OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.  
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Scarborough, Jessica

eRA COMMONS USER NAME (credential, e.g., agency login): JESSICAA

POSITION TITLE: MD/PhD Candidate, Medical Scientist Training Program (MSTP)

EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)

| INSTITUTION AND LOCATION | DEGREE  (if applicable) | Start Date  MM/YYYY | Completion Date  MM/YYYY | FIELD OF STUDY |
| --- | --- | --- | --- | --- |
| University of San Francisco –  San Francisco, CA | B.S. | 08/2012 | 05/2016 | Biology |
| University of San Francisco –  San Francisco, CA | M.S. | 08/2015 | 05/2017 | Health Informatics |
| Case Western Reserve University – Cleveland, OH | M.D. | 07/2017 | Expected  05/2025 | Medicine |
| Case Western Reserve University – Cleveland, OH | PhD | 07/2017 | Expected  05/2023 | Systems Biology and Bioinformatics |

**A. Personal Statement**

**After beginning my medical education, it became clear to me that the best clinicians think like scientists. They don’t immediately accept the facts laid in front of them. Instead, they look deeper into the data to find out “why” in addition to “what.” I would also argue that the best biomedical scientists think like clinicians. Translational science must answer questions that are being asked today, while improving standards that are not appropriately meeting the needs of our patients. My long-term career goal is to become a physician scientist, integrating my passion for discovery with critical clinical knowledge. My plan is not to simply perform best medical practice; I want to *improve* best medical practice.**

**My academic training began at the University of San Francisco, where I studied biology with a molecular concentration. During this time, I garnered my first experience in computational science, constructing phylogenetic trees to examine the evolutionary history of two human cytomegalovirus genes, US27 and US28. In this work, I was exposed to the struggles and satisfaction of data curation, organization, and analysis. I was also very interested in understanding differences between various algorithms used for sequence alignment, hierarchical clustering, and tree building. It was exciting to realize other scientists had worked to develop these methods and shared them freely to further discovery in more laboratories and fields than they could hope to engage with. Although, I thoroughly enjoyed my time as an undergraduate researcher, I remained steadfast in choosing a career focused on medicine. All of my plans changed, however, when I listened to a talk by Dr. William Bosl regarding the use of machine learning to detect autism from seemingly normal electroencephalograms (EEGs) of children as young as six months old. The idea of finding clinically relevant patterns that are invisible to the naked eye fascinated me. I was hooked, but I lacked the requisite computational skills to join Dr. Bosl’s research team. Although I had previously planned to apply to medical school in just two months, I decided that I couldn’t allow this interest to go unexplored. By the end of that week, I applied to the Masters of Health Informatics program, becoming the *first student at the University of San Francisco to complete a 4+1 program with a B.S. in Biology and an M.S. in Health Informatics*. Throughout my exposure to the computational sciences, I became even more steadfast in my desire to intelligently utilize the vast datasets that our healthcare system generates daily.**

**Moving forward, I took this passion to the Medical Scientist Training Program (MSTP) at Case Western Reserve University. Here, I work in Dr. Jacob Scott’s lab, which focuses on the evolution of cancer using a variety of methods, including theoretical mathematics, data analytics, and experimental biology. Since joining this lab, I have been excited to study how we can take advantage of convergent states of drug response phenotypes to extract biomarkers of chemo-sensitivity or -resistance. Utilizing open-source software and publicly available databases, I have created a method for deriving gene expression signatures predictive of therapeutic sensitivity or resistance. Further, I analyze tightly controlled long-term evolution experiments which examine the changes in collateral drug response over time as cancer cells become resistant to first-line therapy. I am proud to utilize software that is easily transferrable between laboratories, and I will continue to make contributions to these incredible resources. In addition to publishing the results of this work, I will publish all related code and conveniently formatted data in a public GitHub repository. I believe that open science is essential to the progression of translational research, bringing diligent work from one laboratory into the hands of scientists around the world.**

**My educational background gives me a distinct advantage while studying the evolution of cancer. I have a strong *foundation in the biological sciences,* which was bolstered by my undergraduate researchusing phylogenetics to examine viral evolution. I use this knowledge to think critically about the evolutionary mechanisms employed by cancer cells to overcome the selective pressures of chemotherapy and radiation. Further, the *computational skills* I’ve acquired while taking health informatics courses were expanded from the research that went on to shape my Master’s Thesis, where I looked for patterns in large EEG datasets to improve the diagnostic accuracy of various neurologic conditions. This bioinformatic skillset I have acquired (and continue to expand) allows me to responsibly appraise, clean, and analyze the large, messy datasets that are publicly available. And finally, my *clinical perspective* helps inform hypothesis generation and improves the translation of our work to the bedside. With this grant, I am eager to utilize my unique training to explore the evolution of cancer and devise improved treatment plans for the patients of today.**

**B. Positions and Honors**

**Positions and Employment**

|  |  |
| --- | --- |
| **2017-** | **Graduate student, Case Western Reserve University Medical Scientist Training Program** |
| **2016-2017** | **Graduate research assistant, University of San Francisco** |
| **2014-2017** | **Copy Editor and Content Manager, Keas Inc, San Francisco, CA** |
| **2015-2016** | **Undergraduate research assistant, University of San Francisco** |
| **2013** | **Undergraduate research technician, University of San Francisco** |

**Other Experience and Professional Memberships**

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| --- | --- |
| **2020-** | **Case Comprehensive Cancer Center, Trainee Associate Member** |
| **2019-** | **American Association for Cancer Research, Associate Member** |
| **2017-** | **Phi Delta Epsilon, International Medical Fraternity** |

**Honors and Awards**

|  |  |
| --- | --- |
| **2021** | ***NCI Ruth L. Kirschstein National Research service F30 Award (4 years, minimum of $150,000 direct costs per year)*** |
| **2020** | **CWRU Translational Fellowship Awardee—Case Western Reserve University, (20% of salary for 1 year, ~$6,000)** |
| **2019** | **Rising Star Award—Innovators in AYA Cancer Symposium, Case Comprehensive Cancer Center, Cleveland, OH** |
| **2016** | **Dean’s Medal of Excellence—Collage of Arts and Sciences, University of San Francisco** |
| **2016** | **Graduated Summa Cum Laude with Honors—University of San Francisco** |
| **2016** | **Graduate Nursing Merit Scholarship ($3,000 single payment)—Health Informatics Program, Department of Nursing, University of San Francisco** |
| **2012-2016** | **USF President’s Merit Award ($10,000 per year)—University of San Francisco** |
| **2012-2016** | **Dean’s List (all semesters)—Collage of Arts and Sciences, University of San Francisco** |
| **2015** | **Carol Chihara Award—Department of Biology, University of San Francisco** |

**C. Contributions to Science**

1. **Undergraduate Research: Early in my undergraduate education, I joined Dr. Juliet Spencer’s laboratory, where our team examined the interactions between human cytomegalovirus (HCMV) and its host. As a research technician, I gained insight into the day-to-day activities of a bench laboratory and developed an intense curiosity regarding the co-evolution of cancer and HCMV within a host. After this initial exposure, I chose to remain on this team to complete research for an honors thesis in my final undergraduate year. Here, I worked on a bioinformatics-based project that focused on elucidating the evolutionary history between two G-protein-coupled receptor (GPCR) HCMV proteins, pUS27 and pUS28. This work included pulling protein sequences from Genbank, aligning their sequences utilizing the MUSCLE multiple sequence alignment tool, and performing phylogenetic analysis with Bayesian and maximum likelihood methods.** **The phylogenetic analyses showed that using both Bayesian and ML methods, the US27 and US28 protein sequences clustered together with a single human GPCR, CX3CR1, as their common ancestor. From these results, I concluded that the two genes likely evolved via a gene duplication event with further neofunctionalization of US27 after duplication.** Moving forward with this work, I defended my honors thesis and went on to write and publish my first, first-author manuscript.
   1. **Publications:** 
      1. **Jessica A. Scarborough, John R. Paul, Juliet V. Spencer, Evolution of the ability to modulate host chemokine networks via gene duplication in human cytomegalovirus (HCMV), *Infection, Genetics and Evolution*, Volume 51, 2017, Pages 46-53, ISSN 1567-1348,** <http://dx.doi.org/10.1016/j.meegid.2017.03.013>**.**
   2. **Abstracts:** 
      1. **Scarborough J.A., Paul J.R., Spencer J. Virus-Host Co-evolution: Determining the origin of Human Cytomegalovirus US27 and US28 (2016). Poster presentation. Collage of Arts and Sciences, University of San Francisco Creative Activity and Research Day. San Francisco, CA.**
2. **Graduate (Masters) Research:** I worked in Dr. William Bosl’s laboratory at the University of San Francisco when completing a capstone research project to satisfy requirements for an M.S. in Health Informatics. The goal of our project was to develop a method for the rapid detection of benign partial epilepsy of childhood with centrotemporal spikes (BECTS). This condition can be difficult to diagnose as symptoms typically appear at night, requiring a 72-hour sleep study to confirm. Therefore, our method would require the detection of subacute disease from EEG readings that appear normal. A neurophysiology resident at Boston Children’s Hospital selected 30 second EEG segments from control and BECTS patients that all appeared normal. The readings were transformed using successive averaging of the time series to create new values for each time scale. Next, variables for recurrence quantitative analysis (RQA) were calculated for each scale. It was very exciting to find that plotting the RQA values of each variable against the time scales for a given lead showed distinct differences between controls and awake patients with BECTS. Importantly, this demonstrated that despite appearing normal to medical professionals, mathematical transformation of the EEGs could differentiate between control and BECTS patients. This work became an integral part of my capstone thesis.
   1. Publications:
      1. **Scarborough, Jessica A.,** "The Acquisition and Analysis of Electroencephalogram Data for the Classification of Benign Partial Epilepsy of Childhood with Centrotemporal Spikes" (2017). *Master's Theses*. 221. <https://repository.usfca.edu/thes/221>
   2. Abstracts:
      1. **Scarborough, J.A.,** Loddenkemper, Tobias, Bosl, W.J. Nonlinear Analysis for Detection and Classification of Benign Childhood Epilepsy with Centrotemporal Spikes (2017). Poster presentation. American Clinical Neurophysiology Society Annual Meeting and Conference.
3. **Graduate (PhD) Research:** My ongoing research occurs in the lab of my PhD advisor, Dr. Jacob Scott of the Cleveland Clinic Foundation’s Translational Hematology and Oncology Research Department. My ***doctoral dissertation project*** entails the exploitation of convergent evolution between cancer cell lines and even across cancer subtypes to extract biomarkers of therapeutic response. First, I have developed a novel method for deriving gene signatures. Beginning with differentially expressed genes between cell lines that are resistant and sensitive to a given chemotherapy, a co-expression network is built with the aim of discovering groups of genes that together promote sensitivity or resistance to a drug. This method can be used to predict response to any therapeutic regimen, including antibiotics, chemotherapy, and radiation. Additionally, it has been used for the analysis of two long term evolution experiments within our laboratory. Both of these tightly controlled studies examine the evolution of evolutionary replicates of cell lines repeatedly challenged with various chemotherapies. The first study, a pilot, examined Ewing’s sarcoma cell lines and the second will examine EGFR+ non-small cell lung cancer (NSCLC). In these long-term evolution experiments, evolutionary (biological) replicates of cancer cell lines are evolved to become resistant to standard treatment. In the case of Ewing’s sarcoma, they are exposed to drug combinations of vincristine-doxorubucin-cyclophosphamide and etoposide-cyclophosphamide. With the EGFR+ NSCLC experiment, replicates are exposed to one of two targeted treatments (gefitinib or osimertinib). After each drug exposure, samples are tested for their collateral response to a panel of drugs and a portion of cells will be saved for future RNA-sequencing. This method of deriving gene signatures can be used to examine the differences of gene expression that lead to chemotherapeutic resistance, agnostic of cell line and treatment history.
   1. **Publications:**
      1. **Jessica A. Scarborough**, Erin McClure, Peter Anderson, Andrew Dhawan, Arda Durmaz, Stephen L. Lessnick, Masahiro Hitomi, Jacob G. Scott., Identifying States of Collateral Sensitivity during the Evolution of Therapeutic Resistance in Ewing’s Sarcoma. *iScience*. 2020. PMC7334607.
   2. **Abstracts:** 
      1. **Scarborough, J.A, Dhawan, A., Scott, J., Generating Gene Expression Signatures Predictive of Therapeutic Response in Lung Adenocarcinoma (2018). Poster presentation. Cleveland Clinic Foundation Lerner Research Day. Cleveland, OH.**
      2. **Scarborough, J.A, Dhawan, A., Scott, J.,** A Novel Method For Extracting Gene Signatures Predictive of Chemotherapeutic Response **(2019). Poster presentation. Case Western Reserve University Lepow Research Day. Cleveland, OH.**
      3. **Scarborough, J.A.**, McClure, E., Sedor, G., Hitomi, M., Scott, JG. Identifying States of Collateral Sensitivity During the Evolution of Therapy Resistance in Ewing’s Sarcoma. (2019) Poster Presentation. **Innovators in AYA Cancer Symposium. Cleveland, OH.**
      4. **Scarborough, J.A, Dhawan, A., Scott, J.,** Deriving Robust Gene Signatures Predictive of Chemotherapeutic Response **(2020). Poster presentation. American Association for Cancer Research 2020 Virtual Annual Meeting II. Virtual Meeting due to COVID-19.**
      5. **Scarborough, J.A., Tom, M., Scott, J.G. Revisiting a Null Hypothesis: Exploring the parameters of oligometastasis treatment (2020) Poster Presentation. Case Western Reserve University Biomedical Graduate Student Symposium. Cleveland, OH.**

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| **D. Additional Information: Research Support and/or Scholastic Performance**  MCAT Score: 34  USMLE Step 1 Score: 245   |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | | University of San Francisco  B.S. Biology (Cumulative GPA 3.91) | | | University of San Francisco  M.S. Health Informatics (Cumulative GPA 4.00) | | | | **YEAR** | **COURSE TITLE** | **GRADE** | **YEAR** | **COURSE TITLE** | **GRADE** | | **2012** | Written & Oral Communication | **A-** | **2015** | **Perspectives in Health Informatics** | **A** | | **2012** | **FYS: Dance in San Francisco** | **A-** | **2015** | **Medical Microbiology\*** | **A** | | **2012** | **General Chemistry I + Lab** | **B** | **2015** | **Medical Microbiology Lab\*** | **A** | | **2012** | **General Biology I + Lab** | **A-** | **2016** | **Health Data Security, Privacy, and Confidentiality** | **A** | | **2013** | **Written & Oral Communication** | **A+** | **2016** | **CS for Health Inf. Professionals** | **A+** | | **2013** | **Latin American Perspectives** | **A-** | **2016** | **Human Physiology\*** | **A+** | | **2013** | **General Chemistry II + Lab** | **A+** | **2016** | **Human Physiology + Lab\*** | **A+** | | **2013** | **General Biology II + Lab** | **A** | **2016** | **Capstone Project in Health Informatics** | **P** | | **2013** | **Second Semester Spanish** | **A** | **2016** | **Ethics and Policy Considerations of Health and Bioinformatics** | **A** | | **2013** | **Biostatistics** | **A-** | **2016** | **Semantic Organization of Health Data Information and Data Semantics** | **A** | | **2013** | **Organic Chemistry I** | **A** | **2017** | **Capstone Project in Health Informatics** | **P** | | **2013** | **Organic Chemistry Lab I** | **A** | **2017** | **Digital Health Entrepreneurship** | **A** | | **2013** | **Cell Physiology** | **A** | **2017** | **Statistical Computing for Biomedical Data Analytics** | **A+** | | **2014** | **Calculus & Analytic Geometry** | **A-** | **2017** | **Clinical Decision Support & Health Data Analytics** | **A** | | **2014** | **Urban Agriculture: Spring** | **A** | **Case Western Reserve University**  **Medical Scientist Training Program (GPA 4.00)** | | | | **2014** | **Organic Chemistry II** | **A** | **YEAR** | **COURSE TITLE** | **GRADE** | | **2014** | **Organic Chemistry Lab II** | **A** | **2017** | **Introduction to MSTP** | **P** | | **2014** | **Genetics + Lab** | **A** | **2017** | **Integrated Biol Sciences I\*\*** | **A** | | **2014** | **Great Works: Spirit of Romance** | **A+** | **2017** | **Clinical Science I\*\*** | **A** | | **2014** | **Mystery of God & Human Person** | **A** | **2017** | **Research Rotation in MSTP** | **P** | | **2014** | **Introductory Physics I + Lab** | **A+** | **2018** | **Integrated Biol Sciences II\*\*** | **A** | | **2014** | **Ethics** | **A** | **2018** | **Clinical Science II\*\*** | **A** | | **2015** | **Introductory Physics II + Lab** | **A** | **2018** | **Research Rotation in MSTP** | **P** | | **2015** | **Gymnastics-Tumbling** | **A** | **2018** | **Research Rotation in MSTP** | **P** | | **2015** | **Undergraduate Sem in Biology** | **A** | **2018** | **Integrated Biol Sciences III\*\*** | **A** | | **2015** | **Special Topic: Forensic Gen** | **A** | **2018** | **Clinical Science III\*\*** | **A** | | **2015** | **Medical Microbiology\*** | **A** | **2019** | **SYBB Research** | **P** | | **2015** | **Medical Microbiology Lab\*** | **A** | **2019** | **Statistical Methods I** | **A** | | **2015** | **Great Philosophical Questions** | **A+** | **2019** | **Technologies in Bioinformatics** | **A** | | **2015** | **Fundamentals of Biochemistry** | **A** | **2019** | **Data Integration in Bioinformatics** | **A** | | **2015** | **Honors Research in Biology** | **A** | **2019** | **Translational Bioinformatics** | **A** | | **2015** | **Conservation Biology** | **A** | **2019** | **Fundamentals Clinical Informtn** | **A** | | **2015** | **Conservation biology Lab** | **A** | **2020** | **Bioinformatics for Sys Biology** | **A** | | **2016** | **Human Physiology\*** | **A+** | **2020** | **Current Issues in Genetic Epi:**Design and Analysis of Seq Studies | **A** | | **2016** | **Human Physiology Lab\*** | **A+** | **2020** | **Biomedical Informatics and Systems Biology Journal Club** | **P** | | **2016** | **Evolution** | **A** |  |  |  | | **2016** | **Honors Thesis Writing** | **A** |  |  |  | |  |  |

**University of San Francisco grading**:

B.S.: Passing is D- or better

M.S.: Capstone projects are graded P (pass) or F (fail). In all other courses, passing is C- or better.

\* These courses overlapped as elective courses in both the B.S. in Biology and M.S. in Health informatics

**Case Western Reserve University grading**:

Research rotations and SYBB Research are graded as P (pass) or F (fail). In all other courses, passing is D- or better; IP = In progress

\*\*These courses comprise the first two-years of pre-clinical curriculum at the CWRU School of Medicine. The medical school curriculum is organized into blocks of organ systems and clinical practices including two graded portfolios of reflections. The block system is described as follows:

Block 8: Foundations of Clinical Medicine

Block 7: Structure

Block 6: Cognition, Sensation, and Movement

Block 5: Host Defense and Host Response

Block 4: Homeostasis

Block 3: Food to Fuel

Block 2: The Human Blueprint

Block 1: Becoming a Doctor