# Giulio Caravagna, PhD

Associate Professor, Head of the *Cancer Data Science Laboratory, University of Trieste*


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


## Academic achievements

### Current positions

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| > 2022 | Associate Professor, Department of Mathematics and Geoscience, University of Trieste, Trieste, Italy. |
| > 2020 | Visiting scientist, Centre for Evolution and Cancer, Institute for Cancer Research, London, UK |

### Previous positions

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| 2020-22 | Tenure track Researcher, Department of Mathematics and Geoscience, University of Trieste, Trieste, Italy. |
| 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). |

### Education

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| 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. |

**Italian qualifications:** National Scientific Habilitation (ASN) as Associate professor in *Informatics* (2021), *Molecular Biology* (2021) and *Computer engineering* (2020) issued by the Ministry of University and Education, Italy.

### Research grants

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| 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* |
| 2023 - 24 | Principal Investigator (5.000 EUR), Microgrant program, University of Trieste |
| 2021 - 22 | Principal Investigator (3.200 EUR), Microgrant program, University of Trieste |
| 2018-23 | Collaborator (5.500.000 EUR, no budget to GC). CRUK-AIRC Accelerator award (#22790. PI Giovanni Tonon, Hospital San Raffaele). *Single-cell cancer evolution in the clinic.* |

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## Awards and patents

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

# Teaching and mentoring

## Teaching

### Graduate and undergraduate level

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| > 2020 | *Computational Biology* (48h), MSc in Data Science and Scientific Computing, University of Trieste, Trieste |
| > 2020 | *Programming* (72h), 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 level

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| > 2020 | *Core faculty.* PhD program in *Applied Data Science and Artificial Intelligence*, University of Trieste, Italy. |
| > 2020 | *Adjoint member.* PhD program in *Theoretical and Scientific Data Science*, SISSA, Italy. |

## Mentoring

### Postdoctoral scientists

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| > 2021 | Nicola Calonaci. *Artificial Intelligence for clonal evolution and plasticity in Chronic Lymphocytic Leukaemia*, University of Trieste. |
| > 2020 | Riccardo Bergamin. *Mathematical modelling for evolutionary processes underlying immune-escape dynamics in Acute Myeloid Leukaemia*, University of Trieste. |

### PhD students

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| 2022-25 | Lucrezia Valeriani. *Statistical models for genome instability from long-read technologies. Applied Data Science and Artificial Intelligence* PhD program, University of Trieste.<br>Co-supervisor: *Alessio Ansuini and Alberto Cazzaniga, Area Science Park, Trieste.* |
| 2022-25 | Giovanni Santacatterina. *Statistical models for phylogenetic inference from long-read technologies. Applied Data Science and Artificial Intelligence* PhD program, University of Trieste.<br>Co-supervisor: *Leonardo Egidi, University of Trieste.* |



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| 2022-25 | Elena Buscaroli. *Statistical models for high-resolution image demultiplexing. Applied Data Science and Artificial Intelligence* PhD program, University of Trieste. |
| 2021-24 | Alice Antonello. *Timing somatic evolution from bulk sequencing data. Applied Data Science and Artificial Intelligence* PhD program, University of Trieste. |
| 2021-25 | Salvatore Milite. *Longitudinal evolution from single-cell barcoding. Computational Biology* PhD program, European School of Molecular Medicine, Italy.<br>Co-supervisor: *Andrea Sottoriva, Human Technopole.* |
| 2020-22 | Lucrezia Patruno. Aneuploidy inference from joint single-cell RNA and ATAC sequencing assays. *Computer Science* PhD program, University of Milan-Bicocca.<br>Co-supervisor: *Alex Graudenzi and Marco Antoniotti, University of Milan-Bicocca.*<br>Subsequent post: *postdoctoral scientist, University College London.* |

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

## Scientific activities

### Committees

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| > 2022 | Steering committee member. GITMO-RELAPSE Investigator Grant to Fabio Ciceri. Italian Association for Cancer Research (AIRC). |
| > 2022 | Faculty Advisor, Regional Student Group of the International Society for Computational Biology. |

### Editorial activity

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

### Organisation of scientific events

**Conferences and Workshops**

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| 2023 | *Co-Chair. The 15th RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB CCB), Istanbul.* |
| 2016 | *Chair. Computational Intelligence methods for Bioinformatics and Biostatistics* (CIBB), University of Stirling |
| 2013 | *Chair. Italian Workshop on Artificial Life and Evolutionary Computation* (WIVACE), University of Milan-Bicocca |

**Summer schools**

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| 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: ISMB/ECCB MLCSB 2023I; 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

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| 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 |



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2017 *Preclinical research into liquid biopsies.* Stand Up To Cancer, Belgium

## Other affiliations

> 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).

## Administrative tasks

> 2023 Junta board member (elected), Department of Mathematics and Geosciences, University of Trieste, Italy.

> 2023 Student-teachers Quality Control board, Department of Mathematics and Geosciences, University of Trieste, Italy.

## Scientific papers

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

**Journal papers (with peer-review)** *Papers with >3 authors appear as "et al".*

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| 2023 | 1. Zapata L *et al.* Immunoediting dynamics determine tumour immunogenicity and drive response to checkpoint inhibitors. **Nature Genetics**, *in press.*<br>2. Zapata L *et al.* Modeling the coevolutionary dynamics of cancer cells and the immune system using dN/dS. **PNAS**, *in press.* |
| 2022 | 3. Scalera S *et al.* Clonal KEAP1 mutations with loss of heterozygosity share reduced immunotherapy efficacy and low immune cell infiltration in lung adenocarcinoma. **Annals of Oncology,** *in press.*<br>*4.* Hernández-Verdin I *et al.* Pan-cancer landscape of AID-related mutations, composite mutations, and their potential role in the ICI response. **npj Precision Oncology,** *in press.*<br>5. Househam J *et al.* Phenotypic plasticity and genetic control in colorectal cancer evolution. **Nature** 611 (7937), 744-753.<br>6. Heide T *et al.* The co-evolution of the genome and epigenome in colorectal cancer. **Nature** 611 (7937), 733-743 .<br>7. Palles C *et al.* Germline MBD4 deficiency causes a multi-tumor predisposition syndrome. **The American Journal of Human Genetics** 109 (5), 953-960<br>8. ❙❙ 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*** 38(9) (2022) :2512-2518.<br>9. Martin A et al. Signatures of TOP1 transcription-associated mutagenesis in cancer and germline. ***Nature***, 602 623-631 (as part of the *Genomics England Research Consortium*).<br>10. Tedesco M *et al*. Chromatin Velocity reveals epigenetic dynamics by single-cell profiling of heterochromatin and euchromatin. ***Nature Biotechnology*** 40: 235-244. |
| 2021 | 11. Angaroni F *et al.* PMCE: efficient inference of expressive models of cancer evolution with high prognostic power. ***Bioinformatics*** 38 (3): 754-762 .<br>12. ❙❙ Caravagna G, Ramazzotti D. Learning the structure of Bayesian Networks via the bootstrap. ***Neurocomputing*** 448: 48-59. |
| 2020 | 13. ❙ Caravagna G *et al*. Subclonal reconstruction of tumors by using machine learning and population genetics. ***Nature Genetics*** 52(9):898-907. |



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| | 14. ❙ Caravagna G *et al*. The MOBSTER R package for tumour subclonal deconvolution from bulk DNA whole-genome sequencing data. ***BMC Bioinformatics*** 21(1):531.<br>15. Acar A *et al*. Exploiting evolutionary steering to induce collateral drug sensitivity in cancer. ***Nature Communications*** 11(1):1923.<br>16. ❙ Caravagna G. Measuring evolutionary cancer dynamics from genome sequencing, one patient at a time. ***Statistical Applications in Genetics and Molecular Biology*** 19(4-6).<br>17. Maspero D *et al*. The influence of nutrients diffusion on a metabolism-driven model of a multi-cellular system. ***Fundamenta Informaticae***;171(1-4):279-295. |
| 2019 | 18. ❙ Spiteri I, Caravagna G *et al*. Evolutionary dynamics of residual disease in human glioblastoma. ***Annals of Oncology*** 30(3):456-463.<br>19. Chkhaidze K *et al*. Spatially constrained tumour growth affects the patterns of clonal selection and neutral drift in cancer genomic data. ***PLoS Computational Biology*** 2019;15(7):e1007243.<br>20. ❙ 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 | 21. Heide T *et al*. Reply to "Neutral tumor evolution?" ***Nature Genetics*** 2018;50(12):1633-1637.<br>22. ❙❙ Caravagna G *et al*. Detecting repeated cancer evolution from multi-region tumor sequencing data. ***Nature Methods*** 2018;15(9):707-714.<br>23. Ramazzotti D *et al*. Modeling Cumulative Biological Phenomena with Suppes-Bayes Causal Networks. ***Evolutionary Bioinformatics*** 14:1176934318785167.<br>24. 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 | 25. ❙❙ Caravagna G *et al*. Algorithmic methods to infer the evolutionary trajectories in cancer progression. ***PNAS***. 2016;113(28):E4025-E4034.<br>26. ❙ 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.<br>27. ❙ 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.<br>28. 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 | 29. Ramazzotti D *et al*. CAPRI: efficient inference of cancer progression models from cross-sectional data. ***Bioinformatics***. 31(18):3016-3026.<br>30. ❙ Rubinacci S *et al*. 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.<br>31. ❙❙ Caravagna G *et al*. Automatising the analysis of stochastic biochemical time-series. ***BMC Bioinformatics*** 16 Suppl 9:S8. |
| 2014 | 32. ❙ Olde Loohuis L *et al*. Inferring tree causal models of cancer progression with probability raising. ***PLoS One***. 9(10):e108358.<br>33. ❙ Graudenzi A *et al*. Investigating the relation between stochastic differentiation, homeostasis and clonal expansion in intestinal crypts via multiscale modeling. ***PLoS One*** 9(5):e97272.<br>34. ❙❙ Caravagna G *et al*. Stochastic Hybrid Automata with delayed transitions to model biochemical systems with delays. ***Information and Computation*** 236:19-34. |
| 2013 | 35. ❙ Caravagna G, Mauri G, d'Onofrio A. The interplay of intrinsic and extrinsic bounded noises in biomolecular networks. ***PLoS One*** 8(2):e51174.<br>36. Antoniotti M *et al*. 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.<br>37. Caravagna G, Graudenzi A, d'Onofrio A. Distributed delays in a hybrid model of tumor-immune system |



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| | interplay. ***Mathematical Biosciences and Engineering*** 10(1):37-57. |
| 2012 | 38. Caravagna G, Barbuti R, d'Onofrio A. Fine-tuning anti-tumor immunotherapies via stochastic simulations. ***BMC Bioinformatics*** 13 Suppl 4:S8.<br>39. Caravagna G, Hillston J. Bio-PEPAd: A non-Markovian extension of Bio-PEPA. ***Theoretical Computer Science*** 419:26-49.<br>40. Barbuti R *et al*. Foundational aspects of multiscale modeling of biological systems with process algebras. ***Theoretical Computer Science*** 431:96-116. |
| 2010 | 41. Caravagna G *et al*. Tumour suppression by immune system through stochastic oscillations. ***Journal of Theoretical Biology*** 265(3):336-345. |
| 2009 | 42. Barbuti R *et al*. An intermediate language for the stochastic simulation of biological systems. ***Theoretical Computer Science*** 410(33):3085-3109. |

**Preprints**

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| 2022 | 43. 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.<br>44. Cornish A, Gruber A, Kinnersley B, Chubb D, Frangou A, Caravagna et al., Whole genome sequencing of 2,023 colorectal cancers reveals mutational landscapes, new driver genes and immune interactions.<br>45. Kayhanian H *et al.* Mutation Rate Evolution Drives Immune Escape In Mismatch Repair-Deficient Cancer. |
| 2021 | 46. 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. |
| 2020 | 47. Cross W *et al*. Stabilising selection causes grossly altered but stable karyotypes in metastatic colorectal cancer. |

**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)**

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|---|---|
| 2022 | - *Winter School on Quantitative Systems Biology,* ICTP-ICTS, Trieste.<br>- *Evolutionary Biology and Ecology of Cancer*, Wellcome Sanger, Cambridge.<br>- *Mathematics of Cancer Evolution*, Centre International de Rencontres Mathématiques, Marseille.<br>- *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. |



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| 2017 | - CODATA-RDA Applied workshop on Bioinformatics. International Centre for Theoretical Physics, Trieste.<br>- School on Cancer: Development and Complexity, Lake Como School of Advanced Studies, Como. |

**Conferences (invited speaker)**

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| 2023 | - *Measuring tumour aneuploidy from single cell sequencing data.* International Symposium on Single-Cell Transcriptomics, Ankara |
| 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.*<br>- *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)**

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| 2021 | - Area Science Park Data Science seminar series, Trieste. |
| 2020 | - Computational and Quantitative Biology PhD Seminars: University of Naples Federico II, Naples.<br>- SISSA Data Science Seminar Series, Trieste.<br>- European Laboratory for Learning and Intelligent Systems (ELLIS) Health, Virtual. |
| 2019 | - Cancer Institute seminar series, University College London, London<br>- MSCA ITN CONTRA initiative on Tumor Heterogeneity, Bertinoro |
| 2018 | - Lyon Cancer research center, Lyon<br>- Gran Sasso Science Institute, L'Aquila |
| < 2016 | - School of Mathematics and Statistics, University of Glasgow, Glasgow<br>- Department of Information Engineering, University of Padua, Pauda<br>- 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 & 2023), 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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