

Yannis Nevers

Curriculum vitae

Centre de recherche en biomédecine
1 Rue Eugène Boeckel,
67000 Strasbourg
Strasbourg, France

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Training & Degrees

- 01/10/2015 - 14/12/2018 **PhD Thesis in Health and Life Sciences - Bioinformatics and System Biology**
Title : “Exploitation of evolutionary markers to explore genotype-phenotype relationships. Application to ciliopathies.”
University of Strasbourg
- 01/09/2013 - 30/06/2015 **Life Sciences Master - Structural biology, bioinformatics and biotechnologies**
University of Strasbourg
Courses in: Phylogenomic, -omics, Programming (Bash, Java, Python), Algorithmics, Database (SQL), Statistics, Structural biology, Molecular modeling
- 01/09/2010 - 30/06/2013 **Life Sciences Bachelor - Biochemistry and molecular biology**
University of Strasbourg
Courses in: Introductory immunology - cell biology - vegetal biology - animal biology - developmental biology. Advanced genetics - biochemistry - molecular biology

Research

Full time

- 01/09/2024- Now **Tenured-track Professor**
University of Strasbourg - Complex System and Translational Bioinformatics team - Laboratoire des sciences de l'ingénieur, de l'informatique et de l'imagerie - ICUBE UMR7357
- Research topics:
- Biodiversity comparative genomics
 - Using AI to boost speed and performance of orthology inference
 - Evolution of exon structure across eukaryotes
- 02/09/2019 - 31/08/2024 **Post-doctoral researcher**
University of Lausanne (UNIL) -Laboratory of Computational Evolutionary Biology, Lausanne.
PI : Christophe Dessimoz
- Research topics :
- Homology determination of alternative transcripts
 - Evaluation of genome annotation quality (protein coding genes)
- 01/10/2018 - 01/08/2019 **Research and Teaching associate**
University of Strasbourg - CSTB - ICube UMR7357, Strasbourg.
Supervisor : Pr Odile Lecompte
- Research topics :
- Exploration of evolutionary and multi-omics networks for biological systems characterization.

01/10/2015 - **PhD**
 14/12/2018 *University of Strasbourg - Complex System and Translational Bioinformatics team - Laboratoire des sciences de l'ingénieur, de l'informatique et de l'imagerie - ICUBE UMR7357*
Supervisor : Pr Odile Lecompte

Research topics :

- *Orthology resource development*
- *Determination of genotype-phenotype relationships by phylogenetic profiling*

Internships

05/01/2015 - **Master Internship (M2S4)**
 31/05/2015 *LBGI Bioinformatics and Integrative Genomics - LBGI - ICube - UMR 7357, Strasbourg.*

Title : Prediction and characterization of ciliary proteins by integration of evolutionary and functional data

04/11/2014 - **Master Internship (M2S3)**
 22/11/2014 *Department of Integrative Structural Biology- Molecular modeling team (IGBMC - UMR 7104), Strasbourg.*

Title : Modeling of the ligand binding domain of PPAR gamma by accelerated molecular dynamics.

23/06/2014 - **Summer internship**
 31/07/2014 *LBGI Bioinformatics and Integrative Genomics - LBGI - ICube - UMR 7357, Strasbourg.*

Title : Implementation and optimization of a phylogenetic profiling protocol.

01/03/2014 - **Master Internship (M1S2)**
 31-03-2014 *LBGI Bioinformatics and Integrative Genomics - LBGI - ICube - UMR 7357, Strasbourg.*

Title : In silico search for molecular patterns recognized by the GGA protein in fungi.

Honors & Awards

21/06/2019 **Thesis prize** of the Université de Strasbourg

22/03/2019 **Thesis prize** of the Strasbourg Society of Biology
"Prize of the Life and Health Sciences Doctoral School"

Teaching & supervision

2019-2022	Post-doctoral teaching missions Practical work supervision and grading. Introduction to programming and introduction to bioinformatics Level: Bachelor 2	~30h / year
2020	SIB Comparative Genomics course Teaching material design and conception(Interactive web interface) and practical work supervision on using tool and public resource for comparative genomics	4h of practicals
2018-2019	Half ATER - Teaching missions Practical work supervision, practicals and exam subject conception Computer science for biologists (Python, Java, Database) Level: L2, L3 Life Science, M1 Bioinformatics	96h

2016-2018	Doctoral contract - Teaching mission Practical work supervision, practicals and exam subject conception Computer science for biologists (Python, Database) and molecular bioinformatics Level: L2, L3 Life Science ; M1, M2 Bioinformatics	64h / years
2016-2022	Master internship supervision and co-supervision 7 students (from 3 weeks to 6 months)	

Other activities & responsibilities

2022	Outreach activity - Mystères de l'UNIL
2022	SATW TecDay, Aarau, Suisse Outreach activity in a highschool. Introduction of comparative genomics's principle around a pedagogic activity.
2018 -2019	CSTB team's PhD students and Post-Docs representation
2017	Science outreach activity - Fête de la Science
2016-2019	Local event planning for ISCB Regional Student Group France - JeBif

Outreach	Journée oser tous les métiers, 2023, Lausanne, Switzerland 2h activity to present the concept of comparative genomics to middle school student Mystères de l'UNIL, 2022, Lausanne, Switzerland Half-day animation of an activity about comparative genomics SATW TecDay, 2022, Aarau, Switzerland One day animation in a high-school. Introduction to the concept of comparative genomics Fête de la Science, 2017, Strasbourg, France Animation of the CSTB team outreach activity
Scientific life	Member of the Quest for Orthologs consortium, 2019- Peer review for <i>Bioinformatics</i>, <i>NAR Genomics and Bioinformatics</i>, <i>Genome Biology</i>, <i>Molecular Biology and Evolution</i>, <i>Methods in evolutionary biology</i>, <i>PLoS Biology</i>
Administrative responsibilities	Assistants (PhD students and Post-Docs) representative for the Dessimoz laboratory at the Assistants Council of the Department, 2023-2024 Representative of the PhD students and Post-Docs for the CSTB team at the PhD students Council of ICube laboratory, 2017-2019
Associative life	Local event organizer for the ISCB Regional Student Group France - JeBif , 2016-2019

Publications in peer-reviewed international journals

As first author

- 01/2024 Y. Nevers, A. Warwick Vesztrocy, V. Rossier, CM. Train, A. Altenhoff, C.Dessimoz, N. Glover
Quality assessment of gene repertoire annotation with OMArk
Nature Biotechnology 2024; on press
- 08/06/2023 Y. Nevers, N. Glover, C.Dessimoz, O. Lecompte
Protein length distribution is remarkably uniform across the tree of life
Genome Biol. 2023 Jun 8;24(1):135. doi: 10.1186/s13059-023-02973-2.
- 22/02/2022 Y. Nevers, T.E.M. Jones, D. Jyothi, B. Yates, M. Ferret, L. Portell-Silva, L. Codo, S. Cosentino, M. Marcet-Houben, A. Vlasova, L. Poidevin, A. Kress, M. Hickman, E. Persson, I. Piližota, C. Guijarro-Clarke, the OpenEBench team, the Quest for Orthologs Consortium, W. Iwasaki, O. Lecompte, E. Sonnhammer, D.S. Roos, T. Gabaldón, D. Thybert, P.D. Thomas, Y. Hu, D.M. Emms, E. Bruford, S. Capella-Gutierrez, M.J. Martin, C. Dessimoz, A. Altenhoff
The Quest for Orthologs orthology benchmark service in 2022
Nucleic Acids Research 2022 Jul 5;50(W1):W623-W632. doi: 10.1093/nar/gkac330
- 28/02/2022 D. Dylus,* Y. Nevers*, AM. Altenhoff, A. Gürtler, C. Dessimoz, NM. Glover
How to build phylogenetic species trees with OMA
F1000Research 2022, 9:511 (<https://doi.org/10.12688/f1000research.23790.2>)
- 08/01/2019 Y. Nevers, A. Kress, A. Defosset, R. Ripp, B. Linard, JD. Thompson, O. Poch, O. Lecompte
OrtholInspector 3.0: open portal for comparative genomics.
Nucleic Acids Research. Database Issue 2019 Jan 8;47(D1):D411-D418. (doi: 10.1093/nar/gky1068)
- 01/08/2017 Y. Nevers, M. Prasad, L. Poidevin, K. Chennen, A. Allot, A. Kress, R. Ripp, H. Dollfus, O. Poch, O. Lecompte
Insights into Ciliary Genes and Evolution from Multi-Level Phylogenetic Profiling
Molecular Biology and Evolution 2017 Aug 1;34(8):2016-2034. (doi: 10.1093/molbev/msx146)

As co-author

- 14/05/2024 V. Rossier, C. Train , Y. Nevers, M. Robinson-Rechavi, C. Dessimoz
Matreex: compact and interactive visualisation for scalable studies of large gene families.
Genome Biol Evol. 2024 May 14:evae100. doi: 10.1093/gbe/evae100. Epub ahead of print. PMID: 38742690.
- 05/01/2024 AM. Altenhoff, A. Warwick Vesztrocy, C. Bernard, CM. Train, A. Nicheperovich, S. Prieto Baños, I. Julca, D. Moi, Y. Nevers, S. Majidian, C. Dessimoz, NM. Glover.
OMA orthology in 2024: improved prokaryote coverage, ancestral and extant GO enrichment, a revamped synteny viewer and more in the OMA Ecosystem.
Nucleic Acids Res. 2024 Jan 5;52(D1):D513-D521. doi: 10.1093/nar/gkad1020.
- 15/04/2022 S. Briand, C. Dessimoz, N. El-Mabrouk, Y. Nevers
A Linear-Time Solution to the Labeled Robinson-Foulds Distance Problem
Systematic Biology, syac028, <https://doi.org/10.1093/sysbio/syac028>
- 05/01/2022 S. Jammali, A. Djossou, WDD. Ouédraogo, Y. Nevers, I. Chegrane, A. Ouangraoua
From pairwise to multiple spliced alignment.
Bioinformatics Advances, Vol. 2, Issue 1, 2022, vbab044. <https://doi.org/10.1093/bioadv/vbab044>

- 22/09/2021 A. Defosset, D. Merlat, L. Poidevin, Y. Nevers, A. Kress, O. Poch, O. Lecompte.
Novel approach combining transcriptional and evolutionary signatures to identify new multiciliation genes
Genes 2021, 12(9), 1452; <https://doi.org/10.3390/genes12091452>
- 02/04/2021 B. Linard, I. Ebersberger, S. McGlynn, N. Glover, T. Mochizuki, M. Patricio, O. Lecompte, Y. Nevers, PD. Thomas, T. Gabaldón, E. Sonnhammer, C. Dessimoz, I. Uchiyama.
Ten years of collaborative progress in the Quest for Orthologs.
Molecular Biology and Evolution. 2021. (<https://doi.org/10.1093/molbev/msab098>)
- 08/01/2021 Altenhoff AM, Train CM, Gilbert KJ, Mediratta I, Mendes de Farias T, Moi D, Nevers Y, Radoykova HS, Rossier V, Warwick Vesztrocy A, Glover NM, Dessimoz C.
OMA orthology in 2021: website overhaul, conserved isoforms, ancestral gene order and more.
Nucleic Acids Res. 2021 Jan 8;49(D1):D373-D379. (doi: 10.1093/nar/gkaa1007.)
- 19/10/2020 A. Defosset, A. Kress, Y. Nevers, R. Ripp, JD. Thompson, O. Poch, O. Lecompte
Proteome-scale detection of differential conservation patterns at protein and sub-protein levels with BLUR.
Genome Biol Evol. 2020 Nov 19;13(1):evaa248. (doi: 10.1093/gbe/evaa248.)
- 04/06/2020 AM.. Altenhoff, J. Garrajo-Ventas, S. Cosentino, D. Emms, NM. Glover, A. Hernández-Plaza, Y. Nevers, V. Sundesha, D. Szklarczyk, JM. Fernández, L. Codó, The Quest For Orthologs Consortium, JL. Gelpi, J. Huerta-Cepas, W. Iwasaki, S. Kelly, O. Lecompte, M. Muffato, MJ. Martin, S. Capella-Gutierrez, PD. Thomas, E. Sonnhammer, C. Dessimoz
The Quest for Orthologs benchmark service and consensus calls in 2020.
Nucleic Acids Res. 2020 Jul 2;48(W1):W538-W545. (doi: 10.1093/nar/gkaa308.)
- 10/02/2020 AL. Ducrest, S. Neuenschwander, E. Schmid-Siegert, M. Pagni, C. Train, D. Dylus, Y. Nevers, A. Warwick Vesztrocy, LM. San-Jose, M. Dupasquier, C. Dessimoz, I. Xenarios, A. Roulin, J. Goudet
New genome assembly of the barn owl (*Tyto alba alba*).
Ecol Evol. 2020 Feb 19;10(5):2284-2298. (doi: 10.1002/ece3.5991.)
- 16/06/2017 A. Allot, K. Chennen, Y. Nevers, L. Poidevin, A. Kress, R. Ripp, JD. Thompson, O. Poch, O. Lecompte
MyGeneFriends: A Social Network Linking Genes, Genetic Diseases, and Researchers.
J Med Internet Res. 2017 Jun 16;19(6):e212. (doi: 10.2196/jmir.6676).

Peer-reviewed book chapter

- 30/10/2020 Y. Nevers, Defosset A., Lecompte O.
Orthology: Promises and Challenges.
In: Pontarotti P. (eds) *Evolutionary Biology—A Transdisciplinary Approach*. Springer, Cham. (https://doi.org/10.1007/978-3-030-57246-4_9)

Preprint

- 31/01/2024 S. Majidian, Y. Nevers, A. Yazdizadeh Kharrazi, A. Warwick Vesztrocy, S. Pascarelli, D.

Moi, N. Glover, A. M Altenhoff, C. Dessimoz
Orthology inference at scale with FastOMA
bioRxiv 2024.01.29.577392 (<https://doi.org/10.1101/2024.01.29.577392>)
Major revisions at Nature Methods

19/09/2023 D. Moi, C. Bernard, M. Steinegger, Y. Nevers, M. Langleib, C. Dessimoz
Structural phylogenetics unravels the evolutionary diversification of communication systems in gram-positive bacteria and their viruses
bioRxiv 2023.09.19.558401 (<https://doi.org/10.1101/2023.09.19.558401>).
In revision for Nature

Communications

Presentations

- 2023 **OMA and OMArk for homology exploration and gene annotation quality control**
Biodiversity Genomics Academy 2023, *Online tutorial*
- 2022 **OMArk: quality assessment of protein-coding gene repertoires**
Biodiversity Genomics 2022, *Online conference*
- Multifacet quality assessment of gene repertoire annotation with OMArk**
Quest for Orthologs 7, *Sitges, Spain*
- 2021 **Protein length distribution is remarkably consistent across Life**
Quest for Orthologs 6.5, *Online conference*
- 2019 **Investigating evolutionary histories with OrtholInspector 3.0**
67th NIBB Conference - 6th Quest for Orthologs Meeting, *Okazaki, Japan*
- Exploitation of large-scale orthology inference for studying genotype-phenotype relationships**
UNIL internal seminar, *Lausanne, Switzerland*
- 2018 **OrtholInspector 3.0: orthology en route to big data**
Strasbourg Bioinformatics meeting, *Strasbourg, France*
- 2016 **Prediction and characterization of ciliary proteins by comparative genomics**
Journées Ouvertes en Biologie, Informatique et Mathématiques 2016, *Lyon, France*
- Prediction and characterization of ciliary proteins by comparative genomics**
Journées de la Fédération de Médecine Translationnelle de Strasbourg, *Strasbourg, France*

Posters

- 2023 **Large scale orthology inference and phylostratigraphy of birds (Aves)**
[BC]2 - Basel Computational Biology Conference, *Basel, Switzerland*
- Multifacet quality assessment of gene repertoire annotation with OMArk**
SMBE23I *Ferrara, Italy*
- 2022 **OMArk: quality assessment of protein-coding gene repertoires**
ECCB 2022, *Sitges, Spain*
- 2020 **HOTs : Hierarchical Orthologous Transcripts**
SIB days 2020, *Online conference*
- 2018 **OrtholInspector 3.0: keeping up with the flow**
[BC]2 - Basel Computational Biology Conference, *Basel, Switzerland*

- 2017 **OrthoInspector 3.0: orthology en route to big data**
Journées Ouvertes en Biologie, Informatique et Mathématiques 2017, *Lille, France*
- 2016 **Prediction and characterization of ciliary proteins by comparative genomics**
Evolutionary Biology Meeting, *Marseille, France*