

Nicolò Gualandi

WORK EXPERIENCE

📍 **SR-TIGET** – MILANO, ITALY

BIOINFORMATICS SCIENTIST – 01/03/2024 – CURRENT

Bioinformatics data analysis
scRNA-seq data analysis
Building bioinformatics pipelines

📍 **UNIVERSITÀ DEGLI STUDI DI UDINE** – UDINE, ITALY

POSTDOCTORAL RESEARCHER – 15/03/2023 – 01/03/2024

- Bioinformatics data analysis
- Building bioinformatics pipeline
- Experimental design

EDUCATION AND TRAINING

01/11/2018 – 13/02/2023 Trieste, Italy

PHD Scuola Internazionale Superiore di Studi Avanzati (SISSA)

Bioinformatics, RNA-seq data analysis, DNA-seq data analysis

Address 34136, Trieste, Italy | **Website** <https://phdgenomics.sissa.it/> | **Field of study** Bioinformatics | **Final grade** Cum Laude |

Level in EQF EQF level 8 | **Thesis** Intron retention dysregulation in Aicardi-Goutières syndrome

2016 – 2018 Trieste, Italy

MASTER'S DEGREE IN FUNCTIONAL GENOMICS (LM-6) University of Trieste (UNITS)

Bioinformatics, sequence analysis, RT-qPCR, PCR, survival assay, RNA extraction, primer design, MTT assay, phylogenetics analysis,

Address 34124, Trieste, Italy | **Website** <https://www.biologia.units.it/corsi/2/Laurea-Magistrale-in-Genomica-funzionale> |

Final grade 110/110 | **Level in EQF** EQF level 7 |

Thesis First evidence of genic presence/absence variation of bioactive mussels peptides

2013 – 2016 Bologna, Italy

BA BIOLOGICAL SCIENCES Alma Mater Studiorum, University of Bologna (UNIBO)

PCR, RT-qPCR, cloning, bacterial cell cultures, data analysis (excel)

Website <https://corsi.unibo.it/laurea/ScienzeBiologiche> | **Final grade** 102/110 | **Level in EQF** EQF level 6 |

Thesis The HopV gene modulates nickel homeostasis in *Helicobacter pylori*

LANGUAGE SKILLS

Mother tongue(s): **ITALIAN**

Other language(s):

	UNDERSTANDING		SPEAKING		WRITING
	Listening	Reading	Spoken production	Spoken interaction	
ENGLISH	B2	B2	B2	B2	B2

Levels: A1 and A2: Basic user; B1 and B2: Independent user; C1 and C2: Proficient user

SKILLS

Data Science, Data Analytics, Data Visualization | Computational genomics

Programming languages

Python3, Python2 | R | biopython | Pandas, Numpy, Scikit-learn, Scipy libraries

Bioinformatics application

NGS Data Analysis | Genomics Bioinformatics Tools | RNA-Seq Analysis | Protein Modelling | Bioinformatics | ChIP-seq | ATAC-seq | Drug Design Tools (Molecular Docking, Computational Chemistry) | scRNA-seq | FACS Analysis | DNA sequencing | Machine Learning

Computer skills

Unix/Linux und Unix Shell | Bash | bash-script | Windows | LibreOffice 3 | Linux

Laboratory skill

PCR and cDNA library preparation. | Quantitative real-time PCR | DNA/RNA Extraction | Bacterial culture

PUBLICATIONS

2022

[Meta-Analysis Suggests That Intron Retention Can Affect Quantification of Transposable Elements from RNA-Seq Data](#)

Gualandi, N.; Iperi, C.; Esposito, M.; Ansaloni, F.; Gustincich, S.; Sanges, R. Meta-Analysis Suggests That Intron Retention Can Affect Quantification of Transposable Elements from RNA-Seq Data. *Biology* **2022**, *11*, 826. <https://doi.org/10.3390/biology11060826>

2023

[Unveiling the Impact of Gene Presence/Absence Variation in Driving Inter-Individual Sequence Diversity within the CRP-I Gene Family in *Mytilus* spp](#)

Gualandi N, Fracarossi D, Riommi D, Sollitto M, Greco S, Mardirossian M, Pacor S, Hori T, Pallavicini A, Gerdol M. Unveiling the Impact of Gene Presence/Absence Variation in Driving Inter-Individual Sequence Diversity within the CRP-I Gene Family in *Mytilus* spp. *Genes* (Basel). 2023 Mar 24;14(4):787. doi: 10.3390/genes14040787. PMID: 37107545; PMCID: PMC10138031.

2022

[TEspeX: consensus-specific quantification of transposable element expression preventing biases from exonized fragments](#)

Federico Ansaloni, Nicolò Gualandi, Mauro Esposito, Stefano Gustincich, Remo Sanges, TEspeX: consensus-specific quantification of transposable element expression preventing biases from exonized fragments, *Bioinformatics*, 2022;, btac526, <https://doi.org/10.1093/bioinformatics/btac526>

2022

[Transposons Acting as Competitive Endogenous RNAs: In-Silico Evidence from Datasets Characterised by L1 Overexpression](#)

Esposito, M.; Gualandi, N.; Spirito, G.; Ansaloni, F.; Gustincich, S.; Sanges, R. Transposons Acting as Competitive Endogenous RNAs: In-Silico Evidence from Datasets Characterised by L1 Overexpression. *Biomedicines* **2022**, *10*, 3279. <https://doi.org/10.3390/biomedicines10123279>

2023

[NRF2 interacts with distal enhancer and inhibits nitric oxide synthase 2 expression in KRAS-driven pancreatic cancer cells](#)

Di Giorgio E, Cortolezzis Y, Gualandi N, Agostini F, Rapozzi V, Xodo LE. NRF2 interacts with distal enhancer and inhibits nitric oxide synthase 2 expression in KRAS-driven pancreatic cancer cells. *Biochim Biophys Acta Mol Cell Res.* 2023 Oct 16;1871(1):119606. doi: 10.1016/j.bbamcr.2023.119606. Epub ahead of print. PMID: 37852325.

2024

[Transcription of endogenous retroviruses in senescent cells contributes to the accumulation of double-stranded RNAs that trigger an anti-viral response that reinforces senescence](#)

Di Giorgio E, Ranzino L, Tolotto V, Dalla E, Burelli M, Gualandi N, Brancolini C. Transcription of endogenous retroviruses in senescent cells contributes to the accumulation of double-stranded RNAs that trigger an anti-viral response that reinforces senescence. *Cell Death Dis.* 2024 Feb 21;15(2):157. doi: 10.1038/s41419-024-06548-2. PMID: 38383514; PMCID: PMC10882003.

2024

[THE 7 STAGES OF NEURONAL DEVELOPMENT IN VITRO: MORPHOLOGICAL AND MOLECULAR SIGNATURES FROM BIRTH TO SENESCENCE](#)

V. Ciraci, E. Saccone, N. Gualandi, O.M. Roggero, E. Tongiorgi

2024

[The DNA-repair protein APE1 participates with hnRNPA2B1 to motif-enriched and prognostic miRNA secretion](#)

Mangiapane G, Notarangelo M, Canarutto G, Fabbiano F, Dalla E, Degrassi M, Antoniali G, Gualandi N, De Sanctis V, Piazza S, D'Agostino VG, Tell G. The DNA-repair protein APE1 participates with hnRNPA2B1 to motif-enriched and prognostic miRNA secretion. *Oncogene.* 2024 Apr 25. doi: 10.1038/s41388-024-03039-8. Epub ahead of print. PMID: 38664500.

2024

[Transcriptomic Module Discovery of Diarrhea-Predominant Irritable Bowel Syndrome: A Causal Network Inference Approach](#)

Guido, D.; Maqoud, F.; Aloisio, M.; Mallardi, D.; Ura, B.; Gualandi, N.; Cocca, M.; Russo, F. Transcriptomic Module Discovery of Diarrhea-Predominant Irritable Bowel Syndrome: A Causal Network Inference Approach. *Int. J. Mol. Sci.* **2024**, *25*, 9322. <https://doi.org/10.3390/ijms25179322>

2024

[Dissecting transposable elements and endogenous retroviruses upregulation by HDAC inhibitors in leiomyosarcoma cells: Implications for the interferon response](#)

Gualandi N, Minisini M, Bertozzo A, Brancolini C. Dissecting transposable elements and endogenous retroviruses upregulation by HDAC inhibitors in leiomyosarcoma cells: Implications for the interferon response. *Genomics.* 2024 Aug 3;110909. doi: 10.1016/j.ygeno.2024.110909. Epub ahead of print. PMID: 39103003.

2024

[Apurinic/Apyrimidinic Endodeoxyribonuclease 1 modulates RNA G-quadruplex folding of miR-92b and controls its expression in cancer cells](#)

Bellina A, Malfatti MC, Salgado G, Fleming AM, Antoniali G, Othman Z, Gualandi N, La Manna S, Marasco D, Dassi E, Burrows CJ, Tell G. Apurinic/Apyrimidinic Endodeoxyribonuclease 1 modulates RNA G-quadruplex folding of miR-92b and controls its expression in cancer cells. *Proc Natl Acad Sci U S A.* 2024 Nov 12;121(46):e2317861121. doi: 10.1073/pnas.2317861121. Epub 2024 Nov 4. PMID: 39495925; PMCID: PMC11572961.

[Gualandi N](#), Bertozzo A, Brancolini C. ProOvErlap: Assessing feature proximity/overlap and testing statistical significance from genomic intervals. J Biol Chem. 2025 May 7:110209. doi: 10.1016/j.jbc.2025.110209. Epub ahead of print. PMID: 40345582.

● DRIVING LICENCE

Driving Licence: B

● CONFERENCES AND SEMINARS

01/07/2021 – 02/07/2021

BITS annual meeting

Poster presentation: "Intron retention can bias accurate transposable elements quantification in RNA-seq data"
[Gualandi N](#), Iperi C, Esposito M, Ansaloni F, Sanges R

Link <https://bioinformatics.it/bits2021>

Cajal Course of "Advanced imaging techniques for cellular and systems neuroscience 2020"

Poster presentation: "A systems pharmacology approach for innovative treatments to promote recovery of neuronal atrophy in Rett syndrome"

Ottavia Maria Roggero, Vittoria Berutto, [Nicolò Gualandi](#), Remo Sanges, Enrico Tongiorgi

Link <https://www.fens.org/careers/training-activities/the-cajal-training-programme>

17/05/2023 – 20/05/2023 Vienna, Austria

ESPGHAN 2023

Poster presentation: "UNDERSTANDING CELIAC DISEASE AT SINGLE CELL RESOLUTION"

Luigina De Leo, Remo Sanges, [Nicolò Gualandi](#), Fabiana Ziberna, Sara Lega, Giuseppe Molinaro, Matteo Bramuzzo

19/06/2023 – 20/06/2023 Trieste, Italy

TRIM-NET Closure Meeting 2023

Poster presentation: "A systems pharmacology approach for innovative treatments to promote recovery of neuronal atrophy in Rett syndrome".

Authors: Roggero Ottavia Maria, Berutto Vittoria, [Gualandi Nicolò](#), Carosati Emanuele, Sanges Remo, Tongiorgi Enrico.

19/06/2023 – 20/06/2023 Trieste, Italy

TRIM-NET Closure Meeting 2023

Poster presentation: "UNDERSTANDING CELIAC DISEASE AT SINGLE CELL RESOLUTION"

Luigina De Leo, Remo Sanges, [Nicolò Gualandi](#), Fabiana Ziberna, Sara Lega, Giuseppe Molinaro, Matteo Bramuzzo

14/09/2023 – 17/09/2023 Torino, Italy

20th national congress of the Italian Society for Neuroscience (SINS),

Poster presentation: "Mirtazapine rescues neuronal atrophy in Rett syndrome by directly binding SOS1 and triggering the MAPK/ERK pathway". Authors: Donegà Stefano, Roggero Ottavia Maria, [Gualandi Nicolò](#), Berutto Vittoria, Colliva Andrea, Masella Gianluca, Carosati Emanuele, Sanges Remo, Baj Gabriele, Tongiorgi Enrico

20/10/2022 – 21/10/2022 Coimbra, Portugal

European Synapse Meeting (ESM)

Poster presentation: "A systems pharmacology approach for innovative treatments to promote recovery of neuronal atrophy in Rett syndrome".

Authors: Roggero Ottavia Maria, Berutto Vittoria, [Gualandi Nicolò](#), Carosati Emanuele, Sanges

Molecular Analysis for Precision Oncology Congress 2024

Poster presentation: "Patient-based models to study infiltration heterogeneity in gliomas"

Authors: Irene Giulia Rolle, Serena Mastantuono, [Nicolò Gualandi](#), Miran Skrap, Marco Vindigni, Antonio Paolo Beltrami, Daniela Cesselli

Background:

Despite advances in understanding the molecular basis of high-grade gliomas, glioblastoma (GBM) still represents a challenge in terms of therapy. Beside tumor heterogeneity, one of the features hindering the efficacy of treatments is the highly infiltrative nature of glioma cells that, by hydrodynamic cellular volume changes, invade brain parenchyma along narrow extracellular routes. GSC have been reported as the putative population responsible for GBM resistance to treatments and recurrences. Aim of the study was to use a Precision Medicine (PM) approach by taking advantage of patient-derived in vitro models to give insight into the heterogeneity of the molecular pathways underlying the infiltration process.

Methods:

GSC were obtained from 15 patients undergoing surgery for a newly diagnosed GBM. GSC were analysed in terms of: 1. invasive attitude by using an ad hoc in vitro migration assay; 2. transcriptional profile, by next generation sequencing. Bioinformatic was employed to define a genetic signature, and to validate its prognostic role in 500 GBM tissues included in TCGA/GTEX datasets.

Results:

The in vitro study revealed that each cell line was characterized by a distinct migratory behavior, confirming that GSC recapitulated the intrinsic heterogeneity of the original tumors. Moreover, migrating and non-migrating GSC showed a distinctive transcriptional profile and, correlating differentially expressed genes with GBM included in TCGA/GTEX datasets, we identified a GSC-based signature predictive of GBM patient's prognosis.

Conclusions:

This study outlines the role of patient-based stem cells models as a tool to deepen insights on GBM features and to discover new biomarkers useful in identifying adjuvant therapies targeting the infiltration process.

Link <https://www.esmo.org/meeting-calendar/molecular-analysis-for-precision-oncology-congress-2024>

Molecular Analysis for Precision Oncology Congress (MAP) 2024

18P Molecular characterization of circulating tumor cells in metastatic breast cancer using shallow whole genome sequencing

Authors: M. Bulfoni, [N. Gualandi](#), G. Vesca, S. Bisetto, M. Turetta, F. Del Ben, S. Bertozzi, F. Curcio, C. Di Loreto, A.P. Beltrami, D. Cesselli.

ESMO Open, Volume 9, Supplement 6, 2024, 103764, ISSN 2059-7029, <https://doi.org/10.1016/j.esmoop.2024.103764>.

Background

Metastatic breast cancer is the leading cause of cancer-related mortality in women, largely due to challenges in early detection of metastasis and limitations of current treatment options. Circulating Tumor Cells (CTC) are critical to metastatic dissemination, making their detection and characterization through liquid biopsy a promising advancement in oncology. While counting CTC can offer insights into prognosis, molecular characterization has the potential to refine therapeutic strategies and enable early detection of treatment resistance. This study focuses on the molecular analysis of CTC using a shallow Whole Genome Sequencing (sWGS) approach to enhance the understanding of CTC in metastatic breast cancer.

Methods

114 CTC were isolated from 10 patients with metastatic luminal breast cancer using DEPArray technology. After sorting, single cells underwent Whole Genome Amplification (WGA) followed by shallow sWGS to identify common copy number alteration (CNA) patterns. Sequencing was performed on the Illumina MiSeq platform. CNA were called using a home-made pipeline. The prognostic value of CNA signatures was evaluated using data from The Cancer Genome Atlas (TCGA) dataset (n=466), with Kaplan-Meier curves generated using the log-rank test.

Results

Six molecular CNA signatures were identified in patients. Notably, four of these signatures were strongly associated with worse prognosis: deletions of chromosome 1, amplifications of chromosome 1, hemizygous deletions of X chromosome, deletions of chromosome 4 and 13. The prognostic significance was confirmed in primary breast carcinomas from the TCGA consortium. The identification of molecular signatures on CTC provides valuable insights into the genetic landscape of breast cancer. The association of specific aberrations with poorer outcomes underscores the potential of these markers for guiding risk assessment and therapeutic strategies. The validation in primary breast

carcinomas further supports the clinical relevance of integrating molecular signatures into personalized treatment and patient management.

Conclusions

Our study demonstrated the utility of molecular signatures in CTC from breast cancer patients in aiding better prognosis.

Link <https://www.sciencedirect.com/science/article/pii/S2059702924015345>

10/09/2025 – 13/09/2025 Pisa

SINS 2025

Poster presentation: "Novel Biomarkers Define Hippocampal Neuron Developmental Stages"

Authors: Ciraci, Viviana; Gualandi, Nicolò; Saccone, Elisabetta; Roggero, Ottavia Maria; Tongiorgi, Enrico

10/09/2025 – 13/09/2025 Pisa

SINS 2025

Poster presentation: "In-silico prediction of novel targets for mirtazapine in Rett syndrom"

Authors: Roggero, Ottavia Maria; Gualandi, Nicolò; Ciraci, Viviana; Berutto, Vittoria; Carosati, Emanuele; Tongiorgi, Enrico

● COURSES

12/06/2019 – 14/06/2019

NGS - Quality control, Alignment, Visualisation - University of Bern, Bern, Switzerland

Python for Data Science, Numpy, Pandas, Matplotlib, Seaborn, Scikit-learn, Linear Regression, Data Engineering & Data Visualization fundamentals

Verification number: 55616079436005

04/06/2020

Applied Machine Learning in Python - Coursera

- Align ChIP-seq and WGBS sequence data to a reference genome
- Identify narrow and broad peaks from ChIP-seq data
- Identify methylated levels from WGBS data
- Visualize and summarize the output of ChIP-Seq and WGBS analyses
- Explore integrative tools for epigenomic data sets

Link coursera.org/verify/8AV3L583JSXU

10/05/2021

Machine Learning: Regression -Coursera

Canadian Bioinformatics Workshops

Link coursera.org/verify/RYZ9H8KAJ2NV

2022

DATA SCIENTIST STARTER KIT - Datamasters

10/07/2020

Introduction to Data Science in Python

Link coursera.org/verify/XGS7XZDJJP6

10/02/2022

Formazione generale dei Laboratori

23/06/2020

Python for Genomic Data Science

Link coursera.org/verify/7TY5N3MUWN4K

Analysis of single cell RNA-seq data

25/11/2022

Impariamo da zero la piattaforma cloud AWS - 2022

11/10/2023 – 13/10/2023

Epigenomics Analysis

Link <https://bioinformatics.ca/workshops-all/2023-epigenomics-analysis/>

20/02/2025 – 21/02/2025

Introductory Spatial 'Omics Analysis: Visium HD

TEACHING AND MENTORING ACTIVITY

2020 – 2021

Exploring the relation between intron retention and gene expression in lymphoblastoid cell lines from public data

Co-supervisor of one student of the Master Degree in Functional Genomics (Units, Trieste, Italy).

Thesis title: "Exploring the relation between intron retention and gene expression in lymphoblastoid cell lines from public data"

Candidate: Cristian Iperi, Co-supervisors: Prof. Remo Sanges and Dott. [Nicolò Gualandi](#), Supervisor: Prof. Marco Gerdol.

2021 – 2022

RePaRe: developing a pangenome building pipeline and its application to the case of *Crassostrea gigas*

Master Thesis reviewer of one student of the Master Degree in Functional Genomics (Units, Trieste, Italy).

Thesis title: "RePaRe: developing a pangenome building pipeline and its application to the case of *Crassostrea gigas*".

Candidate: Nicolò Fogal, Supervisor: Prof. Marco Gerdol, Co-supervisor: Dott. Samuele Greco.

21/11/2023 – 24/11/2023

Introduction to Bioinformatics

Theoretical and practical course for PhD students of the "Molecular Medicine" PhD programme at the University of Udine (UniuD).

Main topics: "Bioinformatics databases, raw reads quality control, reads alignment, gene expression and differential expression analysis, enrichment analysis, linux and bash, R.

SOFTWARE

ProOvErlap

Assessing feature proximity/overlap and testing statistical significance from genomic intervals.

Authors: ProOvErlap was developed by Nicolò Gualandi and Alessio Bertozzo under the supervision of Prof. Claudio Brancolini (Professor of Cell Biology, Department of Medicine, Università degli Studi di Udine)

available at:

GitHub: <https://github.com/ngualand/ProOvErlap>

PyPI: <https://pypi.org/project/prooverlap>

conda: <https://bioconda.github.io/recipes/prooverlap/README.html>

Link <https://github.com/ngualand/ProOvErlap>

Il sottoscritto Gualandi Nicolò, ai sensi e per gli effetti degli articoli 46 e 47 e consapevole delle sanzioni penali previste dall'articolo 76 del d.P.R. 28 dicembre 2000, n. 445 nelle ipotesi di falsità in atti e dichiarazioni mendaci, dichiara che le informazioni riportate nel presente curriculum vitae, redatto in formato europeo, corrispondono a verità.