Scientific production
Marco Di Stefano

March 9, 2026

Contents

1 Personal information

Born: 30 April, 1985 in Rome, Italy
Citizenship: Italian
Married, one child.

Current position
Chargé de recherche - Section 23 Organisation, expression, évolution des génomes
Chromatin and Cell Biology Group
Institut de Génétique Humaine (IGH) - CNRS UMR9002
141, rue de la Cardonille, 34396 Montpellier, France
Tel: +33 434359968 - E-mail: marco.di-stefano@igh.cnrs.fr
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Education
Nov 2010 - Oct 2014 Ph.D. in Physics and chemistry of biological systems
Scuola Internazionale Superiore di Studi Avanzati (SISSA), Trieste, Italy.
Thesis Structure and dynamics of entangled biopolymers: from knotted DNA to chromosomes.
Date of degree October 16th 2014

Oct 2007 - July 2010 M.sc in Physics (Biophysics)
Sapienza Università di Roma, Roma, Italy.
Thesis Study of the elastic properties of the active site of viral neuraminidases via the Gaussian-β model.
Date of degree July 2010

Sept 2004 - Oct 2007 B.sc in Physics
Sapienza Università di Roma, Roma, Italy
Thesis Application of proton magnetic resonance spectroscopy to study neural activation processes.
Date of degree October 2007

Research experience
Oct 2020 - Sept 2023 *Postdoctoral researcher*
Chromatin and Cell Biology Group
Institut de Génétique Humaine (IGH) - CNRS UMR9002
141, rue de la Cardonille, 34396 Montpellier, France

Nov 2014 - Aug 2020 *Postdoctoral researcher*
Structural Genomics Group
Centre for Genomic Regulation (CNAG-CRG)
Baldiri i Reixac 4, 08028 Barcelona, Spain

Nov 2010 - Oct 2014 *PhD student*
Statistical and Biological Physics
Scuola Internazionale Superiore di Studi Avanzati (SISSA)
Via Bonomea, 265, 34136 Trieste, Italy

2   Summary of the Research activity

Since my PhD studies, my research has focused on modeling chromosome structure and dynamics using tools and methods from polymer physics and computer simulations. Since 2020, I have been building new skills in bioinformatics for the analysis of transcriptomics, epigenomics, genomics, and 3D genomics data, which I used to inform and contextualize my modelling strategies. Within the team, we share similar research interests, but my expertise is largely orthogonal to that of my colleagues: having complementary, interdisciplinary expertise is a valuable resource for addressing complex biological questions.

Over the last years, I have investigated a wide variety of biological questions using bottom-up (hypothesis-driven) methods that aim to build parametric, predictive models based on mechanistic rules inferred from data and experimental observations. In close collaboration with experimental biologists of the team, we develop synergistic approaches that trigger a virtuous cycle: experiments help refine mechanistic rules and improve models, while models help test these new mechanisms and generate new hypotheses.

My main interests and contributions have focused on understanding chromatin regulation and 3D structural organization in eukaryotes, with a particular focus on identifying regulators of 3D genome memory, critical processes that trigger epigenetic memory alterations, and the functional consequences for gene expression regulation. By developing models and computer simulations at multiple scales, my work contributes to better characterizing the dynamical coupling among gene expression, chromatin regulation, and 3D genome organization, as well as to studying novel biophysical phenomena.

3   Publications

A star *, ∗∗, or cross [+] indicates (co-)first, co-second or co-corresponding author, respectively.

3.1   International journals

1. Paldi, F, Szalay, M-F, Dufau, S, **Di Stefano, M**∗∗, Reboul, H, Jost, D, Bantignies, F, Cavalli, G *Transient histone deacetylase inhibition induces cellular memory of gene expression and 3D genome folding.* Nat Genet (2026) 58, 404–417 **Contributions:** Bioinformatic analysis of Micro-C experiments; Development and implementation of the 3D modeling method; Analysis and interpretation of the modelling results; Input to the paper writing.

2. Denaud, S, Sabarís, G, **Di Stefano, M**∗, Papadopoulos, G-L, Schuettengruber, B, Cavalli, G *Determining the functional relationship between epigenetic and physical chromatin domains in Drosophila* Genome Biol (2025) 26, 116 **Contributions:** Bioinformatic analyses of multi-omics datasets and cross-correlation analysis of chromatin loops and gene repression; Input to paper writing.

3. Parreno V, Loubiere V, Schuettengruber B, Fritsch L, Rawal CC, Erokhin M, Győrffy B, Normanno D, **Di Stefano M**, Moreaux J, Butova NL, Chiolo I, Chetverina D, Martinez A-M, Cavalli G. *Transient loss of Polycomb components induces an epigenetic cancer fate.* Nature (2024) 629, 688–696. **Contributions:** Bioinformatic analyses of multi-omics datasets and cross-correlation analysis of transcriptomics and epigenetics; Input to paper writing.

4. Denaud S, Bardou M, Papadopoulos G-L, Grob S, **Di Stefano M**, Nollmann M, Schuettengruber B, Cavalli G. *PRE loops constitute a topological chromatin structure that restricts and specifies enhancer promoter communication.* Nat Struct Mol Biol (2024) 31, 1942–1954 **Contributions:** Bioinformatic analyses of multi-omics datasets and cross-correlation analysis of chromatin loops and gene repression; Input to paper writing.

5. **International Nucleome Consortium**. *3DGenBench: a web-server to benchmark computational models for 3D Genomics.* Nucleic Acids Res (2022) 50(W1):W4-W12. **Contributions:** Development of methods in a web-interface; Input to paper writing.

6. Farabella I, **Di Stefano M**, Soler-Vila P, Marti-Marimon M, Marti-Renom MA. *Three-dimensional genome organization via triplex-forming RNAs.* Nat Struct Mol Biol. (2021) 28:945-954. **Contributions:** Development of the 3D modeling method; Analysis and interpretation of the results; Paper writing.

7. Salari H, **Di Stefano M**, Jost D. *Spatial organization of chromosomes leads to heterogeneous chromatin motion and drives the liquid- or gel-like behavior of chromatin.* Genome Res. (2021) doi:10.1101/gr.275827.121. **Contributions:** Analysis and interpretation of the results; Input to the paper writing.

8. Mendieta-Esteban J, **Di Stefano M**, Castillo D, Farabella I, Marti-Renom MA. *3D reconstruction of genomic regions from sparse interaction data.* NAR genom. bioinform. (2021) 3(1):lqab017. **Contributions:** Development of the 3D modeling method; Analysis and interpretation of the results; Input to the paper writing.

9. Franzini S, **Di Stefano M**, Micheletti C. *essHi-C: Essential component analysis of Hi-C matrices.* Bioinformatics (2021) 37(15):2088–2094. **Contributions:** Conceptualization and design of the essHi-C method; Analysis and interpretation of the results; Paper writing.

10. **Di Stefano M**[+], Nützmann HW, Marti-Renom MA, Jost D. *Polymer modelling unveils the roles of heterochromatin and nucleolar organizing regions in shaping 3D genome organization in Arabidopsis thaliana.* Nucleic Acids Res. (2021) 49(4):1840–1858. **Contributions:** Study conceptualization and design; Development and implementation of the 3D modeling method; Data collection; Analysis and interpretation of the results; Paper writing.

11. Vilarrasa-Blasi R, Soler-Vila P, Verdaguer-Dot N, Russinyol N, **Di Stefano M**, *et al. Dynamics of genome architecture and chromatin function during human B cell differentiation and neoplastic transformation.* Nat. Commun. (2021) 12:651. **Contributions:** Analysis and interpretation of the 3D modeling results.

12. **Di Stefano M**[+], Stadhouders R, Farabella I, Castillo D, Serra F, Graf T, Marti-Renom MA. *Transcriptional activation during cell reprogramming correlates with the formation of 3D open chromatin hubs.* Nat. Commun. (2020) 11(1):2564. **Contributions:** Study conceptualization and design; Conceptualization, design, and implementation of the TADdyn method; Data collection; Analysis and interpretation of the results; Paper writing.

13. Nützmann HW, Doerr D, Ramírez-Colmenero A, Sotelo-Fonseca JE, Wegel E, **Di Stefano M**, Wingett SW, Fraser P, Hurst L, Fernandez-Valverde SL, Osbourn A. *Active and repressed biosynthetic gene clusters have spatially distinct chromosome states.* Proc. Natl. Acad. Sci. U. S. A. (2020) 117(24):13800-13809. **Contributions:** TADbit software application; Analysis and interpretation of the 3D modeling results.

14. Soler-Vila P, Cuscó P, Farabella I, **Di Stefano M**[+], Marti-Renom MA. *Hierarchical chromatin organization detected by TADpole.* Nucleic Acids Res. (2020) gkaa087. **Contributions:** Study conceptualization and design; Conceptualization and design of the TADpole method; Analysis and interpretation of the results; Paper writing.

15. **Di Stefano M**, Di Giovanni F, Pozharskaia V, Gomar-Alba M, Baù D, Carey LB, Marti-Renom MA, Mendoza M. *Impact of chromosome fusions on 3D genome organization and gene expression in budding yeast.* Genetics (2020) 214(3):651-667. **Contributions:** Development of the 3D modeling method; Data collection; Analysis and interpretation of the results; Paper writing.

16. Suma A, **Di Stefano M**, Micheletti C. *Electric-Field-Driven Trapping of Polyelectrolytes in Needle-like Backfolded States.* Macromolecules (2018) 51(12): 4462-4470. **Contributions:** Development of the simulation method; Analysis and interpretation of the results; Paper writing.

17. Cattoni DI, Cardozo-Gizzi, AM, Georgieva M, **Di Stefano M**, Valeri A, Chamousset D, Houbron C, Déjardin S, Fiche J-B, González I, Chang J-M, Sexton T, Marti-Renom MA, Cavalli G, and Nollmann M. *Single-cell absolute contact probability detection reveals chromosomes are organized by multiple low-frequency yet specific interactions.* Nat. Commun. (2017) 8(1):1753. **Contributions:** TADbit software application; Analysis and interpretation of the Hi-C results.

18. **Di Stefano M**[+], Paulsen J, Lien TG, Hovig E, Micheletti C. *Hi-C-constrained physical models of human chromosomes recover functionally-related properties of genome organization.* Sci. Rep. (2016) 6:35985. **Contributions:** Study conceptualization and design; Development of the 3D modeling method; Data collection; Analysis and interpretation of the results; Paper writing.

19. Micheletti C, **Di Stefano M**, and Orland H. *Absence of knots in known RNA structures.* Proc. Natl. Acad. Sci. U. S. A. (2015) 112(7): 2052-2057. **Contributions:** Study conceptualization and design; Data collection; Analysis and interpretation of the results; Paper writing.

20. **Di Stefano M**, Tubiana L, Di Ventra M, Micheletti C. *Driving knots on DNA with AC/DC electric fields: topological friction and memory effects.* Soft Matter (2014) 10(34):6491-6498. **Contributions:** Development of the simulation method; Data collection; Analysis and interpretation of the results; Paper writing.

21. **Di Stefano M**, Rosa A, Belcastro V, di Bernardo D, Micheletti C. *Colocalization of coregulated genes: a steered molecular dynamics study of human chromosome 19.* PLoS Comput. Biol. (2013) 9(3): e1003019. **Contributions:** Development of the 3D modeling method; Data collection; Analysis and interpretation of the results; Paper writing.

3.2   Invited review articles and book chapters

MDS selected the topics to discuss and wrote the contribution for each of the entries in this section.

1. Tubiana L, Alexander GP, Barbensi A, Buck D, Cartwright JHE, Chwastyk M, Cieplak M, Coluzza I, Čopar I, Craik DJ, **Di Stefano M**, et al. *Topology in soft and biological matter.* Physics Reports (2024) 1075, 1-137.

2. **Di Stefano M**, Cavalli G. *Integrative studies of 3D genome organization and chromatin structure.* Curr Opin Struct Biol (2022) 77:102493.

3. **Di Stefano M**[+], Nützmann HW. *Modeling the 3D genome of plants.* Nucleus (2021) 12:65-81.

4. **Di Stefano M**[+], Paulsen J, Jost D, Marti-Renom MA. *4D nucleome modeling.* Curr. Opin. Genet. Dev. (2020) 67, 25-32.

5. **Di Stefano M**, Castillo D, Serra F, Farabella I, Goodstadt MN, Marti-Renom MA. *Analysis, Modeling, and Visualization of Chromosome Conformation Capture Experiments.* (2020) In Bodega B, Lanzuolo C (eds) Capturing Chromosome Conformation. Methods in Molecular Biology, vol 2157. Humana, New York, NY.

6. Rosa A, **Di Stefano M**[+], Micheletti C. *Topological constraints in eukaryotic genomes and how they can be exploited to improve spatial models of chromosomes.* Front. Mol. Biosci (2019) 6: 127.

7. **Di Stefano M**, Paulsen J, Hovig E, Micheletti C. *Physical 3D Modeling of Whole Genomes: Exploring Chromosomal Organization Properties and Principles.* (2019) In Tiana, G, Luca G (eds) Modeling the 3D conformation of genomes. CRC Press.

8. **Di Stefano M**, Marti-Renom MA. *Restraint-Based Modeling of Genomes and Genomic Domains Modeling the 3D Conformation of Genomes.* (2019) In Tiana, G, Luca G (eds) Modeling the 3D conformation of genomes. CRC Press.

9. Burton AS, **Di Stefano M**[*], Lehman N, Orland H, Micheletti C. *Elusive quest of RNA knots.* RNA Biology - Point of View article (2016) 13(2):134-139.

10. Serra F, **Di Stefano M**, Spill YG, Cuartero Y, Goodstadt MN, Baù D, Marti-Renom MA. *Restraint-based three-dimensional modeling of genomes and genomic domains.* FEBS Lett. (2015) 7;589(20 Pt A):2987-95.

3.3   Preprints

1. Jerković I, **Di Stefano M**, Reboul H, Szalay MF, Normanno D, Papadopoulos G-L, Bantignies F, Cavalli G. *A Scaffolding Element Rewires Local 3D Chromatin Architecture During Differentiation.* Posted on bioRxiv on May 24th 2024. **Contributions:** Bioinformatic analyses of multi-omics datasets; cross-correlation analysis of chromatin loops, chromatin domains insulation and transcription; biophysical 3D modelling; paper writing.

2. Sabaris G, **Di Stefano M**, Denaud S, Fritsch L, Popmihaylova AM,Papadopoulos G-L, Schuttengruber B, Cavalli G *Looping specificity of Polycomb response elements requires GAF and a combinatorial code of looping factors.* Posted on bioRxiv on Nov 29th 2025 **Contributions:** Bioinformatic analyses of multi-omics datasets; cross-correlations analyses of chromatin loops and transcription.

3. Akilli N, Puel P-S, **Di Stefano M**, Muzzopappa F, Fritsch L, Erdel F, Jost D, Cheutin T, Cavalli G *Loss of SUMOylation drives aberrant PRC1 clustering and 3D genome rewiring independent of H3K27me3.* Posted on bioRxiv on Feb 6th 2026 **Contributions:** Bioinformatic analyses of the multi-omics data, including RNA-seq, CUT&RUN, and Hi-C.

4   Grants and awards

- Nov. 2018 - 2022 **Genigma Citizen Science project H2020 Program.** ORION Open Science Project [H2020-SwafS-04-2016]. PIs: **Di Stefano M** and Rodriguez Perez JA. Co-PI: Marti-Renom MA. **Budget**: 50,000 €
- Jan. 2020 - Mar. 2020 **Short-term scientific mission Eutopia CA17139.** PIs: **Di Stefano M** and Jost D. **Budget**: 2,500 €
- Nov. 2010 - Oct. 2014 **SISSA Funded PhD studentship** in "Physics and Chemistry of biological systems" to **Di Stefano M. Budget**: 50,000 €

5   Prizes, Mentions, and Distinctions

- May 2020 **Editorial highlight** of Di Stefano *et al.* 2020 in Nature Communications.
- Jan. 2020 **Editorial highlight** of Di Stefano *et al.* 2020 in Genetics.
- Nov. 2016 **Paper highlight** of Di Stefano *et al.* Sci. Rep. 2016 in *How to cram your entire genome into a tiny nucleus* by E. Pennisi in the Latest news of Science.
- May 2013 **Best paper award** for Di Stefano *et al.* 2013 from the Bioinformatics Italian Society.
- Mar. 2013 **Monthly cover** of PLoS Comput Biol for Di Stefano *et al.* 2013, PLoS Computational Biology Issue Image — Vol. 9(3) March 2013.

6   Dissemination activities

During my scientific career, I presented my research in 34 international conferences: **11 times as an invited speaker**, including one as keynote speaker and two at prestigious CECAM conferences gathering world's experts in 3D genome modeling, **10 as a selected speaker** after abstract evaluation, and **13 as a poster presenter**.

6.1   Invited seminars

1. 20 Jul. 2025 **StatPhys29 Satellite Meeting *StatPoly: Polymers and Biopolymers***, Palazzo Franchetti, Venice (IT), *Biophysical models of the genome structural organization.*

2. 18 Dec. 2024 **Alumni meeting 2024**, SISSA, Trieste (IT), *Biophysical models of the genome structural organization.*

3. 05 Sept. 2022 **Keynote speaker at Topology, Physics, and Chemistry of Soft Matter**, University of Trento, Trento (IT), *Structure and dynamics of eukaryotic chromosomes.*

4. 17 Dec. 2020 **International Nucleome Consortium (INC) Academy webinars**, *Epigenomics-based modeling of the Arabidopsis thaliana genome.*

5. 08 Dec. 2020 **Making Citizen Science - drivers, challenges and benefits? Online workshops**, Karolinska Institute (SWE), *Genigma Citizen science project.*

6. 04 Dec. 2019 **Chromosome conformation symposium**, INSA, Toulouse (FR), *Exploring the dimensions of the genome organization: 1D chromatin tracks and 2D interaction maps for generating 4D models.*

7. 05 Dec. 2019 **Bioinformatics seminars**, CRCT, Toulouse (FR), *Bridging the epigenetic features and the genome 3D organization in Arabidopsis thaliana.*

8. 25 Feb. 2019 **IRB Research Nodes Retreat: 3D-4D chromatin structure**, IRB, Barcelona (ES), *4D nucleome modelling reveals transcriptional control through spatial chromatin caging.*

9. 22 Jul. 2019 **LifeTime Unconference**, Barcelona (ES), *Dynamics of gene expression.*

10. 22 Oct. 2018 **Multiscale analysis and reconstruction of chromatin and nuclear organization**, Scuola Normale Superiore, Pisa (IT), *Exploring the time-dependent structural rearrangements of reprogramming loci in mouse using the TADdyn tool.*

11. 02 May 2018 **Epigenetics and Multiscale Genomics**, EPFL-CECAM, Lausanne (CH), *Exploring the time-dependent structural rearrangements of SOX2 locus in mouse using the TADdyn tool.*

12. 22 Jun. 2015 **Integrating genomics with hierarchical physical models of DNA and chromosomes**, ENS de Lyon - CECAM, Lyon (FR), *Colocalization of coregulated genes: A steered molecular dynamics study of human chromosome 19.*

13. 25 May 2018 **Spring College on the Physics of Complex Systems**, ICTP, Trieste (IT), *Multiscale modeling of biomolecules: from small RNAs to chromosomes.*

6.2   Seminars

1. 10 Apr. 2025 **5ème réunion annuelle du GDR Architecture et Dynamique du Noyau et des Génomes (ADN&G)**, Genopolys, Montpellier (FR), *Biophysical models of the genome structural organization.*

2. 28 Nov. 2023 **Workshop on Genome Organizers**, ENS de Lyon, Lyon (FR), *Epigenetic-driven interactions shape the genome organization in A. thaliana.*

3. 02 Oct. 2023 **5ème Rencontre scientifique des Grands Causses**, GDR Architecture et Dynamique du Noyau et des Génomes (ADN&G), Millau (FR), *Unraveling the principles regulating chromosome spatial organization during differentiation.*

4. 04 Jan. 2023 **Workshop around the Mitotic Chromosome**, ENS de Lyon, Lyon (FR), *Biophysical models of the genome structural organization.*

5. 04 Nov. 2019 **II meeting of the European Topology inter-disciplinary Initiative**, Centro de Fisica de Materiales, San Sebastian (ES), *Bridging the epigenetic features and the genome 3D-organization in A. thaliana.*

6. 03 Oct. 2019 **4D Epigenome, University of Padua**, Venice (IT), *Dynamics of gene expression.*

7. 22 Mar. 2019 **IX Annual Chromatin and Epigenetics symposium**, Societat Catalana de Biologia, Barcelona (ES), *Bridging the epigenetic features and the genome 3D organization in Arabidopsis thaliana.*

8. 20 Dec. 2017 **V Jornada de Bioinformàtica i Genòmica**, Societat Catalana de Biologia, Barcelona (ES), *Exploring the time dependent structural rearrangements of SOX2 locus in mouse using the TADdyn tool.*

9. 16 Dec. 2013 **8th Christmas Biophysics Workshop**, Jozef Stefan Institute, Dobrna (SI), *Colocalization of coregulated genes: a steered molecular dynamics approach.*

10. 21 May 2013 **10th Annual BITS meeting**, University of Udine, Udine (IT), *Colocalization of coregulated genes: a steered molecular dynamics study of human chromosome 19.*

11. 24 May 2012 **8th Seminar SIBBM: Frontiers in Molecular Biology**, SIBBM, Palermo (IT), *Gene co-regulation and co-localization in human chromosome 19: a knowledge-based computational approach.*

6.3   Poster presentations

1. 21 Jan. 2026 **Workshop on genome Organizers**, Genopolys, Montpellier (FR), *Biophysical models of the genome compartmentalization.*

2. 03 June 2024 **Polymer physics in cellular organization and function**, CECAM-ES, Zaragoza (ES), *Unraveling the principles regulating chromosome spatial organization.*

3. 30 May 2024 **Quatrième réunion annuelle du GDR ADN&G**, Centre de Biologie Intégrative Toulouse (CBI), Toulouse (FR), *Biophysical models of the Zfp608 locus in mouse cells.*

4. 09 Oct. 2022 **EMBO Conference Series on Nuclear Structure and Dynamics**, Montpellier (FR), *Unraveling the principles regulating chromosome spatial organization.*

5. 13 Nov. 2017 **Multidimensional Genomics: The 3D/4D organization of chromatin**, CRG, Barcelona (ES), *Rearrangement of 3D chromosome position without altered transcription in budding yeast.*

6. 26 Sept. 2016 **Workshop on Knots and Links in Biological and Soft Matter Systems**, ICTP, Trieste (IT), *The elusive quest of RNA knots.*

7. 22 Sept. 2016 **Dynamics of Genome Structure ERC Synergy Project "4DGenome" Workshop**, CRG, Barcelona (ES), *Robustness of gene expression after induced large-scale chromosomal rearrangements in budding yeast.*

8. 20 June 2016 **Genome Architecture in Space and Time**, ICTP, Trieste (IT), *Knowledge-based modelling of Arabidopsis thaliana genome.*

9. 07 Oct. 2015 **EMBO Conference Series on Nuclear Structure and Dynamics**, L'Isle sur la Sorgue (FR), *Knowledge-based modelling of the Arabidopsis thaliana genome.*

10. 10 July 2015 **14th European Conference on Computational Biology**, ISMB, Dublin (IE), *Knowledge-based modelling of the Arabidopsis thaliana genome.*

11. 02 Oct. 2013 **EMBO Conference Series on Nuclear Structure and Dynamics**, L'Isle sur la Sorgue (FR), *Colocalization of coregulated genes: a steered molecular dynamics study of human chromosome 19.*

12. 03 June 2013 **4th Young Research Meeting**, SISSA, Trieste (IT), *Colocalization of coregulated genes: a steered molecular dynamics study of human chromosome 19.*

13. 21 Oct. 2013 **Venice meeting on Fluctuations in small complex systems**, University of Padua, Venice (IT), *Colocalization of coregulated genes: a knowledge-based chromosome model.*

14. 21 Oct. 2013 **Workshop on Physical Virology**, ICTP, Trieste (IT), *Colocalization of coregulated genes: a knowledge-based chromosome model.*

7   Mentoring and supervising activities

- June 2023 - Sept. 2023 **Co-supervisor** with G Cavalli visiting PhD student from Javierre's lab at the Josep Carreras Leukaemia Research Institute (IJC, Barcelona, ES). *Deciphering the role and regulation of spatial-temporal genome architecture in B cells.*

- Nov. 2023 - Jul. 2024 **Co-supervisor** with A Zippo of the Master student M Gilioli from University of Trento - *Reproducing 3D chromatin organization using coarse-grained models based on ATAC and CTCF data.*

- Mar. 2019 - Aug 2020 **Scientific mentor** PhD student M Gonzalez Ramirez in the CRG mentoring program.

- Oct. 2015 - Dec. 2019 **Co-supervisor** with MA Marti-Renom of the PhD student P Soler Villa from CNAG-CRG - *Multi-scale study of the genome architecture and its dynamical facets.*
- Jun. 2019 - Nov. 2019 **Co-supervisor** with MA Marti-Renom of the Visiting PhD student A Merlotti from University of Bologna - *Analysis of genomic alterations in cancer cells via network and statistical approaches.*
- Oct. 2015 - Nov. 2016 **Co-supervisor** with MA Marti-Renom and M Mendoza of the PhD student F Di Giovanni from CRG - *The impact of chromosome positionings in nuclear functions.*

8   Methods and software development

1. **TADphys**. Building on the LAMMPS software, TADphys is a Python library to perform biophysical 3D modelling of genomic regions using molecular dynamics simulations. TADphys has been used for the simulations in Jerković I *et al.* 2024 and it is currently under development for ongoing projects, such as Paldi *et al.* 2026.
   Contributions: Conceptualization, design, development, and implementation.
   Website: https://github.com/cavallifly/TADphys

2. **TADdyn**. Building on the LAMMPS software, TADdyn is a Python library to perform restraint-based genome modeling with molecular dynamics simulations. TADdyn allows quantitative genome structures analysis to characterize the 3D genome over time.
   Contributions: Conceptualization, design, development, and implementation.
   Website: https://github.com/3DGenomes/TADdyn

3. **TADbit**. TADbit is a Python library for Hi-C data analysis and restraint-based modeling of genomes and genomic domains.
   Contributions: Development and implementation.
   Website: https://github.com/3DGenomes/TADbit

4. **TADpole**. TADpole is an R package for identifying the hierarchy of topologically associating domains (TADs) in Hi-C interaction maps.
   Contributions: Conceptualization, design, development, and implementation.
   Website: https://github.com/3DGenomes/TADpole

5. **essHi-C**. essHi-C is a method to extract the specific or essential component of Hi-C matrices from the non-specific portion of the signal that is compatible with random matrices. This method allows for a neat comparison between the experiments in the same or different cell lines in bulk and single-cell Hi-C.
   Contributions: Conceptualization, design, and development.
   Website: https://github.com/stefanofranzini/essHIC

9   Teaching and training activity

- Nov. 2022 **Bioinformatics trainer** in the 3D modeling course *3DAROC22: 3C-based data analysis and 3D reconstruction of chromatin folding* at Instituto Gulbenkian de Ciência (IGC) in Oeiras (PT) for 17 attendants, including PhD students and postdoctoral researchers.
- Oct. 2021 **Bioinformatics trainer** in the 3D modeling online course *3DAROC21: 3C-based data analysis and 3D reconstruction of chromatin folding* at Instituto Gulbenkian de Ciência (IGC) in Oeiras (PT) for 10 attendants, including PhD students and postdoctoral researchers.

- Oct. 2016 **Bioinformatics trainer** in the 3D modeling course *3DAROC16: 3C-based data analysis and 3D reconstruction of chromatin folding* at Instituto Gulbenkian de Ciência (IGC) in Oeiras (PT) for 10 attendants, including PhD students and postdoctoral researchers.

10   Professional activities

Articles for Faculty Opinion

- Cavalli G and **Di Stefano M**: Faculty Opinions Recommendation of [Pang B et al., Nat. Genet. 2020 52(3):254-263]. In Faculty Opinions, 16 May 2021
- Cavalli G, **Di Stefano M** and Bantignies F: Faculty Opinions Recommendation of [Takei Y et al., Nature 2021 590(7845):344-350]. In Faculty Opinions, 30Aug 2021
- Cavalli G, **Di Stefano M** and Bantignies F: Faculty Opinions Recommendation of [Su JH et al., Cell 2020 182(6):1641-1659.e26]. In Faculty Opinions, 31 Aug 2021
- Cavalli G, **Di Stefano M** and Bantignies F: Faculty Opinions Recommendation of [Zenk F et al., Nature 2021 593(7858):289-293]. In Faculty Opinions, 24 Feb 2022

Reviewer for international journals

Nature Communications, Advanced Science, Genome Biology, Biophysical Journal, Nucleic Acids Research, Cell Genomics, PLoS Computational Biology, Journal of Molecular Biology, Genes, Physical Review E, and PLoS One.

Conference organizer

- 06-09 Sept. 2021 **XI Young Researcher Meeting**, University of Trento, Trento (IT)
- 18-21 Jun. 2019 **X Young Researcher Meeting**, Tor Vergata University, Roma (IT)
- 27-28 Sept. 2018 **17th CRG Symposium**, CRG, Barcelona (ES)
- 10-13 Jul. 2018 **IX Young Researcher Meeting**, University of Salerno, Salerno (IT)
- 01 Jun. 2017 **VIII Young Researcher Meeting**, University of Cagliari, Cagliari (IT)

Editor

- 2017-2020 **Proceedings of the Young researcher Meetings editions VIII to XI**

Scientific associations and actions

- 2018 - Present **Member** of the COST actions INC (CA18127) and EUTOPIA (CA17139)
- 2016 - 2022 **Founder and board member** of the International Physicists Network
- 2018 - 2020 **Member** of the COST action INDEPTH (CA16212)

11   Outreach activities

- 28 Nov. 2020 **European Researchers' Night 2020**, CRG (virtual) round table *¿Qué es una comunicación científica efectiva?*, Barcelona (ES). **Contributions**: Invited to the round-table discussion to present the Genigma project. **Audience**: General public.
- 21-22 May 2019 **SURf: Días de Ciencia y Deportes**, Centre Obert Adolescent Raval, Barcelona (ES). **Contributions**: Speaker to explain my research in 3D genomics **Audience**: School-age audience.
- 23 May 2019 **Genigma beta-testing event**, Creative Research Park, Barcelona (ES)
- 29 May 2019 **III Genigma co-creation event**, ENTI PRO campus, Barcelona (ES)
- 09 Mar. 2019 **II Genigma co-creation event**, Sagrada Familia Library, Barcelona

- 23 Jan. 2019 **I Genigma co-creation event**, CRG, Barcelona (ES).
  Contributions: Co-organizer, seminar speaker. **Audience**: Scientists, cancer patients, care-givers, designers, storytellers, software developers, and professional gamers.

- 23 Sept. 2011 **European Researchers' Night 2011**, SISSA, Trieste (IT).
  Contributions: Co-organizer of the SISSA stand and speaker. **Audience**: General public.