

Dr Marco J. Morelli

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PROFESSIONAL EXPERIENCE:

5/2021-present

Open Science Consultant, San Raffaele University, Milan, Italy

Open Science and Research Data Management support to the San Raffaele community: writing of Data Management Plans, training of researchers and students, management of the internal data repository.

3/2018-present

Head of Bioinformatics, Center for Translational Genomics and Bioinformatics, San Raffaele Scientific Institute, Milan, Italy

Scientific supervision and management of all Bioinformatics activities in the center (21 members), both in clinical and research environments. Development of shared infrastructures for coordination of members and reproducibility of work. Application of machine learning techniques to genomic data. Coordination of European genomic projects and Italian initiatives from the Health Ministry.

10/2017-12/2018

Research Data Manager, Istituto Italiano di Tecnologia, Genoa, Italy

Design of policies for data management, sharing and storage for IIT.

2/2012-12/2017

Researcher, Center for Genomic Science of IIT@SEMM, Milan, Italy

NGS data analysis and integration: development of novel analysis methods, computational infrastructures and quantitative models in close interaction with wet-lab scientists. Management of computational resources for computational genomics, supervision of PhD students and postdocs in computational biology, training and supervision of wet-lab scientists in NGS data analysis.

9/2008-12/2011

Postdoctoral Researcher, Theoretical Biology group, University of Glasgow, UK

NGS data analysis of foot-and-mouth disease virus (detection of minority variants). Bayesian modelling the spread of RNA virus with epidemiologic and genetic data.

11/2007-4/2008:

Postdoctoral Researcher, Biochemical Networks group at AMOLF Institute, Amsterdam, the Netherlands

Modelling the bacteriophage λ lysis-to-lysogeny genetic switch.

EDUCATION:

Ph.D. in Biophysics - October 2007

AMOLF Institute, Amsterdam, The Netherlands

Thesis: Fluctuations in Genetic Networks: a Computational Study
Advisors: Prof. D. Frenkel and Prof. P.R. ten Wolde

Diploma of the International School of Advanced Studies (*cum laude*) - November 2002
University of Pavia, Italy

Final project: Complexity in biological and financial systems: analogies and differences

Laurea (M.Sc.) in Theoretical Physics (full grade 110/110 *cum laude*) - June 2002
University of Pavia, Italy
Average grade: 29.8/30

Thesis: Stochastic Processes and Neural Networks to Model Complex Systems
Advisors: Prof. G. Montagna and Prof. O. Nicosini

PROFESSIONAL ACTIVITIES:

Referee for numerous scientific journals (most notable: PLoS Computational Biology, Bioinformatics, BMC Bioinformatics, Journal of Theoretical Biology, Physical Review Letters, Biophysical Journal, PNAS) and BBSRC David Phillips Fellowship.

Speaker at numerous international scientific events (most notable: International Conference for Systems Biology, Cancer Genomics EMBL conference)

TEACHING EXPERIENCE:

- 2021-2022: Lectures in Statistics and Research Integrity (Open Science) for San Raffaele University, Milan
- 2015-2022: Lectures in the “Genomics” and “Bioinformatics” course for SEMM PhD students, Milan
- 2014-2018: Course “R language and genomic applications” for wet-lab scientists.

SKILLS:

Computational

- 10+ years of experience with Unix/Linux O.S.
- Extensive experience of C programming language
- Extensive experience of R programming language
- Knowledge of Mathematica and Matlab environment
- Extensive knowledge of a wide range of software packages for analyzing next-generation sequencing data
- Dynamical models and machine learning (“artificial intelligence”) methods

Soft

- Extensive experience of presenting at international scientific events
- Proficient in scientific writing
- Excellent in building productive work relationships
- Focus-driven, problem solver, mediator, team builder

LIST OF PUBLICATIONS

Papers published on peer-reviewed journals

- 1) F. Frasca, M. Matteucci, M. Leone, **M.J. Morelli**, M. Masseroli, “Accurate and highly interpretable prediction of gene expression from histone modifications”, *BMC Bioinformatics*, **23**, 1 (2022).
- 2) N. Zambrano, G. Froechlich, D. Lazarevic, M. Passariello, A. Nicosia, C. De Lorenzo, **M.J. Morelli**, E. Sasso, “High-Throughput monoclonal antibody discovery from phage libraries: challenging the current preclinical pipeline to keep pace with the increasing mAb demand”, *Cancer*, **14**, 1325 (2022).
- 3) F. Colombo, F. Calesella, M.G. Mazza, E.M.T. Melloni, **M.J. Morelli**, G.M. Scotti, F. Benedetti, I. Bollettini, B. Vai, “Machine learning approaches for prediction of bipolar disorder based on biological, clinical and neuropsychological markers: a systematic review and meta-analysis”, *Neuroscience and Biobehavioral Reviews*, 10455 (2022).
- 4) F. Cianflone, D. Lazarevic, A. Palmisano, G. Fallara, A. Larcher, M. Freschi, G. Dell’Antonio, G.M. Scotti, **M.J. Morelli**, A.M. Ferrara, F. Trevisani, A. Cinque, A. Esposito, A. Briganti, C. Tacchetti, C. Doglioni, A. Del Maschio, F. de Cobelli, R. Bertini, A. Salonia, F. Montorsi, G. Tonon, U. Capitanio, “Radiomic and gEnomic approaches for the enhanced Diagnosis of clear cell Renal Cancer (REDIRECT): a translational pilot methodological study, *Translational Andrology and Urology*, **11**, 149 (2022).
- 5) A.G. Milano, E. Bezzecchi, C. Socci, M. Bissolati, C. Corsini, A. Terulla, G.M. Scotti, S. Cardellini, A. Saibene, **M.J. Morelli**, E. Ruggiero, A. Petrelli, “Fat tissue-derived PD1+ CD4 T Cells are pro-inflammatory and recirculating in obese patients with T2D”, *Obesity*, **29**, 99-100 (2021).
- 6) S. Makieva, G.M. Scotti, D. Lazarevic, E. Giacomini, J. Ottolina, L. Bartiromo, M. Schimberni, A. Alteri, V. Pavone, E. Papaleo, **M.J. Morelli**, G. Tonon, P. Vigano, “Human extracellular vesicles secreted by aneuploid embryos potentiate development of non-invasive PGT-A RNA biomarkers and stimulated MUC1 up-regulation in primary endometrial stromal cells”, *Human reproduction*, **36**, 244-244 (2021).
- 7) P. Pellanda, M. Dalsass, M. Filipuzzi, A. Loffreda, A. Verrecchia, V. Castillo Cano, M. Doni, **M.J. Morelli**, M. Beaulieu, L. Soucek, D. Mazza, M. Mapelli, T. Kress, B. Amati, A. Sabò, “Integrated requirement of non-specific and sequence-specific DNA binding in MYC-driven transcription”, *EMBO journal*, **40** (10), e105464 (2021).
- 8) A. Palmisano, G.M. Scotti, D. Ippolito, **M.J. Morelli**, D. Vignale, D. Gandola, S. Sironi, F. de Cobelli, L. Ferrante, M. Spessot, G. Tonon, C. Tacchetti, A. Esposito, “Chest CT in the emergency department for suspected COVID-19 pneumonia”, *La radiologia medica*, **126** (3), 498-502 (2021).
- 9) A. Bisso, M. Filipuzzi, G.P. Gamarra Figueroa, G. Brumana, F. Biagioni, M. Doni, G. Ceccotti, N. Tanaskovic, **M.J. Morelli**, V. Pendino, F. Chiacchiera, D. Pasini, D. Olivero, S. Campaner, A. Sabò, B. Amati, “Cooperation between MYC and beta-Catenin in liver tumorigenesis requires Yap/Taz”, *Hepatology*, **72** (4), 1430-1433 (2020).
- 10) A. Tesi, S. De Pretis, M. Furlan, M. Filipuzzi, **M.J. Morelli**, A. Andronache, M. Doni, A. Verrecchia, M. Pelizzola, B. Amati, A. Sabò, “An early Myc-dependent transcriptional program orchestrates cell growth during B-cell activation”, *EMBO Reports*, 20(9) (2019).

- 11) G. Maroni, V. Tkachuk, A. Egorov, **M.J. Morelli**, R. Luongo, E. Levantini, F. Blasi, M.C. Magli, D. Penkov, "Prep1 prevents premature adipogenesis of mesenchymal progenitors", *Scientific Reports*, **7** 15573 (2017).
- 12) S. de Pretis, T.R. Kress, **M.J. Morelli**, A. Sabò, C. Locarno, A. Verrecchia, M. Doni, S. Campaner, B. Amati, M. Pelizzola, "Integrative analysis of RNA Polymerase II and transcriptional dynamics upon Myc activation", *Genome Research*, **27**, 1658-1664 (2017).
- 13) S. Rohban, **M.J. Morelli**, F. D'adda di Fagagna, A. Cerutti, S. Campaner, "The cohesin complex prevents Myc-induced replication stress", *Cell Death and Disease*, **8**, e2956 (2017).
- 14) A. Parodi, L. Sangalli, S. Vantini, B. Amati, P. Secchi, **M.J. Morelli**: "FunChIP: an R/Bioconductor package for functional classification of ChIP-seq shapes", *Bioinformatics*, **33**, 2570 (2017).
- 15) M. Rava, A. D'Andrea, M. Doni, T.R. Kress, R. Ostuni, V. Bianchi, **M.J. Morelli**, A. Collino, S. Ghisletti, P. Nicoli, C. Recordati, M. Iascone, A. Sonzogni, L. D'Antiga, R. Shukla, G.J. Faulkner, G. Natoli, S. Campaner, B. Amati, "Mutual epithelium-macrophage dependency in liver carcinogenesis, mediated by ST18", *Hepatology*, **65**, 1708-1719 (2017).
- 16) C. Tonelli, **M.J. Morelli**, A. Sabò, A. Verrecchia, L. Rotta, T. Capra, S. Bianchi, S. Campaner, B. Amati, "Genome-wide analysis of p53-regulated transcription in Myc-driven lymphomas", *Oncogene*, **36**, 2921-2929 (2017).
- 17) E. Donato, O. Croci, A. Sabò, H. Muller, **M.J. Morelli**, M. Pelizzola, S. Campaner, "Compensatory RNA Polymerase 2 loading determines the efficacy and transcriptional selectivity of JQ1 in Myc driven tumours", *Leukemia*, **31**, 479-490 (2016).
- 18) D. Walerych, K. Lisek, R. Sommaggio, S. Piazza, Y. Ciani, E. Dalla, K. Rajkowska, K. Gaweda-Walerych, E. Ingallina, C. Tonelli, **M.J. Morelli**, A. Amato, V. Eterno, A. Zambelli, A. Rosati, B. Amati, J.R. Wisniewski, G. Del Sal, "Proteasome machinery is instrumental in a common gain-of-function program of the p53 missense mutants in cancer", *Nature cell biology*, **18**, 897-909 (2016).
- 19) V. Jalili, M. Matteucci, **M.J. Morelli**, M. Masseroli, "MuSERA: Multiple Sample Enriched Region Assessment", *Briefings in Bioinformatics*, bbw029 (2016).
- 20) V. Bianchi, A. Ceol, A.G. Ogier, S. de Pretis, E. Galeota, K. Kishore, P. Bora, O. Croci, S. Campaner, B. Amati, **M.J. Morelli**, M. Pelizzola, "Integrated systems for NGS data management and analysis: open issues and available solutions", *Frontiers in Genetics*, **7**, 00075 (2016).
- 21) L. D'Artista, A. Bisso, A. Piontini, M. Doni, A. Verrecchia, T.R. Kress, **M.J. Morelli**, G. Del Sal, B. Amati, S. Campaner, "Pin1 is required for sustained B cell proliferation upon oncogenic activation of Myc", *Oncotarget*, **7**, 21786-21798 (2016).
- 22) C. Tonelli, B. Amati, **M.J. Morelli**, "p53 transcriptional programs in B cells upon exposure to genotoxic stress *in vivo*: computational analysis of next-generation sequencing data", *Genomics Data*, **7**, 29-31 (2016).
- 23) K. Kishore, S. de Pretis, R. Lyster, **M.J. Morelli**, V. Bianchi, B. Amati, J.R. Ecker, M. Pelizzola, "methylPipe and compEpiTools: a suite of R packages for the integrative analysis of epigenomics data", *BMC Bioinformatics* **16**, 313 (2015).
- 24) V. Jalili, M. Matteucci, M. Masseroli, **M.J. Morelli**: "Using combined evidence from replicates to evaluate ChIP-seq peaks", *Bioinformatics*, btv293 (2015).

- 25) C. Tonelli, **M.J. Morelli**, S. Bianchi, L. Rotta, T. Capra, A. Sabò, S. Campaner, B. Amati, “Genome-wide analysis of p53 transcriptional programs in B cells upon exposure to genotoxic stress *in vivo*”, *Oncotarget*, **6**, 24611-24626 (2015).
- 26) L. Dardaei, D. Penkov, L. Mathiasen, P. Bora, **M.J. Morelli**, F. Blasi, “Tumorigenesis by Meis1 overexpression is accompanied by a change of DNA target-sequence specificity which allows binding to the AP-1 element, *Oncotarget*, **6**, 25175-25187 (2015).
- 27) S. de Pretis, T. Kress, **M.J. Morelli**, G.E.M Melloni, L. Riva, B. Amati, M. Pelizzola, “INSPECT: a computational tool to infer mRNA Synthesis, Processing and Degradation Dynamics from RNA- and 4sU-seq time course experiments”, *Bioinformatics*, **btv288** (2015).
- 28) M. Pelizzola, **M.J. Morelli**, A. Sabo, T.R. Kress, S. de Pretis, B. Amati, “Selective transcriptional regulation by Myc: experimental design and computational analysis of high-throughput sequencing data”, *Data in brief*, **3**, 40-46 (2015).
- 29) R.J. Orton, C.F. Wright, **M.J. Morelli**, D.J. King, D.J. Paton, D.P. King, D.T. Haydon, “Distinguishing low frequency mutations from RT-PCR and sequencing errors in viral deep sequencing data”, *BMC Genomics*, **16**, 229 (2015).
- 30) I. Barozzi, P.Bora, **M.J. Morelli**: “Comparative evaluation of DNase-seq footprint identification strategies”, *Frontiers in Genetics*, **5**, 278 (2014).
- 31) A. Sabo, T.R. Kress, M. Pelizzola, S. de Pretis, M.M. Gorski, A. Tesi, **M.J. Morelli**, P. Bora, M. Doni, A. Verrecchia, C. Tonelli, G. Faga, V. Bianchi, A. Ronchi, D. Low, H. Muller, E. Guccione, S. Campaner, B. Amati: “Selective transcriptional regulation by cellular growth control and lymphomagenesis”, *Nature*, **511**, 488 (2014).
- 32) R.J. Orton, C.F. Wright, **M.J. Morelli**, N. Juleff, G. Thebaud, N.J. Knowles, B. Valdazo-Gonzales, D.J. Paton, D.P. King, D.T. Haydon: “Observing micro-evolutionary processes of viral populations at multiple scales”, *Philosophical Transactions of the Royal Society B: Biological Sciences*, **368**, 1614 (2013).
- 33) **M.J. Morelli**, C.F. Wright, N.J. Knowles, N. Juleff, D.J. Paton, D.P. King, D.T. Haydon: “Evolution of foot-and-mouth disease virus intra-sample diversity during serial transmission in bovine hosts”, *Veterinary Research*, **44**, 1 (2013).
- 34) **M.J. Morelli**, G. Thebaud, J. Chadoeuf, D.P. King, D.T. Haydon, S. Soubeyrand: “A Bayesian inference framework to reconstruct transmission trees using epidemiological and genetic data”: *PLoS computational biology*, **8**, e1002768 (2012).
- 35) F. Martinez, G. Lafforgue, **M.J. Morelli**, F. Gonzalez-Candelas, N.H. Chua, J.A. Daros, S.F. Elena: “Ultradeep sequencing analysis of population dynamics of virus escape mutants in RNAi-mediated resistant plants”, *Molecular Biology and Evolution*, **mss135** (2012).
- 36) **M.J. Morelli**, R.J. Allen. P.R. ten Wolde: “Effects of macromolecular crowding on genetic networks”, *Biophysical Journal* **101**, 2882 (2011).
- 37) **M.J. Morelli**, C.F. Wright, N.J. Knowles, G. Thebaud, P. Herzyk, D. J. Paton, D.T. Haydon, D.P. King: “Beyond the consensus: dissecting within-host viral population diversity of foot-and-mouth disease virus using next-generation genome sequencing”, *Journal of Virology*, **85**, 2266 (2011).
- 38) G. Thebaud, J. Chadoeuf, **M.J. Morelli**, J.W. McCauley, and D.T. Haydon: “The relationship between mutation frequency and replication strategy in positive-sense single-stranded RNA viruses”, *Proceedings of the Royal Society B-Biological Sciences* **277**, 1682, 809-817 (2010).

- 39) **M.J. Morelli**, P.R. ten Wolde, R.J. Allen: "Modeling the bacteriophage lambda switch: DNA looping causes stability and robustness", *Proceedings of the National Academy of Science USA*, **20**, 8101-8106 (2009).
- 40) **M.J. Morelli**, P.R. ten Wolde: "Reaction Brownian dynamics and the effect of spatial fluctuations on the gain of a push-pull network", *Journal of Chemical Physics*, **129**, 054112 (2008).
- 41) **M.J. Morelli**, R.J. Allen, S. Tanase-Nicola, P.R. ten Wolde, "Eliminating fast reactions in stochastic simulations of biochemical networks: a bistable genetic switch", *Journal of Chemical Physics*, **128**, 045105 (2008).
- 42) **M.J. Morelli**, R.J. Allen, S. Tanase-Nicola, P.R. ten Wolde, "Reaction coordinates for the flipping of genetic switches", *Biophysical Journal*, **94**, 3413 (2008).
- 43) C. Valeriani, **M.J. Morelli**, R.J. Allen, P.R. ten Wolde, D. Frenkel: "Computing stationary distributions in equilibrium and nonequilibrium systems with Forward Flux Sampling", *Journal of Chemical Physics*, **127**, 114109 (2007). Selected for the Virtual Journal of Biological Physics Research, **14**, Oct 1st 2007
- 44) J.S. van Zon, **M.J. Morelli**, P.R. ten Wolde, "Diffusion of transcription factors enhances the noise in gene expression", *Biophysical Journal*, **91**, 4350 (2006).
- 45) **M.J. Morelli**, G. Montagna, O. Nicrosini, M. Treccani, M. Farina, P. Amato, "Pricing financial derivatives with neural networks", *Physica A*, **338**, 160 (2004).
- 46) G. Montagna, **M.J. Morelli**, O. Nicrosini, P. Amato, M. Farina: "Pricing financial derivatives by path integral and neural networks", *Physica A*, **324**, 189 (2003).

Milano, 31/5/2023