

From Cancer to Pathogens: Interactions Between Microbial Population Biology and Medicine

Jake Scott - introducing:

Dmitri Petrov, Pleuni Pennings, Kevin Wood, Oana Carja



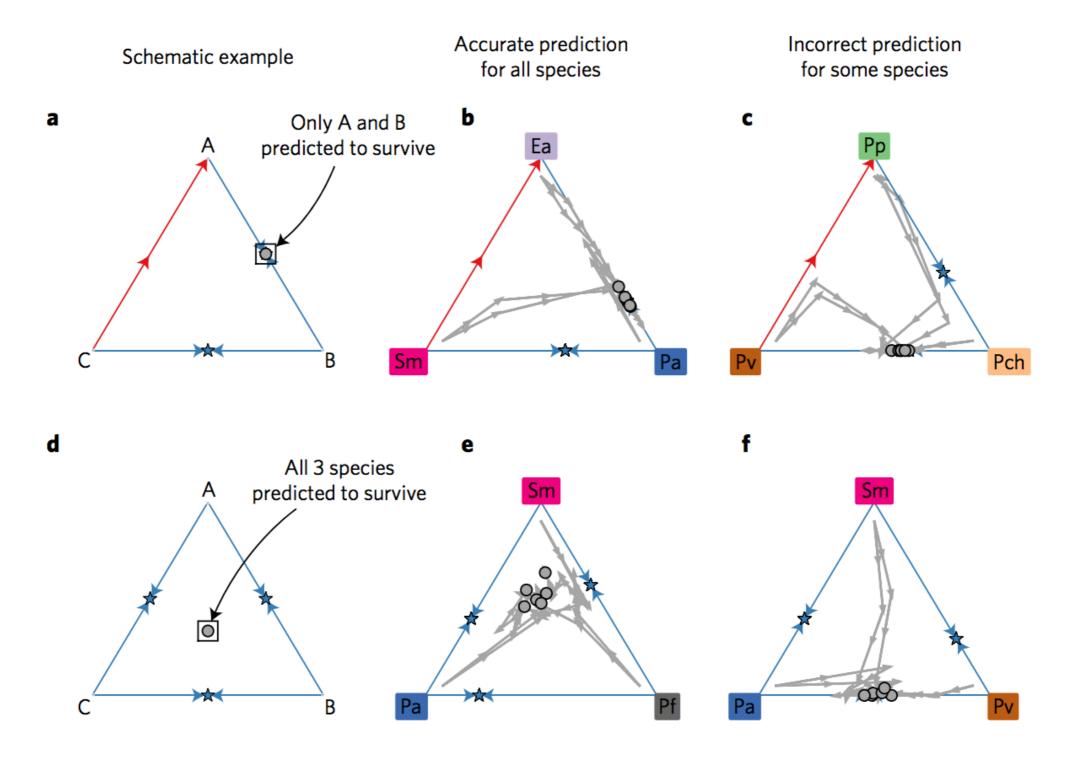
Microbial Population Biology Gordon Research Conference 10 July 2019

https://www.lerner.ccf.org/thor/scott/lab/

scottj10@ccf.org



The results of simple co-culture yielded intuition about competition in more complex mixtures in diverse bacteria



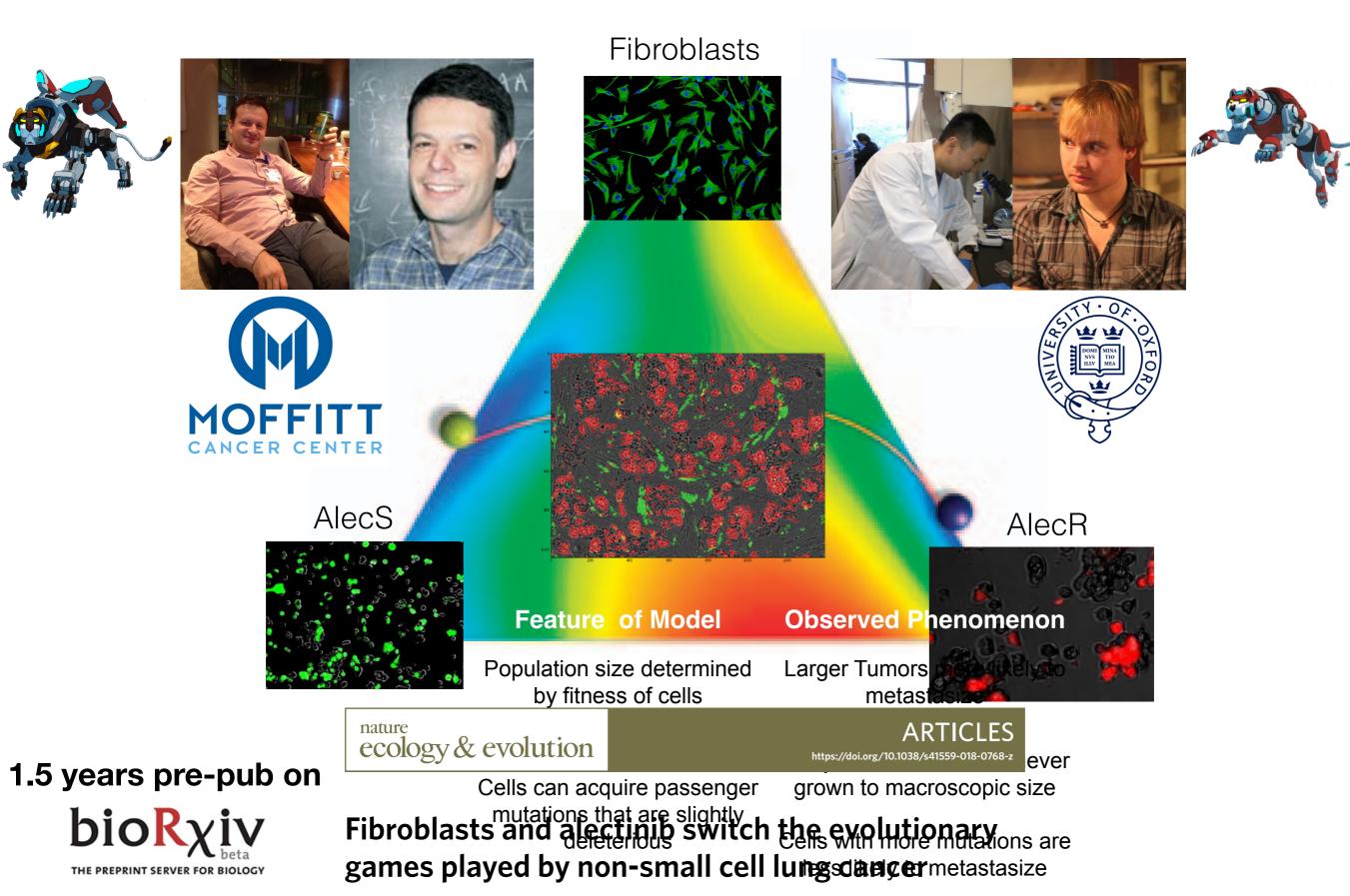
Community structure follows simple assembly rules in microbial microcosms

Jonathan Friedman^{1*}, Logan M. Higgins^{1,2} and Jeff Gore^{1*}

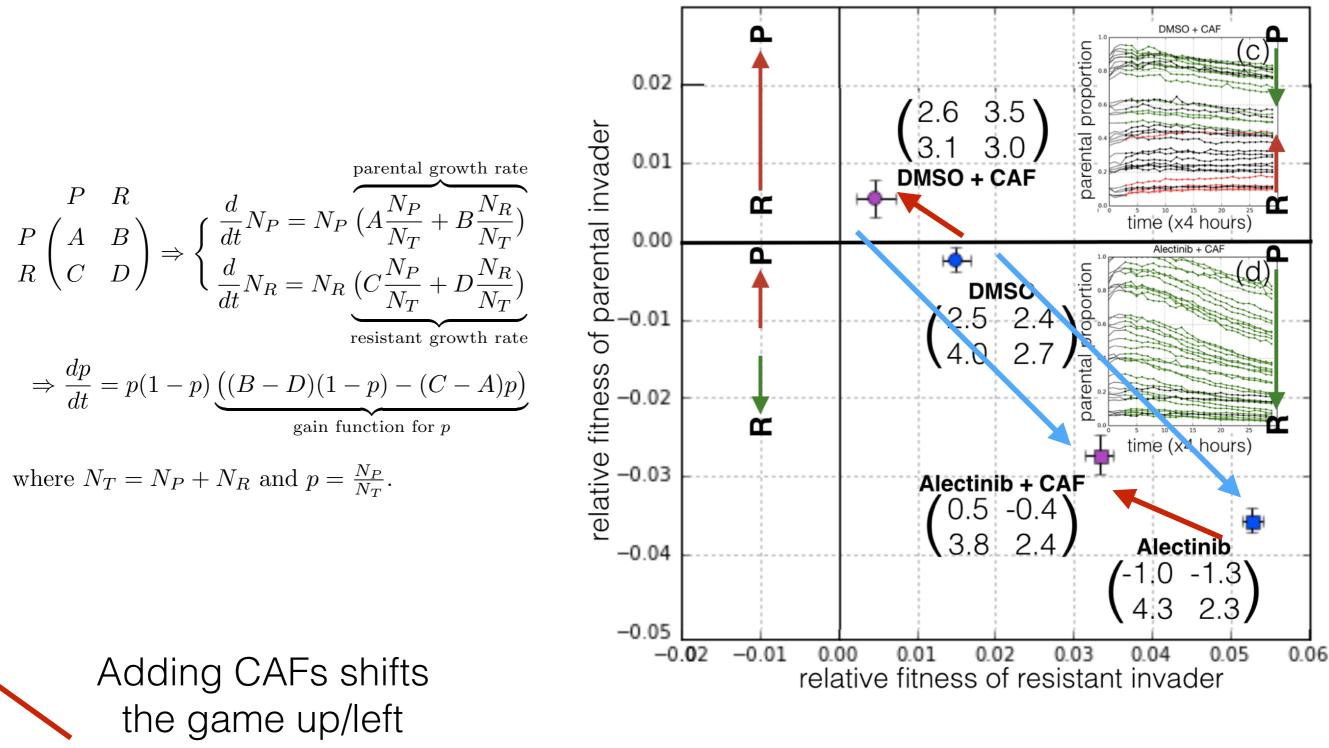
ecology & evolution

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What about a GAME ASSAY to directly measure the effective game cancer cells are playing?



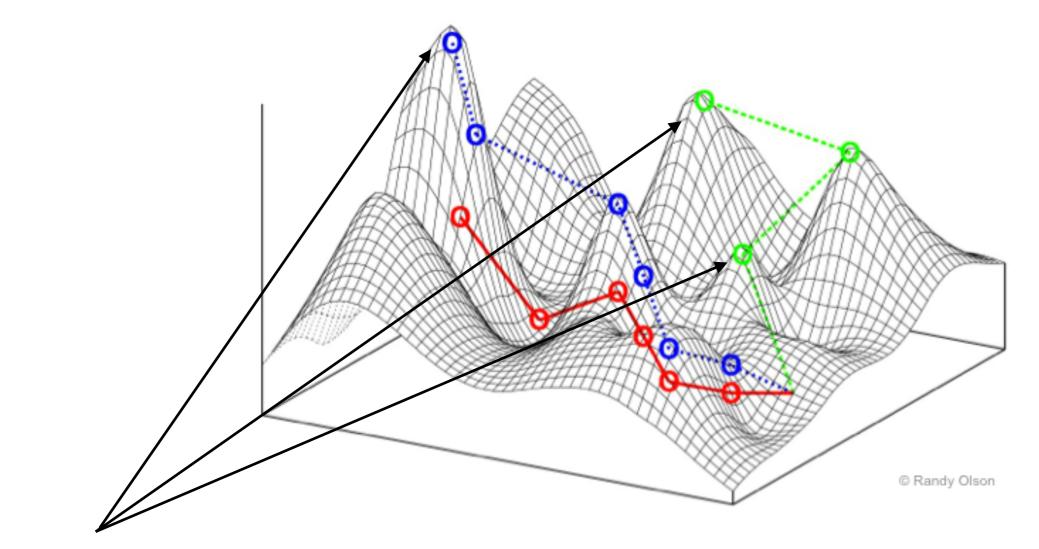
Plotting the fitness functions in a game space reveals a qualitative shift in the game



Adding alectinib shifts the game down/right

Can we think of drugs in this new way to steer evolution rationally?

Key questions:

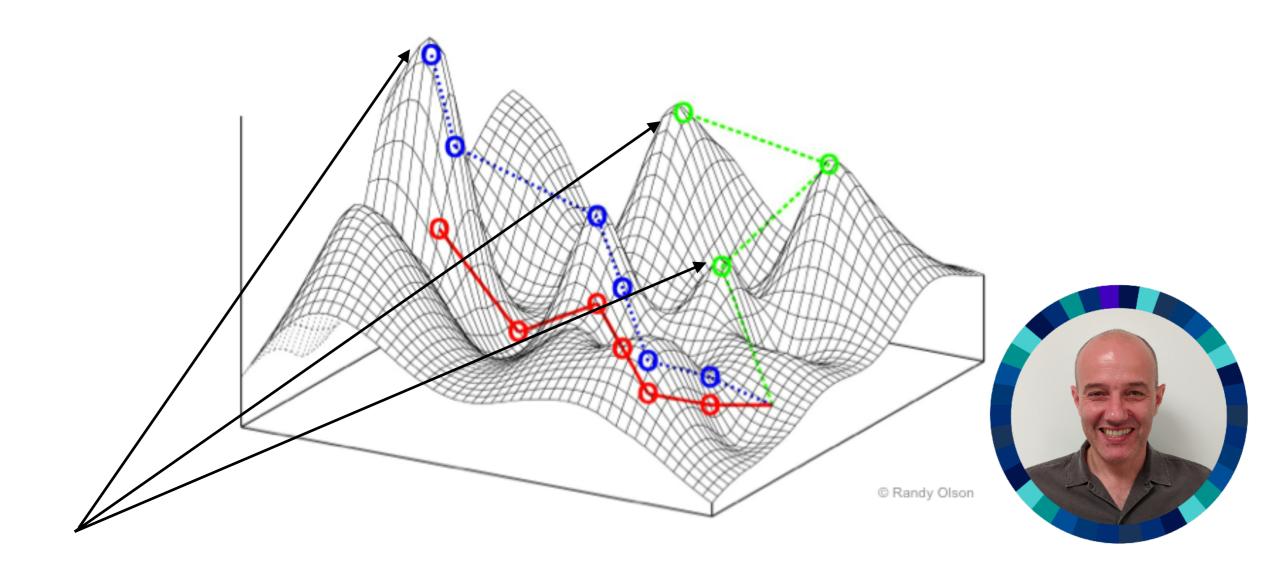


 Where will evolution drive a disease? (and what are the evolutionary consequences - e.g. CS)

2. How fast will it go?

3. Can we *control* these things?

GP maps in yeast and cancer



1. Where will evolution drive a disease?

Dmitri Petrov, PhD Stanford

Development of a Comprehensive Genotype-to-Fitness Map of Adaptation-Driving Mutations in Yeast

Venkataram et al., 2016, Cell *167*, 1–12 September 22, 2016 © 2016 Elsevier Inc. http://dx.doi.org/10.1016/j.cell.2016.08.002

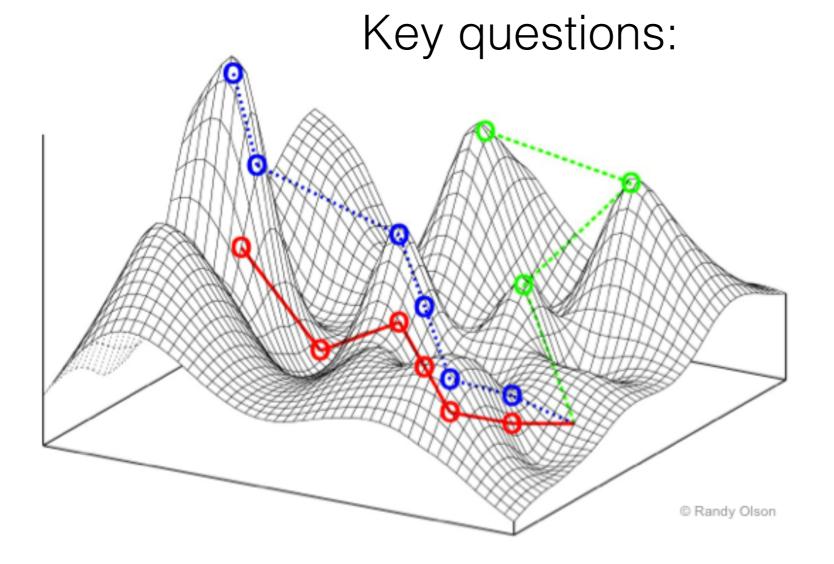
Mapping the in vivo fitness landscape of lung adenocarcinoma tumor suppression in mice

Zoë N. Rogers^{1,8}, Christopher D. McFarland^{2,8}, Ian P. Winters^{®1}, Jose A. Seoane^{1,3,4}, Jennifer J. Brady¹, Stephanie Yoon⁵, Christina Curtis^{®1,3,4,6}, Dmitri A. Petrov^{® 2*} and Monte M. Winslow^{®1,4,6,7*}



Single Nucleotide Mapping of the Locally Accessible Trait Space in Yeast Reveals Pareto Fronts that Constrain Initial Adaptation Yuping Li, Dmitri A. Petrov*, Gavin Sherlock*







2. How fast will it go? and in what order?

https://abetterscientist.wordpress.com/2019/02/01/sequentialevolution-of-hiv-drug-resistance-against-two-drug-treatments/

Challenging conventional wisdom on the evolution of resistance to multi-drug HIV treatment: Lessons from data and modeling.

Alison Feder, Kristin Harper, Pleuni Pennings

Pleuni Pennings, PhD SFSU

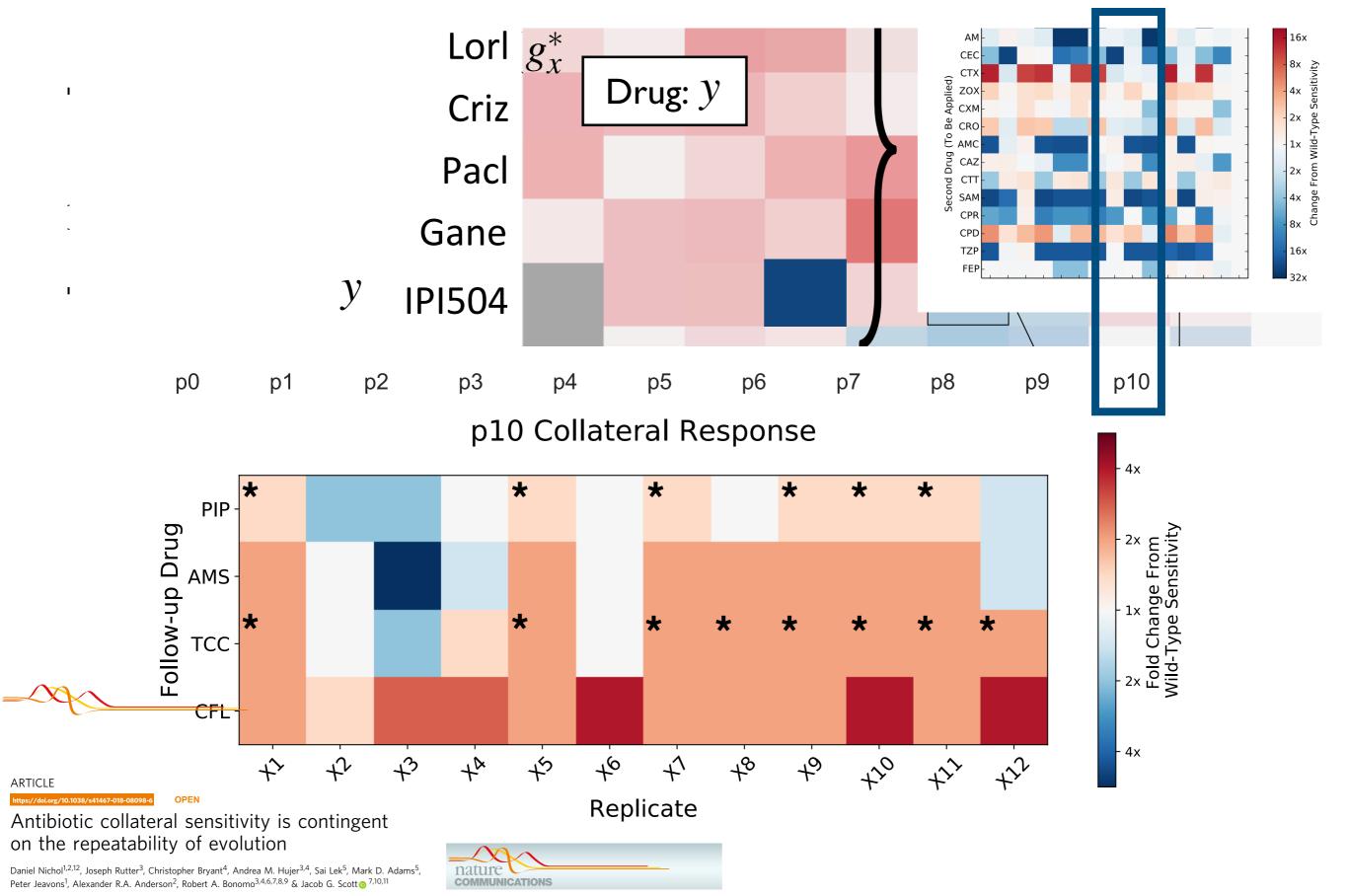
Imperfect drug penetration leads to spatial monotherapy and rapid evolution of multidrug resistance

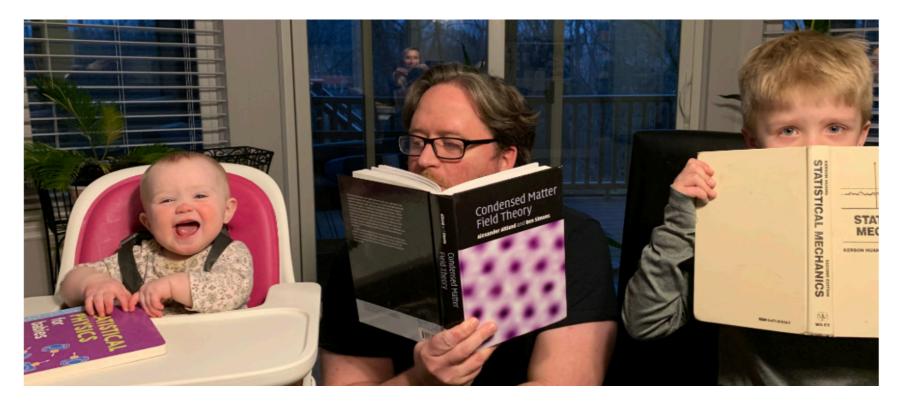
Stefany Moreno-Gamez^{a,b,1}, Alison L. Hill^{a,1}, Daniel I. S. Rosenbloom^{a,c}, Dmitri A. Petrov^d, Martin A. Nowak^a, and Pleuni S. Pennings^{d,e,f,2}



www.pnas.org/cgi/doi/10.1073/pnas.1424184112

in vitro: evolution under cefotaxime is not repeatable, and collateral sensitivity varies with genetic divergence





Kevin Wood, PhD UMichigan

PHYSICAL REVIEW LETTERS 120, 238102 (2018)

Antibiotics can be used to contain drug-resistant bacteria by maintaining sufficiently large sensitive populations

Elsa Hansen, Jason Karslake, Robert J. Woods, Andrew F. Read, 💿 Kevin B. Wood doi: https://doi.org/10.1101/638924

> Cold Spring Harbor

Tuning Spatial Profiles of Selection Pressure to Modulate the Evolution of Drug Resistance

Maxwell G. De Jong¹ and Kevin B. Wood^{1,2,*}

Pervasive and diverse collateral sensitivity profiles inform optimal

strategies to limit antibiotic resistance

Jeff Maltas, 🝺 Kevin B. Wood

doi: https://doi.org/10.1101/24107

bioRχiv Laboratory THE PREPRINT SERVER FOR BIOLOGY

How can heterogeneity be maintained?

Are there other ways to move through genotype space?



Theoretical Population Biology Volume 86, June 2013, Pages 29-42 Oana Carja, PhD Carnegie Mellon

Evolution with stochastic fitnesses: A role for recombination

Oana Carja ^a [∧] [∞], Uri Liberman ^b, Marcus W. Feldman ^a

Evolutionary Rescue Through Partly Heritable Phenotypic Variability

GENETICS | INVESTIGATION Oana Carja*1 and Joshua B. Plotkin1

Genetics, Vol. 211, 977–988 March 2019