

# Daniel A Cuevas, PhD

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## EDUCATION

**Doctor of Philosophy (PhD), Computational Biology and Bioinformatics** 08/12 – 02/18  
San Diego State University with Claremont Graduate University

**Bachelor of Science (BS), Computer Science** 08/05 – 05/11  
San Diego State University

## GRADUATE RESEARCH

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

**Mentor:** Professor Robert Edwards

## PROFESSIONAL EXPERIENCE

**Bioinformatician** 03/18 – Present  
Progenity, Inc. R&D

**Graduate Research Assistant** 07/12 – 03/18  
Robert Edwards Bioinformatics Lab, San Diego State University

- Led production of PyFBA to identify novel metabolic pathways and transporters within bacterial genomes. PyFBA is a systems biology Python software integrating genomes, phenotypes, and the ModelSEED database to build and test genome-scale metabolic models, then amended with pathways missed by traditional genome annotation platforms
- Developed PMAalyzer to profile bacterial phenotypes across thousands of growth curves from monoculture or microbial community assays. PMAalyzer is an automated web-interface and pipeline that rapidly processes growth data using model parameterization
- Participated in design and development of a full NGS metagenome/metatranscriptome computational pipeline used for emergency Cystic Fibrosis patient sputum sequencing data: includes read QA, species profiling, functional profiling, virulence factor/antibiotic resistance identification, and custom sequencing statistics scripts with graph visualizations
- Supported microbiology researchers through consulting and analyzing biological datasets consisting of hundreds of variables, including sequencing, metabolomics, time-series growth data, and RNA expression. Analyses include regressions, classifications, feature importance, and custom data visualizations

**Bioinformatics Scientist and Software Engineer** 09/11 – 07/12  
Life Technologies, Ion Torrent R&D

- Developed a Django web-interface search engine for hundreds of internal sequencing results produced by all Ion Torrent R&D across the country, increasing ease of access and accepted as an integral tool for comparative studies throughout the company
- Developed a variety of C, Python, and Perl programs for customer facing Torrent Suite plugins. Utilized JIRA software tracking and version control for all products
- Supported scientists with custom pipelines to analyze sequence quality and mapping statistics for deficiencies in sequencing protocols and the Ion Torrent AmpliSeq primer design algorithm, including GC bias, primer-strand preferences, targeted sequencing efficacy

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

05/11 – 08/11

- Created and presented analyses measuring the quality of sequencing experiments testing various sequencing polymerase mutants for longer reads and higher Phred quality scores
- Led and supervised sequencing and mapping runs that produced variant calls, mapping statistics, and mapping quality summaries for the SOLiD Collaborations team
- 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

- Developed several Java programs interfacing with a web service API for the SEED genome annotation database
- Constructed a search hash-algorithm in Java to accurately identify DNA sequence similarity between multiple sequence files
- Co-developed a front-end Android app producing figures and statistics for the Real Time Metagenomics server-side annotation tool
- 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

**FIRST AUTHOR PUBLICATIONS**

1. **Cuevas, D.A.** (2018). *Bridging the genomic gaps: genome-scale metabolic network tools for bioinformatics analyses*. Dissertation. (In submission).
2. **Cuevas, D.A.** and Edwards, R.A. (2018). *Growth Score: a single metric to define growth in 96-well phenotype assays*. *PeerJ* 6:e4681.
3. **Cuevas, D.A.** and Edwards, R.A. (2017). *PMAnalyzer: a new web interface for bacterial growth curve analysis*. *Bioinformatics* 33(12), 1905-1906.
4. **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.
5. **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., and Edwards, R.A. (2014). *Elucidating genomic gaps using phenotypic profiles*. *F1000Research* 3, 210.

**CO-AUTHOR PUBLICATIONS**

1. Boling, L., **Cuevas, D.A.,** Kang, H.S., Knowles, B., Maughan, H., McNair, K., Rojas, M.I., Sanchez, S.E., Smurthwaite, C., and Rohwer, F. (2018). *Dietary Antimicrobials and Prophage Inducers – Towards Landscaping of the Human Gut Microbiome*. (In submission).
2. Silveira, C.B., Coutinho, F.H., Cobián-Güemes, A.G., Cantu, V.A., **Cuevas, D.A.,** Knowles, B., Cavalcanti, G.S., Soares, A.C., Silva, G.G.Z., Doane, M., Francini-Filho, R., Thompson, C., Dinsdale, E., Edwards, R., Gregoracci, G., Rohwer, F., and Thompson, F. (2018). *Phage-mediated transfer of bacterial virulence genes in coral reefs*. (In submission).

3. Silva, G.G.Z., Haggerty, J.M., **Cuevas, D.A.**, Doane, M., Dinsdale, E.A., Dutilh, B.E., and Edwards, R.A. (2018). *Ecological Implications of Metagenomics Data Analysis*. (In submission).
4. Sczyrba, A., Hofmann, P., Belmann, P., Koslicki, D., Janssen, S., Dröge, J., Gregor, I., Majda, S., Fiedler, J., Dahms, E., Bremges, A., Fritz, A., Garrido-Oter, R., Jørgensen, T.S., Shapiro, N., Blood, P.D., Gurevich, A., Bai, Y., Turaev, D., DeMaere, M.Z., Chikhi, R., Nagarajan, N., Quince, C., Meyer, F., Balvočiūtė, M., Hansen, L.H., Sørensen, S.J., Chia, B.K.H., Denis, B., Froula, J.L., Wang, Z., Egan, R., Kang, D.D., Cook, J.J., Deltel, C., Beckstette, M., Lemaitre, C., Peterlongo, P., Rizk, G., Lavenier, D., Wu, Y.W., Singer, S.W., Jain, C., Strous, M., Klingenberg, H., Meinicke, P., Barton, M.D., Lingner, T., Lin, H.H., Liao, Y.C., Silva, G.G.Z., **Cuevas, D.A.**, Edwards, R.A., Saha, S., Piro, V.C., Renard, B.Y., Pop, M., Klenk, H.P., Göker, M., Kyrpides, N.C., Woyke, T., Vorholt, J.A., Schulze-Lefert, P., Rubin, E.M., Darling, A.E., Rattei, T., and McHardy, A.C. (2017). Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. *Nature Methods*, 14(11), 1063–1071.
5. 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.
6. 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., Edwards, R.A., Burgin, A.B., Segall, A.M., and Rohwer, F. (2015). *Phage Phenomics: Physiological Approaches to Characterize Novel Viral Proteins*. *Journal of Visualized Experiments*, e52854.
7. 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., Harkins, T.T., Lee, C.C., Tom, W., Sandin, S.A., Smith, J.E., Zgliczynski, B., Vermeij, M.J.A., Rohwer, F., and Edwards, R.A. (2014). *Sequencing at sea: challenges and experiences in Ion Torrent PGM sequencing during the 2013 Southern Line Islands Research Expedition*. *PeerJ* 2, e520.
8. 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.**, Garza, D.R., Okeke, I.N., Aboderin, A.O., Spangler, J., Ross, T., Dinsdale, E.A., Thompson, F.L., Harkins, T.T., and Edwards, R.A. (2014). *Comparative genomics of 274 Vibrio cholerae genomes reveals mobile functions structuring three niche dimensions*. *BMC Genomics* 15, 654.
9. 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.
10. 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.

## AWARDS

**14<sup>th</sup> Annual SDSU ACSESS Poster Award**

04/17

Tioga Research, Inc.

**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

<b>11<sup>th</sup> Annual Rocky Mountain Bioinformatics Conference Poster Prize</b> F1000Research	12/13
<b>Statistical Biomedical Informatics Scholarship, Two Semesters</b> Biomedical Informatics Research Center, San Diego State University	08/12 – 05/13
<b>NIH New Interdisciplinary Workforce Fellow</b> Computational Science Research Center, San Diego State University	07/09 – 07/10
<b>Dean's Honors List, Six Semesters</b> San Diego State University	08/08 – 05/11

## 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 REVIEWER

PLoS One

## TALKS AND POSTER PRESENTATIONS

<b>Unraveling metabolism network models of kelp-associated bacteria</b> (Talk) San Diego State University Student Research Symposium, San Diego, CA	03/18
<b>Metabolic model and data-driven exploration linking genotypes to phenotypes</b> (T) 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) ARCS Scientist of the Year Award Dinner, 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