Package 'ExpGenetic'

January 20, 2025

Type Package

Title Non-Additive Expression Analysis of Hybrid Offspring

Version 0.1.0

Description Three functional modules, including genetic features, differential expression analysis and non-additive expression analysis were integrated into the package. And the package is suitable for RNA-seq and small RNA sequencing data. Besides, two methods of non-additive expression analysis were provided. One is the calculation of the additive (a) and dominant (d), the other is the evaluation of expression level dominance by comparing the total expression of the gene in hybrid offspring with the expression level in parents. For non-additive expression analysis of RNA-seq data, it is only applicable to hybrid offspring (including two subgenomes) species for the time being.

License AGPL (>= 3)

Encoding UTF-8

LazyData true

Imports DESeq2 (>= 1.34.0), futile.logger (>= 1.4.3), ggplot2 (>= 3.3.6), ggsci (>= 2.9), plyr (>= 1.8.7), VennDiagram (>= 1.7.3)

Depends R (>= 2.10)

RoxygenNote 7.2.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2022-09-09 07:13:01 UTC

Contents

`basepreplot` *Plot the base frequency distribution diagram for small RNA (sRNA)*

Description

Plot the base frequency distribution diagram for small RNA (sRNA)

Usage

```
basepreplot(sRNAdata, width = 0.6, font_size = 10, title_size = 12)
```

Arguments

`sRNAdata`	A data frame. Base frequency distribution of sRNAs.
`width`	A numeric. Bar width, and default is 0.6.
`font_size`	A numeric. Size of axis ticks and legend item labels, and default is 10.
`title_size`	A numeric. Size of axis titles and legend titles, and default is 12.

Value

Base frequency distribution plot of sRNAs.

Examples

```
#F1
F1_miRNA <- F1_miRNA_count[,1]
F1_bf <- mirnapredata(sRNAseq = F1_miRNA)
basepreplot(sRNAdata = F1_bf)
```

`Countfilter` *Filtering out lowly expressed genes based on count*

Description

Regarding the criteria for filtering out lowly expressed genes, no less than the count threshold in all replicates.

Usage

```
Countfilter(
  P1_count,
  P2_count,
  F1_count,
  type,
  homoeologs,
  count_threshold = 5
)
```

Arguments

`P1_count`	A data frame. The count table of genes in P1 species. For the count table, the first column is the gene identifier, and other columns are read counts of the gene in each biological replicate.
`P2_count`	A data frame. The count table of genes in P2 species.
`F1_count`	A data frame. The count table of genes in F1 species.
`type`	A character. "sRNA" or "mRNA".
`homoeologs`	A data frame. Orthologous relationships of genes within the parental species and their progeny. Only required when the 'type' is 'mRNA'.
`count_threshold`	A numeric. Threshold for filtering out the lowly expressed genes. The default is 5 (the count values in all replicates).

Details

The 'homoeologs' table contains the orthologs pairs. In detail, the first column is the group name (unique) of homoeologs among three species (Parents: P1; P2, Progeny: F1), the second column is the Gene ID of P1, the third column is the Gene ID of P2. And the fourth column and fifth columns are the identifier of F1 orthologs derived from P1 and P2 ancestors, respectively (e.g. "Homoeolog1 BraA01t00004Z BolC01g000040.2J BnA01g0000030.1 BnC01g0424620.1").

Value

A data frame.

Examples

```
Count5result <- Countfilter(P1_count = P1_miRNA_count,
                            P2_count = P2_miRNA_count,
                            F1_count = F1_miRNA_count,
                            type = "sRNA", count_threshold = 5)
```

F1_miRNA_count *Count table of miRNAs in F1 (F1: the polyploid progeny).*

Description

Count table of miRNAs in F1 species. The "F1" represents the polyploid progeny.

Examples

```
head(F1_miRNA_count)
#                 sequence     BF1.1    BF1.2    BF1.3
#1  TTTGGATTGAAGGGAGCTCTA     20233     6388    16732
#2  TTTCCAAATGTAGACAAAGCA     19909     5157    16076
#3    TCCCAAATGTAGACAAAGC        82       33      103
#4 CTTTGTCTATCGTTTGGAAAAG      2367     1040     3203
#5  TTGGACTGAAGGGAGCTCCTT        34        9       21
#6  TCGGACCAGGCTTCATTCCCC      3281      607     1289
```

F1_miRNA_rpm *RPM table of miRNAs in F1 (F1: the polyploid progeny).*

Description

RPM table of miRNAs in F1 species. The "F1" represents the polyploid progeny.

Examples

```
head(F1_miRNA_rpm)
#                 sequence     BF1.1    BF1.2     BF1.3
#1  TTTGGATTGAAGGGAGCTCTA   1512.16  1086.35   2032.97
#2  TTTCCAAATGTAGACAAAGCA   1487.94   877.01   1953.27
#3    TCCCAAATGTAGACAAAGC      6.13     5.61     12.51
#4 CTTTGTCTATCGTTTGGAAAAG    176.90   176.86    389.17
#5  TTGGACTGAAGGGAGCTCCTT      2.54     1.53      2.55
#6  TCGGACCAGGCTTCATTCCCC    245.21   103.23    156.62
```

F1_sRNA_seq *All sRNA sequences in F1 (F1: the polyploid progeny).*

Description

All sRNA sequences in F1 (F1: the polyploid progeny).

Get12Bins *Non-additive expression analysis*

Description

Rapp et al. proposed the classification of 12 expression patterns in allopolyploids, including additivity (I, XII), ELD (II, XI, IV, IX), transgressive down-regulation (III, VII, X) and transgressive up-regulation (V, VI, VIII).

Usage

```
Get12Bins(
  P1_count,
  P2_count,
  F1_count,
  type,
  homoeologs,
  count_threshold = 5,
  Pvalue = 0.05,
  log2FC = 1
)
```

Arguments

P1_count	A data frame. The count table of genes in P1 species. For the count table, the first column is the gene identifier, and other columns are the corresponding expression levels of the genes in each biological replicate.
P2_count	A data frame. The count table of genes in P2 species.
F1_count	A data frame. The count table of genes in F1 species.
type	A character. "sRNA" or "mRNA".
homoeologs	A data frame. Orthologous relationships of genes in the parental species and their progeny. Only required when the 'type' is 'mRNA'.
count_threshold	A numeric. Threshold for filtering out the lowly expressed genes. The default is 5 (the count values in all replicates).
Pvalue	A numeric. The P value of differential expression analysis using DESeq2. Default is 0.05.
log2FC	A numeric. The log2-transformed expression fold of differential expression analysis using DESeq2. Default is 1.

Details

pv11: P value of differential expression analysis using DESeq2. Parental P1 was used as the control group and F1 was used as the treatment group. pv12: P value of differential expression analysis using DESeq2. Parental P2 was used as the control group and F1 was used as the treatment group. pv21: P value of differential expression analysis using DESeq2. Parental P1 was used as the control group and P2 was used as the treatment group. Besides, "fc" represents the log2FoldChange of differential expression analysis.

Value

A data frame. Classification results of non-additive analysis based on the ELD method.

References

Rapp RA, Udall JA, Wendel JF. Genomic expression dominance in allopolyploids. BMC Biol. 2009 May 1;7:18.

Examples

```
miRNA_12bin <- Get12Bins(P1_count = P1_miRNA_count,
                         P2_count = P2_miRNA_count,
                         F1_count = F1_miRNA_count,type = "sRNA")
```

`GetDAtable` *Non-additive expression analysis*

Description

About the classification method based on |d/a|, the additive (a) and dominant (d) values were calculated by the expression level of each miRNA. Edwards et al. proposed that the "|d/a|" can be used as the criterion to estimate the expression patterns of miRNAs. Specific classification criteria are as follows, |d/a| <= 0.2, additivity; |d/a| > 0.2 and |d/a| <= 0.8, partial dominance; |d/a| > 0.8 and |d/a| <= 1.2, dominance; |d/a| > 1.2, overdominance.

Usage

```
GetDAtable(P1_RPM, P2_RPM, F1_RPM, type, homoeologs, rpm_threshold = 1)
```

Arguments

`P1_RPM`	A data frame. The RPM table of genes in P1 species. For the RPM table, the first column is the gene identifier, and other columns are the RPM values of the genes in each biological replicate.
`P2_RPM`	A data frame. The RPM table of genes in P2 species.
`F1_RPM`	A data frame. The RPM table of genes in F1 species.
`type`	A character. "sRNA" or "mRNA".

homoeologs	A data frame. Orthologous relationships of genes in the parental species and their progeny. Only required when the 'type' is 'mRNA'.
rpm_threshold	A numeric. Threshold for filtering out the lowly expressed genes. The default is 1 (the average RPM of all replicates).

Details

The 'homoeologs' table contains the orthologs pairs. In detail, the first column is the group name (unique) of homoeologs among three species (Parents: P1; P2, Progeny: F1), the second column is the Gene ID of P1, the third column is the Gene ID of P2. And the fourth column and fifth columns are the identifier of F1 orthologs derived from P1 and P2 ancestors, respectively (e.g. "Homoeolog1 BraA01t00004Z BolC01g000040.2J BnA01g0000030.1 BnC01g0424620.1").

Value

A data frame. Classification results of non-additive expression analysis based on |d/a|.

References

Edwards MD, Stuber CW, Wendel JF. Molecular-marker-facilitated investigations of quantitative-trait loci in maize. I. Numbers, genomic distribution and types of gene action. Genetics. 1987 May;116(1):113-25.

Examples

```
DAresult <- GetDAtable(P1_RPM = P1_miRNA_rpm,
                       P2_RPM = P2_miRNA_rpm,
                       F1_RPM = F1_miRNA_rpm,
                       type = "sRNA", rpm_threshold = 1)
```

GetDEdata *Get the results of differential expression analysis.*

Description

Extract the results of differential expression analysis.

Usage

```
GetDEdata(
  P1_count,
  P2_count,
  F1_count,
  output_type,
  type,
  homoeologs,
  count_threshold = 5
)
```

Arguments

P1_count	A data frame. The count table of genes in P1 species. For the count table, the first column is the gene identifier, and other columns are the corresponding expression levels of the genes in each biological replicate.
P2_count	A data frame. The count table of genes in P2 species.
F1_count	A data frame. The count table of genes in F1 species.
output_type	A character. "F1_vs_P1", "F1_vs_P2" or "P2_vs_P1".
type	A character. "sRNA" or "mRNA".
homoeologs	A data frame. Orthologous relationships of genes in the parental species and their progeny. Only required when the 'type' is 'mRNA'.
count_threshold	A numeric. Threshold for filtering out the lowly expressed genes. The default is 5 (the count values in all replicates).

Details

F1_vs_P1: Results of differential expression analysis using DESeq2. Parental P1 was used as the control group and F1 was used as the treatment group. If the log2FoldChange of a gene is positive, it means that the expression level of the gene in F1 is higher than that in P1. F1_vs_P2: Results of differential expression analysis using DESeq2. Parental P2 was used as the control group and F1 was used as the treatment group. P2_vs_P1: Results of differential expression analysis using DESeq2. Parental P1 was used as the control group and P2 was used as the treatment group.

Value

A data frame. Differential expression analysis results.

Examples

```
P2_vs_P1 <- GetDEdata(P1_count = P1_miRNA_count,
                      P2_count = P2_miRNA_count,
                      F1_count = F1_miRNA_count,
                      output_type = "P2_vs_P1", type="sRNA")
```

---

lenplot *Plot the length distribution diagram for small RNAs (sRNAs)*

Description

There are two types of pictures: bar plot (type = "bar") and line plot (type = "line"). For the bar plot, the Y-axis displays the proportion of sRNAs in a certain length, the X-axis represents sRNAs in different length. And for line plot, the Y-axis displays the abundance of sRNAs in a certain length, the X-axis represents sRNAs in different length.

Usage

```
lenplot(sRNAdata, type, width = 0.6, font_size = 10, title_size = 12)
```

Arguments

sRNAdata	A data frame. Frequency distribution of sRNAs in different length.
type	A character. "bar" or "line".
width	A numeric. Bar width, and default is 0.6. if the type is "line", the parameter does not need to be given.
font_size	A numeric. Size of axis ticks and legend item labels, and default is 10.
title_size	A numeric. Size of axis titles and legend titles, and default is 12.

Value

Length distribution plot of sRNAs.

Examples

```
#P1(B.napus)
B.napu_sRNA <- srnapredata(sRNAseq = P1_sRNA_seq,Group = "B.napus(AACC)")
#P2(B.rapa)
B.rapa_sRNA <- srnapredata(sRNAseq = P2_sRNA_seq,Group = "B.rapa(AA)")
#F1(B.napus X B.rapa)
B.nr_sRNA <- srnapredata(sRNAseq = F1_sRNA_seq,Group = "B.napus x B.rapa(AAAACC)")
#intergrate these data for length distribution plot
sRNA_data <- rbind(B.napu_sRNA,B.rapa_sRNA,B.nr_sRNA)
#plot
lenplot(sRNAdata = sRNA_data,type = "line")
lenplot(sRNAdata = sRNA_data,type = "bar")
```

---

mirnapredata *Base frequency distribution of small RNA (sRNA)*

Description

Get the base frequency distribution table.

Usage

```
mirnapredata(sRNAseq)
```

Arguments

sRNAseq	Character. All sRNA sequences in vector format.

Value

A data frame. The output consists of three columns, i.e., base, base frequency and position.

Examples

```
#F1
F1_miRNA <- F1_miRNA_count[,1]
F1_bf <- mirnapredata(sRNAseq = F1_miRNA)
#output result
head(F1_bf)
#  Base Frequency Position
#1    A        32        1
#2    C        27        1
#3    G        31        1
#4    T       115        1
#5    A        27        2
#6    C        50        2
```

`P1_miRNA_count` *Count table of miRNAs in P1 (P1: one of the parents).*

Description

Count table of miRNAs in P1 species. The "P1" represents one of parents.

Examples

```
head(P1_miRNA_count)
#                 sequence   Bnapus.1   Bnapus.2   Bnapus.3
#1  TTTGGATTGAAGGGAGCTCTA      29848      12094      10685
#2  TTAGATTCACGCACAAACTCG        986        571        456
#3  TGAAGCTGCCAGCATGATCTA       3152       1436       1091
#4 CTTTGTCTATCGTTTGGAAAAG       2449       1307       1116
#5  GATCATGTTCGCAGTTTCACC       1364        650        656
#6  TTTCCAAATGTAGACAAAGCA      11658       3914       4123
```

`P1_miRNA_rpm` *RPM table of miRNAs in P1 (P1: one of the parents).*

Description

RPM table of miRNAs in P1 species. The "P1" represents one of parents.

Examples

```
head(P1_miRNA_rpm)
#                 sequence    Brapa.1    Brapa.2    Brapa.3
#1 TTTGGATTGAAGGGAGCTCTA    1641.18    1116.03    1014.37
#2 TGAAGCTGCCAGCATGATCTA     129.33     103.23     103.68
#3 TTTCCAAATGTAGACAAAGCA     905.23     920.57    1180.51
#4 TCGGACCAGGCTTCATCCCCC      24.71      14.38      15.03
#5 AGAATCTTGATGATGCTGCAG      48.64      41.09      41.60
#6 TTGACAGAAGAAAGAGAGCAC      86.96      81.23      67.41
```

P1_sRNA_seq *All sRNA sequences in P1 (P1: one of the parents).*

Description

All sRNA sequences in P1 (P1: one of the parents).

P2_miRNA_count *Count table of miRNAs in P2 (P2: one of the parents).*

Description

Count table of miRNAs in P2 species. The "P2" represents one of parents.

Examples

```
head(P2_miRNA_count)
#                 sequence  Bnapus.1  Bnapus.2  Bnapus.3
#1  TTTGGATTGAAGGGAGCTCTA     29848     12094     10685
#2  TTAGATTCACGCACAAACTCG       986       571       456
#3  TGAAGCTGCCAGCATGATCTA      3152      1436      1091
#4 CTTTGTCTATCGTTTGGAAAAG      2449      1307      1116
#5  GATCATGTTCGCAGTTTCACC      1364       650       656
#6  TTTCCAAATGTAGACAAAGCA     11658      3914      4123
```

P2_miRNA_rpm *RPM table of miRNAs in P2 (P2: one of the parents).*

Description

RPM table of miRNAs in P2 species. The "P2" represents one of parents.

Examples

```
head(P2_miRNA_rpm)
#                 sequence   Bnapus.1   Bnapus.2   Bnapus.3
#1  TTTGGATTGAAGGGAGCTCTA    1804.35    1362.88    1439.22
#2  TTAGATTCACGCACAAACTCG      59.60      64.35      61.42
#3  TGAAGCTGCCAGCATGATCTA     190.54     161.82     146.95
#4 CTTTGTCTATCGTTTGGAAAAG     148.04     147.29     150.32
#5  GATCATGTTCGCAGTTTCACC      82.46      73.25      88.36
#6  TTTCCAAATGTAGACAAAGCA     704.74     441.07     555.35
```

P2_sRNA_seq *All sRNA sequences in P2 (P2: one of the parents).*

Description

All sRNA sequences in P2 (P2: one of the parents).

polyDESeq *Make a Triangle Diagram*

Description

The count matrix of different species as the input data to perform differential expression analysis using DESeq2. And the number of differentially expressed genes between any two species is marked on the triangle diagram.

Usage

```
polyDESeq(
  P1_count,
  P2_count,
  F1_count,
  P1_name,
  P2_name,
  F1_name,
  type,
  homoeologs,
  count_threshold = 5,
  Pvalue = 0.05
)
```

Arguments

P1_count	A data frame. The count table of genes in P1 species. For the count table, the first column is the gene identifier, and other columns are the read counts of the genes in each biological replicate.
P2_count	A data frame. The count table of genes in P2 species.
F1_count	A data frame. The count table of genes in F1 species.
P1_name	A character. Category names of P1 species.
P2_name	A character. Category names of P2 species.
F1_name	A character. Category names of F1 species.
type	A character. "sRNA" or "mRNA".

homoeologs A data frame. Orthologous relationships of genes in the parental species and their progeny. Only required when the 'type' is 'mRNA'.

count_threshold A numeric. Threshold for filtering out the lowly expressed genes. The default is 5 (the count values in all replicates).

Pvalue A numeric. Threshold for significance test in differential expression analysis. Default is 0.05.

Details

The 'homoeologs' table contains the orthologs pairs. In detail, the first column is the group name (unique) of homoeologs among three species (Parents: P1;P2, Progeny: F1), the second column is the Gene ID of P1, the third column is the Gene ID of P2. And the fourth column and fifth columns are the identifier of F1 orthologs derived from P1 and P2 ancestors, respectively (e.g. "Homoeolog1 BraA01t00004Z BolC01g000040.2J BnA01g0000030.1 BnC01g0424620.1").

Value

Triangle Diagram

Examples

```
polyDESeq(P1_count = P1_miRNA_count,
          P2_count = P2_miRNA_count,
          F1_count = F1_miRNA_count,
          P1_name = "B.napus(AACC)",
          P2_name = "B.rapa(AA)",
          F1_name = "B.napus x B.rapa (AAAACC)",type="sRNA")
```

Rpmfilter *Filtering out lowly expressed genes based on RPM*

Description

Regarding the criteria for filtering out lowly expressed genes, no less than the RPM threshold in all replicates.

Usage

```
Rpmfilter(P1_RPM, P2_RPM, F1_RPM, type, homoeologs, rpm_threshold = 1)
```

Arguments

P1_RPM	A data frame. The RPM table of genes in P1 species. For the RPM table, the first column is the gene identifier (e.g. sequences of sRNA, Gene ID), and other columns are the RPM values of the gene in each biological replicate.
P2_RPM	A data frame. The RPM table of genes in P2 species.
F1_RPM	A data frame. The RPM table of genes in F1 species.
type	A character. "sRNA" or "mRNA".
homoeologs	A data frame. Orthologous relationships of genes within the parental species and their progeny. Only required when the 'type' is 'mRNA'.
rpm_threshold	A numeric. Threshold for filtering out the lowly expressed genes. The default is 1 (the average RPM of all replicates).

Details

The 'homoeologs' table contains the orthologs pairs. In detail, the first column is the group name (unique) of homoeologs among three species (Parents: P1; P2, Progeny: F1), the second column is the Gene ID of P1, the third column is the Gene ID of P2. And the fourth column and fifth columns are the identifier of F1 orthologs derived from P1 and P2 ancestors, respectively (e.g. "Homoeolog1 BraA01t00004Z BolC01g000040.2J BnA01g0000030.1 BnC01g0424620.1").

Value

A data frame.

Examples

```
Rpm1result <- Rpmfilter(P1_RPM = P1_miRNA_rpm,
                        P2_RPM = P2_miRNA_rpm,
                        F1_RPM = F1_miRNA_rpm,
                        type = "sRNA", rpm_threshold = 1)
```

---

srnapredata *Length distribution of small RNAs (sRNAs)*

Description

Get the length distribution of sRNAs.

Usage

```
srnapredata(sRNAseq, Group)
```

Arguments

sRNAseq	Character. All sRNA sequences in vector format.
Group	Character. Group name.

Value

A data frame. The output consists of three columns, i.e., length, frequency and group name.

Examples

```
#P1(B.napus)
B.napu_sRNA <- srnapredata(sRNAseq = P1_sRNA_seq, Group = "B.napus(AACC)")
#P2(B.rapa)
B.rapa_sRNA <- srnapredata(sRNAseq = P2_sRNA_seq, Group = "B.rapa(AA)")
#F1(B.napus X B.rapa)
B.nr_sRNA <- srnapredata(sRNAseq = F1_sRNA_seq, Group = "B.napus x B.rapa(AAAACC)")
#intergrate these data for length distribution plot
sRNA_data <- rbind(B.napu_sRNA, B.rapa_sRNA, B.nr_sRNA)
#output result
head(sRNA_data)
#  Length Frequency         Group
#1     15         8 B.napus(AACC)
#2     16         7 B.napus(AACC)
#3     17        13 B.napus(AACC)
#4     18        16 B.napus(AACC)
#5     19        25 B.napus(AACC)
#6     20        33 B.napus(AACC)
```

VennData *Get the details of the Venn Diagram*

Description

Get the information for each region of the venn diagram.

Usage

```
VennData(
  P1_RPM,
  P2_RPM,
  F1_RPM,
  type,
  homoeologs,
  rpm_threshold = 1,
  output_file = "venn_list"
)
```

Arguments

P1_RPM	A data frame. The RPM table of genes in P1 species. For the RPM table, the first column is the gene identifier, and other columns are the RPM values of the genes in each biological replicate.
P2_RPM	A data frame. The RPM table of genes in P2 species.

F1_RPM	A data frame. The RPM table of genes in P2 species.
type	Character. "sRNA" or "mRNA".
homoeologs	A data frame. Orthologous relationships of genes in the parental species and their progeny. Only required when the 'type' is 'mRNA'.
rpm_threshold	A numeric. Threshold for filtering out the lowly expressed genes. The default is 1 (the average RPM of all replicates).
output_file	"venn_list", "P1_specific", "P2_specific", "F1_specific", or "all_common".

Details

The 'homoeologs' table contains the orthologs pairs. In detail, the first column is the group name (unique) of homoeologs among three species (Parents: P1; P2, Progeny: F1), the second column is the Gene ID of P1, the third column is the Gene ID of P2. And the fourth column and fifth columns are the identifier of F1 orthologs derived from P1 and P2 ancestors, respectively (e.g. "Homoeolog1 BraA01t00004Z BolC01g000040.2J BnA01g0000030.1 BnC01g0424620.1").

Value

A data frame.

Examples

```
#output_file = "venn_list"
venn_list <- VennData(P1_RPM = P1_miRNA_rpm,
                      P2_RPM = P2_miRNA_rpm,
                      F1_RPM = F1_miRNA_rpm,
                      type="sRNA",rpm_threshold = 1,
                      output_file = "venn_list")
##output_file = "P1_specific"
P1_specific <- VennData(P1_RPM = P1_miRNA_rpm,
                        P2_RPM = P2_miRNA_rpm,
                        F1_RPM = F1_miRNA_rpm,
                        type="sRNA",rpm_threshold = 1,
                        output_file = "P1_specific")
##output_file = "P2_specific"
P2_specific <- VennData(P1_RPM = P1_miRNA_rpm,
                        P2_RPM = P2_miRNA_rpm,
                        F1_RPM = F1_miRNA_rpm,
                        type="sRNA",rpm_threshold = 1,
                        output_file = "P2_specific")
##output_file = "F1_specific"
F1_specific <- VennData(P1_RPM = P1_miRNA_rpm,
                        P2_RPM = P2_miRNA_rpm,
                        F1_RPM = F1_miRNA_rpm,
                        type="sRNA",rpm_threshold = 1,
                        output_file = "F1_specific")
##output_file = "all_common"
all_common <- VennData(P1_RPM = P1_miRNA_rpm,
                       P2_RPM = P2_miRNA_rpm,
                       F1_RPM = F1_miRNA_rpm,
```

```
type="sRNA",rpm_threshold = 1,
output_file = "all_common")
```

VennPlot *Make a three-set Venn Diagram*

Description

This function creates a Venn Diagram to display the overlap of expressed genes between three sets (parents and progeny).

Usage

```
VennPlot(
  P1_RPM,
  P2_RPM,
  F1_RPM,
  P1_name,
  P2_name,
  F1_name,
  type,
  homoeologs,
  rpm_threshold = 1
)
```

Arguments

P1_RPM	A data frame. The RPM table of genes in P1 species. For the RPM table, the first column is the gene identifier, and other columns are the RPM values of the genes in each biological replicate.
P2_RPM	A data frame. The RPM table of genes in P2 species.
F1_RPM	A data frame. The RPM table of genes in F1 species.
P1_name	Character. Category names of P1 species.
P2_name	Character. Category names of P2 species.
F1_name	Character. Category names of F1 species.
type	Character. "sRNA" or "mRNA".
homoeologs	A data frame. Orthologous relationships of genes in the parental species and their progeny. Only required when the 'type' is 'mRNA'.
rpm_threshold	A numeric. Threshold for filtering out the lowly expressed genes. The default is 1 (the average RPM of all replicates).

Details

The 'homoeologs' table contains the orthologs pairs. In detail, the first column is the group name (unique) of homoeologs among three species (Parents: P1; P2, Progeny: F1), the second column is the Gene ID of P1, the third column is the Gene ID of P2. And the fourth column and fifth columns are the identifier of F1 orthologs derived from P1 and P2 ancestors, respectively (e.g. "Homoeolog1 BraA01t00004Z BolC01g000040.2J BnA01g0000030.1 BnC01g0424620.1").

Value

Venn diagram.

Examples

```
#miRNA
VennPlot(P1_RPM = P1_miRNA_rpm,
         P2_RPM = P2_miRNA_rpm,
         F1_RPM = F1_miRNA_rpm,
         P1_name = "B.napus(AACC)",
         P2_name = "B.rapa(AA)",
         F1_name = "B.napus x B.rapa(AAAACC)",type="sRNA")
```

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