

Guillaume Achaz

Professor (Univ Paris-Cité), GDR director (CNRS), co-head of the SMILE group (Collège de France)

Born on 1974; married with 3 children

Professor at Université de Paris

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<http://bioinfo.mnhn.fr/abi/people/achaz/>

Research topics

Molecular evolution, mathematical modeling, genomics, bioinformatics *sensu lato*, philosophy and history of biology.

Positions & affiliations

2019-...	professor at Univ Paris-Cité (UMR 7142 CIRB, Collège de France)
2016-...	director of the research network AIEM <i>Approche Interdisciplinaire de l'Évolution Moléculaire</i> (GDR CNRS 3765)
2021-...	co-head of the <i>SMILE</i> group (UMR7241, Collège de France)
2021-...	elected member of the teaching council (Conseil d'Enseignement, Univ. Paris-Cité)
2019-...	research associate at the <i>Anthropologie Génétique</i> group (UMR7206, Musée de l'Homme)
2019-...	research associate at the <i>Atelier de Bioinformatique</i> group (UMR7205, Muséum)
2016-...	monthly discussion group of philosophy and history of biology (IHPST)
2012-2021	research associate at the <i>SMILE</i> group (UMR7241, Collège de France)
2015-2019	head of the <i>Atelier de Bioinformatique</i> group (UMR7205, Muséum)
2005-2019	associate professor at Sorbonne Univ (UMR7138 then UMR7205)
2009-2010	CNRS research sabbatical (Kyoto University)
2002-2005	postdoctoral fellow (Harvard University, Boston)
1998-2002	PhD (Institut Jacques Monod, Paris)

Diplomas

2009	HDR <i>Évolution moléculaire: des données aux modèles, et vice-versa</i> (Sorbonne Univ)
2002	PhD <i>Etude de la dynamique des génomes: les répétitions intrachromosomiques</i> (Sorbonne Univ)

Teaching

- **M2 EvoGEM, 2022-....**: Phylogeny (12h), Population genetics (30h).
- **Univ Paris-Cité, 2019-....**: *Bachelor students*: Mathematics (40h, L1), Population Genetics (30h, L2, L3), Statistics (10h, L3). *Master and graduate students*: Mathematical modelling (20h, M1), Bioinformatics (10h, M2).
- **Ecole Normale Supérieur, 2019-....**: Population genetics (L3, 12h).

- **Muséum, 2016-...:** Evolutionary models (grad students 4h).
- **Ecole Normale Supérieure, 2017-2021:** Population genetics (M2, 30h).
- **Sorbonne Univ, 2014-2022:** Population genetics (Med School 2 yr, 2h).
- **Pasteur Institut, 2019:** One 8min MOOC lecture on demographical inference.
- **Sorbonne Univ, 2005-2019:** *Bachelor students:* Computer science (20h), Mathematics and modeling (60h), Biochemistry (20h in 2011-2014) and L1 research project (ARE) (20h since 2017). *Master and graduate students:* Molecular evolution (population genetics, phylogeny, comparative genomics) (50h) et Bioinformatics (20h).

Organization of scientific events

[org= organization committee, sc= scientific committee, head= main organizer]

International

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|------|--|
| 2019 | Summer school, Institut Pascal (Orsay, org). |
| 2017 | Workshop “Coevolution, Fitness Landscapes and epistasis” (Muséum, head). |
| 2015 | Mathematical Models for Ecology and Evolution 2015 (Collège de France, org). |
| 2011 | Conférence Jacques Monod <i>Theoretical and empirical advances in evolutionary genomics</i> (Roscoff, one session) |

National

- | | |
|------|--|
| 2023 | Empirisme et Théorie en Écologie et Évolution (9th AIEM, Gif-s-Yvette, org) |
| 2022 | joint AIEM+ALPHY meeting (8th AIEM, Grenoble, org)
From reads to genomes and variants, GDR ³ event (Muséum, org) |
| 2021 | joint AIEM+ALPHY meeting (7th AIEM, Rennes, org) |
| 2020 | 6th AIEM meeting (Video-conf, org) |
| 2019 | 5th AIEM meeting (Toulouse, org)
ALPHY 2019 (Muséum, org) |
| 2018 | 4th AIEM meeting (Lille, org)
JOBIM 2018 (Marseille, sc)
Inferences in evolution from genomic data (Muséum, org) |
| 2017 | SMBE regional meeting in Lyon (3rd AIEM, org) |
| 2016 | Approche Interdisciplinaire en Évolution (2nd AIEM, Montpellier, org) |
| 2015 | Empirisme et Théorie en Écologie et Évolution (1st AIEM, Paris, org) |
| 2011 | JOBIM 2011 (sc) |

Recurrent local events

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|-----------|---|
| 2018-... | Evolution à Paris (Muséum, coordinator) |
| 2014-2020 | “EvolMol” Molecular Evolution seminars (ENS, org) |

Scientific committees

[E= examinateur, R=rapporteur (manuscript report), P=président (defense report)]

PhD thesis

2022	A Louvet (Ecole Polytechnique Paris, P), T Virgoulay (Univ Montpellier, E), M Leduc (Université Angers, R), T Grohens (INSAE Lyon, P)
2021	P Ecoffet (Sorbone Univ, R), A Desbiez-Piat (Univ Paris-Saclay, R), J Voznica (Univ Paris, E), J Chouin (Sorbonne Univ, E), A Arredondo (Toulouse, R)
2020	C Paris (Univ Toulouse, E), L Marrec (Sorbone Univ, R), G Louvel (Sorbone Univ, P),
2019	M Silver (Sorbonne Univ, P), N Cerisier (Univ Paris, P), N Saclier (Univ Lyon, R), P Zacharias (Muséum, P)
2018	M Tiret (Agro ParisTech, E), J Fouret (Univ Lyon, E), P Barlat-Charlaix (Sorbonne Univ, E), T Naidoo (Uppsala Univ, Sweden, opponent)
2017	N Harmand (Univ Montpellier, E), M Barbier (EPHE, E), C Giner (UAB, Barcelona, R)
2016	F Gascuel (Sorbonne Univ, E), F Pouyet (Univ Lyon 1, R), A Launay (Sorbonne Univ, E), J Fumey (UPSud, R)
2015	M Fagny (Sorbonne Univ, E).
2014	C Delaporte (Sorbonne Univ, E), B Batut (Univ Lyon 1, R).

HDR

2020	E Pelletier (Genoscope, R)
2019	F Debarre (CNRS - Sorbonne Univ, E)
2018	E Patin (CNRS - Institut Pasteur, R), S Mona (EPHE, R)
2017	S Boitard (INRA Toulouse, R)
2013	D Dupuy (Univ Bordeaux, R)

(Assistant) Prof Recruitment

2022	Bioinformatics (Sorbonne Univ), Evolutionary genomics (Univ Paris-Saclay)
2020	Population genomics (Univ Paris-Saclay), History of Sciences (Univ Paris)
2019	Bioinformatics (Univ Denis Diderot), ATER (Sorbonne Univ), Population genomics (EPHE)
2018	Mathematics & Biology (Sorbonne Univ), Population Genetics (Univ Lille 1)
2017	Theoretical Population Genetics (Univ Lyon 1)
2016	Evolutionary Microbiology (Univ Denis Diderot)
2010	Statistics (Univ Rouen)
2009	Statistics (Univ Rouen), Molecular Evolution (Univ Lille 1)

Other

2020-	member of the COMESP (committee for the evaluation/promotion of Faculty members of Pasteur Institute)
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Grants

2021-2023	120 kE	Labex "Who Am I?" (partner)
2020-2022	100 kE	Inception Program (partner)
2019-2022	90 kE	Fondation François Sommer grant (coord)
2012-2016	250 kE	young researcher ANR grant <i>TempoMut</i> (coord)
2012-2016	20 kE	ANR project <i>Demochips</i> (partner)

2008-2011	20 kE	ANR project <i>Flavophylogenomics</i> (partner)
2010	15 kE	CNRS grant (Projets Exploratoires / Premier Soutien) (coord)
2010	20 kE	JSPS fellowship for doing research in Japan
2003	90 kFr	Fondation Singer Polignac fellowship.
2002	1 yr sal.	Post-doctoral fellowshsip - Fondation pour la Recherche Médicale.

Scientific mentoring

Postdoc

2021-2023	Jean-Noël Lorrenzi
2020-2022	Maxime Godfroid
2013-2015	Luca Ferretti

PhDs

2022-2025	Augustin Chen : <i>Evolution Somatique</i> , shared with A. Lambert and S. Baulac
2020-2023	Thomas Forest: <i>Détecer les espèces en voie de disparition par l'approche génomique</i> , shared with A. Lambert and J. Fuchs
2017-2021	Elise Kerdoncuff: <i>Détecer les espèces en voie de disparition par l'approche génomique</i> , shared with A. Lambert (now post-doc in Berkley)
2017-2021	Karen Salazar: <i>Does and how the environment impact the biodiversity: contrasting european and south american ladybird beetles</i> , shared with R. Nattier
2014-2017	Marguerite Lapierre: <i>Modèles de référence en évolution moléculaire</i> , shared with A. Lambert (now high-school teacher agrégée)
2012-2015	Abdelkader Bedhenna: <i>Inférence des interactions entre processus évolutifs</i> , shared with A. Lambert (now IT)
2006-2009	Etienne Loire: <i>Impact des microsatellites codants chez les primates</i> (now researcher at CIRAD).

Masters

2023	N Vitorelli
2022	A Omarjee, A Chen
2021	P Imbert, L Manceron
2011-2020	D Klein, D Ramesh, V Cabocel, L Fourteau, R Clodion, J Bac, E Kerdoncuff, Y Chen, M N'debi, X Maynadier, L Bouteille, P Petot, G Li Cavoli, T Van Meter, Y Ben Chehida, M Lapierre, B Rocques, A Bedhenna, D Monet, S Houari, A Foucal

Publications track record

55 published articles: 13 as last author, 3 as unique author, 13 as (co-)first author
h-index: 27 ; ~ 5,500 citations (src: Google Scholar 01/2023)

Submitted

- Y Ben Chehida, M Eleaume, C Gallut and **G Achaz**. The rapid divergence of the antarctic crinoid species *Promachocrinus kerguelensis*. [Sc. Reports](#). in revision.
- F Freund*, E Kerdoncuff*, S Matuszewski, M. Lapierre, M Hildebrandt, J.D. Jensen, L Ferretti, A. Lambert, T. Sackton and **G Achaz**. Interpreting the pervasive observation of U-shaped Site Frequency Spectra. [PLoS Genetics](#), in revision.

- M Godfroid, C Coluzzi, A Lambert, P Glaser, EPC Rocha and **G Achaz**. Evo-Scope: Fully automated assessment of correlated evolution on phylogenetic trees. [Methods in Ecology and Evolution](#), submitted.

Pre-print (no review)

- S Brouillet, A Hannoni, L Ferretti and **G Achaz** MAGELLAN: a tool to explore small fitness landscapes. [bioRxiv](#). <https://doi.org/10.1101/031583>

Reviews / book chapters

55. **G Achaz** and JY Dutheil. Correlated evolution: models and methods. (2020), [Étude de l'Évolution par l'approche Mathématique et Informatique](#) (2022). ISTE Editions.
54. **G Achaz**. Which model(s) explain(s) biodiversity. In: [Biodiversity & Evolution](#) (2018), ISTE Editions & Wiley Blackwell, 39-61.
53. **G Achaz**, A Rodriguez-Verdugo, BS Gaut and O Tenaillon. The reproducibility of adaptation in the light of experimental evolution with whole genome sequencing. [Advances in Experimental Medicine and Biology](#) (2014), 781:211-31

Original articles

1. I Overcast, **G Achaz**, R Aguilée, ... and H Morlon (24 co-authors). Toward a Genetic Theory of Island Biogeography: Inferring Processes from Multi-Dimensional Community-Scale Data, submitted to [Global Ecology and Biogeography](#), in press.
2. J Guez, **G Achaz**, F Bienvenu, J Cury, B Toupance, E Heyer, F Jay, and F Austerlitz. Cultural transmission of reproductive success impacts genomic diversity, coalescent tree topologies and demographic inferences, submitted to [Genetics](#), in press.
3. A Fedosov, **G Achaz** and N Puillandre. MOLD, a novel software to compile accurate and reliable DNA diagnoses for taxonomic descriptions. [Mol Ecol Res](#) (2022). 22(5):2038-2053.
4. A Behdenna, M Godfroid, P Petot, J Pothier, A Lambert and **G Achaz**. A minimalist yet flexible likelihood framework to assess correlated evolution. [Syst Biol](#) (2022). 71(4):823-838.
5. M Dahawi, , ... , **G Achaz**, ... and E Leguern [17 co-authors]. Involvement of ADGRV1 Gene in Familial Forms of Genetic Generalized Epilepsy. [Front Neurol](#) (2021). 12:738272
6. J van Helden, C D Butler, **G Achaz**, D Casane, ..., E Decroly and J Halloy [16 co-authors]. An appeal for an objective, open, and transparent scientific debate about the origin of SARS-CoV-2 [Lancet](#) (2021). 98:1402-1404.
7. J Cury, BC Haller, **G Achaz** and F Jay. Simulation of bacterial populations with SLiM. [bioRxiv](#), version 5 peer-reviewed and recommended by [Peer community in Evolutionary Biology](#) (2021). [Peer Community Journal](#) (2022), 2:e7.

8. N Puillandre, S Brouillet and **G Achaz**. ASAP: Assemble your Species by Automatic Partitioning. [Mol Ecol Res](#) (2021). 21:609–620.
9. B Adbi, T Nguyen, S Brouillet, ..., **G Achaz**, ..., G Marcelin, C Soulie [17 co-authors]. No HIV-1 Molecular Evolution On Long Term Antiretroviral Therapy Initiated During Primary HIV-1 Infection. [AIDS](#) (2020), 34(12):1745-1753.
10. J Marin, **G Achaz**, A Crombach and A Lambert. The genomic view of diversification. [Journal of Evolutionary Biology](#) (2020), 33(10):1387-1404.
11. E Kerdoncuff, A Lambert and **G Achaz**. Testing for population decline using maximal linkage disequilibrium blocks. [Theoretical Population Biology](#) (2020), 134:171-181.
12. C Moreau, B Danis, Q Jossart, M Eléaume, C Sands, **G Achaz**, A Agüera and T Saucède. Is reproductive strategy a key factor in understanding the evolutionary history of Southern Ocean Asteroidea (Echinodermata)? [Ecology and Evolution](#) (2019), 9(15):8465-8478.
13. **G Achaz**, S Gangloff and B. Arcangioli. The quiescent X, the replicative Y and the Autosomes. bioRxiv 351288, ver 3 peer-reviewed and recommended by [PCI Evol Biol](#) (2019). [Peer Community Journal](#) (2022), 2:e18.
14. Z Landoulsi, F Laatar, E Noé, S Mrabet, M Ben Djebara, **G Achaz**, C Nava, S Baulac, I Kacem, A Gargori-Berrechidi, R Gouider, E Leguern. Clinical and genetic study of Tunisian families with Genetic Generalized Epilepsy: contribution of CACNA1H and MAST4 genes. [Neurogenetics](#) (2018), 19(3):165-178
15. L Ferretti, D Weinreich, F Tajima and **G Achaz**. Evolutionary constraints in fitness landscapes. [Heredity](#) (2018), 121:466-481.
16. **G Achaz**, A Lambert and E Schertzer. The sequential loss of the allelic diversity. [Advances in Applied Probability](#) (2018), 50(A):13-29.
17. L Ferretti, A Klassman, AM Ferrer, E Raineri, T Wiehe, S Ramos-Onsins and **G Achaz**. The neutral frequency spectrum of linked sites. [Theoretical Population Biology](#) (2018), 123:70-79.
18. S Baldassari, F Picard, ..., **G Achaz**, ... and S Baulac [87 co-authors] The landscape of epilepsy-related GATOR1 variants. [Genetics in Medicine](#) (2018).
19. N Vakirlis, AS Hebert, DA Oplente, **G Achaz**, CT Hittinger, G Fischer, JJ Coon, and I Lafontaine. A Molecular Portrait Of De Novo Genes, [Mol Biol Evol](#) (2018), 35(3):631-645.
20. S Bridel, AB Olsen, H Nilsen, J-F Bernardet, **G Achaz**, R Avendaño-Herrera and E Duchaud. Comparative genomics of *Tenacibaculum dicentrarchi* and “*Tenacibaculum finnmarkense*” highlights intricate evolution of fish-pathogenic species. [Genom Biol Evol](#) (2018), 10 (2), 452-457.
21. S Matuszewski, ME Hildebrandt, **G Achaz** and JD Jensen. Coalescent Processes With Skewed Offspring Distributions And Non-Equilibrium Demography, [Genetics](#) (2018), 208(1):323-338.

22. S Gangloff*, **G Achaz***, S Miled, C Denis A Villain and B Arcangioli. Quiescence unveils a novel mutational force in fission yeast, [eLife](#) (2017), 6:e27469 [* equal contribution].
23. L Ferretti, A Ledda, T Wiehe, **G Achaz** and S Ramos-Onsins. Decomposing the site frequency spectrum: the impact of tree topology on neutrality tests. [Genetics](#) (2017), 207(1):229-240.
24. M Lapierre, A Lambert and **G Achaz**. Accuracy of demographic inferences from Site Frequency Spectrum: The case of the Yoruba population. [Genetics](#) (2017), 206(1):439-449.
25. M Lapierre, C Blin, A. Lambert, **G Achaz** and EPC Rocha. The impact of selection, gene conversion, and biased sampling on the assessment of microbial demography. [Molecular Biology and Evolution](#) (2016), 33(7):1711-25.
26. L Ferretti, D Weinreich, B Schmiegel, Y Kobayashi, A Yamaushi, F Tajima and **G Achaz**. Measuring epistasis in fitness landscapes: the correlation of fitness effects of mutations. [Journal of Theoretical Biology](#) (2016), 396:132-43
27. A Behdenna, J Pothier, S Abby, A Lambert and **G Achaz**. Testing for independence between evolutionary processes. [Systematic Biology](#) (2016), 65(5):812-23
28. C Delaporte, **G Achaz** and A Lambert. Mutational pattern of a sample from a critical branching population. [Journal of Mathematical Biology](#) (2016), 73(3), 627-664.
29. M Suez, A Behdenna, S Brouillet, P Graça, D Higuete and **G Achaz**. MicNeSs: genotyping microsatellite loci from (NGS) sequences of specific amplifications. [Molecular Ecology Resources](#) (2016), 16(2):524-33.
30. C Régnier*, **G Achaz***, A. Lambert, RH Cowie, P Bouchet and B Fontaine. Mass extinction in poorly known taxa. [PNAS](#) (2015), 112:7761-7766. [* equal contribution]
31. F Blanquart, **G Achaz**, T Bataillon and O Tenaillon. Properties of selected mutations and emergence of complex genotypic landscapes under Fisher's geometric model. [Evolution](#) (2014), 68:3537-54.
32. E Loire, D Higuete, P Netter and **G Achaz**. Evolution of coding microsatellites in primate genomes. [Genome Biology and Evolution](#) (2013), 5(2):283-295.
33. S Ishida, F Picard, G Rudolf, E Noé, **G Achaz**, P Thomas, P Genton, E Mundwiler, M Wolff, C Marescaux, R Mieles, M Baulac, E Hirsch, E Leguern and S Baulac. Mutations of DEPDC5 cause autosomal dominant focal epilepsies. [Nature Genetics](#) (2013), 45(5):552-5
34. N Puillandre, A Lambert, S Brouillet and **G Achaz**. ABGD, Automatic Barcode Gap Discovery for Primary Species Delimitation. [Molecular Ecology](#) (2012), 21(8), 1864-1877.
35. Y Kobayashi, **G Achaz** and A Telschow. Effect of Parasitic Sex Ratio Distorters on Host Gene Frequencies in a Mainland-Island Context. [Journal of Evolutionary Biology](#) (2011), 24(8):1695-705.
36. G Kutty, **G Achaz**, F Maldarelli, A Varma, R Shroff, S Becker, G Fantoni and JA Kovacs. Characterization of the meiosis-specific recombinase Dmc1 of pneumocystis. [Journal of Infectious Disease](#) (2010), 202(12):1920-9.

37. J Pellet, L Tafforeau, M Lucas-Hourani, V Navratil, L Meyniel, **G Achaz**, ... and Vidalain PO [29 co-authors] ViralORFeome: an integrated database to generate a versatile collection of viral ORFs. [Nucleic Acid Research](#) (2010), 38(Database issue):D371-8
38. **G Achaz**. Frequency spectrum neutrality tests, one for all and all for one. [Genetics](#) (2009), 183(1):249-58.
39. T Treangen, A Darling, **G Achaz**, M Ragan, X Messeguer and EPC Rocha. A novel heuristic for local multiple alignment of interspersed DNA repeats. [IEEE/ACM Transactions on Computational Biology and Bioinformatics](#) (2009), 6(2):180-9.
40. E Loire, F Praz, D Higuët, P Netter, **G Achaz**. Hypermutability of genes in Homo sapiens due to the hosting of long mono-SSR. [Molecular Biology and Evolution](#) (2009), 26(1):111-121
41. **G Achaz**. Testing for neutrality in samples with sequencing errors. [Genetics](#) (2008), 179(3):1409-24
42. P Nicolas, S Mondot, **G Achaz**, C Bouchenot, JF Bernardet and E Duchaud. Population structure of the fish-pathogenic bacterium *Flavobacterium psychrophilum*. [Applied Environmental Microbiology](#) (2008), 74(12):3702-9.
43. G Kutty, F Maldarelli, **G Achaz** and JA Kovacs. Variation in the major surface glycoprotein genes in *Pneumocystis jirovecii*. [Journal of Infectious Disease](#) (2008), 198(5):741-9.
44. J-F Rual, N Klitgord and **G Achaz**. Novel insights into RNAi off-target degradation using *C. elegans* paralogs. [BMC Genomics](#) (2007), 8(1):106.
45. **G Achaz**, F Boyer, EPC Rocha, A Viari and E Coissac. Repseek, a tool to retrieve non-exact repeats from large DNA sequences. [Bioinformatics](#) (2007), 23(1):119-21
46. SJ Potter, P Lemey, **G Achaz**, CB Chew, AM Vandamme, DE Dwyer and NK Saxena. HIV-1 compartmentalization in diverse leukocyte populations during antiretroviral therapy. [Journal of Leukocytes Biology](#) (2004), 76(3):562-70.
47. CI Castillo-Davis, DL Hartl and **G Achaz**. Cis-regulatory and protein evolution in orthologous and duplicate genes. [Genome Research](#) (2004), 14(8):1530-1536.
48. **G Achaz**, S Palmer, M Kearney, F Maldarelli, JW Mellors, JM Coffin and J Wakeley. A robust measure of HIV-1 population turnover within chronically infected individuals. [Molecular Biology and Evolution](#) (2004), 21(10):1902-12.
49. **G Achaz**, P Netter and E Coissac and EPC Rocha. Associations between inverted repeats and the structural evolution of bacterial genomes. [Genetics](#) (2003), 164(4):1279-89.
50. **G Achaz**, EPC Rocha, P Netter and E Coissac. Origin and fate of repeats in bacteria. [Nucleic Acid Research](#) (2002), 30(13):2987-94.
51. **G Achaz**, P Netter and E Coissac. Study of intrachromosomal duplications among eukaryotes genomes. [Molecular Biology and Evolution](#) (2001), 18(12):2280-2288.

52. **G Achaz**, E Coissac, A Viari and P Netter. Analysis of intrachromosomal duplications in yeast *Saccharomyces cerevisiae*: a possible model for their origin. [Molecular Biology and Evolution](#) (2000), 17(8):1268-1275.

Scientific communications

Invited conferences (14)

- 2023 Chaire Mathematical Models in Biology (Aussois, FR)
2022 Société Française de Systématique (Rennes, FR)
2021 Phylogeny and inference: from models to data and back (IHP, Paris, FR)
2019 Ecosystem dynamics (Institut Pascal, Orsay, FR)
Journées à la mémoire de JP Bocquet-Appel (Aix-en-Provence, FR)
Human genome variation (summer school in Rabat, Morocco)
Le hasard, le calcul et la vie (Cerisy, FR)
2017 Mathematical Models in Ecology and Evolution 2017 (University of London, UK)
ALPHY 2017 (INSA-Lyon)
Rencontres "Génétique et Bioinformatique" (Sorbonne Univ, Paris)
2016 Journée Évolution et Biodiversité (Muséum, Paris)
2015 Approches théoriques et modélisation de la diversité biologique et résilience dynamique des systèmes complexes organisés multi-échelles (Institut des Systèmes Complexes, Paris)
2014 Journées Memo-Life (Ecole Normale Supérieure, Paris)
2011 Mind the Gap 2011 (University of Cologne, Allemagne)

Invited seminars (38)

- 2022 Vienna Population Genetics Graduate Program (Austria) ; Musée de l'Homme (Paris) ; Vienna Mathematical department (Austria)
2021 Uppsala Univ (Sweden)
2020 AMIS (Toulouse)
2019 Musée de l'Homme (Paris) ; chaire MMB (Muséum, Paris) ; Moulon semideev (Ferme du Moulon, Saclay)
2018 Séminaire de Biophysique (ESPCI, Paris),
2017 Laboratoire de Biologie Computationnelle et Quantitative (Sorbonne Univ, Paris) ; Excoffier lab (Berne, Suisse)
2016 Jensen Lab (Lausanne, Suisse) ; Bioinformatics Research Centre (Aarhus, Danemark); Séminaires Mathématique-Évolution-Biologie (Marseilles)
2015 SaMMBA (Institut Pasteur, Paris) ; MaIAGE (INRA, Jouy-en-Josas)
2014 Agents, Interaction and Complexity group (Southampton University, UK) ; Institut des Sciences de l'Évolution de Montpellier (ISEM, Montpellier)
2013 Journée ANR MANEGE (Paris)
2012 Evol Mol (ENS, Paris)
2011 Séminaire de mathématiques-biologie de Paris 13 (Paris) ; Statistical Department at Oxford University (UK) ; Centre for Research in Agricultural Genomics (Barcelona, Espagne)
2010 Evol Mol (Paris)

- 2009 Population Biology (Tokyo University, Japan) ; Center for Ecological Research (Kyoto University, Japan) ; Musée de l'Homme (Paris) ; Laboratoire d'Ecologie Alpine (Grenoble)
- 2008 Mathématiques, Informatique et Génomes (Jouy-en-Josas)
- 2007 Museum, renouvellement du quadriennal (Paris) ; séminaires Génomique (Institut Henri Poincaré, Paris)
- 2006 Midi-pile (Orsay) ; Institut Jacques Monod, séminaire de département (Paris) ; Séminaires de l'UMR 8016 (Lille)
- 2004 Harvard Center for Cancer Systems Biology (Boston, USA) ; Harvard Center for Genomic Research (Cambridge, USA) ; Tuft New England Medical Center (Somerville, USA)

Contributed talks (last 5 years)

- 2023 PopGroup 56 (London, UK)
- 2021 Mathematical and Computational Evolutionary Biology (Porquerolles, FR)
- 2020 PopGroup 53 (Leicester, UK)
- 2019 PopGroup 52 (Oxford, UK)
- 2018 Evolution Montpellier

Popularization of science (general public)

- 2022 TV interview **France Info** on origin of SARS-Cov2
Oral presentation **Pint of Science** on origin of SARS-Cov2
- 2021 TV interview **France TV** (C dans l'air) + **BFM-TV** on origin of SARS-Cov2
- 2020 written interview for **Le Monde** on origin of SARS-Cov2
written interview for **Figaro** on red pandas
- 2019 conference at the **Centre d'Alembert** (Orsay) [www.youtube.com/watch?v=oklzE4oRgSs]
- 2018 article in **The Conversation: Espèces en voie d'extinction: le compte n'y est pas.**
- 2017 oral interview for the JeBif association (young bioinformaticians)
- 2015 written interview for **Sciences & Vie** on the book *Les Animaux du Futur*
radio interview at **France Inter** on the 6th mass extinction

Journals & Reviews

Managing board

- 2017-... PCI Evolutionary Biology

Scientific review (last 3 years)

- 2022 Theoretical Population Biology, Journal of Theoretical Biology, eLife, G3, PCI Evol Biol, Genetics, Philosophical Transactions B, Biological Theory
- 2021 Genom Biol Evol, PCI Evol Biol, Evolution
- 2020 Conservation Genetics Resources, PCI Evol Biol, Evolution x3

Grant evaluation

2016-2018 ATM - Actions Thématiques du Muséum (evaluation committee)
2017 ERC (Europe)
2015 NSTA (China)
2012 ANR (France)

Softwares development

2023 **EvoSCOP**, quantify co-evolution in phylogeny - Godfroid et al., subm, [Meth Evo Eco](#)
2021 **epocs**, quantify co-evolution in phylogeny - Bedhenna et al., 2022, [Sys Biol](#)
2020 **ASAP**, species delimitation (2nd software) - Puillandre et al., 2020. [Mol Ecol Res](#)
2016 **micness**, genotyping microsatellites from NGS - Suez et al., 2016, [Mol Ecol Res](#)
2016 **epics**, detecting of co-evolution in a phylogeny - Bedhenna et al., 2016, [Sys Biol](#)
2015 **magellan**, exploring small fitness landscapes - Brouillet et al., 2015. [biorxiv](#)
2012 **ABGD**, species delimitation - Puillandre et al., 2012. [Mol Ecol](#)
2010 **ViralORFEome**, a human-virus interacting proteins D.B.- Pellet et al., 2010. [NAR](#)
2007 **repseek**, *de novo* repeats detection in chrmosomes - Achaz et al., 2007. [Bioinformatics](#)
2004 **sharmot**, detect small conserved motifs - Castillo-Davis et al., 2004. [Genom Res](#)