Recap and biological replicates

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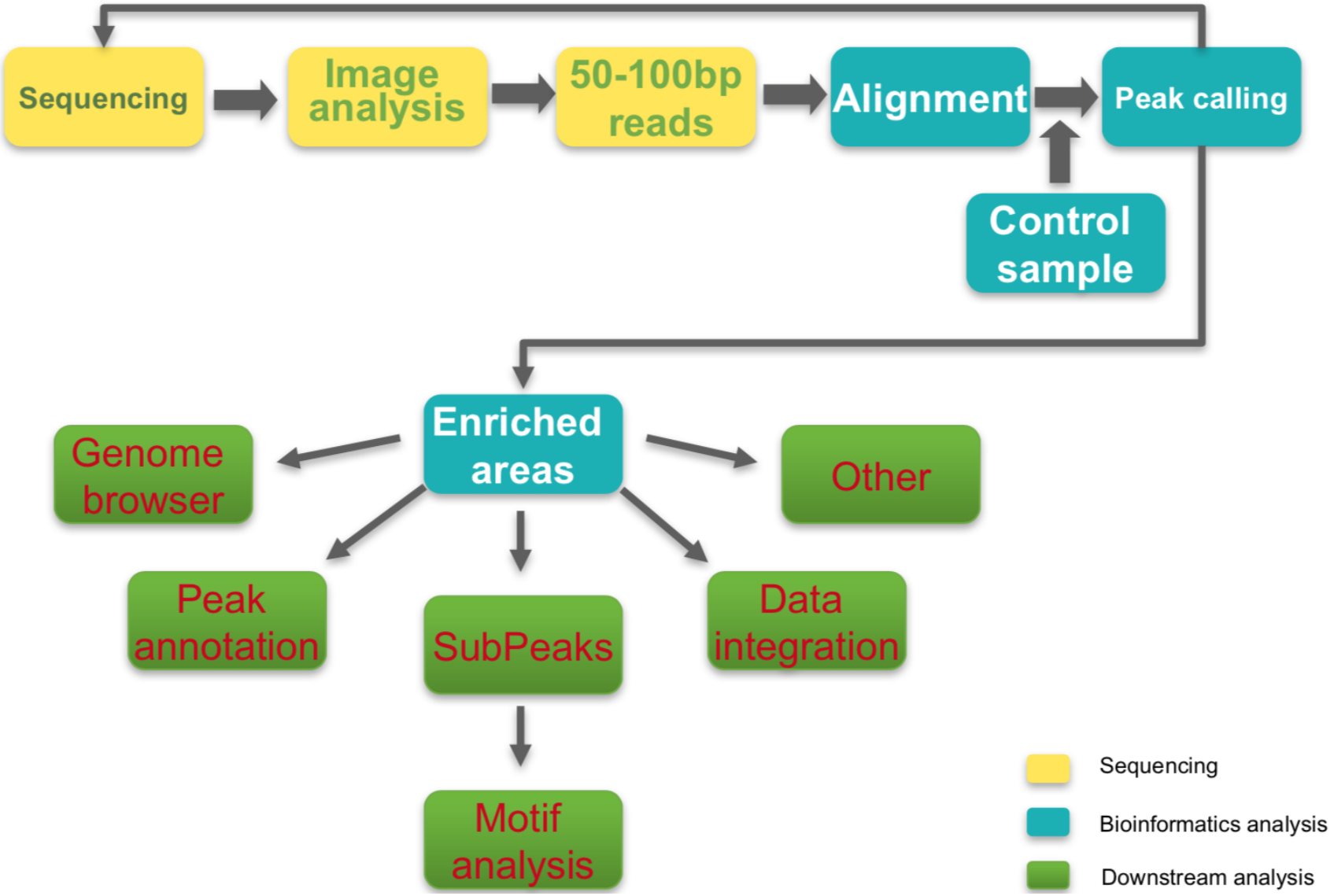
Based on slides by Myrto Kostadima


Sequencing
Image analysis
50-100bp reads
Alignment
Peak calling
Control sample
Enriched areas
Genome browser
Other
Peak annotation
SubPeaks
Data integration
Motif analysis
Sequencing
Bioinformatics analysis
Downstream analysis

• Quality check	*fastqc*
• Alignment	*bwa, bowtie*
• Filtering	*samtools*
• Peak calling	*macs2*
• Peak annotation	*ChIPseeker*
• Sequence motif discovery	*MEME tools*
• Signal (non-peak) analysis	*deepTools*
• Visualisation	*IGV*

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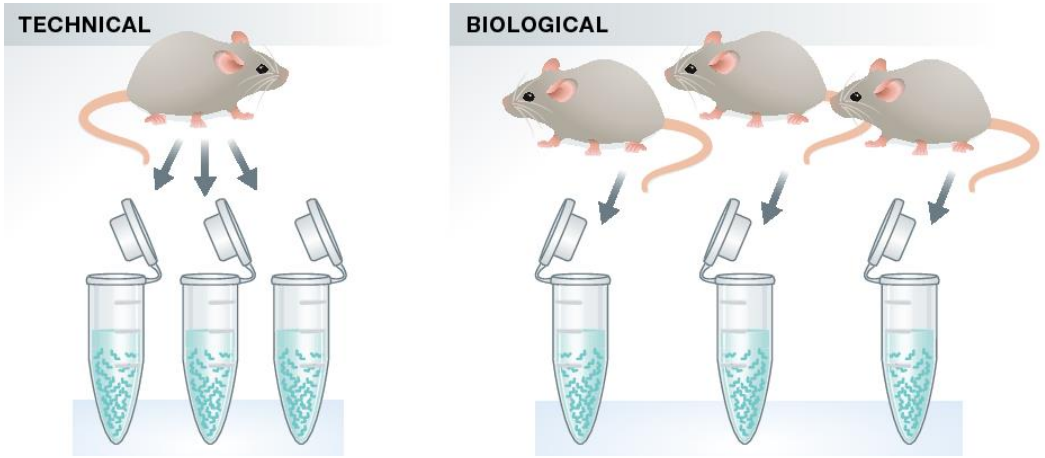

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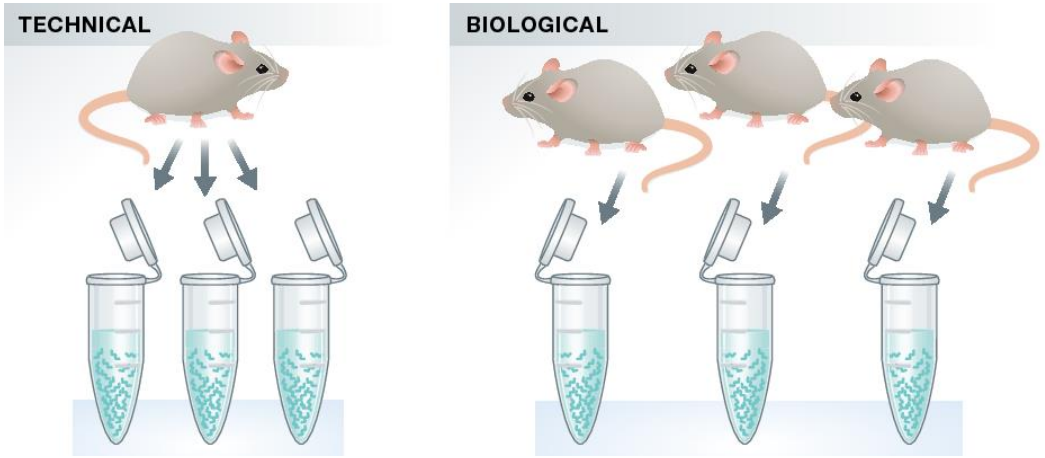

Increase the significance of peaks by using more replicates

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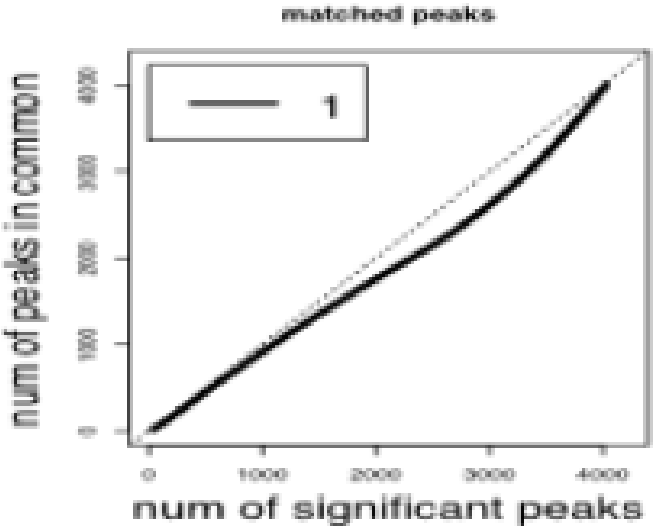
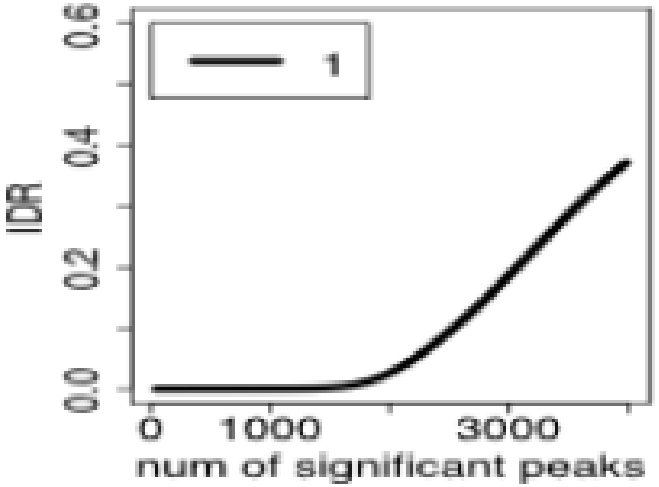
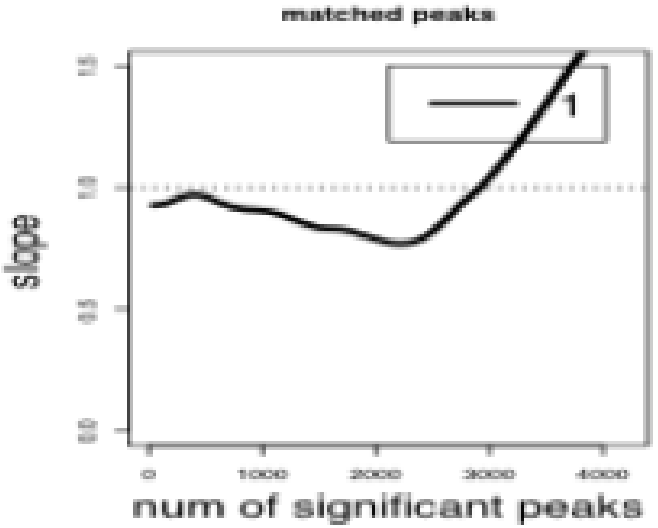
Developed in Qunhua Li and Peter Bickel as part of the ENCODE project

IDR

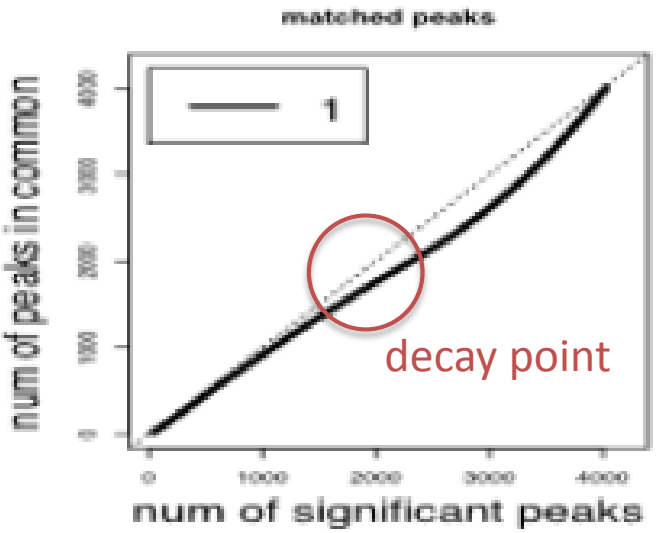


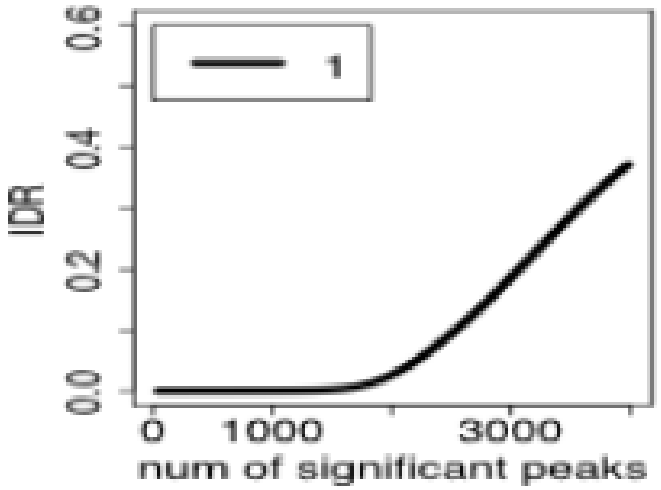


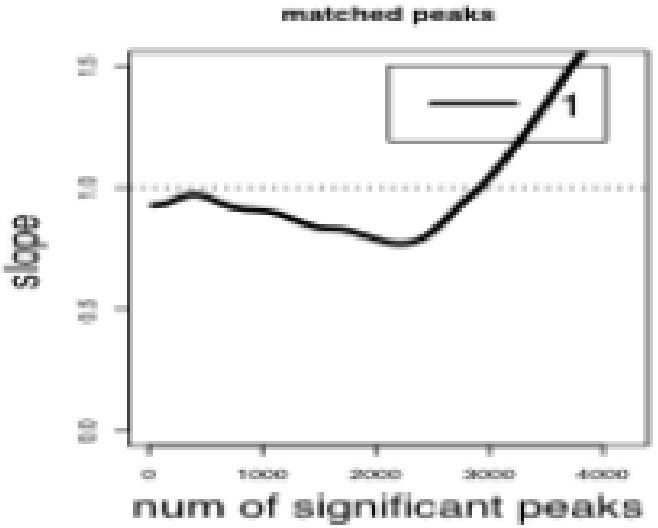


reasonable consistency

IDR







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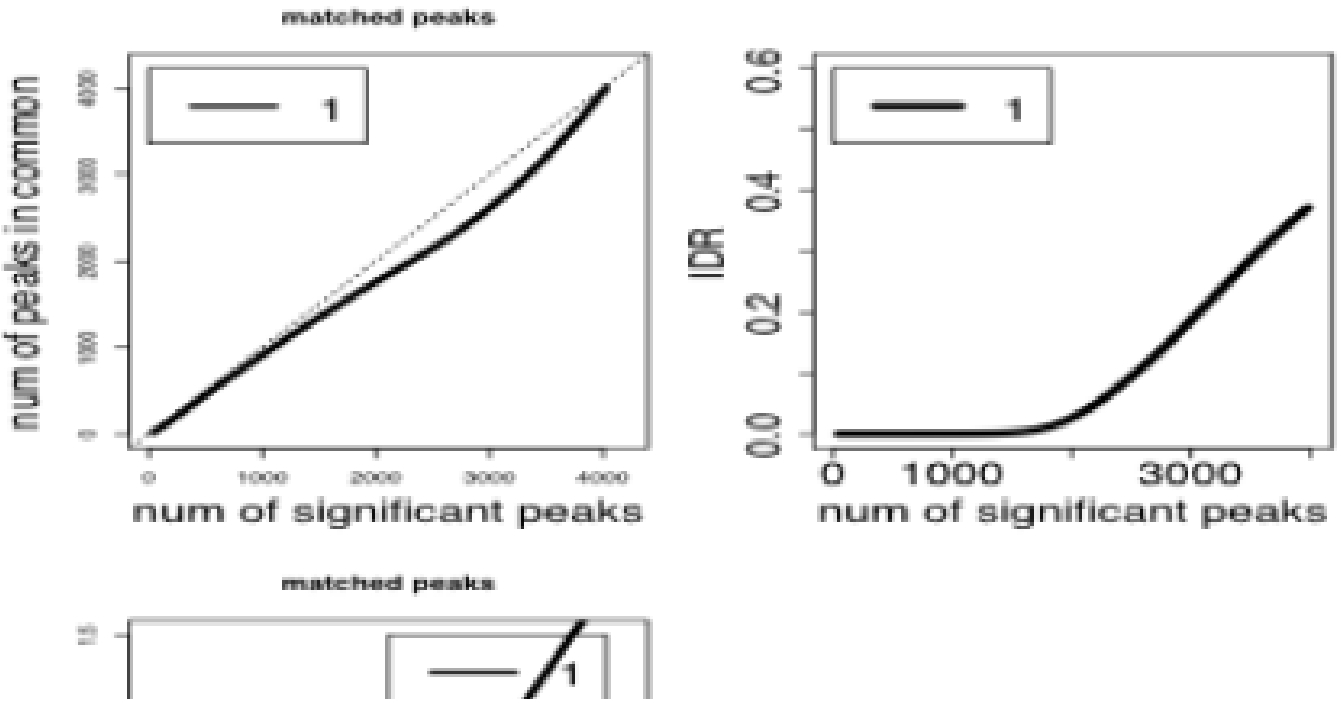
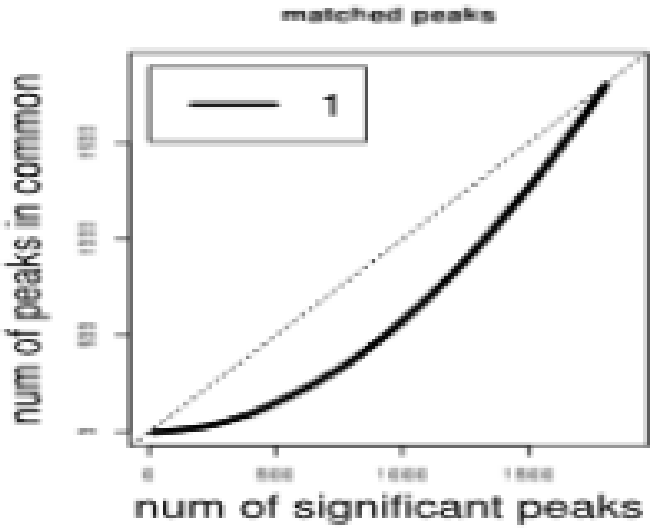
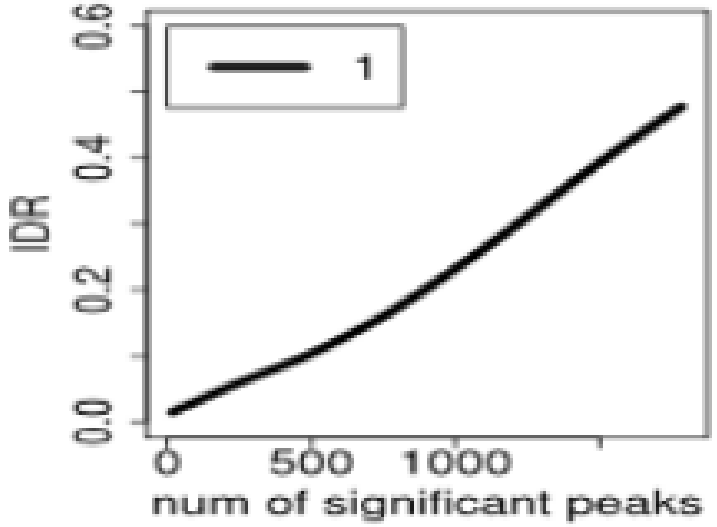
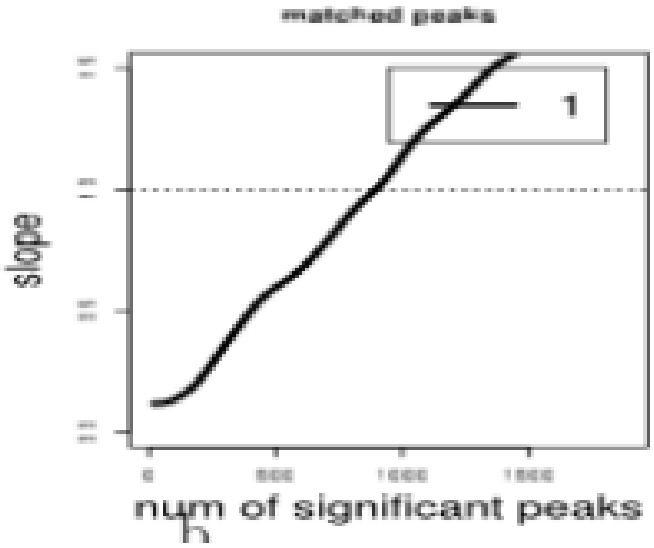


The IDR score represents the *probability of a peak to belong to the irreproducible group*

IDR







poor consistency

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Li and Bickel have used this principle to define numerical cutoffs on peaks called after merging the replicates (**IDR thresholds**) where an IDR of 0.05 means that there is a 5% chance that a called peak is irreproducible.

Li et al., The Annals of Applied Statistics (2011)