Alexander G. Lucaci

email: alexander.lucaci@temple.edu website: aglucaci.github.io ORCiD: 0000-0002-4896-6088

EDUCATION

Ph.D. Candidate in Bioinformatics

2018 - Present

Temple University

Institute for Genomics Evolutionary Medicine (iGEM)

Dissertation mentored by Dr. Sergei Pond

M.S. in Biology 2016 - 2018

New York University

B.S. in Biochemistry 2011

Stony Brook University

EXPERIENCE

Temple University

Spring 2022 - Present

Graduate Research Assistant

• Development, validation, and application of statistical methods which evaluate the effects of mutational events on the inference of evolutionary rates.

Maxim Group Fall 2021 - Present

Intern - Biotechnology Equity Research

Initiate coverage on companies with investment recommendations based on fundamental analysis. Modeling companies using a three-statement model and DCF valuation methods, and report on company earnings.

Temple University Fall 2021

Graduate Teaching Assistant - Genomics in Medicine

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

ROTH Capital Partners

Spring 2018

Intern - Healthcare Investment Banking

 Participated in the IPO process for a NASDAQ listed company. Responsible for current healthcare IPO market data, curating pitch decks for senior managers, and research for M&A deals.

SELECTED PUBLICATIONS

- 1. Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa (Accepted at Nature)
- 2. The emergence and ongoing convergent evolution of the N501Y lineages coincides with a major global shift in the SARS-CoV-2 selective landscape (Accepted at Cell)
- **3.** Extra base hits: widespread empirical support for instantaneous multiple-nucleotide changes (Accepted at PLOS One)
- **4.** Human HspB1, HspB3, HspB5 and HspB8: Shaping these Disease Factors during Vertebrate Evolution (submitted)
- **5.** RASCL: Rapid assessment of SARS-COV-2 clades enabled through molecular sequence analysis (manuscript in preparation)