

## Nolwenn Le Meur - Rouillard

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EHESP

Avenue du Professeur-Léon-Bernard  
CS 74312 35043 Rennes Cedex  
France

Tel: +33 (0) 2 99 02 25 14

Nolwenn.LeMeur-Rouillard@ehesp.fr  
<http://www.nlmr.free.fr>

### Research

EHESP - Dpt InfoBioStat

Associate professor

Teaching in Biostatistics

Research in data integration via graphs concept

Rennes, FR

November 2010 – present

INSERM-IRISA-Biogenouest

Post-Doctoral Research Associate

*Coordinator of the Biogenouest Integrative Genomics Project.*

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

Dr N. Théret, IRSET EA 4427 SeRAIC.

Rennes, FR

March. 2008 – October 2010

Fred Hutchinson Cancer Center Research

Post-Doctoral Research Associate

*The role of multiprotein complexes in determining phenotype in Yeast.*

*Quality assessment of flow cytometry data.*

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

Seattle, USA

Jul. 2005–Feb. 2008

### Education

2001-2005 Ph.D. in Bioinformatics, INSERMU533, Supervisor Jean Léger, University of Nantes, France.

2000-2001 Master in Genomics and Bioinformatics, University of Rennes I, France.

1997-2000 Engineering School of Microbiology and Food Safety, Brest, France.

1996-1997 Biology Diploma, University of Brest, France.

### Main publications

N. Le Meur *et al.* R and Bioconductor packages in Bioinformatics: toward systems biology. *In* Statistical Bioinformatics: A Guide for Life and Biomedical Science researchers. John Wiley & Sons (2010).

N. LeMeur\* , F. Hahne\* *et al.* flowCore: a Bioconductor package for high throughput flow cytometry. BMC Bioinformatics 2009, 10:106 (\* Equal contributors).

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

N. Le Meur *et al.* Quality assessment of ungated Flow cytometry data in high throughput

experiments, *Cytometry A*. 2007, 71A(6):393-403.

N. Le Meur *et al.* 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.

## Teaching Experience

### Teaching

- 2011 Biostatistics, Fondamentaux établissements, EHESP (TD 15h)
- 2010 Biostatistics, Fondamentaux école, EHESP (TD 18h)
- 2010 Biostatistics, Master I Gouvernance, EHESP-University of Rennes I (18h)
- 2010 R and Bioconductor, 3 day course, University of Rennes I (21h)
- 2009 Flow cytometry data analysis, practical course  
Immunology Center, Marseille Luminy (4h)
- 2008 Introductory courses: R and Bioconductor, University de Rennes I
- 2006-2008 Introductory courses: R and Bioconductor, lectures and practicals  
Fred Hutchinson Cancer Center Research, Seattle (13h30)
- 2004 Introductory course in R, practical course, Rennes (4h)
- 2002-2003 High-throughput data management and analysis, lecture, Rennes

### E-learning

- screencast for the Analysis Tool Pack for Excel(r)

### Monitoring

- 2009-2010 Master 2 Modeling biological systems, University of Rennes I
- 2004 IUP Technologies Avancés des Sciences du Vivant,  
Louis Pasteur University, Strasbourg
- 2003-2004 IUT, Statistics et Data mining, Vannes

## Language Skills

- French (native)
- English (fluent)

## Computer Skills

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

## Organisations

- 2010-2011 Coordinator of the Biogenouest Integrative Genomics Project.
- 2010 Scientific meeting on modeling approaches in systems biology (IRISA Symbiose, Rennes)
- 2005-2007 Weekly scientific seminars of the computational biology group, Fred Hutchinsons Cancer Research Center, Seattle.
- 2005-2008 Member of the International Society for Advancement of Cytometry (ISAC)  
Member of the Flow Informatics and Computational Cytometry Society (FICCS)

## **Honors and Scholarship**

- 2008-2010 LA LIGUE CONTRE LE CANCER. Post-doctoral grant for young scientists.
- 2009 Travel grant for oral presentation at the 19th APASL congress (Asian Pacific Association for the Study of the Liver), Hong Kong, Feb 2009.
- 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.

## Publications

2011

**N. Le Meur** and R. Gentleman. Analyzing statistical properties of networks with R. [Book chapter in press]

D. Gilot, **N. Le Meur**, et al RNAi-based screening identifies kinases interfering with dioxin-mediated up-regulation of CYP1A1 activity [PLoS ONE in press]

2010

**N. Le Meur**, M. Lawrence, M. Tewari, R. Gentleman. R and Bioconductor in bioinformatics: toward systems biology. In: Statistical Bioinformatics: A Guide for Life and Biomedical Science Researchers. John Wiley & Sons.

G. Lamirault, **N. Le Meur** et al. *Molecular risk stratification in advanced heart failure patients*. J Cell Mol Med. 2010 Jun;14(6B):1443-52.

2009

**N. Le Meur**, M Le Borgne, J Gruel and N Thret. *Multi-clock discrete modelling of biological systems*. ECCS, Warwick 2009.

J. Gruel, M. LeBorgne, **N. LeMeur**, N. Théret. In silico investigation of ADAM12 effect on TGF-beta receptors trafficking. BMC Res Notes. 2009 Sep 24;2(1):193.

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. BMC Systems Biology 2009, 3:80

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).

2008

**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.

2007

**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*, CytometryA.

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.

## 2006

**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.

## 2005

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.

#### 2004

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.(2010)

#### 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](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](http://www.ogepucesadnant.es.org/publis_fr.php))

#### Selected Presentations (seminars, symposium, congress)

High throughput flow cytometry analysis with Bioconductor. UseR 2009, Rennes, 8-10 July 2009.

Modeling the influence of EGF and TGF- $\beta$  pathways in tumor progression of hepatocellular carcinoma. Asian Pacific Association for the Study of the Liver (APASL), Hong Kong, 13-16 Feb 2009

The flowCore package. Tutorial, ISAC XXIV International Congress, Budapest, Mai 2008.

Multi-protein complexes and synthetic lethality. Symbiose seminars, IRISA, Rennes, April 2008.

Flow cytometry data analysis with R: the flowCore package, BioC2007 conference, FHCRC, Seattle, August 2007.

Data quality assessment in flow cytometry experiment. Genetics and Genomics Group seminars, FHCRC, Seattle, March 2006.

Outils pour l'analyse et la gestion des données de puces AND (R, Base), Journée Réseau National des Génomies, Toulouse, 2005.

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

The challenges of Bioinformatics for Microarray Data Analysis, Le Croisic, 2004.

Beyond Microarrays Data Acquisition, OuestChips, 2003.

Data Analysis: Numerical treatment and knowledge Extraction, Université Paris XI-Hôpital Marie Lannelongue, 2003.

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.

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

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

#### **Poster presentation (seminars, symposium, congres)**

Discrete multi-clock modelling of biological systems. Lyon's International Multidisciplinary Meeting on Integrative Post-Genomics (IPG), Lyon, 19-21 Nov., 2008.

The role of multi-protein complexes in synthetic lethality, **15th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB) & 6th European Conference on Computational Biology (ECCB)**, Vienna, Autriche 2007.

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

**GRRC**, Des maladies du Coeur et des vaisseaux - Journal d'expression de la société française de cardiologie, La Baule, France 2004.

MADTOOLS: management tools for the mining of microarray data, **ECCB**, Paris, 2003 ; **Cambridge Healthtech Institute's**, Baltimore, 2003; **MGED 6**, Aix-en-Provence, 2003; **Amersham Biosciences**. Villejuif, 2003; **Chips to Hits**, Philadelphia, USA 2002.

### Software development

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

**N. Le Meur**, R. Gentleman. PCpheno RBioconductor 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, RBioconductor 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, RBioconductor 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 RBioconductor 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>)