**Criteria 1 script**

Purpose: To pair Watson peaks with the Crick peaks on the opposing strand.

INPUT

1. Genetrack peak calls

>files are always tab delimited

>do not hardcode the extension because sometimes it is .idx or .tab or .txt

User specified parameters

Peak-pair distance range

-u -50 #Upstream distance for Crick (- strand) peak relative to Watson (+ strand) peak

-d 100 #Downstream distance for Crick (- strand) peak relative to Watson (+ strand) peak

Script instructions

1. Sort the Watson and Crick peaks separately from max to min values.
2. Start with the max Watson peak and search in the user defined window for the max Crick peak. 🡪 Pair these peaks and write to output.
3. If a Watson or Crick peak have no pair in the user specified window, write out to OUTPUT\_orphan\_peaks.txt

OUTPUT

1. Peak pair result
2. Peak pair detailed report
3. Frequency distribution plot

Special notes

>When calling peak-pair midpoint, only use integers (NO decimals).

>The peak height (value) can be floating (decimals)

>Allow for batch processing of multiple input files at once, either with a shell script or built into the main script.

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