Hua-Ting YAO

Born August 26th, 1994 From Taipei, Taiwan htyao.gitlab.io Mobile +33 6 64 87 51 53 E-mail hua-ting.yao@polytechnique.edu

Gitlab https://gitlab.com/htyao

Ph.D. candidate in Computer Science mainly working on RNA Design problem with decompositions and structural motifs. The project consists of designable secondary structure enumeration and RNA Design tool development. The defence will be held at 15th December. My research interest is to apply computer science or mathematics methods on biological problems.

EXPERIENCE

Since 2019 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

2018 Visiting intern

Gene selection with network based a priori BCI team at CEA Grenoble, France Supervised by Laurent Guyon

2017-2018 M2 in Bioinformatics (AMI2B)

University of Paris-Saclay, Orsay, France

2017 Visiting Intern

Model-based clustering on Tuberculosis strains during an outbreak Simom Fraser University, Vancouver, Canada Co-supervised by Cedric Chauve & Leonid Chindelevitch

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

Until 2012 Secondary education in Taiwan.

Publication

- 2021 <u>Yao H-T</u>, 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 Ponty, Y., Hammer, S., <u>Yao H-T</u>, & Will, S. Advanced design of structural RNAs using RNARedPrint. In E. Picardi (Ed.), RNA Bioinformatics.
- 2020 Sarrazin-Gendron, R., <u>Yao H-T</u>, 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 <u>Yao H-T</u>, 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.
- 2017 Feijao P, <u>Yao H-T</u> et al. *MentaLiST A fast MLST caller for large MLST schemes*. Microbial Genomics. doi:10.1099/mgen.0.000146

Talks

Mar 2021 ALÉA2021 (theoretical computer science, discrete mathematics seminar), Online
Feb 2021 TBI Winterseminar'21, Online
Feb 2020 TBI Winterseminar'20, Bled
Sep 2019 ACM-BCB'19 (bioinformatics conference), Niagara Falls, New York
Nov 2018 International Conference on Systems Biology, Lyon (Contributed)

Posters

Sep 2019 RiboClub'19, Sherbrooke, Québec

TEACHING EXPERIENCE

- 2020 Teaching assistant (36h), INF442 Algorithms data analysis in C++, École Polytechnique 2020 Teaching assistant (24h), CSE103 Introduction to Algorithms, École Polytechnique Fall 2019 Teaching assistant (80h), COMP251 Algorithms and Data Structures, McGill University
- Contributions to the scientific community
 - 2020 Review for RECOMB'21
 - since 2020 Development of RNAPOND, RNA negative design tool using positive design approach
 - since 2020 Maintenance & deployment of Infrared, A generic C++/Python hybrid library for FPT Boltzmann sampling.
 - since 2019 Development of BayesPairing 2, RNA 3D modules identification in sequence and alignments

AWARDS AND HONORS

- ${\rm Jan~2018~~Project~competition~Meet-U~2018~(on~protein~docking) -- First~Prize}$
- Jan 2011 Taiwan International Science Fair Fourth Prize in zoology.

SKILLS

- ${\bf Languages \quad Mandarin \ (native), \ English \ (fluent), \ French \ (fluent), \ Korean \ (basic),}$
 - Japanese (basic)
- Programming C++, OCaml, Python3, Java, R, Julia
 - Web Dev HTML, CSS, php, SQL, JavaScript, AngularJS, Django, Ocsigen
 - Software Coq, Scilab Other Git, Linux, LATEX

References

- * 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
- * Laurent Guyon laurent.guyon@cea.fr Research faculty – CEA – Laboratory of Cancer and Infection
- * Cedric Chauve cedric.chauve@sfu.ca Professor – Simon Fraser University – Department of Mathematics