Qing Zhou

Department of Statistics
University of California, Los Angeles.

Constructing sparse binding landscapes by penalized posterior sampling.

We develop a penalized posterior sampling method to construct binding landscapes of DNA-binding factors from ChIP-seq data, nucleosome occupation models, and often a large set of position-specific weight matrices (PWMs). The method uses penalty counts to achieve a sparse selection of PWMs and a more accurate prediction of binding site locations. Applications to mouse ChIP-seq data demonstrate the effectiveness of this method compared to other scanning-based approaches.