

# Daniel A. Cuevas

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

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## 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**  
Ph.D., Computational Biology  
Cumulative GPA: 3.85

*08/12 – 12/17*

**San Diego State University**  
B.S., Computer Science  
Major GPA: 3.89 | Cumulative: 3.23

*08/05 – 05/11*

## PROFESSIONAL EXPERIENCE

### **Graduate Research Assistant**

*07/12 – Present*

**Robert Edwards Bioinformatics Lab, San Diego State University**

- Generated a diverse set of bacterial genome-scale metabolic models to perform comparative analyses alongside investigation into common and unique difficulties in metabolism-based annotations
- Developed automated pipeline named PMAnalyzer that performs logistic model fitting onto bacterial growth curves using Python's SciPy optimization libraries and Pandas data structures, eliminating manual execution and increasing throughput
- Developed genome-scale metabolic model software named PyFBA that performs Flux-Balance Analysis and a customizable model reconciliation heuristic to improve bacterial metabolism accuracy and robustness
- Led a team of student researchers to produce a bacterial database and API that consist of a variety of data, including taxonomic-based phenotypes, experimental observations, and model-predicted results
- Performed various statistical and machine learning techniques (e.g., regressions, SVM, random forest) 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, and other quantitative biological/environmental measurements

**Software Engineer and Bioinformatics Scientist**  
**Life Technologies, Ion Torrent R&D**

*09/11 – 07/12*

- Developed a web-interface serving as a hub that aggregated the entirety of experimental results and analysis conducted by all Ion Torrent R&D sites across the country and was absorbed as an integral tool for comparative studies throughout the company
- Performed deep analysis on sequence quality and mapping statistics (e.g., GC bias, primer-strand preferences, targeted sequencing efficacy) that identified deficiencies in the sequencing protocols and the Ion Torrent AmpliSeq primer design algorithm
- Trained team members to use bioinformatics tools (e.g., in-house bash scripts, the Integrated Genomics Viewer, Torrent Suite plugins) for investigations within various aspects of the Ion Torrent technology
- Exercised interdisciplinary skills by bridging communication between molecular biology and bioinformatics scientists to assess the effectiveness of library preparation procedures in producing longer read lengths, higher quality sequences, and other far reaching goals

**Molecular Biology and Bioinformatics Internship**  
**Life Technologies, Ion Torrent R&D and SOLiD Collaborations**

*05/11 – 08/11*

- 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 sequencing runs, prepared and initialized PGM sequencing instruments, and resolved server-related issues to improve the flow of experiments

**Undergraduate Research Assistant**  
**Robert Edwards Bioinformatics Lab, San Diego State University**

*05/09 – 05/11*

- Constructed a search hash-algorithm in Java to accurately identify DNA sequence similarity between multiple sequence files
- Collaborated with a group member to develop an Android mobile application operating as a front-end interface to illustrate statistics metrics and figures for a server-side application that performed metagenome data analysis
- Developed a social network web application to access and distribute metagenomics data while leveraging the network's API and infrastructure to connect with colleagues and collaborators

**AWARDS**

**14<sup>th</sup> Annual SDSU ACSESS Poster Award**  
 Tioga Research, Inc.

*04/17*

**ARCS Foundation Scholar, Two Years**  
 ARCS San Diego Chapter

*09/15-05/17*

**2014 GEN TEN Award**  
 Genetic Engineering and Biotechnology News Publisher

*06/14*

**Graduate S-STEM Scholarship, Two Years**  
 National Science Foundation via SDSU Computational Science Research Center

*01/14 – 01/16*

**11<sup>th</sup> Annual Rocky Mountain Bioinformatics Conference Poster Prize**  
 F1000Research

*12/13*

**Statistical Biomedical Informatics Scholarship, Two Semesters**  
 Biomedical Informatics Research Center, San Diego State University

*08/12 – 05/13*

**NIH New Interdisciplinary Workforce Fellow**  
 Computational Science Research Center, San Diego State University

*07/09 – 07/10*

## MEMBERSHIPS

Sigma Xi Scientific Society — Full member	05/16
Society for Industrial and Applied Mathematics	10/15
San Diego State University Science Alumni Network	05/15
San Diego State University Biomedical Technology Student Association — Webmaster	09/12

## PEER REVIEWED PUBLICATIONS

Boling, L., **Cuevas, D.**, McNair, K., Smurthwaite, C., Sanchez, S., Kang, H.S., and Rohwer F. (2017). Dietary Antimicrobials and Prophage Inducers – Towards Landscaping of the Human Gut Microbiome. (In preparation).

Kang, H.S., McNair, K., **Cuevas, D.**, Bailey, B., Segall, A.M., and Edwards, R.A. (2017). Prophage genomics reveals patterns in phage genome organization and replication. *bioRxiv*, 114819. (In submission).

Silva, G.G.Z., Haggerty, J.M., **Cuevas, D.A.**, Doane, M., Dinsdale, E.A., Dutilh, B.E., and Edwards, R.A. (2017). Ecological Implications of Metagenomics Data Analysis. (In submission).

Sczyrba A., et al. (2017). Critical Assessment of Metagenome Interpretation – a benchmark of computational metagenomics software. *Nature Methods*. (Accepted).

**Cuevas, D.A.**, and Edwards, R.A. (2017). PMAalyzer: a new web interface for bacterial growth curve analysis. *Bioinformatics* 33(12), 1905-1906.

**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., Chimetto, 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**

<b>Metabolic model and data-driven exploration linking genotypes to phenotypes</b> (Talk) SDSU Computational Science Research Center Colloquium, San Diego, CA	07/17
<b>Metabolic model and data-driven exploration linking genotypes to phenotypes</b> (Poster) SDSU Applied Computational Science and Engineering Student Support, San Diego, CA	04/17
<b>Metabolic model and data-driven exploration linking genotypes to phenotypes</b> (P) San Diego State University Student Research Symposium, San Diego, CA	03/17
<b>From DNA to FBA: how to build your own genome-scale metabolic model</b> (P) SDSU Applied Computational Science and Engineering Student Support, San Diego, CA	04/16
<b>From DNA to FBA: how to build your own genome-scale metabolic model</b> (P) ARCS Scientist of the Year Award Dinner, San Diego, CA	04/16
<b>From DNA to FBA: how to build your own genome-scale metabolic model</b> (T) San Diego State University Student Research Symposium, San Diego, CA	03/16
<b>Phenotyping Diverse Bacteria for Metabolic Network Reconstruction</b> (P) General Meeting of the American Society for Microbiology, New Orleans, LA	06/15
<b>Phenotyping Diverse Bacteria for Metabolic Network Reconstruction</b> (P) SDSU Applied Computational Science and Engineering Student Support, San Diego, CA	04/15
<b>Phenotyping Diverse Bacteria for Metabolic Network Reconstruction</b> (T) San Diego State University Student Research Symposium, San Diego, CA	03/15
<b>High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization</b> (T) Biotechnology Industry Organization International Convention, San Diego, CA	06/14
<b>High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization</b> (P) General Meeting of the American Society for Microbiology, Boston, MA	05/14
<b>High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization</b> (T) San Diego State University Student Research Symposium, San Diego, CA	03/14
<b>High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization</b> (P) Southern California Systems Biology Conference, Irvine, CA	01/14
<b>High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization</b> (T & P) Rocky Mountain Bioinformatics Conference, Snowmass, CO	12/13
<b>Measuring Growth Quality of Bacteria Using Phenotypic Microarrays</b> (P) San Diego Microbiology Group All-day Meeting, San Diego, CA	05/13
<b>Characterizing Phenotypic Properties of Unexplored Viral Genes</b> (T) San Diego State University Student Research Symposium, San Diego, CA	03/13
<b>Compiling Genome Metadata for Comparative Analysis</b> (T) Rocky Mountain Bioinformatics Conference, Snowmass, CO	12/12
<b>Rapid Sequence Searching Using Hashing</b> (T) San Diego State University Student Research Symposium, San Diego, CA	03/11

<b>Real-Time Metagenomics</b> (P) General Meeting of the American Society for Microbiology, San Diego, CA	05/10
<b>Real-Time Metagenomics</b> (P) San Diego Microbiology Group All-day Meeting, San Diego, CA	05/10
<b>Real-Time Metagenomics</b> (P) SDSU Applied Computational Science and Engineering Student Support, San Diego, CA	03/10
<b>Real-Time Metagenomics</b> (T) San Diego State University Student Research Symposium, San Diego, CA	03/10

## **LECTURES**

Guest lecture at San Diego State University. Course: BIOL549 - Microbial Genetics and Physiology <i>Flux-balance analysis using genome-scale metabolic models</i>	11/16
Guest speaker at the ARCS General Meeting, Rancho Santa Fe, CA <i>Metabolic modeling in the era of genomics</i>	06/16
Summer workshop at San Diego State University <i>Introduction to Python programming for microbiology scientists</i>	Summer 2016