Olivier Croce - Research Engineer (IRHC) – CNRS
Institute for Research on Cancer and Aging of Nice (IRCAN)
INSERM U1081 - CNRS UMR 7284 - UNS
Faculty of Medicine - Pasteur tower
28, av. Valombrose
06107 Nice Cedex 2, France

Phone: +33(0)4 93 37 70 00
E-mail: olivier.croce@cnrs.fr
http://bioinfomed.fr | www.ircan.org

Current position

I am the head of the Bioinformatics & Informatics service of IRCAN ("Institute for Research on Cancer and Aging of Nice"). The main part of the service activity is to interpret and analyze the data coming from IRCAN's teams experiments such as NGS data generated by our high throughput sequencers. More generally, I perform *in silico* biology to find hidden relevant biological information in the flow of binary digits !

Competences - by keywords

- **Biology & Bioinformatics:** genomics - microbiology & eucaryota/epigenomics -, sequences / NGS data analysis, transcriptomics, genomes assembly and annotation, evolution & phylogeny, bioinfo softwares development and more !
- **Computer science:** systems architecture, servers administration (web, Cloud, virtualization), multimedia, networks, development (Python, C, C++, Tcl, Perl, VB, smattering Java), GUI (Qt, Gtk, WxWidgets, Tk), parallelization (MPI), web technologies (PHP, HTML, JavaScript, CGI, CSS), databases (MySql, Sqlite, NoSQL, Access), average concepts in statistics and R language.
- **Physics & Biomedical:** Monte Carlo simulation (PENELOPE code), basis on dosimetrics measurements /interaction of radiation with matter, medical images (Dicom format).

Publications (in peer-reviewed journals)

ORCID: 0000-0002-7342-3157

- [68] **2026** ; Chevalier A, Ben Khedher M, Tran A, Coin M, Pousse M, Tazi A, Eleni Dit Trolli S, Lanotte P, Follet C, Pichon M, Dubois D, Herbulot L, Potron A, Aberrane S, Birgy A, Boutillier B, Pantel A, Di Maio M, Dubourg G, Boyer P, Corvec S, Groshenry G, Bonis M, Saissi M, Gallet A, Boyer L, Croce O, Lotte R, Ruimy R. ; Genomic determinants of Bacillus cereus and outcomes of infection in preterm neonates: a multicentre retrospective study. *Clin Microbiol Infect.*
- [67] **2025** ; Andreoni-Pham R, Johnston H, Warner JF, Nedoncelle K, Carvalho JE, Hofmänner K, Maugeri A, Croce O, Amiel A, Röttinger E ; Whole body regeneration deploys a rewired

embryonic gene regulatory network logic ; *Nature Communications* doi PubMed

- [66] **2025** ; Iltis C, Moskalevska I, Debiesse A, Seguin L, Fissoun C, Cervera L, Moudombi L, Ardin M, Ferrari A, Eliott C, Pisani D, Ottaviani A, Bourinet M, Luci C, Gual P, Makulyte G, Bernard D, Durandy M, Duret LC, Hamidouche T, Kunz S, Croce O, Delannoy C, Guérardel Y, Allain F, Hofman P, Benarroch-Popivker D, Bianchini L, Dadone-Montaudie B, Cosson E, Guglielmi J, Pourcher T, Braud VM, Shkreli M, Pers YM, Jorgensen C, Brondello JM, Féral CC, Michallet MC, Gilson E, Cherfils-Vicini J. ; A ganglioside-based immune checkpoint enables senescent cells to evade immunosurveillance during aging ; *Nat Aging* doi PubMed
- [65] **2024** ; Colson D, Yalvac B, Weterings J, Verrijssen AS, Van Haaren P, Bellezzo M, Berbée M, Van Limbergen EJ, Croce O, Verhaegen F, Reniers B ; Dosimetry and Monte Carlo modelling of the Papillon+ contact X-ray brachytherapy device ; *Brachytherapy* doi PubMed
- [64] **2022** ; Mendez-Bermudez A, Lototska L, Pousse M, Tessier F, Croce O, Latrick C, Cherdyntseva V, Nassour J, Xiaohua J, Lu Y, Abbadie C, Gagos S, Ye J, Gilson E; Selective pericentromeric heterochromatin dismantling caused by TP53 activation during senescence ; *Nucleic Acids Res.* doi PubMed
- [63] **2022** ; Ben Khedher M, Ghedira K, Rolain JM, Ruimy R, Croce O ; Application and Challenge of 3rd Generation Sequencing for Clinical Bacterial Studies ; *International Journal of Molecular Sciences* doi PubMed
- [62] **2022** ; Montandon M, Hamidouche T, Yart L, Duret LC, Pons C, Soubeiran N, Pousse M, Cervera L, Vial V, Fassy J, Croce O, Gilson E, Shkreli M ; Telomerase is required for glomerular renewal in kidneys of adult mice ; *NPJ Regen Med.* doi PubMed
- [61] **2021** ; Ben Khedher M, Nindo F, Chevalier A, Bonacorsi S, Dubourg G, Fenollar F, Casagrande F, Lotte R, Boyer L, Gallet A, Rolain JM, Croce O, Ruimy R; Complete Circular Genome Sequences of Three Bacillus cereus Group Strains Isolated from Positive Blood Cultures from Preterm and Immunocompromised Infants Hospitalized in France ; *Microbiology Resource Announcement* doi PubMed
- [60] **2020** ; Robin JD, Jacome Burbano MS, Peng H, Croce O, Thomas JL, Laberthonniere C, Renault V, Lototska L, Pousse M, Tessier F, Bauwens S, Leong W, Sacconi S, Schaeffer L, Magdinier F, Ye J, Gilson E ; Mitochondrial function in skeletal myofibers is controlled by a TRF2-SIRT3 axis over lifetime ; *Aging Cell* doi PubMed
- [59] **2019** ; Cherfils-Vicini J, Iltis C, Cervera L, Pisano S, Croce O, Sadouni N, Győrffy B, Collet R, Renault VM, Rey-Millet M, Leonetti C, Zizza P, Allain F, Ghiringhelli F, Soubeiran N, Shkreli M, Vivier E, Biroccio A, Gilson E ; Cancer cells induce immune escape via glycocalyx changes controlled by the telomeric protein TRF2 ; *EMBO Journal* doi PubMed
- [58] **2018** ; Tissot F, Estrach S, Boulter E, Cailleteau L, Tosello L, Seguin L, Pisano S, Audebert S, Croce O, Féral C ; Dermal fibroblast SLC3A2 deficiency leads to premature aging and loss of epithelial homeostasis ; *Journal of Investigative Dermatology* doi PubMed
- [57] **2018** ; Mendez-Bermudez A, Lototska L, Bauwens S, Giraud-Panis MJ, Croce O, Jamet K, Irizar A, Mowinckel M, Koundrioukoff S, Nottet N, Almouzni G, Teulade-Fichou MP, Schertzer M, Perderiset M, Londoño-Vallejo A, Debatisse M, Gilson E, Ye J. ; Genome-wide Control of

Heterochromatin Replication by the Telomere Capping Protein TRF2. ; *Mol Cell* doi PubMed

- [56] **2017** ; Bouam A., Robert C., Croce O., Levasseur A., Drancourt M. ; Draft genome sequence of Mycobacterium boenickei CIP 107829 ; *Genome Announcements* doi PubMed
- [55] **2017** ; Drancourt M., Aboudharam G., Croce O., Armougom F., Robert C., Raoult D. ; Dental pulp as a source of low-contaminated DNA ; *Microbial Pathogenesis* doi PubMed
- [54] **2016** ; Cassir N., Benamar S., Croce O., La Scola B. ; Clostridium species identification by 16S rRNA pyrosequencing metagenomics ; *Clinical Infectious Diseases* doi PubMed
- [53] **2016** ; Khelaifia S., Lagier J.C., Bibi F., Azhar E.I., Croce O., Padmanabhan R., Jiman-Fatani A.A., Yasir M., Robert C., Andrieu C., Fournier P.E., Raoult D. ; Microbial Culturomics to Map Halophilic Bacterium in Human Gut: Genome Sequence and Description of Oceanobacillus jeddahense sp. nov. ; *OMICS* doi PubMed
- [52] **2016** ; Bou Khalil J., Benamar S., Baudoin J.P., Croce O., Blanc-Tailleur C., Pagnier I., Raoult D., La Scola B. ; Developmental Cycle and Genome Analysis of “Rubidus massiliensis,” a New Vermamoeba vermiformis Pathogen ; *Frontiers in in Cellular and Infection Microbiology* doi PubMed
- [51] **2016** ; Armougom F., Bitam I., Croce O., Merhej V., Barassi L., Nguyen T.T., La Scola B. and Raoult D. ; Genomic insights into a new Citrobacter koseri strain revealed gene exchanges with the virulence-associated Yersinia pestis pPCP1 plasmid ; *Frontiers in Microbiology* doi PubMed
- [50] **2016** ; Seck E.H., Sankar S.A., Khelaifia S., Croce O., Robert C., Couderc C., Di Pinto F., Sokhna C., Fournier P.E., Raoult D., Lagier J.C. ; Noncontiguous finished genome sequence and description of Planococcus massiliensis sp. nov., a moderately halophilic bacterium isolated from the human gut ; *New microbes and new infections* doi PubMed
- [49] **2016** ; Vayssier-Taussat M., Moutailler S., Féménia F., Raymond P., Croce O., La Scola B., Fournier P.E., Raoult D. ; Identification of Novel Zoonotic Activity of Bartonella spp. ; *Emerging infectious diseases* ; doi PubMed
- [48] **2016** ; Moumene M., Drissi F., Croce O., Djebbari B., Robert C., Angelakis E., Benouareth D.E., Raoult D., Merhej V. ; Complete genome sequence and description of Lactococcus garvieae M14 isolated from Algerian fermented milk ; *New microbes and new infections* doi PubMed
- [47] **2015** ; Albrengues J., Bertero T., Grasset E., Bonan S., Maiel M., Bourget I., Philippe C., Herraiz Serrano C., Benamar S., Croce O., Sanz-Moreno V., Meneguzzi G., Feral C.C., Cristofari G., Gaggioli C. ; Epigenetic switch drives the conversion of fibroblasts into proinvasive cancer-associated fibroblasts ; *Nature Communications* doi PubMed
- [46] **2015** ; Asmar S., Robert C., Croce O., Caputo A., Drancourt M.; Draft Genome Sequence of Mycobacterium neworleansense Strain ATCC 49404T ; *Genome Announcements* doi PubMed
- [45] **2015** ; Seck E.H., Rathored J., Khelaifia S., Croce O., Robert C., Couderc C., Di Pinto F., Sokhna C., Raoult D., Lagier J.C.; Virgibacillus senegalensis sp. nov. A new moderately halophilic bacterium isolated from the human gut ; *New microbes and new infections* doi PubMed

- [44] **2015** ; Lagier J.C., Khelaifia S., Azhar E.I., Croce O., Bibi F., Jiman-Fatani A.A., Yasir M., Helaby H.B., Robert C., Fournier P.E., Raoult D.; Genome sequence of Oceanobacillus picturae strain S1, an halophilic bacterium first isolated in human gut. ; 10:91 ; *Stand Genomic Sci.* doi PubMed
- [43] **2015** ; Khelaifia S., Croce O., Lagier J.C., Robert C., Couderc C., Di Pinto F., Davoust B., Djossou F., Raoult D., Fournier P.E. ; Noncontiguous finished genome sequence and description of Virgibacillus massiliensis sp. nov., a moderately halophilic bacterium isolated from human gut ; *New microbes and new infections* doi PubMed
- [42] **2015** ; Caputo A., Merhej V., Georgiades K., Fournier P.E., Croce O, Robert C., Raoult D. ; Pan-genomic analysis to redefine species and subspecies based on quantum discontinuous variation: the Klebsiella paradigm ; *Biology Direct* doi PubMed
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- [40] **2015** ; Phelippeau M., Croce O., Robert C., Raoult D., Drancourt M. ; Draft Genome Sequence of Mycobacterium lentiflavum CSUR P1491 ; *Genome Announcements* doi PubMed
- [39] **2015** ; Phelippeau M., Croce O., Robert C., Raoult D., Drancourt M. ;Draft genome sequence of Mycobacterium europaeum strain CSUR P1344 ; *Genome Announcements* doi PubMed
- [38] **2015** ; Cassir N., Benamar S., Bou Khalil J., Croce O., Saint-Faust M., Jacquot A., Gotthard G., Armstrong N., Henry M., Jardot P., Robert C., Garbi A., Lagier J.C., Ghigo E., Chabrière E., Marchandin H., Sartor C., Boutte P., Cambonie G., Simeoni U., Raoult D. and La Scola B. ; Clostridium butyricum strains and dysbiosis linked to necrotizing enterocolitis in preterm neonates ; *Clinical Infectious Diseases* doi PubMed
- [37] **2015** ; Aboubaker Osman D., Phelippeau M., Musso D., Robert C., Michelle C., Croce O., Drancourt M. ; Draft Genome Sequence Mycobacterium tuberculosis strain MT43, representative of the Manu2 genotype ; *Genome Announcements* doi PubMed
- [36] **2015** ; Aboubaker Osman D., Phelippeau M., Musso D., Robert C., Michelle C., Croce O., Drancourt M. ; Draft Genome Sequence of Mycobacterium tuberculosis strain MT11 representative of a new lineage ; *Genome Announcements* doi PubMed
- [35] **2015** ; Pagnier I., Yutin N., Croce O., Makarova K.S., Wolf Y.I., Benamar S., Raoult D., Koonin E.V., La Scola B. ; Babela massiliensis, a representative of a widespread bacterial phylum with unusual adaptations to parasitism in amoebae ; *Biology Direct* doi PubMed
- [34] **2015** ; Caputo A., Dubourg G., Croce O., Gupta S., Robert C., Papazian L., Rolain J.M., Raoult D. ; Whole-genome assembly of Akkermansia muciniphila sequenced directly from human stool ; *Biology Direct* doi PubMed
- [33] **2014** ; Benamar S., La Scola B., Croce O.; Genome sequence of Afipia felis strain 76713, isolated in hospital water using an amoeba co-culture procedure ; *Genome Announcements* ; doi PubMed

- [32] **2014** ; Croce O., Hugon P., Lagier JC., Bibi F., Robert C., Azhar E., Raoult D., Fournier PE.; Genome sequence of Bacillus simplex strain P558, isolated from human faeces sample ; *Genome Announcements*
- [31] **2014** ; Pagnier I., Croce O., Robert C., Raoult D., La Scola B. ; Genome sequence of Legionella massiliensis, isolated from a cooling tower water sample ; *Genome Announcements*
- [30] **2014** ; Phelippeau M., Robert C., Croce O., Raoult D., Drancourt M. ; Draft genome sequence of Mycobacterium neoaurum strain DSM 44074 T ; *Genome Announcements*
- [29] **2014** ; Croce O., Robert C., Raoult D., Drancourt M. ; Draft genome sequence of Mycobacterium farcinogenes NCTC 10955 ; May 29;2(3). pii: e00523-14 ; *Genome Announcements*
- [28] **2014** ; M. Sassi, Croce O., Robert C., Raoult D., Drancourt M. ; Draft Genome Sequence of Mycobacterium triplex DSM 44626 ; May 29;2(3). pii: e00499-14 ; *Genome Announcements*
- [27] **2014** ; Croce O., Robert C., Raoult D., Drancourt M. ; Draft Genome Sequence of Mycobacterium vulneris DSM 45247T ; May 8;2(3): e00370-14 ; *Genome Announcements*
- [26] **2014** ; Gaia M., Benamar S., Boughalmi M., Pagnier I., Croce O., Colson P., Raoult D., La Scola B.; Zamilon, a Novel Virophage With Mimiviridae Host Specificity ; Apr 18;9(4):e94923 ; *PLoS One*
- [25] **2014** ; Croce O., Robert C., Raoult D., Drancourt M.; Draft genome sequence of Mycobacterium austroafricanum DSM 44191 ; Apr 17;2(2) ; *Genome Announcements*
- [24] **2014** ; Croce O., Robert C., Raoult D., Drancourt M.; Draft Genome Sequence of Mycobacterium margeritense DSM 44476T; *Genome Announcements*
- [23] **2014** ; Croce O., Robert C., Raoult D., Drancourt M.; Draft genome sequence of Mycobacterium asiaticum DSM 44297 strain ; Apr 17;2(2) ; *Genome Announcements*
- [22] **2014** ; Croce O., Robert C., Raoult D., Drancourt M.; Draft Genome Sequence of Mycobacterium cosmeticum DSM 44829; Apr 10;2(2) ; *Genome Announcements* ;
- [21] **2014** ; Gorlas A., Croce O., Oberto J., Gauliard E., Forterre P., Marguet E. ; Thermococcus nautili sp. nov., a hyperthermophilic archaeon isolated from a hydrothermal deep sea vent (East Pacific Ridge) ; May;64(Pt 5):1802-10 ; *Int J Syst Evol Microbiol.*
- [20] **2014** ; Fournier P.E., Levy P.Y., Million M., Croce O., Blanc-Tailleur C., Brouqui P., Raoult D. ; Genome of a chronic osteitis-causing Clostridium tetani ; 2:25–26 ; *New Microbes and New Infections.*
- [19] **2014** ; Pagnier I., Croce O., Robert C., Raoult D., La Scola B. ; Non-contiguous finished genome sequence and description of Anaerococcus provencensis sp. nov. ; 9(3) ; *Stand*

Genomic Sci. doi PubMed

- [18] **2014** ; Pagnier I., Croce O., Robert C., Raoult D., La Scola B. ; Genome Sequence of Legionella anisa, Isolated from a Respiratory Sample, Using an Amoebal Coculture Procedure. ; Feb 27;2(1) ; *Genome Announcements* ; doi PubMed
- [17] **2014** ; Cassir N., Croce O., Pagnier I., Benamar S., Couderc C., Robert C., Raoult D., La Scola B. ; Non-contiguous finished genome sequence and description of Bacteroides neonati sp. nov., a new species of anaerobic bacterium ; 9(3) ; *Stand Genomic Sci.* doi PubMed
- [16] **2013** ; Pagnier I., Croce O., Robert C., Raoult D., La Scola B. ; Non-contiguous finished genome sequence and description of Fenollaria massiliensis gen. nov., sp. nov., a new genus of anaerobic bacterium ; 9(3); *Stand Genomic Sci.* doi PubMed
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- [14] **2012** ; Merhej V., Croce O., Robert C, Raoult D. ; Genome sequence of Bartonella rattimassiliensis, a bacterium isolated from European Rattus norvegicus ; 194(24):7013 ; *J Bacteriol.* doi PubMed
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- [12] **2012** ; Merhej V., Croce O., Robert C, Rolain J.M., Raoult D. ; Genome sequence of Bartonella rattaustraliani, a bacterium isolated from an Australian rat ; 194(24):7012 ; *J Bacteriol.* doi PubMed
- [11] **2012** ; Gardès J., Bachar D., Croce O., Christen R. ; Patho-Genes.org: a website dedicated to gene sequences of potential bioterror bacteria and PCR primers used to amplify them ; 5(5):594-8 ; *Microb Biotechnol.* doi PubMed
- [10] **2012** ;Pagnier I., Boughalmi M., Croce O., Robert C., Raoult D., La Scola B. ; Genome Sequence of Legionella tunisiensis strain LegMT, a new Legionella species isolated from hypersaline lake water ; 194(21):5978 ; *J Bacteriol.* doi PubMed
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- [8] **2012** ; Gardès J., Croce O., Christen R. ; In silico analyses of primers used to detect the pathogenicity genes of Vibrio cholerae ; 27(3):250-6 ; *Microbes Environ.* doi PubMed
- [7] **2012** ; Gérard J.P., Marcie S., Croce O., Hachem S., Trimaud R., Bordy J.M., Denoziere M., Courdi A., Benezery K., Hannoun Levi J.M., Barbet N. ; Development of a new Papillon 50TM machine with dedicated applicators used for 50 kV X-ray radiotherapy of rectal and skin cancers ; 33(2):109-116 ; *IRBM.* doi
- [6] **2012** ; Croce O., Hachem S., Franchisseur E., Marcié S., Gérard J.P. ; Contact radiotherapy using a 50 kV X-ray system : Evaluation of absorbed-dose with the monte-carlo code PENELOPE and comparison with measurements ; 81(6):609-617 ; *Radiation Physics and Chemistry.* doi

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- [4] **2010** ; Croce O.; Chevenet F.; Christen R. ; A new web-server for the rapid identification of microorganisms ; 2(3):84-88 ; *Journal of Microbial and Biochemical Technology.* doi
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Conferences and communications

- **2026** ; Nanopore Full-Length 16S versus WGS for Gut Microbiome Sequencing: A Breast Cancer Case Study ; Fontanille-Kulhanek E., Lavagna C., Abdurahim M., Alsharhan M., Ghazi E., Hachim M.Y., Czerucka D., Croce O. ; *Biennale Monégasque de Cancérologie* ; Monaco
- **2025** ; New sequencing technologies for microbiome analysis: the Nanopore long-read revolution ; Croce O. ; *Pelvic Health* ; Monaco
- **2023** ; Genomic identification of human pathogenic bacteria in the marine environment ; Croce O. ; *Colloque LIA-ROPSE 2023* ; Monaco
- **2021** ; Guidelines for creating a user-friendly and open-access gene expression database for comparing embryonic development and regeneration in Nematostella vectensis ; Croce O., Rottinger E. ; *Methods in Molecular Biology* ; Book chapter 39 – Whole Body Regeneration ; HAL
- **2020** ; ISSI: IRCAN's Satellite Signature Project ; Argentin J., Croce O. ; *JOBIM 2020*
- **2018** ; Comparative study of RNA-Seq analyses based on the genome or transcriptome as reference ; Tessier F., Croce O. ; *JOBIM 2018* ; Marseille (France)
- **2016** ; Comparison of Monte Carlo computed 50 kV X-rays radiation therapy and EBRT for rectal cancer ; Vidal M., Gauthier M., Croce O., Gerard J.P., Benezery K. ; *ESTRO* ; Turin (Italy) ; Presented by M. Vidal
- **2014** ; Genome analysis of a new virophage to highlight the specificity with its host ; Benamar S., Gaïa M., Raoult D., La Scola B., Croce O. ; *ECCB / JOBIM* ; Strasbourg (France) ; Presented by S. Benamar
- **2012** ; Interest of Monte Carlo simulations for dosimetric evaluation of the 50 kVp device “Papillon50” ; *World Congress of Brachytherapy* ; Barcelona (Spain)
- **2011** ; In silico analyses of primers used since 1990 to detect the pathogenicity genes of Vibrio cholerae ; Gardès J., Croce O. ; *JOBIM* ; Paris (France)
- **2011** ; Dosimetric aspects of the X-rays 50 kV machine “Papillon50™” ; Marcié S., Croce O. ; *ESTRO* ; London (United Kingdom)

- **2008** ; Identification of pathogens: BLAST and Blast2TreeDyn ; Croce O. ; *Healthy-Water Project* ; Sitges (Spain)
- **2007** ; 16S rRNA bacterial identification: a BLAST server to query 16S rRNA sequences on cultured bacteria ; Croce O. ; *Healthy-Water Project* ; Budapest (Hungary)
- **2005** ; Conception de puces à ADN pour l'identification de champignons : récupération des séquences, classification et recherche de rapporteurs ; Croce O. ; *JOBIM* ; Lyon (France)
- **2005** ; EmblEX: parse and extract data from EMBL entries ; Croce O. ; *ALPHY – Alignement et Phylogénie* ; Montpellier (France)
- **2004** ; Chips designed to analyze biodiversity in environmental samples or identify micro-organisms ; Croce O. ; Villefranche-sur-Mer (France)

Activities

Main activity

- Responsible of the “Bioinformatics and Informatics” service at the IRCAN institute (service including 3 to ~8 people, depending of students and contractual)

Administrative responsibilities, other

Current commitments

- Regular jury expert for ITA & ITRF concours, BAP A and BAP E (ITRF - BAP A & BAP E), INRAe
- Regular expert for inter-ranking committee for engineers (ITA)
- Member at “Commission régionale du développement professionnel et social” (CRDPS, ex. CRFP) at DR20 CNRS, elected since 2022
- CSSI (Correspondant Sécurité des Systèmes d'Information) for UMR7284
- External expert for CSU of ISA (“Comité Scientifique Utilisateurs” bioinformatics @ Institut Sophia Agrobiotech / INARe).
- Member of the IRCAN lab council : 1 elected seat (ITA representative) + as responsible of service
- Teaching at the University Côte d'Azur since 2006 until now (50-60 hrs/year, for 3 Masters).
- Other attached networks: SFBI, Bioinfo-Unica

Past commitments

- Member of the CNRS INSB CSI (Conseil Scientfique d'Institut) - 5 yrs mandate from 2019 to 2023
- Qualification for “Maître de conférences” (=Assistant Professor) *since 2010, still not available* - Section 65 (Cell biology)

Students supervision

Current students trainees

- Emmanuelle Kulhanek Fontanille - Master 2 Sciences de la vie & de la santé, parcours BBC - UniCA - 2024-2025
  Etude du microbiote intestital chez des atteintes atteintes d'un cancer du sein
- Idrissi Monssef - Ecole Ing. Mohamed 6, 5e année, génie bioinformatique - 2024-2025 - Co-responsible P. Lenormand (Pagès team, IRCAN)
  Études des séquences NTAR et détection de signatures
- Paola Andrea Barrera Rodriguez - Master in Computational Biology - Universitad des Los Andes, Colombia 2024-2025 - co-responsible D. Czerucka (CSM / Monaco) - LIA-ROPSE
  Exploring the Gut-Breast Microbiota Axis in Breast Cancer: Immune Modulation and Bioinformatics Analysis of Microbiota Diversity in the UAE Population
- Marion Mateos - Master 1, Sciences de la vie & de la santé, parcours BBC - UniCA - 2024-2025 - Co-responsible with Julien Cherfils team
  Effet d’une immunothérapie anti-GD3 dans le vieillissement : Analyse par approche RNA-seq

Alumni

- Léa David - Master 2 Sciences de la vie & de la santé, parcours BBC - UniCA - 2023-2024 - co-responsible D. Czerucka (CSM / Monaco) - LIA-ROPSE
  Bacterial shotgun metagenomic analysis using new R10 Nanopore technology
- Emmanuelle Kulhanek Fontanille - Master 2 Sciences de la vie & de la santé, parcours BIM - UniCA - 2022-2024
  Détection de signatures dans les données brutes de séquençage
- Mathieu Ferraud - PolyTech' Nice-Sophia engineer school (5th yr, Artificial Intelligence) - co-responsible E. Rottinger (IRCAN team)
  Structuring and manipulating multi-omics data underlying the extreme regeneration process
- Pierre Marchal - Ecole ingénieur agronome, 5e année (ENSAT) - Co-responsible : Dorota Czerucka (centre scientifique de Monaco), stage via LIA-ROPSE (UCA / CSM) - 2023 -
  Identification et étude de l’expression des facteurs de virulence des bactéries pathogènes pour l’homme en milieu marin : approche bio-informatique
- Mariem Ben Kheder - Bioinformatics PhD - Aix-Marseille University & IHU Infection pôle Sud Méditerrannée - co-responsible : R. Ruimy, JM Rolain - 2019 -2021
  Séquençage haut débit pour le diagnostic et le traitement des infections bactériennes
- Chan SOITHONG - Master 2 Sciences de la vie & de la santé, parcours BIM - UCA - co-responsible : E. Gilson / M. Pousse - 2022
  Recherche de correlations dans des jeux de séquences sub-télomériques
- Faten SLAIMI - Ecole Supérieure d'Ingénieurie et de Technologies, Tunis - 2022
  Développement de webtools pour l'Intranet de l'IRCAN (internship starting from April 2022)
- Eunbae AN - Master 1 Bioinformatique et Biostatistique, Université de Nantes - 2022
  Développement d’un pipeline d’assemblage de génomes bactériens (internship starting from

April 2022)

- Fredrick Nindo - Postdoc bioinfo - IHU Infection pôle Sud Méditerrannée - co-responsible : R. Ruimy - 2 yrs contract 2020 & 2021
  Long reads assembling and annotation of Bacillus cereus strains collection
- Lilian Leblanc - IUT 2 Informatique, Univversité Nice - 2021
  Mise en place d'un système de ticket openSource sur nos serveurs du type OSTicket ou Zammad, sous Docker et intégration à notre intranet NextCloud
- Déborah Braud - Master 2 Sciences de la vie & de la santé, parcours BIM - UCA - co-responsible : E. Rottinger - 2021
  Développement d'une banque de données pour l'analyse d'expression spatio-temporelle et/ou de mutants/transgènes
- Joris Argentin - M2 “apprenti” (2 years contract) - Master 2 Bioinformatics - Rouan University 2018,2019,2020
  Search for signatures in big set of Whole Genome Sequencing (WGS)
- Paul Bachelerie - M2 “apprenti” (1 year contract) - PolyTech' Nice-Sophia (engineer school) 2017/2018
  Rebuild of the management information system of the IRCAN institute
- Guillamaury Debras - Master 2 Bioinformatics - Bordeaux University - 2017/2018
  “Motifs finding in big set of data”
- Nori Sadouni - Master 2 Sciences de la vie & de la santé, parcours BIM - UCA - co-responsible : R. Ruimy - 2016/2017
  “Automatisation des analyses de routine en génomique et métagénomique bactérienne”
- Emilien Ledant - Master 2 Bioinformatique, parcours Biologie computationnelle - Université de Bordeaux - co-responsible: D. Van-Essen - 2016/2017
  “Decyphering hidden relationships between genome-wide datasets”
- Christopher Chevallier - Master 2 BBSG (Bioinformatique Biochimie Structure Génomique) - Aix-Marseille Université - Co-responsible: G. Cristofari - 2016/2017
  “Développement base de données variants génétiques”
- Samia Benamar - Bioinformatics PhD - Aix-Marseille University - co-responsible with Pr. B. LaScola (Samia Benamar pub.) ⇒ PhD - July 6th 2017
- Ludovick Kosthowa - Master 2 BBSG (Bioinformatique Biochimie Structure Génomique) - Aix-Marseille Université - Co-responsible: F. Pedeutour - 2015/2016
  “VarAn : créateur de rapport personnalisé en médecine de précision”
- Amandine Audino - Master 2 GBM (Génie BioMédical) - Université de Nice - 2015/2016
  “Gestion et partage de données sur la plateforme CYTOMED”
- Nori Sadouni - Master 1 Sciences de la vie & de la santé, parcours BIM - Nice Université - Co-responsible: E. Gilson - 2015/2016
  “Etude In Silico de l’effet enhancer de la fixation de TRF2 sur les régions extra-télomériques”
- Sidwell Rigade - Master 2 Bioinformatics - Rennes - Co-responsible: C. Gaggioli - 2015/2016
  “Construction du réseau génique de la carcinogenèse pulmonaire : Identification de la voie de signalisation P38 MAP kinase dans les cellules tumorales et le stroma”
- Duran Audrey - INSA Lyon - co-responsible: E. Gilson - 2015/2016

“Etude de la dynamique de fixation de la proteine telomerique TRF2 par approche ChIP-Seq”

- Amna Bardi - Master 2 BBSG (Bioinformatique Biochimie Structure Génomique) - Aix-Marseille Université - 2014/2015
  “*Développement d'un outil bio-informatique pour l'identification des plasmides”*
- Samia Benamar - Master 2 Biologie-Informatique - Paris Diderot - 2012/2013
  “Analyse de données de méta-génomes de selles de nouveau-nés prématurés atteintes de l'entérocolite nécrosantes de l'agent déclencheur de cette pathologie : Clostridium butyricum”
- Nicolas Girard - Master 1 Bioinformatique - Nantes - 2013/2014
  “RunE. A tool for a fast quality evaluation of NGS runs”

Teaching experiences

Current teachings

- L2,L3,M1 - UniCA - Medicine, UE Microbiology. Since 2019 (4h / year ⇒ 5h eq. TD).
  Content: “High Throughput Sequencing and its applications to the microbiote studies”.
- Master of Life and Health Sciences, mention “BIM” (Biologie Informatique Mathematique) - UniCA. Since 2019 (10h / year ⇒ 15h eq. TD).
  Content: Introduction to MetaGenomics ; Genomes assembling ; rRNA 16S Barcoding.
- Master 1 EE (Economic Expertise), SIED (Social Interactions and Economic Dynamics), Cognitive Sciences (CS) - UniCA. Since 2017 (18h / year ⇒ 22.5h eq. TD).
  Content: Introduction to Python : courses, tutorial, project.

Past teachings

- Master 2 Sciences Technologies and Health, mention “Génie Bio-Médical”. Since 2006 until present (28 h / year ⇒ 30h eq.TD).
  Content: Usage of networks, algorithmic, object-oriented programming (C++).
- License 3 pro. Health, mention “Dosimétrie et Radioprotection Médicale”. Since 2006 until 2018 (24 h / year ⇒ 30h eq.TD).
  Content: Coding of information, programing (Python), medical files (dosimetry using Dicom format).
- Bioinformatics training. 2013 to 2015 (2 sessions per year, for 2 days). Courses and exercises in bioinformatics for employers (technicians, engineers and physicians) or students (Master 2, phD). Faculty of medicine, la Timone, Marseille.
  Content: Assembly and finishing of bacterial genomes sequences from NGS, primers design for PCR.
- Master 1 et 2 Sciences de la Vie, option bioinformatique. 2006 (32 h).
  Content: Biological data recovering, Blast, databases (Access), project in genomics.
- Master 2 Génie biologique, École Polytechnique Sophia Antipolis. 2009 (9 h).
  Content: Data mining, parsing using python.
- Licence 1 Sciences et Technologies, mention « Biologie Mathématiques Informatique ». 2010 à

2011 (18 h / year).
Content: Modeling, bioinformatics and databases.

- Other: private lessons in mathematics (college students).

Professional experiences

- **Since July 2015**: Research Engineer at CNRS (permanent position), IRCAN Nice.

Responsible of the “Bioinformatics and Informatics” service at the IRCAN institute -
Institute for Research on Cancer and Aging of Nice, Nice, Faculty of Medicine, CNRS UMR 7284. I mainly explore and examine biological data from several disparate sources. See my current works for more !

- **March 2012 to June 2015** : Research Engineer at CNRS (permanent position), IHU Marseille.

Bioinformatics plateform of the IHU (Institut hospitalo-universitaire) at Marseille, located at medical school, La Timone (previously the Rickettsia unit, URMITE - UMR 7278). The institute is headed by Pr. Didier Raoult.
I was in charge of the analysis of the data produced from our NGS platform. The platform currently comprises many pyrosequencing machines: 3 Roche 454 (GS20, XL+ and a Titanium), 1 ABI SOLiD, 1 IonTorrent PGM, 2 MiSeq Illumina).
My interests are also to look inside the genomes of prokaryotes and virus using *in silico* existing or homemade tools for discovering meaningful cryptic information.

- **June 2009 to February 2012**: Post-doctoral, University of Nice, Centre Antoine Lacassagne

“Laboratoire de planification assistée par ordinateurs en radiothérapie des cancers (PAORC)”.
Modeling of the radiotherapy device « Papillon 50 » and simulations of the absorbed dose using Monte Carlo code PENELOPE (project ANR- 08-TECS-015, centre Antoine Lacassagne, Nice).

- **2006 to June 2009**: Post-doctoral , CNRS – UMR 6543, Bioinformatics laboratory

Developing new approaches to design PCR primers, development of a software to exchange biological data, achieving database of bacterial sequences (European project: “HealthyWater” FOOD-CT-2006-036306).

- **2004 to 2005**: Research assistant, University of Nice, Bioinformatics laboratory (phD)

DNA chip design for micro organisms identification.

- **2001 to 2003**: Engineer, CNRS – UMR 6078 (part of phD)

Development of bioinformatics softwares and databases (project « Aquachip »: identification of pathogenics bacteria in water).

> - **2001**: Trainee in computer sciences (Master2), INRIA Sophia-Antipolis.
>   Developing of a prototype software to control an experimental marine simulator device (project «COMORE»).
> - **During 2001 to 2003** : Miscellaneous Informatics

- Trainings: Linux administration, Perl programming, training centre PCS Avolys
- Individual project: creating a management software for legal information, Gubernatis lawyers institute
- Assistant network administrator : intrusions detection on the university network, University of Corte.

- **During 1999 to 2000** : Miscellaneous Biology - Ecology

- Technician in bacteriological analyzes: Environmental Laboratory of Nice
- Training of Master 2: Environmental Impact of wild ungulate populations, Office National de la Chasse
- Training in ethology: ethology wolf in the wild, Mercantour National Park
- Training in ecology: analysis of the littoral fauna of the island of Embiez, Study Centre for Marine Animal Resources
- Training in entomology: study of the biodiversity of arthropods alpine meadows, Natural Park of Queyras

Education

- **2005 : PhD in Bioinformatics - Nice Sophia Antipolis University**

Title: “DNA chip design for the identifcation of micro-organisms”. novembre 30, 2005 - Nice.
Jury: M. Gouy, J.M. François, G. Perrière, R. Christen.

Identification of organisms are still often based on phenotypical characters. However, such as an identification is approximate and difficult for micro-organisms. DNA micro-arrays appear to be a solution for a fast and reliable identification of a large number of species. This technique is relatively recent and it is still necessary to improve it, in particular at the conceptual level. Within this framework, the objective of my thesis was to implement new means for chip design. This work was completed through two projects: The project “Aquachip” aimed in designing a DNA array for the identification of pathogenic bacteria present in bathing and drinking water. The project grouped several European laboratories that had to exchange a large amount of data. Such significant flow of information is often badly managed and slows down research. Consequently, we developed a dynamic numerical platform, the “E-dashboard” (MySQL, PHP), allowing all partners to manage data. This tool made it possible on the one hand to follow the progress of the various steps of the project and on the other hand to optimize exchanges between partners. In a second project, “Mycochip”, the objective was to develop a DNA array to identify ectomychorizian fungi. ITS sequences (Internal Transcribed Spacers) from a very divergent area located between ribosomal RNA genes are used for this study. The project initially required the development of a tool to retrieve sequences, « EmblEx » (Perl, MySQL), which is more specific and powerful than Entrez, SRS or ACNUC. Then, the ambiguous taxonomy of fungi led us to conceive a new method of classification through partitioning without alignment. Biological experiments showed that reliable probes could be determined by this approach.

- **2001 : DESS (=Master 2) - “Additional competences in computer sciences” - University of Corsica**

Mention « Databases and advanced programming ».

- **2000 : Master 1 - “Biology of populations and ecosystems” - Aix-Marseille III University**
  Mention « Biology of conservation et systems modeling ».
- **1999 : Licence 3 - “Biology of organisms” - Aix-Marseille III University**
  Mention « Research and specialization in animal biology ».
- **1998 : DEUG (=Licence 1&2) - “Biology and geology” - Nice Sophia Antipolis University**
  Mention « Sciences of life ».

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