Hugo Talibart

27 years old

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EDUCATION

November 2017- February 2021

PhD in Computer Science

Dyliss team, Inria, Université de Rennes 1 (France)

supervised by François Coste and Jacques Nicolas

Introduction of an optimal method to align models representing protein sequences with coevolution information, with application to homology search.

2016 – 2017

Master's Degree in Theoretical Computer Science

Université de Rouen, France

Automata theory, String Algorithms in Bioinformatics

2012 – 2017

Engineering Degree in Mathematics

Institut National des Sciences Appliquées de Rouen (INSA Rouen), France

Statistics, Artificial Intelligence, Operations Research

EXPERIENCE

September 2021 - now

Postdoctoral researcher

Institut de Systématique, Évolution, Biodiversité, MNHN Paris (France)

Research project: introduction of models representing protein sequences with coevolution information specifically designed for pairwise comparison.

Main supervisor of an internship: computation of pairwise amino acid substitution probabilities.

March - April 2021

Research engineer

Dyliss team, Inria, Université de Rennes 1 (France)

Additional development on the protein sequence alignment method designed during my PhD.

May - October 2017

End-of-studies internship

LITIS Lab, Université de Rouen (France)

supervised by Pierrick Tranouez

Supervised learning of emergent structures in agent-based simulations using neural networks.

June - September 2016

International internship

Algorithms & Bioinformatics Team, King's College London (United Kingdom)

supervised by Kathleen Steinhöfel

RNA meta-stable secondary structures clustering.

ARTICLES

- H. Talibart and F. Coste. "PPalign: optimal alignment of Potts models representing proteins with direct coupling information". In: *BMC bioinformatics* 22.1 (2021), pp. 1–22
- W. Dyrka, M. Pyzik, F. Coste and H. Talibart. "Estimating probabilistic context-free grammars for proteins using contact map constraints". In: *PeerJ* 7 (2019), e6559

COMMUNICATIONS

- H. Talibart, M. Carpentier and F. Coste. "PPalign: optimal alignment of Potts models representing proteins with direct coupling information". In: *ISMB 2022 - Conference on Intelligent Systems for Molecular Biology*. 2022
- H. Talibart and F. Coste. "ComPotts: Optimal alignment of coevolutionary models for protein sequences". In: *JOBIM 2020-Journées Ouvertes Biologie, Informatique et Mathématiques*. 2020
- H. Talibart and F. Coste. "Using residues coevolution to search for protein homologs through alignment of Potts models". In: *JOBIM 2019-Journées Ouvertes Biologie, Informatique et Mathématiques*. 2019

SKILLS

Languages

- French – native speaker
- English – fluent (TOEIC: 975/990)
- Spanish – notions

Computer skills

- Python
- C/C++
- LaTeX
- Matlab
- Java
- Linux

MISCELLANEOUS

Science outreach and teaching experience

- *Le Langage comme Inspiration*: short film for the *Sciences en Cour[t]s* 2018 festival
  First jury prize and "Audience's favorite" award
- Tutorials for bachelor students: Introduction to computer progamming in Python
  2017-2018 (ISTIC, Université de Rennes 1)