



# Curriculum Vitae

## BACCHI SARA

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 3939171566

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Date of birth: 09/03/1992

Nationality: Italian

### EDUCATION AND TRAINING

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|                     |   |
|---------------------|---|
| 2011                | <b>High School Diploma</b>  |
| at                  | Enrico Fermi scientific high school of Pavia  |
| vote achieved       | 94/100  |
| Nov 2014 – Feb 2015 | <b>Laboratory internship</b>  |
| at                  | Laboratory of Microbiology and Clinical Microbiology of the Department of Clinical-Surgical, Diagnostic and Pediatric Sciences of the University of Pavia |
| Apr 2015            | <b>Bachelor's Degree in Biotechnology</b>   |
| thesis              | <i>Diagnostica delle beta-lattamasi a spettro esteso nelle Enterobacteriaceae</i>   |
| at                  | University of Pavia   |
| vote achieved       | 91/110  |
| Feb 2017 – Nov 2017 | <b>Laboratory practical Internship</b>  |
| at                  | Genetic Analysis Laboratory of the Department of Earth and Environmental Sciences of the University of Pavia.   |
| Nov 2017            | <b>Master's Degree in Medical and Pharmaceutical Biotechnologies</b>  |
| at                  | University of Pavia   |
| thesis              | <i>Metagenomic analysis of intestinal microbiota in subjects suffering from Alzheimer's disease</i>   |

# Curriculum Vitae

|                         |   |
|-------------------------|---|
| vote achieved           | 110/110   |
| Nov 2017 - May 2018     | <b>Research activities</b> at the Genetic Analysis Laboratory/Department of Earth and Environmental Sciences and Centre for Health Technologies - University of Pavia   |
| activity                | Nucleic acids extraction (DNA, RNA) from different biological matrices including soil and biological traces; production of metagenomics amplicons; sequence analysis; application of bioinformatics and statistical analysis of sequence data. Participation to the research project <i>STUDY OF MICROBIOT COMPOSITION IN ADULT CELIAC DISEASE</i> funded by AIC (FC Call for Proposals 2015), P.I. Rachele Ciccocioppo |
| May 2018 - July 2018    | <b>Laboratory Technicians</b> at LabAnalysis s.r.l. of Casanova Lonati PV   |
| activities              | Research and identification of bacterial and fungal contaminants in food samples, identification and dosage of allergens, reaserch of nitrosamines, vevaluation of the stability of pharmaceutical preparations, determination of particle size of pharmaceutical and food industry samples   |
| Aug 2018 - today        | <b>Research collaborator</b>  |
| at                      | Genetic Analysis Laboratory of the Department of Earth and Environmental Sciences of the University of Pavia  |
| activities              | Statistical analysis for the final report of the research project <i>STUDY OF MICROBIOT COMPOSITION IN ADULT CELIAC DISEASE</i> funded by AIC (FC Call for Proposals 2015). Collaboration in research on pathogenic fungi responsible for onychomycosis: analysis of data derived from NGS sequencing and statistical processing  |
| Nov 2018 - today        | <b>Master's organizational secretariat</b>  |
| at                      | University of Pavia, Department of Internal Medicine and Medical Therapy  |
| performed activity      | Organizational secretarial activities for second level masters in "Oxygen-Ozone Therapy" and "Geriatric medicine and territorial cardiology and RSA coordinator" and for the first level master in "Management of health emergencies in hostile environments"   |
| 5 Feb 2019 - 8 Feb 2019 | BMR Genomics (Padua-Italy) "Bioinformatics for 16S-NGS" course  |

# Curriculum Vitae

## topics addressed

### Introduction to bioinformatic analyzes for NGS data

- Introduction to the course
- Utility with Linux for analysis
- Analysis mode with client / server model
- FASTA format
- FASTQ format
- SAM format
- BED format
- GFF / GTF format
- VCF format
- Commands for manipulating text files

### Introduction to programming in Python

- Introduction to Python
- Data structures
- Flow control instructions (if, for and while)
- Writing a program to change the format of a 16S sequence database

### Quality Analysis of a race

- Demultiplexing output
- Use of FastQC from the command line
- Merging of coupled readings
- Removal of adapters with cutadapt

### Analysis of 16S amplicons

- Introduction to the method and theory
- Introduction to QIIME and USEARCH as a work environment
- Introduction to the experiment
- Analysis with QIIME 2
- Analysis with USEARCH 10
- Comparison of results

## PERSONAL SKILLS

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### Acquired knowledges

- Methods of extraction of nucleic acids from different biological matrices (blood, tissue, feces, soil)
- Quantitative and qualitative analysis of DNA and RNA extracts (spectrophotometric and colorimetric method)
- Amplification methods using PCR, real time PCR, PCR-RFLP and nested PCR
- Metagenomic approach for selective amplification of bacterial and fungal communities for NGS analysis on illumina

## Curriculum Vitae

- Electrophoretic analysis of amplification and extraction products of nucleic acids from band
- Sanger sequencing and cleaning of sequences using dedicated software
- Identification of nucleotide sequences using BLAST algorithm (NCBI)
- Final analysis of metagenomic amplicon sequencing: taxonomic analysis, statistics analysis (Student's t test, ANOVA) and biodiversity analysis (alpha diversity with practical knowledge of species richness and Shannon index and understanding of the Chao1 metric, UniFrac metric and PCoA technique)

Known and used tools: thermocycler, thermocycler for real time analysis, fluorometer, spectrophotometer, SDS page, DNA electrophoretic analysis, ELISA test, granulometer, gas chromatograph, Sanger method sequencer.

Basic knowledge of the shell, R language, Python, qiime2 and usearch10 commands

|                     |  |
|---------------------|--|
| English language    | Good   |
| Digital Skills      | Good   |
| Research activities | Member of the working group of Genetic analysis laboratory of the Department of Earth and Environmental Sciences - University of Pavia, involved in the project: <i>STUDY OF MICROBIOT COMPOSITION IN ADULT CELIAC DISEASE</i> funded by AIC (FC Call for Proposals 2015), PI Rachele Ciccocioppo, lasting two years |
| Pubblications       | <p><i>Study of the bacteriome composition in Alzheimer disease</i>, Bacchi S. et al., article in preparation</p> <p><i>Metagenomic analysis as a support to clinical diagnosis of onychomycosis</i>, Guglielminetti M.L., Bacchi S., Lupo G., Capelli E. 2018, article in preparation</p>                            |

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### FURTHER INFORMATION

# Curriculum Vitae

I feel good to work both in a team and in an autonomous way and I willingly learn any new procedures. I have my own car and I do not have a pressing need to respect schedules.

## Driver's license

Driving license B

## Personal data

I authorize the processing of my personal data in the cv pursuant to Legislative Decree 30 June 2003, n. 196 "Code regarding the protection of personal data" and the GDPR (EU Regulation 2016/679).