

34 Publications (Nombre total en première ou dernière auteure: 9)

1. Lalloué, B., Deguen, S. , Monnez, J. , Padilla, C. , Kihal, W. , Zmirou-Navier, D. and Le Meur, N. (2015) SesIndexCretoR: An R Package for Socioeconomic Indices Computation and Visualization. Open Journal of Statistics.2015 June 8; 5, 291-302. doi: 10.4236/ojs.2015.54031.
2. Le Meur N, Gao F, Bayat S. Mining care trajectories using health administrative information systems: the use of state sequence analysis to assess disparities in prenatal care consumption. BMC Health Serv Res. 2015 May 15;15(1):200. doi: 10.1186/s12913-015-0857-5. PubMed PMID: 25976089.
3. P. Nizard, F. Ezan, D. Bonnier, N. Le Meur, S. Langouet, G. Baffet, Y. Arlot-Bonnemains et al. Integrative analysis of high-throughput RNAi screen data identifies the FER and CRKL tyrosine kinases as new regulators of the mitogenic ERK-dependent pathways in transformed cells. BMC Genomic (Accepted Dec 2014)
4. M. Louazel, F. Gao, L. Ferrat, F. Quidu, N. Le Meur. Le secteur privé non lucratif face à la recomposition hospitalière. Cahier de l'Institut de formation supérieure des cadres dirigeants de la FEHAP 2014 Nov.(4)
5. O. Dameron, C. Bettembourg, N. Le Meur. Measuring ontology quality variations: the Gene Ontology complexity case study. PLoS One. 2013 Oct 11;8(10):e75993.
6. Lalloué B, Monnez JM, Padilla C, Kihal W, Le Meur N, Zmirou-Navier D, Deguen S. A statistical procedure to create a neighborhood socioeconomic index for health inequalities analysis. Int J Equity Health. 2013 Mar 28;12:21.
7. Le Meur N. Computational methods for evaluation of cell-based data assessment--Bioconductor. Curr Opin Biotechnol. 2013 Feb;24(1):105-11.
8. Roussel M, Gros A, Gacouin A, Le Meur N, Le Tulzo Y, Fest T. Toward new insights on the white blood cell differential by flow cytometry: A proof of concept study on the sepsis model. Cytometry B Clin Cytom. 2012 Apr 16.
9. N. Le Meur and R. Gentleman. Analyzing biological data using R: methods for graphs and networks. Methods Mol Biol. 2012; 804:343-73.
10. J. Gruel, M. LeBorgne, N. Le Meur, N. Théret. Simple Shared Motifs (SSM) in conserved region of promoters: a new approach to identify co-regulation patterns. BMC Bioinformat- ics. 2011 Sep 12;12:365.
11. D. Gilot, N. Le Meur, F. Giudicelli, M. Le Vée, D. Lagadic-Gossmann, N. Théret, O. Fardel. RNAi-Based Screening Identifies Kinases Interfering with Dioxin-Mediated Up- Regulation of CYP1A1 Activity. PLoS One. 2011 Mar 29;6(3):e18261.
12. Lamirault G, N Le Meur, Roussel JC, Cunff MF, Baron D, Bihouée A, Guisle I, Raharijaona M, Ramstein G, Teusan R, Chevalier C, Gueffet JP, Trochu JN, Léger JJ, Houlgatte R, Steenman M. Molecular risk stratification in advanced heart failure patients. J Cell Mol Med. 2010 Jun;14(6B):1443-52
13. Gruel J., LeBorgne M, LeMeur N, Théret N. In silico investigation of ADAM12 effect on TGF-beta receptors trafficking. BMC Res Notes. 2009 Sep 24;2(1):193.

14. Bankhead A, Sach I, Ni C, LeMeur N, Kruger M, Ferrer M, Gentleman R, Rohl C. Knowledge based identification of essential signaling from genome-scale siRNA experiments. *BMC systems biology* 2009 vol. 3 pp. 80
15. Hahne* F, Le Meur* N, Brinkman R, Ellis B, Haaland P, Sarkar D, Spidlen J, Strain E, Gentleman R. flowCore: a Bioconductor package for high throughput flow cytometry. *BMC Bioinformatics*. 2009 10:106. (*Equal contributors)
16. Le Meur N and Gentleman R. Modeling synthetic lethality. *Genome Biology*. 2008 Sep; 9:R135.
17. Sarkar D, Le Meur N and Gentleman R. FlowViz: Visualization tool for high throughput flow cytometry data. *Bioinformatics*. 2008 Mar; 24(6):878-879
18. Le Bécheuc A, Zindy P, Sierocinski T, Petritis D, Bihouée A, Le Meur N, Léger J, N. Théret. M@IA: A modular open-source application for microarray workflow and integrative datamining. *In Silico Biology*. 2007; 8, 0007.
19. Le Meur N, Rossini A, Gasparetto M, Smith C, Brinkman RR, Gentleman R. Data quality assessment of ungated flow cytometry data in high throughput experiments. *Cytometry A*. 2007 Jun;71(6):393-403.
20. Cardin S, Libby E, Pelletier P, Le Bouter S, Shiroshita-Takeshita A, Le Meur N, Léger J, Demolombe S, Ponton A, Glass L, Nattel S. Contrasting gene expression profiles in two canine models of atrial fibrillation. *Circ Res*. 2007 Feb 16;100(3):425-33. Epub 2007 Jan 18.
21. Le Meur N, Hahne F. Analyzing Flow Cytometry Data with Bioconductor, *Rnews*. 2006 Dec; 6(5):27-32.
22. Buitink J, Leger JJ, Guisle I, Vu BL, Wuillème S, Lamirault G, Le Bars A, Le Meur N, Becker A, Küster H, Leprince O. Transcriptome profiling uncovers metabolic and regulatory processes occurring during the transition from desiccation-sensitive to desiccation-tolerant stages in *Medicago truncatula* seeds. *Plant J*. 2006 Sep;47(5):735-50.
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24. Blanchard Y, Le Meur N, Le Cunff M, Blanchard P, Léger J, Jestin A. Cellular gene expression survey of PseudoRabies Virus (PRV) infected Human Embryonic Kidney cells (HEK-293). *Vet Res*. 2006 Sep-Oct;37(5):705-23. Epub 2006 Jul 6.
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26. Troadec MB, Glaise D, Lamirault G, Le Cunff M, Guérin E, Le Meur N, Détivaud L, Zindy P, Leroyer P, Guisle I, Duval H, Gripon P, Théret N, Boudjema K, Guguen-Guillouzo C, Brissot P, Léger JJ, Loral O. Hepatocyte iron loading capacity is associated with differentiation and repression of motility in the HepaRG cell line. *Genomics*. 2006 Jan;87(1):93-103. Epub 2005 Dec 1.
27. Lamirault G, Gaborit N, Le Meur N, Chevalier C, Lande G, Demolombe S, Escande D, Nattel S, Léger JJ, Steenman M. 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. Epub 2005 Oct 19
28. Steenman M, Lamirault G, Le Meur N, Léger JJ. Gene expression profiling in human cardiovascular disease. *Clin Chem Lab Med*. 2005;43(7):696-701. Review.
29. Gaborit N, Steenman M, Lamirault G, Le Meur N, Le Bouter S, Lande G, Léger J, Charpentier F, Christ T, Dobrev D, Escande D, Nattel S, Demolombe S. Human atrial ion channel and transporter subunit gene-

expression remodelling associated with valvular heart disease and atrial fibrillation. *Circulation*. 2005 Jul 26;**112**(4):471-81. Epub 2005 Jul 18.

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32. Lamirault G, Steenman M, Le Meur N, Demolombe S, Trochu JN, Léger JJ. DNA chip technology in cardiovascular research. *Arch Mal Coeur Vaiss*. 2004 Dec;**97**(12):1251-5. Review.
33. Le Meur N, Lamirault G, Bihouée A, Steenman M, Bédrine-Ferran H, Teusan R, Ramstein G, Léger JJ. A dynamic, web-accessible resource to process raw microarray scan data into consolidated gene expression values: importance of replication. *Nucleic Acids Res*. 2004 Oct 8;**32**(18):5349-58. Print 2004.
34. Bédrine-Ferran H, Le Meur N, Gicquel I, Le Cunff M, Soriano N, Guisle I, Mottier S, Monnier A, Teusan R, Fergelot P, Le Gall JY, Léger J, Mosser J. Transcriptome variations in human CaCo-2 cells: a model for enterocyte differentiation and its link to iron absorption. *Genomics*. 2004 May;**83**(5):772-89.

Chapitre de livre

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.

Communication orale

Parcours de soins des femmes enceintes à partir de l'échantillon généraliste des bénéficiaires (EGB), JOSE, Nantes, 4 Septembre 2014.

Coopération hospitalière: Etude pilote modèle matriciel pour l'analyse des flux de patients diabétiques entre établissements de soins bretons. Odissé, Angers, 13 Novembre 2012.

Analyzing large heterogeneous public health data using R. 3rd Conference of the international breast cancer and nutrition (IBCN). Purdue University, West Lafayette, 8-12 October 2012.

The role of socio-territorial inequities on health of pregnant women. Health and Space, Marseille, 19-21 september 2012.

Assessing the role of multi-protein complexes in determining phenotype. 58th Congress of the International Statistical Institute. Dublin, August 2011.

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

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

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

Communication par affiche

Estimation de l'effet cohorte comme interaction multiplicative partielle entre l'âge et la période : application à la mortalité liée à l'alcool en France de 1968 à 2010. Congrès ADELPH-EPITER, Nice, 10-12 Septembre 2014.

The role of socio-territorial inequities on health of pregnant women. Odissé, Angers, 13 Novembre 2012.

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.