In this experiment we mixed up the true epigenome and a randomized epigenome, horizontal alignment was then applied on the mixed epigenome(s).

1   generating of mixed epigenome

Parameter "window size" w is given before this generating process. Then each chromosome is cut into non-overlapping contiguous w base-pair segments. After the segmentation, the chromatin states on one segment is assigned by the chromatin states on the corresponding area of either the true epigenome or the randomized one. For the i'th segment of this chromosome, the true epigenome is chosen if i is odd and the randomized epigenome is chosen if i is even. Iteratively apply the assignment procedure on all the chromosomes, we get the whole mixed epigenome. Horizontal alignment and following analysis are applied onto this mixed epigenome.

To remove the bias of choice, we also flipped the choice rule to true-randomized epigenome. In the second mixed epigenome, for the i'th segment of one chromosome, the true epigenome is chosen if i is even and the randomized epigenome is chosen if i is odd. Horizontal alignment and the following analysis are also applied onto the second epigenome.

2   horizontal alignment on mixed epigenome

Do horizontal alignment on mixed epigenome(s)

3   alignment result