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Three million images and morphological profiles of cells treated with matched chemical and genetic perturbations

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doi: <https://doi.org/10.1101/2022.01.05.475090>

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[James Burgess](#) , [Jeffrey J. Nirschl](#), [Maria-Clara Zanellati](#), [Alejandro Lozano](#), [Sarah Cohen](#) & [Serena Yeung-Levy](#) 

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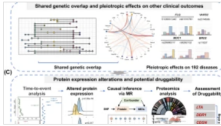
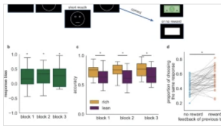
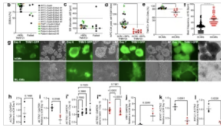
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Three million images and morphological profiles of cells treated with matched chemical and genetic perturbations

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Abstract

Identifying genetic and chemical perturbations with similar impacts on cell morphology can reveal compounds' mechanisms of action or novel regulators of genetic pathways. Research on methods for identifying such similarities has lagged due to a lack of carefully designed and well-annotated image sets of cells treated with chemical and genetic perturbations. Here, we create such a Resource dataset, CPJUMP1, where each perturbed gene is a known target of at least two chemical compounds in the dataset. We systematically explore the directionality of correlations among perturbations that target the same gene, and we find that identifying matches between chemical perturbations and genetic perturbations is a challenging task. Our dataset and baseline analyses provide a benchmark for evaluating methods that measure perturbation similarities and impact, and more generally, learn effective representations of cellular state from microscopy images. Such advancements would accelerate the applications of image-based profiling, such as functional genomics and drug discovery.

Competing Interest Statement

S.S. and A.E.C. serve as scientific advisors for companies that use image-based profiling and Cell Painting (A.E.C.: Recursion, SyzOnc, Quiver Bioscience, S.S.: Waypoint Bio, Dewpoint Therapeutics, Deepcell) and receive honoraria for occasional talks at pharmaceutical and biotechnology companies. Daniel Kuhn and Sakshi Garg are employees of Merck Healthcare KGaA, Darmstadt, Germany.

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