



BIBLIO-WEBOGRAPHIE

SEMAINE 1, COURS 1 - "PLACE DE CET OUTIL ANALYTIQUE DANS LA BIOLOGIE DU XXIEME SIECLE"

Bout B. (2010-2011). L'organisation de la recherche et ses perspectives en matière de prévention et de traitement de l'obésité. Sénat, rapport n°158. Repéré à <http://www.senat.fr/rap/r10-158/r10-15831.html#toc652>.

Inserm. (2011) Reproduction et environnement. LES EDITIONS INSERM, XXI-713 p. Repéré à http://www.ipubli.inserm.fr/bitstream/handle/10608/222/Chapitre_20.html

San Cristobal, M., Sanchez M.P., Mercat M.J., Rohart F., Liaubet L., Tribout T., Canlet C., Muller N., Molina J., Ianucelli B., Laurent B., Villa-Vialaneix N., Paris A., Milan D. (2014). Le métabolome, un moyen pour trouver de nouveaux biomarqueurs ?. VIANDES & PRODUITS CARNES, VPC-2014-30-2-1. Repéré à https://www.viandesetproduitscarnes.fr/phocadownload/vpc_vol_30/3021_sancristobal_metabolomique.pdf

SEMAINE 1, COURS 2 - "OBJET, DIMENSIONS ET FINALITES DE LA METABOLOMIQUE"

C Sévin D., Kuehne A., Zamboni N., Sauer U. (2014) Biological insights through nontargeted metabolomics. CURRENT OPINION IN BIOTECHNOLOGY. <https://doi.org/10.1016/j.copbio.2014.10.001>

Krastanov A. (2010). Metabolomics - The State of Art. BIOTECHNOLOGY & BIOTECHNOLOGICAL EQUIPMENT. <https://doi.org/10.2478/V10133-010-0001-Y>

Patti G.J., Yanes O, Siuzdak G. (2012). Innovation : Metabolomics : the apogee of the omics trilogy. NATURE REVIEWS MOLECULAR CELL BIOLOGY. <https://doi.org/10.1038/nrm3314>



SEMAINE 1, COURS 3 - "DEMARCHE ANALYTIQUE ET TECHNOLOGIES : DU PLAN D'EXPERIENCE AU TRAITEMENT DES DONNEES"

Courant, F., Antignac J.-P., Dervilly-Pinel G., Le Bizec B. (2014). Basics of mass spectrometry based metabolomics. PROTEOMICS.

<https://doi.org/10.1002/pmic.201400255>

SEMAINE 1, COURS 4 - "L'ANALYSE BIOINFORMATIQUE : PRE-TRAITEMENT DES DONNEES, ANALYSES STATISTIQUES ET ANNOTATION"

Kumar Barupal, D., Fan, S., Fiehn, O. (2018). Integrating bioinformatics approaches for a comprehensive interpretation of metabolomics datasets, CURRENT OPINION IN BIOTECHNOLOGY, 54 : 1-9.

<https://doi.org/10.1016/j.copbio.2018.01.010>.

Spicer, R., Salek, R.M., Moreno, P. et al. (2017). Navigating freely-available software tools for metabolomics analysis. METABOLOMICS, 13 : 106.

<https://doi.org/10.1007/s11306-017-1242-7>.



SEMAINE 2, COURS 1 - "PRINCIPE DE LA RESONANCE MAGNETIQUE NUCLEAIRE (RMN)"

Akoka, S. (2018). Introduction à la RMN. Repéré à <http://www.sciences.univ-nantes.fr/CEISAM/index.php?page=43&lang=FR>

Akoka, S. (2018). Une introduction à la RMN. Repéré à <https://www.youtube.com/channel/UCQMIPesU94tj2QGiSmGDQMA>

SEMAINE 2, COURS 2 - "PRINCIPE DE LA SPECTROMETRIE DE MASSE (SDM)"

Courant, F., Antignac J.-P., Dervilly-Pinel G., Le Bizec B. (2014). Basics of mass spectrometry based metabolomics. PROTEOMICS.
<https://doi.org/10.1002/pmic.201400255>

SEMAINE 2, COURS 3 - "PREPARATION DES ECHANTILLONS (RMN, SDM)"

Deborde, C., (scénariste) et Girard A. (réalisateur). 2018. Cryobroyage de pélicarpe de tomate. Broyeur cryogénique Freezer Mill (Cryogenic Grinder). UMR Biologie & Pathologie du Fruit, Bordeaux : INRA.

Deborde, C. Moing, A., Roch, L., Jacob, D., Rolin, D., Giraudeau, P. (2017). Plant metabolism as studied by NMR spectroscopy. PROGRESS IN NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY, 102-103, 61-97. <https://doi.org/10.1016/j.pnmrs.2017.05.001>

Haid M., Muschet C., Wahl S., Römisch-Margl W., Prehn C., Möller et Adamski J. (2018). Long-term stability of human plasma metabolites during storage at -80°C. JOURNAL OF PROTEOM RESEARCH, 17 (1), 203-211. doi : 10.1021/ACS.JPROTEOME.7B00518

Les constituants de l'organisme. 16-21. <http://extranet.editis.com/images/300/art/doc/f/fbabe06ba6e3494a333433343234363834333239.pdf>



SEMAINE 2, COURS 4 - "ACQUISITION ET PRE-TRAITEMENT DES DONNEES RMN"

Akoka, S., Giraudeau, P. (2016). A la découverte des applications de la résonance magnétique nucléaire. Repéré à <http://webtv.univ-nantes.fr/fiche/8391/a-la-decouverte-des-applications-de-la-resonance-magnetique-nucleaire>

Marchand, J., Martineau, E., Guitton, Y., Dervilly-Pinel, G., et Giraudeau, P. (2017). Multidimensional NMR approaches towards highly resolved, sensitive and high-throughput quantitative metabolomics. CURRENT OPINION IN BIOTECHNOLOGY, 43, 49-55. <https://doi.org/10.1016/j.copbio.2016.08.004>

SEMAINE 2, COURS 5 - "ACQUISITION ET PRE-TRAITEMENT DES DONNEES SDM)"

Courant F., Antignac J.-P., Dervilly-Pinel G., Le Bizec B. (2014). Basics of mass spectrometry based metabolomics. PROTEOMICS, 14 (21-22), 2369-88. <https://doi.org/10.1002/pmic.201400255> <https://doi.org/10.1021/ACS.JPROTEOME.7B00518>

Madalinski, G., Godat, E., Alves, S., Lesage, D., Genin, E., Levi, P., Labarre, J., Tabet, J.-C., Ezan, E. and Junot, C. (2008) Direct introduction of biological samples into a LTQ-Orbitrap hybrid mass spectrometer as a tool for fast metabolome analysis. ANAL. CHEM., 80, 3291–303. <https://doi.org/10.1021/ac7024915>



SEMAINE 3, COURS 4 - "LA MODELISATION PLS POUR LA PREDICTION"

Cornillon P. and Matzner-Lober E. (2007). Régression : théorie et applications. SPRINGER.

Tenenhaus M. (1999). L'approche PLS. REVUE DE STATISTIQUES APPLIQUEES, 47, 5-40.

Tenenhaus M. (1998). La régression PLS : théorie et pratique. TECHNIP.

Thévenot EA. (2015). The ropls package: PCA, PLS(-DA) and OPLS(-DA) for multivariate analysis and feature selection of omics data. Repéré à <https://doi.org/10.18129/B9.bioc.ropls>

Vancolen S. (2004). La régression PLS. Université de Neuchâtel, Suisse.

Wold S., Sjöström M. and Eriksson L. (2001). PLS-regression: a basic tool of chemometrics. Chemom. Intell. Lab. Syst. 58, 109-130. Repéré à [https://doi.org/10.1016/S0169-7439\(01\)00155-1](https://doi.org/10.1016/S0169-7439(01)00155-1)

SEMAINE 3, COURS 5 - "LES DONNEES DE METABOLOMIQUE REPETEES : DES DONNEES APPARIEES AUX DONNEES LONGITUDINALES"

Choo JM, Kanno T, Zain NMM, Leong LEX, Abell GCJ, Keeble JE, Bruce KD, Mason AJ, Rogers GB. 2017. Divergent relationships between fecal microbiota and metabolome following distinct antibiotic-induced disruptions. MSPHERE 2:E00005-17. <https://doi.org/10.1128/mSphere.00005-17>.

Ewoud J. J. van Velzent†, Johan A. Westerhuist†, John P. M. van Duynhoven, Ferdi A. van Dorsten, Huub C. J. Hoefsloott†, Doris M. Jacobs§ Suzanne Smitt†, Richard Draijer§, Christine I. Kroner and Age K. Smildet†. Multilevel Data Analysis of a Crossover Designed Human Nutritional Intervention Study. BIOSYSTEMS DATA ANALYSIS, SWAMMERDAM INSTITUTE FOR LIFE SCIENCES, UNIVERSITEIT VAN AMSTERDAM, NIEUWE ACHTERGRACHT 166, 1018 WV AMSTERDAM, THE NETHERLANDS. Unilever Food and Health Research; Institute, Olivier van Noortlaan 120, 3133 AT Vlaardingen, The Netherlands.



MOOC La métabolomique : enjeux technologiques et scientifiques

Boccard J., Rudaz S. 2016. Exploring Omics data from designed experiments using analysis of variance multiblock Orthogonal Partial Least Squares. School of Pharmaceutical Sciences, University of Geneva, University of Lausanne, Geneva, Switzerland.

SEMAINE 3, COURS 6 - "LES RESEAUX METABOLOMIQUE"

Cottret, L., Frainay, C., Chazalviel, M., Cabanettes, F., Gloaguen, Y., Camenen, E., Jourdan, F. (2018). MetExplore : collaborative edition and exploration of metabolic networks. NUCLEIC ACIDS RESEARCH, 46(WEB SERVER ISSUE), W495–W502. <http://doi.org/10.1093/nar/gky301>

Thiele, I., & Palsson, B. Ø. (2010). A protocol for generating a high-quality genome-scale metabolic reconstruction. NATURE PROTOCOLS, 5(1), 93–121. <http://doi.org/10.1038/nprot.2009.203>



SEMAINE 4, COURS 2 - "METABOLOMIQUE ET SOCIETE : LE CAS DE LA LUTTE ANTI-DOPAGE"

Casana M. *Quelles sont les différentes méthodes de dopage ?*. Maxisciences, Août 2012. Repéré à https://www.maxisciences.com/dopage/quelles-sont-les-differentes-methodes-de-dopage_art26264.html.

Devillard D. *Après les aveux de Lance Armstrong, comment agit l'EPO ?*. Science et Avenir, Janvier 2013. Repéré à https://www.sciencesetavenir.fr/sante/apres-les-aveux-de-lance-armstrong-comment-agit-l-epo_25792.

Les ingénieuses méthodes de dopage de l'équipe de Lance Armstrong. AFP - L'Express, Octobre 2012. Repéré à https://www.lexpress.fr/actualite/sport/dopage-les-ingenieuses-methodes-de-l-equipe-de-lance-armstrong_1173465.html.

SEMAINE 4, COURS 3 - "DECOUVRIR ET MANIPULER 3 OUTILS ET METHODES DE LA COMMUNAUTE FRANÇAISE"

Cottret, L., Frainay, C., Chazalviel, M., Cabanettes, F., Cloaguen, Y., Camenen, E., Merlet, B., Heux, S., Portais, J.-C., Poupin, N., Vinson, F., Jourdan, F. MetExplore : collaborative edition and exploration of metabolic networks. NUCLEIC ACIDS RESEARCH, Volume 46, Issue W1, 2 July 2018, Pages W495–W502. <https://doi.org/10.1093/nar/gky301>

Dittami, S.M. et al. (2012) Towards deciphering dynamic changes and evolutionary mechanisms involved in the adaptation to low salinities in Ectocarpus (brown algae) : Adaptation to low salinities in Ectocarpus. THE PLANT JOURNAL, DOI : <https://doi.org/10.1111/j.1365-3113X.2012.04982.x>

Frainay, C., Jourdan, F. Computational methods to identify metabolic sub-networks based on metabolomic profiles. BRIEFINGS IN BIOINFORMATICS, Volume 18, Issue 1, 1 January 2017, Pages 43–56, <https://doi.org/10.1093/bib/bbv115>

Giacomoni, F., Le Corguillé, G., Monsoor, M., Landi, M., Pericard, P., Pétéra, M., Duperier, C., Tremblay-Franco, M., Martin, J.-F., Jacob, D., Goulitquer, S., Thévenot, E., Caron, C. Workflow4Metabolomics : a collaborative research infrastructure for



computational metabolomics. (2014). BIOINFORMATICS, Volume 31, Issue 9, May 2015, 1493-1495, <https://doi.org/10.1093/bioinformatics/btu813>.

Guillon, Y., Tremblay-Franco, M., Le Corguillé, G., Martin, J.-F., Pétera, M., Roger-Mele, P., Delabrière, A., Goulitquer, S., Monsoor, M., Duperier, C., Canlet, C., Servien, R., Tardivel, P., Caron, C., Giacomoni, F., Thévenot, A. (2017). Create, run, share, publish, and reference your LC-MS, FIA-MS, GC-MS, and NMR data analysis workflows with the Workflow4Metabolomics 3.0 Galaxy online infrastructure for metabolomics. THE INTERNATIONAL JOURNAL OF BIOCHEMISTRY & CELL BIOLOGY, 2017, ISSN 1357-2725, <http://dx.doi.org/10.1016/j.biocel.2017.07.002>.

Jacob, D., Deborde, C., Lefebvre, M. et al. NMRProcFlow : a graphical and interactive tool dedicated to 1D spectra processing for NMR-based metabolomics. METABOLOMICS (2017) 13: 36. <https://doi.org/10.1007/s11306-017-1178-y>

Madalinski, G., Godat, E., Alves, S., Lesage, D., Genin, E., Levi, P., Labarre, J., Tabet, J.-C., Ezan, E. and Junot, C. (2008) Direct introduction of biological samples into a LTQ-Orbitrap hybrid mass spectrometer as a tool for fast metabolome analysis. ANAL. CHEM., 80, 3291–303. <https://doi.org/10.1021/ac7024915>