

Nacho Molina

CNRS Research Director and Principal Investigator

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Professional Summary

I lead a research team that bridges generative deep learning with biophysical modeling to create large-scale, interpretable models of gene regulation. By integrating single-cell sequencing and imaging data, we generate testable predictions and uncover mechanisms driving gene expression dynamics in health and disease. Our innovative approach has secured more than 3 million Euros in research funding and established strong collaborations with leading labs worldwide. Over the past eight years, we have published more than 20 papers in high-impact journals, developed 5 open-source software, and mentored more than 20 undergraduate and graduate students, while actively contributing to teaching and scientific leadership at IGBMC and the University of Strasbourg.

Research Positions

Group Leader and Research Director

2016 – Now | CNRS – IGBMC. France.

Faculty Lecturer

2016 – Now | University of Strasbourg. France.

Group Leader and Lecturer

2013 – 2016 | University of Edinburgh. UK.

Postdoctoral Researcher

2009 – 2013 | École Polytechnique Fédérale de Lausanne. Switzerland.

Postdoctoral Researcher

2008 – 2009 | University of Basel. Switzerland.

PhD Researcher

2004 – 2008 | University of Basel. Switzerland.

Education and Diplomas

2019 | Habilitation to Direct Research. University of Strasbourg. France.

2013 | Research Leader Program. Institute of Academic Development. University of Edinburgh. UK.

2008 | PhD in Computational Biology. University of Basel. Switzerland.

2004 | MSc Thesis in Quantum Field Theory and Cosmology. NIKHEF. Amsterdam. Netherlands.

2003 | MSc in Fundamental Physics. Universidad Complutense Madrid. Spain.

2001 | BSc in Physics. Universidad Complutense Madrid. Spain.

Fellowships and Awards

2021 | USIAS Fellowship. University of Strasbourg Institute for Advanced Study. France.

2021 | Theory@EMBL Fellowship. EMBL Heidelberg. Germany.

2016 | IDEX Chair for Attracting Research. University of Strasbourg. France.

2016 | INRT LabEx Chair of Excellence. IGBMC. France.

2013 | Chancellor's Fellowship. University of Edinburgh. UK.

2011 | SIB Young Bioinformatician Award. Swiss Institute of Bioinformatics. Switzerland.

2011 | Award for Best Contribution. Centro Stefano Franscini (ETH). Switzerland.

Research Projects and Funding

Current funded projects

- 2025 – 2027 | **The Chan Zuckerberg Initiative: Single-Cell Biology Data Insights** (200K €)
Space-time regulation of biological cycles in cancer. Developing an interpretable VAE to model context-dependent periodic manifold and decipher circadian and cell cycle dynamics in cancer: from regulation to new opportunities for chrono-treatments.
- 2025 – 2028 | **ANR – PRC. Project CellPath** (160K €)
Tracking cellular transitions during natural direct reprogramming at the unique cell level. Novel machine learning approach to identify regulatory activity dynamics during in vivo reprogramming.
- 2024 – 2027 | **ANR – PRCI. Project ChromOrigami** (116K €)
DNA Origami-based nanomachines for epigenetic manipulation of gene transcription. Developing deep learning tools and biophysical modeling to perform imaging analyses and estimate fundamental kinetic rates of transcription controlled by DNA origami nanomachines.
- 2023 – 2027 | **ANR – PRC. Project IKAROS** (160K €)
Linking protein-protein interactions to regulatory function. Modeling protein monomer and dimer DNA binding, and their effects on transcriptional regulation, by combining machine learning and statistical mechanics.
- 2022 – 2026 | **ANR – PRC. Project HUBDYN** (160K €)
Nuclear diffusion of cis-regulatory hubs in transcriptional control. Computational framework based on Gaussian processes and fractional Brownian motion to extract diffusion properties of chromatin and regulatory proteins.
- 2022 – 2025 | **ANR – PRC. Project ECC** (100K €)
Enteroendocrine cells: differentiation and function. Inference of stochastic gene expression dynamics and regulatory activity using RNA velocity and Markov processes on cell networks.
- 2021 – 2024 | **USIAS Fellowship. Project DeepCycle** (140K €)
Modeling gene regulation dynamics across the cell cycle in single embryonic stem cells. Autoencoder-based modeling of RNA velocity to accurately infer gene expression dynamics throughout the cell cycle.
- 2020 – 2024 | **ANR – PRC. Project COACTIVATOR** (150K €)
Determinants of transcription regulation by co-activator complexes. Developing a biophysical model combining dynamical systems, machine learning and Bayesian statistics to elucidate the regulatory roles of co-activators.

Past funded projects

- 2018 – 2022 | **EU International Training Network. PEP-NET** (250K €)
Predictive epigenetics: fusing theory and experiment. Modeling transcription factor mitotic bookmarking in a dynamic chromatin structure.
- 2017 – 2021 | **AAP Systems Biology – Plan Cancer. Project MethTF** (95K €)
Identification of transcription factors causing aberrant DNA methylation in cancer cells. Modeling transcription factor networks underlying cancer conditions.
- 2017 – 2019 | **AAP Osez l'interdisciplinarité! CNRS. Project ChromoDiff** (140K €)
Experimental and theoretical study of nuclear diffusion of transcription factors. Combining genetic engineering, live imaging, stochastic modeling, and Bayesian statistics to uncover how chromatin influences nuclear diffusion.
- 2016 – 2020 | **IDEX Chair Research Attractively** (200K €)
Biophysical models of gene regulation: from chromatin diffusion to transcriptional bursting. Stochastic modeling of transcription factor diffusion on chromatin networks.
- 2016 – 2021 | **INRT LabEx Chair of Excellence package** (400K €)
Towards an integrative biophysical model of gene regulation: Integration of high-throughput ChIP-seq, Hi-C, and single-cell RNA sequencing data using advanced computational models of transcription factor dynamics, stochastic gene expression, and RNA synthesis.
- 2013 – 2016 | **Chancellor's Fellowship package** (200K £).
Stochastic gene regulation and chromatin remodeling: Developing models of gene regulation based on stochastic processes and Bayesian statistics to uncover the impact of chromatin on gene expression stochasticity.
- 2016 – 2027 | **4 PhD Fellowships & 2 Postdoc Fellowships** (630K €)

Teaching Experience

Faculty Lecturer. University of Strasbourg. France

2016 – Now | *Statistical Analysis and Modeling* (PhD course):

Bayesian statistics; machine learning; linear regression models; neural networks. Python programming with scikit-learn and PyTorch.

2020 – 2024 | *Introduction to Systems Biology* (MSc course):

Reaction kinetics; dynamical systems; stochastic processes; stochastic simulations; machine learning; biophysics-informed neural networks; python programming.

Faculty Lecturer. University of Edinburgh. UK

2020 – 2024 | *Quantification in Life Sciences* (Bsc course):

Introduction to systems biology; biological networks; reaction kinetics; introduction to python programming.

2020 – 2024 | *Practical Systems Biology* (MSc course):

Advanced reaction kinetics; stochastic modeling; stochastic simulations; Python programming.

Teaching Assistant. EPFL. Switzerland

2020 – 2024 | *Research Rotational Modules* (MSc course):

Dynamical systems in biology; Matlab programming.

2020 – 2024 | *Project in Bioinformatics and Genomics* (MSc course):

Reproducing bioinformatic analysis from papers.

Workshops and Summer Schools

2020 – 2020 | *EU-ITN PEP-NET Strasbourg Summer School*:

Predictive Epigenetics: Hybrid and stochastic modeling applied to epigenetics; Bayesian inference; machine learning; agent based modeling; research projects.

2015 – 2015 | *Advance Lecture Course on Computational Systems Biology*

Model-based analysis of time series in Biology: Stochastic processes; master equation; hidden Markov models; Markov chain Monte Carlo.

2017 – 2017 | *Summer School: Epigenetics meets Mathematics*. Humboldt University.

Biophysical modeling of gene regulation by integrating live-cell imaging and genome-wide data

2011 – 2011 | *Tutorial at the International Conference on Systems Biology*. Edinburgh.

Theory and analysis of stochastic gene expression: chemical master equation; hidden Markov models; imaging analysis; Bayesian inference.

Supervision and Mentorship

Former Team Members

2022 – 2024 | ANAÏS BARDET: CNRS researcher → Group leader at IGBMC

Understanding transcription factor binding in the context of chromatin

2022 – 2024 | DAVID DE SANTIAGO: Postdoc → Lab head at IGBMC

Decoding cell cycle and differentiation Interplay to enhance cell therapy protocols through single-cell multiomics

2019 – 2023 | KAREN AMARAL: PhD student → Postdoc at University of Stuttgart

Modeling molecular diffusion in the nucleus and its role in gene regulation

2018 – 2022 | SARA JIMENEZ: PhD student → Postdoc at Helmholtz Zentrum München

Computational modeling of the gene regulatory network dynamics during endocrine cell differentiation

2019 – 2020 | CONIC SASCHA: Postdoc → Postdoc at HI-STEM Heidelberg

Analysis of gene regulation dynamics in single living cells using a novel antibody-based imaging approach

2017 – 2022 | ANDREA RIBA: Postdoc → Data Scientist at Leroy Merlin

Deep learning framework to uncover gene regulatory dynamics throughout the cell cycle using RNA velocity

2017 – 2020 | ATTILA ORAVECZ: Postdoc → Postdoc at IGBMC

Characterization of gene regulatory dynamics throughout the cell cycle in single pluripotent stem cells

2017 – 2021 | GUILHERME OLIVEIRA: PhD student → Software Engineer at MathWorks
Modeling chromatin dynamics using Gaussian processes and polymer physics

2017 – 2021 | SERGIO SARNATARO: PhD student → Coordinator of data analysis at Spatial-Cell-ID Lyon
Transcription reactivation kinetics and chromatin structure reorganization after mitosis

2015 – 2016 | NESLIHAN AVCU: Postdoc → Assistant Professor at Dokuz Eylül University
Transcription reactivation kinetics and chromatin structure reorganization after mitosis

2014 – 2018 | URIEL URQUIZA-GARCÍA: co-supervised PhD student → Group leader at University of Düsseldorf
Mathematical model in absolute units for the Arabidopsis circadian oscillator

2014 – 2024 | Supervision of 10 MSc students

Current Team Members

2024 – Now | SOUFIANE OUAHI: PhD student
Modeling gene regulatory networks using biophysics-informed neural networks

2024 – Now | GUIANNI ZANARDELLI: PhD student
Developing an interpretable variational autoencoder to model context-dependent periodic manifold in cancer

2022 – Now | MAULIK NARIYA: Postdoc
A novel dynamical variational autoencoder to uncover the interplay between the cell cycle and cell differentiation

2022 – Now | LASHA DALAKISHVILI : PhD student
Computational modeling of the gene regulatory network dynamics during endocrine cell differentiation

2021 – Now | HUSAIN MANAOGRI: PhD student
Analysis of gene regulation dynamics in single living cells using a novel antibody-based imaging approach

2016 – Now | OLIVIER TASSY: Engineer
Developing databases and web tools to implement the team's computational methods and explore the results

Institutional Responsibilities

2021 – Now | Member of the Artificial Intelligence PhD program of Unistra. France.

2019 – Now | Member of the Scientific Council. IGBMC. France.

2019 – 2021 | Member of the LabEx committee. IGBMC. France.

2019 – 2020 | Organizer of the DSC Department Seminar Series. IGBMC. France.

2018 – 2019 | Member of the Life Sciences Doctoral School selection committee of Unistra. France.

2017 – 2019 | Member of the Data Science Council. University of Strasbourg. France.

2015 – 2016 | Organizer of the SynthSys Seminars Series. University of Edinburgh. UK.

2006 – 2008 | Organizer of the Computational Biology Seminar. University of Basel. Switzerland.

Software and Website

DeepCycle is autoencoder to infer underlying cycling structure in scRNA-seq data and uncover gene regulation during the cell cycle in single cells.

<https://github.com/MolinaLab-IGBMC/DeepCycle>

FateCompass is a flexible computational framework to estimate dynamic stochastic trajectories of gene expression and transcription factor activities during cell-fate decision using single-cell RNA-seq data.

<https://github.com/MolinaLab-IGBMC/fatecompass>

GP-Tool is an user-friendly interphase to analyze the diffusion dynamic of particles in the living cells using Gaussian processes and fractional Brownian motion.

<https://github.com/MolinaLab-IGBMC/GP-Tool>.

FurierCycle is a novel computational approach to uncover fundamental rates of RNA metabolism and chromatin accessibility dynamics during the cell cycle. Results can be explored online.

<https://github.com/MolinaLab-IGBMC/FourierCycle> | <https://molina.igbmc.science/FourierCycle.html>

HiddenFoot is an efficient thermodynamic model to reveal transcription factor and nucleosome binding patterns on single DNA molecules using dynamical programming and stochastic gradient decent

<https://github.com/MolinaLab-IGBMC/HiddenFoot>

Publications

(@) Corresponding senior author. (*) First author. Full list of publications available on Google Scholar

1. *Single-Cell multiomics reveals the oscillatory dynamics of mRNA metabolism during the cell cycle.*
M. K. Nariya, D. Santiago-Algarra, O. Tassy, M. Cerciat, T. Ye, A. Riba and N. Molina[@].
bioRxiv 2024 (Under review in Cell Systems).
2. *Gene-specific RNA homeostasis revealed by perturbation of coactivator complexes.*
F. Forouzanfar, F. Plassard, A. Furst, D. F. Moreno, K. A. Oliveira, L. Tora, N. Molina[@] and M. Mendoza[@].
bioRxiv 2024 (Under revision in Science Advances).
3. *Mammalian promoters are characterised by low occupancy and high turnover of RNA polymerase II*
K. Chatsirisupachai, C. J. I. Moene, R. Kleinendorst, E. Kreibich, N. Molina[@], A. Krebs[@]
bioRxiv 2024 (Under revision in Molecular Systems Biology).
4. *Abundant clock proteins point to missing molecular regulation in the plant circadian clock*
U. Urquiza-Garcia, N. Molina, K.J. Halliday, A.J. Millar
bioRxiv 2024 (Under revision in Molecular Systems Biology).
5. *Competition between transcription and loop extrusion modulates promoter and enhancer dynamics.*
A. Platania, C. Erb, M. Barbieri, B. Molcrette, E. Grandgirard, M. AC. de Kort, K. Meaburn, T. Taylor, V. M. Shchuka, S. Kocanova, G. M. Oliveira, J. A. Mitchell, E. Soutoglou, T. L. Lenstra, N. Molina, A. Papantonis, K. Bystricky, T. Sexton.
Science Advances 2023: In press. (Citations: 14).
6. *Characterization of cell-fate decision landscapes by estimating transcription factor dynamics.*
S. Jiménez, V. Schreiber, R. Mercier, G. Gradwohl[@], N. Molina[@].
Cell Reports Methods 2023: 3 (7), 100512. (Citations: 3).
7. *Cell cycle gene regulation dynamics revealed by RNA velocity and deep-learning.*
A. Riba, A. Oravec, M. Durik, S. Jiménez, M. Cerciat, M. Jung, C. Keime, W. M. Keyes, and N. Molina[@].
Nature Communications 2022: 13 (2865), 1-13. (Citations: 53).
8. *Precise measurements of chromatin diffusion dynamics by modeling using Gaussian processes.*
G. M. Oliveira, A. Oravec, D. Kobi, M. Maroquenne, K. Bystricky, T. Sexton, and N. Molina[@]
Nature Communications 2021: 12 (6184), 1-11. (Citations: 12).
9. *Regulation of transcription reactivation dynamics exiting mitosis.*
S. Sarnataro, A. Riba, and N. Molina[@]
PLoS Computational Biology 2021: 17 (10), e1009354. (Citations: 8).
10. *Molecular co-occupancy identifies transcription factor binding cooperativity in vivo.*
C. Sönmezer, R. Kleinendorst, D. Imanci, G. Barzaghi, L. Villacorta, D. Schübeler, N. Molina, A. Krebs.
Molecular Cell 2021: 81 (2), 255-267. (Citations: 119).
11. *First responders shape a prompt and sharp NFκB-mediated transcriptional response to TNFα.*
S. Zambrano, A. Loffreda, E. Carelli, G. Stefanelli, E. Bertrand, M. E. Bianchi, N. Molina[@], and D. Mazza[@]
iScience 2020: 101529. (Citations: 14).
12. *Temporal specificity and heterogeneity of Drosophila immune cells.*
P. B. Cattenoz, R. Sakr, A. Pavlidaki, C. Delaporte, A. Riba, N. Molina, N. Hariharan, T. Mukherjee, and A. Giangrande.
The EMBO Journal 2020: 29, 24-39. (Citations: 111).
13. *Rfx6 promotes the differentiation of peptide-secreting enteroendocrine cells while repressing genetic programs.*
Piccand, C. Vagne, F. Blot, A. Meunier, A. Beucher, P. Strasser, M. L. Lund, S. Ghimire, L. Nivlet, C. Lapp, N. Petersen, M. S. Engelstoft, C. Thibault-Carpentier, C. Keime, S. J. Correa, V. Schreiber, N. Molina, T. W. Schwartz, A. De Arcangelis, and G. Gradwohl.
Molecular Metabolism 2019: 29, 24-39. (Citations: 56).
14. *Visualization of Endogenous Transcription Factors in Single Cells Using VANIMA.*
S. Conic, D. Desplancq, A. Ferrand, N. Molina, E. Weiss, and L. Tora.
Springer Protocols: Imaging Gene Expression 2019. (Citations: 4).
15. *Imaging of native TFs and histone phosphorylation at high resolution in live cells.*
S. Conic, D. Desplancq, A. Ferrand, V. Fischer, V. Heyer, B. Reina San Martin, J. Pontabry, M. Oulad-Abdelghani, K. Babu N, G. D. Wright, N. Molina, E. Weiss, and L. Tora.
Journal of Cell Biology 2018: 217 (4), 1537-1552. (Citations: 42).

16. *Multiple inputs ensure yeast cell size homeostasis during cell cycle progression.*
C. Garmendia-Torres, O. Tassy, A. Matifas, N. Molina, and G. Charvin.
eLife 2018: 7, e34025. (Citations: 58).
17. *Circadian clock-dependent and-independent posttranscriptional regulation in mouse liver.*
J. Wang, L. Symul, J. Yeung, C. Gobet, J. Sobel, S. Lück, N. Molina, and F. Naef.
PNAS 2018: 115 (8), E1916-E1925. (Citations: 75).
18. *Revealing assembly of a pore forming complex using single-cell kinetic analysis and modeling.*
M. Bischofberger, I. Iacovache, D. Boss, F. Naef, G. van der Goot[®], and N. Molina[®].
Biophysical Journal 2016: 110 (7) 1574-1581. (Citations: 8).
19. *Chromatin structure shapes the search process of transcription factors.*
N. Avcu and N. Molina[®].
bioRxiv 2016. (Citations: 4).
20. *Temperature regulates splicing efficiency of the cold-inducible RNA-binding protein gene Cirbp.*
Gotic, S. Omid, F. Fleury-Olela, N. Molina, F. Naef, and U. Schibler.
Genes & Development 2016: 30 (17) 2005-2017. (Citations: 80).
21. *Interplay between stochasticity and negative feedback leads to pulsed dynamics and distinct gene activity patterns.*
S. Zambrano, M. E. Bianchi, A. Agresti, and N. Molina[®]
Physical Review E 2015: 92 (2) 022711. (Citations: 11).
22. *Structure of silent transcription intervals and noise characteristics of mammalian genes.*
B. Zoller, D. Nicolas, N. Molina, and F. Naef.
Molecular Systems Biology 2015: 11 (7) 1-15. (Citations: 124).
23. *Stimulus-induced modulation of transcriptional bursting in a single mammalian gene.*
N. Molina^{*}, D. M. Suter^{*}, R. Cannavo, B. Zoller, I. Gotic, and F. Naef
PNAS 2013: 110 (51) 20563–20568. (Citations: 159).
24. *MotEvo: Integrated Bayesian probabilistic methods for inferring regulatory sites and motifs on multiple alignments of DNA sequences.*
P. Arnold, I. Erb, M. Pachkov, N. Molina, and E. van Nimwegen.
Bioinformatics 2012: 28 (4) 487-494. (Citations: 112).
25. *Circadian Dbp transcription relies on highly dynamic BMAL1-CLOCK interaction with E boxes and requires the proteasome.*
M. Stratmann, D.M. Suter, N. Molina, F. Naef, U. Schibler.
Molecular Cell 2012: 48 (2), 277-287. (Citations: 115).
26. *Mammalian genes are transcribed with widely different bursting kinetics.*
D. M. Suter^{*}, N. Molina^{*}, D. Gatfield, K. Schneider, U. Schibler, and F. Naef.
Science 2011: 332 (6028) 472-474. (Citations: 1052).
27. *Origins and consequences of transcriptional discontinuity.*
D. M. Suter, N. Molina, F. Naef, and U. Schibler.
Current Opinion in Cell Biology 2011: 23 (6) 657-662. (Citations: 54).
28. *Scaling laws in the functional content of genome across bacterial clades and life-styles.*
N. Molina^{*} and E. van Nimwegen.
Trends in Genetics 2009: 25 (6) 243-247. (Citations: 80).
29. *The evolution of domain-content in bacterial genomes.*
N. Molina^{*} and E. van Nimwegen.
Biology Direct 2008: 3 51. (Citations: 37).
30. *Universal patterns of purifying selection at noncoding positions in bacteria.*
N. Molina^{*} and E. van Nimwegen.
Genome Reserach 2008: 18 (1) 148-160. (Citations: 75).
31. *SwissRegulon: a database of genome-wide annotations of regulatory sites.*
M. Pachkov, I. Erb, N. Molina, and E. Van Nimwegen
Nucleic Acids Research 2007: 35 (1) D127-D131. (Citations: 161).

Selected Conferences and Seminars

2025 Statistical Methods for Post Genomic Data. University of Heidelberg. Germany.	<i>Chair</i>
2025 Seminars Barcelona Collaboratorium for Modeling and Predictive Biology. Spain.	<i>Invited speaker</i>
2024 Quantitative Biology to Molecular Mechanisms. EMBL. Heidelberg. Germany.	<i>Invited speaker</i>
2024 Spatial-Cell-ID Day. ENS Lyon. France.	<i>Keynote speaker</i>
2024 IRMIA: Research in Mathematics, Interactions and Applications. Strasbourg. France.	<i>Keynote speaker</i>
2024 Systems Biology: Global Regulation of Gene Expression. CSHL. USA.	<i>Selected speaker</i>
2023 Basel Computational Seminar Series. Biozentrum. Switzerland.	<i>Invited speaker</i>
2023 Basel Conference on Computational Biology. Switzerland.	<i>Selected speaker</i>
2023 CHORD Workshop on Epigenetic Data Analysis. Lausanne. Switzerland.	<i>Invited speaker</i>
2023 Single Cell Genomics Moving Forward. Barcelona. Spain.	<i>Invited speaker</i>
2022 Keystone Symposium: Single Cell Biology: New Frontiers in the Life Sciences. Italy.	<i>Selected speaker</i>
2022 Biological Oscillators: Design, Mechanism, Function. EMBL Germany.	<i>Selected speaker</i>
2022 Strasbourg Soft Matter Meeting. France.	<i>Invited speaker</i>
2021 FMI Young Investigator Seminar Series. Basel. Switzerland.	<i>Invited speaker</i>
2021 EMBL Blue Seminar Series. Heidelberg. Germany.	<i>Invited speaker</i>
2020 EU-ITN PEP-NET Strasbourg Summer School. Strasbourg. France.	<i>Organizer and lecturer</i>
2019 LabEx: Summer School on Immunology and Genomic Medicine. Strasbourg. France.	<i>Invited speaker</i>
2019 Regulatory Epigenomics: From large data to useful models. EMBO. India.	<i>Invited speaker</i>
2018 EMBL Transcription and Chromatin. Heidelberg. Germany.	<i>Invited speaker</i>
2017 Basel Conference on Computational Biology. Basel. Switzerland.	<i>Selected speaker</i>
2017 Summer School: Epigenetics meets Mathematics. Berlin. Germany.	<i>Co-organizer and lecturer</i>
2017 Chromatin and Epigenetics: from Mechanism to Function. Munich. Germany.	<i>Selected speaker</i>
2016 2nd Computational RNA Biology. Cambridge. UK.	<i>Invited speaker</i>
2016 Bioengineering Seminars. EPFL. Switzerland.	<i>Invited speaker</i>
2015 Advanced Lecture Course on Computational Systems Biology. Aussois. France.	<i>Invited speaker</i>
2014 2nd International SystemsX Conference. Lausanne. Switzerland.	<i>Invited speaker</i>
2014 Bayes Lectures. Edinburgh. UK.	<i>Invited speaker</i>
2014 Conference on Stochastic Biology. Vienna. Austria.	<i>Invited speaker</i>
2014 Biomathematics Seminars. Imperial Collage. London. UK.	<i>Invited speaker</i>
2013 MathBio Seminars. University of Edinburgh. UK.	<i>Invited speaker</i>
2013 Plenary Seminars. San Raffael Scientific Institute. Milan. Italy.	<i>Invited speaker</i>
2013 IGMM Seminars Series. University of Edinburgh. UK.	<i>Invited speaker</i>
2012 Bison Seminars. ETH Zurich. Switzerland.	<i>Invited speaker</i>
2011 Biomath Seminars. INRIA Lyon. Switzerland.	<i>Invited speaker</i>
2011 International Workshop on Stochasticity in Biochemical Reaction Networks. Banff. Canada.	<i>Invited speaker</i>
2010 Tutorial at the International Conference on Systems Biology. Edinburgh.	<i>Organizer and lecturer</i>
2010 Noise in Life. Benasque. Spain.	<i>Selected speaker</i>
2009 CECAM-EPFL Workshop on Computational Systems Biology. Lausanne. Switzerland.	<i>Selected speaker</i>
2009 Conference on Information Processing in Cells and Tissues. Ascona. Switzerland.	<i>Selected speaker</i>
2008 Computational and Experimental Molecular Biology Summer Meeting. Berlin. Germany.	<i>Selected speaker</i>
2007 Conference Biology without Borders. Innsbruck. Vienna.	<i>Selected speaker</i>
2006 Otto Warburg International Summer School. Berlin. Germany.	<i>Selected speaker</i>

References

Institutional Directors and Department Heads:

- **Dr. Manuel Mendoza** | Head of Department and Collaborator
Group Leader at IGBMC – INSERM – University of Strasbourg.
e-mail: mendozam@igbmc.dr phone: +33 388 65 33 13.
- **Prof. Gilles Charvin** | Former Head of Department and Collaborator and Collaborator
Group Leader at GMGM – CNRS – University of Strasbourg.
e-mail: charvin@unistra.fr phone: +33 368 85 19 26.
- **Prof. Andrew Millar** | Former Director head of SynthSys Center and Collaborator
Group Leader at SynthSys Center. University of Edinburgh.
e-mail: andrew.millar@ed.ac.uk phone: +44 131 651 3325.

Teaching and Mentorship:

- **Dr. Daniel Riveline** | Director of the MSc Cell Physics
Group Leader at IGBMC – CNRS – University of Strasbourg.
e-mail: riveline@unistra.fr phone: +33 388 65 51 42.
- **Dr. Leonie Ringrose** | Coordinator of the European Innovative Training Network *PEP-NET*
Head of Science-Kitchen and former Professor at Humboldt University.
e-mail: leonie.ringrose@gmail.com phone: +49 30 2093 49772.

Mentors:

- **Prof. Felix Naef** | Postdoc mentor
Group Leader at Institute of Bioengineering. Ecole Polytechnique Fédérale de Lausanne.
e-mail: felix.naef@epfl.ch phone: +41 21 693 16 21.
- **Prof. Ueli Schibler** | Postdoc mentor
Emeritus at Department of Molecular Biology. University of Geneva.
e-mail: ueli.schibler@unige.ch phone: +41 22 379 61 75.
- **Prof. Erik van Nimwegen** | PhD mentor
Group Leader at Biozentrum. University of Basel.
e-mail: erik.vannimwegen@unibas.ch phone: +41 61 267 15 76.

Collaborators:

- **Dr. Gerard Gradwohl** | Collaborator
Group Leader at IGBMC – INSERM – University of Strasbourg.
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- **Dr. Arnaud Krebs** | Collaborator
Group Leader at European Molecular Biology Laboratory Heidelberg.
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- **Prof. David Suter** | Collaborator
Group Leader at Institute of Bioengineering. Ecole Polytechnique Fédérale de Lausanne.
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- **Prof. Davide Mazza** | Collaborator
Group Leader at Imaging of Gene Regulation. San Raffaele Scientific Institute Milan.
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