NICHOLAS A. CLARK
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EDUCATION:

XAVIER UNIVERSITY – B.S. Cum Laude, Mathematics (May 2010 – GPA: 3.670)
GPA in Mathematics courses: 3.874
University of Cincinnati – PhD student, Biostatistics and Bioinformatics (Big Data Track)
GPA: 3.796 (August 2014 – present)

COURSEWORK RELEVANT TO BIOSTATISTICS*:

UNDERGRADUATE: (2006 – 2010)

- COMPUTER SCIENCE I CSCI 170
- COMPUTER SCIENCE II CSCI 180
- PROBABILITY MATH 311
- STATISTICAL INFERENCE MATH 312
- OPTIMAL CONTROL THEORY (APPLIED TO BIOLOGICAL MODELS) MATH 396
- INTRODUCTION TO MATHEMATICAL BIOLOGY MATH 598 (TAKEN AT UNIVERSITY OF CINCINNATI)
  *I have also taken a plethora of upper-level mathematics courses in Calculus, Differential Equations, Linear Algebra, etc. that may be of use or would at least prepare one well to study a quantitative discipline.

GRADUATE: (2014 – 2016)

- INTRODUCTION TO BIOSTATISTICS BE 7022 – A
- REGRESSION ANALYSIS BE 7088 – A
- EXPERIMENTAL DESIGN BE 7089 – A-
- DESIGN AND ANALYSIS OF ALGORITHMS CS 4071 – A
- MATHEMATICAL STATISTICS I STAT 6021 – A
- MATHEMATICAL STATISTICS II STAT 6022 – A-
- INTRODUCTION TO BIOINFORMATICS CS 7099– A
- INTRODUCTION TO FUNCTIONAL GENOMICS GNTD 8001 – A
- LINEAR MODELS AND MULTIVARIATE ANALYSIS I STAT 7023 – B
- LINEAR MODELS AND MULTIVARIATE ANALYSIS II STAT 7024 – A-
- DATABASE THEORY CS 6051 – A

AWARDS AND HONORS:

- **Full scholarship and stipend support** under LINCS-BD2K grant with Dr. Mario Medvedovic (2015 – present)
- **Full scholarship and stipend support** to University of Cincinnati Biostatistics PhD program (2014 – 2015)
- **Patterson Prize recipient** for **“outstanding undergraduate student presentation”** from the Mathematics Association of America **(MAA) SE Section Meeting** (2009)
- **Kramer-Miller Outstanding Mathematics Student Award** recipient from Xavier Math/CS Department (2009)
- **Academic Honors Convocation Award** from Xavier Math/CS Department (2009)
- Inducted into **Pi Mu Epsilon** Mathematics Fraternity (2008)
- **St. Francis Xavier full tuition Scholarship** recipient (2006)
- **National Merit Scholar** (2006)

STANDARDIZED TEST SCORES:

GRE: Quantitative – 800/800 Verbal – 650/800 Analytical Writing – 4.0/6.0

INTERNSHIPS:

- NSF Summer 2009 Research internship at Texas A&M University (Algebraic Geometry)
- Summer 2008 Research internship at Xavier University (Applied Mathematics)

RESEARCH AND PRESENTATIONS:

GRADUATE:

- ***"GRcalculator: an online tool for calculating and mining drug response data"*** – upcoming publication (planning to submit to BMC Cancer as first author)
- **NIH Library of Integrated Network-Based Cellular Signatures (LINCS) Meeting** held on March 10-11, 2016 at the University of California, Irvine. Poster presentation.
- **BD2K-LINCS Systems Biology Data Science Symposium** held on January 19-20, 2016 at the University of Miami. Oral presentation: "Internal benchmarking of connectivity between LINCS L1000 Level 5 signatures"

UNDERGRADUATE:

- **Mathematics Association of America (MAA) SE Section Meeting 2009 Presenter** at Belmont University. *"Modeling and Optimizing HIV Treatment"*
- **TIMBER (The Institute for Mathematical Biology Education and Resources) Conference 2008 Presenter** at Appalachian State University. *"Modeling and Optimizing HIV Treatment"*
- **Summer 2008 Research internship at Xavier University under advisor Dr. Hem Joshi**, studying mathematical models of HIV treatment (Using optimal control theory and numerical methods in MATLAB to find optimal solutions to ODE systems).

COMPUTER SKILLS:

Programs/Languages in order of experience:
R, Shiny, Python, MATLAB
Summary of Experience:
R/Shiny
I have used R daily for the past two years. I recently led development of an R/Shiny application in conjunction with a group at Harvard Medical School as a companion to a paper published in *Nature Methods* (Hafner et al. "Growth rate inhibition metrics correct for confounders in measuring sensitivity to cancer drugs"). The website for the application can be found at http://www.grcalculator.org.
Python
I learned and used Python for my Design and Analysis of Algorithms class. I also used Python in Introduction to Bioinformatics for two projects: 1) writing a modified Needleman-Wunsch algorithm for DNA sequence alignment 2) reading in the DNA sequence of Bacillus anthracis and searching for all tandem repeats.
MATLAB
I recently translated MATLAB scripts to R code for the GR Calculator project. I also used MATLAB in my undergraduate Optimal Control Theory class and in related research I wrote a program to numerically solve and graph the solution to a system of ODEs using a Runge-Kutta method.