

## 1 Curriculum Vitae

**Name:** Fenix Wenda Huang  
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### Education:

2011.7 Ph.D. in Applied Mathematics,  
Center for Combinatorics, Nankai University,  
Tianjin, China,  
supervised by Prof. Christian M. Reidys

### Doctoral Dissertation:

Folding of structures with cross-serial interactions

### Work Experience:

2011.7- 2013.8 Postdoc in Department of Mathematics and Computer science,  
University of Southern Denmark, Denmark  
2013.9- 2015.4 Assistant professor (tenure track) in Department of Mathematics and  
Computer science, University of Southern Denmark, Denmark  
2015.5- 2018.10 Research assistant professor in Biocomplexity Institute of Virginia  
Tech, USA  
2018.11- present Research assistant professor in Biocomplexity Institute & Initiative,  
University of Virginia, USA

### Research Interests:

- RNA structure and RNA-RNA interaction prediction
- Computational biology
- Bioinformatics

## 2 Publications List

### submitted:

- Barrett, C.L., Bura, A., He Q., Huang, F.W, Li, T.J.X. and Reidys, C.M., 2023, *Motifs in SARS-CoV-2 evolution*. Submitted to RNA, under review. [bioRxiv, pp.2023-01](#).
- Barrett, C.L., Huang, F.W, Li, T.J., Warren, A.S. and Reidys, C.M., 2022, *Rapid threat detection in SARS-CoV-2* Submitted to PlosOne, under review. [medRxiv, pp.2022-08](#).

### Published:

- Barrett, C.L., Bura, A., He Q., Huang, F.W and Reidys, C.M., 2023, *The arithmetic topology of genetic alignments* [Journal of Mathematical Biology, 86\(3\), p.34](#).
- Parikh, R., Wilson, B., Marrah, L., Su, Z., Saha, S., Kumar, P., Huang, F. and Dutta, A., 2022, *tRForest: a novel random forest-based algorithm for tRNA-derived fragment target prediction*. [NAR Genomics and Bioinformatics, 4\(2\), p.lqac037](#).
- Kocher, M.A., Huang, F.W., Le, E. and Good, D.J., 2021, *Snord116 post-transcriptionally increases Nhlh2 mRNA stability: implications for human Prader-Willi syndrome*. [Human Molecular Genetics, 30\(12\), pp.1101-1110](#).
- Huang F.W.D, Barrett, C.L. and Reidys, C.M., 2021, *The energy-spectrum of bicompatible sequences* [Algorithm for Molecular Biology, 16\(1\):1-8](#).
- He, Q.J., Barrett, C, Huang F.W.D and Reidys, C.M., 2019 *Genetic robustness of let-7 miRNA sequence-structure pairs* [RNA, 25\(12\), 1592-1603](#)
- Barrett, C, He, Q.J., Huang F.W.D and Reidys, C.M., 2018, *A Boltzmann sampler for 1-pairs with double filtration* [J. Comput. Biol., 26\(3\), 173-192](#)
- Barrett, C, He, Q.J., Huang F.W.D and Reidys, C.M., 2018, *An efficient dual sampling algorithm with Hamming distance filtration* [J. Comput. Biol., 25\(11\), 1179-1192](#)
- Huang, F.W.D. and Reidys, C.M., 2017, *A topological framework for signed permutations* [Discrete Mathematics, 340\(9\), 2161-2182](#).
- Huang F.W.D, Rezagaden, R and Reidys, C.M., 2017, *Fatgraph models of RNA structure* [Molecular Based Mathematical Biology, 5, 1-20](#)
- Barrett, C, Huang F.W.D and Reidys, C.M., 2017, *Sequence-structure relations of biopolymers* [Bioinformatics, 33\(3\), 382-389](#).
- Huang, F.W.D and Reidys, C.M., 2016, *Topological language for RNA* [Mathematical Biosciences, 282, 109-120](#).
- Huang, F.W.D. and Reidys, C.M., 2015, *Shape of topological RNA structures* [Mathematical Biosciences, 270\(Pt A\) 57-65](#).
- Huang, F.W.D., Nebel,M.E. and Reidys C.M., 2013, *Generation of RNA pseudoknot structures with topological genus filtration* , [Mathematical Biosciences, 245\(2\) 216-225](#)
- Huang, F.W.D. and Reidys, C.M., 2012, *On the combinatorics of sparsification*, [Algorithm. Mol. Biol., 7\(28\) doi:10.1186/1748-7188-7-28](#)
- Andersen, J.E., Huang, F.W.D., Penner, R.C. and Reidys, C.M., 2012, *Topology of RNA-RNA interaction structures*, [J. Comput. Biol., 19\(7\), 928-943](#)
- Reidys, C.M., Huang, F.W.D., Andersen, J.E., Penner, R.C., Stadler, P.F. and Nebel, M.E., 2011, *Topology and prediction of RNA pseudoknots*, [Bioinformatics 27\(8\), 1076-1085](#)
- Huang, F.W.D, Qin, J., Reidys, C.M., and Stadler, P.F., 2010, *Target prediction and a statistical sampling algorithm for RNA-RNA interaction*, [Bioinformatics, 26\(2\), 175-181](#).
- Huang, F.W.D., Qin, J., Reidys, C.M., and Stadler, P.F., 2009, *Partition function and base pairing probabilities for RNA-RNA interaction prediction*, [Bioinformatics, 25\(20\), 2646-2654](#).
- Huang, F.W.D. and Reidys, C.M., 2010, *On the uniform generation of modular diagrams*, [E. J. Combin., 17\(1\), R175](#)
- Huang, F.W.D., Li, L.Y.M., Reidys, C.M., 2009, *Sequence-structure relations of pseudoknot RNA*, [BMC Bioinformatics, 10, Suppl 1, S39](#)
- Huang, F.W.D., Peng W.W.J., Reidys, C.M. 2009, *Folding 3-noncrossing RNA pseudoknot struc-*

*tures*, *J. Comput. Biol.*, **16(11)**, 1549-1575

• Huang, F.W.D., Reidys, C.M., 2008, *Statistics of canonical RNA Pseudoknot Structures*, *J. Theoret. Biol.*, **(253)**, 570-578