

Daniel A. Cuevas

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GRADUATE RESEARCH

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

Mentor: Professor Robert Edwards

EDUCATION

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

08/12 – 05/18

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

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
- Participated in design and development of a metagenome/metatranscriptome analysis pipeline used for Cystic Fibrosis patient sputum paired-end sequencing data: read QA, species profiling, functional profiling, virulence factor and antibiotic resistance identification, and a suite of custom DNA sequence analysis and data visualization Python and R scripts
- 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

05/11 – 08/11

Life Technologies, Ion Torrent R&D and SOLiD Collaborations

- 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

05/09 – 05/11

Robert Edwards Bioinformatics Lab, San Diego State University

- 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
- 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

FIRST AUTHOR PUBLICATIONS

Cuevas, D.A., and Edwards, R.A. (2018). *Growth Score: a single metric to define growth in 96-well phenotype assays*. (In submission).

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.

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

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).

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).

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).

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., Kypides, 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.

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.

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.

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.

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.**, 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.

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.

AWARDS

14th Annual SDSU ACSESS Poster Award
Tioga Research, Inc.

04/17

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

Metabolic model and data-driven exploration linking genotypes to phenotypes

07/17

(Talk) 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

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 03/14
(T) San Diego State University Student Research Symposium, San Diego, CA

High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization 01/14
(P) Southern California Systems Biology Conference, Irvine, CA

High-Throughput Phenotype Profiling for Bacterial Flux-Balance Model Optimization 12/13
(T & P) Rocky Mountain Bioinformatics Conference, Snowmass, CO

Measuring Growth Quality of Bacteria Using Phenotypic Microarrays 05/13
(P) San Diego Microbiology Group All-day Meeting, San Diego, CA

Characterizing Phenotypic Properties of Unexplored Viral Genes 03/13
(T) San Diego State University Student Research Symposium, San Diego, CA

Compiling Genome Metadata for Comparative Analysis 12/12
(T) Rocky Mountain Bioinformatics Conference, Snowmass, CO

Rapid Sequence Searching Using Hashing 03/11
(T) San Diego State University Student Research Symposium, San Diego, CA

Real-Time Metagenomics 05/10
(P) General Meeting of the American Society for Microbiology, San Diego, CA

Real-Time Metagenomics 05/10
(P) San Diego Microbiology Group All-day Meeting, San Diego, CA

Real-Time Metagenomics 03/10
(P) SDSU Applied Computational Science and Engineering Student Support, San Diego, CA

Real-Time Metagenomics 03/10
(T) San Diego State University Student Research Symposium, San Diego, CA

LECTURES

Guest lecture at San Diego State University. Course: BIOL549 - Microbial Genetics and Physiology 11/16
Flux-balance analysis using genome-scale metabolic models

Guest speaker at the ARCS General Meeting, Rancho Santa Fe, CA 06/16
Metabolic modeling in the era of genomics

Summer workshop at San Diego State University Summer 2016
Introduction to Python programming for microbiology scientists