Manuel **Razo-Mejia**

PhD Candidate · Biochemistry & Molecular Biophysics

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Education

California Institute of Technology (Caltech)   *Pasadena, California*

PhD Biochemistry & Molecular Biophysics   *2014 - present*

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

Instituto Politecnico Nacional   *Silao, Guanajuato, Mexico*

BSc Biotechnological Engineering   *2009 - 2014*

Awards & Scholarships

PhD

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

2014	**Valedictorian**, Class of 2014	*IPN, Mexico*
2013	**Research Fellowship**, Summer Kupcinet-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, M. Lewis, and R. Phillips   *2018*

- Despite lacking a nervous system, single bacterial cells are capable of making decisions given signals from their surroundings. How can individual molecules sense and transmit these signals? The answer comes from one of the crowning scientific achievements of the past century: allostery. Simply stated, allostery is the property of certain macromolecules to exist in multiple conformations with different properties. For example, transcription factors —proteins that control gene expression— can be active (able to bind the DNA) or inactive (unable to bind DNA) depending on the concentration of a signaling molecule.
  In a 2018 paper, I wrote down a theoretical model that predicts the expression level of a gene regulated by an allosteric transcription factor. I then tested the model experimentally, showing that the model was able to predict how changes to the regulation of the gene translate to changes in the cellular response.
  As we strive to turn synthetic biology into a predictive engineering discipline, this work brings us closer to be able to design input-output functions for biological circuits. The better models become, the easier it will be to design biological systems to address modern society problems.

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*

- Living organisms are constantly sensing intra and extracellular cues and responding accordingly. The quality and precision of such responses can mean the difference between surviving or not certain challenges; therefore, there is a constant selection pressure for cells to gather enough information from any stimulus in order to build an adequate response. In this context, the information that cells can obtain has a precise mathematical definition measured —just as in computers— in bits.
  In a recent publication our goal was to predict how many bits of information can a cell harboring a simple genetic circuit process. To do so, I wrote down a theoretical model to predict the full distribution of gene expression based on the physics of this molecular process. I calibrated our model with previous information in order to perform parameter-free predictions. To test the model, I compared the predictions with experimental single-cell gene expression data finding great agreement.
  This work puts us a step closer towards understanding the intriguing idea for a general principle in biology: information, in its mathematical definition, is a quantity that cells try to maximize over evolutionary time.

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*. ArXiv. `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 {at} pboc {dot} caltech {dot} edu

Dianne Newman *Caltech*

THESIS COMMITTEE

- Email: dkn {at} caltech {dot} edu

Faculty Member
- Email: bois {at} caltech {dot} 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.