

Bioconductor - TransView

A brief introduction to TransView

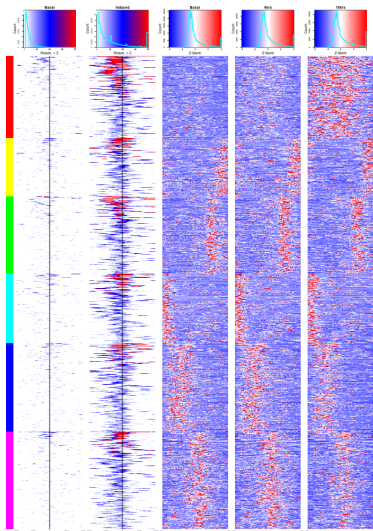
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Motivation and use case I



- Analytical tool to visualize ChIP-Seq data along with PolII activity.
- Continuous view on a region can be combined with the fragmented view of a corresponding gene or an ordinary matrix.
- Comparison of replicates, experiments and assays
- Clustering of multiple samples and visual indication of the outcome.
- Facilities for import and annotation of results from MACS ChIP-Seq algorithm.
- Consistent usage of popular formats, tools and classes such as GRanges.

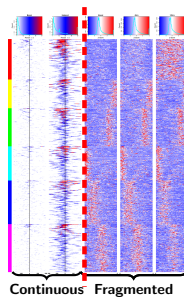
```
> hifhyp<-parseReads(hiff,description="HIF1a",min_quality=30)
Reading chrY (21 of 22)
Warning: the following chromosomes have no reads
chrM
About 7 seconds passed. 6199639 reads processed
> hifhyp
class: DensityContainer
  Experiment: HIF1a
  Source: HIF1a_hyp/hif1a_raw264_hyp.bam
  Spliced: FALSE
  Paired: FALSE
  Filtered: FALSE
  Reads in file: 6199639
  Reads used: 5951538
  Coverage: 0.080702
  Local Coverage: 1.358501
  Max Score: 4855
  Local Max Score: 4855
  Low Quality / Unmapped: 248101
  Strands: both
  Memory usage [MB]: 339.23
  Available Slots:
data_pointer histogram size env ex_name origin spliced paired
  Chromosomes: chr10|chr11|chr12|chr13|chr14|chr15|chr16|chr17
```

- Many ($> 1k$) repeated random slicing operations from a density map.
- Learn about the outcome of a mapping run.
- Assemble density maps of whole transcripts.
- However: Current design choice 16bit integers \rightarrow pile ups $> 65k$ reads will be capped.

NGS Experiment

Densities
[List/Rle]

Other
Assays



Workflow

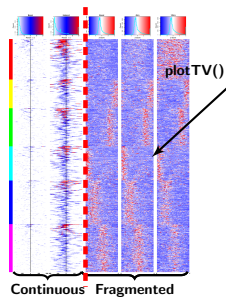
NGS Experiment

Densities
[List/Rle]

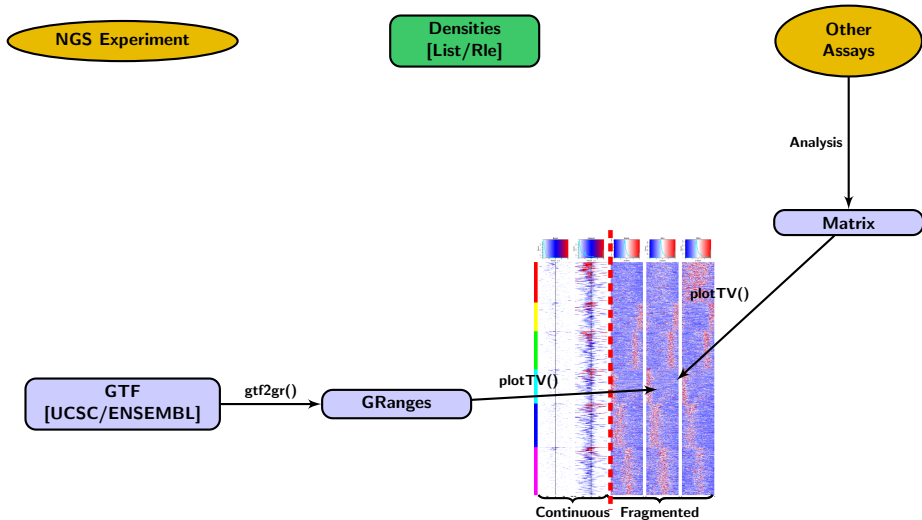
Other
Assays

Analysis

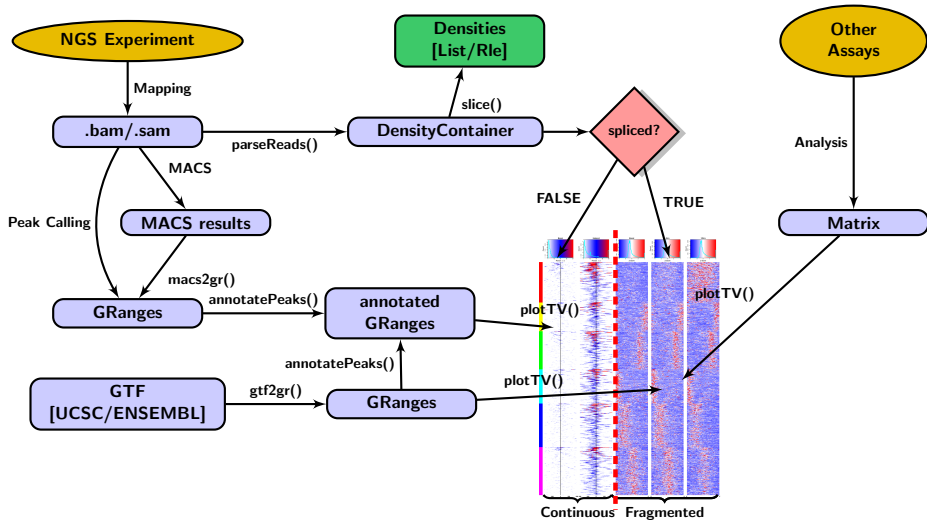
Matrix



Workflow



Workflow



- Further development is ongoing and a major release is planned for the next bioconductor version.
- Allow merging, subtraction and division of DensityContainer classes.
- Extend the functionality of the major class (DensityContainer class) holding the density maps to enable special functions such as strand specific plotting.
- Merge nearby peaks and transcripts.
- Improve documentation

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