Andrew Tupper | PhD Biochemistry

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Scientist and software engineer. My PhD thesis focused on the developement of computational modeling software to simulate chemical reaction mixtures and the process of RNA replication as it relates to the RNA World hypothesis for the origin of life. As a postdoc, I was employed as a research associate for the United States Department of Agriculture - Agricultural Research Services, where I developed bioinformatic software tools for the detection of plant pathogens using CRISPR-based diagnostics.

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*

Relevant Coursework

- Software Design and Documentation (Capstone)
- SHARCNET Advanced Research Computing
- Parallel Programming
- Machine Learning
- Advanced Algorithm Design
- Numerical Computing
- Graph Theory
- Data Structures

Research Experience

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

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

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

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

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 to simulate prebiotic Earth conditions

Publications

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., . . . 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*

Technical and Personal Skills

- **Programming Languages:** Python, C, C++, R, Bash
- **Parallel Languages:** openMPI / MPICH, openMP, CUDA, python3-multiprocessing
- **Human Languages:** English, French (limited)
- **Python Libraries:** NumPy, SciPy, SKLearn (Machine Learning), PyMC3 (Bayesian)
- **Other Skills:** Git, Docker, Conda, Linux, LaTeX

References

Dr. Niklaus J. Grünwald
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Dr. Paul G. Higgs
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McMaster University
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