

# Guido Uguzzoni

## CONTACTS

<i>Institute</i>	CEA-IRIG-BGE
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## CURRENT POSITION

CEA RESEARCHER	FROM DEC 2024
Interdisciplinary Research Institute of Grenoble (IRIG)	
Biosciences and bioengineering for Health unit (BGE)	
<i>Artificial Intelligence for health. Protein design. Functional genomics.</i>	

## PREVIOUS APPOINTMENTS

2024	Researcher
<i>Institute</i>	Candiolo Cancer Institute - Turin
<i>lab</i>	Pr. S. Marchiò - AI, Bioinformatics, Oncology <i>AI applications to design antitumor peptides</i>
2022 - 2023	Postdoc
<i>Institute</i>	Italian Institute for Genomic Medicine - Turin
<i>lab</i>	Pr. A. Pagnani - AI, Computational Biology <i>AI framework to design therapeutical proteins</i>
2018 - 2022	Postdoc
<i>Institute</i>	Polytechnic University of Turin
<i>lab</i>	Dipartimento Scienza Applicata e Tecnologia Pr. A. Pagnani - AI, Computational Biology <i>Generative AI models of protein sequences</i>
2016 - 2017	Research Engineer
<i>Institute</i>	Institut Curie - Paris
<i>lab</i>	Laboratoire Physico Chimie Curie Pr. H. Isambert - Pr. A. Pagnani - Bioinformatics <i>Causal graphs inference from clinical records</i>
2014 - 2016	Postdoc
<i>Institute</i>	Université Pierre et Marie Curie (Sorbonne Universités) - Paris
<i>lab</i>	Laboratoire de Biologie Computationnelle et Quantitative Pr. M. Weigt - Statistical Genomics and Biological Physics <i>Structural predictions from homologous protein sequences</i>

## EDUCATION

2022	<b>Master of Business Administration</b>
<i>Institute</i>	MIB Trieste School of Management EXECUTIVE MBA IN BUSINESS INNOVATION
2014	<b>Ph.D</b>
<i>Institute</i>	Università di Parma
Thesis	STATISTICAL PHYSICS AND COMPUTATIONAL BIOLOGY. <i>Statistical mechanics models for biological systems: cooperativity in biochemistry and maturation of antibodies.</i>
2010	<b>Master's degree</b>
<i>Institute</i>	Università di Roma "La Sapienza"
	PHYSICS
<i>Mark</i>	110/110 with praise
2007	<b>Bachelor's degree</b>
<i>Institute</i>	Università di Roma "La Sapienza"
	PHYSICS
<i>Mark</i>	110/110

## ACADEMIC ACTIVITIES AND CONTRIBUTIONS

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- 18 peer-reviewed scientific articles (12 first author, 2 last author)
- 1 patent (WO2020255058A1)
- Oral contribution to 20 conferences and workshops
- Grant €100k Proof-of-Concept Program “Vertis Venture 3 Tech Transfer” (VV3TT) 2020
- Fellowships for my PhD at University of Parma
- Scientific journal editor (Elsevier - Computer Methods and Programs in Biomedicine)
- Referee for many scientific journals (PLoS Comput. Biol., MBE, Bioinformatics, ..)
- Co-tutoring Ph.D. and master students
- Served as a teaching assistant
- Award for startup Business Plan development (Piemonte Startup 2022)

## RELEVANT PUBLICATIONS

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Jorge Fernandez-de-Cossio-Diaz\*, Guido Uguzzoni\*, Kévin Ricard, Andrea Pagnani, Francesca Anselmi, Clément Nizak, and Olivier Rivoire *Inference and design of antibody specificity: from experiments to models and back* **PLoS Comp. Biol.** (2024) <https://doi.org/10.1101/2023.10.23.563570>

A multi-stage approach combining phage display experiments with machine learning to predict antibody binding profiles and design sequences with customized specificity. Successfully demonstrated the computational design of antibodies with tailored specificity profiles for specific targets or with cross-specificity for multiple ligands.

Jeanne Trinquier\*, Guido Uguzzoni, Andrea Pagnani, Francesco Zamponi, and Martin Weigt. *Efficient generative modeling of protein sequences using simple autoregressive models.*

**Nature communications** (2021) <https://www.nature.com/articles/s41467-021-25756-4>

Development of simple autoregressive models for protein sequence generation that match performance of more complex approaches at reduced computational cost. The models estimate sequence likelihood and quantify functional sequence space.

Fernandez-de-Cossio-Diaz\*, Jorge, Guido Uguzzoni\*, and Andrea Pagnani. *Unsupervised inference of protein fitness landscape from deep mutational scan.* **Molecular Biology and Evolution** (2020) <https://academic.oup.com/mbe/article/38/1/318/5889958>

A data-driven maximum likelihood approach for modeling genotype-phenotype relationships from experimental data. The resulting fitness landscape demonstrates robustness against experimental variations and superior generalization capabilities for exploring sequence space and predicting high-fitness variants.

Guido Uguzzoni\*, Shalini John Lovis\*, Francesco Oteri, Alexander Schug, Hendrik Szurmant, Martin Weigt. *Large-scale identification of coevolution signals across homo-oligomeric protein interfaces by direct coupling analysis.* **PNAS** (2017) <https://www.pnas.org/doi/abs/10.1073/pnas.1615068114>

Application of statistical inference techniques to identify protein contacts from coevolution patterns in sequence databases. Focusing on homo-oligomeric protein assemblies, the study provides systematic evidence of the method's effectiveness across nearly 2,000 protein families.

## PUBLICATIONS

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J. Fernandez-de-Cossio-Diaz, G. Uguzzoni, K. Ricard, F. Anselmi, C. Nizak, A. Pagnani, O. Rivoire, **PLoS Computational Biology**, 20, e1012522, 2024.

L. Sesta, A. Pagnani, J. Fernandez-de-Cossio-Diaz, G. Uguzzoni, **PLOS Computational Biology**, 20, 1-16, 2024.

M. De Leonardis, J. Fernandez-de-Cossio-Diaz, G. Uguzzoni, A. Pagnani, **BMC Bioinformatics**, 25, 229, 2024.

G. Uguzzoni, A. Pagnani, J. Fernandez de Cossio Dia, US Patent App. 17/620,768, 2022.

J. Trinquier, G. Uguzzoni, A. Pagnani, F. Zamponi, M. Weigt, **Nature Communications**, 12, 5800, 2021.

J. Fernandez-de-Cossio-Diaz, G. Uguzzoni, A. Pagnani, **Molecular Biology and Evolution**, 38, 318-328, 2021.

L. Sesta, G. Uguzzoni, J. Fernandez-de-Cossio-Diaz, A. Pagnani, **International Journal of Molecular Sciences**, 22, 10908, 2021.

V. Cabeli, L. Verny, N. Sella, G. Uguzzoni, M. Verny, H. Isambert, **PLoS Computational Biology**, 16, e1007866, 2020.

N. Sella, L. Verny, G. Uguzzoni, S. Affeldt, H. Isambert, **Bioinformatics**, 34, 2311-2313, 2018.

G. Uguzzoni, S. John Lovis, F. Oteri, A. Schug, H. Szurmant, M. Weigt, **Proceedings of the National Academy of Sciences**, 114, E2662-E2671, 2017.

L. Asti, G. Uguzzoni, P. Marcatili, A. Pagnani, **PLoS Computational Biology**, 12, e1004870, 2016.

A. Coucke, G. Uguzzoni, F. Oteri, S. Cocco, R. Monasson, M. Weigt, **The Journal of Chemical Physics**, 145, 17, 2016.

E. Agliari, A. Barra, R. Burioni, A. Di Biasio, G. Uguzzoni, **Scientific Reports**, 3, 3458, 2013.

E. Agliari, L. Asti, A. Barra, R. Burioni, G. Uguzzoni, **Journal of Physics A: Mathematical and Theoretical**, 45, 365001, 2012.

A. De Martino, D. De Martino, R. Mulet, G. Uguzzoni, **PLoS ONE**, 7, e39849, 2012.

E. Agliari, R. Burioni, G. Uguzzoni, **New Journal of Physics**, 14, 063027, 2012.