CV: Olivier GASCUEL
Directeur de Recherche au CNRS (DRCE2)
Institut de Systématique, Evolution, Biodiversité (ISYEB)
UMR 7205 - CNRS & Muséum National d'Histoire Naturelle
olivier.gascuel@mnhn.fr

February 3, 1956
Married – Four children

EDUCATION

1990 – Habilitation à Diriger des Recherches (HDR), Computer Science, Montpellier
1981 – PhD thesis, Artificial Intelligence – Computer Science, Paris
1975-1979 – Ecole Normale Supérieure, Mathematics, Cachan

RESEARCH AND PROFESSIONAL EXPERIENCE

2016-20 – PI of the Evolutionary Biology Research Unit, Institut Pasteur, Paris
2015-20 – Head of the Dpt. of Computational Biology (formerly C3BI), Institut Pasteur, Paris
2013-20 – Directeur de Recherche de Classe Exceptionnelle (DRCE2), CNRS
2011-15 – Head of the Institute for Computational Biology (IBC), Univ. Montpellier, France
2000-15 – Head of the Methods and Algorithms for Bioinformatics team, LIRMM, Montpellier

SCIENTIFIC ACTIVITIES   GOOGLE SCHOLAR

155 publications, 53 invited lectures, H-index 45, >50,000 citations (Google Scholar)
Associate Editor of *Systematic Biology* (Oxford University Press, IF>10)
Board on *BMC Bioinformatics*, *BMC Evolutionary Biology*, *NAR Genomics and Bioinformatics*
Chair of yearly conference *Mathematical and Computational Evolutionary Biology*, since 2012
Initiator as Chair or Co-Chair of the following still running conferences:
    2000 – JOBIM, the French Bioinformatics conference
    2001 – WABI, one of the main conferences on algorithms in bioinformatics
    2007 – ISCB Africa ASBCB, the African bioinformatics conference
Reviewer (2018-Now) for: Nature, PNAS, Plos Computational Biology, Bioinformatics, Virus,
    Molecular Biology and Evolution, Systematic Biology, Welcome Open Research

TEACHING ACTIVITIES

32 PhDs with successful defense, 3 ongoing PhDs, 15 Post Doc supervisions
Scientific Director of yearly course on Molecular Phylogenetics, Institut Pasteur & ENS Paris
This course is run every year in the Int. Network of Pasteur Institutes (2019 Montevideo, 2018 HK)
Invited to teach all around the world (Cuba: 2019, Vietnam: 2015-16-17, Crete: 2016 etc.)

ADMINISTRATIVE RESPONSIBILITIES AND EXPERTISE

2019 – Scientific Evaluation of MAIAGE Laboratory, Institut National de la Recherche Agronomique
2018-2019 – Professor and Tenure Assessor reporting for Univ. Tasmania (AUS), Simon Fraser
    University (CA), Australian University (AU), University of Otago (NZ)
2008-2012 Head of the Systems Biology and Bioinformatics Committee of the CNRS
2006-2011 President of the Scientific Council of the LIRMM (>500 members), Montpellier, France

AWARDS AND DISTINCTIONS

2019 – Elected member of the French Academy of Science
2017 – Grand Prix Inria - Académie des Sciences for Numerical Sciences
2009 – Silver Medal of the CNRS
2007-11 – Current Classic (Thomson Reuter, most cited paper in Environment and Ecology)
2005 – Fast breaking paper (Thomson Reuter, highest citation growth in Environment and Ecology)

MAIN RECENT RESEARCH FUNDING

2020-24 **PRAIRIE** (Artificial Intelligence Call 3IA – ANR), Chair Holder (488 K€)
2017-25 **INCEPTION** (Convergence Call PIA – ANR), Director until 2020 (12 M€)
2015-18 **VIROGENESIS** (EU H2020), Coordinator for France/CNRS (450 K€)
2011-17 **Inst. Biologie Computationnelle** (Bioinformatics Call PIA – ANR), Coordinator (3 M€)

INVITED PRESENTATIONS IN INTERNATIONAL CONFERENCES AND SCHOOLS

2019 **Keynote Speaker**, 13th Aykut Kence Evolution Conference, Ankara, 2019
2017 **Invited Speaker**, Algebraic and Combinatorial Phylogenetics, Barcelona,
2017 **Invited Speaker**, Math. Approaches to Evolutionary Trees and Networks, BIRS, Banff CA
2009-16 **Invited Speaker**, EMBO Course Computational Molecular Evolution, Heraklion/Hinxton
2015 **Invited Speaker**, Society for Molecular Biology and Evolution (SMBE), Vienna

TEN YEARS TRACK RECORDS

In 2011, I initiated and then headed until 2015 the Institute for Computational Biology (IBC) in Montpellier, France. This transversal structure involved ~100 researchers (permanent positions, PhDs, postdocs) from a number of laboratories belonging to a large scope of domains, ranging from mathematics and computer science to biology, medicine and ecology.

In 2015, I moved to the Institut Pasteur, Paris, to create and direct the Centre for Bioinformatics, Biostatistics and Integrative Biology (C3BI). We started with a small group of less than 10 people, but hired a number of PIs and bioinformaticians. In 2019, the C3BI became the new Computational Biology Department that is affiliated to both the Institut Pasteur and the CNRS. The C3BI/Dpt. comprises 5 Research Units (sequence algorithms, modelling, Bayesian computation, statistical genetics, and my Unit in evolutionary bioinformatics) and a large core facility, the Bioinformatics and Biostatistics HUB, with 50 engineers having a broad spectrum of expertise, ranging from software development to machine learning and biological data analysis.

MAJOR CONTRIBUTIONS TO EARLY CARREERS

1. **Celine Scornavacca** (PhD - defence 2009): Permanent researcher position CNRS – Institut des Sciences de l'Evolution, Montpellier, France. Celine is working on the algorithmics of phylogenetic trees and networks. More than 2,500 citations, H-index 21, SCHOLAR.

2. **Stéphane Guindon** (PhD - defence 2003): Permanent researcher position CNRS – Laboratoire d'Informatique, de Robotique et de Microélectronique de Montpellier, France. Stéphane is the first author of PhyML, started during his PhD. He's working on algorithms and models in phylogenetics and population genetics. More than 38,000 citations, H-index 21, SCHOLAR.

3. **Olivier Elemento** (PhD - defence 2002): Director, Englander Institute for Precision Medicine, Weill Cornell Medicine, NY - USA. Olivier is working on functional genomics, precision medicine and cancer. More than 16,000 citations, H-index 65, URL SCHOLAR.

4. **Richard Nock** (PhD - defence 1998): Professor Université des Antilles, France. Richard is working on both the theory and applications of machine learning. He's has been invited all around the word, and received the Grand Prix ANR for Numerical Sciences. More than 4,000 citations, H-index 29 URL SCHOLAR.

5. **Maria Anisimova** (Postdoc 2003-2004): Head of Applied Computational Genomics team, Zurich University of Applied Sciences. Maria is working on phylogenetics and its applications to functional genomics. More than 14,000 citations, H-index 27 URL SCHOLAR.

6. **David Bryant** (Postdoc 1999-2000). Professor of Mathematics, Director Computational Modeling, Otago University, New Zealand. David is working on a number of topical questions in mathematical phylogenetics. More than 13,000 citations, H-index 39 URL SCHOLAR.

DEVELOPING COUNTRIES

For fifteen years, I have been involved in bioinformatics collaborations and training in developing countries. I initiated with local organizers and a large community of researchers the first African bioinformatics conference, Nairobi, Kenya, 2007 (URL). This conference became ISCB Africa ASBCB, and is still run every two years (Kumasi, Ghana, in 2019). I taught bioinformatics courses intended for students and researchers from developing and emerging countries in a number of places: South Africa, Brazil, Uruguay, Morocco, Tunisia, Cambridge, Grece, Vietnam, Paris, Hong Kong… Via the Institut Pasteur International Network, I organize several bioinformatics courses every year (Hanoi, Cuba and Tunis in 2019), and I regularly host young researchers in my group (2 from Cambodia, 1 from Brazil and 1 from Cuba in 2019).

TEN MOST SIGNIFICANT PUBLICATIONS IN THE LAST TEN YEARS

1. **Gascuel O**, Steel M. 2020. *A Darwinian Uncertainty Principle*. **Systematic Biology** 69 (3), 521-529
   PDF

2. Lemoine F, Correia D, Lefort V, Doppelt-Azeroual O, Mareuil F, Cohen-Boulakia S, **Gascuel O**. 2019. NGPhylogeny.fr: *new generation phylogenetic services for non-specialists*. **Nucleic Acids Research**, 47(W1):W260-W265. **Google Scholar: 34 citations** PDF

3. Ishikawa SA, Zhukova A, Iwasaki W, **Gascuel O**. 2019. *A Fast Likelihood Method to Reconstruct and Visualize Ancestral Scenarios*. **Molecular Biology and Evolution**, 36(9):2069-85. PDF

4. Lemoine F, Domelevo Entfellner JB, Wilkinson E, Correia D, Dávila Felipe M, De Oliveira T, **Gascuel O**. 2018. *Renewing Felsenstein's phylogenetic bootstrap in the era of big data*", **Nature**, 556(7702):452-456. **Google Scholar: 94 citations** NATURE PDF

5. Lefort V, Longueville JE, **Gascuel O**. 2017. *SMS: Smart Model Selection in PhyML*. **Molecular Biology and Evolution**, 34(9):2422-24. **Google Scholar: 543 citations** PDF

6. Cassan E, Arigon-Chifolleau AM, Mesnard JM, Gross A, **Gascuel O**. 2016. Concomitant Emergence of the AntiSense Protein Gene of HIV-1 and of the Pandemic. **Proc. National Academy of Science USA**, 113(41):11537-42. **Google Scholar: 39 citations** PDF

7. To TH, Jung M, Lycett S, **Gascuel O**. 2016. Fast Dating Using Least-Squares Criteria and Algorithms. **Systematic Biology**, (1):82-97. **Google Scholar: 136 citations** PDF

8. Le SQ, Dang CC, **Gascuel O**. 2012. Modeling protein evolution with several amino acid replacement matrices depending on site rates. **Molecular Biology and Evolution**, 29(10):2921-36. **Google Scholar: 119 citations** PDF

9. Gouy M, Guindon S, **Gascuel O**. 2010. SeaView version 4: A multiplatform graphical user interface for sequence alignment and phylogenetic tree building. **Molecular Biology and Evolution**, 27(2):221-4. **Google Scholar: 4,143 citations** PDF

10. Guindon S, Dufayard JF, Anisimova M, Hordijk W, Lefort V, **Gascuel O**. 2010. *New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0*. **Systematic Biology**, 59:307-21. **Google Scholar: 10,356 citations** PDF

HIGHLY CITED PUBLICATIONS MORE THAN TEN YEARS OLD

1. Dereeper A., …, **Gascuel O**. 2008 - *Phylogeny. fr: robust phylogenetic analysis for the non-specialist* - **Nucleic acids research** 36 (suppl_2), W465-W469 **Google Scholar: 3,830 citations**

2. SQ L., **Gascuel O**. 2008 - *An improved general amino acid replacement matrix* -**Molecular biology and evolution** 25 (7), 1307-1320 **Google Scholar: 1,947 citations**

3. Anisimova A, **Gascuel O**. 2006 - *Approximate likelihood-ratio test for branches: a fast, accurate, and powerful alternative* - **Systematic biology** 55 (4), 539-552 **Google Scholar: 2,121 citations**

4. Guindon S., **Gascuel O**. 2003 - *A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood* - **Systematic biology** 52 (5), 696-704 **Google Scholar: 16,122 citations**

5. **Gascuel O.** 1997 - *BIONJ: an improved version of the NJ algorithm based on a simple model of sequence data.* - **Molecular Biology and Evolution** 14 (7), 685-695 **Google Scholar: 1,736 citations**