

Daniel A. Cuevas

dcuevas08@gmail.com

Website: <http://daniel-cuevas.com>

RESEARCH INTERESTS

I aim to furnish my analytical skill set with education and extensive, collaborative research in advanced mathematics, statistics, biology, and bioinformatics. The primary areas of focus in my doctoral curriculum are to develop bioinformatics tools, algorithms, and data visualization methods concentrated on DNA sequence analysis and bacterial metabolic modeling. These can be comprehensively applied toward various areas of biological research where data aggregation and investigation is required to answer scientific queries.

GRADUATE RESEARCH

Edwards Bioinformatics Lab
San Diego State University
5500 Campanile Drive, San Diego, CA 92182

Mentor: Professor Robert Edwards

EDUCATION

San Diego State University with Claremont Graduate University *05/13 – 12/17*
Ph.D., Computational Biology
Cumulative GPA: 3.85

San Diego State University *08/12 – 05/13*
M.S., Bioinformatics (transferred to Ph.D. program)
Cumulative GPA: 3.80

San Diego State University *08/05 – 05/11*
B.S., Computer Science
Major GPA: 3.89 | Cumulative: 3.23

G. R. E.
V: 148 | Q: 159 | A: 4.0

PROFESSIONAL EXPERIENCE

Graduate Research Assistant *07/12 – Present*
Robert Edwards Bioinformatics Lab, San Diego State University
Advisor: Professor Robert Edwards

- Generated a diverse set of bacterial genome-scale metabolic models to investigate common and unique difficulties in metabolism-based annotations
- Developed automated pipeline performing logistic model fitting onto bacterial growth curves, eliminating manual execution and increasing throughput
- Implemented the use of metabolic models and multi-phenotype growth curves to improve model accuracy and robustness using the Flux-Balance Analysis method
- Led a team of student researchers to produce bacterial databases that consist of a variety of data, including taxonomic-based phenotypes, experimental observations, and model-predicted results
- Performed various statistical and machine learning techniques on numerous biological data sets, such as DNA/amino acid sequences, mass spectroscopy-based metabolomics data, optical density biomass measurements, and DNA microarray expression levels

Software Engineer and Bioinformatician

09/11 – 07/12

Life Technologies, Ion Torrent R&D

Supervisor: Ellen Beasley

- Performed deep analysis on sequence quality and mapping statistics that identified deficiencies in the sequencing protocols and the AmpliSeq primer design algorithm
- Trained team members to use bioinformatics tools for investigations within various aspects of the Ion Torrent technology
- Exercised interdisciplinary skills of molecular biology and bioinformatics to assess the effectiveness of library preparation procedures in producing longer read lengths, higher quality sequences, and other far reaching goals
- Developed a multi-site accessible web-interface for experimental results and analysis that was absorbed as an integral tool for comparative studies throughout the company

Molecular Biology and Bioinformatics Internship

05/11 – 08/11

Life Technologies, Ion Torrent R&D and SOLiD Collaborations

Supervisor: Marie Callahan

- Performed multiple studies to measure the quality of several sequencing experiments by focusing on the performance of various sequencing polymerase mutants
- Led projects through supervision of sequencing and mapping runs to produce variant calls, mapping statistics, and mapping quality summaries for Collaborations group
- Assisted team members with scheduling sequencing runs, initializing PGM instruments, and resolving server-related issues to improve the flow of experiments

Undergraduate Research Assistant

05/09 – 05/11

Robert Edwards Bioinformatics Lab, San Diego State University

Advisor: Professor Robert Edwards

- Constructed a search hash-algorithm used to accurately identify DNA sequence similarity among multiple files
- Collaborated with a group member in developing an Android mobile application that effectively extracted metagenomic information from a DNA sequence file
- Developed a social network web application to access and distribute metagenomic data while leveraging the network's facilities to connect with colleagues and collaborators

AWARDS**ARCS Foundation Scholar, Two Years**

09/15-05/17

ARCS San Diego Chapter

2014 GEN TEN Award

06/14

Genetic Engineering and Biotechnology News Publisher

Graduate S-STEM Scholarship, Two Years

01/14 –01/16

National Science Foundation via SDSU Computational Science Research Center

11th Annual Rocky Mountain Bioinformatics Conference Poster Prize

12/13

F1000Research

Statistical Biomedical Informatics Scholarship, Two Semesters

08/12 – 05/13

Biomedical Informatics Research Center, San Diego State University

NIH New Interdisciplinary Workforce Fellow

07/09 – 07/10

Computational Science Research Center, San Diego State University

Dean's Honors List, Six Semesters

08/08 – 05/11

MEMBERSHIPS

Sigma Xi Scientific Society — Associate member	05/16
San Diego State University Science Alumni Network	05/15
San Diego State University Biomedical Technology Student Association — Webmaster	09/12

PEER REVIEWED PUBLICATIONS

Kang, H.S., McNair, K., **Cuevas, D.A.**, Bailey, B., Segall, A.M., and Edwards, R.A. (2016). Comprehensive analysis of curated prophage genomes from PhiSpy for assessment of phage genome mosaicism and tRNA dependencies. (In preparation).

Silva, G.G.Z., **Cuevas, D.A.**, Haggerty, J.M., Doane, M., Dinsdale, E.A., Dutilh, B.E., and Edwards, R.A. (2016). FOCUS2: agile and sensitive classification of metagenomics data using a reduced database. (In preparation).

Boling, L., **Cuevas, D.**, McNair, K., Smurthwaite, C., Sanchez, S., Kang, H.S., and Rohwer F. (2016). Dietary Antimicrobials and Prophage Inducers – Towards Landscaping of the Human Gut Microbiome. (In preparation).

Cuevas, D.A., and Edwards, R.A. (2016). PMAnalyzer 2.0: an online bacterial growth curve analysis pipeline. (In preparation).

Cuevas, D. A., Edirisinghe, J., Henry, C. S., Overbeek, R., O’Connell, T. G., and Edwards, R. A. (2016). From DNA to FBA: How to Build Your Own Genome-Scale Metabolic Model. *Systems Microbiology*, 907.

Sanchez, S.E., **Cuevas, D.A.**, Rostron, J.E., Liang, T.Y., Pivaroff, C.G., Haynes, M.R., Nulton, J., Felts, B., Bailey, B.A., Salamon, P., et al. (2015). Phage Phenomics: Physiological Approaches to Characterize Novel Viral Proteins. *Journal of Visualized Experiments*. e52854.

Cuevas, D.A., Garza, D., Sanchez, S.E., Rostron, J., Henry, C.S., Vonstein, V., Overbeek, R.A., Segall, A., Rohwer, F., Dinsdale, E.A., et al. (2014). Elucidating genomic gaps using phenotypic profiles. *Fl000Research*. (In review).

Lim, Y.W., **Cuevas, D.A.**, Silva, G.G.Z., Aguinaldo, K., Dinsdale, E.A., Haas, A.F., Hatay, M., Sanchez, S.E., Wegley-Kelly, L., Dutilh, B.E., et al. (2014). Sequencing at sea: challenges and experiences in Ion Torrent PGM sequencing during the 2013 Southern Line Islands Research Expedition. *PeerJ* 2, e520.

Dutilh, B.E., Thompson, C.C., Vicente, A.C., Marin, M.A., Lee, C., Silva, G.G., Schmieder, R., Andrade, B.G., Chimento, L., **Cuevas, D.**, et al. (2014). Comparative genomics of 274 *Vibrio cholerae* genomes reveals mobile functions structuring three niche dimensions. *BMC Genomics* 15, 654.

Silva, G.G.Z., **Cuevas, D.A.**, Dutilh, B.E., and Edwards, R.A. (2014). FOCUS: an alignment-free model to identify organisms in metagenomes using non-negative least squares. *PeerJ* 2, e425.

Disz, T., Akhter, S., **Cuevas, D.**, Olson, R., Overbeek, R., Vonstein, V., Stevens, R., and Edwards, R.A. (2010). Accessing the SEED Genome Databases via Web Services API: Tools for Programmers. *BMC Bioinformatics* 11, 319.

TALKS AND POSTER PRESENTATIONS

From DNA to FBA: how to build your own genome-scale metabolic model

04/16

SDSU Applied Computational Science and Engineering Student Support, San Diego, CA

From DNA to FBA: how to build your own genome-scale metabolic model San Diego State University Student Research Symposium, San Diego, CA	03/16
Phenotyping Diverse Bacteria for Metabolic Network Reconstruction General Meeting of the American Society for Microbiology, New Orleans, LA	06/15
Phenotyping Diverse Bacteria for Metabolic Network Reconstruction SDSU Applied Computational Science and Engineering Student Support, San Diego, CA	04/15
Phenotyping Diverse Bacteria for Metabolic Network Reconstruction San Diego State University Student Research Symposium, San Diego, CA	03/15
High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization Biotechnology Industry Organization International Convention, San Diego, CA	06/14
High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization General Meeting of the American Society for Microbiology, Boston, MA	05/14
High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization San Diego State University Student Research Symposium, San Diego, CA	03/14
High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization Southern California Systems Biology Conference, Irvine, CA	01/14
High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization Rocky Mountain Bioinformatics Conference, Snowmass, CO	12/13
Measuring Growth Quality of Bacteria Using Phenotypic Microarrays San Diego Microbiology Group All-day Meeting, San Diego, CA	05/13
Characterizing Phenotypic Properties of Unexplored Viral Genes San Diego State University Student Research Symposium, San Diego, CA	03/13
Compiling Genome Metadata for Comparative Analysis Rocky Mountain Bioinformatics Conference, Snowmass, CO	12/12
Rapid Sequence Searching Using Hashing San Diego State University Student Research Symposium, San Diego, CA	03/11
Real-Time Metagenomics General Meeting of the American Society for Microbiology, San Diego, CA	05/10
Real-Time Metagenomics San Diego Microbiology Group All-day Meeting, San Diego, CA	05/10
Real-Time Metagenomics SDSU Applied Computational Science and Engineering Student Support, San Diego, CA	03/10
Real-Time Metagenomics San Diego State University Student Research Symposium, San Diego, CA	03/10