

## PERSONAL INFORMATION

## Andrea Silverj



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🌐 <https://andrea-silverj.github.io/>

✉ @silverjand

Sex: Male | Date of birth: 26/03/1993 | Place of birth: Rome | Nationality: Italian

## CURRENT POSITION

## PhD candidate in Agrifood and Environmental Sciences at the University of Trento

## ABOUT ME

I'm a computational evolutionary biologist specialised in viral metagenomics and phylogenomics. I study arboviruses, such as West Nile virus, and phages of the human microbiome. Interested in mobile genetic elements, such as plasmids and transposons.

## EDUCATION AND TRAINING

November 2019 - Ongoing

### PhD in Agrifood and Environmental Sciences

University of Trento, Italy

Thesis title: "Viral metagenomics and phylogenomics for One Health"

Supervisors: Prof. Omar Rota-Stabelli and Prof. Nicola Segata

During my PhD, I developed new metagenomic and phylogenomic pipelines for the study of viruses, working mainly with animal metagenomes and viromes. I worked at the Evolutionary Genomics laboratory (C3A department) and at the Computational Metagenomics laboratory (CIBIO department).

March 2018 - March 2019

### Internship

Edmund Mach Foundation (Italy) – Agrarian Entomology laboratory

Supervisor: Prof. Omar Rota-Stabelli

- Molecular evolution
- Arboviruses
- R and Python programming

October 2016 - March 2019

### Master of Science in Evolutionary Biology

University of Padova, Italy

Thesis title: "An evolutionary analysis of codon usage bias in Zika virus to identify possible vectors and host"

Supervisor: Prof. Giuseppe Fusco

Final grade: 110/110 cum laude

October 2012 - March 2016

### Bachelor of Science in Biological Sciences

University of L'Aquila, Italy

Thesis title: "Aging in vertebrates: an evolutionary point of view"

Supervisor: Prof. Adriano Angelucci

Final grade: 110/110 cum laude

## PERSONAL SKILLS

Mother tongue(s)

Italian

## Other language(s)

UNDERSTANDING		SPEAKING		WRITING
Listening	Reading	Spoken interaction	Spoken production	
English	C2	C2	C2	C2

PhD course held in English, involving numerous participations at conferences, and writing of scientific papers.

Levels: A1/A2: Basic user - B1/B2: Independent user - C1/C2: Proficient user  
[Common European Framework of Reference for Languages](#)

## Position-related skills

- Experience with large-scale analyses of biological sequence data, molecular evolution, comparative methods, phylogenomics and molecular clocks using maximum likelihood and Bayesian methods.

## Digital skills

- UNIX shell scripting
- R and Python programming
- Git
- HPC computing; Containers (Singularity, Docker)
- HTML and CSS
- GIS
- Advanced command of Microsoft Office™ tools
- Very good knowledge of Windows/Linux/macOS operative systems
- Most used softwares: BEAST, PhyloBayes, IQ-TREE, RAxML, MAFFT, bioBakery tools, OrthoFinder, RDP4, Prokka, BLAST, Bowtie2, BRAKER, MaSuRCA, BUSCO, BlobTools

## Developed software

- SiDcal (<https://github.com/andrea-silverj/SiDcal>)

## Scientific interests

- Evolutionary biology, phylogenomics, computational biology, bioinformatics, viral metagenomics, mobilome, philosophy of biology

## ADDITIONAL INFORMATION

## Memberships

- Member of the Society for Molecular Biology and Evolution (since 2019)
- Member of the Italian Society for Evolutionary Biology (since 2017)

## Awards

- Best talk at the XVI FISV congress (2022) - Environmental, Evolutionary and Developmental Biology section
- Winner of the "Golden Charley Prize" for the best creative performance in the outreach of Evolutionary Biology at the 8<sup>th</sup> congress of the Italian Society for Evolutionary Biology (2019)

## Outreach

- European Researcher's Night at the MUSE Science Museum in Trento
- Outreaching the behaviour of *Drosophila suzukii* (2018)
- Molecular clocks to study the evolution of life on Earth (2021)

## Organised workshops

- Founder and organiser of the Italian Phylogenetics Workshop (ITA\*PHY)  
The first edition, held in June 2023, has seen more than 30 participants from different parts of the world, with three invited speakers (Sandra Álvarez Carretero, Benoît Morel and Omar Rota-Stabelli).

## Driving license

- Italian driving licence (B)

## References

- Prof. Omar Rota-Stabelli, PhD. E-mail: [omar.rota@fmach.it](mailto:omar.rota@fmach.it)
- Prof. Nicola Segata, PhD. E-mail: [nicola.segata@unitn.it](mailto:nicola.segata@unitn.it)
- Annapaola Rizzoli, PhD. E-mail: [annapaola.rizzoli@fmach.it](mailto:annapaola.rizzoli@fmach.it)
- Prof. Giuseppe Fusco, PhD. E-mail: [giuseppe.fusco@unipd.it](mailto:giuseppe.fusco@unipd.it)

## List of publications

### Published in peer-reviewed journals

Silverj\* A., Rota-Stabelli O. (2020) On the correct interpretation of similarity index in codon usage studies: comparison with four other metrics and implications for Zika and West Nile virus. *Virus Research*. 286, 198097. <https://doi.org/10.1016/j.virusres.2020.198097>

Bianco L., Moser M., Silverj A., Micheletti D., Lorenzin G., Collini L., Barbareschi M., Lanzafame P., Segata N., Pindo M., Franceschi P., Rota-Stabelli O., Rizzoli A., Fontana P., Donati C. (2022) On the origin and propagation of the COVID-19 outbreak in the Italian province of Trento, a tourist region of Northern Italy. *Viruses*. Mar 11;14(3):580. <https://doi.org/10.3390/v14030580>

Mencattelli\* G., Silverj\* A., Iapaolo F., Ippoliti C., Teodori C., Di Gennaro A., Curini V., Candeloro L., Conte A., Polci A., Morelli D., Perrotta M.G., Marini G., Rosà R., Monaco F., Segata N., Rizzoli A., Rota-Stabelli O., Savini G., West Nile Working Group (2022) Epidemiological and evolutionary analysis of West Nile virus lineage 2 in Italy. *Viruses*. 15(1), 35. <https://doi.org/10.3390/v15010035>

Marchesini A., Silverj A., Torre S., Rota-Stabelli O., Girardi M., Passeri I., Fracasso I., Sebastiani F., Vernesi C. (2023) First genome-wide data from Italian European beech (*Fagus sylvatica* L.): Strong and ancient differentiation between Alps and Apennines. *PLOS ONE*. 18(7): e0288986 <https://doi.org/10.1371/journal.pone.0288986>

Mencattelli\* G., Ndione\* H.D., Silverj\* A., Diagne M.M., Curini V., Teodori L., Di Domenico M., Mbaye R., Leone A., Marcacci M., Gaye A., Ndiaye E., Diallo D., Ancora M., Secondini B., Di Lollo V., Mangone I., Bucciaccchio A., Polci A., Marini G., Rosà R., Segata N., Fall G., Cammà C., Monaco F., Diallo M., Rota-Stabelli O., Faye O., Rizzoli A., Savini G. (2023) Spatial and temporal dynamics of West Nile virus between Africa and Europe. *Nature communications*. 14, 6440. <https://doi.org/10.1038/s41467-023-42185-7>.

### Submitted or available on bioRxiv

Pinto F., Zolfo M., Beghini F., Armanini F., Asnicar F., Silverj A., Boscaini A., Salmaso N., Segata N. (2020) A step-by-step sequence-based analysis of virome enrichment protocol for freshwater and sediment samples. *Applied and Environmental Microbiology*. Preprint available on *bioRxiv*: <https://doi.org/10.1101/2020.09.17.302836>

Silverj\* A., Mencattelli\* G., Monaco F., Iapaolo F., Teodori L., Leone A., Polci A., Curini V., Di Domenico M., Secondini B., Di Lollo V., Ancora M., Di Gennaro A., Morelli D., Perrotta M.G., Marini G., Rosà R., Segata N., Rota-Stabelli O., Rizzoli A., Savini G. (2023) Origin and evolution of West Nile virus lineage 1 in Italy. *Submitted in Epidemiology&Infection*

Zadra N., Tatti A., Silverj A., Piccinno R., Devilliers J., Lewis C., Arnoldi D., Montarsi F., Escuer P., Fusco G., De Sanctis V., Feuda R., Sánchez-Gracia A., Rizzoli A., Rota-Stabelli O. Genome skimming of *Aedes japonicus* and *Aedes koreicus* from Italy and an updated picture of their evolution based on mitogenomics and barcoding. *Submitted in Insects*

### In preparation

Silverj\* A., Alfano N., Tagliapietra V., Rosso F., Segata N., Rota-Stabelli O. and Rizzoli A. Evolutionary analysis of viral metagenome-assembled genomes from Italian tick populations detects pathogens and reveals new viral species.

Zolfo M., Silverj A., Blanco-Míguez A., Manghi P., Rota-Stabelli O., Pinto F., Ciciani M., Cereseto A., Asnicar F., Yamada T., Segata, N. Discovering and exploring the hidden diversity of the human gut viruses using highly enriched virome samples.

Silverj\* A., Zolfo M., Asnicar F., Blanco-Míguez A., Cumbo F., Huang K.D., Pinto F., Rota-Stabelli O., Segata N. Large-scale genome reconstructions from human gut metagenomes to study phage-host relationships.

Silverj\* A., Zadra N., Martelossi J., Tatti A., Battista M., Fouani J., Scala M., Roselli G., Pedrazzoli F., Vicelli B., Pindo M., Anfora G., Mazzoni V., Luchetti A. and Rota-Stabelli O. The short-read genome of two populations of the parasitoid wasp *Trissolcus japonicus* from Italy: male haploidy, genome of harbored *Wolbachia*, and identical mitogenomes.

**Note:** the symbol “\*” indicates first or co-first authorship.

## Conferences

### SMBE2023

19/03/2023 – 21/03/2023 – Ferrara (Italy)

“Evolutionary analysis of viral metagenome-assembled genomes from Italian tick populations sampled on a latitudinal gradient.” Poster presentation.

### ARES/EVA-G joint session

19/03/2023 – 21/03/2023 – Padua (Italy)

“Evolutionary analysis of viral metagenome-assembled genomes from Italian tick populations.” and “Eco-epidemiological and genetic evolutionary features of WNV L1 and L2 in Italy.” Oral presentation as invited speaker.

### Cell Symposium: Viruses in health and disease

19/03/2023 – 21/03/2023 – Sitges (Spain)

"Large-scale genome reconstructions from human gut metagenomes to study phage-host relationships." Oral presentation.

9<sup>th</sup> SIBE/ISEB (Italian Society for Evolutionary Biology) congress

04/09/2022 – 07/09/2022 – Ancona (Italy)

"Large scale genome reconstructions from human gut metagenomes reveal weak coevolution between phages and their bacterial hosts." Oral presentation.

FISV2022 congress

09/2022 – Naples (Italy)

"Large scale genome reconstructions from human gut metagenomes reveal weak coevolution between phages and their bacterial hosts." Oral presentation.

SMBEv2021

2021 – Online

"Large scale genome reconstructions from human gut metagenomes reveal weak coevolution between phages and their bacterial hosts." Oral presentation.

Virtual FISV symposium on SARS-CoV-2 biology and COVID-19: current research and perspectives.

16 September 2020.

"Tracing the SARS-CoV-2 outbreak in Trentino using Nanopore sequencing". Abstract.

8<sup>th</sup> SIBE/ISEB (Italian Society for Evolutionary Biology) congress

09/2019 – Padua (Italy)

"Codon usage indicates that amphibians, reptiles and birds are major hosts for Zika and other arboviruses: implications for epidemiology and surveillance." Oral presentation.

EuroScitizen WG5 Meeting

04/2019 – Paris (France)

Project contribution.

XI European congress of entomology

07/2018 – Naples (Italy)

"Using codon usage bias to investigate the role of alternative vectors in the spread of Zika." Poster presentation.

7<sup>th</sup> SIBE/ISEB (Italian Society for Evolutionary Biology) congress

28/08/2017 – 31/08/2017 – Rome (Italy)

"404 Error: (Evolutionary) Page Not Found." Poster presentation.

## **Seminars, courses, workshops, summer schools**

Bridging Phylogeny and Population genetics: Inferring divergence and selection at both interspecies and intraspecies level (summer school)

Held at the Campus of Fondazione Edmund Mach in San Michele all'Adige from 27/08/2019 to 01/09/2019

Laboratory health and safety (LHS) - Specific training

Held at Edmund Mach Foundation by C3A and FEM health and safety officers and consultants in 01/2020 (8 hours)

Hit the Ground Running with SNP Calling for PopGen and Evolutionary Analyses

Held online on 11/09/2020

Large-scale Biological Network Analysis and Visualization Using CyVerse

Held online on 05/03/2021

AGS Virtual Symposium Spring 2021

Held online on 13/04/2021

Molecular Phylogenetics: from genes to communities to kingdoms

Hosted by the University of Pavia and held online from 26/04/2021 to 30/04/2021

I Simposio Virtuale FISV "Life Science and Society"

Held online on 28/04/2021

DrosEU workshop

Held online on 21/06/2021 and 22/06/2021

High-Performance Computing summer School 2021

Held in Trento, Italy, from August 30<sup>th</sup> to September 3<sup>rd</sup>, 2021 (24 hours)

Emerging viral threats in a globalized society: molecular, epidemiological, clinical and social aspects of emerging viral diseases

Hosted by the University of Pavia and held online from 06/09/2021 to 10/09/2021