



## Benjamin Good

Assistant Professor of Applied Physics and, by courtesy, of Biology

### Bio

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#### BIO

Benjamin Good is a theoretical biophysicist with a background in experimental evolution and population genetics. He is interested in the short-term evolutionary dynamics that emerge in rapidly evolving microbial populations like the gut microbiome. Technological advances are revolutionizing our ability to peer into these evolving ecosystems, providing us with an increasingly detailed catalog of their component species, genes, and pathways. Yet a vast gap still remains in understanding the population-level processes that control their emergent structure and function. Our group uses tools from statistical physics, population genetics, and computational biology to understand how microscopic growth processes and genome dynamics at the single cell level give rise to the collective behaviors that can be observed at the population level. Projects range from basic theoretical investigations of non-equilibrium processes in microbial evolution and ecology, to the development of new computational tools for measuring these processes in situ in both natural and experimental microbial communities. Through these specific examples, we seek to uncover unifying theoretical principles that could help us understand, forecast, and eventually control the ecological and evolutionary dynamics that take place in these diverse scenarios.

#### ACADEMIC APPOINTMENTS

- Assistant Professor, Applied Physics
- Assistant Professor (By courtesy), Biology
- Member, Bio-X

#### HONORS AND AWARDS

- Stanford Prize in Population Genetics and Society, Stanford University (2025-2026)
- Philippe Meyer Prize in Theoretical Physics, École normale supérieure (2024)
- Alden H. and Winifred Hubbard Brown Faculty Fellow, Stanford University (2024-2025)
- Chan Zuckerberg Biohub Investigator Award, Chan Zuckerberg Biohub (2022-2027)
- Alfred P. Sloan Research Fellowship, Alfred P. Sloan Foundation (2021-2023)
- Terman Fellowship, Stanford University (2019)
- Miller Research Fellowship, Miller Institute for Basic Research in Science (2016-2019)

#### PROFESSIONAL EDUCATION

- Ph. D., Harvard University , Physics (2016)
- B.A., Swarthmore College , Physics/Mathematics (2010)

#### LINKS

- Research group website: <https://bgoodlab.github.io>

## Teaching

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### COURSES

#### 2025-26

- Introduction to Biophysics: APPPHYS 205, BIO 126, BIO 226 (Win)
- Quantitative Evolutionary Dynamics and Genomics: APPPHYS 237, BIO 251 (Spr)

#### 2024-25

- Introduction to Biophysics: APPPHYS 205, BIO 126, BIO 226 (Win)
- Simulating Collective Dynamics in Living Systems: From Enzymes to Bird Flocks: BIOS 430 (Spr)

#### 2023-24

- Introduction to Biophysics: APPPHYS 205, BIO 126, BIO 226 (Win)
- Quantitative Evolutionary Dynamics and Genomics: APPPHYS 237, BIO 251 (Spr)

#### 2022-23

- Introduction to Biophysics: APPPHYS 205, BIO 126, BIO 226 (Win)
- Quantitative Evolutionary Dynamics and Genomics: APPPHYS 237, BIO 251 (Spr)

### STANFORD ADVISEES

#### Doctoral Dissertation Reader (AC)

Javan Tahir, Julie Zhu

#### Postdoctoral Faculty Sponsor

Andrew Pyo

#### Doctoral Dissertation Advisor (AC)

James Ferrare, Olivia Ghosh, Anastasia Lyulina, John McEnany, Jello Zhou

#### Doctoral Dissertation Co-Advisor (AC)

Andrea Gaspert, Sophie Walton

#### Doctoral (Program)

Antti Asikainen, Misha Bilokur, Manh-Quan Nguyen, Erkan Nurdun

#### Postdoctoral Research Mentor

Jamie Lopez

### GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biophysics (Phd Program)

## Publications

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### PUBLICATIONS

- **Predicting the first steps of evolution in randomly assembled communities.** *Nature communications*  
McEnany, J., Good, B. H.  
2024; 15 (1): 8495
- **Abundance measurements reveal the balance between lysis and lysogeny in the human gut microbiome.** *bioRxiv : the preprint server for biology*

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- Lopez, J., McKeithen-Mead, S., Shi, H., Nguyen, T. H., Huang, K. C., Good, B. H.  
2024
- **Evolution of evolvability in rapidly adapting populations.** *Nature ecology & evolution*  
Ferrare, J. T., Good, B. H.  
2024
  - **Linkage equilibrium between rare mutations.** *Genetics*  
Lyulina, A. S., Liu, Z., Good, B. H.  
2024
  - **Linkage equilibrium between rare mutations.** *bioRxiv : the preprint server for biology*  
Lyulina, A. S., Liu, Z., Good, B. H.  
2024
  - **Quantifying the adaptive landscape of commensal gut bacteria using high-resolution lineage tracking.** *Nature communications*  
Wong, D. P., Good, B. H.  
2024; 15 (1): 1605
  - **Dynamics of bacterial recombination in the human gut microbiome.** *PLoS biology*  
Liu, Z., Good, B. H.  
2024; 22 (2): e3002472
  - **Predicting the First Steps of Evolution in Randomly Assembled Communities.** *bioRxiv : the preprint server for biology*  
McEnany, J., Good, B. H.  
2023
  - **Competition for shared resources increases dependence on initial population size during coalescence of gut microbial communities.** *bioRxiv : the preprint server for biology*  
Goldman, D. A., Xue, K. S., Parrott, A. B., Jeeda, R. R., Franzese, L. R., Lopez, J. G., Vila, J. C., Petrov, D. A., Good, B. H., Relman, D. A., Huang, K. C.  
2023
  - **Eco-evolutionary feedbacks in the human gut microbiome.** *Nature communications*  
Good, B. H., Rosenfeld, L. B.  
2023; 14 (1): 7146
  - **Prolonged delays in human microbiota transmission after a controlled antibiotic perturbation.** *bioRxiv : the preprint server for biology*  
Xue, K. S., Walton, S. J., Goldman, D. A., Morrison, M. L., Verster, A. J., Parrott, A. B., Yu, F. B., Neff, N. F., Rosenberg, N. A., Ross, B. D., Petrov, D. A., Huang, K. C., Good, et al  
2023
  - **A mutant fitness compendium in Bifidobacteria reveals molecular determinants of colonization and host-microbe interactions.** *bioRxiv : the preprint server for biology*  
Shiver, A. L., Sun, J., Culver, R., Violette, A., Wynter, C., Nieckarz, M., Mattiello, S. P., Sekhon, P. K., Friess, L., Carlson, H. K., Wong, D., Higginbottom, S., Weglarz, et al  
2023
  - **Quantifying the local adaptive landscape of a nascent bacterial community.** *Nature communications*  
Ascensao, J. A., Wetmore, K. M., Good, B. H., Arkin, A. P., Hallatschek, O.  
2023; 14 (1): 248
  - **Within-host evolution of the gut microbiome.** *Current opinion in microbiology*  
Dapa, T., Wong, D. P., Vasquez, K. S., Xavier, K. B., Huang, K. C., Good, B. H.  
2023; 71: 102258
  - **Emergent evolutionary forces in spatial models of luminal growth and their application to the human gut microbiota.** *Proceedings of the National Academy of Sciences of the United States of America*  
Ghosh, O. M., Good, B. H.  
2022; 119 (28): e2114931119

- **Competition for fluctuating resources reproduces statistics of species abundance over time across wide-ranging microbiotas.** *eLife*  
Ho, P., Good, B. H., Huang, K. C.  
2022; 11
- **Population genetics of polymorphism and divergence in rapidly evolving populations.** *Genetics*  
Melissa, M. J., Good, B. H., Fisher, D. S., Desai, M. M.  
2022
- **Linkage disequilibrium between rare mutations.** *Genetics*  
Good, B. H.  
2022
- **Eco-evolutionary feedbacks in the human gut microbiome**  
Good, B. H., Rosenfeld, L. B.  
biorxiv.  
2022
- **Quantifying the Adaptive Potential of a Nascent Bacterial Community**  
Ascensao, J. A., Wetmore, K. M., Good, B. H., Arkin, A. P., Hallatschek, O.  
biorxiv.  
2022
- **Quantifying rapid bacterial evolution and transmission within the mouse intestine.** *Cell host & microbe*  
Vasquez, K. S., Willis, L., Cira, N. J., Ng, K. M., Pedro, M. F., Aranda-Diaz, A., Rajendram, M., Yu, F. B., Higginbottom, S. K., Neff, N., Sherlock, G., Xavier, K. B., Quake, et al  
2021
- **Longitudinal linked-read sequencing reveals ecological and evolutionary responses of a human gut microbiome during antibiotic treatment.** *Genome research*  
Roodgar, M., Good, B. H., Garud, N. R., Martis, S., Avula, M., Zhou, W., Lancaster, S. M., Lee, H., Babveyh, A., Nesamoney, S., Pollard, K. S., Snyder, M. P.  
2021
- **Competition for fluctuating resources reproduces statistics of species abundance over time across wide-ranging microbiotas**  
Ho, P., Good, B. H., Huang, K. C.  
biorxiv.  
2021
- **Emergent evolutionary forces in spatial models of microbial growth in the human gut microbiota**  
Ghosh, O. M., Good, B. H.  
biorxiv.  
2021
- **Population genetics of polymorphism and divergence in rapidly evolving populations**  
Melissa, M. J., Good, B. H., Fisher, D. S., Desai, M. M.  
biorxiv.  
2021
- **Evolutionary dynamics of bacteria in the gut microbiome within and across hosts.** *PLoS biology*  
Garud, N. R., Good, B. H., Hallatschek, O., Pollard, K. S.  
2019; 17 (1): e3000102
- **Adaptation limits ecological diversification and promotes ecological tinkering during the competition for substitutable resources** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Good, B. H., Martis, S., Hallatschek, O.  
2018; 115 (44): E10407–E10416
- **Effective models and the search for quantitative principles in microbial evolution** *CURRENT OPINION IN MICROBIOLOGY*  
Good, B. H., Hallatschek, O.

2018; 45: 203–12

- **The Effect of Strong Purifying Selection on Genetic Diversity** *GENETICS*  
Cvijovic, I., Good, B. H., Desai, M. M.  
2018; 209 (4): 1235–78
- **The dynamics of molecular evolution over 60,000 generations** *NATURE*  
Good, B. H., McDonald, M. J., Barrick, J. E., Lenski, R. E., Desai, M. M.  
2017; 551 (7678): 45-+
- **Evolution of Mutation Rates in Rapidly Adapting Asexual Populations** *GENETICS*  
Good, B. H., Desai, M. M.  
2016; 204 (3): 1249–66
- **Fate of a mutation in a fluctuating environment** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Cvijovic, I., Good, B. H., Jerison, E. R., Desai, M. M.  
2015; 112 (36): E5021–E5028
- **The Evolutionarily Stable Distribution of Fitness Effects** *GENETICS*  
Rice, D. P., Good, B. H., Desai, M. M.  
2015; 200 (1): 321–U599
- **The Impact of Macroscopic Epistasis on Long-Term Evolutionary Dynamics** *GENETICS*  
Good, B. H., Desai, M. M.  
2015; 199 (1): 177–U639
- **Deleterious Passengers in Adapting Populations** *GENETICS*  
Good, B. H., Desai, M. M.  
2014; 198 (3): 1183–1208
- **The Fates of Mutant Lineages and the Distribution of Fitness Effects of Beneficial Mutations in Laboratory Budding Yeast Populations** *GENETICS*  
Frenkel, E. M., Good, B. H., Desai, M. M.  
2014; 196 (4): 1217-+
- **Genetic Diversity in the Interference Selection Limit** *PLOS GENETICS*  
Good, B. H., Walczak, A. M., Neher, R. A., Desai, M. M.  
2014; 10 (3): e1004222
- **Fluctuations in fitness distributions and the effects of weak linked selection on sequence evolution** *THEORETICAL POPULATION BIOLOGY*  
Good, B. H., Desai, M. M.  
2013; 85: 86–102
- **Distribution of fixed beneficial mutations and the rate of adaptation in asexual populations** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Good, B. H., Rouzine, I. M., Balick, D. J., Hallatschek, O., Desai, M. M.  
2012; 109 (13): 4950–55
- **Performance of modularity maximization in practical contexts** *PHYSICAL REVIEW E*  
Good, B. H., de Montjoye, Y., Clauset, A.  
2010; 81 (4): 046106