Package: RareComb (via r-universe)

September 15, 2024

Title Combinatorial and Statistical Analyses of Rare Events

Version 1.1

Description A custom implementation of the apriori algorithm and binomial tests to identify combinations of features (genes, variants etc) significantly enriched for simultaneous mutations/events from sparse Boolean input, see Vijay Kumar Pounraja, Santhosh Girirajan (2021). Version 1.1 includes a minor adjustment to the number of combinations to be considered for multiple testing correction. This updated version is more conservative in its approach and hence more selective. <doi:10.1101/2021.10.01.462832>.

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Encoding UTF-8

LazyData true

Depends R (>= 2.10)

Imports magrittr, arules, dplyr, methods, pwr, stringr, tidyr, reshape2, sqldf

RoxygenNote 7.1.1

NeedsCompilation no

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Contents

`analyze_in_out_simultaneity` *Analyze relationships between rare events among multiple input and output variables*

Description

This function takes a Boolean dataframe as input and analyzes the relationship between input and output variables for the combinations that that include at least a single output variable andmeet all the input criteria specified by the user.

Usage

```
analyze_in_out_simultaneity(boolean_input_mult_df, combo_length, min_output_count,
                        max_output_count, min_indv_threshold, max_freq_threshold,
                              input_format, output_format, pval_filter_threshold,
                              adj_pval_type)
```

Arguments

`boolean_input_mult_df`	An input Boolean dataframe with multiple input and outcome variables
`combo_length`	The length of the combinations specified by the user
`min_output_count`	Minimum number of output variables present in the combination
`max_output_count`	Maximum number of output variables present in the combination
`min_indv_threshold`	Minimum number of instances that support the combination

`max_freq_threshold`	Maximum fraction of the cohort size that could support a combination (i.e., filter out highly frequent events)
`input_format`	Optional | Naming convention used for input variables (Default = 'Input_')
`output_format`	Optional | Naming convention used for output variables (Default = 'Output_')
`pval_filter_threshold`	Optional | p-value cut-off to use to identify significant combinations (Default = 0.05)
`adj_pval_type`	Optional | Type of multiple testing corrections to use (Default = 'BH'; Alternative option = 'bonferroni')

Value

A dataframe with the list of multiple-testing adjusted statistically significant combinations along with quantitative measures (frequencies, p-values etc) that support the findings.

Author(s)

Vijay Kumar Pounraja

Examples

```
analyze_in_out_simultaneity(boolean_input_mult_df, 3, 1, 2, 5, 0.25,
                            input_format = 'Input_', output_format = 'Output_',
                            pval_filter_threshold = 0.05, adj_pval_type = 'BH')
```

`boolean_input_df` *Sparse Boolean dataframe with rare variant information and a single outcome variable*

Description

A synthetic dataset containing information about 5000 individuals (rows) and 1000 rare variants (columns).

Usage

```
boolean_input_df
```

Format

A data frame with 5000 rows and 1002 variables:

Sample_Name Unique identifier of the samples
Input_1 Presence and absense of rare variant 1
Input_2 Presence and absense of rare variant 2
Input_3 Presence and absense of rare variant 3
Input_4 Presence and absense of rare variant 4
Input_5 Presence and absense of rare variant 5
Input_6 Presence and absense of rare variant 6
Input_7 Presence and absense of rare variant 7
Input_8 Presence and absense of rare variant 8
Input_9 Presence and absense of rare variant 9
Input_10 Presence and absense of rare variant 10
Input_11 Presence and absense of rare variant 11
Input_12 Presence and absense of rare variant 12
Input_13 Presence and absense of rare variant 13
Input_14 Presence and absense of rare variant 14
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Input_483	Presence and absense of rare variant 483
Input_484	Presence and absense of rare variant 484
Input_485	Presence and absense of rare variant 485
Input_486	Presence and absense of rare variant 486
Input_487	Presence and absense of rare variant 487
Input_488	Presence and absense of rare variant 488
Input_489	Presence and absense of rare variant 489
Input_490	Presence and absense of rare variant 490
Input_491	Presence and absense of rare variant 491
Input_492	Presence and absense of rare variant 492
Input_493	Presence and absense of rare variant 493
Input_494	Presence and absense of rare variant 494
Input_495	Presence and absense of rare variant 495
Input_496	Presence and absense of rare variant 496
Input_497	Presence and absense of rare variant 497
Input_498	Presence and absense of rare variant 498
Input_499	Presence and absense of rare variant 499
Input_500	Presence and absense of rare variant 500
Output_1	Disease outcome or phenotype

`boolean_input_mult_df` *Sparse Boolean dataframe with rare variant information and multiple outcome variables*

Description

A synthetic dataset containing information about 5000 individuals (rows) and 1000 rare variants (columns) and 3 outcome variables.

Usage

```
boolean_input_mult_df
```

Format

A data frame with 5000 rows and 1004 variables:

Sample_Name Unique identifier of the samples
Input_1 Presence and absense of rare variant 1
Input_2 Presence and absense of rare variant 2
Input_3 Presence and absense of rare variant 3
Input_4 Presence and absense of rare variant 4
Input_5 Presence and absense of rare variant 5
Input_6 Presence and absense of rare variant 6
Input_7 Presence and absense of rare variant 7
Input_8 Presence and absense of rare variant 8
Input_9 Presence and absense of rare variant 9
Input_10 Presence and absense of rare variant 10
Input_11 Presence and absense of rare variant 11
Input_12 Presence and absense of rare variant 12
Input_13 Presence and absense of rare variant 13
Input_14 Presence and absense of rare variant 14
Input_15 Presence and absense of rare variant 15
Input_16 Presence and absense of rare variant 16
Input_17 Presence and absense of rare variant 17
Input_18 Presence and absense of rare variant 18
Input_19 Presence and absense of rare variant 19
Input_20 Presence and absense of rare variant 20
Input_21 Presence and absense of rare variant 21
Input_22 Presence and absense of rare variant 22
Input_23 Presence and absense of rare variant 23
Input_24 Presence and absense of rare variant 24
Input_25 Presence and absense of rare variant 25
Input_26 Presence and absense of rare variant 26
Input_27 Presence and absense of rare variant 27
Input_28 Presence and absense of rare variant 28
Input_29 Presence and absense of rare variant 29
Input_30 Presence and absense of rare variant 30
Input_31 Presence and absense of rare variant 31
Input_32 Presence and absense of rare variant 32
Input_33 Presence and absense of rare variant 33
Input_34 Presence and absense of rare variant 34

Input_35	Presence and absense of rare variant 35
Input_36	Presence and absense of rare variant 36
Input_37	Presence and absense of rare variant 37
Input_38	Presence and absense of rare variant 38
Input_39	Presence and absense of rare variant 39
Input_40	Presence and absense of rare variant 40
Input_41	Presence and absense of rare variant 41
Input_42	Presence and absense of rare variant 42
Input_43	Presence and absense of rare variant 43
Input_44	Presence and absense of rare variant 44
Input_45	Presence and absense of rare variant 45
Input_46	Presence and absense of rare variant 46
Input_47	Presence and absense of rare variant 47
Input_48	Presence and absense of rare variant 48
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Input_50	Presence and absense of rare variant 50
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Input_61	Presence and absense of rare variant 61
Input_62	Presence and absense of rare variant 62
Input_63	Presence and absense of rare variant 63
Input_64	Presence and absense of rare variant 64
Input_65	Presence and absense of rare variant 65
Input_66	Presence and absense of rare variant 66
Input_67	Presence and absense of rare variant 67
Input_68	Presence and absense of rare variant 68
Input_69	Presence and absense of rare variant 69
Input_70	Presence and absense of rare variant 70
Input_71	Presence and absense of rare variant 71

Input_72	Presence and absense of rare variant 72
Input_73	Presence and absense of rare variant 73
Input_74	Presence and absense of rare variant 74
Input_75	Presence and absense of rare variant 75
Input_76	Presence and absense of rare variant 76
Input_77	Presence and absense of rare variant 77
Input_78	Presence and absense of rare variant 78
Input_79	Presence and absense of rare variant 79
Input_80	Presence and absense of rare variant 80
Input_81	Presence and absense of rare variant 81
Input_82	Presence and absense of rare variant 82
Input_83	Presence and absense of rare variant 83
Input_84	Presence and absense of rare variant 84
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Input_86	Presence and absense of rare variant 86
Input_87	Presence and absense of rare variant 87
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Input_89	Presence and absense of rare variant 89
Input_90	Presence and absense of rare variant 90
Input_91	Presence and absense of rare variant 91
Input_92	Presence and absense of rare variant 92
Input_93	Presence and absense of rare variant 93
Input_94	Presence and absense of rare variant 94
Input_95	Presence and absense of rare variant 95
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Input_97	Presence and absense of rare variant 97
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Input_99	Presence and absense of rare variant 99
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Input_102	Presence and absense of rare variant 102
Input_103	Presence and absense of rare variant 103
Input_104	Presence and absense of rare variant 104
Input_105	Presence and absense of rare variant 105
Input_106	Presence and absense of rare variant 106
Input_107	Presence and absense of rare variant 107
Input_108	Presence and absense of rare variant 108

Input_109	Presence and absense of rare variant 109
Input_110	Presence and absense of rare variant 110
Input_111	Presence and absense of rare variant 111
Input_112	Presence and absense of rare variant 112
Input_113	Presence and absense of rare variant 113
Input_114	Presence and absense of rare variant 114
Input_115	Presence and absense of rare variant 115
Input_116	Presence and absense of rare variant 116
Input_117	Presence and absense of rare variant 117
Input_118	Presence and absense of rare variant 118
Input_119	Presence and absense of rare variant 119
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Input_127	Presence and absense of rare variant 127
Input_128	Presence and absense of rare variant 128
Input_129	Presence and absense of rare variant 129
Input_130	Presence and absense of rare variant 130
Input_131	Presence and absense of rare variant 131
Input_132	Presence and absense of rare variant 132
Input_133	Presence and absense of rare variant 133
Input_134	Presence and absense of rare variant 134
Input_135	Presence and absense of rare variant 135
Input_136	Presence and absense of rare variant 136
Input_137	Presence and absense of rare variant 137
Input_138	Presence and absense of rare variant 138
Input_139	Presence and absense of rare variant 139
Input_140	Presence and absense of rare variant 140
Input_141	Presence and absense of rare variant 141
Input_142	Presence and absense of rare variant 142
Input_143	Presence and absense of rare variant 143
Input_144	Presence and absense of rare variant 144
Input_145	Presence and absense of rare variant 145

Input_146	Presence and absense of rare variant 146
Input_147	Presence and absense of rare variant 147
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Input_179	Presence and absense of rare variant 179
Input_180	Presence and absense of rare variant 180
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Input_495	Presence and absense of rare variant 495
Input_496	Presence and absense of rare variant 496
Input_497	Presence and absense of rare variant 497
Input_498	Presence and absense of rare variant 498
Input_499	Presence and absense of rare variant 499
Input_500	Presence and absense of rare variant 500
Output_1	Disease outcome or phenotype 1
Output_2	Disease outcome or phenotype 2
Output_3	Disease outcome or phenotype 3

`compare_enrichment` *Compare the enrichment in combinations of input variables between the binary outcomes (case/control)*

Description

This function takes a Boolean dataframe as input and quantifies the enrichment in the observed frequency of combinations that meet the criteria specified by the users compared to their corresponding expectation derived under the assumption of independence between the constituent elements of each combination. The function then reports the multiple-testing adjusted significant combinations in which enrichment is observed in cases but not in controls.

Usage

```
compare_enrichment(boolean_input_df, combo_length, min_indv_threshold,
                   max_freq_threshold, input_format, output_format,
                   pval_filter_threshold, adj_pval_type, min_power_threshold,
                   sample_names_ind)
```

Arguments

`boolean_input_df`	An input Boolean dataframe with multiple input and a single binary outcome variable
`combo_length`	The length of the combinations specified by the user
`min_indv_threshold`	Minimum number of instances that support the combination
`max_freq_threshold`	Maximum fraction of the cohort size that could support a combination (i.e., filter out highly frequent events)
`input_format`	Optional | Naming convention used for input variables (Default = ’Input_’)
`output_format`	Optional | Naming convention used for output variables (Default = ’Output_’)
`pval_filter_threshold`	Optional | p-value cut-off to use to identify significant combinations in cases (Default = 0.05)
`adj_pval_type`	Optional | Type of multiple testing corrections to use (Default = ’BH’; Alternative option = ’bonferroni’)
`min_power_threshold`	Optional | Minimum statistical power (at 5% sig.threshold) required for significant combinations to be returned in the results (Default = 0.7)
`sample_names_ind`	Optional | Indicator to specify if the output should includes row names that support each significant combination (Default = ’N’; Alternative option = ’Y’)

Value

A dataframe with the list of multiple-testing adjusted statistically significant combinations along with quantitative measures (frequencies, p-values etc) that support the findings.

Author(s)

Vijay Kumar Pounraja

Examples

```
compare_enrichment(boolean_input_df, 3, 5, 0.25, input_format = 'Input_',
                   output_format = 'Output_', adj_pval_type = 'bonferroni',
                   sample_names_ind = 'N')
```

`compare_enrichment_depletion`

Compare the enrichment in combinations of input variables between the binary outcomes (case/control)

Description

This function takes a Boolean dataframe as input and quantifies the enrichment in the observed frequency of combinations that meet the criteria specified by the users compared to their corresponding expectation derived under the assumption of independence between the constituent elements of each combination. The function then reports the multiple-testing adjusted significant combinations in which enrichment is observed in cases and depletion is observed in controls.

Usage

```
compare_enrichment_depletion(boolean_input_df, combo_length, min_indv_threshold,
                             max_freq_threshold, input_format, output_format,
                      pval_filter_threshold, adj_pval_type, min_power_threshold,
                             sample_names_ind)
```

Arguments

`boolean_input_df`	An input Boolean dataframe with multiple input and a single binary outcome variable
`combo_length`	The length of the combinations specified by the user
`min_indv_threshold`	Minimum number of instances that support the combination
`max_freq_threshold`	Maximum fraction of the cohort size that could support a combination (i.e., filter out highly frequent events)
`input_format`	Optional | Naming convention used for input variables (Default = 'Input_')
`output_format`	Optional | Naming convention used for output variables (Default = 'Output_')
`pval_filter_threshold`	Optional | p-value cut-off to use to identify significant combinations in cases (Default = 0.05)
`adj_pval_type`	Optional | Type of multiple testing corrections to use (Default = 'BH'; Alternative option = 'bonferroni')
`min_power_threshold`	Optional | Minimum statistical power (at 5% sig.threshold) required for significant combinations to be returned in the results (Default = 0.7)
`sample_names_ind`	Optional | Indicator to specify if the output should includes row names that support each significant combination (Default = 'N'; Alternative option = 'Y')

Value

A dataframe with the list of multiple-testing adjusted statistically significant combinations along with quantitative measures (frequencies, p-values etc) that support the findings.

Author(s)

Vijay Kumar Pounraja

Examples

```
compare_enrichment_depletion(boolean_input_df, 3, 5, 0.25, input_format = 'Input_',
                             output_format = 'Output_', adj_pval_type = 'bonferroni',
                             sample_names_ind = 'N')
```

---

compare_enrichment_modifiers

Compare the enrichment in combinations of input variables between the binary outcomes (case/control)

Description

This function takes a Boolean dataframe as input and quantifies the enrichment in the observed frequency of combinations that include at least one of the input variables supplied by the user as well as meet other user-specified criteria compared to their corresponding expectation derived under the assumption of independence between the constituent elements of each combination. The function then reports the combinations in which enrichment is observed in cases but not in controls.

Usage

```
compare_enrichment_modifiers(boolean_input_df, combo_length, min_indv_threshold,
                          max_freq_threshold, primary_input_entities, input_format,
                               output_format, pval_filter_threshold, adj_pval_type,
                                 min_power_threshold, sample_names_ind)
```

Arguments

`boolean_input_df`	An input Boolean dataframe with multiple input and a single binary outcome variable
`combo_length`	The length of the combinations specified by the user
`min_indv_threshold`	Minimum number of instances that support the combination
`max_freq_threshold`	Maximum fraction of the cohort size that could support a combination (i.e., filter out highly frequent events)

`primary_input_entities`	List of variables that MUST be part of the combinations identified by the method
`input_format`	Optional | Naming convention used for input variables (Default = 'Input_')
`output_format`	Optional | Naming convention used for output variables (Default = 'Output_')
`pval_filter_threshold`	Optional | p-value cut-off to use to identify significant combinations in cases (Default = 0.05)
`adj_pval_type`	Optional | Type of multiple testing corrections to use (Default = 'BH'; Alternative option = 'bonferroni')
`min_power_threshold`	Optional | Minimum statistical power (at 5% sig.threshold) required for significant combinations to be returned in the results (Default = 0.7)
`sample_names_ind`	Optional | Indicator to specify if the output should includes row names that support each significant combination (Default = 'N'; Alternative option = 'Y')

Value

A dataframe with the list of multiple-testing adjusted statistically significant combinations along with quantitative measures (frequencies, p-values etc) that support the findings.

Author(s)

Vijay Kumar Pounraja

Examples

```
compare_enrichment_modifiers(boolean_input_df, 2, 4, 0.25, input_format = 'Input_',
                        output_format = 'Output_', primary_input_entities = input_list,
                              adj_pval_type = 'bonferroni', sample_names_ind = 'N')
```

`compare_expected_vs_observed`

Compare the observed frequencies of combinations with their expected frequencies under the assumption of independence within a single group

Description

This function takes a Boolean dataframe as input and compares the observed frequency of combinations that meet the criteria specified by the users with their corresponding expectation derived under the assumption of independence between the constituent elements of each combination

Usage

```
compare_expected_vs_observed(boolean_input_df, combo_length, min_indv_threshold,
                             max_freq_threshold, input_format,
                             pval_filter_threshold, adj_pval_type)
```

Arguments

`boolean_input_df`	An input Boolean dataframe with multiple input variables
`combo_length`	The length of the combinations specified by the user
`min_indv_threshold`	Minimum number of instances that support the combination
`max_freq_threshold`	Maximum fraction of the cohort size that could support a combination (i.e., filter out highly frequent events)
`input_format`	Optional | Naming convention used for input variables (Default = 'Input_')
`pval_filter_threshold`	Optional | p-value cut-off to use for multiple testing adjustment (Default = 0.05)
`adj_pval_type`	Optional | Type of multiple testing corrections to use (Default = 'BH'; Alternative option = 'bonferroni')

Value

A dataframe with the list of multiple-testing adjusted statistically significant combinations along with quantitative measures (frequencies, p-values etc) that support the findings.

Author(s)

Vijay Kumar Pounraja

Examples

```
compare_expected_vs_observed(boolean_input_df, 2, 10, 0.25, 0.05,
                             input_format = 'Input_', adj_pval_type = 'BH')
```

`custom_left_join` *Perform successive left joins to fetch information about the constituent elements of the combinations*

Description

Fetching the frequency of multiple individual elements that make up the combinations of varying length and hence varying variable names or to join two similar data frames using identical variable names necessitates this function that supplements and joins data based on the length of the combinations.

Usage

```
custom_left_join(
  left_df,
  right_df,
  combo_length = combo_length,
  diff_colnames = diff_colnames
)
```

Arguments

`left_df`	The data frame with information about the combinations
`right_df`	The data frame with information either about the combinations or their constituent elements
`combo_length`	The length of the combinations specified by the user used to determine the number of successive joins to attempt
`diff_colnames`	Indicator that specifies if the joins are to be made based on same or different column names

Value

An output dataframe with the results of the join operation

Author(s)

Vijay Kumar Pounraja

`input_list` *A list of 50 random input variables*

Description

A list of 50 random input variables

Usage

```
input_list
```

Format

A list of 50 random input variables:

`run_apriori_freqitems` *Generate frequent items using the apriori algorithm*

Description

This function takes in a factorized Boolean matrix and generate frequent itemsets that meet all the user provided criteria provided by the calling function.

Usage

```
run_apriori_freqitems(
  apriori_input_df,
  combo_length,
  support_threshold,
  input_colname_list,
  confidence_threshold = confidence_threshold,
  include_output_ind = include_output_ind,
  output_colname_list = output_colname_list
)
```

Arguments

`apriori_input_df`	An input factorized Boolean dataframe with multiple input and outcome variables
`combo_length`	The length of the combinations specified by the user
`support_threshold`	Minimum support value calculated based on the minimum absolute observed frequency threshold specified by the user
`input_colname_list`	A list of column names that identify the input variables
`confidence_threshold`	Minimum confidence threshold specified by the user
`include_output_ind`	Specifies if the outcome variables must also be made part of the analysis using the algorithm
`output_colname_list`	A list of column names that identify the outcome variables

Details

This is a function leveraged by few of the four main methods available to the users.

Value

A list of frequent item sets that meet all the constraints supplied to the apriori algorithm

Author(s)

Vijay Kumar Pounraja

`run_apriori_rules` *Generate rules using the apriori algorithm*

Description

This function takes in a factorized Boolean matrix and generate rules that meet all the user provided criteria while restricting the RHS of the rule based on the list of variables allowed in RHS provided by the calling function.

Usage

```
run_apriori_rules(
  apriori_input_df,
  combo_length,
  support_threshold,
  input_colname_list,
  confidence_threshold = confidence_threshold,
  output_colname_list = output_colname_list
)
```

Arguments

`apriori_input_df`	An input factorized Boolean dataframe with multiple input and outcome variables
`combo_length`	The length of the combinations specified by the user
`support_threshold`	Minimum support value calculated based on the minimum absolute observed frequency threshold specified by the user
`input_colname_list`	A list of column names that identify the input variables
`confidence_threshold`	Minimum confidence threshold specified by the user
`output_colname_list`	Optional | A list of column names that identify the outcome variables

Details

This is a function leveraged by few of the four main methods available to the users.

Value

A list of rules that meet all the constraints supplied to the apriori algorithm

Author(s)

Vijay Kumar Pounraja

`run_apriori_rules_inout_simult`
Generate rules using the apriori algorithm

Description

This function takes in a factorized Boolean matrix and generate rules that meet all the user provided criteria while allowing the outcome variables to be part of either LHS or RHS of the rules but restricting the input variables to the LHS of the rules.

Usage

```
run_apriori_rules_inout_simult(
  apriori_input_df,
  combo_length,
  support_threshold,
  input_colname_list,
  output_colname_list = output_colname_list
)
```

Arguments

`apriori_input_df`	An input factorized Boolean dataframe with multiple input and outcome variables
`combo_length`	The length of the combinations specified by the user
`support_threshold`	Minimum support value calculated based on the minimum absolute observed frequency threshold specified by the user
`input_colname_list`	A list of column names that identify the input variables
`output_colname_list`	Optional | A list of column names that identify the outcome variables

Details

This is a function leveraged by few of the four main methods available to the users.

Value

A list of rules that meet all the constraints supplied to the apriori algorithm

Author(s)

Vijay Kumar Pounraja

`run_apriori_rules_modifiers`
Generate rules using the apriori algorithm

Description

This function takes in a factorized Boolean matrix and generate rules that meet all the user provided criteria while restricting the RHS of the rule based on the list of variables allowed in RHS provided by the calling function.

Usage

```
run_apriori_rules_modifiers(
  apriori_input_df,
  combo_length,
  support_threshold,
  input_colname_list,
  output_colname_list = output_colname_list
)
```

Arguments

`apriori_input_df`	An input factorized Boolean dataframe with multiple input and outcome variables
`combo_length`	The length of the combinations specified by the user
`support_threshold`	Minimum support value calculated based on the minimum absolute observed frequency threshold specified by the user
`input_colname_list`	A list of column names that identify the input variables
`output_colname_list`	Optional | A list of column names that identify the outcome variables

Details

This is a function leveraged by few of the four main methods available to the users.

Value

A list of rules that meet all the constraints supplied to the apriori algorithm

Author(s)

Vijay Kumar Pounraja

---

run_apriori_w_sample_names

Generate frequent items along with the names of supporting observations using the apriori algorithm

---

Description

This function takes in a factorized Boolean matrix and generate frequent item sets that meet all the user provided criteria provided by the calling function. This function includes in it's output the identifiers of observations that support each significant combination.

Usage

```
run_apriori_w_sample_names(
  apriori_input_df,
  combo_length,
  support_threshold,
  input_colname_list,
  input_sample_list,
  confidence_threshold = confidence_threshold,
  include_output_ind = include_output_ind,
  output_colname_list = output_colname_list
)
```

Arguments

`apriori_input_df`	An input factorized Boolean dataframe with multiple input and outcome variables
`combo_length`	The length of the combinations specified by the user
`support_threshold`	Minimum support value calculated based on the minimum absolute observed frequency threshold specified by the user
`input_colname_list`	A list of column names that identify the input variables
`input_sample_list`	A list of row names that identify the samples/observations
`confidence_threshold`	Minimum confidence threshold specified by the user
`include_output_ind`	Specifies if the outcome variables must also be made part of the analysis using the algorithm
`output_colname_list`	A list of column names that identify the outcome variables

Details

This is a function leveraged by few of the four main methods available to the users.

Value

A list of frequent item sets that meet all the constraints supplied to the apriori algorithm

Author(s)

Vijay Kumar Pounraja

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