

CummeRbund: Visualization and Exploration of Cufflinks High-throughput Sequencing Data

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1 Requirements

NOTE: cummeRbund 2.0 was designed in conjunction with the release of cufflinks 2.0. While we attempted to preserve backwards-compatibility, it is highly recommended that you update your cufflinks version ≥ 2.0 to take full advantage of the improvements in modeling, reporting, and visualization that have been incorporated.

- Cufflinks \geq v2.0.0
- SQLite
- R \geq v2.7.0
- Packages:
 - RSQLite
 - ggplot2 v0.9.2
 - reshape2
 - plyr
 - fastcluster
 - rtracklayer
 - Gviz
 - Recommended:
 - * Hmisc

2 Introduction

cummeRbund is a visualization package for Cufflinks high-throughput sequencing data. It is designed to help you navigate through the large amount of data produced from a Cuffdiff RNA-Seq differential expression analysis. The results of this analysis are typically a large number of inter-related files that are not terribly intuitive to navigate through. cummeRbund helps promote rapid analysis of RNA-Seq data by aggregating, indexing, and allowing you easily visualize and create publication-ready figures of your RNA-Seq data while maintaining appropriate relationships between connected data points. CummeRbund is a multifaceted suite for streamlined analysis and visualization of massively parallel RNA differential expression data sequencing data.

CummeRbund begins by re-organizing output files of a cuffdiff analysis, and storing these data in a local SQLite database. CummeRbund indexes the data to speed up access to specific feature data (genes, isoforms, TSS, CDS, etc.), and preserves the various relationships between these features. Access to data elements is managed via the RSQLite package and data are presented in appropriately structured R classes with various convenience functions designed to streamline your workflow. This persistent database storage means that inter-connected expression values are rapidly accessible and quickly searchable in future analyses.

CummeRbund defines two types of data classes, 'pointer' or reference classes describe SQL connections to the database without directly containing data, and 'data' classes that retrieve a subset of related data points such as associated features from a given gene or gene set. Each class type has methods for direct access to FPKM values, differential expression information, statistical test results, raw and normalized fragment counts, individual replicate FPKM values, and additional annotation information for features. Output formats allow for browsing and analysis of data in standard R objects (data.frame, list, etc). CummeRbund was designed to provide analysis and visualization tools analogous to microarray data. In this regard, numerous plotting methods are provided for visualization of RNA-Seq data quality and global statistics, and simple routines for plotting expression levels for one or thousands of genes, their isoforms, TSS groups, or CDS groups.

The base class, *cuffSet* is a 'pointer' to cuffdiff data that are stored out-of-memory in a sqlite database.

3 CummeRbund Classes

3.1 CuffSet Class

A pointer class to control access to the sqlite tables holding the Cufflinks data. The primary slot is DB which contains the RSQLite connection object. This can be accessed using the *DB()* accessor. The additional slots (genes, isoforms, TSS, and CDS) are each instances of the *CuffData* class and are pointers to sets of tables for each data subtype. They can be accessed with similar accessor wrappers. This is the default class created by *readCufflinks*. By default, *CuffData* accessor methods applied to a *CuffSet* class will operate on the 'genes' slot. The *runInfo()* method can be used to retrieve information about the actual cuffdiff run itself, including command-line arguments used to generate the results files.

3.2 CuffData Class

The *CuffData* class is also a pointer class to the SQL backend, but each instance is specific for a data subtype (genes, isoforms, TSS, CDS). Again, there is an DB slot (accessible using *DB()*) that contains the RSQLite connection object. There are several accessor, setter, and plotting methods that allow for global analysis of all features within a *CuffData* class. Subsetting is currently being re-written, however, it is primarily done through the 'gene_id' field. Available slots for the CuffData class are:

- DB: RSQLite connection object
- tables: A *list* of tables in the SQLite DB that contain the cufflinks data.
- filters: A *list* of filters for subsetting (not implemented yet).
- type: A *character* field describing the data (ie. 'genes', 'isoforms', 'TSS', 'CDS', 'other')
- idField: The name of the identifying index field for this object (eg. 'gene_id' for type='gene', or 'isoform_id' for type='isoform')

Making the best use of either the CuffSet or CuffData classes will enable you to keep the entire dataset out of memory and significantly improve performance for large cufflinks datasets.

3.3 CuffDist Class

The *CuffDist* class is an pointer class that contains the results of the various 'distribution tests' performed by cuffdiff. These include differential promoter usage, differential splicing, and differential CDS usage. These are independent tests from the differential analysis of gene-, isoform-, TSS-, and CDS-level features and therefore have their own container type to distinguish them as such. The 'promoters', 'relCDS', and 'splicing' slots of a *CuffSet* class are all *CuffDist* instances.

Available slots for the CuffDist class are:

- DB: RSQLite connection object
- tables: A *list* of tables in the SQLite DB that contain the distribution test data.
- type: A *character* field describing the data (ie. 'promoters', 'relCDS', 'splicing')
- idField: The name of the identifying index field for this object (eg. 'TSS_group_id' for type='promoters', or 'CDS_id' for type='relCDS', etc.)

3.4 CuffFeatureSet Class

The *CuffFeatureSet* class is a data-storage container that holds all available data for a pre-determined list of features. Slots for FPKM data, differential regulation data, and feature-level annotation are all available. Unlike the previous classes, this class contains no connection information to the SQL database, but rather contains several slots with *data.frame* objects storing multiple-features worth of information. There are available accessors, and plotting methods that are designed to present multiple-features worth of information (eg. heatmaps, scatterplots, etc) Available slots for a *CuffFeatureSet* object include:

- annotation: Holds all feature-level annotation information for all features in object.

- fpkm: A data frame of FPKM data across all conditions, for all features in object.
- repFpkm: A data frame of deconvolved FPKM values across individual replicates, for all features in object.
- diff: A data frame of differential expression/regulation data for all features in object.
- count: A data frame containing raw and normalized fragment counts, variance, dispersion, and uncertainty for all features in object.
- genome: A character string indicating which build of the genome the associated features are derived from. (e.g. 'hg19', 'mm9')

A specialized sub-class of *CuffFeatureSet* is the *CuffGeneSet* class. This subclass adds additional slots to contain all isoforms, TSS, and CDS information for a given set of gene_ids. The *CuffGeneSet* class is designed to aggregate all relevant information for a set of genes into one object for easy analysis and/or manipulation. The *CuffGeneSet* object adds the following slots:

- ids: A 'character' list of all gene_ids used in object.
- isoforms: A *CuffFeatureSet* object for all isoforms of genes in object.
- TSS: A *CuffFeatureSet* object for all TSS of genes in object.
- CDS: A *CuffFeatureSet* object for all CDS of genes in object.

3.5 CuffFeature Class

The *CuffFeature* class is designed for single-feature-level data analysis and plotting. The methods available for this object are designed to analyze or visualize information about a specific feature. This is a 'data' object, as opposed to a 'pointer' object to the database backend. There is a validity requirement that a *CuffFeature* object only point to data from a single feature. Available slots for a *CuffFeature* object include:

- annotation: Holds feature-level annotation information for a given feature.
- fpkm: A data frame of FPKM data across all samples for a given feature.
- repFpkm: A data frame of deconvolved FPKM values across all replicates for a given feature.
- diff: A data frame of differential expression/regulation data for a given feature.
- count: A data frame containing raw and normalized fragment counts, variance, dispersion, and uncertainty for a given feature.

A specialized sub-class of *CuffFeature* is the *CuffGene* class. This subclass adds additional slots to contain all isoform, TSS, and CDS information for a given gene. The *CuffGene* object adds the following slots:

- id: The common 'gene_id' for all data in object
- isoforms: A *CuffFeature* object for all isoforms of a given gene.
- TSS: A *CuffFeature* object for all TSS of a given gene.
- CDS: A *CuffFeature* object for all CDS of a given gene.
- features: A *data.frame* object containing feature information for the transcript models describing the gene.

4 Reading cuffdiff output

cummeRbund was designed to process the multi-file output format for a 'cuffdiff' differential expression analysis. In this type of analysis, a user will use a reference .gtf file (either known annotation or a .gtf file created from a cufflinks assembly or merge of assemblies) and quantitate the expression values and differential regulation of the annotation(s) in the .gtf file across two or more SAM/BAM files. By design, cuffdiff produces a number of output files that contain test results for changes in expression at the level of transcripts, primary transcripts, and genes. It also tracks changes in the relative abundance of transcripts sharing a common transcription start site, and in the relative abundances of the primary transcripts of each gene. Tracking the former allows one to see changes in splicing, and the latter lets one see changes in relative promoter use within a gene.

Note: Early versions of Cuffdiff required that transcripts in the input GTF be annotated with certain attributes in order to look for changes in primary transcript expression, splicing, coding output, and promoter use. This is no longer the case with $\geq v1.1.1$ of cummeRbund, however we still recommend the use of both the following attributes in your GTF file to enable all downstream features of cummeRbund.

These attributes are:

- **tss_id**: The ID of this transcript's inferred start site. Determines which primary transcript this processed transcript is believed to come from. Cuffcompare appends this attribute to every transcript reported in the .combined.gtf file.
- **p_id**: The ID of the coding sequence this transcript contains. This attribute is attached by Cuffcompare to the .combined.gtf records only when it is run with a reference annotation that include CDS records. Further, differential CDS analysis is only performed when all isoforms of a gene have p_id attributes, because neither Cufflinks nor Cuffcompare attempt to assign an open reading frame to transcripts.

cuffdiff calculates the FPKM of each transcript, primary transcript, and gene in each sample. Primary transcript and gene FPKMs are computed by summing the FPKMs of transcripts in each primary transcript group or gene group. The results are output in FPKM tracking files, the structure of which can be found in the cufflinks manual.

There are four FPKM tracking files:

- *isoforms.fpkm_tracking* Transcript FPKMs
- *genes.fpkm_tracking* Gene FPKMs. Tracks the summed FPKM of transcripts sharing each gene_id
- *cds.fpkm_tracking* Coding sequence FPKMs. Tracks the summed FPKM of transcripts sharing each p_id, independent of tss_id
- *tss_groups.fpkm_tracking* Primary transcript FPKMs. Tracks the summed FPKM of transcripts sharing each tss_id

cuffdiff also performs differential expression tests between supplied conditions. This tab delimited file lists the results of differential expression testing between samples for spliced transcripts, primary transcripts, genes, and coding sequences. For detailed file structure see cufflinks manual.

Four .diff files are created:

- *isoform_exp.diff* Transcript differential FPKM.
- *gene_exp.diff* Gene differential FPKM. Tests difference in the summed FPKM of transcripts sharing each gene_id
- *tss_group_exp.diff* Primary transcript differential FPKM. Tests differences in the summed FPKM of transcripts sharing each tss_id
- *cds_exp.diff* Coding sequence differential FPKM. Tests differences in the summed FPKM of transcripts sharing each p_id independent of tss_id

In addition, cuffdiff also performs differential splicing, CDS usage, and promoter usage tests for each gene across conditions:

- *splicing.diff* Differential splicing tests.
- *CDS.diff* Differential coding output.
- *promoters.diff* Differential promoter use.

All of these output files are related to each other through their various tracking_ids, but parsing through individual files to query for important result information requires both a good deal of patience and a strong grasp of command-line text manipulation. Enter cummeRbund, an R solution to aggregate, organize, and help visualize this multi-layered dataset.

One of the principle benefits of using cummeRbund is that data are stored in a SQLite database. This allows for out-of-memory analysis of data, quick retrieval, and only a one-time cost to setup the tables. By default, cummeRbund assumes that all output files from cuffdiff are in the current working directory. To read these files, populate the 'cuffData.db' database backend, and return the *CuffSet* pointer object, you can do the following.

```
> library(cummeRbund)
> cuff<-readCufflinks()
> cuff

CuffSet instance with:
  3 samples
  400 genes
  1203 isoforms
  662 TSS
  906 CDS
  1062 promoters
  1986 splicing
  990 relCDS
```

Again, by default *dir* is assumed to be the current working directory and `cuff<-readCufflinks()` should work if all appropriate files are in the current working directory. We now also recommend that you use both the *genome* and *gtfFile* arguments to `readCufflinks()`. This will allow cummeRbund to archive the transcript structure information located in the .gtf file associated with your particular cuffdiff run, as well as associate these transcripts with an appropriate genome build (e.g. 'hg19', 'mm9', etc) so as to allow for transcript-level visualizations and future integration with other external resources. Should you need to rebuild the SQLite backend for any reason, you can add the option *rebuild=T* to `readCufflinks`. Once the database is created, `readCufflinks` will default to using the SQL backend and should not need to rebuild this database. Each R session should begin with a call to `readCufflinks` so as to initialize the database connection and create an object with the appropriate RSQLite connection information.

4.1 Adding additional feature annotation

Gene- or feature-level annotation can be permanently added to the database tables for future querying. If you have a data.frame where the first column contains the 'tracking_id' (eg. 'gene_id' for genes, 'isoform_id' for isoforms, etc). You can easily add feature level annotation using the `addFeatures()` function:

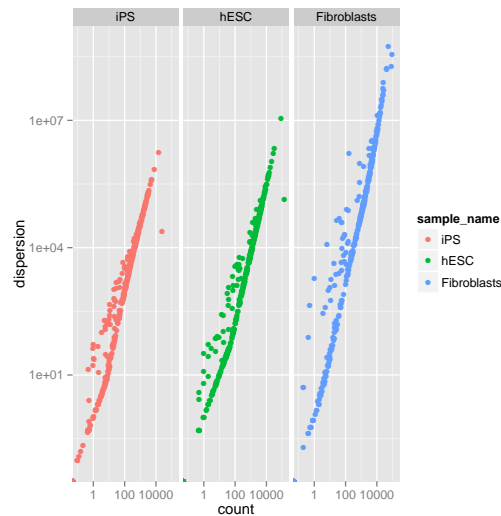
```
> #annot<-read.table("gene_annotation.tab",sep="\t",header=T,na.string="-")
> #addFeatures(cuff,annot,level="genes")
```

By default, features added to a *CuffSet* object are assumed to be gene-level annotations, but the level can be selected using the argument *level*. Features added to a *CuffData* object are assumed to be of the same type as the 'type' value for that given object (e.g. gene-level features for 'genes', isoform-level features for isoforms, etc.)

5 Global statistics and Quality Control

Several plotting methods are available that allow for quality-control or global analysis of cufflinks data. A good place to begin is to evaluate the quality of the model fitting. Overdispersion is a common problem in RNA-Seq data. As of cufflinks *v2.0* mean counts, variance, and dispersion are all emitted, allowing you to visualize the estimated overdispersion for each sample as a quality control measure.

```
> disp<-dispersionPlot(genes(cuff))
> disp
```



(a) Count vs dispersion plot by condition for all genes.

The squared coefficient of variation is a normalized measure of cross-replicate variability that can be useful for evaluating the quality your RNA-seq data. Differences in CV^2 can result in lower numbers of differentially expressed genes due to a higher degree of variability between replicate fpkm estimates.

```
> genes.scv<-fpkmSCVPlot(genes(cuff))
> isoforms.scv<-fpkmSCVPlot(isoforms(cuff))
```

To assess the distributions of FPKM scores across samples, you can use the *csDensity* plot (Figure 1).

```
> dens<-csDensity(genes(cuff))
> dens
> densRep<-csDensity(genes(cuff),replicates=T)
> densRep
```

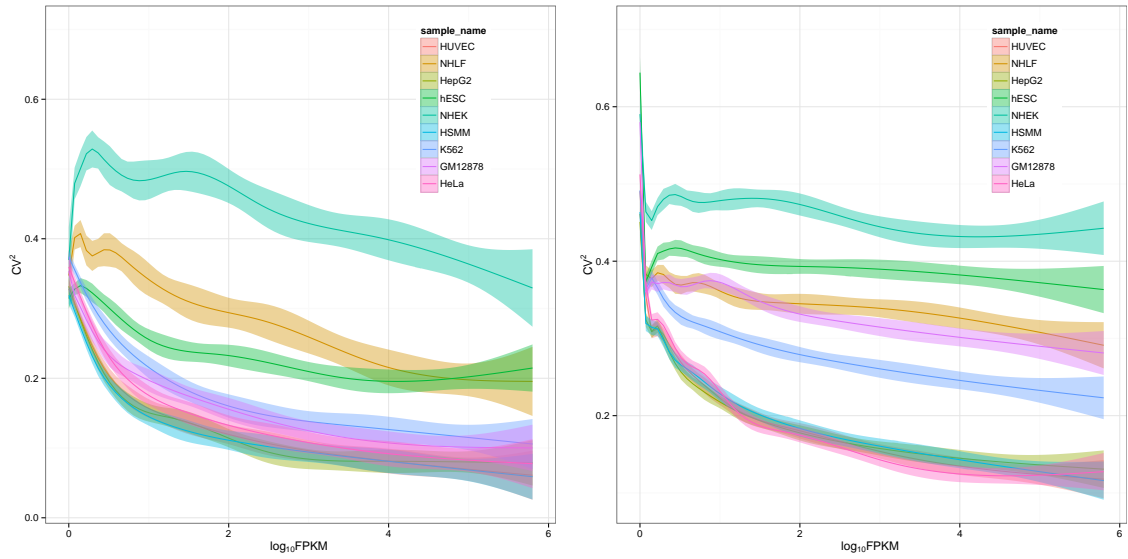
Boxplots can be visualized using the *csBoxplot* method (Figure 2).

```
> b<-csBoxplot(genes(cuff))
> b
> brep<-csBoxplot(genes(cuff),replicates=T)
> brep
```

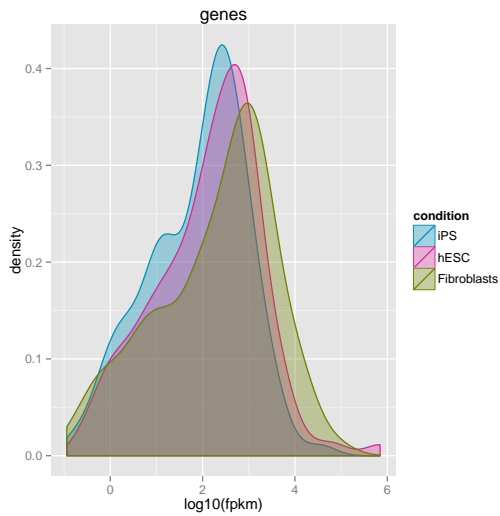
A matrix of pairwise scatterplots can be drawn using the *csScatterMatrix()* method.

```
> s<-csScatterMatrix(genes(cuff))
>
```

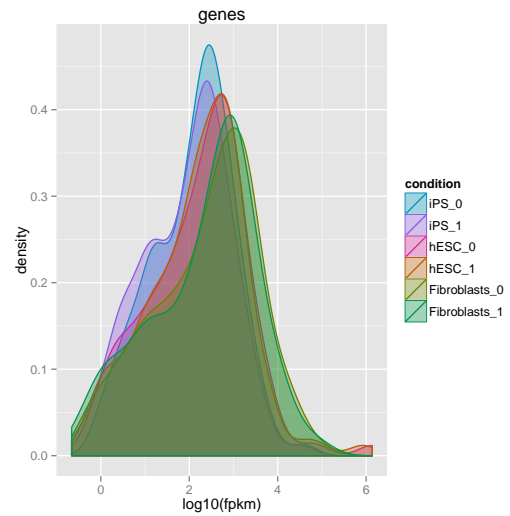
Individual Pairwise comparisons can be made by using *csScatter*. You must specify the sample names to use for the *x* and *y* axes:



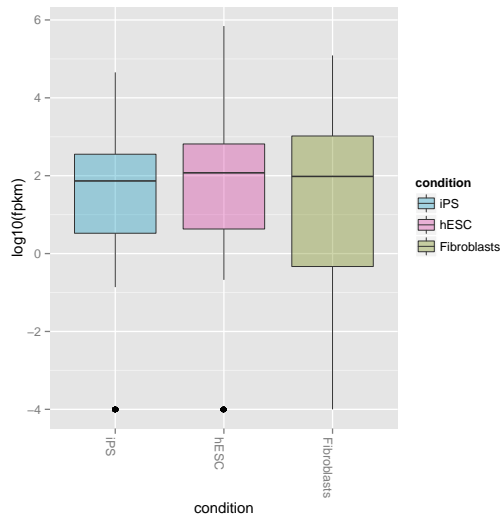
(a) The squared coefficient of variation allows visualization of cross-replicate variability between conditions and can be a useful metric in determining data quality at the gene level (left) or isoform level (right). Here we demonstrate the variability of each individual ENCODE project RNA-seq conditions.



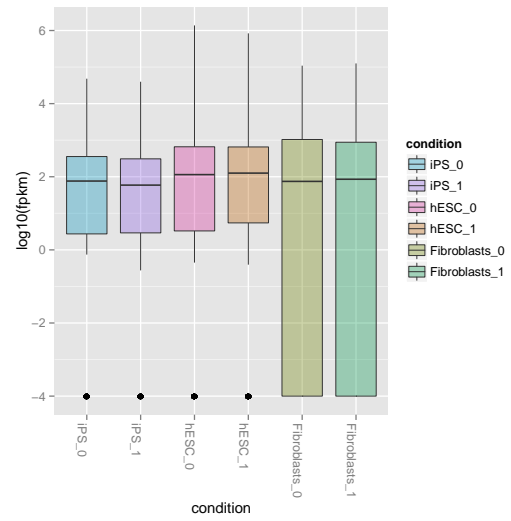
(a) Density plot of individual conditions.



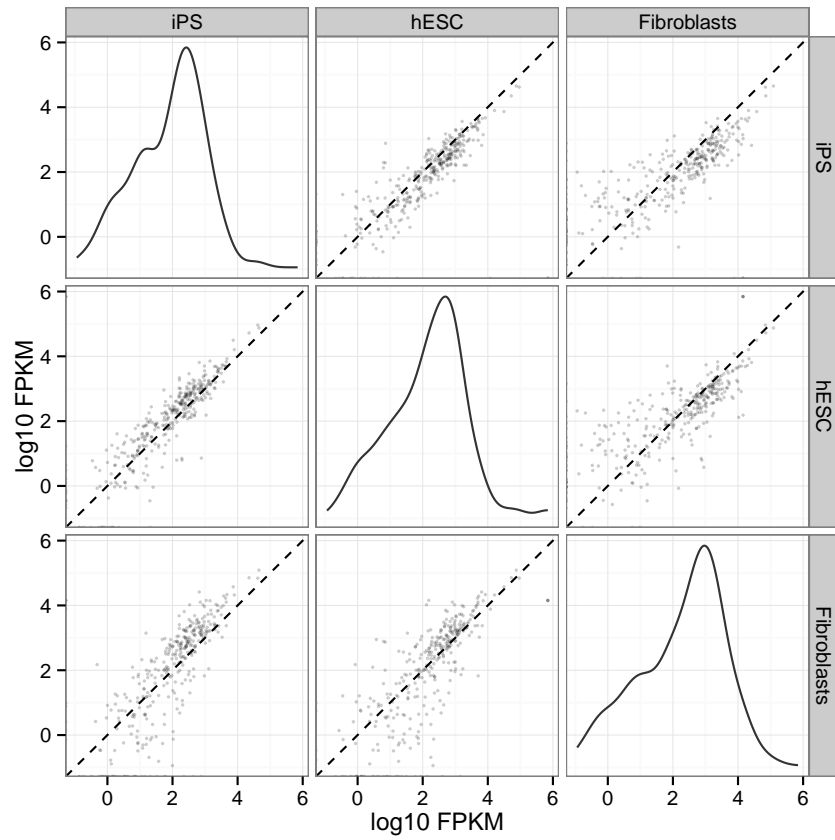
(b) Density plot with replicates=TRUE exposes individual replicate FPKM distributions.



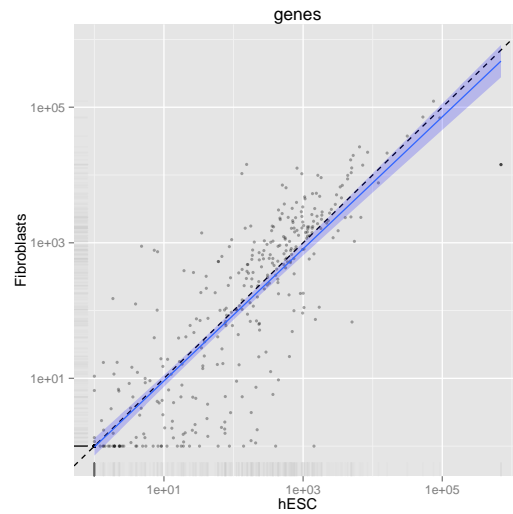
(a) Box plot of FPKM distributions for individual conditions.



(b) Box plot with replicates=TRUE exposes individual replicate FPKM distributions.



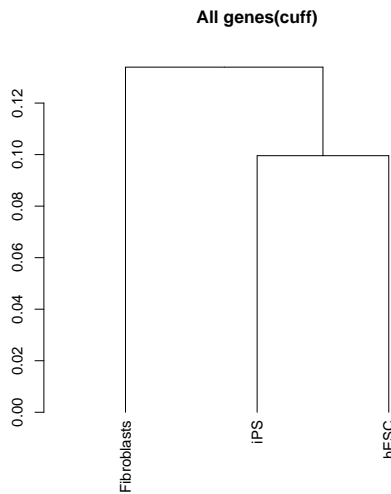
(a) Scatterplots can be useful to identify global changes and trends in gene expression between pairs of conditions.



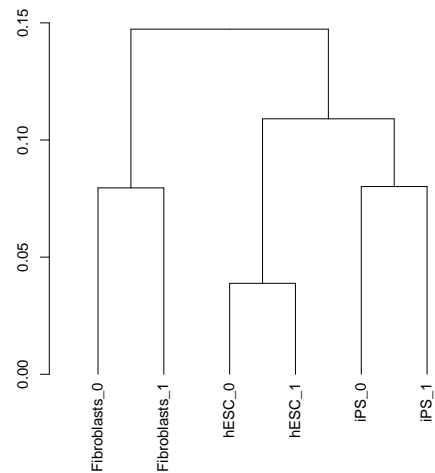
(a) Pairwise scatterplots can identify biases in gene expression between two particular conditions.

```
> s<-csScatter(genes(cuff),"hESC","Fibroblasts",smooth=T)
> s

> dend<-csDendro(genes(cuff))
> dend.rep<-csDendro(genes(cuff),replicates=T)
```



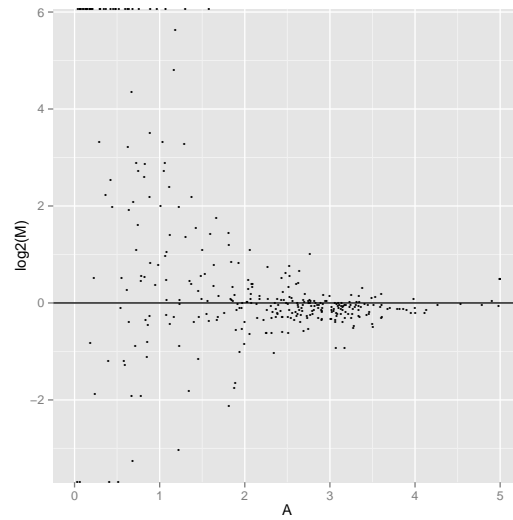
(a) Dendrogram of JS distances between conditions.



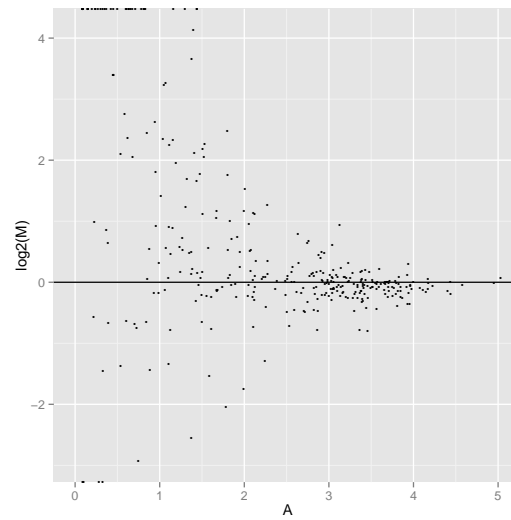
(b) Dendrogram with replicates=TRUE can identify outlier replicates.

MvsA plots can be useful to determine any systematic bias that may be present between conditions. The CuffData method `MAplot()` can be used to examine these intensity vs fold-change plots. You must specify the sample names to use for the pairwise comparison with *x* and *y*:

```
> m<-MAplot(genes(cuff),"hESC","Fibroblasts")
> m
> mCount<-MAplot(genes(cuff),"hESC","Fibroblasts",useCount=T)
> mCount
```



(a) MA plots can identify biases across ranges of intensity and fold-change.



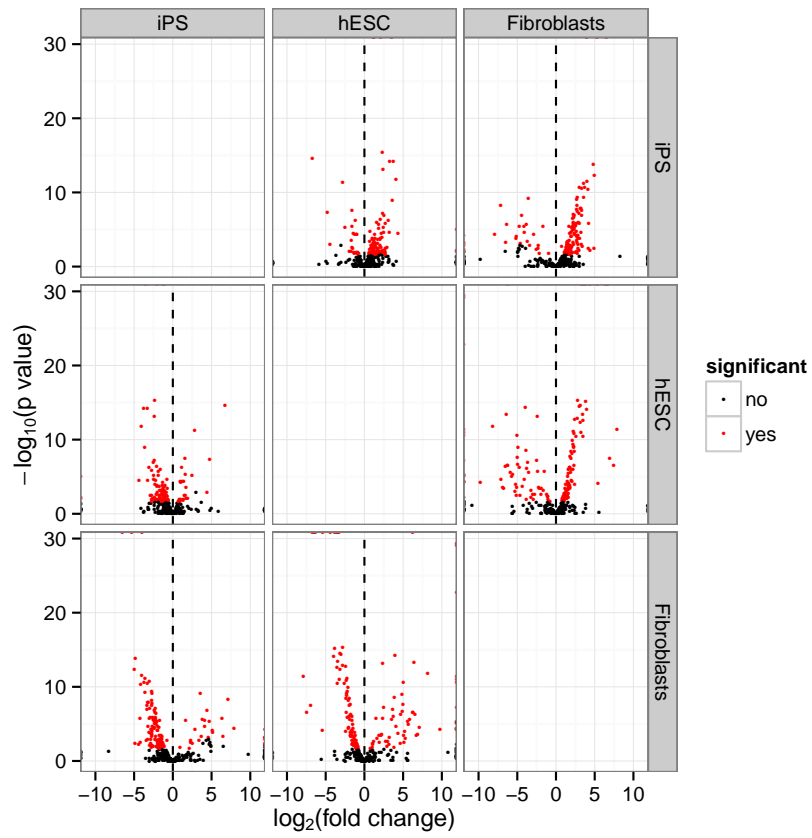
(b) MA plot drawn on normalized count values instead of FPKM.

Volcano plots are also available for the *CuffData* objects.

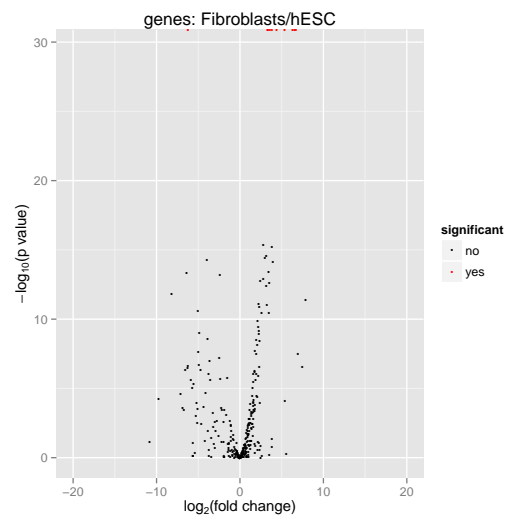
```
> v<-csVolcanoMatrix(genes(cuff))
> v
```

For individual pairwise comparisons, you must specify the comparisons by sample name.

```
> v<-csVolcano(genes(cuff),"hESC","Fibroblasts")
> v
```



(a) Volcano plots explore the relationship between fold-change and significance.



(a) Volcano plots explore the relationship between fold-change and significance.

6 Accessing Data

Cuffdiff run information

Run-level information such as run parameters, and sample information can be accessed from a *CuffSet* object by using the *runInfo* and *replicates* methods:

```
> runInfo(cuff)
```

```
      param
1  cmd_line
2  version
3  SVN_revision
4 boost_version
5    genome
```

```
1 cuffdiff -L iPS,hESC,Fibroblasts -p 6 chr1_snippet.gtf -o iPS_hESC_fibro iPS_rep1.bam,iPS_rep2.bam H1_rep
2
3
4
5
```

```
> replicates(cuff)
```

	file	sample_name	replicate	rep_name	total_mass
1	iPS_rep1.bam	iPS	0	iPS_0	173431
2	iPS_rep2.bam	iPS	1	iPS_1	173007
3	H1_rep1.bam	hESC	0	hESC_0	754749
4	H1_rep3.bam	hESC	1	hESC_1	762643
5	NHLF_rep1.bam	Fibroblasts	0	Fibroblasts_0	876775
6	NHLF_rep2.bam	Fibroblasts	1	Fibroblasts_1	1412130

	norm_mass	internal_scale	external_scale
1	706934	0.958068	0.584877
2	706934	1.037970	0.584877
3	706934	0.989851	1.513060
4	706934	1.010250	1.513060
5	706934	0.840416	1.223240
6	706934	1.198470	1.223240

Features/Annotation

Feature-level information can be accessed directly from a *CuffData* object using the *fpkm*, *repFpkm*, *count*, *diffData*, or *annotation* methods:

```
> gene.features<-annotation(genes(cuff))
```

```
> head(gene.features)
```

	gene_id	class_code	nearest_ref_id	gene_short_name
1	XL0C_000001	<NA>	<NA>	<NA>
2	XL0C_000002	<NA>	<NA>	OR4F5
3	XL0C_000003	<NA>	<NA>	<NA>
4	XL0C_000004	<NA>	<NA>	<NA>
5	XL0C_000005	<NA>	<NA>	<NA>
6	XL0C_000006	<NA>	<NA>	OR4F16

	locus	length	coverage
1	chr1:11873-29961	NA	NA
2	chr1:69090-70008	NA	NA
3	chr1:321083-321114	NA	NA
4	chr1:321145-321223	NA	NA
5	chr1:322036-328580	NA	NA
6	chr1:367658-368595	NA	NA

```
> gene.fpk<-fpkm(genes(cuff))
```

```
> head(gene.fpk)
```

	gene_id	sample_name	fpkm	conf_hi	conf_lo
1	XL0C_000001	Fibroblasts	16.1506	182.9240	0.00000
2	XL0C_000002	Fibroblasts	0.0000	0.0000	0.00000
3	XL0C_000003	Fibroblasts	0.0000	0.0000	0.00000
4	XL0C_000004	Fibroblasts	14237.7000	78180.9000	0.00000
5	XL0C_000005	Fibroblasts	48.0566	90.6526	5.46055
6	XL0C_000006	Fibroblasts	0.0000	0.0000	0.00000

	quant_status	stdev
1	OK	83.3867
2	OK	0.0000
3	OK	0.0000
4	OK	31971.6000
5	OK	21.2980
6	OK	0.0000

```
> gene.repFpk<-repFpk(genes(cuff))
```

```
> head(gene.repFpk)
```

	gene_id	sample_name	replicate	rep_name	raw_frags
1	XL0C_000001	Fibroblasts	0	Fibroblasts_0	12.000100
2	XL0C_000002	Fibroblasts	0	Fibroblasts_0	0.000000
3	XL0C_000003	Fibroblasts	0	Fibroblasts_0	0.000000
4	XL0C_000004	Fibroblasts	0	Fibroblasts_0	0.333333
5	XL0C_000005	Fibroblasts	0	Fibroblasts_0	137.100000
6	XL0C_000006	Fibroblasts	0	Fibroblasts_0	0.000000

	internal_scaled_frags	external_scaled_frags	fpkm
1	14.278800	11.672900	11.1815
2	0.000000	0.000000	0.0000
3	0.000000	0.000000	0.0000
4	0.396629	0.324245	28475.5000
5	163.134000	133.362000	57.8929
6	0.000000	0.000000	0.0000

	effective_length	status
1	NA	OK
2	NA	OK
3	NA	OK
4	NA	OK
5	NA	OK
6	NA	OK

```
> gene.counts<-count(genes(cuff))
```

```
> head(gene.counts)
```

	gene_id	sample_name	count	variance	uncertainty
1	XL0C_000001	Fibroblasts	20.072500	1.05160e+04	1.77636e-15
2	XL0C_000002	Fibroblasts	0.000000	0.00000e+00	0.00000e+00
3	XL0C_000003	Fibroblasts	0.000000	0.00000e+00	0.00000e+00
4	XL0C_000004	Fibroblasts	0.198315	1.98315e-01	0.00000e+00
5	XL0C_000005	Fibroblasts	131.575000	3.35882e+03	5.68434e-14
6	XL0C_000006	Fibroblasts	0.000000	0.00000e+00	0.00000e+00

	dispersion	status
1	1311.870000	OK
2	0.000000	OK
3	0.000000	OK
4	0.198315	OK

```
5 2161.890000 OK
6 0.000000 OK
```

```
> isoform.fpkms<-fpkm(isoforms(cuff))
```

```
> head(isoform.fpkms)
```

	isoform_id	sample_name	fpkm	conf_hi	conf_lo
1	TCONS_00000001	Fibroblasts	10.99630	118.178	0
2	TCONS_00000002	Fibroblasts	0.00000	0.000	0
3	TCONS_00000003	Fibroblasts	5.15434	132.926	0
4	TCONS_00000004	Fibroblasts	0.00000	0.000	0
5	TCONS_00000005	Fibroblasts	0.00000	0.000	0
6	TCONS_00000006	Fibroblasts	14237.70000	78180.900	0

	quant_status	stdev
1	OK	53.59085
2	OK	0.00000
3	OK	63.88583
4	OK	0.00000
5	OK	0.00000
6	OK	31971.60000

```
> gene.diff<-diffData(genes(cuff))
```

```
> head(gene.diff)
```

	gene_id	sample_1	sample_2	status	value_1	value_2
1	XL0C_0000001	iPS	hESC	NOTEST	20.21750	3.47386e-01
2	XL0C_0000002	iPS	hESC	NOTEST	0.00000	0.00000e+00
3	XL0C_0000003	iPS	hESC	NOTEST	0.00000	0.00000e+00
4	XL0C_0000004	iPS	hESC	OK	0.00000	6.97259e+05
5	XL0C_0000005	iPS	hESC	OK	355.82300	6.96704e+02
6	XL0C_0000006	iPS	hESC	NOTEST	1.51396	0.00000e+00

	log2_fold_change	test_stat	p_value	q_value
1	-5.86292e+00	7.13525e-01	0.47552100	1.00000000
2	0.00000e+00	0.00000e+00	1.00000000	1.00000000
3	0.00000e+00	0.00000e+00	1.00000000	1.00000000
4	1.79769e+308	1.79769e+308	0.00857693	0.02109120
5	9.69385e-01	-2.98373e+00	0.00284757	0.00840284
6	-1.79769e+308	-1.79769e+308	0.24382400	1.00000000

	significant
1	no
2	no
3	no
4	yes
5	yes
6	no

Condition and feature names

Vectors of sample names and feature names are available by using the *samples* and *featureNames* methods:

```
> sample.names<-samples(genes(cuff))
```

```
> head(sample.names)
```

```
[1] "iPS" "hESC" "Fibroblasts"
```

```
> gene.featurenames<-featureNames(genes(cuff))
```

```
> head(gene.featurenames)
```

```
[1] "XL0C_0000001" "XL0C_0000002" "XL0C_0000003" "XL0C_0000004"
[5] "XL0C_0000005" "XL0C_0000006"
```


Convenience functions

To facilitate Bioconductor-like operations, an 'FPKM-matrix' can be returned easily using the *fpkmMatrix* method:

```
> gene.matrix<-fpkmMatrix(genes(cuff))
> head(gene.matrix)
```

	iPS	hESC	Fibroblasts
XLOC_000001	20.21750	3.47386e-01	16.1506
XLOC_000002	0.00000	0.00000e+00	0.0000
XLOC_000003	0.00000	0.00000e+00	0.0000
XLOC_000004	0.00000	6.97259e+05	14237.7000
XLOC_000005	355.82300	6.96704e+02	48.0566
XLOC_000006	1.51396	0.00000e+00	0.0000

A matrix of replicate FPKM values can be retrieved by using *repFpkmMatrix*

```
> gene.rep.matrix<-repFpkmMatrix(genes(cuff))
> head(gene.rep.matrix)
```

	iPS_0	iPS_1	hESC_0	hESC_1
XLOC_000001	17.2049	22.92880	0.000	6.21918e-01
XLOC_000002	0.0000	0.00000	0.000	0.00000e+00
XLOC_000003	0.0000	0.00000	0.000	0.00000e+00
XLOC_000004	0.0000	0.00000	1377990.000	8.35811e+05
XLOC_000005	319.0300	390.45500	687.563	7.21983e+02
XLOC_000006	0.0000	3.02791	0.000	0.00000e+00

	Fibroblasts_0	Fibroblasts_1
XLOC_000001	11.1815	20.6009
XLOC_000002	0.0000	0.0000
XLOC_000003	0.0000	0.0000
XLOC_000004	28475.5000	0.0000
XLOC_000005	57.8929	38.0084
XLOC_000006	0.0000	0.0000

Similarly, a matrix of normalized counts can be generated by using *countMatrix*

```
> gene.count.matrix<-countMatrix(genes(cuff))
> head(gene.count.matrix)
```

	iPS	hESC	Fibroblasts
XLOC_000001	11.440900	0.494996	20.072500
XLOC_000002	0.000000	0.000000	0.000000
XLOC_000003	0.000000	0.000000	0.000000
XLOC_000004	0.000000	5.680560	0.198315
XLOC_000005	486.456000	2495.560000	131.575000
XLOC_000006	0.481711	0.000000	0.000000

6.1 Writing your own SQL accessors

Since the cuffData.db is a SQLite database backend, if you are familiar with SQL and/or RSQLite query construction, you can simply design your own SQL queries to access the data that you are after.

7 Creating Gene Sets

Gene Sets (stored in a *CuffGeneSet* object) can be created using the *getGenes* method on a *CuffSet* object. You must first create a vector of 'gene_id' or 'gene_short_name' values to identify the genes you wish to select:

```
> data(sampleData)
> myGeneIds<-sampleIDs
> myGeneIds

[1] "XLOC_001363" "XLOC_001297" "XLOC_001339" "XLOC_000132"
[5] "XLOC_001265" "XLOC_000151" "XLOC_001359" "XLOC_000069"
[9] "XLOC_000170" "XLOC_000105" "XLOC_001262" "XLOC_001348"
[13] "XLOC_001411" "XLOC_001369" "XLOC_000158" "XLOC_001370"
[17] "XLOC_001263" "XLOC_000115" "XLOC_000089" "XLOC_001240"

> myGenes<-getGenes(cuff,myGeneIds)
> myGenes
```

CuffGeneSet instance for 20 genes

Slots:

annotation	
fpkm	
repFpkm	
diff	
count	
isoforms	CuffFeatureSet instance of size 45
TSS	CuffFeatureSet instance of size 23
CDS	CuffFeatureSet instance of size 36
promoters	CuffFeatureSet instance of size 20
splicing	CuffFeatureSet instance of size 23
relCDS	CuffFeatureSet instance of size 20

The same *fpkm*, *repFpkm*, *count*, *annotation*, *diffData*, *samples*, and *featureNames* methods are available for instances of the *CuffGeneSet* class, but additional accessor methods are available for the *promoters*, *relCDS*, and *splicing* slot data as well.

```
> #FPKM values for genes in gene set
> head(fpkm(myGenes))

  gene_id sample_name      fpkm    conf_hi  conf_lo
1 XLOC_000069 Fibroblasts 2.05083e-01 8.94501e-01  0.000
2 XLOC_000069      hESC 1.77686e+02 2.15888e+02 139.484
3 XLOC_000069      iPS 1.90000e+01 3.88149e+01  0.000
4 XLOC_000089 Fibroblasts 1.39701e+04 2.19187e+04 6021.450
5 XLOC_000089      hESC 7.18339e+03 7.92296e+03 6443.810
6 XLOC_000089      iPS 1.41690e+03 1.96558e+03  868.215
  quant_status      stdev
1          OK    0.344709
2          OK   19.101000
3          OK    9.907450
4          OK 3974.300000
5          OK  369.785000
6          OK  274.340000

> #Isoform-level FPKMs for gene set
> head(fpkm(isoforms(myGenes)))
```

	isoform_id	sample_name	fpkm	conf_hi	conf_lo
1	TCONS_00000179	Fibroblasts	0.205083	0.894501	0.00000
2	TCONS_00000179	hESC	20.360900	33.840500	6.88119
3	TCONS_00000179	iPS	7.694340	16.356900	0.00000
4	TCONS_00000180	Fibroblasts	0.000000	0.000000	0.00000
5	TCONS_00000180	hESC	157.325000	198.673000	115.97800
6	TCONS_00000180	iPS	11.305600	27.105700	0.00000

	quant_status	stdev
1	OK	0.344709
2	OK	6.739800
3	OK	4.331280
4	OK	0.000000
5	OK	20.674000
6	OK	7.900050

```
> #Replicate FPKMs for TSS groups within gene set
> head(repFpkm(TSS(myGenes)))
```

	TSS_group_id	sample_name	replicate	rep_name	raw_frags
1	TSS128	iPS	0	iPS_0	987.0
2	TSS128	iPS	1	iPS_1	1065.0
3	TSS128	hESC	1	hESC_1	13196.0
4	TSS128	hESC	0	hESC_0	13588.0
5	TSS128	Fibroblasts	1	Fibroblasts_1	18899.5
6	TSS128	Fibroblasts	0	Fibroblasts_0	22201.0

	internal_scaled_frags	external_scaled_frags	fpkm
1	1030.20	1761.39	1412.22
2	1026.04	1754.29	1404.74
3	13062.10	8632.91	7131.86
4	13727.30	9072.58	7500.15
5	15769.70	12891.80	10368.60
6	26416.70	21595.70	17372.90

	effective_length	status
1	NA	OK
2	NA	OK
3	NA	OK
4	NA	OK
5	NA	OK
6	NA	OK

```
>
```

As of *cummeRbund v2.0* *CuffGeneSet* classes can be created from any type of identifier ('gene_id', 'isoform_id', 'TSS_group_id', or 'CDS_id'). When you pass a list of identifiers that are not *gene_id* to *getGenes()*, the function attempts to lookup the parent *gene_id* for each feature and returns *all* relevant information for the given genes and all of their sub-features (not just the sub-features passed to *getGenes()*). If you are interested in just retrieving information for a given set of features, please use the new *getFeatures()* method described later.

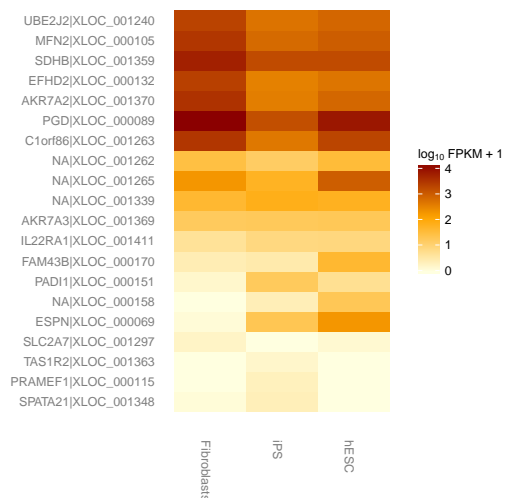
7.1 Geneset level plots

There are several plotting functions available for gene-set-level visualization:

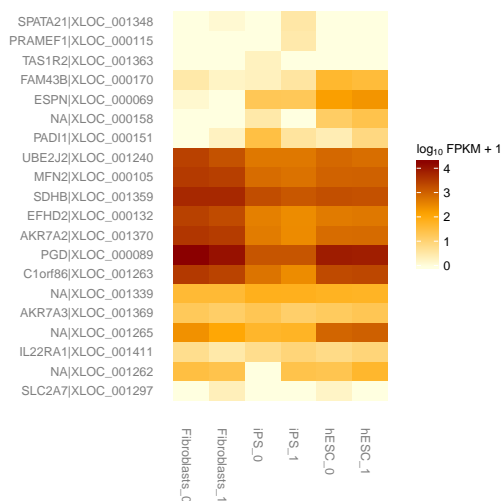
The *csHeatmap()* function is a plotting wrapper that takes as input either a *CuffGeneSet* or a *CuffFeatureSet* object (essentially a collection of genes and/or features) and produces a heatmap of FPKM expression values. The 'cluster' argument can be used to re-order either 'row', 'column', or 'both' dimensions of this matrix. By default, the Jensen-Shannon distance is used as the clustering metric, however, any function that produces a *dist* object can be passed to the 'cluster' argument as well.

```
> h<-csHeatmap(myGenes,cluster='both')
> h
```

```
> h.rep<-csHeatmap(myGenes,cluster='both',replicates=T)
> h.rep
```



(a) Heatmaps provide a convenient way to visualize the expression of entire gene sets at once.



(b) Same heatmap, with replicates=T can help to visualize variance between replicates.

If you prefer barplots over heatmaps for genesets (although this is not necessarily recommended for large gene sets). You can use the *expressionBarplot()* method on a *CuffFeatureSet* or a *CuffGeneSet* object.

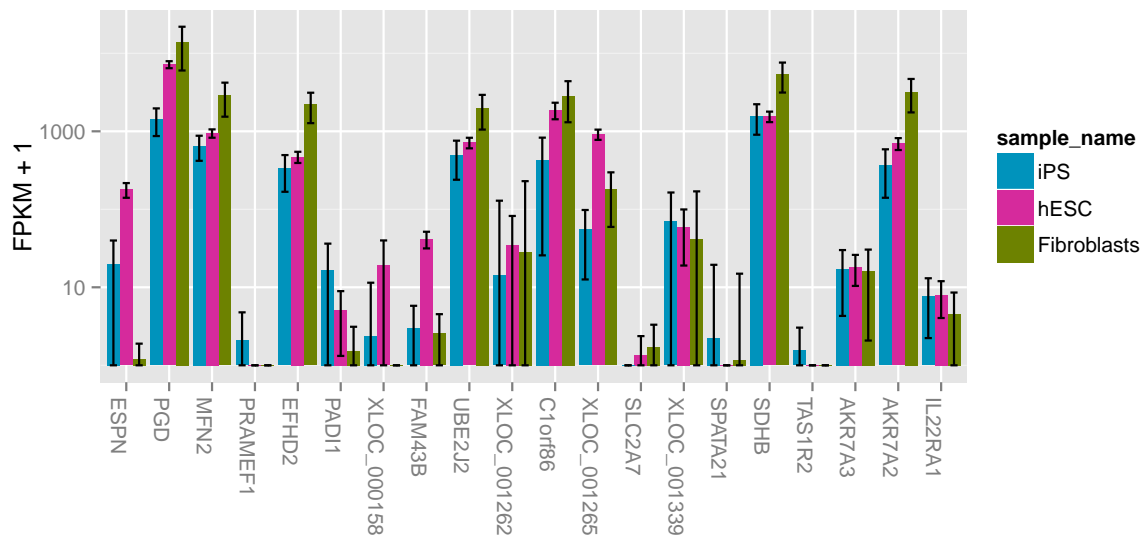
```
> b<-expressionBarplot(myGenes)
> b
```

The *csScatter()* method can be used to produce scatter plot comparisons between any two conditions.

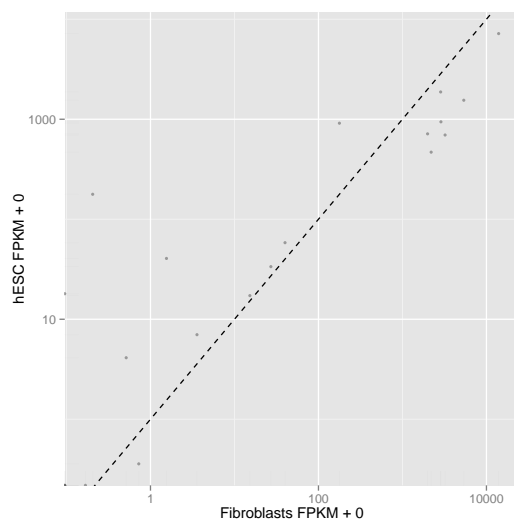
```
> s<-csScatter(myGenes,"Fibroblasts","hESC",smooth=T)
> s
```

The volcano plot is a useful visualization to compare fold change between any two conditions and significance (-log P-values).

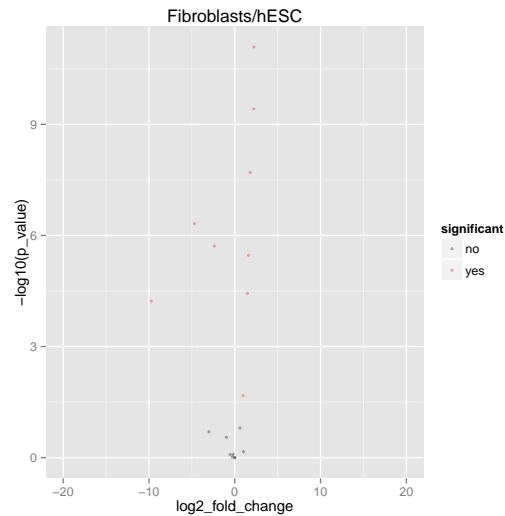
```
> v<-csVolcano(myGenes,"Fibroblasts","hESC")
> v
```



(a) A (somewhat crowded) barplot for all genes in a CuffGeneSet object.



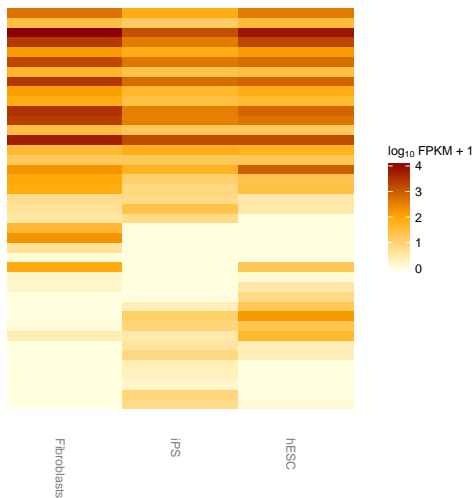
(a) Scatterplot showing relationship between two conditions for genes in a CuffGeneSet.



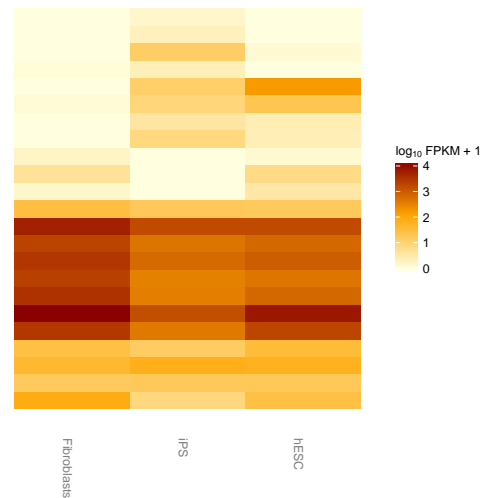
(a) Fold-change vs significance for genes in a *CuffGeneSet* object.

Similar plots can be made for all sub-level features of a *CuffGeneSet* class by specifying which slot you would like to plot (eg. *isoforms(myGenes)*, *TSS(myGenes)*, *CDS(myGenes)*).

```
> ih<-csHeatmap(isoforms(myGenes),cluster='both',labRow=F)
> ih
> th<-csHeatmap(TSS(myGenes),cluster='both',labRow=F)
> th
```



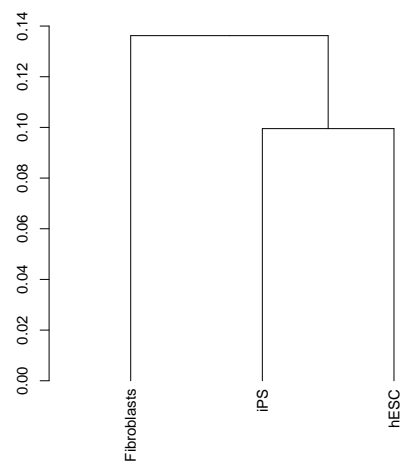
(a) A heatmap of isoform-level FPKM values for all genes in a *CuffGeneSet* object.



(b) A heatmap of TSS-level FPKM values for all genes in a *CuffGeneSet* object.

Dendrograms can provide insight into the relationships between conditions for various genesets (e.g. significant genes used to draw relationships between conditions). As of v1.1.3 the method *csDendro()* can be used to plot a dendrogram based on Jensen-Shannon distances between conditions for a given *CuffFeatureSet* or *CuffGeneSet*.

```
> den<-csDendro(myGenes)
```



(a) A dendrogram of the relationship between conditions based on the expression of genes in a CuffGeneSet.

8 Individual Genes

An individual CuffGene object can be created by using the `getGene()` function for a given 'gene_id' or 'gene_short_name'. As of cummeRbund $\geq v2.0$ you can also use `isoform_id`, `tss_group_id`, or `cds_id` values to retrieve the corresponding parent gene object.

```
> myGeneId<-"PINK1"
> myGene<-getGene(cuff,myGeneId)
> myGene

CuffGene instance for gene XLOC_000172
Short name:      PINK1
Slots:
  annotation
  features
  fpkm
  repFpkm
  diff
  count
  isoforms      CuffFeature instance of size 2
  TSS           CuffFeature instance of size 2
  CDS           CuffFeature instance of size 2

> head(fpkm(myGene))

      gene_id sample_name      fpkm  conf_hi  conf_lo
1 XLOC_000172 Fibroblasts 3045.930 4529.840 1562.020
2 XLOC_000172          hESC  441.939  523.916  359.961
3 XLOC_000172          iPS  640.208  914.562  365.853
quant_status
1          OK
2          OK
3          OK

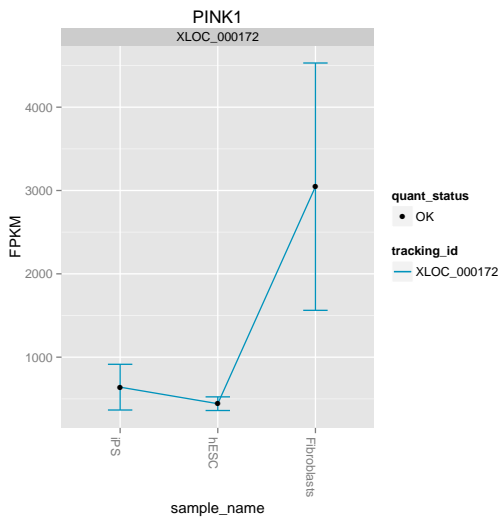
> head(fpkm(isoforms(myGene)))

      isoform_id sample_name      fpkm  conf_hi  conf_lo
1 TCONS_00000480 Fibroblasts 2213.850 3284.980 1142.7100
2 TCONS_00000480          hESC  326.979  388.108  265.8500
3 TCONS_00000480          iPS  640.208  914.562  365.8530
4 TCONS_00000481 Fibroblasts  832.083 1760.820    0.0000
5 TCONS_00000481          hESC  114.960  166.530   63.3891
6 TCONS_00000481          iPS    0.000    0.000    0.0000
quant_status
1          OK
2          OK
3          OK
4          OK
5          OK
6          OK
```

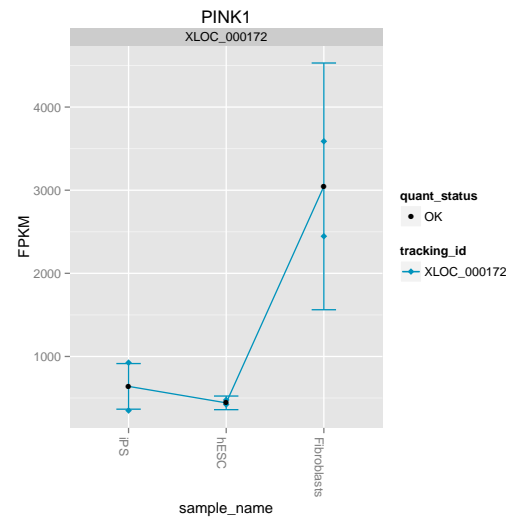
8.1 Gene-level plots

```
> gl<-expressionPlot(myGene)
> gl
> gl.rep<-expressionPlot(myGene,replicates=TRUE)
> gl.rep
> gl.iso.rep<-expressionPlot(isoforms(myGene),replicates=T)
> gl.iso.rep
```

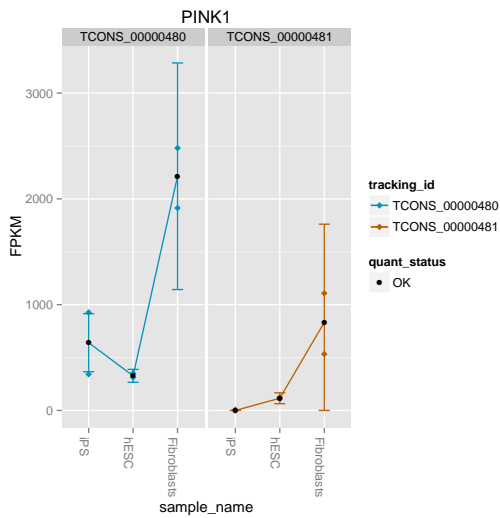
```
> gl.cds.rep<-expressionPlot(CDS(myGene),replicates=T)
> gl.cds.rep
```



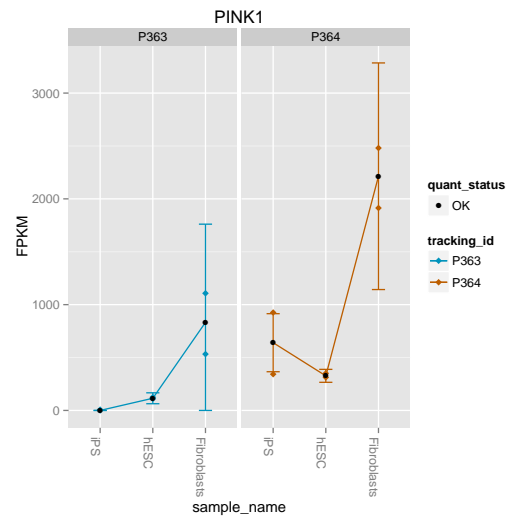
(a) Expression plot of a single gene.



(b) Expression plot of a single gene with replicate FPKMs exposed.



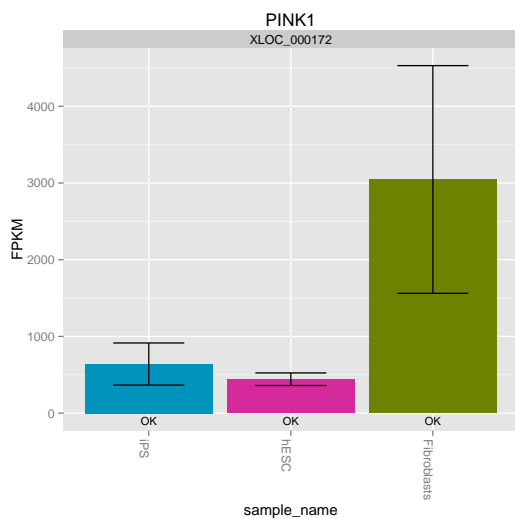
(c) Expression plot of all isoforms of a single gene with replicate FPKMs exposed.



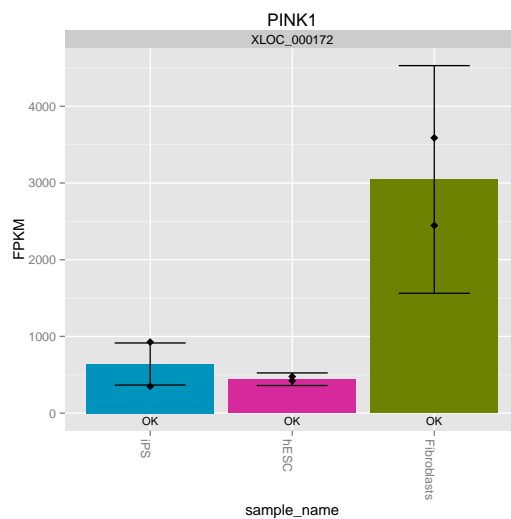
(d) Expression plot of all CDS for a single gene with replicate FPKMs exposed.

```
> gb<-expressionBarplot(myGene)
> gb
> gb.rep<-expressionBarplot(myGene,replicates=T)
> gb.rep

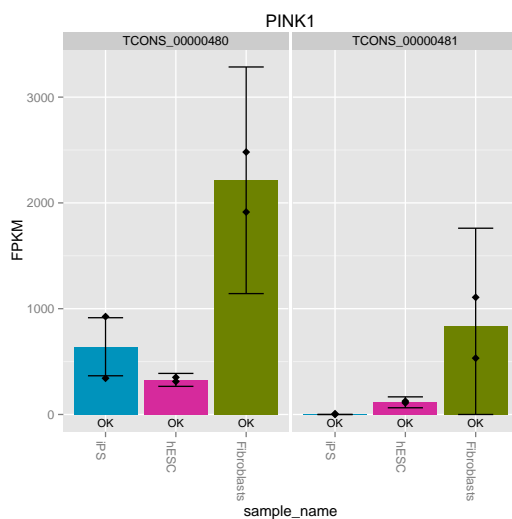
> igb<-expressionBarplot(isoforms(myGene),replicates=T)
> igb
```



(a) Expression Barplot of a single gene.



(b) Expression Barplot of a single gene with replicate FPKMs exposed.



(a) Expression Barplot of all isoforms single gene with replicates exposed.

8.1.1 Gene Feature plots

If you included both the genome build and `gtfFile` in your call to `readCufflinks()` then you will be able to access some of the transcript-structure level features that are now being integrated into `cummeRbund`. For now, these features are extended only to the single gene, *CuffGene* objects.

Feature data are loaded into the `features` table of the `cuffData.db` database. When a *CuffGene* object is created using `getGene()`, all relative features are selected from this table and a `features` slot is added to the resulting object.

```
> head(features(myGene))
```

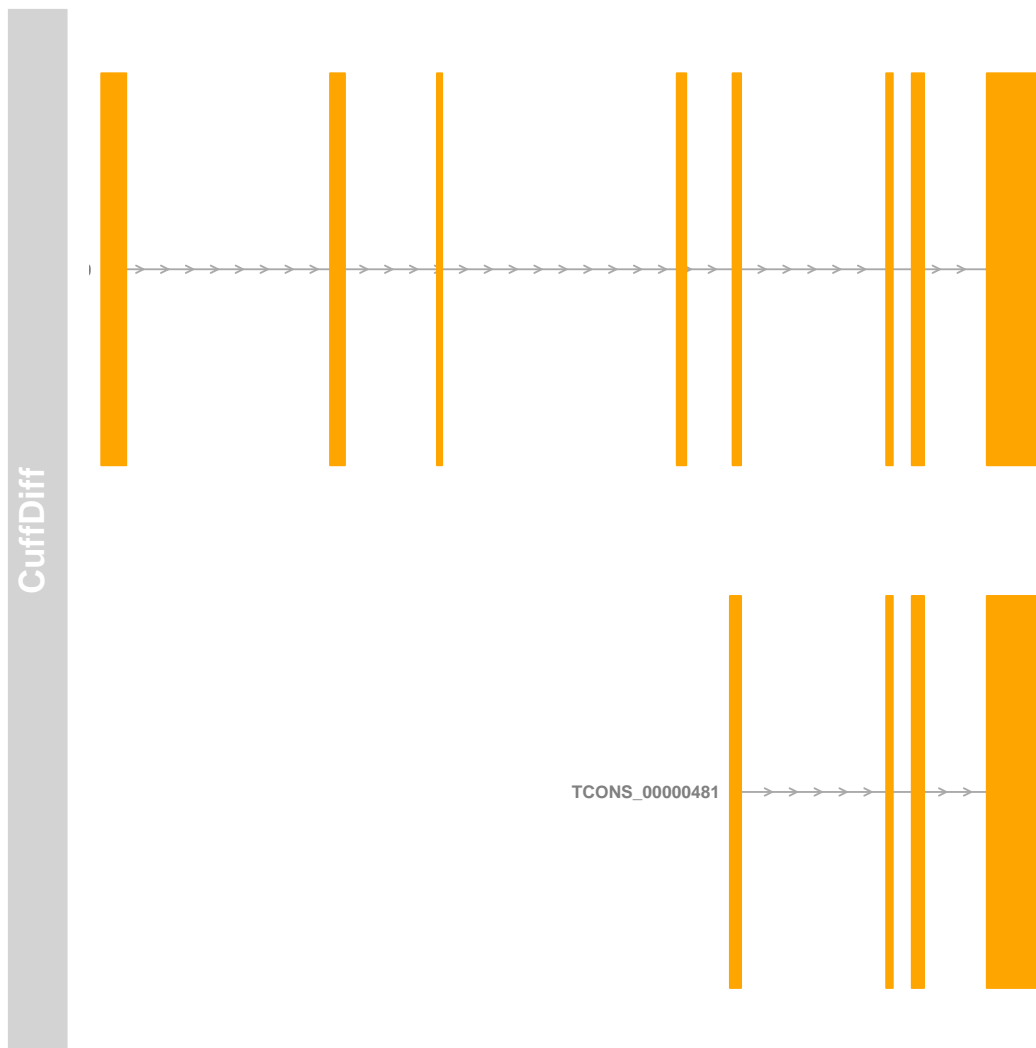
	seqnames	start	end	width	strand	source	type	score
1	chr1	20959948	20960428	481	+	coding	exon	NA
2	chr1	20964335	20964622	288	+	coding	exon	NA
3	chr1	20966385	20966485	101	+	coding	exon	NA
4	chr1	20970983	20971165	183	+	coding	exon	NA
5	chr1	20972053	20972216	164	+	coding	exon	NA
6	chr1	20974998	20975125	128	+	coding	exon	NA

	phase	class_code	exon_number	gene_id	gene_name	nearest_ref
1	NA	=	1	XLOC_000172	PINK1	uc001bdm.2
2	NA	=	2	XLOC_000172	PINK1	uc001bdm.2
3	NA	=	3	XLOC_000172	PINK1	uc001bdm.2
4	NA	=	4	XLOC_000172	PINK1	uc001bdm.2
5	NA	=	5	XLOC_000172	PINK1	uc001bdm.2
6	NA	=	6	XLOC_000172	PINK1	uc001bdm.2

	oId	CDS_id	isoform_id	TSS_group_id
1	uc001bdm.2	P364	TCONS_00000480	TSS264
2	uc001bdm.2	P364	TCONS_00000480	TSS264
3	uc001bdm.2	P364	TCONS_00000480	TSS264
4	uc001bdm.2	P364	TCONS_00000480	TSS264
5	uc001bdm.2	P364	TCONS_00000480	TSS264
6	uc001bdm.2	P364	TCONS_00000480	TSS264

The `Gviz` package can be used to display features in a 'track'-like format. In particular, the *GeneRegionTrack* class creates a mechanism by which we can start to visualize transcript-level structures in their genomic context. `cummeRbund` implements the `makeGeneRegionTrack()` method to quickly create a *GeneRegionTrack* from the gene features.

```
> genetrack<-makeGeneRegionTrack(myGene)
> plotTracks(genetrack)
```



We can then use some of the additional features from the Gviz package to add additional tracks from an external data source.

```
> trackList<-list()
> myStart<-min(features(myGene)$start)
> myEnd<-max(features(myGene)$end)
> myChr<-unique(features(myGene)$seqnames)
> genome<-'hg19'
> ideoTrack <- IdeogramTrack(genome = genome, chromosome = myChr)
> trackList<-c(trackList,ideoTrack)
> axtrack<-GenomeAxisTrack()
> trackList<-c(trackList,axtrack)
> genetrack<-makeGeneRegionTrack(myGene)
> genetrack

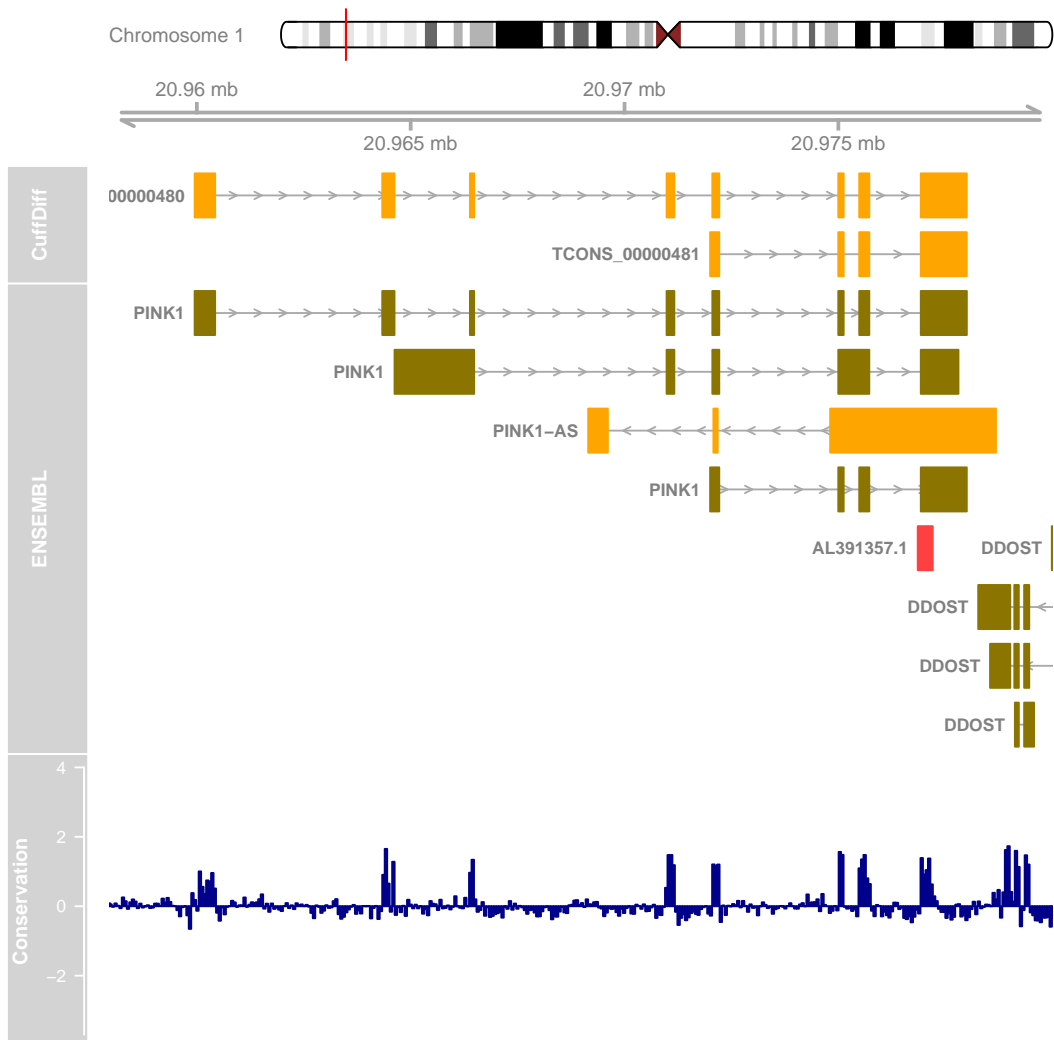
GeneRegionTrack 'CuffDiff'
| genome: hg19
| active chromosome: chr1
| annotation features: 12

> trackList<-c(trackList,genetrack)
> biomTrack<-BiomartGeneRegionTrack(genome=genome,chromosome=as.character(myChr),
+                               start=myStart,end=myEnd,name="ENSEMBL",showId=T)
> trackList<-c(trackList,biomTrack)
```

```

> conservation <- UcscTrack(genome = genome, chromosome = myChr,
+   track = "Conservation", table = "phyloP46wayPlacental",
+   from = myStart-2000, to = myEnd+2000, trackType = "DataTrack",
+   start = "start", end = "end", data = "score",
+   type = "hist", window = "auto", col.histogram = "darkblue",
+   fill.histogram = "darkblue", ylim = c(-3.7, 4),
+   name = "Conservation")
> trackList<-c(trackList,conservation)
> plotTracks(trackList,from=myStart-2000,to=myEnd+2000)
>

```



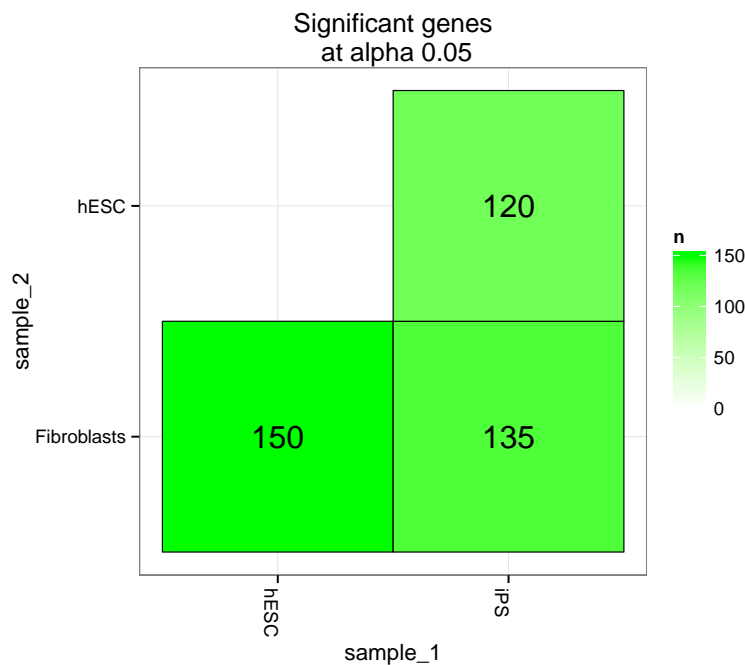
9 Data Exploration

The `cummeRbund` package is more than just a visualization tool as well. We are working to implement several different means of data exploration from gene and condition clustering, finding features with similar expression profiles, as well as incorporating Gene Ontology analysis.

9.1 Overview of significant features

The `sigMatrix()` function can provide you with a “quick-and-dirty” view of the number of significant features of a particular type, and at a given alpha (0.05 by default). For example:

```
> mySigMat<-sigMatrix(cuff,level='genes',alpha=0.05)
>
```



(a) Significant features overview matrix. This plot describes the number of significant genes at a 5%FDR for each pairwise interaction tested.

9.2 Creating gene sets from significantly regulated genes

One of the primary roles of a differential expression analysis is to conduct significance tests on each feature (genes, isoforms, TSS, and CDS) for appropriate pairwise comparisons of conditions. The results of these tests (after multiple testing correction of course) can be used to determine which genes are differentially regulated. `cummeRbund` makes accessing the results of these significance tests simple via `getSig()`. This function takes a `CuffSet` object and will scan at various feature levels ('genes' by default) to produce a *vector* of feature IDs. By default `getSig()` outputs a vector of tracking IDs corresponding to all *genes* that reject the null hypothesis in any condition tested. The default feature type can be changed by adjusting the 'level' argument to `getSig()`. In addition, a alpha value can be provided on which to filter the resulting list (the default is 0.05 to match the default of `cuffdiff`).

```
> mySigGeneIds<-getSig(cuff,alpha=0.05,level='genes')
> head(mySigGeneIds)
```

```
[1] "XLOC_000004" "XLOC_000005" "XLOC_000008" "XLOC_000009"
[5] "XLOC_000011" "XLOC_000013"
```

```
> length(mySigGeneIds)
```

```
[1] 207
```

By default *getSig()* outputs a vector of tracking IDs corresponding to all *genes* that reject the null hypothesis in any condition tested. The default feature type can be changed by adjusting the 'level' argument to *getSig()*. In addition, a alpha value can be provided on which to filter the resulting list (the default is 0.05 to match the default of *cuffdiff*). Significance results for specific pairwise comparisons can be retrieved as well by specifying the two conditions as 'x' and 'y'. In this case, p-values are adjusted to reduce the impact of multiple-testing correction when only one set of tests is being conducted.

```
> hESC_vs_iPS.sigIsoformIds<-getSig(cuff,x='hESC',y='iPS',alpha=0.05,level='isoforms')
> head(hESC_vs_iPS.sigIsoformIds)
```

```
[1] "TCONS_00000006" "TCONS_00000013" "TCONS_00000015"
[4] "TCONS_00000018" "TCONS_00000034" "TCONS_00000041"
```

```
> length(hESC_vs_iPS.sigIsoformIds)
```

```
[1] 118
```

The values returned for each level of this list can be used as an argument to *getGenes*, to create a *CuffGeneSet* object of significantly regulated genes (or features).

```
> mySigGenes<-getGenes(cuff,mySigGeneIds)
> mySigGenes
```

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
```

```
>
```

Alternatively, you can use the *getSigTable()* method to return a full test-table of 'significant features' x 'pairwise tests' for all comparisons. Only features in which the null hypothesis can be rejected in at least one test are reported.

```
> mySigTable<-getSigTable(cuff,alpha=0.01,level='genes')
> head(mySigTable,20)
```

	hESCvsFibroblasts	iPSvsFibroblasts	iPSvshESC
XLOC_000005	1	1	1
XLOC_000008	0	1	1
XLOC_000009	1	1	1
XLOC_000011	0	1	1
XLOC_000013	0	1	0
XLOC_000014	1	NA	0

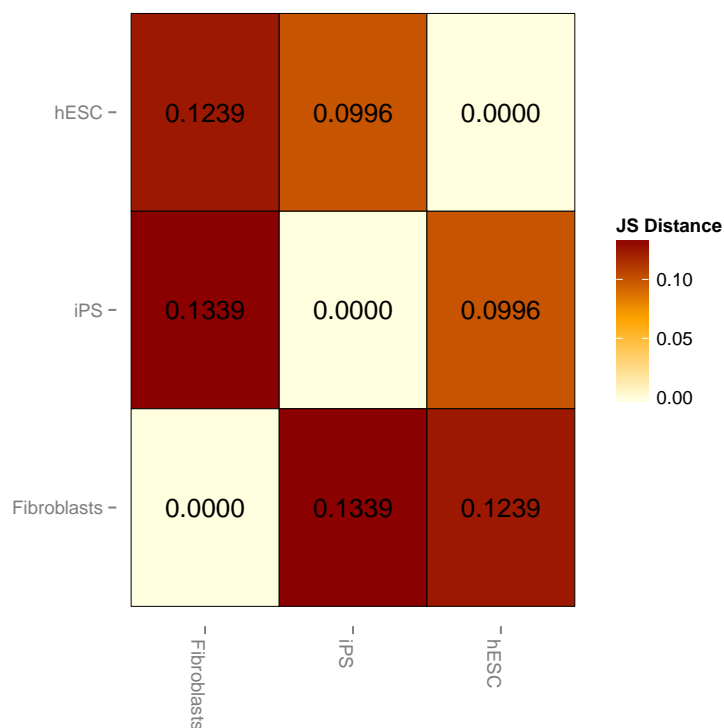
XL0C_000016	0	0	1
XL0C_000017	0	1	0
XL0C_000018	1	1	0
XL0C_000019	0	1	1
XL0C_000025	1	NA	1
XL0C_000026	1	1	0
XL0C_000027	0	1	1
XL0C_000029	1	1	0
XL0C_000032	1	NA	0
XL0C_000034	1	0	1
XL0C_000036	0	1	1
XL0C_000044	1	NA	1
XL0C_000047	1	1	1
XL0C_000048	1	1	0

9.3 Exploring the relationships between conditions

9.3.1 Distance matrix

Similarities between conditions and/or replicates can provide useful insight into the relationship between various groupings of conditions and can aid in identifying outlier replicates that do not behave as expected. `cummeRbund` provides the `csDistHeat()` method to visualize the pairwise similarities between conditions:

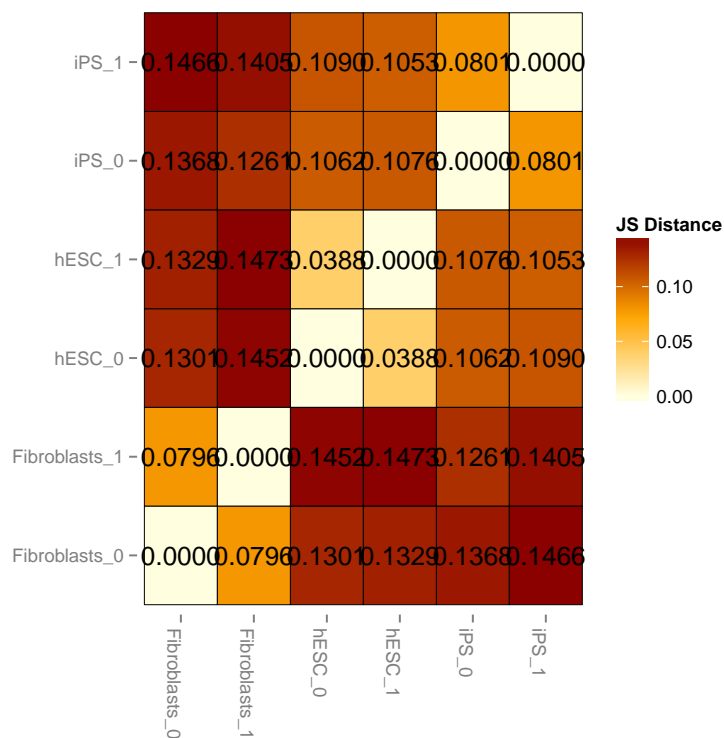
```
> myDistHeat<-csDistHeat(genes(cuff))
>
```



(a) JS distance heatmap between conditions across all gene features.

Again with the `replicates` argument, distances between individual replicates can be presented.

```
> myRepDistHeat<-csDistHeat(genes(cuff),replicates=T)
>
```



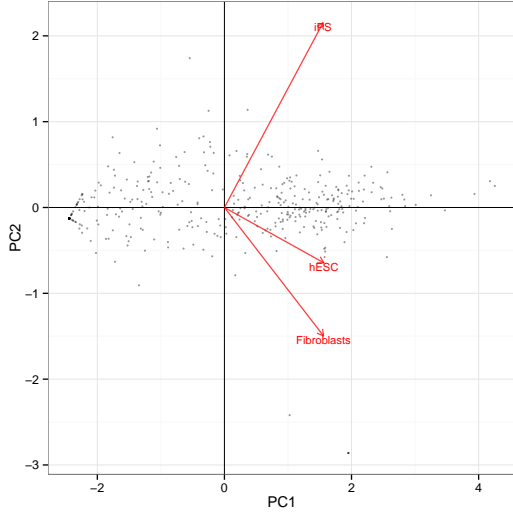
(a) JS distance heatmap between replicate samples across all gene features.

This method can be used to explore similarities between conditions for all features, or just those features contained within a *CuffGeneSet* class. Additionally, the *samples.not.genes=F* argument will display distances between individual genes or features across conditions.

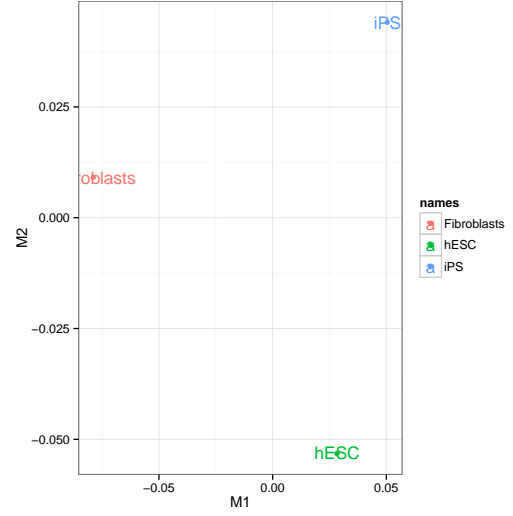
9.3.2 Dimensionality reduction

Dimensionality reduction is an informative approach for clustering and exploring the relationships between conditions. It can be useful for feature selection as well as identifying the sources of variability within your data. To this end, we have applied two different dimensionality reduction strategies in *cummeRbund*: principal component analysis (PCA) and multi-dimensional scaling (MDS). We provide the two wrapper methods, *PCApplot* and *MDSplot*

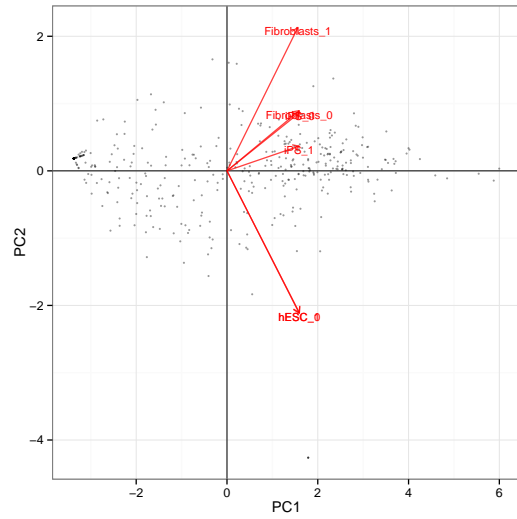
```
> genes.PCA<-PCApplot(genes(cuff),"PC1","PC2")
> genes.MDS<-MDSplot(genes(cuff))
> genes.PCA.rep<-PCApplot(genes(cuff),"PC1","PC2",replicates=T)
> genes.MDS.rep<-MDSplot(genes(cuff),replicates=T)
```



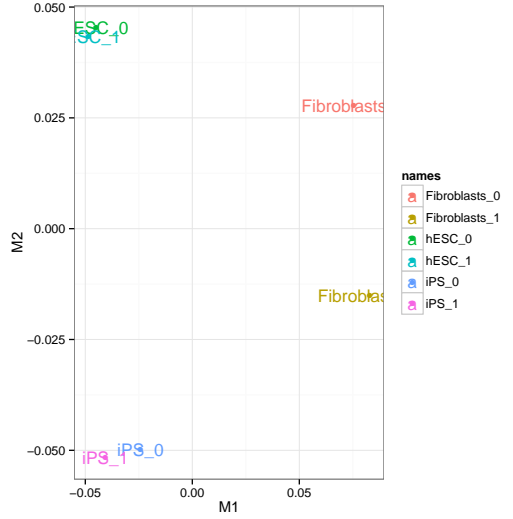
(a) PCA plot for gene-level features



(b) MDS plot for gene-level features



(c) Individual replicate level PCA plot for gene-level features



(d) Individual replicate level MDS plot for gene-level features

9.4 Partitioning

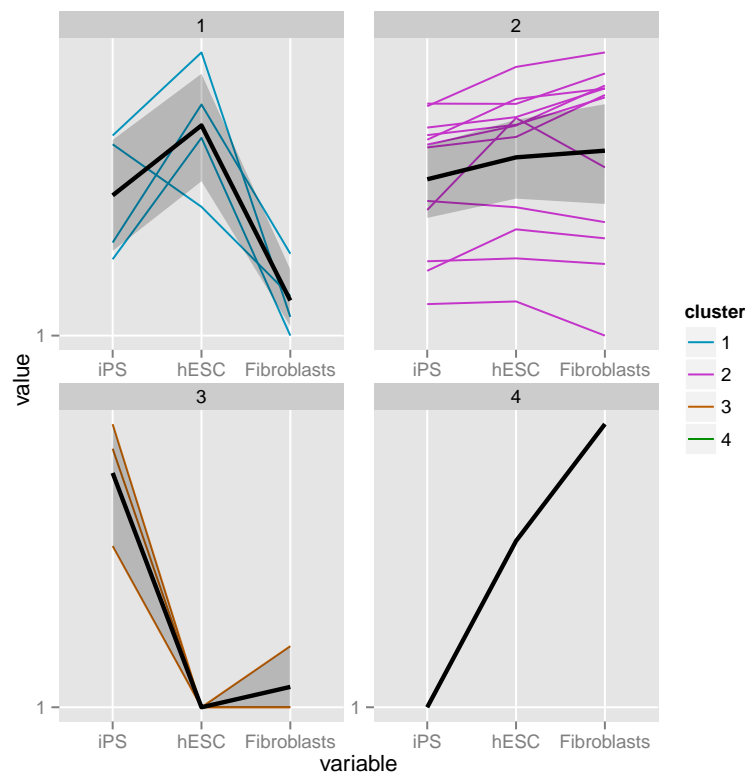
K-means clustering is a useful tool that can be helpful in identifying clusters of genes with similar expression profiles. In fact, these profiles are learned from the data during the clustering. *csCluster()* uses the *pam()* method from the *clustering* package to perform the partitioning around medoids. In this case however, the distance metric used by default is the Jensen-Shannon distance instead of the default Euclidean distance. Prior to performing this particular partitioning, the user must choose the number of clusters (K) into which the expression profiles should be divided.

```
> ic<-csCluster(myGenes,k=4)
> head(ic$cluster)

XLOC_000069 XLOC_000089 XLOC_000105 XLOC_000115 XLOC_000132
           1           2           2           3           2
XLOC_000151
           1

> icp<-csClusterPlot(ic)
> icp
```

As of v1.1.1 of *cummeRbund*, the output of *csCluster* is a modified *pam* object. This replaces the default plotting behavior of the original *csCluster* plot to allow for further analysis of the clustering results. The original plotting behavior has been recapitulated in the *csClusterPlot()* method.



(a) PAM clustering with JS distance for a CuffGeneSet.

9.5 Specificity

In some cases, a researcher may be interested in identifying features that are 'condition-specific'. Or, more likely, producing an ordered list of genes based on their specificity for a given condition. We define a specificity score (S) as the following:

$$S_{g,i} = 1 - JSD(p_g, \hat{q}_i) \quad (1)$$

Where JSD is the Jensen-Shannon distance, p_g is the expression profile of a given gene g expressed as a density (probability) of $\log_{10}FPKM + 1$, and \hat{q}_i is the unit vector of 'perfect expression' in a particular condition i .

We have created a method, `csSpecificity()` that outputs a matrix (with identical shape to that produced by `fpkmMatrix()`) of specificity scores (S) across all conditions for all features in a `CuffFeatureSet` or `CuffGeneSet`.

```
> myGenes.spec<-csSpecificity(myGenes)
> head(myGenes.spec)
```

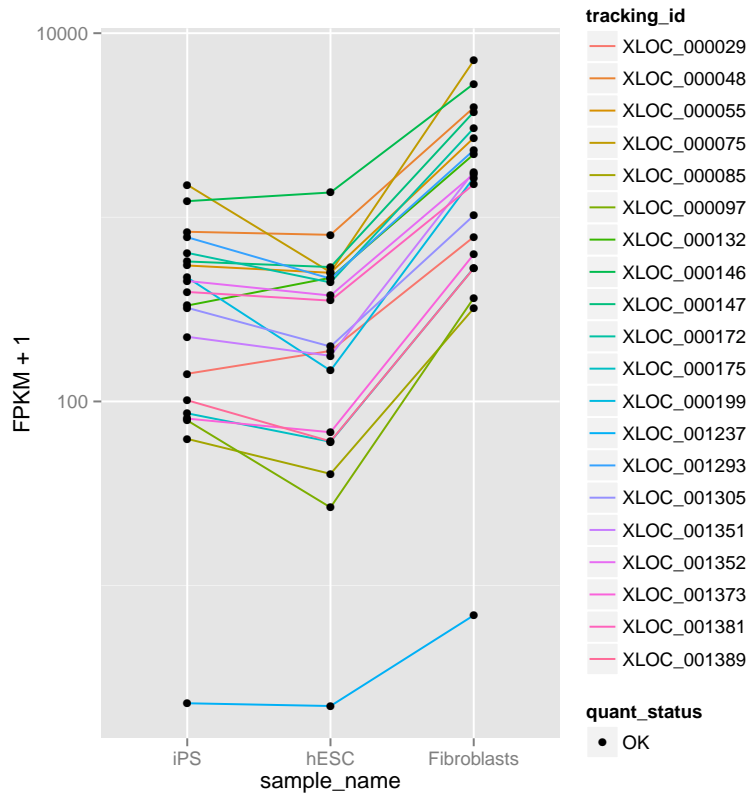
	iPS_spec	hESC_spec	Fibroblasts_spec
XL0C_000069	0.6381500	0.7411063	0.4730055
XL0C_000089	0.6073556	0.6332403	0.6435982
XL0C_000105	0.6163066	0.6235261	0.6445646
XL0C_000115	1.0000000	0.4513380	0.4513380
XL0C_000132	0.6126800	0.6199645	0.6514962
XL0C_000151	0.7244614	0.6295328	0.5141304

$S = 1.0$ if the feature is expressed exclusively in that condition. The `findSimilar()` method outlined below is another method that can be used to identify genes based on specificity but has the added feature that you can determine similarity to a more complex q expression profile.

9.6 Finding similar genes

Another common question in large-scale gene expression analyses is 'How can I find genes with similar expression profiles to gene x ?'. We have implemented a method, *findSimilar* to allow you to identify a fixed number of the most similar genes to a given gene of interest. For example, if you wanted to find the 20 genes most similar to "PINK1", you could do the following:

```
> mySimilar<-findSimilar(cuff,"PINK1",n=20)
> mySimilar.expression<-expressionPlot(mySimilar,logMode=T,showErrorbars=F)
```



(a) Top 20 most similar genes to 'PINK1'.

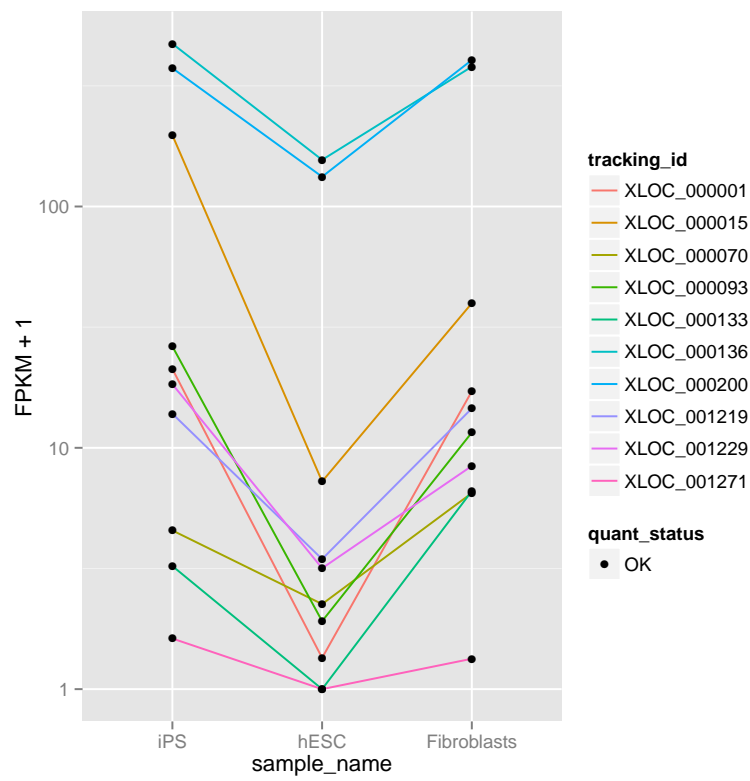
By default, *findSimilar* will return a *CuffGeneSet* of similar genes matching your criteria. Recently a few additional features have been added as well to enhance this type of exploration:

- If 'returnGeneSet' is set to FALSE, then *findSimilar* returns a data.frame of distance-ranked similar genes with distances. This is useful if you would like to see a rank-ordered list of similar genes.
- The 'distThresh' argument allows you to pass a value [between 0-1] to be used as a distance threshold instead of an arbitrary 'n' number of genes. setting *distThresh*=1.0 will return all genes ranked by their distance to your gene of interest.

You are also able to provide your own expression profile in lieu of a 'gene_id'. The vector provided must match the order and length of *samples()*.

```
> myProfile<-c(500,0,400)
> mySimilar2<-findSimilar(cuff,myProfile,n=10)
> mySimilar2.expression<-expressionPlot(mySimilar2,logMode=T,showErrorbars=F)
```

findSimilar() also uses the Jensen-Shannon distance between the probability distributions of each gene across conditions to determine the similarity. We have found this to be a more robust way to determine distance between genes using the high dynamic range of FPKM data. Future versions may allow for other dissimilarity measures to be used instead.



(a) Top 10 genes most similar genes to a provided expression profile.

10 Miscellaneous

- In appropriate plots, using the argument `replicates=T` will allow you to visualize replicate-level FPKM values either in lieu of or in addition to condition-level FPKMs.
- As of v1.1.3 we attempt to provide new visual cues in most plots that will indicate the quantification status for a particular feature in each given condition. We have enabled this feature by default for most plots to suggest a measure of reliability for each feature in a particular condition. In most cases, this feature can be disabled by setting `'showStatus=FALSE'`.
- `CummeRbund` will now work with the hidden `'-no-diff'` argument for `cuffdiff`. This will quantify features against .bam files but not do differential testing. This is useful when you want to aggregate very large numbers of conditions, and cannot afford the time or space for the differential test results. (Not recommended unless you have a SPECIFIC need for this).
- All plotting functions return `ggplot` objects and the resulting objects can be manipulated/faceted/alted using standard `ggplot2` methods.
- There are occasional DB connectivity issues that arise. Not entirely sure why yet. If necessary, just `readCufflinks` again and this should solve connectivity issues with a new `RSQLite` connection object. If connectivity continues to be a problem, try `cuff<-readCufflinks(rebuild=T)`
- I am still working on fully documenting each of the methods. There are a good number of arguments that exist, but might be hard to find without looking at the reference manual.

11 Known Issues

- Large cuffdiff runs (e.g. ≥ 10 conditions) produce very large results files. These will take some time to parse and populate the cuffData.db sqlite database. While this is only a one time cost, the process can take a while. We are working on making the table writes and indexing significantly faster.
- Cuffdiff does not 'require' that gene_ids, isoform_ids, TSS_group_ids, or CDS_ids be unique in your reference gtf file. In fact, duplicate IDs will be aggregated by cummeRbund in the indexing phase and will produce undesirable effects. Please ensure that all of your IDs are unique prior to running cuffdiff (see cuffmerge for help) to avoid this issue.

12 Session info

```
> sessionInfo()

R version 2.15.1 (2012-06-22)
Platform: x86_64-unknown-linux-gnu (64-bit)

locale:
 [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
 [3] LC_TIME=en_US.UTF-8      LC_COLLATE=C
 [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
 [7] LC_PAPER=C               LC_NAME=C
 [9] LC_ADDRESS=C            LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C

attached base packages:
[1] splines    grid      stats      graphics  grDevices  utils
[7] datasets  methods   base

other attached packages:
 [1] Hmisc_3.9-3      survival_2.36-14
 [3] cluster_1.14.2   cummeRbund_2.0.0
 [5] Gviz_1.2.0       rtracklayer_1.18.0
 [7] GenomicRanges_1.10.0 IRanges_1.16.2
 [9] fastcluster_1.1.7 reshape2_1.2.1
[11] ggplot2_0.9.2.1  RSQLite_0.11.2
[13] DBI_0.2-5        BiocGenerics_0.4.0

loaded via a namespace (and not attached):
 [1] AnnotationDbi_1.20.0
 [2] BSgenome_1.26.0
 [3] BSgenome.Hsapiens.UCSC.hg19_1.3.19
 [4] Biobase_2.18.0
 [5] Biostrings_2.26.0
 [6] GenomicFeatures_1.10.0
 [7] MASS_7.3-21
 [8] RColorBrewer_1.0-5
 [9] RCurl_1.95-0.1.2
[10] Rsamtools_1.10.1
[11] XML_3.95-0.1
[12] biomaRt_2.14.0
[13] biovizBase_1.6.0
[14] bitops_1.0-4.1
[15] colorspace_1.1-1
[16] dichromat_1.2-4
[17] digest_0.5.2
[18] gtable_0.1.1
[19] labeling_0.1
[20] lattice_0.20-10
[21] memoise_0.1
[22] munsell_0.4
[23] parallel_2.15.1
[24] plyr_1.7.1
[25] proto_0.3-9.2
[26] scales_0.2.2
[27] stats4_2.15.1
[28] stringr_0.6.1
[29] tools_2.15.1
```

[30] zlibbioc_1.4.0