Combined CRISPRa and CRISPRn screening platform reveals directional cellular pathways

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While many genomes from healthy humans and patients have been sequenced, we still lack a systematic understanding of how human genes function in health and disease, and how they interact in pathways. Interactions of human genes can be elucidated using systematic genetic interaction maps, using an approach pioneered by Dr. Martin Kampmann [1] and colleagues at UCSF. In a new publication in *Nature Biotechnology* [2], the Kampmann lab teamed up with the McManus lab at UCSF to establish a strategy to determine directional pathways from genetic interaction maps. This innovative platform combines two uses of CRISPR/Cas9 technology in the same cell: Activation of genes using CRISPRa (previously co-developed by Dr. Kampmann) and inactivation of genes using CRISPR knockout. The development of the quantitative approach that enables the reconstruction of directional pathways from the resulting data was spearheaded by Ruilin Tian [3], a Biophysics graduate student in the Kampmann lab.

Reference:


Links: