2002.

N. Le Meur. Signaux d'hybridation : captures, logiciels, traitement. Atelier Genopole Ouest, Initiation à la technologies des puces ADN, Nantes, 2001.

Poster presentation

N. Le Meur, Le Borgne M, Gruel J, Thret N. Discrete multi-clock modelling of biological systems. Lyon's International Multidisciplinary Meeting on Integrative Post-Genomics (IPG), Lyon, 19-21 Nov., 2008.

Data quality assessment in flow cytometry experiment, **XXIII International Congress of the International Society for Analytical Cytology (ISAC)**, Québec City, Canada, 2006.

MADTOOLS : management tools for the mining of microarray data, Archives Congrès **GRRRC**, Des maladies du Coeur et des vaisseaux - Journal d'expression de la société française de cardiologie, La Baule, 2004.

MADTools : management tool for the mining of microarray data, 'Details on MADSENSE, a gene comprehension support system'. **ECCB**, Paris, 2003.

MADTOOLS : management tools for the mining of microarray data, **Cambridge Healthtech Institute's**, Baltimore, 2003 .

MADTOOLS : management tools for the mining of microarray data, **MGED 6**, Aix-en-Provence, 2006.

MADTOOLS : management tools for microarray data. Rencontres Microarray, **Amersham Biosciences**. Villejuif, 2003.

Dynamic procedure for numerical analysis of microarray data, **Chips to Hits**, Philadelphia, 2002.

Software development

N. Le Meur, Z. Jiang, T-Y. Liu, J. Mar, R. Gentleman. SLGI R/Bioconductor package for the analysis of synthetic genetic interactions. (<http://www.bioconductor.org>)

N. Le Meur, R. Gentleman. PCpheno R/Bioconductor package to integrate, annotate, and link phenotypes to cellular organizational units such as protein complexes and pathways. (<http://www.bioconductor.org>)

N. Le Meur, B. Ellis, F. Hahne, R. Gentleman, P.D. Haaland. flowCore, R/Bioconductor package that proposes S4 data structures and basic functions to deal with flow cytometry

data. (<http://www.bioconductor.org>)

B. Ellis, R. Gentleman, F. Hahne, **N. Le Meur**, D. Sarkar. `flowViz`, R/Bioconductor package that provides visualization tools for flow cytometry data. (<http://www.bioconductor.org>)

N. Le Meur, R. Gentleman, F. Hahne, J. Kettman, M. Tang. `flowQ` R/Bioconductor package that provides quality control and quality assessment tools for flow cytometry data. (<http://www.bioconductor.org>)

A.J. Rossini, J.Y. Wan, Z. Moodie and **N. Le Meur** (Maintainer). `rflowcyt` Bioconductor R package for flow cytometry experiment. (<http://www.bioconductor.org>)

MADSCAN MicroArray Data Suite of Computed Analysis is a web service for two color microarray pre-processing I developed during my PhD and maintain. (<http://www.madtools.org>)

Grants

2008-2010 LA LIGUE CONTRE LE CANCER. Post-doctoral grant for young scientists.

Honors and Scholarship

2005 Ph.D. in Bioinformatics, *Honors Status*. University of Loire Atlantique, Nantes, France.

2002 Scholarship from the University of Bretagne Occidentale for thesis in Genomics and Bioinformatics, Rennes, France.

2000-2001 Scholarship from the University of Bretagne Occidentale for a Master in Bioinformatics, Rennes, France.

2000 Engineering Diploma in Microbiology and Food Safety, University of Bretagne Occidentale, Brest, France.

1997 Biology Diploma, *Cum Laude*. University of Bretagne Occidentale, Brest, France.

1995 Baccalaureate of Sciences, *Honors Status*. Quimper, France

Language Skills

- French (native)
- English (fluent)

Computer Skills

- Operating systems: UNIX, Linux, Macintosh and Windows.
- Languages: R, Python, Perl, CGI technology, PHP, HTML, \LaTeX