

Alexander G. Lucaci

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EDUCATION

Ph.D. Candidate in Bioinformatics

2018 - Present

Temple University

Institute for Genomics Evolutionary Medicine (iGEM)

Thesis mentored by Dr. Sergei Pond:

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 to Cell)*

3. *RASCL: Rapid assessment of SARS-COV-2 clades enabled through molecular sequence analysis (manuscript in preparation)*

4. *Extra base hits: Widespread empirical support for instantaneous multiple-nucleotide changes, accepted at PLOS One*

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, Jupyter, Observable