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**A generalized errors-in-variables model, with application to
single-cell CRISPR screens**

1 Introduction

CRISPR is a genome engineering tool that has enabled scientists to precisely edit human and nonhuman genomes, opening the door to new therapies for diseases [1, 2] and accelerating basic biology research [3]. Recently, scientists have paired CRISPR genome engineering with single-cell sequencing [4, 5]. The resultant assays, known as a “single-cell CRISPR screens,” link specific genetic perturbations to changes in cellular phenotypes, illuminating regulatory networks underlying human diseases and other traits [6].

Despite their extraordinary promise, single-cell CRISPR screens present substantial statistical and computational challenges.

2 Background and analysis challenges

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3 Thresholding method

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References

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