Alexander G. Lucaci

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EDUCATION

Ph.D. Candidate in Bioinformatics   2018 - Present
Temple University
Institute for Genomics Evolutionary Medicine (iGEM)
Thesis:
The influence of multi-nucleotide instantaneous mutations on evolutionary dynamics.

M.S. in Biology   2018
New York University

B.S. in Biochemistry   2011
Stony Brook University

EXPERIENCE

Graduate Research Assistant   Present
Temple University

- Conducting research in molecular evolution evaluating the effect of multinucleotide mutational events on the inference of parameters of gene adaptation.
- This work involves the use and development of statistical models, algorithms and computational software. Our current implementation is available as an extension in the Hypothesis Testing using Phylogenies (HyPhy) software suite.

Graduate Teaching Assistant: Genomics in Medicine   Fall 2020
Temple University

- Directed over one hundred and sixty students in a cross-listed (Graduate and Undergraduate) course in a virtual format.
- Responsible teaching material, grading, quizzes and exams, holding office hours and guidance on assignments

SELECTED PUBLICATIONS

1. *Human HspB1, HspB3, HspB5 and HspB8: Shaping these Disease Factors during Vertebrate Evolution (manuscript in preparation)*
2. *The emergence and ongoing convergent evolution of the N501Y lineages coincides with a major global shift in the SARS-CoV-2 selective landscape (manuscript submitted*
3. *RASCL: Rapid assessment of SARS-COV-2 clades enabled through molecular sequence analysis and its application to B.1.617.1 and B.1.617.2 (manuscript in preparation)*
4. *Extra base hits: Widespread empirical support for instantaneous multiple-nucleotide changes*

SKILLS

Scientific knowledge: Biochemistry, Neuroscience, Virology, Molecular Evolution
Programming languages: Perl, Python, R, Java, C++, JavaScript
Statistics and Machine learning: statsmodels, pymc3, scikit-learn, tensorflow
Data Science: numpy, scipy, pandas, matplotlib, plotly, altair
Science communication: LaTeX, Adobe suite, Markdown
Sequencing informatics: Illumina, Oxford Nanopore, Consensus genomes
Other tools: Git, Github, Bash, Snakemake workflows, Jupyter, Observable