CummeRbund workflow

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This document is a work in progress and will continually be updated as new features or analyses are integrated into the cummeRbund pipeline. This guide is being released as is, with the understanding that existing gaps will be completed in due time. Please bear with us as we work to expand this resource.

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Overview

Workflow Summary

Reading cuffdiff output

Quality Assessment of data

4.1 Evaluating model fit
4.2 Identifying outlier replicates

```r
> pBoxRep <- csBoxplot(genes(cuff), replicates = T)
> pBoxRep

> pDendro <- csDendro(genes(cuff), replicates = T)
> pDendro

'dendrogram' with 2 branches and 6 members total, at height 0.2685017
'dendrogram' with 2 branches and 6 members total, at height 0.2685017
'dendrogram' with 2 branches and 6 members total, at height 0.2685017
4.3 Determining relationships between conditions

> pBox<-csBoxplot(genes(cuff))
> pBox
5 Analysis of differential expression

5.1 Identifying differentially expressed genes

```r
> sigGeneIds <- getSig(cuff, alpha=0.05, level="genes")
> head(sigGeneIds)
[1] "XLOC_000004" "XLOC_000005" "XLOC_000008" "XLOC_000009"
[5] "XLOC_000011" "XLOC_000013"
> length(sigGeneIds)
[1] 207
```

```r
> hESCvsFibroblast.sigGeneIds <- getSig(cuff, "hESC","Fibroblasts",alpha=0.05,level="genes")
> head(hESCvsFibroblast.sigGeneIds)
[1] "XLOC_000005" "XLOC_000009" "XLOC_000013" "XLOC_000014"
[5] "XLOC_000018" "XLOC_000025"
> length(hESCvsFibroblast.sigGeneIds)
[1] 151
```
5.1.1 Creating significant gene sets

```r
> sigGenes<-getGenes(cuff,sigGeneIds)
> sigGenes

CuffGeneSet instance for 207 genes

Slots:
annotation
fpkm
repFpkm
diff
count
isoforms CuffFeatureSet instance of size 717
TSS CuffFeatureSet instance of size 399
CDS CuffFeatureSet instance of size 577
promoters CuffFeatureSet instance of size 207
splicing CuffFeatureSet instance of size 399
relCDS CuffFeatureSet instance of size 207
```

5.1.2 Visualization of significant gene sets

5.2 Identifying differentially expressed features

```r
> sigGeneIds<-getSig(cuff,alpha=0.05,level="isoforms")
> head(sigGeneIds)

[1] "TCONS_00000007" "TCONS_00000008" "TCONS_00000021"
[4] "TCONS_00000022" "TCONS_00000033" "TCONS_00000041"

> length(sigGeneIds)

[1] 256
```

5.2.1 Creating significant feature sets

5.2.2 Visualization of significant feature sets

5.3 Analysis of individual genes

5.3.1 Subsetting individual genes

5.3.2 Creating a CuffGene object

```r
> Pink1<-getGene(cuff,'PINK1')
> Pink1

CuffGene instance for gene XLOC_000172
Short name: PINK1
Slots:
```
5.3.3 Visualization of individual genes

6 Data Exploration

6.1 Identifying patterns of gene expression

Partitioning around medoids as e.g.

6.2 Similarity analysis

findSimilar

6.3 Specificity analysis

csSpecificity

7 Analysis of differential splicing

8 Analysis of differential promoter usage

9 Linking with additional analyses

9.1 Gene Ontology Analysis (clusterProfiler)

In this particular example, the reference .gtf file that was used has the official gene symbol (HUGO) stored in the gene name attribute field. This value is carried over by cuffdiff and cummeRbund into the gene_short_name field for each feature. We will exploit this ID and use it to map genes to their Entrez ID to be able to use the very nice clusterProfiler package.

The first step is to translate

9.2 Gene Set Enrichment Analysis (Preranked)

We will generate .rnk and .gmx files for use in the GSEA Preranked analysis.
9.3 Principal component analysis

10 Visualization Tips/Tricks

10.1 Faceting

11 Session Info