

COMPUTATIONAL DISSECTION OF MAMMALIAN REGULATION NETWORKS

MICHAEL ZHANG
mzhang@cshl.edu

Cold Spring Harbor Laboratory , USA

Abstract

Identification of direct targets of an individual or a combination of transcription factors (TFs) is central to determination of regulatory network architecture. Experimental approaches require a combination of expression profiling and binding assay to accurately identify direct targets.

Here we propose an adaptive determination of the gene activation thresholds by using regression splines. Since the thresholds are learnt adaptively from the expression data, the identified targets depend on the physiological condition under which the mRNA sample was obtained. It can work with data from a single condition and no separation of genes into foreground and background sets is necessary. Using human cell-cycle as an example, we show that the E2F targets that we identify at the G1/S phase are significantly different from those at the G2/M phase. We verify known targets and find several novel direct targets of E2F in the G2/M phase.