ALESSANDRO BARBERIS

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EXPERIENCE

2024 - now **Senior Computational Biologist & Project Manager, WhiteLab Genomics**
Computational Biology Team

- Analysing single-cell data to identify cell surface markers for adeno-associated virus (AAV) mediated gene therapy in the retina within the GEAR consortium (**Python**, **R**)
- Defining internal strategy and leading projects on synthetic promoter design to improve transgene transcriptional control for genetic engineering (**R**, **Python**)
- Contributing to the implementation of single-cell RNA-seq computational pipelines (**Python**, **Terra**, **Google Cloud Platform**, **Nextflow**)
- Contributing to code quality by reviewing and providing feedback on code written by junior team members
- Mentoring junior team members

2024 - now **Consultant, Nuffield Department of Surgical Sciences, University of Oxford**
Insulin-like Growth Factor (IGF) laboratory

- Characterising functional effects of IGFs on prostate tumour intrinsic and extrinsic components of the anti-tumour immune response (**R**). Leading role in the analysis of the RNA-seq data generated in the WINGMEN trial (NCT05110495)
- Guiding bioinformatics analysis of in vitro and in vivo prostate cancer samples
- Designing and overseeing the implementation of portable and reproducible bulk RNA-seq computational pipelines (**Nextflow**, **bash**, **R**)
- Supervising and mentoring one junior postdoctoral researcher

2024 - now **Visitor, Nuffield Department of Surgical Sciences, University of Oxford**

- Identifying **unimodal**/**multimodal** prognostic signatures for radical radiotherapy in oesophageal cancer via **artificial intelligence** (AI) techniques, such as **random forests**, **boosted machines**, and **neural networks** (**Python**)
- Evaluating the performance of hypoxia gene signatures using multiple summarisation methods in microarray and bulk/single-cell RNA-seq data across cancer types (**R**)
- Unravelling the relationship between lipidomics and transcriptomics in castration resistant prostate cancer using **AI** techniques (**R**)
- Developed **AI-based models** of hypoxia in breast cancer single-cell RNA-seq data via several **AI** techniques, including least absolute shrinkage and selection operator (**lasso**), **ridge**, and **elastic-net** (**R**)
- Co-supervising one PhD student

2022 - 2023 Senior Researcher, Nuffield Department of Surgical Sciences, University of Oxford
Insulin-like Growth Factor (IGF) laboratory

- Identified immunosuppressive effects of high level of IGF in prostate cancer (**R**)
- Implemented portable and reproducible bulk RNA-seq computational pipelines (**Nextflow**, **bash**, **R**)
- Performed bioinformatics analysis to support different research projects (**R**)

2014 - 2022 Post-doctoral Researcher, Department of Oncology, University of Oxford
Computational Biology and Integrative Genomics (CBIG) group

- Studied the relationship between obesity and gene expression in cancer via **AI** techniques, such as **generalised linear models with L1/L2 penalisation** (**R**). Performed **integrative multi-omics** analysis (methylation, copy number variations, miRNAs, proteomics, genetic variants) and identified potential pleiotropic effects
- Identified robust **AI** model for diagnosing SETD2-mutated renal cancers (**R**)
- Investigated functional consequences of TP53 mutations in human cancers via **AI** (R)
- Developed software to extract genomic data from large public repositories (**R**)
- Implemented novel computational pipelines to analyse microarray and next-generation sequencing data (**R**)
- Created software for robust and reproducible biomedical analysis via **AI** (**R**)
- Identified **machine learning** model of response to radiation in rectal cancer (**R**)
- Designed and implemented frontend/backend of web-based platform for biomarker discovery (**R, HTML5, CSS, Java, JavaScript, jQuery, Spring Framework, Hibernate**)
- Contributed to design and implementation of database for storing health data (**MySQL**)
- Contributed to creation of software for quality control of gene signatures by writing code and reviewing code developed by collaborators (**R**)
- Published in top-tier peer-reviewed journals
- Supported grant applications
- Collaborated with different research groups

2010 - 2013 PhD Research
Custom Computing and Programmable Systems laboratory, University of Pavia

- Gained experience in data processing and high-performance computing using multicore processors, graphics processing units (GPUs), field programmable gate arrays (FPGAs), clusters
- Utilised GPUs and FPGAs technologies to develop real time solutions for image analysis
- Modified popular imaging algorithm to lower computational complexity and developed first-ever parallel solution using different programming languages (**C/C++**, **OpenCL**, **VHDL**, **MATLAB**) and libraries (**BLAS**, **CUDA**, **cuBLAS**, **OpenMP**, **MPI**)
- Created parallel implementation of Monte Carlo simulations code (**C**, **OpenMP**, **MPI**)

- Collaborated with the Hyperspectral Computing Laboratory (University of Extremadura, Spain) and the Laboratory of Complex Fluids and Molecular Biophysics (University of Milan, Italy)

Extra-curricular activities

- Attended extra courses (e.g., in Histology, Physiology, Biology) held either at the University of Pavia and online (e.g., MITx)

HIGHER EDUCATION

2013 **PhD in Electronics, Computer Science and Electrical Engineering**
Faculty of Engineering, University of Pavia (Italy)
Thesis: High-performance computing for highly demanding applications

2010 **MSc in Automation Engineering (110/110 *cum laude*)**
Faculty of Engineering, University of Pavia (Italy)
Thesis: Identification of an order parameter in Monte Carlo simulations of dipolar systems on hexagonal lattices

2007 **BSc in Computer Science Engineering**
Faculty of Engineering, University of Pavia (Italy)
Thesis: Automated fingerprint recognition: software for data handling and validation

PRIZES & AWARDS

2020 Contributed to Medical Research Council Capital Bid (awarded to Department of Oncology, £92,000)
2013 4th position over 40 proposals in the national Altera Design Contest Innovate Italy
2010 Awarded 1 of 6 fully funded PhD scholarships by the University of Pavia for the PhD course in Electronics, Computer Science and Electrical Engineering (~ €45000)

PATENT PENDING

Medical e-Research Linking genomic with clinical data: Merlin, a web-based platform for biomarkers discovery

INVITED TALKS & SEMINARS

2024 Seminar on “Introduction to AI learning in biomedical science” (University of Pisa, Italy)
2019 Seminar on “Obesity and Cancer Metabolism” (University of Oxford, UK)
2018 Invited talk on “Big data in genomics: towards personalised medicine” (Technical University of Madrid, Spain)

TEACHING EXPERIENCE

INTERNATIONAL COURSES

2018 - 2019 *Teaching Assistant* for the RNA transcriptomics course (Wellcome Connecting Science, UK)
2011 *Lecturer* for the Summer School on Data Fusion and High-Performance Computing onboard aircraft (University of Pavia, Italy)

UNIVERSITY LECTURING AND SUPERVISION

University of Pisa (Italy)

2024 - 2025 *Lecturer in Machine Learning* for MSc in Clinical Trials and Methodology

University of Oxford (UK)

2020 - now *Lecturer* in Bioinformatics for MSc in Precision Cancer Medicine
Internal Assessor for MSc in Precision Cancer Medicine
2020 - 2021 *Lecturer* in Statistics for MSc in Radiation Biology
Teaching Assistant for MSc in Radiation Biology
2014 - now *Research co-supervision* at MSc and PhD level, training junior lab members in statistics and bioinformatics

University of Pavia (Italy)

2010 - 2013 *Research co-supervision* at MSc level

PUBLICATIONS

JOURNAL ARTICLES, PEER REVIEWED

1. **Barberis, A.†**, Aerts, H., Buffa, F. M.†, *Robustness and reproducibility for AI learning in biomedical sciences: RENOIR.* Scientific Reports (2024)
2. Rodriguez-Berriguete, G., Puliyadi, R., **Barberis, A.**, Nassiris, I., Prevo, N., McLaughlin, M., Buffa, F. M., Harrington, K., Higgins, G., and Machado, N., *Antitumour effect of the mitochondrial complex III inhibitor Atovaquone in combination with anti-PD-L1 therapy in mouse cancer models*. Cell Death & Disease (2023)
3. **Barberis, A.***, Pasqualetti, F.*, Zanotti, S., Montemurro, N., Lombardi, G., De Salvo, G. L., Soffietti, R., Mazzanti, C. M., Ius, T., Caffo, M., Paiar, F., Bocci, G., Harris, A., Buffa, F. M., *The impact of survivorship bias in recurrent glioblastoma research*. Critical Reviews in Oncology/Hematology 188 (2023)
4. Triantafyllidis, C. P., **Barberis, A.**, Cuervo, A. M., Charlton, P., Hartley, F., Van Bijsterveldt, L., Gjerga, E., Rodriguez, J. S., Buffa, F. M., *A machine learning and directed network optimization approach to uncover TP53 regulatory patterns.* iScience (2023)
5. Javaid, H., **Barberis, A.**, Chervova, O., Voloshin, V., Buffa, F. M., and Humphrey, T., *A role for SETD2 loss in tumorigenesis through DNA methylation dysregulation*. BMC Cancer 23, 721 (2023)
6. Kawashima, M., Bensaad, K., Zois, C., **Barberis, A.**, Bridges, E., Lagerholm, C., Dmitriev, R. I., Toi, M., Papkovsky, D. B., Buffa, F. M., Harris, A. L., *Disruption of hypoxia-inducible fatty acid binding protein 7 induces beige fat-like differentiation and thermogenesis in breast cancer cells.* Cancer & Metabolism 8, 13 (2020)
7. Dhawan, A., **Barberis, A.**, Cheng, W.-C., Domingo, E., West, C., Maughan, T., Scott, J. G., Harris, A. L., Buffa, F. M., *Guidelines for using sigQC for systematic evaluation of gene signatures*. Nature Protocols 14, 1377–1400 (2019)

8. Chen, L., Zeng, X., Kleibeuker, E., Buffa, F. M., **Barberis, A.**, Leek, R. D., Roxanis, I., Zhang, W., Worth, A., Beech, J. S., Harris, A. L., Cai, S., *Paracrine effect of GTP cyclohydrolase and angiopoietin-1 interaction in stromal fibroblasts on tumor Tie2 activation and breast cancer growth*. Oncotarget 7, 9353–9367 (2016)
9. Raducu, M., Fung, E., Serres, S., Infante, P., **Barberis, A.**, Fischer, R., Bristow, C., Thézénas, M. L., Finta, C., Christianson, J.C., Buffa, F. M., Kessler, B. M., Sibson, N. R., Di Marcotullio, L., Toftgård, R., D'Angiolella, V., *SCF (Fbxl17) ubiquitylation of Sufu regulates Hedgehog signaling and medulloblastoma development*. EMBO J. 35,1400–1416 (2016)
10. **Barberis, A.***, Harris, B. H. L.*, West, C. M. L., Buffa, F. M., *Gene expression signatures as biomarkers of tumour hypoxia*. Clinical Oncology, 27, 547–560 (2015)
11. **Barberis, A.**, Danese, G., Leporati, F., Plaza, A., Torti, E., *Real-Time Implementation of the Vertex Component Analysis Algorithm on GPUs*. IEEE Geosci. Remote Sens. Lett. 10, 251–255 (2013)

UNDER REVIEW

Domingo, E., Rathee, S., Blake, A., … **Barberis, A.**, … Buffa, F.M., Maughan, T., S:CORT, *A machine learning model of complete response to radiation in rectal cancer reveals immune infiltrate and TGFβ signalling as key predictors.*

Alonso-Calvo, R., Hernandez-Ibarburu, G., **Barberis, A.**, Buffa, F. M., Manso, L., Pedrera-Jimenez, M., Perez-Rey, D., *Automated calculation of endpoints using semantically homogenized real-world data for adjuvant breast cancer clinical trials*.

*co-first †co-corresponding

CONFERENCE PRESENTATIONS & POSTERS

Nandakumar, A., **Barberis, A.**, Kim, J., Lang, C., Taylor, A., Macaulay, V., *IGFs Regulate Tumour-Intrinsic Components of the Immune Response to Promote an Immunosuppressive Microenvironment in Prostate Cancer*. IGF and Insulin System in Physiology and Disease Gordon Research Conference; Ventura Beach Marriott, CA, USA; 12-17 March (2023)

Barberis, A., Alonso-Calvo, R., Blake, A., Buffa, F. M., *Merlin: a web-based platform to derive robust gene signatures and evaluate existing patient classifiers*. Poster presented at: CRUK/MRC Oxford Institute for Radiation Oncology Symposium; Saïd Business School, Oxford; 7-8 September (2017)

Domingo, E., Blake, A., Richman, S., Stewart, P., **Barberis, A.**, Haider, S., Cheng, W.-C., Dunne, P., Buffa, F. M., Gollins, S., Maughan, T., *Multi-omic profiling and radiotherapy response in rectal cancer biopsies of COPERNICUS trial: results from SCORT (Stratification in COloRecTal cancer).* Poster presented at: 15th International Wolfsberg Meeting on Molecular Radiation Biology/Oncology; Wolfsberg Castle, Ermatingen, Lake Constance, Switzerland; 17-19 June (2017)

Barberis, A., Buffa, F. M., *Medical eResearch LINking 'omic signatures*. Poster presented at: 3rd International Course on Post-Transcriptional Gene Regulation; Institut Curie, Paris; 27-31 March (2017)

Lim, S. H.-S., Ip, E., Chua, W., Ng, W., Henderson, C., Shin, J.-S., Harris, B. H. L., **Barberis, A.**, Cowley, M., De Souza, P.L., Spring, K., *Serum microRNA expression during neoadjuvant chemoradiation for rectal cancer*. J. Clin. Oncol. 35, e15081–e15081 (2017)

Barberis, A., Voukantsis, D., Buffa, F. M., *In-silico modelling of the tumour microenvironment*. Poster presented at: CRUK/MRC Oxford Institute for Radiation Oncology Quinquennial Review; Old Road Campus Research Building, Oxford; 21 July (2016)

Barberis, A., Leporati, F., *QR Decomposition via Householder Reflectors on FPGA Technology.* DSD & SEAA Euromicro Conference, Santander, Spain, 4-6 Sept. (2013)

ADMINISTRATIVE EXPERIENCE

- Member of the interview panel for Oncology IT Manager (University of Oxford)
- CBIG group management: weekly meeting organizer and purchase manager (University of Oxford)
- Invigilating examinations (University of Pavia)
- Talking to students, teachers and parents at Open Days

COMMITTEE PARTICIPATION

2021	Member of the evaluation committee for the Transfer of Status (ToS) from probationer research student (PRS) to either full MSc by Research status or full DPhil status
2019 - 2021	Oxford University Italian Society senior committee member
2017 - 2019	Oxford University Italian Society junior committee member
2015 - 2017	New College Boat Club committee member (IT Secretary)

IT SKILLS

- Experienced in several programming languages (e.g., **R**, **Python**, **Java**, **C**, **Matlab**)
- Experienced in **SQL** for database querying, **MySQL** for managing relational databases, and **Hibernate** for object-relational mapping
- Proficient in pipelines development using **Nextflow** workflow management system
- Familiar with **high-performance computing** solutions such clusters, GPUs, and FPGAs
- Familiar with **Git** and **Bitbucket** for version control and code collaboration
- Confident in web-based design using **html**, **css**, **php**, **javascript**, **jquery**
- Working knowledge of machine learning frameworks such as **PyTorch** and **TensorFlow**

RELEVANT SKILLS

- Effective communicator able to engage specialist and non-expert audiences
- Confident, independent scientist with experience in conducting his own research
- Excellent team player experienced in working in groups with different backgrounds
- Creative problem solver with track record in implementing innovative scientific solutions
- Trustful scientist who constantly meets deadlines

RELEVANT TRAINING

ongoing	Neural Networks and Deep Learning (DeepLearning.AI) Develop Your Skills in Agile Software Development (LinkedIn Learning)

2024 Advancing Teaching and Learning (University of Oxford)
2023 Preparing for Learning and Teaching – Tutorials Teaching (University of Oxford)
2022 Preparing for Learning and Teaching – Taught Masters (University of Oxford)
2018 CRUK-CI Bioinformatics Summer School (Cambridge, UK)
2017 Molecular Biology – Transcription and Transpositions (MITx)
Post-Transcriptional Gene Regulation International Course (Institut Curie, France)
PACRI Symposium on the Future of Oncology (Paris, France)
2016 Further Topics in Statistics and Bioinformatics (University of Oxford)
2015 Teaching and Learning Skills Development – Part 2 (University of Oxford)
2014 Teaching and Learning Skills Development – Part 1 (University of Oxford)
2013 Introduction to Biology – The Secret of Life (MITx)
Summer School on Parallel Computing (CINECA, Italy)
2011 Caspur – CILEA GPU Programming Course (Italy)

REFEREE ACTIVITY

Referee in the Computational Biology field (Computational and Structural Biotechnology Journal, International Journal of Environmental Research and Public Health)

MEMBERSHIPS

2014 - 2015 European Project “Personalised Medicine (P-MEDICINE)” – FP7-ICT-2009.5.3 270089 – Member of the research unit of the University of Oxford
2014 - 2015 European Project “Enabling information re-Use by linking clinical REsearch and CAre (EURECA)” – FP7-ICT-2011-5.3 288048 – Member of the research unit of the University of Oxford
2012 High Performance, Edge And Cloud computing (HiPEAC) Network
2011 Board of Engineers – Licensed Computer Science Engineer (Italy)

CONSULTING ACTIVITY

2024 Bioinformatics consultancy for University of Oxford

2023 Bioinformatics consultancy for biotechnology company (Senya Therapeutics)