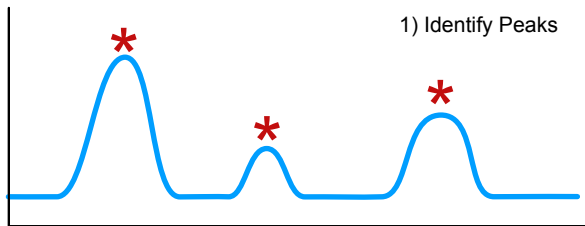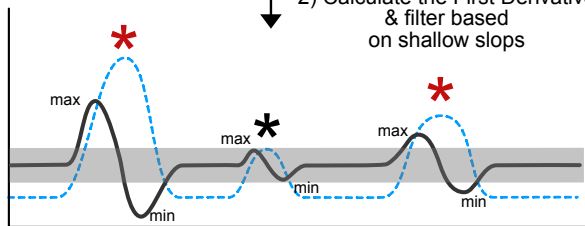NGS Peak Calling Using the First Derivative

* Peaks   * Peaks that do not meet cutoffs
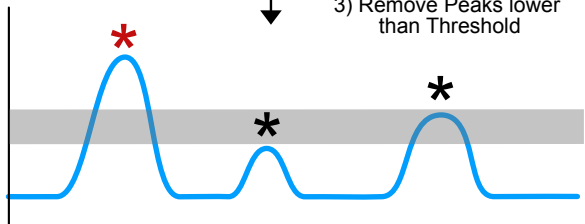
1) Identify Peaks

2) Calculate the First Derivative & filter based on shallow slops

max   max   max   min   min   min

3) Remove Peaks lower than Threshold

ChIP-Seq Analysis with WonderPeaks

Tagged Sample

t

$\frac{t}{u}$ > threshold

u

Untagged Control

C. albicans Genes

Score Peak Size & Associate with Genes
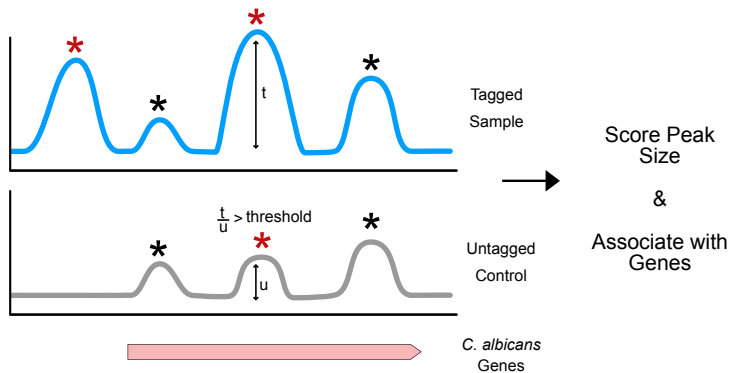
3'UTR Annotation with PeakStream

PeakStream annotation

Forward Reads

C. albicans Genes

Reverse Reads

novel transcript

Create new annotation for Genes & annotate novel transcripts & Count Reads using new annotation