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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, transcriptomic, 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)

- [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*  
- [59] **2019** ; Cherfils-Vicini J, Iltis C, Cervera L, Pisano S, [Croce O](#), Sadouni N, Gyórfy 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 glycoalyx changes controlled by the telomeric protein TRF2 ; *EMBO Journal*  
- [58] **2018** ; Tissot F, Estrach S, Boulter E, Cailleateau 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*  
- [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*  
 - [56] **2017** ; Bouam A., Robert C., Croce O., Levasseur A., Drancourt M. ; Draft genome sequence of *Mycobacterium boenickei* CIP 107829 ; *Genome Announcements*  
 - [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*  
 - [54] **2016** ; Cassir N., Benamar S., Croce O., La Scola B. ; Clostridium species identification by 16S rRNA pyrosequencing metagenomics ; *Clinical Infectious Diseases*  
 - [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*  
 - [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 Cellular and Infection Microbiology*  
 - [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*  
 - [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*  
 - [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* ;  
 - [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*  
 - [47] **2015** ; Albregues 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*  
 - [46] **2015** ; Asmar S., Robert C., Croce O., Caputo A., Drancourt M.; Draft Genome Sequence of











- Mycobacterium neworleansense Strain ATCC 49404T ; *Genome Announcements*  
- [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*  
 - [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.*  
 - [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*  
 - [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*  
 - [41] **2015** ; Asmar S.; Phelippeau M., Croce O., Robert C., Drancourt M. ; Draft genome sequence of *Mycobacterium bohemicum* strain DSM 44277T ; *Genome Announcements*  
 - [40] **2015** ; Phelippeau M., Croce O., Robert C., Raoult D., Drancourt M. ; Draft Genome Sequence of *Mycobacterium lentiflavum* CSUR P1491 ; *Genome Announcements*  
 - [39] **2015** ; Phelippeau M., Croce O., Robert C., Raoult D., Drancourt M. ;Draft genome sequence of *Mycobacterium europaeum* strain CSUR P1344 ; *Genome Announcements*  
 - [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*  
 - [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*  
 - [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*  
 - [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*  
 - [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*  

- [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* ;  
- [32] **2014** ; Croce O., Hugon P., Lagier J.C., Bibi F., Robert C., Azhar E., Raoult D., Fournier P.E.; 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 mageritense* 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., Gaudiard 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.*  
 - [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* ;  
 - [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.*  
 - [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.*  
 - [15] **2013** ; Pagnier I., Croce O., Robert C., Raoult D., La Scola B. ; Non-contiguous finished genome sequence and description of *Anaerococcus pacaensis* sp. nov., a new species of anaerobic bacterium ; 8(3):548-60 ; *Stand Genomic Sci.*  
 - [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.*  
 - [13] **2012** ; Pagnier I, Croce O., Robert C, Raoult D, La Scola B. ; Genome sequence of *Afipia birgiae*, a rare bacterium associated with Amoebae ; 194(24):7018 ; *J Bacteriol.*  
 - [12] **2012** ; Merhej V., Croce O., Robert C, Rolain J.M., Raoult D. ; Genome sequence of *Bartonella rattaaustraliani*, a bacterium isolated from an Australian rat ; 194(24):7012 ; *J Bacteriol.*  
 - [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.*  
 - [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.*  
 - [9] **2012** ; Pagnier I., Croce O., Robert C, Raoult D, La Scola B. Genome Sequence of *Reyranelia massiliensis*, a Bacterium Associated with Amoebae ; 194(20):5698 ; *J Bacteriol.*  
 - [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.*  
 - [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*. 

- [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*. 
- [5] **2011** ; Gérard J.P., Sun Myint A., [Croce O.](#), Marcié S. ; Renaissance of contact x-ray therapy for treating rectal cancer; 8(4):483-92 ; *Expert Rev Med Devices*.  
- [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*. 
- [3] **2010** ; Chevenet F., [Croce O.](#), Hebrard M., Christen R., Berry V. ; ScripTree: scripting phylogenetic graphics ; 26(8):1125-6 ; *Bioinformatics*.  
- [2] **2008** ; [Croce O.](#); Chevenet F.; Christen R.; OligoHeatMap (OHM): an online tool to estimate and display hybridizations of oligonucleotides onto DNA sequences; 36: W154-W156. ; *Nucleic Acids Research*.  
- [1] **2006** ; [Croce O.](#); Lamarre M.; Christen R. ; Querying the public databases for sequences using complex keywords contained in the feature lines; 7:45 ; *BMC Bioinformatics*.  

Conferences and communications

- **2016** ; Comparison of Monte-Carlo computed 50 kV X-rays radiation therapy and EBRT for rectal cancer ; M. Vidal, M. Gauthier, O. Croce, J.P. Gerard, K. Benezery ; ESTRO (Turin - Italia) - Supported by M. Vidal.
- **2014** ; Genome analysis of a new virophage to highlight the specificity with its host ; S. Benamar, M. Gaïa, D. Raoult, B. La Scola, O. Croce ; ECCB / JOBIM (Strasbourg France) - Supported by S. Benamar
- **2012** ; Interest of the Monte Carlo simulations for dosimetric evaluation of the 50 kVp device "Papillon50" ; World Congress of Brachytherapy (Barcelone - Espagne).
- **2011** ; In silico analyses of primers used since 1990 to detect the pathogenicity genes of *Vibrio cholerae* ; JOBIM (Paris - France) - Supported by Gardès J.
- **2011** ; Dosimetric aspects of the X-rays 50 kV machine "Papillon50TM"; ESTRO (London - England) - Supported by Marcié S.
- **2008** ; Identification of pathogens : Blast and Blast2TreeDyn ; Healthy-Water project (Sitges - Espagne).
- **2007** ; 16S rRNA bacterial identification: A Blast server to blast 16S rRNA sequences on cultured bacteria; Healthy-Water project (Budapest - Hongrie).
- **2005** ; Conception de puces à ADN pour l'identification de champignons, récupération des séquences, classification et recherche de rapporteurs; Journées Ouvertes Biologie Informatique Mathématiques JOBIM (Lyon - France).
- **2005** ; EmblEX : Parse and extract data from EMBL entries; colloque Alignement et Phylogénie

ALPHY (Montpellier - France).

- **2004** ; Chips designed to analyse the biodiversity of samples or to identify micro-organisms; (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)

Other

- Elected member of the INSB Scientific Council (CSI) - since 2019
- Jury expert for ITRF concours, BAP A and BAP E ([ITRF - BAP A & BAP E](#)).
- Teacher assistant at the University of Nice Sophia Antipolis (since 2006 until now, 50-60 hrs/year).
- Qualification for “Maître de conférences” (=Assistant Professor) 2010-2014 - Section 65 (Cell biology) (*still not available, have to repass*)
- Member of “Tara Pacific” consortium

Students supervision

Current students trainees

- [Joris Argentin](#) - M2 “apprenti” (1 year contract) - Master 2 Bioinformatics - Rouan University 2018,2019,2020
Search for signatures in big set of WGS

Former students trainees

- [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 - co-responsable : 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. Pedoutour - 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-téломériques"
- [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 protéine télomérique 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-génomés 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

- [Licence 3 pro. Health](#), mention "Dosimétrie et Radioprotection Médicale". Since 2006 until present (24 h / year ⇒ 30h eq.TD).
Content: Coding of information, programming (Python), medical files (dosimetry using Dicom format).
- [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++).

Past teachings

- 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 Technologie, 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 institue - 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 platform 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 informations.

- **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 informations, 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 identification 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.

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- **1998 : DEUG (=Licence 1&2) - “Biology and geology” - Nice Sophia Antipolis University**
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