Containers for Experimental and Integrative Data

Martin Morgan (mtmorgan@fhcrc.org)
Fred Hutchinson Cancer Research Center

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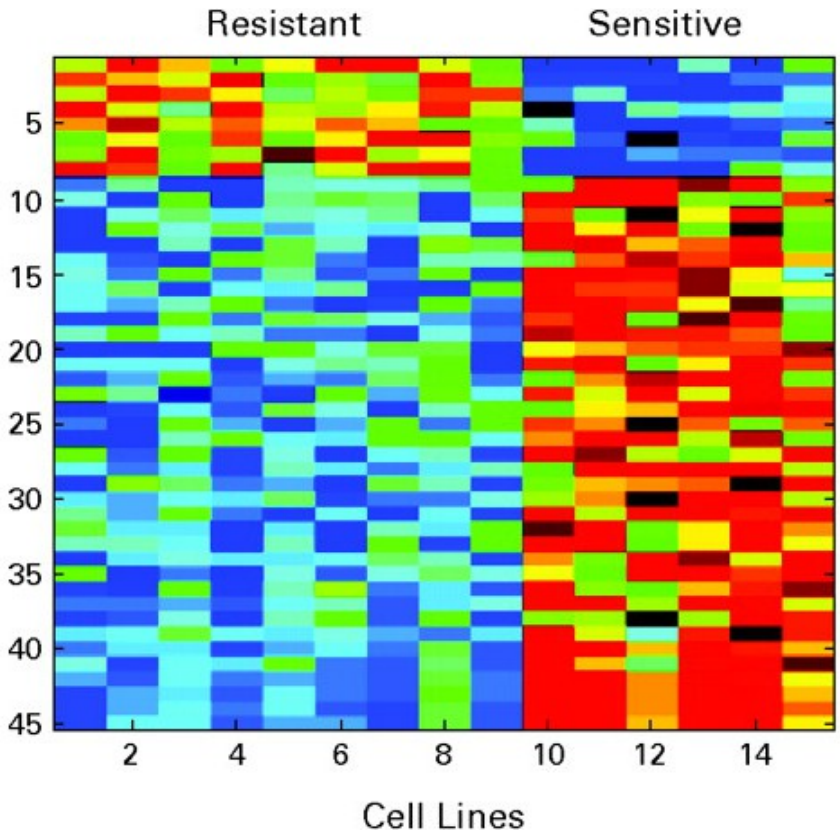
What we want?



Hsu *et al.* 2007 J Clin Oncol 25: 4350-4357 (retracted)

- Provenance
  - Sample and row 'metadata'
- Book-keeping, e.g., during subset
- Integration
  - With annotation resources
  - With *GenomicRanges*
- Re-use

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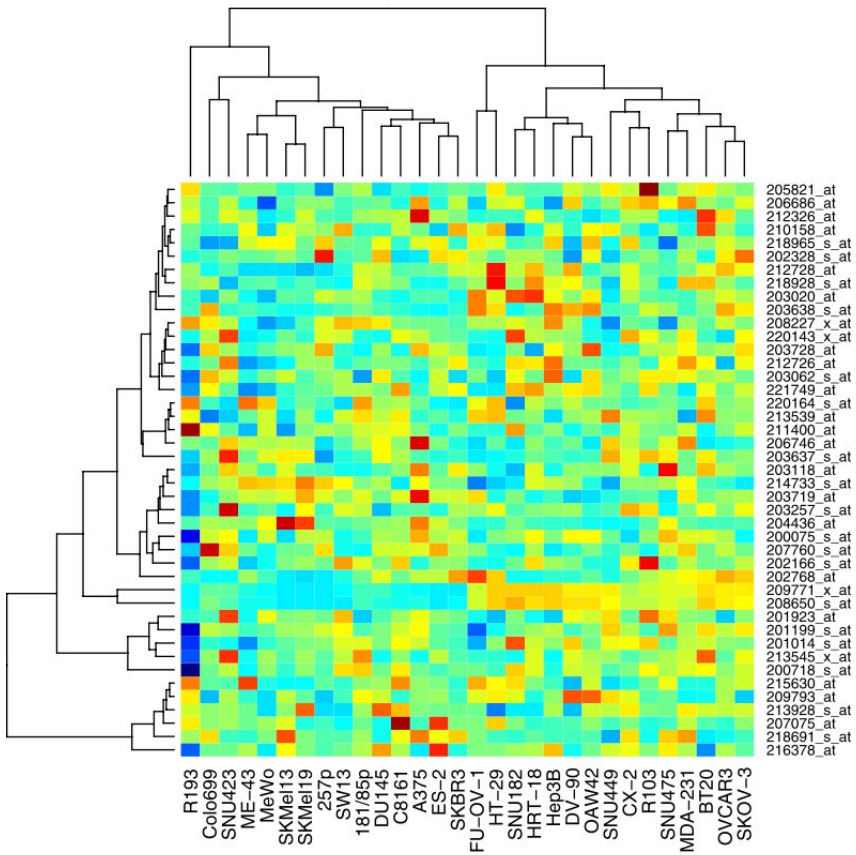

Baggerly & Coombes 2009 Ann Appl Stat 3: 1309-1334

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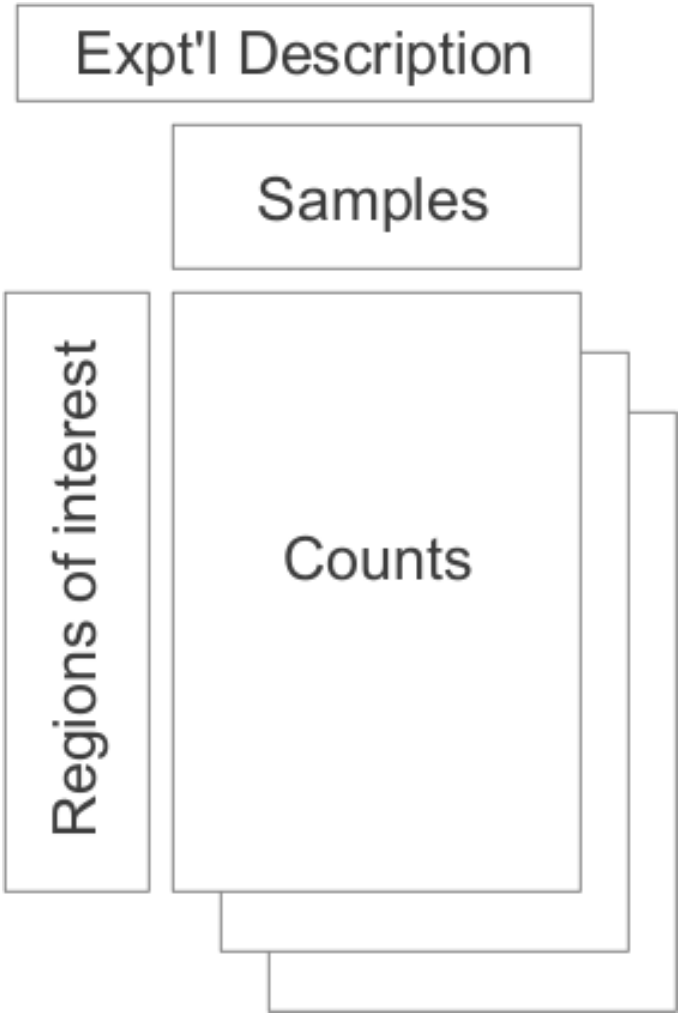
What we have?

- *SummarizedExperiment*
  - Range-based rows; *IRanges* data structures
- *eSet*-derived
  - E.g., *DESeq countDataSet*
- Other, e.g., *edgeR*
  - Simple lists wrapped as S4 classes
- ...
- *BamViews*

Design

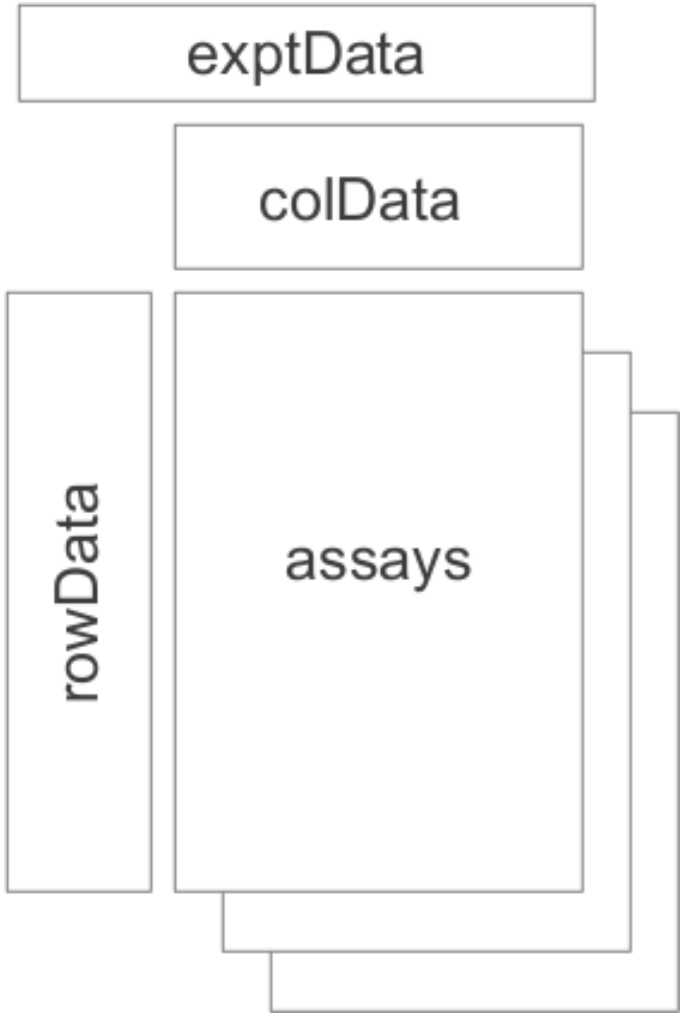


SummarizedExperiment

- Experiment data
- Regions of interest
- Samples
- Assay(s)

Assays implemented to avoid unnecessary copy

Design



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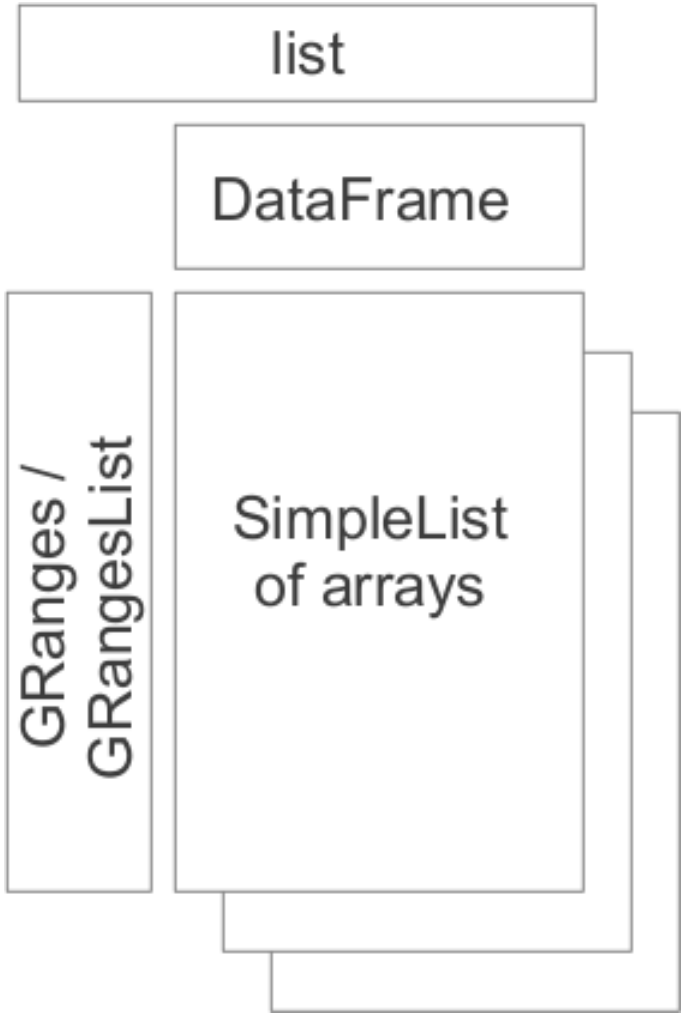

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Use & re-use

Use

- Accessors, `rowData(se)`
- Subset, `se[, se$Treatment == "ChIP"]`
- Annotation, `seqinfo(se)`, `mcols(se)`
- Overlap, e.g., `subsetByOverlaps` to select rows within regions of interest

```
> roi <- GRanges("chr1", IRanges(1, 2e6))
> subsetByOverlaps(se, roi)
```

Re-use

- *easyRNASeq*, *ggbio*, *Gviz*, ...
- *VariantAnnotation* *VCF* class; *minfi*, ...

Limitations and Alternatives

SummarizedExperiment

- Ranges required? Not really, but a bit of a hack (*GRangesList* as `rowData`).
- Rectangular; not suitable for 'ragged' data
- Equal-sized arrays as assays
- In-memory

eSet-derived

- No ranges, so harder to integrate.
- Inherits sub-optimal representations, e.g., *annotatedDataFrame* rather than *DataFrame*

Other, e.g., *edgeR*

- Simple, but limited interoperability with *Bioconductor* resources

Ideas and needs?