

# Dr Cédric Notredame, PhD.



Dr Cedric Notredame  
Group Leader  
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## Personal Information

Nationality: French

Born 30/10/70, Married

## Education

**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.

**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 developed 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 most 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

## 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. Chenivresse, 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. Beaudoin, **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. 1187-92.
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. Orbitg, F. Guirardo, 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. Beaudoin, 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 Tommaso, P., S. Morreti, I. Xenarios, M. Orobittg, 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. Eyra, 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.

## 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 *Evolutionary 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.

#### 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](http://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, 2002
- SwissProt Twenty Years Celebration, Foz de Iguaçu, Brazil, 2006
- Intelligent System in Molecular Biology, Fortaleza, 2006

- German Conference in Bioinformatics, Tübingen, 2006
- Horizons in Bioinformatics, Göttingen, 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 Fédérale de Lausanne, 2010
- Sinica Academia, Taiwan, 2010
- EMBO conference on RNA translocation, Tuscany, 2011
- Italian Bioinformatics Conference (BITS), Pisa, 2011
- EMBO Bioinformatics Summer school, Tangier, 2011

#### **Member of Program Committees**

- 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)

#### **Editorial Responsibilities**

- Associate Editor of "Applied Bioinformatics"
- Associate Editor of "BMC Bioinformatics"

#### **Languages**

**French:** maternal.

**English:** fluently spoken, read and written.

**Spanish:** spoken, read

**Greek:** notions.