

Uniquely mapped paired-end reads

1. Extract each fragment's start position and end position in chromosome i
2. Sort each fragment by start position

Use each fragment's start position and end position to compute the fragment pileup value of each point in chromosome i

Construct signal map
ranging from baseline 1 till t

1. Signal map when
 - a) $p \leq p_threshold$
 - b) $fold \geq fold_threshold$
 - c) $baseline = t$ or with *a single global maximum* when $baseline < t$
will be called as candidate binding site
2. Reserve the signal map with the highest *fold* from the same summit position signal maps.

Report as a binding site