Hugo Talibart

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Profile

Computer scientist with 8+ years of expertise in algorithm design and implementation, with experience building and shipping software. Looking for a software engineering role where rigorous algorithmic thinking meets concrete development.

Experience

Postdoctoral Researcher *Université Libre de Bruxelles*, Brussels (Belgium) 2023 – Present

- Designed ILP formulations for bias-controlled machine learning benchmark construction – applied to drug-target interaction prediction.
- Designed and trained a large-scale Transformer VAE for molecular generation – architecture design, training at scale. Released as a pip package.
  github.com/3BioCompBio/chembed
- Collaborated on a sparse structure-informed probabilistic graphical model with C++ solver and Python interface, achieving orders of magnitude speedup over fully-connected models – applied to mutation effect prediction, state-of-the-art on standard benchmarks. Released as a pip package.
  github.com/3BioCompBio/StructureDCA
- Supervised two Master's students and an intern on benchmark design and deep learning topics.

Postdoctoral Researcher *Muséum National d'Histoire Naturelle, Sorbonne Université*, Paris (France) 2021 – 2023

- Extended my PhD's probabilistic graphical model alignment framework with a redesigned statistical inference pipeline – faster inference, improved robustness on shallow data.

PhD Researcher *INRIA, Université de Rennes*, Rennes (France) 2017 – 2021

- Introduced PPalign: first exact ILP-based alignment of probabilistic graphical models, solved in tractable time – applied to protein remote homology detection, outperforming HMM baselines.

Education

PhD in Computer Science *INRIA, Université de Rennes 1*, Rennes (France) 2017 – 2021

Master in Theoretical Computer Science *Université de Rouen*, Rouen (France) 2016 – 2017

Engineering Degree in Mathematics *Institut National des Sciences Appliquées (INSA)*, Rouen (France) 2012 – 2017

Skills

Languages Python, C/C++, JavaScript, Bash
ML & Data PyTorch, NumPy, SciPy, Pandas, scikit-learn
Tools git, conda, docker/Singularity
Environment Linux, cluster computing (Slurm)

Personal projects

wikiddle.com *Daily Wikipedia puzzle game*

- JavaScript frontend
- Python backend with FastAPI and SQL
- Self-hosted on a self-administered server
- github.com/htalibart/wikiddle

Selected publications

- **Talibart H**, Gilis D. *Learning a chemistry-aware latent space for molecular encoding and generation with a large-scale Transformer Variational Autoencoder.* bioRxiv, 2025.
- Tsishyn M, **Talibart H**, Rooman M, Pucci F. *Structure-informed direct coupling analysis improves protein mutational landscape predictions.* bioRxiv, 2026.
- **Talibart H**, Coste F. *PPalign: optimal alignment of Potts models representing proteins with direct coupling information.* BMC Bioinformatics, 2021.

Languages

French: Native
English: Fluent