



Marco Chiapello

DATA SCIENTIST - BIOINFORMATICIAN

Department of Life Sciences And Systems Biology @ University of Turin

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About myself

I am **currently working as Senior PostDoc** at the University of Turin (Department of Life Sciences And Systems Biology). My daily focus is on **bioinformatics analysis** and **method standardization** for fungi/heavy-metals interaction and analysis of NGS samples. I am a big **supporter of reproducible and open research**. My main tools are R, git, vim and docker. I am a **curious person** and a **dedicated worker**, I love the challenges of **computational biology** and teaching the principle of **data analysis and visualization**.

Functional Experience

DATA SCIENCE

- I developed analysis reports to advise companies to product price changes (Evo)
- I developed analysis reports to help companies to understand the current selling situation (University of Turin)
- I developed R script for data analysis automatisation with docker (ProteiQ)
- I taught more than 10 courses in several European Universities about Data science in R. I also develop a docker container to deliver the course during the covid-19 lockdown.

WET LAB

- During my PhD I focused my attention on fungal protein extraction, separation and identification via immunoblotting or mass spectrometry
- During my PostDoc in Switzerland I consolidated my skill in molecular biology techniques, like PCR, qPCR and cloning
- During my last PostDoc, at the Institute for Sustainable Plant Protection, I worked with viruses in the frame of Viroplant project (H2020 project)

BIOINFORMATICS

- Co-founder of IBiG (IPSP Bioinformatics group in Turin). The group has three missions: education, support and service.
- At Institute of Sustainable Plant Protection I worked on viruses identification in complex metatranscriptomics samples, developing an automatic pipeline from raw data cleaning, read assembly, viruses identification, reads mapping, uniconfigs identification to phylogenetic tree and genome structure draw (in R)
- At Cambridge Center for proteomics I worked on proteomics data interpretation from data imputation, data clustering to differential expression (in R)
- At Cambridge Center for proteomics I developed interactive data analysis report for customers
- I developed two R packages
- I conducted my analysis both on servers and dockers

CLIENT RELATIONS

- Present results and recommendations from data analysis to senior management (Evo, University of Cambridge)
- Advise clients of best strategies to adopt after data analysis (Evo)
- Pre-Post data analysis meeting on experimental design strategy and data analysis interpretation (University of Cambridge)

COMMUNICATION SKILLS

- I took two courses in teaching and communication techniques with: The Carpentries and Elixir Train-the-Trainers programs
- I present regularly results of my data analysis to my supervisor and colleagues
- I used to run a monthly seminar about statistics at the Institute of Sustainable Plant Protection

Computer Skills

BIOINFORMATICS

- Basic: Bioconda
- Intermediate: Galaxy, ncbi edirect
- Advance: Trinity, bwa, bowtie2, samtools, CLARK, Kraken, Diamond, Megan, Mega, Clustalo, IQTree, Bioconductor, Mascot, Protein Discoverer, Scaffold, Blast2GO, KEGG, MaxQuant, NCBI toolbox, Bioconductor

GRAPHICS

- Advance: InkScape, Scribus, Adobe Illustrator, Adobe Photoshop, Adobe Indesign, Adobe Premiere, Adobe After Effects

OPEN SCIENCE

- Intermediate: pandoc, Docker, CircleCI, Travis, MySQL
- Advance: R, Nvim-R, RStudio, Unix Bash, tmux, Rmarkdown

OPERATING SYSTEM

- Advance: Linux, MacOS, Windows

TEXT EDITOR

- Advance: Vim, Microsoft Office, LibreOffice, OpenOffice, Atom

WEB APPS

- Basic: Shiny, HTML, CSS, Javascript, PHP, blogdown, pkgdown

COLLABORATION SOFTWARE

- Basic: HackMD, Asana
- Intermediate: Zoom, GoToMeeting, Meet, Webex, TeamViewer, Trello, Etherpad
- Advance: Version control (git), GitLab, GitHub, Bitbucket, Google Drive, Dropbox, Mega, Skype, Slack

Technical Skills

WET LAB

- Protein extraction from cells and tissues, analysis of protein patterns using gel (mono- or two-dimension), Immunoblotting
- DNA/RNA extraction and manipulation, PCR, Analysis of gene expression (qPCR), Cloning (classical and gateway)
- Protein extraction, in-gel separation, in-gel digestion, gel-free separation, gel-free digestion, membrane protein purification, FASP and MED-FASP

DRY LAB

- Proteomics data analysis from protein identification to data interpretation
- Transcriptomics data analysis for virus identification in complex metatranscriptomics samples
- Transcriptomics analysis from assembly to data quantification and statistical analysis
- R package development (CI Travis, Codecov, unit test)
- R markdown report for each analysis
- Bash script development
- Version Control (git), repository on GitHub, GitLab, BitBucket
- Containerization with: docker and anaconda

Education

University of Turin

PHD IN BIOLOGY AND BIOTECHNOLOGY OF FUNGI

Turin
2005 - 2009

University of York

EXCHANGE

York
2007 - 2008

University of Calgary

EXCHANGE

Calgary
2005 - 2005

University of Turin

B. SC. PLANT BIOTECHNOLOGY

Turin
1999 - 2005

Liceo Scientifico "A. Einstein"

HIGH SCHOOL GRADUATE

Turin
1994 - 1999

Work experience

Department of Life Sciences And Systems Biology

POSTDOCTORAL RESEARCH FELLOW

University of Turin, Italy
2021–Present

- Responsible for the project: Mechanisms of gene regulation during the ericoid endomycorrhizal interaction
- RNA-seq data analysis
- Bioinformatics analysis (shell, R, git)

Institute for Sustainable Plant Protection

POSTDOCTORAL RESEARCH FELLOW

National Research Council, Italy
2018–2021

- Bioinformatics analysis (shell, R, git)
- RNA-seq data analysis of metatranscriptomics samples for virus identification
- Molecular analysis and cloning (viral samples)

Institute for Sustainable Plant Protection

CO-FOUNDER AND MEMBER OF INSTITUTE BIOINFORMATICS GROUP (I-BiG)

- Teaching activities
- Bioinformatics data analysis
- Core facility

National Research Council, Italy

2018–Present

Revelo

CONSULTANT

- Bioinformatics analysis
- Teaching R courses

Milan

2020–Present

Frontiers

REVIEW EDITOR

- Review Editor on the Editorial Board of Microbe and Virus Interactions with Plants
- Review Editor on the Editorial Board of Plant Symbiotic Interactions

Lausanne, Switzerland

2020–Present

Life

SPECIAL ISSUE EDITOR

- Editor of special issue “Plant Proteomics”

Basel, Switzerland

2020–Present

The Carpentries

MENTORING CHAIR

- Recruit mentors/mentees
- Managing The Carpentries Mentoring Groups

Worldwide

2019–2020

Department of Life Sciences And Systems Biology

MENTOR

- Student mentoring

University of Turin, Italy

2019–2020

Department of Life Sciences And Systems Biology

LECTURER

- Teaching data analysis principles
- Hands-on coding with R

University of Turin, Italy

2019

ProteIQ Biosciences GmbH

DATA ANALYST

- Proteomics data analysis
- Analysis automatization using R

Berlin

2018

Department of Life Sciences And Systems Biology

DATA ANALYST

- Next generation sequencing analysis: from raw data to result interpretation

University of Turin, Italy

2018

Liceo Scientifico “Majorana”

TEACHER

- Frontal teaching

Turin, Italy

2018

Evo Pricing

DATA SCIENTIST

- Business intelligence and data analysis
- Liaise with customers
- Ensure accuracy of data analysis
- Data analysis automatization using R and SQL

Turin, Italy

2018

Cambridge Centre for Proteomics

RESEARCH DATA TECHNICIAN

- Bioinformatics analysis
- Proteomics data collection and results interpretation
- Liaise with the principal investigators, other members of the CCP and internal/external users of the facility
- Collaborate with other CCP staff to ensure accuracy of data analysis
- Data analysis using R

University of Cambridge, United Kingdom

2017–2018

Department of Biotechnology and Life Science

POSTDOCTORAL RESEARCH FELLOW

- Bioinformatics analysis
- Proteomics data analysis
- MySQL database for data storage and R for statistical analysis
- Mentoring of M.Sc/PhD scientists

University of Insubria, Varese, Italy

2016

Department of Life Sciences And Systems Biology

University of Turin, Italy

POSTDOCTORAL RESEARCH FELLOW

2013–2016

- Plan experiments
- Managing the project from plants growth to protein identification and quantification
- Molecular analysis and cloning
- Data analysis (proteomics and transcriptomics data)
- Mentoring of M.Sc/PhD scientists

Department of Molecular Plant Physiology

University of Zurich, Switzerland

POSTDOCTORAL RESEARCH FELLOW

2013

- Plan experiments
- Data analysis (proteomics and transcriptomics data)
- MySQL database for data storage and R for statistical analysis

Department of Plant Molecular Biology

University of Lausanne, Switzerland

POSTDOCTORAL RESEARCH FELLOW

2010–2013

- Responsible for the project: Towards the arbusculated cell membrane proteome
- Plan experiments
- Manage the project from plants growth to protein identification and quantification
- Molecular analysis and cloning
- MySQL database for data storage and R for statistical analysis

Department of Life Sciences And Systems Biology

University of Turin, Italy

POSTDOCTORAL RESEARCH FELLOW

2009–2010

- Responsible for the project: Molecular and cellular interaction between soil fungi and heavy metals
- Manage the project from fungal growth to protein identification and quantification
- Perform 2DE-SDS-PAGE
- Computational analysis of the 2DE gels
- Responsible for data analysis and interpretation
- Develop scripts in Perl and R

Certifications

This section contains the areas on which I have obtained certifications, through University courses (eg. Cambridge University (UK)) or online services (eg. Coursera, DataCamp, etc.).

EDUCATION

- 24 training credits in anthropo-psycho-pedagogical disciplines and teaching methodologies and technologies
- Data Carpentry instructor training (Data Carpentry foundation)
- Software Carpentry instructor training (Software Carpentry foundation)
- Bioinformatics for Core Facility Managers (European Bioinformatics Institute)
- ELIXIR-EXCELERATE Train the Trainer course (ELIXIR-IT)

STATISTICAL MODELLING AND MACHINE LEARNING

- Statistical Modeling in R (DataCamp)

DATA ANALYSIS

- R object-oriented programming and package development (University of Cambridge)
- The Data Scientists Toolbox (Coursera)
- R Programming (Coursera)
- Reproducible Research (Coursera)
- Getting and Cleaning Data (Coursera)
- The Basics of Data for Analytics (Lynda.com)
- Data Visualization for Data Analysts (Lynda.com)

TIME SERIES DATA ANALYSIS

- ARIMA Modeling with R (DataCamp)
- Introduction to time series analysis (DataCamp)

BIOLOGICAL DATA ANALYSIS

- Analysis of single cell RNA-seq data (University of Cambridge)
- Molecular Phylogenetics (University of Cambridge)
- Using the Ensembl Genome Browser (University of Cambridge)
- An Introduction to Solving Biological Problems with PERL (University of Cambridge)
- Statistics and R for the Life Sciences (University of Cambridge)
- Exploring Protein Sequence and Functional Information with UniProt (University of Cambridge)
- International Course in Automated Functional Annotation and Data Mining (BioBam Company)

RELATIONAL DATABASES

- Relational Database Design (University of Cambridge)
- MySQL: Implementing a Relational Database Design (University of Cambridge)
- Relational Database Fundamentals (Lynda.com)

OTHER COURSES

- Docker for reproducibility (Elixir Workshop - University of Turin)
- Beginners guide to version control with git (University of Cambridge)
- Git Essential Training (Lynda.com)
- Up and Running with vi (Lynda.com)
- Foundations of UX: Content Strategy (Lynda.com)
- Falcon: An Introduction for Content and Site Managers (University of Cambridge)
- Web Authoring: HTML - Cascading Style Sheets (University of Cambridge)

Teaching Activities

I am a certified instructor for “The Carpentries” [<https://carpentries.org/>] and a certified trainer for Elixir [<https://elixir-europe.org/>].

University of Turin (IT)

5 days course

JAN 2022

- Class: PhD students
- Subject: Reproducible research and R

University of Strasbourg (FR)

16 hours online course

NOV 2021

- Class: PostDocs & PIs
- Subject: R data Carpentry

University of Turin (IT)

8 hours online course

NOV 2021

- Class: Master students – Laurea Magistrale in Biologia dell'Ambiente
- Subject: Microbiota analysis

University of Turin (IT)

8 hours online course

OCT 2021

- Class: Master students – Laurea Magistrale in Biologia dell'Ambiente
- Subject: Biological data analysis

National Research Council (IT)

online course

OCT 2021

- Class: PostDocs & PIs
- Subject: Base R course and Statistics (<https://2021-09-cnr-r-base.github.io/2021-CNR-Rbasic/>)

University of Turin (IT)

8 hours online course

DEC 2020

- Class: Master students – Laurea Magistrale in Biologia dell'Ambiente
- Subject: Biological data analysis

University of Turin (IT)

8 hours online course

NOV 2020

- Class: Master students – Laurea Magistrale in Biologia dell'Ambiente
- Subject: Microbiota analysis

National Research Council (IT)

1 day course

OCT 2020

- Class: PostDocs & PIs
- Subject: Bioinformatics analysis of viromes

Nord university in Bodø (N)

18 hours online course

SEP 2020

- Class: PostDocs & PIs
- Subject: R data Carpentry

University of Turin (IT)

16 hours online course

JUN 2020

- Class: PhD students
- Subject: Reproducible research and R

National Research Council (IT) FEB 2020 <ul style="list-style-type: none"> • Class: PostDocs & PIs • Subject: Graphical visualization 	Half day course
National Research Council (IT) JAN 2020 <ul style="list-style-type: none"> • Class: PostDocs & PIs • Subject: Statistical uncertainty 	Half day course
University of Turin (IT) JUN 2019 <ul style="list-style-type: none"> • Class: Master students - Controllo Biologico dei processi e dei prodotti dell'industria • Subject: Data analysis with R 	24 hours course
Université Catholique de Louvain MAY 2019 <ul style="list-style-type: none"> • Class: PostDocs & PIs • Subject: R data Carpentry 	2 days course
University of Naples (IT) FEB 2019 <ul style="list-style-type: none"> • Class: PostDocs & PIs • Subject: R data Carpentry 	2 days course
University of Debrecen (H) DEC 2018 <ul style="list-style-type: none"> • Class: PostDocs & PIs • Subject: R data Carpentry 	2 days course
National Research Council (IT) NOV 2018 <ul style="list-style-type: none"> • Class: Senior scientist • Subject: Project management Course 	1 day course
National Research Council (IT) OCT 2018 <ul style="list-style-type: none"> • Class: Senior scientist • Subject: Introduction to Git 	1 day course
University of Turin (IT) JAN 2018 <ul style="list-style-type: none"> • Class: PhD students • Subject: Reproducible research and R 	3 days course
University of Cambridge (UK) SEP 2017 <ul style="list-style-type: none"> • Class: PostDocs & PIs • Subject: R data Carpentry 	2 days course
University of Cambridge (UK) SEP 2017 <ul style="list-style-type: none"> • Class: PostDocs & PIs • Subject: Data analysis with R 	1 day course
The Francis Crick Institute (UK) JUN 2017 <ul style="list-style-type: none"> • Class: PostDocs & PIs • Subject: R data Carpentry 	2 days course
University of Turin (IT) JAN 2017 <ul style="list-style-type: none"> • Class: PhD students • Subject: Reproducible research and R 	4 days course
University of Turin (IT) JUL 2016 <ul style="list-style-type: none"> • Class: PhD students • Subject: Reproducible research and R 	3 days course

intRo.Esercizi

<https://github.com/2021-09-CNR-R-base/intRo.Esercizi>

A PACKAGE TO SUPPORT ENTRY-LEVEL R STUDENT LEARNING

- Developed for R course at CNR (OCT 2021)

Ramf

<https://github.com/mchiapello/Ramf>

A PACKAGE FOR ARBUSCULAR MYCORRHYZAL FUNGI COLONIZATION SCORING

- Published

Rwaves

<https://github.com/mchiapello/Rwaves>

A PACKAGE TO ANALYZE ELECTROPENETROGRAPHY DATA

- Under develop

Publications

1. Muleya, V., Lois, L. M., Chahtane, H., Thomas, L., Chiapello, M., & Marondedze, C. (2022). (De)activation (ir)reversibly or degradation: Dynamics of post-translational protein modifications in plants. *Life*, 12(2). <https://doi.org/10.3390/life12020324>
2. Crucitti, D., Chiapello, M., Oliva, D., Forgia, M., Turina, M., Carimi, F., La Bella, F., & Pacifico, D. (2022). Identification and molecular characterization of novel mycoviruses in saccharomyces and non-saccharomyces yeasts of oenological interest. *Viruses*, 14(1), 52.
3. Carretero-Rodriguez, L., Gujónsdóttir, R., Poparic, I., Reilly, M. L., Chol, M., Bianco, I. H., Chiapello, M., Feret, R., Deery, M. J., & Guthrie, S. (2021). The rac-GAP alpha2-chimaerin signals via CRMP2 and stathmins in the development of the ocular motor system. *Journal of Neuroscience*, 41(31), 6652–6672.
4. Chiapello, M., Bosco, L., Ciuffo, M., Ottati, S., Salem, N., Rosa, C., Tavella, L., & Turina, M. (2021). Complexity and local specificity of the virome associated with tospovirus-transmitting thrips species. *Journal of Virology*, 95(21), e00597–21.
5. Martino, G., Holtappels, D., Vallino, M., Chiapello, M., Turina, M., Lavigne, R., Wagemans, J., & Ciuffo, M. (2021). Molecular characterization and taxonomic assignment of three phage isolates from a collection infecting pseudomonas syringae pv. Actinidiae and p. Syringae pv. Phaseolicola from northern Italy. *Viruses*, 13(10), 2083.
6. Kuhn, J. H., Adkins, S., Agwanda, B. R., Al Kubrusli, R., Alkhovsky, S. V., Amarasinghe, G. K., Avsic-Zupanc, T., Ayllon, M. A., Bahl, J., Balkema-Buschmann, A., others. (2021). 2021 taxonomic update of phylum negarnaviricota (riboviria: Orthornavirae), including the large orders bunyavirales and mononegavirales (aug, 10.1007/s00705-021-05143-6, 2021). *Archives Of Virology*, 166(12), 3567–3579.
7. Peracchio, C., Forgia, M., Chiapello, M., Vallino, M., Turina, M., & Ciuffo, M. (2020). A complex virome including two distinct emaraviruses associated with virus-like symptoms in camellia japonica. *Virus Research*, 286, 197964.
8. Chiapello, M., Rodríguez-Romero, J., Nerva, L., Forgia, M., Chitarra, W., Ayllón, M. A., & Turina, M. (2020). Putative new plant viruses associated with plasmopara viticola-infected grapevine samples. *Annals of Applied Biology*, 176(2), 180–191.
9. Chiapello, M., Zampieri, E., & Mello, A. (2020). A small effort for researchers, a big gain for soil metaproteomics. *Frontiers in Microbiology*, 88.
10. Ottati, S., Chiapello, M., Galetto, L., Bosco, D., Marzachì, C., & Abbà, S. (2020). New viral sequences identified in the flavescence dorée phytoplasma vector scaphoideus titanus. *Viruses*, 12(3), 287.
11. Procopio, N., Ghignone, S., Voyron, S., Chiapello, M., Williams, A., Chamberlain, A., Mello, A., & Buckley, M. (2020). Soil fungal communities investigated by metabarcoding within simulated forensic burial contexts. *Frontiers in Microbiology*, 1686.
12. Chiapello, M., Rodríguez-Romero, J., Ayllón, M., & Turina, M. (2020). Analysis of the virome associated to grapevine downy mildew lesions reveals new mycovirus lineages. *Virus Evolution*, 6(2), veaa058.

13. Sutela, S., Forgia, M., Vainio, E. J., Chiapello, M., Daghino, S., Vallino, M., Martino, E., Girlanda, M., Perotto, S., & Turina, M. (2020). The virome from a collection of endomycorrhizal fungi reveals new viral taxa with unprecedented genome organization. *Virus Evolution*, 6(2), veaa076.
14. Daghino, S., Sutela, S., Forgia, M., Vainio, E. J., Chiapello, M., Vallino, M., Martino, E., Girlanda, M., Perotto, S., & Turina, M. (2020). Molecular investigations of ericoid and orchid mycorrhizal fungi reveal new mycoviral taxa. *115th Conference of the Italian Botanical Society*.
15. Kuhn, J. H., Adkins, S., Alioto, D., Alkhovsky, S. V., Amarasinghe, G. K., Anthony, S. J., Avšič-Županc, T., Ayllón, M. A., Bahl, J., Balkema-Buschmann, A., others. (2020). 2020 taxonomic update for phylum negarnaviricota (riboviria: Orthornavirae), including the large orders bunyavirales and mononegavirales. *Archives of Virology*, 165(12), 3023–3072.
16. Zampieri, E., Chiapello, M., & Mello, A. (2020). A small effort for researchers, a big gain for soil metaproteomics. *Frontiers in Microbiology*.
17. Russo, G., Carotenuto, G., Fiorilli, V., Volpe, V., Chiapello, M., Van Damme, D., & Genre, A. (2019). Ectopic activation of cortical cell division during the accommodation of arbuscular mycorrhizal fungi. *New Phytologist*, 221(2), 1036–1048.
18. Roth, R., Hillmer, S., Funaya, C., Chiapello, M., Schumacher, K., Lo Presti, L., Kahmann, R., & Paszkowski, U. (2019). Arbuscular cell invasion coincides with extracellular vesicles and membrane tubules. *Nature Plants*, 5(2), 204–211.
19. Picarelli, M. A. S., Forgia, M., Rivas, E. B., Nerva, L., Chiapello, M., Turina, M., & Colariccio, A. (2019). Extreme diversity of mycoviruses present in isolates of rhizoctonia solani AG2-2 LP from zoysia japonica from brazil. *Frontiers in Cellular and Infection Microbiology*, 244.
20. Chiapello, M., Das, D., & Gutjahr, C. (2019). Ramf: An open-source R package for statistical analysis and display of quantitative root colonization by arbuscular mycorrhiza fungi. *Frontiers in Plant Science*, 1184.
21. Nerva, L., Forgia, M., Ciuffo, M., Chitarra, W., Chiapello, M., Vallino, M., Varese, G., & Turina, M. (2019). The mycovirome of a fungal collection from the sea cucumber holothuria polii. *Virus Research*, 273, 197737.
22. Russo, G., Carotenuto, G., Fiorilli, V., Volpe, V., Faccio, A., Bonfante, P., Chabaud, M., Chiapello, M., Van Damme, D., & Genre, A. (2019). TPLATE recruitment reveals endocytic dynamics at sites of symbiotic interface assembly in arbuscular mycorrhizal interactions. *Frontiers in Plant Science*, 1628.
23. Thomson, N. M., Shirai, T., Chiapello, M., Kondo, A., Mukherjee, K. J., Sivaniah, E., Numata, K., & Summers, D. K. (2018). Efficient 3-hydroxybutyrate production by quiescent escherichia coli microbial cell factories is facilitated by indole-induced proteomic and metabolomic changes. *Biotechnology Journal*, 13(5), 1700571.
24. Chialva, M., Salvioli di Fossalunga, A., Daghino, S., Ghignone, S., Bagnaresi, P., Chiapello, M., Novero, M., Spadaro, D., Perotto, S., & Bonfante, P. (2018). Native soils with their microbiotas elicit a state of alert in tomato plants. *New Phytologist*, 220(4), 1296–1308.
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27. Alqurashi, M., Chiapello, M., Bianchet, C., Paolocci, F., Lilley, K. S., & Gehring, C. (2018). Early responses to severe drought stress in the arabidopsis thaliana cell suspension culture proteome. *Proteomes*, 6(4), 38.
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29. Garcia-Seco, D., Chiapello, M., Bracale, M., Pesce, C., Bagnaresi, P., Dubois, E., Moulin, L., Vannini, C., & Koebnik, R. (2017). Transcriptome and proteome analysis reveal new insight into proximal and distal responses of wheat to foliar infection by xanthomonas translucens. *Scientific Reports*, 7(1), 1–13.
30. Thomson, N. M., Shirai, T., Chiapello, M., Kondo, A., Mukherjee, K. J., Sivaniah, E., Summers, D. K., & Numata, K. (2016). Metabolomic and proteomic analyses of a quiescent escherichia coli cell factory reveal the mechanisms behind its production efficiency. *bioRxiv*, 82305.

31. Zampieri, E., Chiapello, M., Daghino, S., Bonfante, P., & Mello, A. (2016). Soil metaproteomics reveals an inter-kingdom stress response to the presence of black truffles. *Scientific Reports*, 6(1), 1–11.
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34. Gutjahr, C., Radovanovic, D., Geoffroy, J., Zhang, Q., Siegler, H., Chiapello, M., Casieri, L., An, K., An, G., Guiderdoni, E.others. (2012). The half-size ABC transporters STR1 and STR2 are indispensable for mycorrhizal arbuscule formation in rice. *The Plant Journal*, 69(5), 906–920.
35. Chiapello, M., Daghino, S., Martino, E., & Perotto, S. (2010). Cellular response of *fusarium oxysporum* to crocidolite asbestos as revealed by a combined proteomic approach. *Journal of Proteome Research*, 9(8), 3923–3931.
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37. Vallino, M., Martino, E., Boella, F., Murat, C., Chiapello, M., & Perotto, S. (2009). Cu, zn superoxide dismutase and zinc stress in the metal-tolerant ericoid mycorrhizal fungus *oidiodendron maius zn*. *FEMS Microbiology Letters*, 293(1), 48–57.
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Languages

ITALIAN

- ILR: 5
- CEFR: Native
- ACTFL: Distinguished

ENGLISH

- ILR: 3+
- CEFR: C1
- ACTFL: Advanced High

FRENCH

- ILR: 1
- CEFR: A2
- ACTFL: Intermediate Mid

Interests and Activities

Technology, Open-Source, Programming, Reproducible Research, Mountainbiking, Volleyball, Travelling

References

Dr. Mike Deery

University of Cambridge (UK)

CAMBRIDGE CENTER FOR PROTEOMICS

- Email: md289@cam.ac.uk
- Tel: +44 (0) 1223 760253

Prof. Uta Paszkowski

University of Cambridge (UK)

DEPARTMENT OF PLANT SCIENCES

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Marco Chiapello

A handwritten signature in black ink, reading "Marco Chiapello". The signature is fluid and cursive, with a long horizontal stroke at the end.