Andrew Tupper — PhD Biochemistry

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Education

McMaster University — **Hamilton, ON (Canada)**
PhD Biochemistry and Astrobiology — *2015–2020*

Rensselaer Polytechnic Institute — **Troy, NY (USA)**
BS Interdisciplinary Science – summa cum laude — *2011–2015*

Technical Skills

Programming

- Proficient in Python, C, C++, R, and Bash. Basic knowledge of HTML, CSS, and javascript
- Parallel programming paradigms: MPI (MPICH and openMPI), threading (POSIX and openMP), and GPU (NVIDIA-CUDA)
- Python libraries: NumPy, SciPy, SymPy, Scikit-learn (Machine learning), and PyMC3 (Bayesian leaning)
- Code development on Unix clusters: Docker and Conda, job scheduling with SLURM and SGE
- Dedicated to software development best practices such as Git/GitHub and test-driven developement
- Server admin for the USDA, deployment and maintenance of databases and R-shiny websites
- Coded exclusively in VIM for 1-2 years

Problem Solving

- Numerical analysis of stiff and ordinary differential equations using Runge-Kutta methods
- Monte-Carlo and Gillespie based simulations of chemical kinetics and thermodynamics

Problem Solving (Cont.)

- Surface and lattice based models of nearest-neighbor stochastic processes
- Kmer based algorithms for the analysis of genomic and population genetic data
- Development of CRISPR-based diagnostic assays of pathogens using SHERLOCK protocol

Communication

- Proficient in scientific writing and presentations
- Author of 7 published papers (4 as first author)
- Awarded best PhD seminar twice, best poster once
- Mentored 5 graduate and 4 undergraduate students
- Led research lab during final year of PhD

Relevant Coursework

- SHARCNET Advanced Research Computing
- Software Design and Documentation
- Parallel Programming
- Numerical Computing
- Machine Learning

Professional Experience

BenchSci — **Potsdam, NY (USA)**
Bioinformatics Software Engineer (remote) — *2022–present*

- Development of ETL pipelines using Apache beam and Google cloud infrastructure
- Extraction and analysis of large scale bioinformatics databases
- Development of novel bioinformatics tools to aid drug discovery

Horticultural Crops Research Laboratory — **Corvallis, OR (USA)**
Research Associate with Dr. Niklaus J. Grünwald — *2020–2021*

- Development of python software packages for CRISPR-based diagnostic assays
- System administrator for the *'oomy'* compute cluster and web server
- Population genetics of *P. ramorum*, causal agent of sudden oak death

McMaster University — **Hamilton, ON (Canada)**
Graduate Researcher with Dr. Paul G. Higgs — *2015–2020*

- Software development of massively parallel programs for high performance computing
- Designing computational models of non-enzymatic and enzymatic RNA replication
- Lipid-catalyzed polymerization of unactivated RNA monomers in the *'Planet Simulator'* - Origins lab

Professional Experience (continued)

Rensselaer Polytechnic Institute **Troy, NY (USA)**
Undergraduate Researcher with Dr. James P. Ferris *2012–2013*

- Clay-catalyzed polymerization of activated RNA monomers
- Banin protocol - Quantitative ion exchange of clay minerals
- Data analysis of chemical experiments

Publications

Foster, Z. S., **Tupper**, A. S., Press, C. M., & Grunwald, N. J. (2023). Krisp: A python package for designing crispr and amplification-based diagnostic assays from whole genome data. *bioRxiv*, 2023–11.

Tupper, A. S., & Higgs, P. G. (2021). Rolling-circle and strand-displacement mechanisms for non-enzymatic rna replication at the time of the origin of life. *Journal of Theoretical Biology*, 110822.

Cauret, C. M., Gansauge, M.-T., **Tupper**, A. S., Furman, B. L., Knytl, M., Song, X.-Y., Greenbaum, E., Meyer, M., & Evans, B. J. (2020). Developmental systems drift and the drivers of sex chromosome evolution. *Molecular Biology and Evolution*, *37*(3), 799–810.

Tupper, A. S., Pudritz, R. E., & Higgs, P. G. (2019). Can the RNA world still function without cytidine? *Molecular biology and evolution*.

Shah, V., de Bouter, J., *Pauli, Q., **Tupper**, A. S., & Higgs, P. G. (2019). Survival of RNA replicators is much easier in protocells than in surface-based, spatial systems. *Life*, *9*(3), 65.

Pearce, B. K., **Tupper**, A. S., Pudritz, R. E., & Higgs, P. G. (2018). Constraining the time interval for the origin of life on earth. *Astrobiology*, *18*(3), 343–364.

Tupper, A. S., & Higgs, P. G. (2017). Error thresholds for RNA replication in the presence of both point mutations and premature termination errors. *Journal of theoretical biology*, *428*, 34–42.

Tupper, A., *Shi, K., & Higgs, P. (2017). The role of templating in the emergence of RNA from the prebiotic chemical mixture. *Life*, *7*(4), 41.

***** *mentored undergraduate student*

Select Conferences

Gordon Research Conference for the Origins of Life **Galveston, TX (USA)**
Poster Presentation *2020*
Non-enzymatic Rolling-circle Replication in an RNA World

- Andrew S. Tupper & Paul G. Higgs

Astrobiology Science Conference (AbSciCon) **Bellevue, WA (USA)**
Poster Presentation *2019*
Can the RNA World still function without cytidine?

- Andrew S. Tupper, Ralph E. Pudritz & Paul G. Higgs

Science of Early Life Conference **Hamilton, ON (Canada)**
Poster Presentation *2018*
Assessing the Plausibility of an AUG Alphabet for RNA Secondary Structure Formation and Replication

- Andrew S. Tupper, Ralph E. Pudritz, & Paul G. Higgs

Astrobiology Science Conference (AbSciCon) **Mesa, AZ (USA)**
Oral Presentation *2017*
Error thresholds for RNA replication in the presence of point mutations and premature termination errors

- Andrew S. Tupper & Paul G. Higgs

Astrobiology Science Conference (AbSciCon) **Mesa, AZ (USA)**
Oral Presentation – *By Supervisor* *2017*
The role of templating in the emergence of RNA from the prebiotic chemical mixture

- Andrew S. Tupper, Kevin Shi, & Paul G. Higgs