

# Hua-Ting YAO

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## EXPERIENCE

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- Since 2022 ***Post-doc in Bioinformatics***  
TBI, University of Vienna, Vienna, Austria
- 2019–2021 ***Joint Ph.D. candidate in Computer Science***  
*Local Decomposition In RNA Structural Design*  
AMIBio, LIX, École Polytechnique, Palaiseau, France  
School of Computer Science, McGill University, Montreal, Canada  
Co-supervised by Yann Ponty & Jérôme Waldispühl
- 2017–2018 ***M2 in Bioinformatics (AMI2B)***  
University of Paris-Saclay, Orsay, France
- 2014–2018 ***Cycle d'ingénieur***  
École Polytechnique, Palaiseau, France  
*Bioinformatics, Computer Science, Math Application*
- 2012–2014 ***Classe préparatoire aux grandes écoles (CPGE)***  
Lycée Louis le Grand, Paris, France.  
*Mathematic, Physics, Computer Science*

## (Co-)SUPERVISION EXPERIENCE

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- Since 2025 S. Gardelle, M2 intern (ENS Lyon), University of Vienna
- Since 2025 P. Holotova, Master student, University of Vienna
- Since 2025 P. Koller, Master student, University of Vienna
- Since 2025 D. Skibinski, doctoral student, University of Vienna
- Since 2024 Y. Cai, doctoral student, University of Vienna
- Since 2023 L. Sidl, doctoral student, University of Vienna

## TEACHING EXPERIENCE

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- 2025 Lecturer (30h), 2025S 270034-1 Practical Course Bioinformatics of Nucleic Acids, University of Vienna
- 2025 Lecturer (5h), 2025S 270056-1 Algorithms and program development for biological chemistry, University of Vienna
- 2025 Lecturer (1.5h), 2025S 270054-1 Bioinformatics of nucleic acids, University of Vienna
- 2024 Supervisor, 2024W 053531-1 Master Bioinformatic software project, University of Vienna
- 2023 Supervisor, 2023W 053531-1 Master Bioinformatic software project, University of Vienna
- 2020 Teaching assistant (36h), *INF442 Algorithms data analysis in C++*, École Polytechnique
- 2020 Teaching assistant (24h), *CSE103 Introduction to Algorithms*, École Polytechnique
- 2019 Teaching assistant (80h), *COMP251 Algorithms and Data Structures*, McGill University

## CONTRIBUTIONS TO THE SCIENTIFIC COMMUNITY

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- since 2022 Review for journals Bioinformatics, DMTCS, RNA, NARGAB, ALMOB
- since 2020 Review for conferences RECOMB, ISMB, IJCAI, CMSB

## PUBLICATION (JOURNAL)

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- 2025 Sidl, L., Faissner, M., Uhler, M., Velandia-Huerto, C. A., Waldl, M., Yao H-T, Hofacker I. L., & Stadler, P. F.. Computational complexity, algorithmic scope, and evolution. *Journal of Physics: Complexity*.
- 2024 von Löhneysen, S., Spicher, T., Varenky, Y., Yao H-T, Lorenz, R., Hofacker, I., & Stadler, P. F. Phylogenetic and Chemical Probing Information as Soft Constraints in RNA Secondary Structure Prediction. *Journal of Computational Biology*, 31(6), 549-563.
- 2024 Yao H-T, Marchand, B., Berkemer, S. J., Ponty, Y., & Will, S. Infrared: a declarative tree decomposition-powered framework for bioinformatics. *Algorithms for Molecular Biology*, 19(1), 13.
- 2023 Yao H-T, Lorenz, R., Hofacker, I. L., & Stadler, P. F. Mono-valent salt corrections for RNA secondary structures in the ViennaRNA package. *Algorithms for Molecular Biology*, 18(1), 8.
- 2017 Feijao P, Yao H-T et al. *MentaLiST - A fast MLST caller for large MLST schemes*. *Microbial Genomics*. doi:10.1099/mgen.0.000146

## PUBLICATION (CONFERENCE)

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- 2025 Skibinski, D., Spicher, T., Sidl, L., Holotová, P., Pan, Y., Faissner, M., Velandia-Huerto, C. A., Lorenz, R., Waldl, M., Yao H-T & Stadler, P. F. Integrating High-Throughput RNA-RNA Interaction Data into RNA Secondary Structure Prediction. *ISBRA 2025*.
- 2025 Boury, T., Sidl, L., Hofacker, I. L., Ponty, Y., & Yao H-T. Old dog, new tricks: Exact seeding strategy improves RNA design performances. *RECOMB 2025 - 29th International Conference on Research in Computational Molecular Biology*.
- 2023 von Löhneysen, S., Spicher, T., Varenky, Y., Yao H-T, Lorenz, R., Hofacker, I., & Stadler, P. F. Phylogenetic Information as Soft Constraints in RNA Secondary Structure Prediction. In *International Symposium on Bioinformatics Research and Applications* (pp. 267-279). Singapore: Springer Nature Singapore.
- 2021 Yao H-T, Waldispühl, J., Ponty, Y., & Will, S. Taming Disruptive Base Pairs to Reconcile Positive and Negative Structural Design of RNA. *RECOMB 2021 - 25th International Conference on Research in Computational Molecular Biology*.
- 2020 Sarrazin-Gendron, R., Yao H-T, Reinharz, V., Oliver, C. G., Ponty, Y., & Waldispühl, J. Stochastic Sampling of Structural Contexts Improves the Scalability and Accuracy of RNA 3D Modules Identification. *RECOMB 2020 - 24th Annual International Conference on Research in Computational Molecular Biology*.
- 2019 Yao H-T, Chauve, C., Regnier, M., & Ponty, Y. Exponentially few RNA structures are designable. *ACM-BCB 2019 - 10th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics*, 289–298.

## BOOK CHAPTER

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- 2024 Waldl, M.<sup>†</sup>, Yao H-T<sup>†</sup> & Hofacker, I. (2024). Sequence design for RNA-RNA interactions.
- 2022 Yao H-T, Ponty, Y., & Will, S. Developing complex RNA design applications in the Infrared framework.
- 2020 Ponty, Y., Hammer, S., Yao H-T, & Will, S. Advanced design of structural RNAs using RNARedPrint. In E. Picardi (Ed.), *RNA Bioinformatics*.

## CONFERENCE TALKS

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- Aug 2021 RECOMB'21, Online
- Sep 2019 ACM-BCB'19 (bioinformatics conference), Niagara Falls, New York

Yao H-T, Chauve, C., Regnier, M., & Ponty, Y.. Undesignable rna motifs and combinatorial consequence. *Submitted to Journal of Mathematical Biology*

Skibinski, D., Sidl, L., Yao H-T, Parry, R. H., & Wolfinger, M. T.. Evolutionary conservation of exoribonuclease-resistant rnas in tick-borne flaviviruses. *In preparation*

## SEMINAR TALKS

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Jul 2025 Bioinformatics Leipzig seminar, Leipzig  
Sep 2024 RNA research center seminar, Seoul  
Aug 2024 Computational Approaches to RNA Structure and Function, Benasque  
Oct 2022 18th Herbstseminar der Bioinformatik, Doubice  
Sep 2022 Rational Design of RiboNucleic Acids, Dagstuhl Seminar 22381  
Aug 2022 Computational Approaches to RNA Structure and Function, Benasque  
Mar 2021 ALÉA2021 (theoretical computer science, discrete mathematics seminar), Online  
since 2020 TBI Winterseminar'20 21 22 23, Bled

## POSTERS

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2025 RECOMB'25, Seoul, South Korea  
2024 GFV'24, Vienna, Austria  
2024 RNAMedI symposium, Montréal, Québec  
Sep 2019 RiboClub'19, Sherbrooke, Québec

## SOFTWARES

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since 2024 VARNAjs, javascript library for RNA visualization  
since 2022 Contribute to ViennaRNA, library for RNA secondary structure study  
since 2021 VARNA api, a python helper package for RNA visualization tool VARNA  
since 2020 RNAPOND, RNA negative design tool using positive design approach  
since 2020 Infrared, A declarative framework for Bioinformatics.  
since 2019 BayesPairing2, Tool to identify RNA 3D motifs.

## AWARDS AND HONORS

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Jun 2022 IP Paris Best Thesis 2022 related to the IDIA department — IDIA accessits

## SKILLS

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Languages Mandarin (native), English (fluent), French (fluent), Korean (basic)  
Programming C++, Python3, OCaml, Java, R  
Web Dev HTML, CSS, php, SQL, JavaScript, Django  
Other Git, Linux, L<sup>A</sup>T<sub>E</sub>X

## REFERENCES

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- \* Peter F. Stadler -[studla@bioinf.uni-leipzig.de](mailto:studla@bioinf.uni-leipzig.de)  
Professor – University Leipzig – Faculty of Mathematics and Computer Science

- \* Ivo Hofacker – **ivo@tbi.univie.ac.at**  
Professor – University of Vienna – Institute for Theoretical Chemistry
- \* Ronny Lorenz – **ronny@tbi.univie.ac.at**  
Research faculty – University of Vienna – Institute for Theoretical Chemistry
- \* Yann Ponty – **yann.ponty@lix.polytechnique.fr**  
Research faculty – École Polytechnique – Computer Science Department
- \* Jérôme Waldispühl - **jeromew@cs.mcgill.ca**  
Professor – McGill University – School of Computer Science