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CEA Research Director

Team leader Centre National de Recherche en Génomique Humaine (CEA Jacob/CNRGH)

2 Rue Gaston Crémieux

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PROFESSIONAL EXPERIENCE

2021 – present. CEA Research Director.

2019 – present. Member of the executive committee of the CNRGH.

2019 – present. Junior and Senior expert for the CEA in computational genomics.

2018 – present. Team Leader at the CNRGH, computational genomics, 6 FTE.

2015 – present. Senior scientist at the CEA/CNRGH.

2010 – 2015. Research Engineer at the Institut Curie (Paris), in the Team Computational Systems Biology of Cancer.

2001 – 2010. Research Engineer at the VIB Department of Plant Systems Biology, Gent University (Belgium), in the Team Bioinformatics and Evolutionary Genomics.

1997 – 2001. Junior consultant and developer for computer science companies (SSI) in Paris, France.

1997 Post-doc (6 months) at the Laboratoire d'entomologie, Muséum National d'Histoire Naturelle (MNHN, Paris, France) with Dr Christiane Amédégnato.

EDUCATION

2021 HDR (Habilitation à Diriger les Recherches). University of Evry Val d'Essone (UEVE, Paris-Saclay).

1994 - 1996 PhD in computational ecology "Phylogeny and resource sharing in Orthoptera Acrididae". University of Limoges (France), *summa cum laude*, supervisor prof. Daniel Petit.

1989 - 1994 Master's degree in Biology & Neurosciences, University of Poitiers & Toulouse (France).

PUBLICATIONS

(*) indicates co-authorship

Y Poulot-Becq-Giraudon, O Guillemaud, E Degl'Innocenti, V Letenneur, K Bascarane, T Barbay, M Møller Clausen, C Derbois, M Guillermier, L Juricek, M Riquelme-Perez, T Lakomy, L Benhaim, N Dufour, P Gipchtein, F Petit, L Siron, G Aurégan, N Dechamps, MC Gaillard, AP Bemelmans, R Bos, MA Carrillo-de Sauvage, G Milior, N Rouach, S Brohard, K Muret, E Bonnet & C Escartin. (2026) Signaling cascades shape functional subpopulations of cortical astrocytes in male wild-type mice and APP/PS1dE9 Alzheimer's disease model. Nature Communications. <https://doi.org/10.1038/s41467-026-71826-w>.

A Onfroy, F Jean-Louis, P Le Corvoisier, F Couplier, K Muret, E Bonnet, R Arrouasse, C Boucle, S Abid, E Sbidian, C Bergqvist, P Wolkenstein, V Godot, JF Deleuze, Y Levy, P Topilko, E Audureau, S Hue. (2025). Hair follicle stem cell fate supports distinct clinical endotypes in Hidradenitis Suppurativa. Journal of the European Academy of Dermatology and Venereology 40:473–483. <https://doi.org/10.1111/jdv.70302>.

M Mziou-Sallami, P Roger, A Gloaguen, C Dandine-Roulland, T Jiogho Ngaho, S Brohard, K Muret, F Sandron, E Bonnet, JF Deleuze, E Le Floch, V Meyer. (2025). GNNenrich: a novel method for pathway enrichment analysis based on Graph Neural Network. Bioinformatics. <https://doi.org/10.1093/bioinformatics/btaf478>.

K Muret, V Le Goff, C Dandine-Roulland, C Hotz, F Jean-Louis, B Boisson, L Mesrob, F Sandron, D Daian, R Oloso, E Le Floch, V Meyer, P Wolkenstein, JLCasanova, Y Lévy, E Bonnet, JF Deleuze* and S Hue*. (2024). Comprehensive Catalog of Variants Potentially Associated with Hidradenitis Suppurativa, Including Newly Identified Variants from a Cohort of 100 Patients, Int. J. Mol. Sci. , 2024, 25, 10374. <https://doi.org/10.3390/ijms251910374>.

D Derbala, A Garnier, E Bonnet, JF Deleuze, J Tost (2024) Whole-Genome Bisulfite Sequencing Protocol for the Analysis of Genome-Wide DNA Methylation and Hydroxymethylation Patterns at Single-Nucleotide Resolution. *Epigenome Editing: Methods and Protocols*, 353-382. https://doi.org/10.1007/978-1-0716-4051-7_18.

Bonnet E. (2023). La transcriptomique en cellule unique pour étudier des maladies neurodégénératives. *L'Actualité Chimique*, numéro 490, Décembre 2023. <https://cea.hal.science/cea-04394836>.

Derbois C, Palomares MA, Deleuze JF, Cabannes E, Bonnet E. (2023) Single cell transcriptome sequencing of stimulated and frozen human peripheral blood mononuclear cells. *Sci Data*, 2023 Jul 6;10(1):433. <https://doi.org/10.1038/s41597-023-02348-z>.

M Riquelme-Perez, F Perez-Sanz, JF Deleuze, C Escartin, E Bonnet*, S Brohard*. (2023) DEVEA: an interactive shiny application for Differential Expression analysis, data Visualization and Enrichment Analysis of transcriptomics data. *F1000Research*. <https://f1000research.com/articles/11-711>.

Julien Guemri , Morgane Pierre-Jean, Solène Brohard, Nouara Oussada, Caroline Horgues, Eric Bonnet, Florence Mauger and Jean-François Deleuze. (2022) Methylated ccfDNA from plasma biomarkers of Alzheimer's disease using targeted bisulfite sequencing. *Epigenomics*, vol 14, no 8. <https://doi.org/10.2217/epi-2021-0491>.

L. Abjean, L. Ben Haim, M. Riquelme-Perez, P. Gipchtein, C. Derbois, M.A. Palomares, F. Petit, A.S. Hérard, M.C. Gaillard, M. Guillermier, M. Gaudin-Guérif, N. Sagar, N. Dufour, N. Robil, M. Kabani, R. Melki, P. De la Grange, A.P. Bemelmans, G. Bonvento, J.F. Deleuze, P. Hantraye, E. Bonnet, S. Brohard, R. Olaso, E. Brouillet, M.A. Carrillo-de Sauvage, C. Escartin. (2022) The JAK2-STAT3 pathway controls a beneficial proteostasis response of reactive astrocytes in Huntington's disease. *Brain*. <https://doi.org/10.1093/brain/awac068>.

Eric Bonnet. (2021) Using convolutional neural networks for the classification of breast cancer images. *arXiv*. <https://arxiv.org/abs/2108.13661>.

Vidisha Singh, George D.Kallioli, Marek Ostaszewski, Maëva Veyssiere, Eleftherios Pilalis, Piotr Gawron, Alexander Mazein, Eric Bonnet, Elisabeth Petit-Teixeira and Anna Niarakis. (2020) RA-map: building a state-of-the-art interactive knowledge base for rheumatoid arthritis. Database. <https://doi.org/10.1093/database/baaa017>.

Marie-Ange Palomares*, Cyril Dalmasso*, Eric Bonnet*, Céline Derbois, Solène Brohard-Julien, Christophe Ambroise, Christophe Battail, Jean-François Deleuze, Robert Olasso. (2019) Systematic analysis of TruSeq, SMARTer and SMARTer Ultra-Low RNA-seq kits for standard, low and ultra-low quantity samples. Scientific Reports. <https://doi.org/10.1038/s41598-019-43983-0>.

Eric Bonnet*, Marie-Laure Moutet*, Céline Baulard*, Delphine Bacq-Daian, Florian Sandron, Lilia Mesrob, Bertrand Fin, Marc Delépine, Marie-Ange Palomares, Claire Jubin, Hélène Blanché, Vincent Meyer, Anne Boland, Robert Olasso, Jean-François Deleuze. (2018) Performance comparison of three DNA extraction kits on human whole-exome data from formalin-fixed paraffin-embedded normal and tumor samples. PLOS One. <https://doi.org/10.1371/journal.pone.0195471>.

Pau Erola, Eric Bonnet, Tom Michoel. Learning differential module networks across multiple experimental conditions. (2018) book chapter, Gene regulatory network inference, Humana Press. <https://arxiv.org/abs/1711.08927>.

Kernaleguen M., Daviaud C., Shen Y., Bonnet E., Renault V., Deleuze J.F., Mauger F. and Tost J. Whole genome bisulfite sequencing for the analysis of genome-wide DNA methylation and hydroxymethylation patterns at single-nucleotide resolution. (2018) Methods Mol Biol. 1767:311-349. https://doi.org/10.1007/978-1-4939-7774-1_18.

Fatemeh Seyednasrollah, Devin C. Koestler, Tao Wang, Stephen R. Piccolo, Roberto Vega, Russell Greiner, Christiane Fuchs, Eyal Gofer, Luke Kumar, Russell D. Wolfinger, Kimberly Kanigel Winner, Chris Bare, Elias Chaibub Neto, Thomas Yu, Liji Shen, Kald Abdallah, Thea Norman, Gustavo Stolovitzky, Howard R. Soule, Christopher J. Sweeney, Charles J. Ryan, Howard I. Scher, Oliver Sartor, Laura L. Elo, Fang Liz Zhou, Justin Guinney, James C. Costello, and Prostate Cancer DREAM Challenge Community. A DREAM Challenge to Build Prediction Models for Short-Term Discontinuation of Docetaxel in Metastatic Castration-Resistant Prostate Cancer.(2017) JCO Clinical Cancer Informatics web (as contributing team with JP Vert). <https://doi.org/10.1200/CCI.17.00018>.

Arnau Montagud, Pauline Traynard, Loredana Martignetti, Eric Bonnet, Emmanuel Barillot, Andrei Zinovyev, Laurence Calzone. Conceptual and computational framework for logical modelling of biological networks deregulated in diseases. (2017) Briefings in Bioinformatics, bbx163. <https://doi.org/10.1093/bib/bbx163>.

Paul Deveau, Emmanuel Barillot, Valentina Boeva, Andrei Zinovyev, Eric Bonnet. Calculating biological module enrichment or depletion and visualizing data on large-scale molecular maps with ACSNMiner and RNavicell R packages. (2016) The R Journal. The R Journal Vol. 8/2, December 2016, ISSN 2073-4859. <https://doi.org/10.32614/RJ-2016-047>.

Loredana Martignetti, Laurence Calzone, Eric Bonnet, Emmanuel Barillot, Andrei Zinovyev. ROMA: representation and quantification of module activity from target expression data. Frontiers in genetics 7, 18. <https://doi.org/10.3389/fgene.2016.00018>.

Inna Kuperstein, Eric Bonnet, Hien-Anh Nguyen, David Cohen, Eric Viara, Luca Grieco, Simon Fourquet, Laurence Calzone, Christophe Russo, Maria Kondratova, Marie Dutreix, Emmanuel Barillot and Andrei Zinovyev. Atlas of Cancer Signaling Network: a systems biology resource for integrative analysis of cancer data with Google Maps. (2015) Oncogenesis. 2015 Jul 20;4:e160. <https://doi.org/10.1038/oncsis.2015.19>.

Eric Bonnet, Eric Viara, Inna Kuperstein, Laurence Calzone, David PA Cohen, Emmanuel Barillot, Andrei Zinovyev. NaviCell Web Service for Network-based Data Visualization. (2015) Nucleic Acids Research Web issue. <https://doi.org/10.1093/nar/gkv450>.

Eric Bonnet, Laurence Calzone, Tom Michoel. Integrative multi-omics module network inference with Lemon-Tree. (2015) PLoS Comput Biol 11(2): e1003983. <https://doi.org/10.1371/journal.pcbi.1003983>.

Laurence Calzone, Inna Kuperstein, David Cohen, Luca Grieco, Eric Bonnet, Nicolas Servant, Philippe Hupé, Andrei Zinovyev, Emmanuel Barillot. Modélisation de réseaux biologiques et médecine de précision en oncologie. (2014) Bulletin du Cancer Vol. 101, Issue 1, pp 18-21.

Dagmar Waltemath, Frank T Bergmann, Claudine Chaouiya, Tobias Czauderna, Padraig Gleeson, Carole Goble, Martin Golebiewski, Mickael Hucka, Nick Juty, Olga Krebs, Nicolas Le Novère, Huaiyu Mi, Ion I Moraru, Chris J Myers, David Nickerson, Brett G Olivier, Nicolas Rodriguez, Falk Schreiber, Lucian Smith, Fengkai Zhang, Eric Bonnet. Meeting report from the fourth meeting of the Computational Modeling in Biology Network (COMBINE). (2014) Standards in Genomic Sciences. Vol 9, No 3. <https://doi.org/10.4056/sigs.5279417>.

Margolin AA, et al. Systematic analysis of challenge-driven improvements in molecular prognostic models for breast cancer. (2013) Sci Transl Med. Apr 17;5(181):181re1. web (as a contributing team with JP Vert). <https://doi.org/10.1126/scitranslmed.3006112>.

Vera-Licona, P., Bonnet, E., Barillot, E., Zinovyev, A. (2013) OCSANA: Optimal Combinations of Intervention Strategies for Network Analysis. Bioinformatics. 29 (12), 1571-1573. <https://doi.org/10.1093/bioinformatics/btt195>.

Bonnet, E., Calzone, L., Rovera, D., Stoll, G., Barillot, E., Zinovyev, A. (2013) BiNoM, a Cytoscape plugin for accessing and analyzing pathways using standard systems biology formats, BMC Systems Biology, 7:18. <https://doi.org/10.1186/1752-0509-7-18>.

Bonnet, E., Calzone, L., Rovera, D., Stoll, G., Barillot, E., Zinovyev, A. (2013) Practical use of BiNoM, a Biological Network Manager software. In In silico Systems Biology: A systems-based approach to understanding biological processes , Humana Press, pp 127-146. https://doi.org/10.1007/978-1-62703-450-0_7.

The Ectocarpus genome consortium. The Ectocarpus genome and brown algal genomics. (2012) In Genomic insights gained into the Diversity, Biology and Evolution of Algae, Advances in Botanical Research, Vol. 64, pp 143-174, Elsevier, ISSN 0065-2296. <https://hal.inrae.fr/hal-02649287v1>.

Grbić, M., Thomas Van Leeuwen, T., Clark, R.M., Rombauts, S., Rouzé, P., Grbić, V., Osborne, E.J., Dermauw, W., Phuong Cao, T.N., Ortego, F., Hernández-Crespo, P., Diaz, I., Martinez, M., Navajas, M., Sucena, E., Magalhães, S., Nagy, L., Pace, R.M., Djuranović, S., Smagghe, G., Iga, M., Christiaens, O., Veenstra, J.A., Ewer, J., Mancilla Villalobos, R., Hutter, J.L., Hudson, S.D., Velez, M., Yi, S.Y., Zeng, J., Pires-daSilva, A., Roch, F., Cazaux, M., Navarro, M., Zhurov, V., Acevedo, G., Bjelica, A., Fawcett, J.A., Bonnet, E., Martens, C., Baele, G., Wissler, L., Sanchez-

Rodriguez, A., Tirry, L., Blais, C., Demeestere, K., Henz, S.R., Gregory, T.R., Mathieu, J., Verdon, L., Farinelli, L., Schmutz, S., Lindquist, E., Feyereisen, R., Van de Peer, Y. The genome of *Tetranychus urticae* reveals herbivorous pest adaptations. (2011) *Nature* 479, 487-492. <https://doi.org/10.1038/nature10640>.

Bonnet, E. Integrating microRNA expression data and other sources in module network reconstruction. (2010) In *Proceedings of the 6th workshop on computation of biochemical pathways and genetic networks*, Logos Verlag Berlin GmbH.

Bonnet, E., Michoel, T. and Van de Peer, Y. Prediction of a gene regulatory network linked to prostate cancer from gene expression, microRNA and clinical data. (2010) *Bioinformatics*, 26 (18): i638-i644. <https://doi.org/10.1093/bioinformatics/btq395>.

Michoel, T., Joshi, A., Bonnet, E., Vermeirssen, V. and Van de Peer, Y. Towards system level modeling of functional modules and regulatory pathways using genome-scale data. (2010) *Proceedings of the Seventh International Workshop on Computational Systems Biology, WCSB*.

Bonnet, E., Tatari, M., Joshi, A., Michoel, T., Marchal, K., Beerx, G., Van de Peer, Y. Module network inference from cancer expression dataset identifies microRNAs as high scoring regulators. (2010) *PLoS ONE* 5(4). <https://doi.org/10.1371/journal.pone.0010162>.

Bonnet, E., He, Y., Billiau, K., Van de Peer, Y. TAPIR, a web server for the prediction of plant microRNA targets, including target mimics. (2010) *Bioinformatics*, 26(12), 1566-1568. <https://doi.org/10.1093/bioinformatics/btq233>.

Cock, M., Sterck, L., Rouzé, P., Scornet, D., Allen, A., Amoutzias, G., Anthouard, V., Artiguenave, F., Aury, J., Badger, J., Beszteri, B., Billiau, K., Bonnet, E., Bothwell, J., Bowler, C., Boyen, C., Brownlee, C., Carrano, C., Charrier, B., Youn Cho, G., Coelho, A., Colln, J., Corre, E., Da Silva, C., Delage, L., Delaroque, N., Dittami, S., Doulebeau, S., Elias, M., Farnham, G., Gachon, C., Gschloessl, B., Heesch, S., Jabbari, K., Jubin, C., Kawai, H., Kimura, K., Kloareg, B., Kupper, F., Lang, D., Le Bail, A., Leblanc, C., Lerouge, P., Lohr, M., Lopez, P., Martens, C., Maumus, F., Michel, G., Miranda-Saavedra, D., Morales, J., Moreau, H., Motomura, T., Nagasato, C., Napoli, C., Nelson, D., Nyvall-Collén, P., Peters, S., Pommier, C., Potin, P., Poulain, J., Quesneville, H., Read, B., Rensing, S.A., Ritter, A., Rousvoal, S., Samanta, M.,

Samson, G., Schroeder, D., Sgurens, B., Strittmatter, M., Tonon, T., Tregear, J., Valentin, K., von Dassow, P., Yamagishi, T., Van de Peer, Y., Wincker, P. The Ectocarpus genome and the independent evolution of multicellularity in the brown algae. (2010) *Nature*, 465, 617-621. <https://doi.org/10.1038/nature09016>.

Vermeirssen, V., Joshi, A., Michoel, T., Bonnet, E., Casneuf, T. and Van de Peer, Y. Transcription regulatory networks in *Caenorhabditis elegans* inferred through reverse-engineering of gene expression profiles constitute biological hypotheses for metazoan development. (2009) *Mol. BioSyst.*, 5, 1817-1830. <https://doi.org/10.1039/b908108a>.

Abeel, T., Saeys, Y., Bonnet, E., Rouzé, P., Van de Peer, Y. Generic eukaryotic core promoter prediction using structural features of DNA. (2008) *Genome Research* 18, 310-23. <https://doi.org/10.1101/gr.6991408>.

Van Leene, J., Stals, H., Eeckhout, D., Persiau, G., Van De Slijke, E., Van Isterdael, G., De Clercq, R., Bonnet, E., Laukens, K., Remmerie, N., Hendrickx, K., De Vijlder, T., Abdelkrim, A., Pharazyn, A., Van Onckelen, H., Witters, E., Inzé, D., De Jaeger, G. A Tandem Affinity Purification-based technology platform to study the cell cycle interactome in *Arabidopsis thaliana*. (2007) *Mol. Cel. Prot.* 6(7):1226-38. <https://doi.org/10.1074/mcp.M700078-MCP200>.

Michoel, T., Maere, S., Bonnet, E., Joshi, A., Saeys, Y., Van den Bulcke, T., Van Leemput, K., van Remortel, P., Kuiper, M., Marchal, K., Van de Peer, Y. Validating module networks learning algorithms using simulated data. *BMC* (2007) *Bioinformatics* 8, S5. <https://doi.org/10.1186/1471-2105-8-S2-S5>.

Bonnet, E., Van de Peer, Y., Rouzé, P. The small RNA world of plants. (2006) *New Phytol.* 171, 451-68. (Tansley Review). <https://doi.org/10.1111/j.1469-8137.2006.01806.x>.

Faes, P., Minnaert, B., Christiaens, M., Bonnet, E., Saeys, Y., Stroobandt, D., Van de Peer, Y. A Scalable Hardware Accelerator for Comparing Protein Sequences. (2006) *Proceedings of the First International Conference on Scalable Information Systems*. <https://doi.org/10.1145/1146847.1146880>.

Bonnet, E., Wuyts, J., Rouzé, P., Van de Peer, Y. Evidence that microRNA precursors, unlike other non-coding RNAs, have lower folding free energies than random sequences. (2004) *Bioinformatics* 20, 2911-7. <https://doi.org/10.1093/bioinformatics/bth374>.

Bonnet, E. *, Wuyts, J. *, Rouzé, P., Van de Peer, Y. Detection of 91 potential conserved plant microRNAs in *Arabidopsis thaliana* and *Oryza sativa* identifies important new target genes. (2004) *Proc. Natl. Acad. Sci. USA* 101, 11511-6. <https://doi.org/10.1073/pnas.0404025101>.

Picaud, F., Bonnet, E., Gloaguen, V., Petit, D. Decision Making for Food Choice by Grasshoppers (Orthoptera: Acrididae): Comparison Between a Specialist Species on a Shrubby Legume and Three Graminivorous Species. (2003) *Environmental Entomology*, 32 (3) 680-688. <https://doi.org/10.1603/0046-225X-32.3.680>.

Petit, D., Picaud, F. and Bonnet, E. Les peuplements d'Orthoptéroïdes de la lande sur serpentinite de la Flotte et du Cluzeau (Haute-Vienne). (2003) *Annales Scientifiques du Limousin*, 14, pp 13-28. <https://doi.org/10.25965/asl.794>.

Bonnet, E., Van de Peer, Y. zt: a software tool for simple and partial Mantel tests. (2002) *J. Stat. Soft.* 7, 1-12. <https://doi.org/10.18637/jss.v007.i10>.

Bonnet, E. et Petit D. Diversité, densité et biomasse des Orthoptères de la ZNIEFF des Duges. (1998) *Ann. Sc. du Limousin*, numéro spécial Duges, pp 111-120. <https://doi.org/10.25965/asl.962>.

Bonnet, E., Chabrol, L. et Petit, D. Mise à jour de l'inventaire des Orthoptères du Limousin. Actes du colloque "Cartographie et Inventaire des Invertébrés comme contribution à la gestion des milieux naturels", série Patrimoine Naturel, Muséum National d'Histoire Naturelle.

Bonnet, E., Vilks, A., Lenain, J.F., Petit D. Temporal and structural analysis of the relationships between orthoptera and vegetation. (1997) *Ecologie*, 28 (3) 209-216.

Bonnet, E., Chabrol, L. et Petit, D. Catalogue préliminaire des Orthoptères du Limousin (Orthoptera). (1995) Nouv. Revue Ent., T12, fasc. 1, pp 71-83.

Bonnet, E. et Petit, D. A propos de deux espèces d'Orthoptères remarquables en Haute-Vienne : *Calliptamus italicus* et *Aiolopus thalassinus*. (1994) Annales Scientifiques du Limousin, 10, pp 67-73. <https://doi.org/10.25965/asl.739>.

TALKS

2025 Single cell data analysis for neurodegenerative diseases. Master Recherche, Développement et Innovations Thérapeutiques Univ. Strasbourg, UE Innovations thérapeutiques en Recherche et Développement.

2024 Single cell data analysis for neurodegenerative diseases. Master Recherche, Développement et Innovations Thérapeutiques Univ. Strasbourg, UE Innovations thérapeutiques en Recherche et Développement.

2024 Deep learning et génomique. Séminaire élèves Ecole Centrale de Paris.

2023 Deep learning, big data and biology. Master Life Sciences and Health seminar (Paris-Saclay University).

2022 Analysis of single-cell RNA-seq human PBMC datasets France Génomique Annual Meeting.

2019 Deep learning and GPUs on the cobalt high-performance cluster France Génomique Annual Meeting.

2019 Evolution of transcriptomics. NORBIS bioinformatics network seminar. Bergen, Norway.

2019 Hi-C and whole-genome bisulfite sequencing techniques and analysis. Ecole Pratique des Hautes Etudes, seminar for master students, Paris, France.

2018 NGS and machine learning projects at the CNRGH. Seminar at the Institut de Radioprotection et Sûreté Nucléaire, Fontenay-aux-roses, France.

2018 ATAC-seq, Hi-C and whole-genome bisulfite sequencing techniques. Ecole Pratique des Hautes Etudes, seminar for master students, Paris, France.

2016 WBS: a computational pipeline for the treatment of whole-genome high-throughput bisulfite sequencing data. NGS Symposium 2016, IGBMC, Illkirch, France.

2015 NaviCell and ACSN live software demo!. GIW/InCob 2015, Tokyo, Japan.

2015 NaviCell Web Service for Data Visualization. UseR! Conference, Aalborg, Denmark.

2015 Easy navigation and versatile data visualization for biological networks with NaviCell technology . 2nd Annual BiVi meeting, Invited Keynote Speaker, The Genome Analysis Centre (TGAC), Norwich, UK.

2013 Standards and formats in systems biology. Seminar "Mathematics and Biology of Cancer", 12.06.2013, Institut Curie.

2013 BiNoM 2.0, a versatile tool for accessing and analyzing pathways using standard systems biology formats. NUS - IBENS Workshop "Novel genome-wide approaches to decipher transcriptional and epigenetic regulation in mammalian cells. 30 May 2013. ENS, Paris, France.

2012 NGS and microRNAs. Workshop "Generation and Analysis of Next Generation Sequence (NGS) data". Invited Keynote Speaker, Gent, Belgium.

2012 BiNoM, a Cytoscape plugin for accessing and analyzing pathways using standard systems biology formats. Computational Modeling in Biology Network (COMBINE) 2012. August 2012. The Donnelly Centre, University of Toronto, Canada.

2010 Prediction of a prostate cancer regulatory network from gene expression, microRNA and clinical data. 9th European Conference on Computational Biology (ECCB), Ghent, Belgium.

2010 Integrating MicroRNA Expression Data And Other Sources In Module Network Reconstruction. BIOMS workshop Heidelberg.

2010 Top down systems biology: application to the inference of a module network from cancer data including microRNAs. Institut Curie, Paris.

2010 Module network inference from a cancer gene expression data set identifies microRNA regulated modules. VIB Science Club Genetics IV, Leuven, Belgium.

2009 MicroRNA module network inference from expression data. Institut Pasteur, Paris.

2008 MicroRNA module network inference from expression data. 4th EMBO Conference "From Functional Genomics to Systems Biology", Heidelberg, Germany.

2006 MicroARNs, comparaison et prédiction. Ecole chercheurs phylogénomique, Carry-le-Rouet.

2005 Computational screening for Arabidopsis, rice and poplar microRNAs: have most conserved plant miRNAs been identified? Plant GEMS meeting, Amsterdam.

2004 Computational identification of Arabidopsis microRNAs. Annual VIB seminar, Blankenberge, Belgium.

TRAINING

2025 End-to-End Large Language Model (LLM) Bootcamp. TGCC / NVIDIA training session (2d).

2025 Citizen First Aid. CEA training (1d).

2024 Managing Diversity. CEA training (1d).

2023 Succeed in your annual performance reviews. CEA training (2d).

2023 Psychosocial Risks: Key Elements of Prevention. CEA training (1d).

2023 Occupational Safety and First Aid Responder. CEA training (1d).

2022 FUN MOOC Advances in Stem Cell Biology.

2021 FUN MOOC Epigenetics.

2021 Formation Salarié Secouriste du Travail (SST).

2019 Fundamentals of Accelerated Computing with CUDA C/C++. Online Nvidia course, 8 hours.

2019 Fundamentals of Deep Learning for multi-GPUs. 1 day Nvidia training at the CEA computing centre CCRT.

2019 Workshop GPU CC-IN2P3. CNRS IN2P3 data center Lyon, training 3 days.

2018 Single cell transcriptome tutorial. 4 hours, ISMB 2018.

2018 Deep learning for network biology tutorial. 4 hours, ISMB 2018.

2018 Proximity management. CEA internal training 24 hours.

2018 Management and law. CEA internal training 20 hours.

2016 Deep Learning by Google - Udacity. 2 months.

2015 MOOC Coursera.org The Data Scientist's Toolbox. 4 weeks. Johns Hopkins University.

2015 MOOC Coursera.org Practical Machine Learning. 4 weeks. John Hopkins University.

2014 MOOC Coursera.org Introduction to data science. 8 weeks. University of Washington.

SOFTWARE & MODELS

<https://github.com/erbon7/>

Using convolutional neural networks for the classification of breast cancer images.

ACSNMineR.

RNaviCell, a R package for visualizing large-scale "omics" data on ACSN molecular maps.

JNaviCell, a Java package for visualizing large-scale "omics" data on ACSN molecular maps.

Prostate Cancer DREAM Challenge 2015.

<https://www.synapse.org/Synapse:syn4485029/wiki/234262>.

BiNoM, a toolbox for accessing and analyzing biological pathways.

Lemon-Tree, a Java package for the inference of module networks from high-throuput data sets.

DREAM Breast Cancer Prognosis Challenge 2013.

<http://sagebase.net/WP/blog/2013/01/10/sage-bionetworks-dream-breast-cancer-prognosis-challenge/>

Tapir, a web portal for the prediction of plant microRNA targets.

MirFinder, a computational pipeline designed for the de novo prediction of plant microRNAs.

Randfold, a software for permutation test of microRNA precursor sequences.

zt, a software for testing correlation in distance matrices, using a permutation test.

GRANTS & PROJECTS

2023 Association France Alzheimer & maladies apparentées. Project PrimAstro, "Uncovering the role of astrocytes in Alzheimer pathology in a non-human primate". Project PI, collaboration with Dr Marc Dhenain (CEA MIRCen), Dr Carole Escartin (CEA / MIRCen) and Dr H. Hirbec (IGF Montpellier).

2023 University Paris-Saclay Life Sciences and Health. Funding for the project "Age and Alzheimer's disease-related transcriptomic changes in astrocytes". Project PI, collaboration with with Dr Marc Dhenain (CNRS / MIRCEN, CEA).

2019 CEA grant for PhD project "Glial cells and elimination of toxic aggregates in Huntington disease". Project co-writer with Dr Carole Escartin (CNRS / MIRCEN, CEA).

2019 Fondation Maladie Rares - Transcriptomics for the study of the role of Astrocytes and Glial Cells in Huntington's disease. Co-writer with Dr Carole Escartin (CNRS / MIRCEN, CEA).

2010 Apo-Sys, Apoptosis systems biology applied to cancer and AIDS (workpackage leader).

2010 Experimental validation of gene targets for an inferred module network in Arabisopsis. VIB special fund for novel experimental techniques (project leader).

2008 MoneyMaize, funded by IWT, identification of molecular networks for yield increase in maize (project co-writer, workpackage leader).

2007 Bioframe, funded by IWT, conception of a bioinformatics platform for integrative modeling in systems biology (project co-writer, workpackage leader).

2007 Flexware, funded by IWT, exploitation of flexible hardware platforms for massively parallel bioinformatics application (project co-writer, workpackage leader).

2005 IWT funding for an hardware accelerated BLAST computer system.

2002 Planet, a network of european plant databases FP5 project (ERC funding), workpackage leader.

REFeree EXPERIENCE

Review college panel expert for the Belgian FWO (2021 - 2023).

Grant reviewer for the Canadian FCI, french ANR, belgian IWT, belgian FWO, european ERC, US NSF, US USDA.

Manuscript referee for Nucleic Acids Research, Bioinformatics, RNA, Trends in Genetics, PLOS Computational Biology, PLOS One, Scientific Reports, Scientific Data, Genome Biology, BMC Bioinformatics, BMC Plant Biology, Plant Physiology, Bioessays, The Plant Journal, BMC genomics, Plant Biology, Journal of experimental botany, Tree Genetics and Genomes, Molecular Genetics and Genomics, FEBS Journal.

TEACHING

2025 Seminar for students from the Master Recherche, Développement et Innovations Thérapeutiques Univ. Strasbourg, UE Innovations thérapeutiques en Recherche et Développement. Single cell data analysis for neurodegenerative diseases.

2024 Seminar for students from the Master Recherche, Développement et Innovations Thérapeutiques Univ. Strasbourg, UE Innovations thérapeutiques en Recherche et Développement. Single cell data analysis for neurodegenerative diseases.

2024 Seminar for students from the Ecole Centrale de Paris. Deep learning et génomique.

2023 Seminar for students from the Master Life Sciences and Health (Paris-Saclay University). Deep learning, big data and biology.

2019 Seminar for students from the Ecole Pratique des Hautes Etudes (EPHE) in Paris (Master Biology, Health and Ecology). Hi-C and whole-genome bisulfite analysis.

2019 Internal training for CNRGH researchers. R package methylKit for the analysis of methylome data.

2018 Seminar for students from the Ecole Pratique des Hautes Etudes (EPHE) in Paris (Master Biology, Health and Ecology). ATAC-seq, Hi-C and whole-genome bisulfite analysis.

2008 - 2010 Training for students from Ghent University (Master Biochemistry and Bioinformatics). Unix for bioinformatics (30h).

2008 - 2010 Training for students from Ghent University (Master Biochemistry and Bioinformatics). Relational database systems (30h).

1994 - 1996 Practical training sessions for students from the University of Limoges (undergraduate level). Population biology.

SUPERVISION

2023-2026 Altynbek Zhubanchaliyev, PhD student in bioinformatics (co-supervision with L. Martignetti, Institut Curie).

2023 Clara Cherruau, M1 student & ISEN Brest engineering school.

2022 Jeanne Cherruau, MD student & Master student Biologie et Santé.

2019-2023 Miriam Riquelme-Perez, PhD student in bioinformatics (co-supervision with C. Escartin and S. Brohard).

2018 Maria Kondili, Bioinformatics engineer, (co-supervision with S. Chantalat).

2018 Sarah Benmohammed, Bioinformatics engineer, (co-supervision with S. Chantalat).

2016 - 2018 Yimin Shen, Bioinformatics engineer, (co-supervision with J. Tost).

2014 Nadir Sella, Bioinformatics engineer, U900 Bioinformatics and Computational Biology of Cancer, Institut Curie (co-supervision with Andrei Zinovyev).

2010 Ying He, Bioinformatics engineer, Bioinformatics and Evolutionary research group, Ghent.

2009 Irina Lambertz, Post-doctoral researcher, VIB Department for Molecular Biomedical Research (co-supervision with Jean-Christophe Marine).

2006 J.M. Sanchez, Ghent University, Master 2 student (co-supervision with Dirk Stroobandt and Yvan Saeys).

2005 Sven De Smet, Ghent University, Master 2 student (co-supervision with Dirk Stroobandt and Yvan Saeys).

2005 Bram Minnaert, Ghent University, Master 2 student (co-supervision with Dirk Stroobandt and Yvan Saeys).

WORKSHOPS ORGANIZATION

2016 Co-organiser with Dr A. Joshi and Dr T. Michoel, workshop Network Inference: new methods and new data, 1 day, European Conference on Computational Biology, The Hague, The Netherlands.

2013 Co-organiser of the workshop COMBINE 2013 (Computational Modeling in Biology Network), Institut Curie, Paris, 5 days, more than 100 participants.

PhD AND HDR COMMITTEES

2025 Examiner for Mrs Teresa Gravina's PhD "A computational pipeline for multi-omics regulatory network inference in vascular and glioblastoma models", Department of Translational Medicine, Piemonte Orientale University.

2025 Examiner and jury member for Mr Matthew Ricci's Habilitation to Direct Research (HDR), Paris-Cité University.

2024 Examiner for Mr Gautier Stoll's Habilitation to Direct Research (HDR), Paris-Cité University.

2024 Examiner for the PhD Thesis of Jorge Bretones Santamarina, "Integrated multiomic analysis, synthetic lethality inference and network pharmacology to identify SWI/SNF subunit-specific pathway alterations and targetable vulnerabilities", Institut Curie, Paris-Saclay University.

2023-2026 Member of the individual thesis advisory committee for Jennifer Thamara Mata Orozco, "Therapeutic antibody immunogenicity: large-scale single-cell analysis of adalimumab-specific CD4+ T cells", CEA and Paris-Saclay University.

2024-2027 Member of the individual thesis advisory committee for Clémence Raimond, "Etude de la dégénérescence des cellules oligodendrocytaires et étude des effets de la stimulation magnétique répétitive transspinale dans le développement de la SLA chez la souris", SPPIN and Paris-Cité University.

2023-2026 Member of the individual thesis advisory committee for Liébaut Dudragne, "Genomic Instability in *S. Cerevisiae*", Sorbonne University.

2023-2026 Member of the individual thesis advisory committee for Liangwei Yin, "Bioinformatics and Artificial Intelligence Methods to Assess Organoids and Tumor Spheroids Models", Grenoble-Alpes University.

2022 Reviewer for the PhD thesis of Matthieu Cornet, "Etude informatique des effets cliniques et omiques des modulateurs de CFTR dans la mucoviscidose et recherche de nouvelles cibles", Ecoles des Mines de Paris & PSL University, Paris, France.

2021 Reviewer (examineur) for the PhD thesis of Yunfeng Wang, "Transcriptome and Genome Analysis using Mapping-free Protocols", Paris-Saclay University, Paris, France.

2018 Reviewer (examineur) for the PhD thesis of Stéphane Grison, "Approches omics pour les faibles doses sur un modèle rat multigénérationnel", IRSN, Paris, France.

2016 Reviewer for the mid-thesis report for Adrien Trolet, "Régulation et fonction de la protéine AGO1 au cours du cycle cellulaire dans les cellules BY2 de tabac et chez *Arabidopsis thaliana*", Institut de Biologie Moléculaire des Plantes CNRS, Strasbourg, France.

2010 Reviewer (examineur) for the PhD thesis of Naira Naouar, "Methods for genome-wide expression analysis", VIB department of Plant Systems Biology, Gent, Belgium.