Marco **Chiapello**

DATA SCIENTIST - BIOINFORMATICIAN

Institute for Sustainable Plant Protection @ Italian National Research Council

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About myself

I am **currently working as Senior PostDoc** at the Institute for Sustainable Plant Protection (Italian National Research Council). My daily focus is on **bioinformatics analysis** and **method standardization** for virus identification and analysis in 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 Bioinformatis 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, unicontigs 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-Traniers programs
- I present regularly results of my data analysis to my supervisor and colleagues
- I 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

- 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	*Turin*
PhD in Biology and Biotechnology of Fungi	*2005 - 2009*
University of York	*York*
Exchange	*2007 - 2008*
University of Calgary	*Calgary*
Exchange	*2005 - 2005*
University of Turin	*Turin*
B. Sc. Plant Biotechnology	*1999 - 2005*
Liceo Scientifico "A. Einstein"	*Turin*
high school graduate	*1994 - 1999*

Work experience

Institute for Sustainable Plant Protection	*National Research Council, Italy*
Postdoctoral Research Fellow	*2018–Present*

- 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	*National Research Council, Italy*
Co-Founder and Member of Institute Bioinformatics Group (I-BiG)	*2018–Present*

- Teaching activities
- Bioinformatics data analysis
- Core facility

Revelo
Milan

CONSULTANT
2020–Present

- Bioinformatics analysis
- Teaching R courses

Frontiers
Lausanne, Switzerland

REVIEW EDITOR
2020–Present

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

Life
Basel, Switzerland

SPECIAL ISSUE EDITOR
2020–Present

- Editor of special issue "Plant Proteomics"

The Carpentries
Worldwide

MENTORING CHAIR
2019–2020

- Recruit mentors/mentees
- Managing The Carpentries Mentoring Groups

Department of Life Sciences And Systems Biology
University of Turin, Italy

MENTOR
2019–2020

- Student mentoring

Department of Life Sciences And Systems Biology
University of Turin, Italy

LECTURER
2019

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

ProteiQ Biosciences GmbH
Berlin

DATA ANALYST
2018

- Proteomics data analysis
- Analysis automatisation using R

Department of Life Sciences And Systems Biology
University of Turin, Italy

DATA ANALYST
2018

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

Liceo Scientifico "Majorana"
Turin, Italy

TEACHER
2018

- Frontal teaching

Evo Pricing
Turin, Italy

DATA SCIENTIST
2018

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

Cambridge Centre for Proteomics
University of Cambridge, United Kingdom

RESEARCH DATA TECHNICIAN
2017–2018

- 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

Department of Biotechnology and Life Science
University of Insubria, Varese, Italy

POSTDOCTORAL RESEARCH FELLOW
2016

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

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
- Performe 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, throught 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 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) *4 days course*

JAN 2022

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

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) *Half day course*

FEB 2020

- Class: PostDocs & PIs
- Subject: Graphical visualization

National Research Council (IT)

Half day course

JAN 2020

- Class: PostDocs & PIs
- Subject: Statistical uncertainty

University of Turin (IT)

24 hours course

JUN 2019

- Class: Master students - Controllo Biologico dei processi e dei prodotti dell'industria
- Subject: Data analysis with R

Universitè Catholique de Louvain

2 days course

MAY 2019

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

University of Naples (IT)

2 days course

FEB 2019

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

University of Debrecen (H)

2 days course

DEC 2018

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

National Research Council (IT)

1 day course

NOV 2018

- Class: Senior scientist
- Subject: Project management Course

National Research Council (IT)

1 day course

OCT 2018

- Class: Senior scientist
- Subject: Introduction to Git

University of Turin (IT)

3 days course

JAN 2018

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

University of Cambridge (UK)

2 days course

SEP 2017

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

University of Cambridge (UK)

1 day course

SEP 2017

- Class: PostDocs & PIs
- Subject: Data analysis with R

The Francis Crick Institute (UK)

2 days course

JUN 2017

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

University of Turin (IT)

4 days course

JAN 2017

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

University of Turin (IT)

3 days course

JUL 2016

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

RPackage Development

intRo.Esercizi

A PACKAGE TO SUPPORT ENTRY-LEVEL R STUDENT LEARNING

• Developed for R course at CNR (OCT 2021)

Ramf

A PACKAGE FOR ARBUSCULAR MYCORRHYZAL FUNGI COLONIZATION SCORING

• Published

Rwaves

A PACKAGE TO ANALYZE ELECTROPENETROGRAPHY DATA

• Under develop

Publications

1. 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.

2. 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.

3. Kuhn, J. H., Adkins, S., Agwanda, B. R., Al Kubrusli, R., Amarasinghe, G. K., Avšič-Županc, T., Ayllón, M. A., Bahl, J., Balkema-Buschmann, A., Ballinger, M. J.others. (2021). 2021 taxonomic update of phylum negarnaviricota (riboviria: Orthornavirae), including the large orders bunyavirales and mononegavirales. *Archives of Virology*, 1–54.

4. 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.

5. 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.

6. 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.

7. Chiapello, M., Zampieri, E., & Mello, A. (2020). A small effort for researchers, a big gain for soil metaproteomics. *Frontiers in Microbiology*, *11*, 88.

8. 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.

9. 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*, *11*, 1686.

10. 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.

11. 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.

12. 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*,.

13. Roth, R., Chiapello, M., Montero, H.others. (2020). A serine/threonine receptor-like kinase regulates arbuscular mycorrhizal symbiosis at the peri-arbuscular membrane in rice. *Nature Communications*, *9*.

14. 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.

15. Roth, R., Hillmer, S., Funaya, C., Chiapello, M., Schumacher, K., Presti, L. L., Kahmann, R., & Paszkowski, U. (2019). Arbuscular cell invasion coincides with extracellular vesicles and membrane tubules. *Nature Plants*, *5*(2), 204–211.

16. 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*, *9*, 244.

17. 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*, *10*, 1184.

18. 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.

19. 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*, *10*, 1628.

20. 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.

21. 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.

22. Fiorilli, V., Vannini, C., Ortolani, F., Garcia-Seco, D., Chiapello, M., Novero, M., Domingo, G., Terzi, V., Morcia, C., Bagnaresi, P.others. (2018). Omics approaches revealed how arbuscular mycorrhizal symbiosis enhances yield and resistance to leaf pathogen in wheat. *Scientific Reports*, *8*(1), 1–18.

23. Agboh, K., Lau, C. H., Khoo, Y. S., Singh, H., Raturi, S., Nair, A. V., Howard, J., Chiapello, M., Feret, R., Deery, M. J.others. (2018). Powering the ABC multidrug exporter LmrA: How nucleotides embrace the ion-motive force. *Science Advances*, *4*(9), eaas9365.

24. 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.

25. Roth, R., Chiapello, M., Montero, H., Gehrig, P., Grossmann, J., O'Holleran, K., Hartken, D., Walters, F., Yang, S.-Y., Hillmer, S.others. (2018). A rice serine/threonine receptor-like kinase regulates arbuscular mycorrhizal symbiosis at the peri-arbuscular membrane. *Nature Communications*, *9*(1), 1–12.

26. 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.

27. 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*, 082305.

28. Zampieri, E., Chiapello, M., Daghino, S., Bonfante, P., & Mello, A. (2016). *Soil metaproteomics reveals an interkingdom stress response to the presence of black truffles. Sci rep 6: 25773.*

29. Chiapello, M., Perotto, S., & Balestrini, R. (2015). Symbiotic proteomics—state of the art in plant–mycorrhizal fungi interactions. *Recent Advances in Proteomics Research*, *10*, 61331.

30. Chiapello, M., Martino, E., & Perotto, S. (2015). Common and metal-specific proteomic responses to cadmium and zinc in the metal tolerant ericoid mycorrhizal fungus oidiodendron maius zn. *Metallomics*, *7*(5), 805–815.

31. 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.

32. 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.

33. Salvioli, A., Chiapello, M., Fontaine, J., Hadj-Sahraoui, A. L., Grandmougin-Ferjani, A., Lanfranco, L., & Bonfante, P. (2010). Endobacteria affect the metabolic profile of their host gigaspora margarita, an arbuscular mycorrhizal fungus. *Environmental Microbiology*, *12*(8), 2083–2095.

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35. Tretiach, M., Favero-Longo, S., Crisafulli, P., Gazzano, C., Carbone, F., Baiocchi, C., Giovine, M., Modenesi, P., Rinino, S., Chiapello, M.others. (2008). How do endolithic lichens dissolve carbonates. *Biology of Lichens and Bryophytes: Lichenological Abstracts-Miscellaneous Publication NA of the American Bryological Society and the International Association for Lichenology*, 72.

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)*

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