

Manuel Razo-Mejia

PHD CANDIDATE · BIOCHEMISTRY & MOLECULAR BIOPHYSICS

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Education

California Institute of Technology (Caltech)

PHD BIOCHEMISTRY & MOLECULAR BIOPHYSICS

Pasadena, California

2014 - present

- Thesis Topic: Physical biology of cellular information processing
- Thesis Advisor: Rob Phillips.

Instituto Politecnico Nacional

BSC BIOTECHNOLOGICAL ENGINEERING

Silao, Guanajuato, Mexico

2009 - 2014

Awards & Scholarships

PHD

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| 2019 | Caldwell CEMI graduate Fellowship , Kim and Ginger Caldwell endowed fellowship | Caltech |
| 2018 | Caltech's Breakthrough campaign featured story , Caltech's Breakthrough campaign. Link: https://breakthrough.caltech.edu/story/science-and-serendipity/ | Caltech |
| 2015 | Amgen Graduate Fellowship , Caltech-Amgen Research Collaboration | Caltech |
| 2014 | Benjamin M. Rosen Graduate Fellowship , Benjamin M. Rosen endowed fellowship for incoming students | Caltech |

BSc

- | | | |
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| 2014 | Valedictorian , Class of 2014 | IPN, Mexico |
| 2013 | Research Fellowship , Summer Kupcinec-Getz International Science School | WIS, Israel |
| 2012 | Research Fellowship , Summer Undergraduate Research Fellowship | Caltech |

Research Accomplishments

A Predictive Theory of Allosteric Induction

Cell Systems

WITH S. BARNES, N. BELLIVEAU, T. EINAV, G. CHURE, M. LEWIS, AND R. PHILLIPS

2018

- We wrote down a theoretical model, based on statistical physics, that predicts the expression level of a gene regulated by an allosteric transcription factor. We then tested the model experimentally by measuring the mean gene expression of a series of strains with different biophysical parameters, showing that the model was able to predict how changes to the regulation of the gene translate to changes in the cellular response.

Predictive shifts in free energy couple mutations to their phenotypic consequences

PNAS

WITH G. CHURE, N. BELLIVEAU, T. EINAV, Z. KACZMAREK, S. BARNES, M. LEWIS, AND R. PHILLIPS

2019

- We expanded our model of gene regulation by allosteric transcription factors to explore changes in biophysical parameters due to changes in the amino-acid sequence of the transcription factor. We mutated both the DNA-binding domain and the inducer-binding domain of the protein, and re-fit the corresponding parameters given new gene expression measurements. We then predicted the double-mutants by adding the corresponding free-energy changes for each of the mutations, and found great agreement with the corresponding experimental data.

First-principles prediction of the information processing capacity of a simple genetic circuit

Physical Review E

WITH S. MARZEN, G. CHURE, R. TAUBMAN, M. MORRISON, AND R. PHILLIPS

2020

- With the objective of predicting the amount of information (in bits) that a simple genetic circuit can gather from the state of the environment, we wrote down a non-equilibrium model for the full distribution of gene expression as a function of an external signal. We calibrated our model with previous information in order to perform parameter-free predictions. To test the model, we compared the predictions with experimental single-cell gene expression data finding great agreement.

Reconciling Kinetic and Equilibrium Models of Bacterial Transcription

PLoS Comp. Bio. (accepted)

WITH M. MORRISON AND R. PHILLIPS

2020

- We did an exhaustive analysis of the correspondence between equilibrium models of gene regulation –based on statistical mechanics– and equivalent kinetic models –based on the chemical master equation. We found that both frameworks make indistinguishable predictions at the level of mean gene expression. Only through accounting for higher moments of the distribution we can get mechanistic insights into which scheme better describes the regulation of the gene. We finally used Bayesian inference to show that “the best model” we found can predict single-molecule mRNA counts distributions.

Publications

2020

- **Razo-Mejia, M.**, et al. (2020). *First-principles prediction of the information processing capacity of a simple genetic circuit*. Phys. Rev. E 022404, 1–14. **Paper website** and **GitHub repository**
<http://doi.org/10.1103/PhysRevE.102.022404>
- Morrison, M. J., **Razo-Mejia, M.**, & Phillips, R. (2020). *Reconciling Kinetic and Equilibrium Models of Bacterial Transcription*. PLoS comp. bio. (accepted). **GitHub repository**
<https://arxiv.org/abs/2006.07772v1>

2019

- Chure, G., **Razo-Mejia, M.**, Belliveau, N. M., Einav, T., Kaczmarek, Z. A., Barnes, S. L., Lewis, M., Phillips, R. (2019). *Predictive shifts in free energy couple mutations to their phenotypic consequences*. PNAS, 201907869. **Paper website** and **GitHub repository**
<https://doi.org/10.1073/pnas.1907869116>
- Foster, P. J., **Razo-Mejia, M.**, Phillips, R. (2019). *Measuring the Energetic Costs of Embryonic Development*. Developmental Cell, 48(5), 591?592.
<http://doi.org/10.1016/j.devcel.2019.02.016>
- Phillips, R., Belliveau, N. M., Chure, G., Garcia, H. G., **Razo-Mejia, M.**, Scholes, C. (2019). *Figure 1 Theory Meets Figure 2 Experiments in the Study of Gene Expression*. Annual Review of Biophysics, 48(1), 121?163.
<http://doi.org/10.1146/annurev-biophys-052118-115525>

2018

- **Razo-Mejia, M.**^{*}, Barnes, S. L.^{*}, Belliveau, N. M.^{*}, Chure, G.^{*}, Einav, T.^{*}, Lewis, M., Phillips, R. (2018). *Tuning Transcriptional Regulation through Signaling : A Predictive Theory of Allosteric Induction*. Cell Systems, 1-14. ^{*} These authors contribute equally. **Paper website** and **GitHub repository**
<http://doi.org/10.1016/j.cels.2018.02.004>.

2015

- Zelcbuch, L., **Razo-Mejia, M.**, Herz, E., Yahav S., Antonovsky N., Kroytoro H., Milo R., Bar-Even A. (2015). *An in vivo metabolic approach for deciphering the product specificity of glycerate kinase proves that both E. coli's glycerate kinases generate 2-phosphoglycerate*. Plos One, 10(3), e0122957.
<http://doi.org/10.1371/journal.pone.0122957>

2014

- **Razo-Mejia, M.**, Boedicker, J. Q., Jones, D., DeLuna, a, Kinney, J. B., & Phillips, R. (2014). *Comparison of the theoretical and real-world evolutionary potential of a genetic circuit*. Physical Biology, 11(2), 026005.
<http://doi:10.1088/1478-3975/11/2/026005>

Talks & Posters

TALKS

“From Molecular Basis to Predictability and Control of Evolution”, NORDITA

Stockholm, Sweden

INVITED SPEAKER

2019

- Title: Does evolution care about bits? Information as currency in nature's stock market

“Stochastic Physics in Biology”, Gordon Research Conference

Santa Barbara, CA

INVITED SPEAKER

2019

- Title: Does evolution care about bits? Information as currency in nature's stock market

POSTERS

ASCB

San Diego, CA

PRESENTER

2018

- Title: The physics of information processing of a simple genetic circuit.

Personal References

Rob Phillips

Caltech

THESIS ADVISOR

- Email: phillips@pboc.caltech.edu

Dianne Newman

Caltech

THESIS COMMITTEE

- Email: dkn@caltech.edu

Extracurricular Activity

Clubes de Ciencia Mexico (Science Clubs, Mexico)

Mexico

ORGANIZATION COMMITTEE

2011 - Present

- The emerging non-profit association Clubes de Ciencia Mexico aims to expand the access of young Mexican students to high quality scientific education. For this we design and implement science, technology, engineering and math workshops for high school students and freshman undergrads. Our science clubs are the mechanism to establish a network of mentors that link the most prominent young scientists in Mexico and abroad with other Mexican students interested in science. This international network of mentors tries to catalyze three main objectives:
 - (1) Increase the interest for science among the students.
 - (2) Guide young students towards scientific careers.
 - (3) Develop science-related technical and cognitive abilities.