

a

Observed cleavages

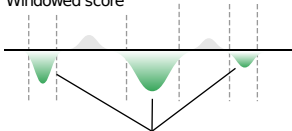
DNase-seq Tag
count

Genomic position
(per nt)

More cleavages
in core than in flank

Fewer cleavages
in core than in flank

Windowed score



Putative footprints

b

TF recognition
sequence occupied?

ACCTAATATCAGAA**ATAGACCA**GCGACTTCTAGA

Observed cleavages

Tag
count

Genomic position
(per nt)

Expected cleavages (not occupied)

Tag
count

$P(\text{motif occupied}) = P(\text{observed}|\text{expected})$