

## Michael A. DeJesus, Ph.D.

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<http://mad-lab.org>  
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### EDUCATION

- *Ph.D.*, Computer Science  
Texas A&M University, College Station, TX
- *M.S.*, Computer Science  
Texas A&M University, College Station, TX
- *B.S.*, Computer Science  
Universidad de Puerto Rico, Mayagüez, PR

### EXPERIENCE

***Senior Computational Biologist*** Summer 2018 - Present  
Rock Lab. Rockefeller University

***Postdoctoral Fellow*** Fall 2016 - Summer 2018  
Ioerger Lab. Texas A&M University

***Ph.D. Student*** Fall 2010 - Fall 2016  
Ioerger Lab. Texas A&M University

- Developed and published statistical models for analyzing and normalizing TnSeq data, to predict gene essentiality.
- Designed and wrote software package providing a graphical interface for the analysis methods developed in the lab (TRANSIT).
- Analyzed TnSeq, RNA-Seq, and sequencing data for the Sacchettini Lab.
- Developed and maintained a website for a NIH-funded project (FLUTE).

***Teaching Assistant*** Fall 2015  
CSCE 625: Artificial Intelligence. Texas A&M University

- Mentored students on assignments and class materials.
- Graded all projects and homework.

***Specialist I*** Fall 2008 - Fall 2009  
Infotech Aerospace Services, Inc., Isabella, PR

- Wrote scripts to test on-board aircraft equipment and automated reports.

### SKILLS

*Programming Languages/Tools*: Python, R, Matlab, C++, J Django, Git  
*Coursework*: Machine Learning, Pattern Recognition, AI, Bayesian Statistics  
*Languages*: English (Fluent), Spanish (Native)

### AWARDS

Lechner Graduate Scholarship (2012)  
Best Paper Award - *ACM-BCB* Conference (2013)  
Best Paper Award - *BICoB* Conference (2015)

## GRANTS

Potts Memorial Foundation

- **Role:** Principal Investigator. **Period:** 2019-2021 **Amount:** \$100,000

Robertson Therapeutic Development Fund

- **Role:** Co-Principal Investigator. **Period:** Jan-July 2020 **Amount:** \$50,000

## PUBLICATIONS

### Journals

- Dutta, E., **DeJesus, M.A.**, Ruecker, N., Zaveri, Z., Koh, E.I., Sassetti, C.M., Schnappinger, D., Ioerger, T.R. (2021). An improved statistical method to identify chemical-genetic interactions by exploiting concentration-dependence. *Plos ONE* (16), 1-24.
- Bosch, B.\*, **DeJesus, M.A.\***, Poulton, N.C., Zhang, W., Engelhart, C.A., Zaveri, A., Lavalette-Levi, S., Ruecker, N., Trujillo, C., Wallach, J.B., Li, S., Ehrt, S., Chait, B.T., Schnappinger, D., Rock, J.M. (2021). Genome-wide titration of essential gene expression reveals diverse vulnerabilities of Mycobacterium tuberculosis. *Cell* 184 (17), 4579-4592. e24. **\*Co-first authors.**
- Jinich, A., Zaveri, A., **DeJesus, M.A.**, Flores-Bautista, E., Smith, C.M., Sassetti, C.M., Rock, J.M., Ehrt, S., Schnappinger, D., Ioerger, T.R., Rhee, K. (2021). The Mycobacterium tuberculosis transposon sequencing database (MtbTnDB): a large-scale guide to genetic conditional essentiality. *bioRxiv* 10.1101/2021.03.05.434127
- Siddharth, S., **DeJesus, M.A.**, Saveri, A., Smith, C.M., Baker, R.E., Ehrt, S., Schnappinger, D., Sassetti, C.M., Ioerger, T.R. (2019). Statistical Analysis of Variability in TnSeq Data Across Conditions Using Zero-Inflated Negative Binomial Regression. *BMC Bioinformatics* 20, 603. doi: 10.1186/s12859-019-3156-z
- **DeJesus, M.A.**, Nambi, S., Smith, C.M., Baker, R.E., Sassetti, C.M., and Ioerger, T.R. (2017). Statistical Analysis of Genetic Interactions in TnSeq Data. *Nucleic Acids Research*, gkx128. doi: 10.1093/nar/gkx128
- Xu, W., **DeJesus, M.A.**, Rucker, N., Engelhart, C., Wright, M.G., Healy, C., Lin, K., Wang, R., Park, S.W., Ioerger, T.R., Schnappinger, D., and Ehrt, S. (2017). Chemical genomic interaction profiling reveals determinants of antibiotic susceptibility in *Mycobacterium tuberculosis*. *Antimicrobial Agents and Chemotherapy*. doi: 10.1128/AAC.01334-17.
- **DeJesus, M.A.**, Gerrick, E.R., Xu, W., Park, S.W., Long, J.E., Boutte, C.C., Rubin, E.J., Schnappinger, D., Ehrt, S., Fortune, S.M., Sassetti, C.M., and Ioerger, T.R. (2017). Comprehensive essentiality analysis of the Mycobacterium tuberculosis genome via saturating transposon mutagenesis. *mBio*, 8(1):e02133-16.
- Korte J, Alber M, Trujillo CM, Syson K, Koliwer-Brandl H, Deenen R, Khrrer K, **DeJesus, M.A.**, Hartman T, Jacobs WR Jr, Bornemann S, Ioerger TR, Ehrt S, Kalscheuer R. *PLoS Pathog*. 2016 Dec 9;12(12):e1006043. doi: 10.1371/journal.ppat.1006043.

- Orsini, C., Setlow, B., **DeJesus, M.A.**, Galaviz, S., Loesch, K., Ioerger, T.R., and Wallis, D. (2016). Behavioral and transcriptomic profiling of mice null for *Lphn3*, a gene implicated in ADHD and addiction. *Molecular Genetics & Genomic Medicine*, 4(3):322-43.
- **DeJesus, M.A.** and Ioerger, T.R. (2016). Normalization of transposon-mutant library sequencing datasets to improve identification of conditionally essential genes. *Journal of Bioinformatics and Computational Biology*, 14(3):1642004.
- **DeJesus, M.A.**, Ambadipudi, C., Baker, R., Sassetti, C., and Ioerger, T.R. (2015). TRANSIT - a Software Tool for Himar1 TnSeq Analysis. *PLoS Computational Biology*, 11(10):e1004401
- Loesch, K., Galaviz, S., Sun, Q., **DeJesus, M.A.**, Ioerger, T.R., Sacchettini, J.C. and Wallis, D. (2015). High-throughput differentiation and screening of a library of mutant stem cell clones defines new host-based genes involved in rabies virus infection. *Stem Cells*, 33(8):2509-22.
- Loesch, K., Clanton, R., Akabani, G., Deveau, M., **DeJesus, M.A.**, Ioerger, T.R., Galaviz, S., Sacchettini, J.C., and Wallis, D. (2015). Functional genomics screening utilizing mutant mouse embryonic stem cells identifies novel radiation-response genes. *PLOS ONE* 10(4): e0120534. doi:10.1371/journal.pone.0120534.
- **DeJesus, M.A.** and Ioerger, T.R. (2014). Capturing uncertainty by modeling local transposon insertion frequencies improves discrimination of essential genes. *IEEE Transactions on Computational Biology and Bioinformatics*. vol.PP, no.99, pp.1,1 doi: 10.1109/TCBB.2014.2326857
- **DeJesus, M.A.** and Ioerger, T.R. (2013). A Hidden Markov Model for identifying essential and growth-defect regions in bacterial genomes from transposon insertion sequencing data. *BMC Bioinformatics* 14:303 DOI: 10.1186/1471-2105-14-303.
- **DeJesus, M.A.**, Zhang, Y.J., Sassetti, C.M., Rubin, E.J., Sacchettini, J.C., and Ioerger, T.R. (2013). Bayesian analysis of gene essentiality based on sequencing of transposon insertion libraries. *Bioinformatics*, 29(6):695-703.
- **DeJesus, M.A.**, Sacchettini, J.C., and Ioerger, T.R. (2012). Reannotation of translational start sites in the genome of *Mycobacterium tuberculosis*. *Tuberculosis*, 93:18-25.
- Griffin, J.E., Gawronski, J.D., **DeJesus, M.A.**, Ioerger, T.R., Akerley, B.J., and Sassetti, C.M. (2011). High-Resolution Phenotypic Profiling Defines Genes Essential for *Mycobacterium tuberculosis* Growth and Cholesterol Catabolism. *PLoS Pathogens* 7, e1002251.

## Conferences

- **DeJesus, M.A.** and Ioerger, T.R. (2015). Reducing type I errors in Tn-Seq experiments by correcting the skew in read count distributions. *7th International Conference on Bioinformatics and Computational Biology (BICoB 2015)*. Best Paper Award.

- **DeJesus, M.A.**, and Ioerger, T.R. (2013). Improving discrimination of essential genes by modeling local insertion frequencies in transposon mutagenesis data. *ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics (ACM-BCB)*, Washington, DC, Sept 22-25, 2013. Best Paper Award.

## Posters

- Maxwell, S.A. and Wallis, D. and Zhou, N. and Baker, D. and Mousavi-Fard, S. and Loesch, K. and Galaviz, S. and Sun, Q. and Threadgill, D.M. and Rojas, C.M. and O'Brien, M. and Clubb, F.J. and Ioerger, T. and **DeJesus, M.A.**, and Dong, W. and Seemann, G. and Fossum, T. and Sacchetti, J.C. (2017). Development of novel, non-toxic Rifamycins that reverse drug resistance in diffuse large b-cell lymphoma (DLBCL). *Hematological Oncology*. vol 35. 10.1002/hon.2438.118

## Book Chapters

- Long, J.E., **DeJesus, M.A.**, Ward, D., Baker, R.E., Ioerger, T.R. and Sassetti, C.M. (2015). Identifying essential genes in Mycobacterium tuberculosis by global phenotypic profiling. *Methods in Molecular Biology: Gene Essentiality*, (Long Jason Lu, ed.), vol. 1279.