Certified Correct, Torredembarra, the 27/06/2024

Dr Cédric Notredame, PhD.

Dr Cedric Notredame
Group Leader
Comparative Bioinformatics Group
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Personal Information

Nationality: French

Born 30/10/70, Married

Education

2013 *Marseilles Medicine School (France)*

Habilitation à Diriger des Recherches.

1998 EMBL-EBI *Heidelberg (Germany) and Cambridge (U.K.)*

PhD in Bioinformatics.

Work carried out in the laboratory of Des Higgins, at the European Molecular Biology Laboratory (EMBL-Heidelberg) and at the European Bioinformatics Institute (EBI-Cambridge)

PhD awarded by Toulouse University with the highest distinction.
Certificate of PhD completion from the European Molecular Biology Laboratory

1993 Université Paul Sabatier *Toulouse, France*

Master in Biotechnologies
With honours

1990-1992 Université Paul Sabatier *Toulouse, France*

Degree of Biochemistry
Degree of Genetics and Molecular Biology

These degrees were both awarded with the highest possible distinction ("Mention Très Bien").

Professional Experience

2009-… UPF *Barcelona, Spain*

Associate Professor in Bioinformatics

2007-… CRG *Barcelona, Spain*

Senior Group Leader, Bioinformatics and Genomics programme, *Centro de Regulacio Genomica*, Barcelona, Spain

My group (10 people) focuses its work in the development of multiple sequence alignment comparisons and their various applications.

2005 - 2007 IBDM-CNRS *Marseilles, France*

Research Investigator, First Class, CNRS-France
Consultant for the Pharmaceutical Industry (Sanofi-Aventis)
Team Leader.

In charge of small group (4 people) funded by Sanofi Aventis. Our work is dedicated to the development of novel sequence analysis method using structural and genomic information.

Visiting Professor, Social Sciences Department, Lausanne University, Switzerland

In collaboration with Profs Eric Widmer and Jacques-Antoine Gauthier, we develop novel methods for the comparison of life trajectories. These methods are inspired by sequence analysis as done in Bioinformatics

2002 - 2003 Aventis Pharna *Paris, France*

Consultant for Aventis-Pharma

Consultation on the setting up of a bioinformatics framework within Aventis. Consultation on punctual projects that require bioinformatics techniques. Expertise on collaborations with the Academia.

2001 - 2005 Lausanne University *Lausanne, Switzerland*

Assistant Professor in Bioinformatics, *Lausanne University*
Group leader at the *Swiss Bioinformatics Institute*
Member of the *Swiss Bioinformatics Institute* Executive Board.

Development of a new pre-graduate curriculum in bioinformatics. Setting up of new projects dedicated to the development of sequence analysis algorithms.

1999 - 2005 IBDM-CNRS, *Marseilles, France*

Research Investigator, Second Class, CNRS-France

Within the group of Jean-Michel Claverie (CNRS-UMR 1889), Development of new algorithms for the combination of sequential and structural information within multiple sequence alignments. Development of new methods for simultaneously comparing several genomes and incorporating heterogeneous sources of experimental information and annotation. Head of a small group (three people) dedicated to the study of the human kinome by bioinformatics means.

1999 - 2001 Université Marseille-Luminy *Marseilles, France*

Assistant Professor in Bioinformatics

Member of the department of bioinformatics, setting up of new courses. Research carried out in the laboratory of Prof. Jean-Michel Claverie. Focus on multiple sequence alignments.

1998 - 1999 National Institute of Medical Research *London, U.K.*

Research Associate

Post Doc with Dr. Jaap Heringa and Dr. Willie Taylor in the department of Mathematical Biology at the National Institute for Medical Research in London. This work was dedicated to the development of new algorithms for sequence and structure analysis.

1998 I.S.R.E.C. *Lausanne, Switzerland*

Post-Doc

Under the supervision of Dr Philip Bücher, I maintained the PROSITE/Profile database, and developped new algorithms for the generation of protein profiles.

1994 - 1998 EMBL-EBI, *Cambridge and Heidelberg*

PhD

Conception of multiple sequence alignment algorithms, under the supervision of Dr. Des Higgins. Strong emphasis on the use of Genetic Algorithms and related techniques.

1992- 1993 Université Paul Sabatier *Toulouse, France*

Pre-graduate

Master degree in the group of Prof F. Amalric at the 'Laboratoire de Biologie Moléculaire des Eucaryotes' in Toulouse. ***wet lab work*** using the mst common molecular biology methods (western, PCR…).

Teaching Experience

EMBO/UNESCO course of Bioinformatics, Lima, Peru, 2003

European Genetics Association annual bioinformatics Course, Bertinoro, Italy, 2001

EMBnet 'Hands on' Courses.
ISREC, Lausanne 1998, 1999,2000, 2001,2002.
SANBI, South Africa, 1999

Master Courses
Marseille University: 1999-2003
Lausanne University: 2001-2005
Madrid University: 2003- 2011
Calgiari University: 2006, 2007
Bergen University, Norway: 2007
UPF-Barcelona: 2007-2011

Publications

Citation Index (01/04/2015): 8700 citations, H-Index 25

Peer Reviewed Publications

Scientific Publications

1. **Notredame, C**. and D.G. Higgins, *SAGA: sequence alignment by genetic algorithm.* Nucleic Acids Res, 1996. **24**(8): p. 1515-24.
2. **Notredame, C**., E.A. O'Brien, and D.G. Higgins, *RAGA: RNA sequence alignment by genetic algorithm.* Nucleic Acids Res, 1997. **25**(22): p. 4570-80.
3. **Notredame, C**., L. Holm, and D.G. Higgins, *COFFEE: an objective function for multiple sequence alignments.* Bioinformatics, 1998. **14**(5): p. 407-22.
4. O'Brien, E.A., C. Notredame, and D.G. Higgins, *Optimization of ribosomal RNA profile alignments.* Bioinformatics, 1998. **14**(4): p. 332-41.
5. **Notredame, C**., D.G. Higgins, and J. Heringa, *T-Coffee: A novel method for fast and accurate multiple sequence alignment.* J Mol Biol, 2000. **302**(1): p. 205-17.
6. Dietmann, S., J. Park, C. Notredame, A. Heger, M. Lappe, and L. Holm, *A fully*

automatic evolutionary classification of protein folds: Dali Domain Dictionary version 3. Nucleic Acids Res, 2001. **29**(1): p. 55-7.

7. **Notredame, C**., *Mocca: semi-automatic method for domain hunting.* Bioinformatics, 2001. **17**(4): p. 373-4.
8. Abergel, C., B. Coutard, D. Byrne, S. Chenivesse, J.B. Claude, C. Deregnaucourt, T. Fricaux, C. Gianesini-Boutreux, S. Jeudy, R. Lebrun, et al. (incl. **Notredame**), *Structural genomics of highly conserved microbial genes of unknown function in search of new antibacterial targets.* J Struct Funct Genomics, 2003. **4**(2-3): p. 141-57.
9. O'Sullivan, O., M. Zehnder, D. Higgins, P. Bucher, A. Grosdidier, and **C. Notredame**, *APDB: a novel measure for benchmarking sequence alignment methods without reference alignments.* Bioinformatics, 2003. **19 Suppl 1**: p. i215-21.
10. Poirot, O., E. O'Toole, and **C. Notredame**, *Tcoffee@igs: a web server for computing, evaluating and combining multiple sequence alignments.* Nucleic Acids Res, 2003. **31**(13): p. 3503-6.
11. Claude, J.B., K. Suhre, C. Notredame, J.M. Claverie, and C. Abergel, *CaspR: a web server for automated molecular replacement using homology modelling.* Nucleic Acids Res, 2004. **32**(Web Server issue): p. W606-9.
12. **Notredame, C**. and K. Suhre, *Computing multiple sequence/structure alignments with the T-coffee package.* Curr Protoc Bioinformatics, 2004. **Chapter 3**: p. Unit3 8.
13. O'Sullivan, O., K. Suhre, C. Abergel, D.G. Higgins, and **C. Notredame**, *3DCoffee: combining protein sequences and structures within multiple sequence alignments.* J Mol Biol, 2004. **340**(2): p. 385-95.
14. Poirot, O., K. Suhre, C. Abergel, E. O'Toole, and **C. Notredame**, *3DCoffee@igs: a web server for combining sequences and structures into a multiple sequence alignment.* Nucleic Acids Res, 2004. **32**(Web Server issue): p. W37-40.
15. Armougom, F., S. Moretti, V. Keduas, and **C. Notredame**, *The iRMSD: a local measure of sequence alignment accuracy using structural information.* Bioinformatics, 2006. **22**(14): p. e35-9.
16. Armougom, F., S. Moretti, O. Poirot, S. Audic, P. Dumas, B. Schaeli, V. Keduas, and **C. Notredame**, *Expresso: automatic incorporation of structural information in multiple sequence alignments using 3D-Coffee.* Nucleic Acids Res, 2006. **34**(Web Server issue): p. W604-8.
17. Armougom, F., O. Poirot, S. Moretti, D.G. Higgins, P. Bucher, V. Keduas, and **C. Notredame**, *APDB: a web server to evaluate the accuracy of sequence alignments using structural information.* Bioinformatics, 2006. **22**(19): p. 2439-40.
18. Moretti, S., F. Reinier, O. Poirot, F. Armougom, S. Audic, V. Keduas, and **C. Notredame**, *PROTOGENE: turning amino acid alignments into bona fide CDS nucleotide alignments.* Nucleic Acids Res, 2006. **34**(Web Server issue): p. W600-3.
19. Wallace, I.M., O. O'Sullivan, D.G. Higgins, and **C. Notredame**, *M-Coffee: combining multiple sequence alignment methods with T-Coffee.* Nucleic Acids Res, 2006. **34**(6): p. 1692-9.
20. Moretti, S., F. Armougom, I.M. Wallace, D.G. Higgins, C.V. Jongeneel, and **C. Notredame**, *The M-Coffee web server: a meta-method for computing multiple sequence alignments by combining alternative alignment methods.* Nucleic Acids Res, 2007. **35**(Web Server issue): p. W645-8.
21. Retelska, D., E. Beaudoing, C. Notredame, C.V. Jongeneel, and P. Bucher, *Vertebrate conserved non coding DNA regions have a high persistence length and a short persistence time.* BMC Genomics, 2007. **8**(1): p. 398.
22. Moretti, S., A. Wilm, D.G. Higgins, I. Xenarios, and C. Notredame, *R-Coffee: a web server for accurately aligning noncoding RNA sequences.* Nucleic Acids Res, 2008. **36**(Web Server issue): p. W10-3.
23. Rausch, T., A.K. Emde, D. Weese, A. Doring, C. Notredame, and K. Reinert, *Segment-based multiple sequence alignment.* Bioinformatics, 2008. **24**(16): p. i187-92.
24. Wilm, A., D.G. Higgins, and **C. Notredame**, *R-Coffee: a method for multiple alignment of non-coding RNA.* Nucleic Acids Res, 2008. **36**(9): p. e52.
25. Gauthier, J.-A., E.D. Widmer, P. Bucher, and **C. Notredame**, *How much does it cost?: Optimization of costs in sequence analysis of social science data* Sociological Methods and Research 2009. **38**(1): p. 197-231.
26. Orbitg, M., F. Guirardo, C. Notredame, and F. Cores, *Exploiting parallelism on progressive alignment methods* Journal of Supercomputing, 2009. **1**(1): p. 1-9.

27. Varas, F., M. Stadtfeld, L. de Andres-Aguayo, N. Maherali, A. di Tullio, L. Pantano, C. Notredame, K. Hochedlinger, and T. Graf, *Fibroblast-derived induced pluripotent stem cells show no common retroviral vector insertions.* Stem Cells, 2009. **27**(2): p. 300-6.
28. Coll, O., A. Villalba, G. Bussotti, C. Notredame, and F. Gebauer, *A novel, noncanonical mechanism of cytoplasmic polyadenylation operates in Drosophila embryogenesis.* Genes Dev, 2010. **24**(2): p. 129-34.
29. Dalloul, R.A., J.A. Long, A.V. Zimin, L. Aslam, K. Beal, L. Ann Blomberg, P. Bouffard, D.W. Burt, O. Crasta, R.P. Crooijmans, et al. (incl. Notredame), *Multi-platform next-generation sequencing of the domestic turkey (Meleagris gallopavo): genome assembly and analysis.* PLoS Biol, 2010. **8**(9).
30. Di Tommaso, P., M. Orobitg, F. Guirado, F. Cores, T. Espinosa, and **C. Notredame**, *Cloud-Coffee: implementation of a parallel consistency-based multiple alignment algorithm in the T-Coffee package and its benchmarking on the Amazon Elastic-Cloud.* Bioinformatics, 2010. **26**(15): p. 1903-4.
31. Gauthier, J.-A., E.D. Widmer, P. Bucher, and **C. Notredame**, *Multichannel Sequence Analysis Applied To Social Science Data.* Sociological Methodology, 2010. **40**(1): p. 1-38.
32. Lingner, T., S. Muhlhausen, T. Gabaldon, C. Notredame, and P. Meinicke, *Predicting phenotypic traits of prokaryotes from protein domain frequencies.* BMC Bioinformatics, 2010. **11**: p. 481.
33. Magis, C., F. Stricher, A.M. van der Sloot, L. Serrano, and **C. Notredame**, *T-RMSD: a fine-grained, structure-based classification method and its application to the functional characterization of TNF receptors.* J Mol Biol, 2010. **400**(3): p. 605-17.
34. Orom, U.A., T. Derrien, M. Beringer, K. Gumireddy, A. Gardini, G. Bussotti, F. Lai, M. Zytnicki, C. Notredame, Q. Huang, et al., *Long noncoding RNAs with enhancer-like function in human cells.* Cell, 2010. **143**(1): p. 46-58.
35. Yau, W.L., T. Blisnick, J.F. Taly, M. Helmer-Citterich, C. Schiene-Fischer, O. Leclercq, J. Li, D. Schmidt-Arras, M.A. Morales, C. Notredame, et al., *Cyclosporin A treatment of Leishmania donovani reveals stage-specific functions of cyclophilins in parasite proliferation and viability.* PLoS Negl Trop Dis, 2010. **4**(6): p. e729.
36. Bussotti, G., E. Raineri, I. Erb, M. Zytnicki, A. Wilm, E. Beaudoing, P. Bucher, and **C. Notredame**, *BlastR--fast and accurate database searches for non-coding RNAs.* Nucleic Acids Res, 2011. **39**(16): p. 6886-95.
37. di Tommasso, P., S. Morreti, I. Xenarios, M. Orobitg, A. Montanyola, J.-M. Chang, J.-F. Taly, and **C. Notredame**, *T-Coffee: a web server for the multiple sequence alignment of protein and RNA sequences using structural information and homology extension.* Nucleic Acids Res, 2011.
38. Erb, I., J.R. Gonzalez-Vallinas, G. Bussotti, E. Blanco, E. Eyras, and **C. Notredame**, Use of ChIP-Seq data for the design of a multiple promoter-alignment method*.* (2012).*Nucleic Acids Res*, 40(7): p. e52.
39. Esteve-Codina, A., R. Kofler, N. Palmieri, G. Bussotti, C. Notredame, and M. Perez-Enciso, *Exploring the gonad transcriptome of two extreme male pigs with RNA-seq.* BMC Genomics, 2011. **12**(1): p. 552.
40. Kemena, C., J.F. Taly, J. Kleinjung, and **C. Notredame**, *STRIKE: Evaluation of Protein Multiple Sequence Alignments using a Single Three Dimensional Structure.* Bioinformatics, 2011.
41. Lin, H.N., C. Notredame, J.M. Chang, T.Y. Sung, and W.L. Hsu, *Improving the alignment quality of consistency based aligners with an evaluation function using synonymous protein words.* PLoS One, 2011. **6**(12): p. e27872.
42. Merhej, V., C. Notredame, M. Royer-Carenzi, P. Pontarotti, and D. Raoult, *The Rhizome of Life: The Sympatric Rickettsia felis Paradigm Demonstrates the Random Transfer of DNA Sequences.* Mol Biol Evol, 2011. **28**(11): p. 3213-23.
43. Rius, J., F. Cores, F. Solsona, J.I. van Hemert, J. Koetsier, and C. Notredame, *A user-friendly web portal for T-Coffee on supercomputers.* BMC Bioinformatics, 2011. **12**: p. 150.
44. Taly, J.F., C. Magis, G. Bussotti, J.M. Chang, P. Di Tommaso, I. Erb, J. Espinosa-Carrasco, C. Kemena, and C. Notredame, *Using the T-Coffee package to build multiple sequence alignments of protein, RNA, DNA sequences and 3D structures.* Nat Protoc, 2011. **6**(11): p. 1669-82.
45. Torrent, M., P. Di Tommaso, D. Pulido, M.V. Nogues, C. Notredame, E. Boix, and D.

Andreu, AMPA: an automated web server for prediction of protein antimicrobial regions. (2012).*Bioinformatics*, 28(1): p. 130-1.

46. Magis, C., A.M. van der Sloot, L. Serrano, and **C. Notredame**, An improved understanding of TNFL/TNFR interactions using structure-based classifications. (2012).*Trends Biochem Sci*.

47. Derrien, T., R. Johnson, G. Bussotti, A. Tanzer, S. Djebali, H. Tilgner, G. Guernec, D. Martin, A. Merkel, D.G. Knowles, et al. (incl. C. Notredame), The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. (2012).*Genome Res*, 22(9): p. 1775-89.

48. Encode Consortium (incl. C. Notredame), An integrated encyclopedia of DNA elements in the human genome. (2012).*Nature*, 7414(489): p. 57-74.

49. Chang, J.M., P. Di Tommaso, J.F. Taly, and C. **Notredame**, Accurate multiple sequence alignment of transmembrane proteins with PSI-Coffee. (2012).*BMC Bioinformatics*, 13 Suppl 4: p. S1

50. Breen, M.S., C. Kemena, P.K. Vlasov, C. Notredame, and F.A. Kondrashov, Epistasis as the primary factor in molecular evolution. (2012).*Nature*, 490(7421): p. 535-8.

51 Rachidi, N., J.F. Taly, E. Durieu, O. Leclercq, N. Aulner, E. Prina, P. Pescher, C. Notredame, L. Meijer, and G.F. Spath, Pharmacological assessment defines the Leishmania donovani casein kinase 1 as a drug target and reveals important functions in parasite viability and intracellular infection. (2013).*Antimicrob Agents Chemother*.

52 Orobitg, M., F. Cores, F. Guirardo, C. Roig, and C. **Notredame**, Improving multiple sequence alignment biological accuracy through genetic algorithms (2013).*Journal of Supercomputing*, 65(3): p. 1076-1088.

53 Monanola, A., C. Roig, F. Guirardo, P. Hernandez, and C. **Notredame**, Performance analysis of computational approaches to solve Multiple Sequence Alignment. (2013).*Journal of Supercomputing*, 64(1): p. 69-78.

54 Magis, C., P. Di Tommaso, and C. **Notredame**, T-RMSD: a web server for automated fine-grained protein structural classification. (2013).*Nucleic Acids Res*, 41(Web Server issue): p. W358-62.

55 Kemena, C., G. Bussotti, E. Capriotti, M.A. Marti-Renom, and C. **Notredame**, Using tertiary structure for the computation of highly accurate multiple RNA alignments with the SARA-Coffee package. (2013).*Bioinformatics*, 29(9): p. 1112-9.

56 Chang, J.M., J.F. Taly, I. Erb, T.Y. Sung, W.L. Hsu, C.Y. Tang, C. Notredame, and E.C. Su, Efficient and interpretable prediction of protein functional classes by correspondence analysis and compact set relations. (2013).*PLoS One*, 8(10): p. e75542.

57 Campo, S., C. Peris-Peris, C. Sire, A.B. Moreno, L. Donaire, M. Zytnicki, C. Notredame, C. Llave, and B. San Segundo, Identification of a novel microRNA (miRNA) from rice that targets an alternatively spliced transcript of the Nramp6 (Natural resistance-associated macrophage protein 6) gene involved in pathogen resistance. (2013).*New Phytol*, 199(1): p. 212-27.

58 Bussotti, G., C. Notredame, and A.J. Enright, Detecting and comparing non-coding RNAs in the high-throughput era. (2013).*Int J Mol Sci*, 14(8): p. 15423-58.

59 Breen, M., C. Kemena, P. Vlasov, C. Notredame, and F. Kondrashov, Reply on The Role of Epistatis in Evolution. (2013).*Nature*, 497(7451): p. E2-E3.

60 Chang JM, Taly JF, Erb I, Sung TY, Hsu WL, Tang CY, Notredame C, Su EC. Efficient and interpretable prediction of protein functional classes by correspondence analysis and compact set relations. PLoS One. 2013 Oct 11;8(10):e75542. doi: 10.1371/journal.pone.0075542. eCollection 2013. PubMed PMID: 24146760; PubMed Central PMCID: PMC3795737

61 Magis C, Taly JF, Bussotti G, Chang JM, Di Tommaso P, Erb I, Espinosa-Carrasco J, **Notredame C**. T-Coffee: Tree-based consistency objective function for alignment evaluation. Methods Mol Biol. 2014;1079:117-29. doi: 10.1007/978-1-62703-646-7_7. PubMed PMID: 24170398.

62 Rachidi N, Taly JF, Durieu E, Leclercq O, Aulner N, Prina E, Pescher P, Notredame C, Meijer L, Späth GF. Pharmacological assessment defines Leishmania donovani casein kinase 1 as a drug target and reveals important functions in parasite viability and intracellular infection. Antimicrob Agents Chemother. 2014 Mar;58(3):1501-15. doi: 10.1128/AAC.02022-13. Epub 2013 Dec 23. PubMed PMID: 24366737; PubMed Central PMCID: PMC3957854.

63 Chang JM, Di Tommaso P, **Notredame C.** TCS: a new multiple sequence alignment reliability measure to estimate alignment accuracy and improve phylogenetic tree reconstruction. Mol Biol Evol. 2014 Jun;31(6):1625-37. doi: 10.1093/molbev/msu117. Epub 2014 Apr 1. PubMed PMID: 24694831.

64 Tommaso PD, Bussotti G, Kemena C, Capriotti E, Chatzou M, Prieto P, **Notredame C.** SARA-Coffee web server, a tool for the computation of RNA sequence and structure multiple alignments. Nucleic Acids Res. 2014 Jun 27. pii: gku459. [Epub ahead of print] PubMed PMID: 24972831.

65 Pervouchine, D.D., S. Djebali, A. Breschi, C.A. Davis, P.P. Barja, A. Dobin, A. Tanzer, J. Lagarde, C. Zaleski, L.H. See, et al., Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. (2015).*Nat Commun*, 6: p. 5903.

66 Orobitg, M., F. Guirardo, F. Cores, J. Llados, and C. Notredame, High Performance computing improvements on bioinformatics consistency-based multiple sequence alignment tools. (2015).*parallel Computing*, 42(1): p. 18-34.

67 Yue, F., Y. Cheng, A. Breschi, J. Vierstra, W. Wu, T. Ryba, R. Sandstrom, Z. Ma, C. Davis, B.D. Pope, et al., A comparative encyclopedia of DNA elements in the mouse genome. (2014).*Nature*, 515(7527): p. 355-64.

68 Magis, C., J.F. Taly, G. Bussotti, J.M. Chang, P. Di Tommaso, I. Erb, J. Espinosa-Carrasco, and C. Notredame, T-Coffee: Tree-based consistency objective function for alignment evaluation. (2014).*Methods Mol Biol*, 1079: p. 117-29.

69 Earl, D., N. Nguyen, G. Hickey, R.S. Harris, S. Fitzgerald, K. Beal, I. Seledtsov, V. Molodtsov, B.J. Raney, H. Clawson, et al., Alignathon: a competitive assessment of whole-genome alignment methods. (2014).*Genome Res*, 24(12): p. 2077-89.

70 Cheng, Y., Z. Ma, B.H. Kim, W. Wu, P. Cayting, A.P. Boyle, V. Sundaram, X. Xing, N. Dogan, J. Li, et al., Principles of regulatory information conservation between mouse and human. (2014).*Nature*, 515(7527): p. 371-5.

Reviews

1. **Notredame, C**., *Recent progress in multiple sequence alignment: a survey.* Pharmacogenomics, 2002. **3**(1): p. 131-44.
2. **Notredame, C**., *Recent evolutions of multiple sequence alignment algorithms.* PLoS Comput Biol, 2007. **3**(8): p. e123.
3. Kemena, C. and **C. Notredame**, *Upcoming challenges for multiple sequence alignment methods in the high-throughput era.* Bioinformatics, 2009. **25**(19): p. 2455-65.

Books and Book Chapters

1. Claverie, J.M. and C. Notredame, *Bioinformatics for dummies*. 2003: Wiley Publishing, Inc.
2. **Notredame, C**., *Using Genetic Algorithms for Pairwise and Multiple Sequence Alignments*, in *Evolutionnary Computation in Bioinformatics*, B.G. Fogel and D.W. Corne, Editors. 2003, Morgan Kaufmann. p. 60-80.
3. **Notredame, C.** and C. Abergel, *Using Multiple Alignment Methods to Assess the Quality of Genomic Data Analysis*, in *Bioinformatics and Genomes: Current Perspectives*, M. Andrade, Editor. 2003, Horizon Scientific Press. p. 30-50.
4. **Notredame, C**. and K. Suhre, *Making Multiple Sequence Alignments with T-Coffee*, in *Current Protocols in Bioinformatics*, Wiley, Editor. 2003. p. 250-275.
5. Claverie, J.M. and C. Notredame, *Bioinformatics for dummies, 2nd*. 2006: Wiley Publishing, Inc.
6. **Notredame, C**., *Computing multiple sequence/structure alignments with the T-coffee package.* Curr Protoc Bioinformatics, 2010. **Chapter 3**: p. Unit 3 8 1-25.

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Competitive Funding

2008-2012 Leishdrug *FP7*

Leishmania Kinome analysis, WP leader, 130.000 Euros

2009-2013 Quantomics *FP7*

Farm animal genomic variability survey, WP Leader, 140.000 Euros

2008-2011 G-Coffee *Plan Nacional (Spain)*

Development of a genomic aligner, Personal project, 120.000 Euros

2012-2014 E-Seq *Plan Nacional (Spain)*

Incorporation of experimental data within genomic sequences, 240.000 Euros

Servers and Programs

www.tcoffee.org

International Conferences and Editorial Responsibilities

Invited Speaker
French Bioinformatics Conference (JOBIM), Toulouse, 2001
Computational Problems in Biology, Lausanne, 2001
Journées Mathématiques, Institut Pointcarré, Paris, 2003
Intelligent System in Molecular Biology, Melbourne, 2003
Spanish Bioinformatics Conference, Salamanca, Spain,
SwissProt Twenty Years Celebration, Fotalezza, Brazil, 2006
Intelligent System in Molecular Biology, Fortalezza, 2006
German Conference in Bioinformatics, Tubingen, 2006
Horizons in Bioinformatics, Goettingen, 2008
Society of Molecular Evolution Annual Conference, Barcelona, 2008
Weizmann Institute, Israel, 2008
Kings College, London, 2009
European Bioinformatic Institute, Cambridge, 2009
Joint Genome Institute, Berkeley, 2010
NCBI, Bethesda, 2010
Ecole Polytechnique Federale de Lausanne, 2010
Sinica Academia, Taiwan, 2010
EMBO conference on RNA translocation, Toscanny, 2011
Italian Bioinformatics Conference (BITS), Pisa, 2011
EMBO Bioinformatics Summer school, Tangier, 2011
Genth Univesity, 2012
IGMM, CNRS, Montpelier, 2012
TEDEx Barcelona, 2012
Harden Confference, Cambridge, UK, 2012
Sinica Academia, Taiwan, 2012
Titissee Borheinger Conference, Germany, 2013
IDIBELL, Barcelona, 2013
Virginia Tech Bioinformatics Conference, 2014

Certified Correct, Bologna, the 21/09/2016

Program Committee Member
JOBIM: French Bioinformatics Conference (2006-2009)
WABI: Workshop On Algorithms in Bioinformatics (2006)
ISMB: Intelligent Systems in Bioinformatics (2005-2011)
ECCB : European Conference on Computational Biology (2010-2011), **track chair (2014)**

Editorial Responsabilities
Section Editor of "Applied Bioinformatics"

Languages

French: maternal.

English: fluently spoken, read and written.

Spanish: spoken, read

Greek: notions.

Certified Correct, Barcelona, the 27/06/2023