

Daniel A Cuevas, PhD

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EDUCATION

Doctor of Philosophy (PhD), Computational Biology and Bioinformatics
San Diego State University with Claremont Graduate University

08/12 – 02/18

Bachelor of Science (BS), Computer Science
San Diego State University

08/05 – 05/11

GRADUATE RESEARCH

Edwards Bioinformatics Lab
San Diego State University
5500 Campanile Drive, San Diego, CA 92182
Mentor: Professor Robert Edwards

PROFESSIONAL EXPERIENCE

Graduate Research Assistant
Robert Edwards Bioinformatics Lab, San Diego State University

07/12 – Present

- 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
Life Technologies, Ion Torrent R&D

09/11 – 07/12

- 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 writing).
2. **Cuevas, D.A.** and Edwards, R.A. (2018). Growth Score: a single metric to define growth in 96-well phenotype assays. *PeerJ Preprints* 6:e26469v1.
3. **Cuevas, D.A.** and Edwards, R.A. (2017). *PMAalyzer: 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

14th 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

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

San Diego State University

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

Unraveling metabolism network models of kelp-associated bacteria

03/18

(Talk) San Diego State University Student Research Symposium, San Diego, CA

Metabolic model and data-driven exploration linking genotypes to phenotypes

07/17

(T) SDSU Computational Science Research Center Colloquium, San Diego, CA

Metabolic model and data-driven exploration linking genotypes to phenotypes

04/17

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

Metabolic model and data-driven exploration linking genotypes to phenotypes

04/17

(P) ARCS Scientist of the Year Award Dinner, San Diego, CA

Metabolic model and data-driven exploration linking genotypes to phenotypes

03/17

(P) San Diego State University Student Research Symposium, San Diego, CA

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

04/16

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

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

04/16

(P) ARCS Scientist of the Year Award Dinner, San Diego, CA

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

03/16

(T) San Diego State University Student Research Symposium, San Diego, CA

Phenotyping Diverse Bacteria for Metabolic Network Reconstruction

06/15

(P) General Meeting of the American Society for Microbiology, New Orleans, LA

Phenotyping Diverse Bacteria for Metabolic Network Reconstruction

04/15

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

Phenotyping Diverse Bacteria for Metabolic Network Reconstruction

03/15

(T) San Diego State University Student Research Symposium, San Diego, CA

High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization

06/14

(T) Biotechnology Industry Organization International Convention, San Diego, CA

High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization

05/14

(P) General Meeting of the American Society for Microbiology, Boston, MA

High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization (T) San Diego State University Student Research Symposium, San Diego, CA	03/14
High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization (P) Southern California Systems Biology Conference, Irvine, CA	01/14
High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization (T & P) Rocky Mountain Bioinformatics Conference, Snowmass, CO	12/13
Measuring Growth Quality of Bacteria Using Phenotypic Microarrays (P) San Diego Microbiology Group All-day Meeting, San Diego, CA	05/13
Characterizing Phenotypic Properties of Unexplored Viral Genes (T) San Diego State University Student Research Symposium, San Diego, CA	03/13
Compiling Genome Metadata for Comparative Analysis (T) Rocky Mountain Bioinformatics Conference, Snowmass, CO	12/12
Rapid Sequence Searching Using Hashing (T) San Diego State University Student Research Symposium, San Diego, CA	03/11
Real-Time Metagenomics (P) General Meeting of the American Society for Microbiology, San Diego, CA	05/10
Real-Time Metagenomics (P) San Diego Microbiology Group All-day Meeting, San Diego, CA	05/10
Real-Time Metagenomics (P) SDSU Applied Computational Science and Engineering Student Support, San Diego, CA	03/10
Real-Time Metagenomics (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