
Formation

- 2015 – 2018 **Doctorat en Informatique**, *Sorbonne Université*
- Laboratoire : Biologie Quantitative et Computationnelle
 - Directeur de thèse: Martin Weigt
 - Titre : *Comprendre et améliorer les modèles statistiques de séquences de protéines*
- 2014 – 2015 **Master de physique ICFP**, *Université Pierre et Marie Curie*
Intitulé: *Physique macroscopique et complexité*
- 2011 – 2014 **Formation d'ingénieur généraliste**, *ENSTA Paristech*
- 2009 – 2011 **Classes Préparatoires**, *Lycée du Parc, Lyon*

Expérience professionnelle

- Depuis 04/2023 **Enseignant-chercheur postdoctoral**, *École Polytechnique de Turin*
Dans l'équipe "Statistical Physics and Interdisciplinary Applications".
- 2019 – 2023 **Chercheur postdoctoral**, *Université de Bâle*
Équipe du professeur Richard Neher.
- 2015 – 2018 **Doctorat**, *Sorbonne Université*
Au Laboratoire de Biologie Computationnelle et Quantitative, sous la direction du professeur Martin Weigt.
- 2014 **Stage**, *ESPCI Paris*
Au Laboratoire de Nanobiophysique, sous la direction du professeur Ulrich Bockelmann.
- 2013 **Stage**, *Schlumberger Doll Research Center*
Stage de recherche, encadré par Nikita Chugunov.

Compétences

Programmation

- Julia
- Python
- Git

Langues

- Français: natif
- Anglais: courant
- Italien: courant
- Allemand: Intermédiaire

Publications

- 2025 M. De Leonardis, A. Pagnani, **P. Barrat-Charlaix**, *Reconstruction of ancestral protein sequences using autoregressive generative models*, accepted in Molecular Biology and Evolution, 2025
- 2024 **P. Barrat-Charlaix**, R. Neher, *Eco-evolutionary dynamics of adapting pathogens and host immunity*, eLife, 2024
- 2022 **P. Barrat-Charlaix**, T. Vaughan, R. Neher, *TreeKnit : Inferring Ancestral Reassortment Graphs of influenza viruses*, PLOS Computational Biology, 2022
- 2021 E. R. Horta, A. Lage-Castellanos, M. Weigt, **P. Barrat-Charlaix**, *Global multivariate model learning from hierarchically correlated data*, Journal of Statistical Mechanics, 2021
- P. Barrat-Charlaix**, A.P. Muntoni, K. Shimagaki, M. Weigt, F. Zamponi, *Sparse generative modeling via parameter reduction of Boltzmann machines : Application to protein-sequence families*, Physical Review E, 2021
- P. Barrat-Charlaix**, J. Huddleston, T. Bedford, R. Neher, *Limited predictability of amino acid substitutions in seasonal influenza viruses*, Molecular Biology and Evolution, 2021
- 2020 J. Huddleston, J. R Barnes, T. Rowe, X. Xu, R. Kondor, D.E Wentworth, L. Whittaker, B. Ermetal, R.S. Daniels, J. W McCauley, S. Fujisaki, K.Nakamura, N. Kishida, S. Watanabe, H. Hasegawa, I. Barr, K. Subbarao, **P. Barrat-Charlaix**, R. A Neher, T. Bedford, *Integrating genotypes and phenotypes improves long-term forecasts of seasonal influenza A/H3N2 evolution*, eLife, 2020
- W. P. Russ, M. Figliuzzi, C. Stocker, **P. Barrat-Charlaix**, M. Socolich, P. Kast, D. Hilvert, R. Monasson, S. Cocco, M. Weigt, R. Ranganathan, *Evolution-based design of chorismate mutase enzymes*, Science, 2020
- 2019 Rodriguez Horta, **P. Barrat-Charlaix**, M. Weigt, *Toward Inferring Potts Models for Phylogenetically Correlated Sequence Data*, MDPI Entropy, 2019
- 2018 Figliuzzi, **P. Barrat-Charlaix**, M. Weigt, *How Pairwise Coevolutionary Models Capture the Collective Residue Variability in Proteins*, Molecular Biology and Evolution, 2018
- 2016 **P. Barrat-Charlaix**, M. Figliuzzi, M. Weigt, *Improving landscape inference by integrating heterogeneous data in the inverse Ising problem*, Scientific Reports, 2016

Brevets

- 2016 N. Chugunov, T.S. Ramakrishnan, **P. Barrat-Charlaix**, *Methods for adaptive optimization of enhanced oil recovery performance under uncertainty*, US Patent App. 14/949,032, 2016

Logiciels

TreeKnit, <https://github.com/PierreBarrat/TreeKnit.jl>

Logiciel permettant d'inférer un Graphe de Réassortiment Ancestral à partir de deux arbres généalogiques.

Conférences

- 2023 *Influenza : Limited predictability of evolution and Ecology of host and pathogen*, Biological Evolution Across Scales, Lausanne, 2023

Influenza : Limited predictability of evolution & Ecology of host and pathogen, Biological sequence variation : from statistical modeling to structure, function, and evolutionary dynamics, Cargèse, 2023

2022 *TreeKnit : Inferring Ancestral Reassortment Graphs of influenza viruses*, SIB days, Bienne, 2022

2019 *Towards inferring Potts models for evolutionary correlated sequence data*, From Molecular Basis to Predictability and Control of Evolution, Stockholm, 2019

Statistical models of protein sequences : Generative models & evolution-guided protein design, BC2 at Basel Life 2019, Basel, 2019

2018 *How pairwise coevolutionary models capture the collective residue variability in proteins*, Regulation and Inference in Biological Networks, Bardonnechia, 2018

2017 *How pairwise coevolutionary models capture the collective residue variability in proteins*, UPMC Young Researcher's Meeting 2017, Paris, 2017

Enseignement

- 2023 – *École Polytechnique de Turin*,
TD, TP et examens du cours *Fisica 1*.
- 2019–2023 *Université de Bâle*,
TD du cours *Physics of Life*.
- 2015–2018 *Polytech Sorbonne*,
- TP d'électronique
 - TP d'informatique
 - TD de mathématiques

Autres activités

Peer-review Pour les journaux suivants:

- PLOS One
- PLOS Computational Biology
- Oxford Bioinformatics
- Chemical Science
- Journal of Statistical moderner-cvhanics : Theory and Experiments
- Journal of Statistical Physics
- Physical Review Research

2019-2023 Co-organisation du séminaire *Basel Computational Biology Seminar Series*.