Giulio Caravagna, PhD

Group Leader, *Cancer Data Science Laboratory, University of Trieste*

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Keywords	*Cancer Data Science; Artificial Intelligence; Bioinformatics; Computational Biology.*

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Academic achievements

Current positions

> 2020	Researcher (tenure track), Department of Mathematics and Geoscience, University of Trieste, Trieste, Italy
> 2020	Visiting scientist, Centre for Evolution and Cancer, Institute for Cancer Research, London, UK

Education

2017 - 20	Institute for Cancer Research, London, UK. Postdoctoral training on *Tumour evolution* with Prof Andrea Sottoriva (Laboratory for evolutionary genomics and modelling).
2015 - 17	University of Edinburgh, Edinburgh, UK. Postdoctoral training on *Machine Learning* with Prof Guido Sanguinetti (Laboratory for Machine Learning for Biology).
2011 - 15	University of Milan-Bicocca, Milan, Italy. Postdoctoral training on *Systems Biology* with Prof Giancarlo Mauri (Milan-Bicocca Bioinformatics Laboratory).
2008 -10	PhD in Computer Science (*with fellowship*), University of Pisa, Italy (with Prof R Barbuti).
2007 & 2005	MSc and BSc *cum laude* in Computer Science, University of Pisa, Italy.

Qualifications: Associate professor in *Informatics* (2021), *Molecular Biology* (2021) and *Computer engineering* (2020) issued by the Ministry of University and Education, Italy.

Research grants

2021 - 25	Principal Investigator (500.000 EUR). My First AIRC Grant, Italian Association for Cancer Research. *Characterising genotype and phenotype clonal evolution of response to therapy with Artificial Intelligence*
2021 - 22	Principal Investigator (3.200 EUR), Microgrant program, University of Trieste

Awards and patents

2016	Travel grant (400 EUR). 15th Symposium Evolution and Medicine, CRG, Barcelona
2016	Silver Award (2.000 USD). Open Source Software World Challenge, Ministry of Science of South Korea
2014	Best interdisciplinary paper of the year, Department of Informatics, University of Milan-Bicocca
2013	US Patent nr. 61896566. *Methods, computer-accessible medium and systems to model disease progression*

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	using biomedical data from multiple patients. Owners: University of Milan-Bicocca & New York University.

Teaching and mentoring

Teaching

Graduate and undergraduate level

> 2020	*Genome Data Analytics* (24h), MSc in Data Science and Scientific Computing, University of Trieste, Trieste
> 2020	*Programming* (48h), BSc in Artificial Intelligence and Data Analytics, University of Trieste, Trieste
2021	*Introduction to Python* (8h), PhD program in Theoretical and Scientific Data Science, SISSA, Trieste
2018	Tumour evolution: essential principles (4h), Institute of Cancer Research, London
2017	Data Science approaches for Cancer Evolution (8h), CODATA-RDA Applied workshop on Bioinformatics, International Centre for Theoretical Physics, Trieste
2010	*Programming* (48h), BSc in Mathematics, University of Pisa, Pisa

PhD faculty

> 2020	*Applied Data Science and Artificial Intelligence*, University of Trieste, Trieste (core)
> 2020	*Theoretical and Scientific Data Science*, SISSA, Trieste (external).

Supervisor experience

Postdoctoral scientists

> 2021	Nicola Calonaci. *Artificial Intelligence for cancer clonal evolution*, University of Trieste
> 2020	Rirccardo Bergamin. *Mathematical modelling for evolutionary processes*, University of Trieste

PhD students

2021-24	Alice Antonello. *Applied Data Science and Artificial Intelligence* PhD program, University of Trieste
2021-25	Salvatore Milite. *Computational Biology and Systems Medicine* PhD program, European School of Molecular Medicine (co-supervised with Andrea Sottoriva, Human Technopole)
2020-22	Lucrezia Patruno. *Computer Science* PhD program, University of Milan-Bicocca (co-supervised with A Graudenzi and M Antoniotti, University of Milan-Bicocca)
2015-18	Daniele Ramazzotti. *Computer Science* PhD program, University of Milan-Bicocca (reader)

Others: supervised >15 BSc projects, MS theses and postgraduate Erasmus+ students.

Scientific activities

Editorial activity

> 2020	Associate editor, Statistical Applications in Genetics and Molecular Biology. de Gruyter, Germany

Organisation of scientific events

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Conferences and Workshops

2016	*Computational Intelligence methods for Bioinformatics and Biostatistics* (CIBB), University of Stirling
2013	*Italian Workshop on Artificial Life and Evolutionary Computation* (WIVACE), University of Milan-Bicocca

Summer schools

2014 & 2015	*Cancer Evolution and Complexity,* Lake Como School of Advanced Studies, Italy

Program Committees: member for the following Computer Science conferences, workshops and symposia: HSB 2019; CIBB 2014 & 2017; BIOINFORMATICS 2017 & 2018; CIBCB 2016; CMSB 2016 & 2018; SASB 2016; DataMod 2016 & 2017; MoKMaSD 2013, 2014 & 2015; WIVACE 2013 & 2014; ECAL 2013.

Expert reviewer

2021	*Continuation Funding.* Rosetree Trusts, UK
2020	*Connect Talent research program*. Région Pays de la Loire, France
2020	*Contributions of mathematics and informatics to oncology*. Aviesan, France
2018	*Methodological Panel*. Medical Research Council, UK
2017	*Preclinical research into liquid biopsies.* Stand Up To Cancer, Belgium

Other affiliations

> 2022	Faculty Advisor, Regional Student Group of the International Society for Computational Biology.
> 2021	National Laboratory of Artificial Intelligence and Intelligent Systems, Italian Informatics Consortium.
> 2019	Genomics England Clinical Interpretation Partnership (GeCIP) member for *colorectal, haematological, endometrial, pediatric and glioma*, Genomics England, UK

Panel member: Bioinformatics manager positions (Human Technopole), postdoctoral positions in Computer Science (University of Trieste) and Statistical Physics (SISSA), Fellowships for the MSc in Data Science and Scientific Computing (University of Trieste, SISSA, Collegio Fonda), Fellowships the MSc in Mathematics (Collegio Fonda).

Scientific papers

Legend: *first or joint-first author* (❙), *senior author* (❙), *corresponding author* (❙), *selected papers* (highlighted)

Journal papers (with peer-review)

2021	1. Angaroni F, Chen K, Damiani C, Caravagna G, Graudenzi A, Ramazotti D. PMCE: efficient inference of expressive models of cancer evolution with high prognostic power. **Bioinformatics** (online). 2. Tedesco M, Giannese F, Lazarević D, Giansanti V, Rosano D, Monzani S, Catalano I, Grassi E, Zanella ER, Botrugno OA, Morelli L, Panina Bordignon P, Caravagna G, Bertotti A, Martino G, Aldrighetti L, Pasqualato S, Trusolino L, Cittaro D, Tonon G. Chromatin Velocity reveals epigenetic dynamics by single-cell profiling of heterochromatin and euchromatin. **Nature Biotechnology** (online). 3. ❙❙ Caravagna G, Ramazzotti D. Learning the structure of Bayesian Networks via the bootstrap. **Neurocomputing** 448
2020	4. ❙ Caravagna G, Heide T, Williams MJ, Zapata L, Nichol D, Chkhaidze K, Cross W, Cresswell GD, Werner B, Acar A, Chesler L, Barnes CP, Sanguinetti G, Graham TA, Sottoriva A. Subclonal reconstruction of tumors by using machine learning and population genetics. ***Nature Genetics*** 52(9):898-907.

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	5. Caravagna G, Sanguinetti G, Graham TA, Sottoriva A. The MOBSTER R package for tumour subclonal deconvolution from bulk DNA whole-genome sequencing data. ***BMC Bioinformatics*** 21(1):531. 6. Acar A, Nichol D, Fernandez-Mateos J, Cresswell GD, Barozzi I, Hong SP, Trahearn N, Spiteri I, Stubbs M, Burke R, Stewart A, Caravagna G, Werner B, Vlachogiannis G, Maley CC, Magnani L, Valeri N, Banerji U, Sottoriva A. Exploiting evolutionary steering to induce collateral drug sensitivity in cancer. ***Nature Communications*** 11(1):1923. 7. Caravagna G. Measuring evolutionary cancer dynamics from genome sequencing, one patient at a time. ***Statistical Applications in Genetics and Molecular Biology*** 19(4-6). 8. Maspero D, Damiani C, Antoniotti M, Graudenzi A, Di Filippo M, Vanoni M, Caravagna G, Colombo R, Ramazzotti D, Pescini D. The influence of nutrients diffusion on a metabolism-driven model of a multi-cellular system. ***Fundamenta Informaticae***;171(1-4):279-295.
2019	9. Spiteri I, Caravagna G, Cresswell GD, Vatsiou A, Nichol D, Acar A, Ermini L, Chkhaidze K, Werner B, Mair R, Brognaro E, Verhaak RGW, Sanguinetti G, Piccirillo SGM, Watts C, Sottoriva A. Evolutionary dynamics of residual disease in human glioblastoma. ***Annals of Oncology*** 30(3):456-463. 10. Chkhaidze K, Heide T, Werner B, Williams MJ, Huang W, Caravagna G, Graham TA, Sottoriva A. Spatially constrained tumour growth affects the patterns of clonal selection and neutral drift in cancer genomic data. ***PLoS Computational Biology*** 2019;15(7):e1007243. 11. Ramazzotti D, Graudenzi A, De Sano L, Antoniotti M, Caravagna G. Learning mutational graphs of individual tumour evolution from single-cell and multi-region sequencing data. ***BMC Bioinformatics*** 2019;20(1):210.
2018	12. Heide T, Zapata L, Williams MJ, Werner B, Caravagna G, Barnes CP, Graham TA, Sottoriva A. Reply to "Neutral tumor evolution?" ***Nature Genetics*** 2018;50(12):1633-1637. 13. Caravagna G, Giarratano Y, Ramazzotti D, Tomlinson I, Graham TA, Sanguinetti G, Sottoriva A. Detecting repeated cancer evolution from multi-region tumor sequencing data. ***Nature Methods*** 2018;15(9):707-714. 14. Ramazzotti D, Graudenzi A, Caravagna G, Antoniotti M. Modeling Cumulative Biological Phenomena with Suppes-Bayes Causal Networks. ***Evolutionary Bioinformatics*** 14:1176934318785167. 15. d'Onofrio A, Caravagna G, de Franciscis S. Bounded noise induced first-order phase transitions in a baseline non-spatial model of gene transcription. ***Physica A: Statistical Mechanics and its Applications*** 492(C), 2018.
2016	16. Caravagna G, Graudenzi A, Ramazzotti D, Sanz-Pamplona R, De Sano L, Mauri G, Moreno V, Antoniotti M, Mishra B. Algorithmic methods to infer the evolutionary trajectories in cancer progression. ***PNAS.*** 2016;113(28):E4025-E4034. 17. De Sano L, Caravagna G, Ramazzotti D, Graudenzi A, Mauri G, Mishra B, Antoniotti M. TRONCO: an R package for the inference of cancer progression models from heterogeneous genomic data. ***Bioinformatics***. 2016;32(12):1911-1913. 18. Paroni A, Graudenzi A, Caravagna G, Damiani C, Mauri G, Antoniotti M. CABeRNET: a Cytoscape app for augmented Boolean models of gene regulatory NETworks. ***BMC Bioinformatics.*** 2016;17:64. 19. de Franciscis S, Caravagna G, Mauri G, d'Onofrio A. Gene switching rate determines response to extrinsic perturbations in the self-activation transcriptional network motif. ***Scientific Reports*** 6:26980.
2015	20. Ramazzotti D, Caravagna G, Olde Loohuis L, Graudenzi A, Korsunsky I, Mauri G, Antoniotti M, Mishra B. CAPRI: efficient inference of cancer progression models from cross-sectional data. ***Bioinformatics***. 31(18):3016-3026. 21. Rubinacci S, Graudenzi A, Caravagna G, Mauri G, Osborne J, Pitt-Francis J, Antoniotti M. CoGNaC: A Chaste Plugin for the Multiscale Simulation of Gene Regulatory Networks Driving the Spatial Dynamics of Tissues and Cancer. ***Cancer Informatics*** 2015;14(Suppl 4):53-65. 22. Caravagna G, De Sano L, Antoniotti M. Automatising the analysis of stochastic biochemical time-series. ***BMC Bioinformatics*** 16 Suppl 9:S8.
2014	23. Olde Loohuis L, Caravagna G, Graudenzi A, Ramazzotti D, Mauri G, Antoniotti M, Mishra B. Inferring tree causal models of cancer progression with probability raising. ***PLoS One.*** 9(10):e108358.

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	24. ❙ Graudenzi A, Caravagna G, De Matteis G, Antoniotti M. Investigating the relation between stochastic differentiation, homeostasis and clonal expansion in intestinal crypts via multiscale modeling. ***PLoS One*** 9(5):e97272. 25. ❙❙ Caravagna G, d'Onofrio A, Antoniotti M, Mauri G. Stochastic Hybrid Automata with delayed transitions to model biochemical systems with delays. ***Information and Computation*** 236:19-34.
2013	26. ❙ Caravagna G, Mauri G, d'Onofrio A. The interplay of intrinsic and extrinsic bounded noises in biomolecular networks. ***PLoS One*** 8(2):e51174. 27. Antoniotti M, Bader GD, Caravagna G, Crippa S, Graudenzi A, Mauri G. GESTODIFFERENT: a Cytoscape plugin for the generation and the identification of gene regulatory networks describing a stochastic cell differentiation process. ***Bioinformatics*** 29(4):513-514. 28. Caravagna G, Graudenzi A, d'Onofrio A. Distributed delays in a hybrid model of tumor-immune system interplay. ***Mathematical Biosciences and Engineering*** 10(1):37-57.
2012	29. ❙ Caravagna G, Barbuti R, d'Onofrio A. Fine-tuning anti-tumor immunotherapies via stochastic simulations. ***BMC Bioinformatics*** 13 Suppl 4:S8. 30. Caravagna G, Hillston J. Bio-PEPAd: A non-Markovian extension of Bio-PEPA. ***Theoretical Computer Science*** 419:26-49. 31. Barbuti R, Caravagna G, Maggiolo-Schettini A, Milazzo P, Tini S. Foundational aspects of multiscale modeling of biological systems with process algebras. ***Theoretical Computer Science*** 431:96-116.
2010	32. Caravagna G, d'Onofrio A, Milazzo P, Barbuti R. Tumour suppression by immune system through stochastic oscillations. ***Journal of Theoretical Biology*** 265(3):336-345.
2009	33. Barbuti R, Caravagna G, Maggiolo-Schettini A, Milazzo P. An intermediate language for the stochastic simulation of biological systems. ***Theoretical Computer Science*** 410(33):3085-3109.

Preprints under review (*the journal where the paper is under review is reported*)

2022	1. ❙❙ Mitchell J, Zarowiecki M, Genomics England Research Consortium, Sosinsky A, Caravagna G. Assessing tumour-in-normal contamination levels in high-quality whole-genome sequencing assays.
2021	2. ❙❙ Milite S, Bergamin R, Patruno L, Calonaci N, Caravagna G. A Bayesian method to cluster single-cell RNA sequencing data using Copy Number Alterations. ***Bioinformatics*** 3. ❙❙ Househam J, Bergamin R, Milite S, Calonaci N, Cross WCH, Caravagna G. Integrated quality control of allele-specific copy numbers, mutations and tumour purity from cancer whole genome sequencing assays. ***Nature Computational Sciences*** 4. Househam J, Heide T, Cresswell GD, Lynn C, Spiteri I, Mossner M, Kimberley C, Gabbutt C, Lakatos E, Fernandez-Mateos J, Chen B, Zapata L, James C, Berner A, Schmidt M, Baker A-M, Nichol D, Costa H, Mitchinson M, Jansen M, Caravagna G, Shibata D, Bridgewater J, Rodriguez-Justo M, Magnani L, Sottoriva A, Graham TA. Phenotypic plasticity and genetic control in colorectal cancer evolution. ***Nature*** 5. Heide T, Househam J, Cresswell GD, Spiteri I, Lynn C, Kimberley C, Mossner M, Zapata L, Gabbutt C, Ramazzotti D, Chen B, Fernandez-Mateos J, James C, Vinceti A, Berner A, Schmidt M, Lakatos E, Baker A-M, Nichol D, Costa H, Mitchinson M, Werner B, Iorio F, Jansen M, Barnes C, Caravagna G, Shibata D, Bridgewater J, Rodriguez-Justo M, Magnani L, Graham TA, Sottoriva A. ***Nature*** 6. Assessment of the evolutionary consequence of putative driver mutations in colorectal cancer with spatial multiomic data. Heide T, Househam J, Cresswell GD, Spiteri I, Lynn C, Mossner M, Kimberley C, Fernandez-Mateos J, Chen B, Zapata L, James C, Barozzi I, Chkhaidze K, Nichol D, Berner A, Schmidt M, Lakatos E, Baker A-M, Costa H, Mitchinson M, Jansen M, Caravagna G, Ramazzotti D, Shibata D, Bridgewater J, Rodriguez-Justo M, Magnani L, Graham TA, Sottoriva A. The co-evolution of the genome and epigenome in colorectal cancer. ***Nature*** 7. Verdin IH, Akdemir KC, Ramazzotti D, Caravagna G. Pan-cancer landscape of AID-related mutations,

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	composite mutations and its potential role in the ICI response. ***Cell Systems***
2020	8. Cross W, Mossner M, Nowinski S, Cresswell G, Banerjee A, Williams M, Gay L, Baker A-M, Kimberley C, Davis H, Martinez P, Traki M, Walther V, Smith K, Caravagna G, Amarasingam S, Elia G, Berner A, Choi RC, Ramagiri P, Chauhan R, Matthews N, Murphy J, Antoniou A, Clark S, Aleong J-AC, Domingo E, Spiteri I, McDonald SAC, Shibata D, Lacle MM, Wang LM, Moorghen M, Tomlinson IPM, Novelli M, Jansen M, Watson A, Wright NA, Bridgewater J, Rodriguez-Justo M, Kocher H, Leedham SJ, Sottoriva A, Graham TA. Stabilising selection causes grossly altered but stable karyotypes in metastatic colorectal cancer. ***Nature Genetics*** 9. Zapata L, Caravagna G, Williams M, Lakatos E, Werner B, Graham TA, Sottoriva A. dN/dS dynamics quantify tumour immunogenicity and predict response to immunotherapy. ***Nature Genetics*** 10. Zapata L, Caravagna G, Williams M, Lakatos E, Werner B, Graham TA, Sottoriva A. *Coevolutionary dynamics of cancer cells and the immune system drives tumor heterogeneity and adaptation.* ***PNAS***

Theses

- Formal modeling and simulation of biological systems with delays. PhD Thesis, University of Pisa, 2011.
- An intermediate language for the simulation of biological systems. MSc Thesis, University of Pisa, 2007.
- Development of a simulator of biological systems. BSc Project, University of Pisa, 2004..

Edited volumes (guest editor)

- A Bracciali, G Caravagna, D Gilbert, R Tagliaferri. Computational Intelligence Methods for Bioinformatics and Bio- statistics. LNCS 10477, 2017 (19 Chapters).
- A Graudenzi, G Caravagna, G Mauri. Artificial Life and Evolutionary Computation. Elsevier Natural Computing 13, 2014 (12 Chapters).

Talks

Invited lecturer (phd or postgraduate level)

2022	- *Evolutionary Biology and Ecology of Cancer*, Wellcome Sanger, Cambridge. - *Mathematics of Cancer Evolution*, Centre International de Rencontres Mathématiques, Marseille. - *Genetic evolution of cancer and access to Big Data,* University of Padua, Padua
2021	- School on Cancer: Development and Complexity, Lake Como School of Advanced Studies, Como
2020	- PhD In Systems Medicine: SEMM European School on Molecular Medicine, Virtual.
2017	- CODATA-RDA Applied workshop on Bioinformatics. International Centre for Theoretical Physics, Trieste - School on Cancer: Development and Complexity, Lake Como School of Advanced Studies, Como

Conferences (invited speaker)

2021	- *Somatic Evolution and Tumour Microenvironment Symposium* (SETM), Crick Institute, Virtual.
2020	- *European Lung Cancer Congress: European Society for Molecular Oncology, cancelled due to COVID-19.* - *Cancer Genomes: Methods and Challenges for the Next Decade*, University College London, London
2018	- From Data to Models and Back (DataMod), University of Toulouse, Toulouse.

Invited seminars (institute-level)

2021	- Area Science Park Data Science seminar series, Trieste.
2020	- Computational and Quantitative Biology PhD Seminars: University of Naples Federico II, Naples. - SISSA Data Science Seminar Series, Trieste. - European Laboratory for Learning and Intelligent Systems (ELLIS) Health, Virtual.
2019	- Cancer Institute seminar series, University College London, London - MSCA ITN CONTRA initiative on Tumor Heterogeneity, Bertinoro

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2018	- Lyon Cancer research center, Lyon - Gran Sasso Science Institute, L'Aquila
2016	- School of Mathematics and Statistics, University of Glasgow, Glasgow
, 2015	Department of Information Engineering, University of Padua, Pauda
2012	Department of Computer Science, University of Stirling, Stirling

Other presentations: Bellinzona Institute of Oncology Research (2015), Universitaat der Saarland (2015); TIGET Centre for Gene Therapy (2015), Italian Institute of Technology (2014); European Institute of Oncology (2009); Imperial College London (2009).

Peer-reviewed conference presentations (area Computer Science): CMSB 2019, CMSB 2016, BITS 2014, WIVACE 2013, TSM 2013, HSB 2012, PASTA 2011, BITS 2011, MeCBIC 2010, CompMod 2009, MC 2009, BWMC 2009, FBTC 2007.

References

The following people have agreed to provide reference letters upon request

- Prof Andrea Sottoriva, Director, Centre of Computational Biology, Human Technopole, Milan, Italy and Director, Centre for Evolution and Cancer, Institute for Cancer Research, London, UK (andrea.sottoriva@fht.org)
- Prof Trevor A Graham, Deputy Centre Lead for the Centre for Cancer Genomics and Computational Biology, Group Leader at the Barts Cancer Institute, Queen Mary University of London, UK (t.graham@qmul.ac.uk)
- Prof Guido Sanguinetti, Chair of Data Science, International School for Advanced Studies (SISSA), Trieste, Italy (gsanguin@sissa.it)

L'originale compilato e sottoscritto è depositato presso gli Uffici dell'Ente

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