

36. Analysis of single-cell CRISPR screens
1 unit, Thomas Norman, November 17, 2025

1. CRISPR screens: design principles, readout
 - a. Quantification of fitness CRISPR screens (MAGECK)
2. High-content readouts for inferring gene function
 - a. Genome-scale Perturb-seq
 - b. Optical screens
3. Guide assignment and incomplete penetrance
 - a. Molecular strategies for barcode capture
 - b. Guide assignment (crispat)
 - c. Incomplete penetrance (Mixscape)
4. Achieving greater capacity through multiplexing
 - a. “CRISPR-QTL” approaches to studying enhancers
 - b. Differential expression (SCEPTRE)
5. Predictive models of perturbations
 - a. Predicting across context (Compositional Perturbation Autoencoder)
 - b. Genetic interactions (GEARS)

Paper discussion:

Mapping information-rich genotype-phenotype landscapes with genome-scale Perturb-seq

<https://www.sciencedirect.com/science/article/pii/S0092867422005979?via%3Dihub>

The datasets from this paper will form the basis of the practical project.

Optional background paper:

High-content CRISPR screening

This is a reasonably up-to-date review covering basics. We will discuss some elements of it in the lecture.

<https://www.nature.com/articles/s43586-021-00093-4>