

Sequence Analysis: Differential Representation

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Sequence Analysis

- Work Flows

- Example data

- Differential Representation

Subsequent Analysis

- Lab activity

- References

Work Flows: Differential Representation

Prior to analysis

- ▶ Biological experimental design – treatments, replication, etc.
- ▶ Sequencing preparation – library preparation, manufacturer protocol, etc.

Analysis

1. Pre-processing (sequencing, alignment, quality assessment)
2. Count, e.g., reads per transcript – ChIP-seq; RNA-seq; novel transcript identification; microbiome; ...
3. Differential representation
4. Annotation
5. ...

<http://bioconductor.org/workflows> for common analyses.

Third-party tools

- ▶ Primary data generation.
- ▶ Aligners
 - ▶ Differing in alignment flexibility (e.g., mismatches vs. indels); error models (e.g., SOLiD homopolymers); performance
 - ▶ *Bowtie*, *BWA*, *SSAHA2*, ...
- ▶ Domain-specific
 - ▶ ChIP-seq: *MACS*; ...
 - ▶ RNA-seq: *GSNAP*, *TopHat* (alignment); *Cufflinks* (isoform assembly), ...
 - ▶ Variants: *samtools*, ...
 - ▶ Microbiome: ?
- ▶ Comprehensive: *GATK*; *BioPerl*, *Biopython*, *HTSeq*
- ▶ SeqAnswers

Bioconductor entry points

- ▶ Quality assessment.
- ▶ Preliminary read processing, e.g., demultiplexing, remediation
- ▶ Specialized alignment, e.g., `matchPDict` in *Biostrings*.
- ▶ ‘Upstream’ domain-specific work flows, e.g., ChIP-seq peak calling (*chipseq*), RNA-seq reads per transcript (*GenomicRanges* / *IRanges* / ...)
- ▶ Statistical analysis of designed experiments, e.g., *edgeR*, *DESeq*
- ▶ Specialized analysis, e.g., microbiome sequence processing and ecological analysis (*vegan*, *ape*, ...)

Example Data

Nagalakshmi et al., 2008. The transcriptional landscape of the yeast genome defined by RNA sequencing, *Science* 320: 1344–1349.

- ▶ Original 'RNA-seq' experiment
- ▶ Two different primers to generate DNA from poly(A) RNA:
 - RH Random hexamer
 - dT oligo(dT)
- ▶ Biological and technical replicates
- ▶ Illumina GAI – relatively small number (<5 million / lane) of short (33bp) reads; poor trailing base quality.

Counting Reads

- ▶ Retrieve results from SRA, reference sequence from UCSC.
- ▶ Align to reference using BWA
- ▶ Use *GenomicFeatures* to identify exons
- ▶ `IRanges::countOverlaps` to count reads
- ▶ See `browseVignette("SeattleIntro2010")`

Bioconductor Solutions

Data

- ▶ Matrix (transcript \times samples) of counts (caution: no special treatment of overlapping transcripts!)
- ▶ Designed experiment – random hexamer vs. oligo(dT)

edgeR [3]

- ▶ Negative binomial error model (originally:(over-dispersed Poisson).
- ▶ Empirical Bayes to moderate over-dispersion.
- ▶ Recently: much more flexible experimental design – negative binomial GLM – `glmFit`

DESeq [1]

- ▶ Negative binomial error model
- ▶ Variance and mean estimation using local regression.

Issues in Analysis

Normalization

- ▶ Between-sample differences in total count
- ▶ Within-sample trade-offs in reads per transcript
- ▶ Approaches: robust estimates via trimmed or geometric mean counts or quantiles (e.g., 75th) per sample

Dispersion: overcoming poor estimates

- ▶ *edgeR*: empirical Bayes, common dispersion.
- ▶ *DESeq*: estimate per-gene mean and variance, then robust fit across genes to model mean / variance relationship

Significance

- ▶ Exact test (single factor; analogous to Fisher exact test)
- ▶ GLM likelihood ratio – comparison of fitted to reduced model

DESeq in a Nutshell

```
> ## counts: matrix of counts
> ## conditions: vector of treatments, corresponding
> ##    to each column of counts
> cds <- newCountDataSet(counts, conditions)
> cds <- estimateSizeFactors(cds)
> cds <- estimateVarianceFunctions(cds)
> ## 'top table' of differentially expressed regions
> res <- nbinomTest(cds, "Condition_1", "Condition_2")
```

Subsequent analysis

- ▶ Annotation work flows
- ▶ Novel domain-specific approaches, e.g., ChIP-seq motif discovery
- ▶ Standard analyses tailored to sequence data, e.g., *goseq*.
- ▶ Application of microarray-style analyses.

Lab Activity

- ▶ Exploratory assessment of 'hits per transcript'
- ▶ *DESeq* work flow
- ▶ Evaluation of results

References



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