Thomas Dupic

PhD

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Research Experience

- 2020-present **Post-doctoral student**, Desai Lab (Harvard, USA), with Michael Desai, Antibodies Evolution, Experimental and computational study of the affinity maturation landscape.
 - 2018-2020 **Post-doctoral student**, *LPENS (ENS, France)*, in the group of Aleksandra Walczak and Thierry Mora, structure and generation of the immune repertoire, relationship and interactions between the two polymer chains composing the T-cell receptor.
 - 2015-2018 **Doctoral student**, LPTHE (UPMC, France) supervised by Yacine Ikhlef and Benoît Estienne, loop models and conformal field theories, study of a particular class of two-dimensional polymer models at criticality, entanglement entropy in critical non-unitary systems.
 - 2015 Internship at the LPTHE (UPMC), with B. Estienne and Y. Ikhlef.
 - 2014 Internship at the LPS (ENS), ABCD group, with J-F. Allemand, Optical microscopy, tracking of a magnetic bead through diffraction patterns, Building of an optical setup.
 - 2013 Internship at the disordered system group in King's College London, with I.P. Castillo, Eigenvalues of product of random matrices; behaviour of vicious brownian walkers.
 - 2012 Internship at the laboratory Kastler Brossel, non-destructive quantum measurement: photons and atoms in cavity with M.Brune and P. Rouchon.

Education

- 2013 Master ICFP, Theoretical Physics.
- 2012 Master ICFP.
- 2011 Bachelors of Science in Mathematics and in Physics.
- 2010-2014 École normale supérieure (ENS, Paris).
- 2009-2010 Classe Préparatoire (Nantes).
 - 2009 A-levels with First Class Honors.

Area of expertise

Scientific

Immunology Immune repertoire, transcriptomics, antibody and T-cell receptor specificity.

Evolutionary Population genetics, fitness landscapes, viral evolution.

biology

Physics Statistical physics, mathematical physics.

Methods

Molecular Flow-cytometry, Sequencing, single-cell methods incl. scRNA-biology seq, transformations, cloning.

Protein Recombinant protein, Column chromatography, Western Blot. fabrication

Cell culture Bacteria, Yeasts, Mammalian cell line.

Programming **Python, C++, Rust, R**, Data analysis, statistics, optimization (LP, MIP), version control

Teaching Experience

- 2015-2018 **UPMC**, Teaching assistant (theoretical and practical), electromagnetism and optics .
 - 2013 Lycée Henri IV, Oral examiner in classe préparatoire.

Oral communications

- July 2023 **EMBO Predicting evolution**, The evolution of the Omicron SARS-CoV-2 variant, Heidelberg, Germany.
- April 2023 **Biological sequence variation**, The evolution of the Omicron SARS-CoV-2 variant, Cargèse, France.
- September **ENS seminar**, The evolution of the Omicron SARS-CoV-2 variant, Paris, 2022 France.
- April 2021 **CSHL virtual conference on Systems Immunology**, *Immune fingerprints*, Online.
- September Harvard Physics Research Scholar Retreat, Immune fingerprints, 2020 Online.
- March 2020 Statistics of the T-cell repertoire, QBio Fellow at Harvard's NSF-Simons Center, Online.
- August 2019 **qBio**, Genesis of the α - β T-cell receptor, San Francisco, US.
 - April 2019 Tumors and immune system, from theory to therapy, Genesis of the α - β T-cell receptor, Cargèse, France.

- August 2018 International Physics of living systems, Genesis of the α - β T-cell receptor, Houston, US.
 - June 2016 ICFT 2016 (UK Meeting on Integrable and Conformal Field Theory), Relation between fully packed loop models and W_3 .
- October 2016 Workshop on exactly solvable models, The fully packed loop model on the honeycomb lattice, Nancy, France.

Publications

2023 Moulana, Alief, Thomas Dupic, Angela Phillips, et al. (2023). "Genotype-Phenotype Landscapes for Immune-Pathogen Coevolution". In: Trends in immunology 44.5.

Moulana, Alief, Thomas Dupic, Angela M Phillips, et al. (2023). "The Landscape of Antibody Binding Affinity in SARS-CoV-2 Omicron BA.1 Evolution". In: *eLife* 12. Ed. by Jos W van der Meer, e83442.

Phillips, Angela M, Daniel P Maurer, et al. (2023). "Hierarchical Sequence-Affinity Landscapes Shape the Evolution of Breadth in an Anti-Influenza Receptor Binding Site Antibody". In: *eLife* 12. Ed. by Tomohiro Kurosaki and Betty Diamond, e83628.

- 2022 Moulana, Alief, Thomas Dupic, Angela M. Phillips, et al. (2022). "Compensatory Epistasis Maintains ACE2 Affinity in SARS-CoV-2 Omicron BA.1". In: *Nature Communications* 13.1, p. 7011.
 - Spisak, Natanael et al. (2022). Combining Mutation and Recombination Statistics to Infer Clonal Families in Antibody Repertoires.
- 2021 Dupic, Thomas, Meriem Bensouda Koraichi, et al. (2021). "Immune Fingerprinting through Repertoire Similarity". In: PLoS genetics 17.1, e1009301.
 - Phillips, Angela M, Katherine R Lawrence, et al. (2021). "Binding Affinity Landscapes Constrain the Evolution of Broadly Neutralizing Anti-Influenza Antibodies". In: eLife 10. Ed. by Sarel Jacob Fleishman et al., e71393.
- 2020 Sethna, Zachary et al. (2020). "Population Variability in the Generation and Selection of T-cell Repertoires". In: *PLoS computational biology* 16.12, e1008394.
- 2019 Dupic, T., B. Estienne, and Y. Ikhlef (2019a). "The Imaginary Toda Field Theory". In: Journal of Physics A: Mathematical and Theoretical 52.10, p. 105201.
 - Dupic, T., B. Estienne, and Y. Ikhlef (2019b). "Three-Point Functions in the Fully Packed Loop Model on the Honeycomb Lattice". In: *Journal of Physics A: Mathematical and Theoretical* 52.20, p. 205003.

- Dupic, Thomas, Quentin Marcou, et al. (2019). "Genesis of the $\alpha\beta$ T-cell Receptor". In: *PLOS Computational Biology* 15.3, e1006874.
- 2018 Dupic, Thomas, Benoit Estienne, and Yacine Ikhlef (2018). "Entanglement Entropies of Minimal Models from Null-Vectors". In: *SciPost Physics* 4.6, p. 031.
- 2016 Dupic, Thomas, Benoît Estienne, and Yacine Ikhlef (2016). "The Fully Packed Loop Model as a Non-Rational W3 Conformal Field Theory". In: Journal of Physics A: Mathematical and Theoretical 49.
- Castillo, Isaac Pérez and Thomas Dupic (2014). "Reunion Probabilities of N One-Dimensional Random Walkers with Mixed Boundary Conditions".
 In: Journal of Statistical Physics 156.3, pp. 606–616.