NAME

ElementalAnalysisTextFiles.pl - Perform elemental analysis using formula column in TextFile(s)

SYNOPSIS

ElementalAnalysisTextFiles.pl TextFile(s)...

ElementalAnalysisTextFiles.pl [-c, --colmode colnum | collabel] [-d, --detail infolevel] [-f, --fast] [-f, --formulacol colnum | collabel] [-h, --help] [--indelim comma | semicolon] [-m, --mode All | "ElementalAnysis, [MolecularWeight, ExactMass]"] [-o, --overwrite] [--outdelim comma | tab | semicolon] [-p, --precision number] [-q, --quote yes | no] [-r, --root rootname] [-s, --startcol colnum | collabel] [--startcolmode before | after] -v --valuecollabels [Name, Label, [Name, Label,...]] [-w, --workingdir dirname] TextFile(s)...

DESCRIPTION

Perform elemental analysis using molecular formula column specified by a column number or label in *TextFile(s)*.

In addition to straightforward molecular formulas - H2O, HCl, C3H7O2N - other supported variations are: Ca3(PO4)2, [PCl4]+, [Fe(CN)6]4-, C37H42N2O6+2, Na2CO3.10H2O, 8H2S.46H2O, and so on. Charges are simply ignored. Isotope symbols in formulas specification, including D and T, are not supported.

The valid file extensions are *.csv* and *.tsv* for comma/semicolon and tab delimited text files respectively. All other file names are ignored. All the text files in a current directory can be specified by **.csv*, **.tsv*, or the current directory name. The --indelim option determines the format of *TextFile(s)*. Any file which doesn't correspond to the format indicated by --indelim option is ignored.

OPTIONS

-c, --colmode *colnum* | *collabel*

Specify how columns are identified in *TextFile(s)*: using column number or column label. Possible values: *colnum or collabel*. Default value: *colnum*.

-d, --detail *infolevel*

Level of information to print about lines being ignored. Default: *1*. Possible values: *1, 2 or 3*.

-h, --help

Print this help message.

--fast

In this mode, the formula column specified using -f, --formulacol option is assumed to contain valid molecular formula data and initial formula validation check is skipped.

-f, --formulacol *col number* | *col name*

This value is mode specific. It specifies molecular formula column to use for performing elemental analysis on *TextFile(s)*. Possible values: *col number or col label*. Default value: *first column containing the word formula in its column label*.

-m, --mode *All* | *"ElementalAnalysis,[MolecularWeight,ExactMass]"*

Specify what values to calculate using molecular formula in *TextFile(s)*: calculate all supported values or specify a comma delimited list of values. Possible values: *All* | *"ElementalAnalysis, [MolecularWeight, ExactMass]"*. Default: *All*

--indelim *comma* | *semicolon*

Input delimiter for CSV *TextFile(s)*. Possible values: *comma or semicolon*. Default value: *comma*. For TSV files, this option is ignored and *tab* is used as a delimiter.

-o, --overwrite

Overwrite existing files.

--outdelim *comma* | *tab* | *semicolon*

Output text file delimiter. Possible values: *comma, tab, or semicolon* Default value: *comma*.

-p, --precision *number*

Precision of calculated values in the output file. Default: up to *2* decimal places. Valid values: positive integers.

-q, --quote *yes* | *no*

Put quotes around column values in output text file. Possible values: *yes or no*. Default value: *yes*.

-r, --root *rootname*

New text file name is generated using the root: <Root>.<Ext>. Default new file name: <InitialTextFileName>ElementalAnalysis.<Ext>. The csv, and tsv <Ext> values are used for comma/semicolon, and tab delimited text files respectively. This option is ignored for multiple input files.

-s, --startcol *colnum* | *collabel*

This value is mode specific. It specifies the column in text files which is used for start adding calculated column values. For

colnum mode, specify column number and for *collabel* mode, specify column label.

Default value: *last*. Start merge after the last column.

--startcolmode *before* | *after*

Start adding calculated column values after the -s, --startcol value. Possible values: *before or after*. Default value: *after*.

-v --valuecollabels *Name,Label,[Name,Label,...]*

Specify column labels to use for calculated values. In general, it's a comma delimited list of value name and column label pairs. Supported value names: *ElementalAnalysis, MolecularWeight, and ExactMass*. Default labels: *ElementalAnalysis, MolecularWeight, and ExactMass*.

-w, --workingdir *dirname*

Location of working directory. Default: current directory.

EXAMPLES

To perform elemental analysis, calculate molecular weight and exact mass using formulas in a column with the word Formula in its column label and generate a new CSV text file NewSample1.csv, type:

```
% ElementalAnalysisTextFiles.pl -o -r NewSample1 Sample1.csv
```

To perform elemental analysis using formulas in column number two, use column label Analysis for calculated data, and generate a new CSV text file NewSample1.csv, type:

```
% ElementalAnalysisTextFiles.pl --m ElementalAnalysis --formulacol 2
  --valuecollabels "ElementalAnalysis,Analysis" -o -r NewSample1
  Sample1.csv
```

To calculate molecular weight using formula in column label Formula with four decimal precision and generate a new CSV text file NewSample1.csv, type

```
% ElementalAnalysisTextFiles.pl --m MolecularWeight --colmode collabel
  --formulacol Formula --precision 4 -o -r NewSample1 Sample1.csv
```

To calculate exact mass using formula in column label Formula with four decimal precision, adding column for exact mass right after Formula column, and generate a new CSV text file NewSample1.csv, type

```
% ElementalAnalysisTextFiles.pl --m ExactMass --colmode collabel
  --formulacol Formula --precision 4 --startcolmode after
  --startcol Formula -o -r NewSample1 Sample1.csv
```

AUTHOR

Manish Sud <msud@san.rr.com>

SEE ALSO

AnalyzeTextFilesData.pl, InfoTextFiles.pl, ExtractFromTextFiles.pl

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