Package 'FIREVAT'

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Type Package

Title FIREVAT, FInding REliable Variants without ArTifacts

Description FIREVAT is a variant filtering tool for cancer sequencing data, which uses mutational signatures to identify sequencing artifacts and low-quality variants.

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Imports data.table,
stringi,
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jsonlite,
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MutationalPatterns,
deconstructSigs,
lsa,
BSgenome.Hsapiens.UCSC.hg19,
BSgenome.Hsapiens.UCSC.hg38,
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rmarkdown,
gtable,
dplyr,
foreach,
doParallel

URL https://github.com/cgab-ncc/FIREVAT

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Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Suggests knitr

VignetteBuilder knitr

R topics documented:

`AnnotateVCFObj` *AnnotateVCFObj*

Description

Annotates a vcf.obj using df.variants.of.interest (from `PrepareAnnotationDB`)

Usage

```
AnnotateVCFObj(vcf.obj, df.annotation.db, columns.to.include,
  include.all.columns = FALSE)
```

Arguments

vcf.obj	ReadVCF
df.annotation.db	A data.frame from PrepareAnnotationDB. This data.frame must have the columns 'CHROM', 'POS', 'REF', 'ALT'
columns.to.include	A character vector of columns to include. Note that existing columns in vcf.obj will not be affected.
include.all.columns	A boolean value. If TRUE, then annotates vcf.obj with all columns present in df.variants.of.interest. If FALSE, columns.to.include must be supplied.

Value

An annotated vcf.obj

CheckIfVariantRefinementIsNecessary

CheckIfVariantRefinementIsNecessary

Description

Checks if variant refinement is necessary by identifying mutational signatures related to sequencing artifact in the vcf.obj (set of original unrefined point mutations).

Usage

```
CheckIfVariantRefinementIsNecessary(vcf.obj, bsg, df.mut.pat.ref.sigs,
  target.mut.sigs, sequencing.artifact.mut.sigs,
  init.artifact.stop = 0.05, verbose = TRUE)
```

Arguments

vcf.obj	A list from ReadVCF
bsg	BSgenome.Hsapiens.UCSC object
df.mut.pat.ref.sigs	A data.frame from MutPatParseRefMutSigs
target.mut.sigs	A character vector of target mutational signatures from reference mutational signatures.

`sequencing.artifact.mut.sigs`
: A character vector of sequencing artifact mutational signatures from reference mutational signatures.

`init.artifact.stop`
: Numeric value less than 1. If the sum of sequencing artifact weights in vcf.obj is less than or equal to this value then this function returns judgment = FALSE, otherwise returns judgment = TRUE.

`verbose`
: If TRUE, provides process detail. Default value is TRUE.

Value

A list with the following elements

- judgmentA boolean value
- seq.art.sigs.weights.sumA numeric value. Sum of sequencing artifact weights.

`Chromosome.Names` *Constant*

Description

Chromosome names for FIREVAT. Chromosome names should be given in the format of "chr" + chromosome number.

Usage

```
Chromosome.Names
```

Format

An object of class `character` of length 25.

`ComputeZScore` *ComputeZScore*

Description

Returns a z-score of x given a distribution of values

Usage

```
ComputeZScore(values, x)
```

Arguments

`values`
: a numeric vector

`x`
: a numeric value

Value

a numeric value corresponding to the z-score of x

`ComputeZScoreEquiValue` *ComputeZScoreEquiValue*

Description

Returns a numeric value that is equivalent to the specified z.score in the distribution of 'values'

Usage

```
ComputeZScoreEquiValue(z.score, values)
```

Arguments

`z.score`	numeric value
`values`	numeric vector

Value

a numeric value corresponding to the specified z.score in the 'values' distribution

---

`DecimalCeiling` *DecimalCeiling*

Description

Returns the ceiling of a decimal value e.g. value = 0.15, decimal = 0.1 returns 0.2

Usage

```
DecimalCeiling(value, decimal)
```

Arguments

`value`	numeric value (decimal)
`decimal`	numeric value (e.g. 0.1, 0.001)

Value

a numeric value

Default.Obj.Fn *Default.Obj.Fn*

Description

Calculates the default objective value for FIREVAT GA optimization.

Usage

```
Default.Obj.Fn(C.refined, A.refined, C.artifactual, A.artifactual)
```

Arguments

C.refined	A numeric value between 0 and 1.
A.refined	A numeric value between 0 and 1.
C.artifactual	A numeric value between 0 and 1.
A.artifactual	A numeric value between 0 and 1.

Value

A numeric value between 0 and 1.

DefaultFilterToBinary *Transform default filtering parameters to a binary vector*

Description

This function transforms default filtering parameter to binary vector which can be used as a suggested solution in GA algorithm.

Usage

```
DefaultFilterToBinary(vcf.filter, params.bit.len)
```

Arguments

vcf.filter	A list generated in MakeFilter
params.bit.len	A list with bit lengths of filtering parameters which is generated from ParameterToBits

Value

A binary vector

`EnumerateTriNucCounts` *EnumerateTriNucCounts*

Description

Returns C>A, C>G, C>T, T>A, T>C, T>G counts

Usage

```
EnumerateTriNucCounts(spectrum)
```

Arguments

`spectrum`	a numeric vector with 96 numeric values

Details

Please note that this function assumes that 'spectrum' is sorted (i.e. 1:16 –> C>A; 17:32 –> C>G; 33:48 –> C>T; 49:64 –> T>A; 65:80 –> T>C; 81:96 –> T>G)

Value

a numeric vector of length 6 corresponding to the counts of each trinucleotide change (C>A, C>G, C>T, T>A, T>C, T>G)

`Euc.Exp.Weighted.Obj.Fn`
Euc.Exp.Weighted.Obj.Fn

Description

Calculates the Euclidean-distance of logarithmically weighted objective value for FIREVAT GA optimization.

Usage

```
Euc.Exp.Weighted.Obj.Fn(C.refined, A.refined, C.artifactual, A.artifactual)
```

Arguments

`C.refined`	A numeric value between 0 and 1.
`A.refined`	A numeric value between 0 and 1.
`C.artifactual`	A numeric value between 0 and 1.
`A.artifactual`	A numeric value between 0 and 1.

Value

A numeric value between 0 and 1.

`Euc.Exp.Weighted.Seq.Art.Only.Obj.Fn.1`
Euc.Exp.Weighted.Seq.Art.Only.Obj.Fn.1

Description

Calculates the Euclidean-distance of logarithmically weighted objective value for FIREVAT GA optimization.

Usage

```
Euc.Exp.Weighted.Seq.Art.Only.Obj.Fn.1(C.refined, A.refined, C.artifactual,
  A.artifactual)
```

Arguments

`C.refined`	A numeric value between 0 and 1.
`A.refined`	A numeric value between 0 and 1.
`C.artifactual`	A numeric value between 0 and 1.
`A.artifactual`	A numeric value between 0 and 1.

Value

A numeric value between 0 and 1.

`Euc.Exp.Weighted.Seq.Art.Only.Obj.Fn.2`
Euc.Exp.Weighted.Seq.Art.Only.Obj.Fn.2

Description

Calculates the Euclidean-distance of logarithmically weighted objective value for FIREVAT GA optimization.

Usage

```
Euc.Exp.Weighted.Seq.Art.Only.Obj.Fn.2(C.refined, A.refined, C.artifactual,
  A.artifactual)
```

Arguments

`C.refined`	A numeric value between 0 and 1.
`A.refined`	A numeric value between 0 and 1.
`C.artifactual`	A numeric value between 0 and 1.
`A.artifactual`	A numeric value between 0 and 1.

Value

A numeric value between 0 and 1.

`Euc.Obj.Fn` *Euc.Obj.Fn*

Description

Calculates the Euclidean-distance based objective value for FIREVAT GA optimization.

Usage

```
Euc.Obj.Fn(C.refined, A.refined, C.artifactual, A.artifactual)
```

Arguments

`C.refined`	A numeric value between 0 and 1.
`A.refined`	A numeric value between 0 and 1.
`C.artifactual`	A numeric value between 0 and 1.
`A.artifactual`	A numeric value between 0 and 1.

Value

A numeric value between 0 and 1.

`Exp.Weighted.Obj.Fn.1` *Exp.Weighted.Obj.Fn.1*

Description

Calculates the exponentially weighted objective value for FIREVAT GA optimization.

Usage

```
Exp.Weighted.Obj.Fn.1(C.refined, A.refined, C.artifactual, A.artifactual)
```

Arguments

`C.refined`	A numeric value between 0 and 1.
`A.refined`	A numeric value between 0 and 1.
`C.artifactual`	A numeric value between 0 and 1.
`A.artifactual`	A numeric value between 0 and 1.

Value

A numeric value between 0 and 1.

`Exp.Weighted.Obj.Fn.2` *Exp.Weighted.Obj.Fn.2*

Description

Calculates the exponentially weighted objective value for FIREVAT GA optimization.

Usage

```
Exp.Weighted.Obj.Fn.2(C.refined, A.refined, C.artifactual, A.artifactual)
```

Arguments

`C.refined`	A numeric value between 0 and 1.
`A.refined`	A numeric value between 0 and 1.
`C.artifactual`	A numeric value between 0 and 1.
`A.artifactual`	A numeric value between 0 and 1.

Value

A numeric value between 0 and 1.

`Exp.Weighted.Refined.Seq.Art.Only.Obj.Fn`
Exp.Weighted.Refined.Seq.Art.Only.Obj.Fn

Description

Calculates the Euclidean-distance of logarithmically weighted objective value for FIREVAT GA optimization.

Usage

```
Exp.Weighted.Refined.Seq.Art.Only.Obj.Fn(C.refined, A.refined,
  C.artifactual, A.artifactual)
```

Arguments

`C.refined`	A numeric value between 0 and 1.
`A.refined`	A numeric value between 0 and 1.
`C.artifactual`	A numeric value between 0 and 1.
`A.artifactual`	A numeric value between 0 and 1.

Value

A numeric value between 0 and 1.

FilterVCF *FilterVCF*

Description

Filter vcf based on the filter Filtering parameters are saved in config.obj Split vcf.obj into vcf.obj.filtered & vcf.obj.artifact based on vcf.filter

Usage

```
FilterVCF(vcf.obj, vcf.filter, config.obj, include.array = NULL,
  force.include = FALSE, verbose = TRUE)
```

Arguments

vcf.obj	A list from ReadVCF
vcf.filter	A list from MakeMuTect2Filter
config.obj	A list from ParseConfigFile
include.array	A boolean vector
force.include	A boolean value. If TRUE, then uses 'include.array'
verbose	If true, provides process detail

Value

A list with the following elements

- 1) Mutations which passed filteringvcf.obj.filtered = vcf.obj (list with data, header, genome)
- 2) Mutations which did not pass filteringvcf.obj.artifact = vcf.obj (list with data, header, genome)

GenerateConfigObj *Generate config.obj by checking vcf header*

Description

This function generate config.obj by checking vcf header. Users should fill in the information needed in console. In current version, only Integers & Float values can be used in config.obj for running FIREVAT.

Usage

```
GenerateConfigObj(vcf.obj, save.config = TRUE,
  config.path = "../temp/FIREVAT_configure.json")
```

Arguments

vcf.obj	A list from ReadVCF
save.config	If true, save config.obj to config.path
config.path	File path to write config.obj (json or yaml)

Value

config.obj

GetCOSMICMutSigs *GetCOSMICMutSigs*

Description

Returns a data.frame of the COSMIC mutational signature reference file from the data directory

Usage

```
GetCOSMICMutSigs()
```

Value

a data.frame of the COSMIC reference mutational signatures

GetCOSMICMutSigsEtiologiesColors *GetCOSMICMutSigsNames*

Description

Returns all COSMIC mutational signature etiologies and colors

Usage

```
GetCOSMICMutSigsEtiologiesColors()
```

Value

data.frame with following columns: signature, group and color.

GetCOSMICMutSigsNames *GetCOSMICMutSigsNames*

Description

Returns all COSMIC mutational signature names

Usage

```
GetCOSMICMutSigsNames()
```

Value

a character vector

GetGASuggestedSolutions *GetGASuggestedSolutions*

Description

Computes suggested solutions

Usage

```
GetGASuggestedSolutions(vcf.obj, bsg, config.obj, lower.upper.list,
  df.mut.pat.ref.sigs, target.mut.sigs, sequencing.artifact.mut.sigs,
  objective.fn, original.muts.seq.art.weights.sum, verbose = TRUE)
```

Arguments

`vcf.obj`	A list from ReadVCF
`bsg`	BSgenome.Hsapiens.UCSC object
`config.obj`	A list from ParseConfigFile
`lower.upper.list`	A list from GetParameterLowerUpperVector
`df.mut.pat.ref.sigs`	A data.frame from MutPatParseRefMutSigs
`target.mut.sigs`	A character vector of the target mutational signatures from reference mutational signatures.
`sequencing.artifact.mut.sigs`	A character vector of the sequencing artifact mutational signatures from reference mutational signatures.

objective.fn	Objective value derivation function.
original.muts.seq.art.weights.sum	A numeric value. 'seq.art.sigs.weights.sum' from CheckIfVariantRefinementIsNecessary
verbose	If TRUE, provides process detail. Default value is TRUE.

Value

A list with the following elements

- judgmentA boolean value
- seq.art.sigs.weightsA numeric value. Sum of sequencing artifact weights.

GetOptimizedSignatures *GetOptimizedSignatures*

Description

This function fetches the last row from the optimization iteration log and returns the target and artifactual mutational signatures for the type of mutations ('refined' or 'artifactual')

Usage

```
GetOptimizedSignatures(data, mutations.type = "refined",
  signatures = "all")
```

Arguments

data	A list of main data from RunFIREVAT
mutations.type	A string for type of mutations ('refined' or 'artifact')
signatures	A string ('all', 'target', 'artifact')

Value

A data.frame with the columns 'signature' and 'weight'

GetParameterLowerUpperVector *GetParameterLowerUpperVector*

Description

Return a lower/upper vector needed to conduct FIREVAT GA real-valued optimization.

Usage

```
GetParameterLowerUpperVector(vcf.obj, config.obj, vcf.filter,
  multiplier = 100)
```

Arguments

vcf.obj	A list from ReadVCF
config.obj	A list from ParseConfigFile
vcf.filter	A list from MakeMuTect2Filter
multiplier	A multiplier for convert fraction to integer (default = 100)

Details

vcf.obj$data: if max(vcf.obj$data[[param]]) < 1, then multiply multiplier to the vector

Value

A list with the elements

- lower.vector A numeric vector. Each element is the minimum value of each parameter
- upper.vector A numeric vector. Each element is the maximum value of each parameter
- vcf.obj vcf.obj with updated data

GetPCAWGMutSigs *GetPCAWGMutSigs*

Description

Returns the PCAWG mutational signatures data

Usage

```
GetPCAWGMutSigs()
```

Value

a data.frame of the PCAWG mutatioanl signatures

GetPCAWGMutSigsEtiologiesColors *GetPCAWGMutSigsEtiologiesColors*

Description

Returns the PCAWG mutational signatures etiologies and colors

Usage

```
GetPCAWGMutSigsEtiologiesColors()
```

Value

a data.frame with the columns 'signature', 'group', 'color'

GetPCAWGMutSigsNames *GetPCAWGMutSigsNames*

Description

Returns the PCAWG mutational signatures names

Usage

```
GetPCAWGMutSigsNames()
```

Value

a character vector of the PCAWG mutational signatures names

InitializeVCF *InitializeVCF*

Description

Initialize VCF with FIREVAT config file This functions selects point mutations and appends filter values to vcf.obj$data

Usage

```
InitializeVCF(vcf.obj, config.obj, verbose = TRUE)
```

Arguments

vcf.obj	A list from ReadVCF
config.obj	A list from ParseConfigFile
verbose	If true, provides process detail

Value

A list with the following elements

- vcf.obj.filteredvcf.obj (high-quality vcf)
- vcf.obj.artifactvcf.obj (low-quality vcf)

MakeFilter *MakeFilter*

Description

Creates a vcf filter from config.obj

Usage

```
MakeFilter(config.obj)
```

Arguments

config.obj	A list from ParseConfigFile (any filter with "use_in_filter" value declared as FALSE is not considered)

Value

A list with the filter parameters

MutaliskParseVCFObj *MutaliskParseVCFObj*

Description

Parses a vcf.obj and prepares it to run Mutalisk.

Usage

```
MutaliskParseVCFObj(vcf.obj)
```

Arguments

vcf.obj	A list from ReadVCF

Value

A data.frame

`MutPatParseRefMutSigs` *MutPatParseRefMutSigs*

Description

Parses a df.ref.mut.sigs and prepares it to run Mutational Patterns.

Usage

```
MutPatParseRefMutSigs(df.ref.mut.sigs, target.mut.sigs,
  signature.start.column.index = 4,
  mutation.type.header = "SomaticMutationType")
```

Arguments

`df.ref.mut.sigs`
: A data.frame of reference mutational signatures

`target.mut.sigs`
: A character vector of target mutational signatures names

`signature.start.column.index`
: = An integer value (e.g. column index corresponding to 'SBS1')

`mutation.type.header`
: = A string value (name of header corresponding to column containing 'A[C>A]A' data))

Value

A data.frame of the format deconstructSigs::signatures.cosmic

---

`MutPatParseVCFObj` *MutPatParseVCFObj*

Description

Parses a vcf.obj and prepares it to run Mutational Patterns.

Usage

```
MutPatParseVCFObj(vcf.obj, bsg, sample.id = "sample")
```

Arguments

vcf.obj	A list from ReadVCF
bsg	BSgenome.Hsapiens.UCSC.hg19::BSgenome.Hsapiens.UCSC.hg19 or BSgenome.Hsapiens.UCSC.hg38
sample.id	A string value

Value

A data.frame with the column sample.id and row names corresponding to 96 substitution types

---

ParameterToBits *ParameterToBits*

Description

Calculate the number of bits needed to conduct FIREVAT GA binary optimization.

Usage

```
ParameterToBits(vcf.obj, config.obj, vcf.filter, multiplier = 100)
```

Arguments

vcf.obj	A list from ReadVCF
config.obj	A list from ParseConfigFile
vcf.filter	A list from MakeMuTect2Filter
multiplier	A multiplier for convert fraction to integer (default = 100)

Details

vcf.obj$data: if max(vcf.obj$data[[param]]) < 1, then multiply multiplier to the vector

Value

A list with the elements

- params.bit.lenA numeric vector. Each element is the bit length of each parameter value
- vcf.objA vcf.obj (ReadVCF) with updated data

ParseConfigFile *ParseConfigFile*

Description

This function returns config.obj from JSON or YAML config file. - Check if the config file is in JSON format or YAML format - Return config.obj

Usage

```
ParseConfigFile(config.path, verbose = TRUE)
```

Arguments

config.path	A string for config file path
verbose	If true, provides process detail

Value

config.obj: list of parameters

Examples

```
## Not run:
ParseConfigFile("example.variant.caller.json")
ParseConfigFile("example.variant.caller.json", verbose=False)

## End(Not run)
```

PCAWG.All.Sequencing.Artifact.Signatures *Constant*

Description

PCAWG mutational signatures reported to be associated with sequencing artifacts

Usage

```
PCAWG.All.Sequencing.Artifact.Signatures
```

Format

An object of class character of length 17.

PCAWG.Known.Sequencing.Artifact.Signatures

Constant

Description

PCAWG mutational signatures reported to be associated with sequencing artifacts

Usage

```
PCAWG.Known.Sequencing.Artifact.Signatures
```

Format

An object of class `character` of length 1.

PCAWG.Likely.Sequencing.Artifact.Signatures

Constant

Description

PCAWG mutational signatures reported to be associated with sequencing artifacts

Usage

```
PCAWG.Likely.Sequencing.Artifact.Signatures
```

Format

An object of class `character` of length 5.

PCAWG.Possible.Sequencing.Artifact.Signatures

Constant

Description

PCAWG mutational signatures reported to be associated with sequencing artifacts

Usage

```
PCAWG.Possible.Sequencing.Artifact.Signatures
```

Format

An object of class `character` of length 11.

PCAWG.Target.Mutational.Signatures
Constant

Description

PCAWG target mutational signatures reported to be unrelated to sequencing artifacts

Usage

```
PCAWG.Target.Mutational.Signatures
```

Format

An object of class `character` of length 49.

PerformStrandBiasAnalysis
PerformStrandBiasAnalysis

Description

Performs strand bias analysis

Usage

```
PerformStrandBiasAnalysis(vcf.obj, ref.forward.strand.var,
  ref.reverse.strand.var, alt.forward.strand.var, alt.reverse.strand.var,
  perform.fdr.correction = TRUE, fdr.correction.method = "BH")
```

Arguments

`vcf.obj` ReadVCF

`ref.forward.strand.var`
: A string value.

`ref.reverse.strand.var`
: A string value.

`alt.forward.strand.var`
: A string value.

`alt.reverse.strand.var`
: A string value.

`perform.fdr.correction`
: If TRUE, then performs false discovery rate correction

`fdr.correction.method`
: A string value. FDR correction method (Refer to p.adjust() function)

Value

An updated vcf.obj

`PlotMutaliskResults` *PlotMutaliskResults*

Description

Plots Mutalisk results

Usage

```
PlotMutaliskResults(mutalisk.results, signatures, trinuc.max.y,
  trinuc.min.y, mut.type.max.y, title)
```

Arguments

`mutalisk.results`	A list obtained from `RunMutalisk`
`signatures`	A character vector of mutational signatures names
`trinuc.max.y`	A numeric value (maximum y-axis value)
`trinuc.min.y`	A numeric value (minimum y-axis value)
`mut.type.max.y`	A numeric value
`title`	A string value

Value

A ggplot object

Examples

```
## Not run:
  df.ref.mut.sigs <- GetPCAWGMutSigs()
  target.mut.sigs <- GetPCAWGMutSigsNames()
  vcf.obj <- ReadVCF(vcf.file = "../data/sample/P-233-CT.final.vcf")
  mutalisk.results <- RunMutalisk(vcf.obj = vcf.obj,
                                  df.ref.mut.sigs = df.ref.mut.sigs,
                                  target.mut.sigs = target.mut.sigs)
  p <- PlotMutaliskResults(mutalisk.results = mutalisk.results)
  print(p)

## End(Not run)
```

PlotMutationTypes *PlotMutationTypes*

Description

Plots a horizontal barplot of mutation types

Usage

```
PlotMutationTypes(mutation.types = c("C>A", "C>G", "C>T", "T>A", "T>C",
  "T>G"), mutation.types.values, mutation.types.colors, max.y.val, title,
  convert.to.percentage = T, show.legend = T, font.size.small = 8,
  font.size.med = 14, plot.margin = unit(c(0.5, 0.5, 0.5, 0.5), "cm"))
```

Arguments

`mutation.types`	Mutation types; Default = c("C>A", "C>G", "C>T", "T>A", "T>C", "T>G")
`mutation.types.values`	Mutation count for each mutation type
`mutation.types.colors`	A color vector for indicating mutation types
`max.y.val`	y axis maximum value
`title`	Plot title
`convert.to.percentage`	if True convert y values to percentage (x 100); Default = T
`show.legend`	If True, show legend; Default = T
`font.size.small`	Small font size; Default = 8
`font.size.med`	Medium font size; Default = 14
`plot.margin`	Margin vector for drawing plot; Default = unit(c(0.5, 0.5, 0.5, 0.5), "cm"))

Value

A ggplot object

Examples

```
## Not run:
p <- PlotMutationTypes(mutation.types = c("C>A", "C>G", "C>T", "T>A", "T>C", "T>G"),
                  mutation.types.values = c(0.3, 0.3, 0.1, 0.1, 0.1, 0.1),
                  mutation.types.colors = TriNuc.Mutation.Type.Hex.Colors,
                  max.y.val = 0.5,
                  convert.to.percentage = T,
                  show.legend = T,
                  font.size.small = 8,
                  font.size.med = 14,
```

```
                  plot.margin = unit(c(0.5, 0.5, 0.5, 0.5), "cm"))
print(p)

## End(Not run)
```

`PlotOptimizationIterations` *PlotOptimizationIterations*

Description

Plots multiple scatter plots into one figure

Usage

```
PlotOptimizationIterations(df, columns.to.plot, x.axis.var, x.axis.title,
  x.max, save.file, title, y.axis.title = "", y.max = 1,
  point.size = 1, connect.dots = T, plot.legend = T,
  legend.ncol = 1, font.size.med = 14, font.size.large = 16,
  plot.margin = unit(c(0.5, 0.5, 0.5, 0.5), "cm"))
```

Arguments

`df`	A data.frame (from reading "FIREVAT_Optimization_Logs.tsv")
`columns.to.plot`	A character vector (of column names to plot)
`x.axis.var`	x axis variable
`x.axis.title`	x axis title
`x.max`	x axis maximum value
`save.file`	Filename (including full path) to which the plot will be saved
`title`	Plot title
`y.axis.title`	y axis title; Default = ""
`y.max`	y axis maximum value; Default = 1
`point.size`	Point size; Default = 1
`connect.dots`	If True draws dots for each iteration; Default = True
`plot.legend`	If True write legend of plot; Default = T
`legend.ncol`	legend.n Default = 1
`font.size.med`	Medium font size; Default = 14
`font.size.large`	Large font size; Default = 16
`plot.margin`	Margin vector for plot; Default = unit(c(0.5, 0.5, 0.5, 0.5), "cm"))

Value

A ggplot object

PlotSignaturesContProbs *PlotSignaturesContProbs*

Description

Plots a horizontal barplot of identified mutational signatures

Usage

```
PlotSignaturesContProbs(df.identified.mut.sigs, df.ref.sigs.groups.colors,
  title, convert.to.percentage = T, font.size.small = 8,
  font.size.med = 14, plot.margin = unit(c(0.5, 0.5, 0.5, 0.5), "cm"))
```

Arguments

df.identified.mut.sigs	A data.frame of identified mutational signatures
df.ref.sigs.groups.colors	A data.frame with 'signature', 'group', and 'color' columns
title	Plot title
convert.to.percentage	If true, convert y values to percentage (x 100); Default = T,
font.size.small	Small font size; Default = 8,
font.size.med	Medium font size; Default = 14,
plot.margin	Margin vector for drawing plot; Default = unit(c(0.5, 0.5, 0.5, 0.5), "cm"))

Value

A ggplot object

Examples

```
## Not run:
 g <- PlotSignaturesContProbs(sigs = c(mutalisk.results$identified.mut.sigs),
 sigs.probs = c(mutalisk.results$identified.mut.sigs.probs),
 df.ref.sigs.groups.colors = GetPCAWGMutSigsEtiologiesColors())
 print(g)

## End(Not run)
```

PlotTable *PlotTable*

Description

Plots basic statistics table

Usage

```
PlotTable(df, padding = 20, font.size = 14)
```

Arguments

df	= A data.frame where the first column is header and the second column is data value
padding	Padding size; Default = 20
font.size	Font size; Default = 14

Value

A plot

PlotTriNucSpectrum *PlotTriNucSpectrum*

Description

Plots the spectrum of 96 trinucleotide distribution (C>A, C>G, C>T, T>A, T>C, T>G) Please note that this function assumes that both sub.types and spectrum are sorted in the following order: C>A, C>G, C>T, T>A, T>C, T>G

Usage

```
PlotTriNucSpectrum(sub.types, spectrum, max.y.val, min.y.val, y.axis.title,
  draw.top.strip = T, draw.x.axis.labels = T, draw.y.axis.labels = T,
  draw.y.axis.title = T, font.size.small = 8, font.size.med = 14,
  plot.margin.top = 0.5, plot.margin.bottom = 0.5,
  plot.margin.left = 0.5, plot.margin.right = 0.5, title)
```

Arguments

sub.types	A character vector (types of 96 trinucleotide substitutions)
spectrum	A numeric vector (96 elements)
max.y.val	y axis maximum value
min.y.val	y axis minimum value
y.axis.title	y axis title
draw.top.strip	If True then draws top strip; Default = T
draw.x.axis.labels	If True then draws x axis labels; Default = T
draw.y.axis.labels	If True then draws y axis labels; Default = T
draw.y.axis.title	If True then draws y axis title; Default = T
font.size.small	Small font size; Default = 8
font.size.med	Medium font size; Default = 14
plot.margin.top	Top margin; Default = 0.5
plot.margin.bottom	Bottom margin; Default = 0.5
plot.margin.left	Left margin; Default = 0.5
plot.margin.right	Right margin; Default = 0.5
title	Plot title

Value

A ggplot object

PlotVCFStatsBoxPlots *PlotVCFStatsBoxPlots*

Description

Plots multiple (original, refined, artifact vcf) boxplots for single filter parameter

Usage

```
PlotVCFStatsBoxPlots(original.vcf.stat.values, refined.vcf.stat.values,
  artifact.vcf.stat.values, xlab, axis.font.size = 10,
  label.font.size = 10, title.font.size = 12)
```

Arguments

original.vcf.stat.values	A numeric vector corresponding to the original vcf.obj values of single filter parameter
refined.vcf.stat.values	A numeric vector corresponding to the refined vcf.obj values of single filter parameter
artifact.vcf.stat.values	A numeric vector corresponding to the artifact vcf.obj values of single filter parameter
xlab	A string value (x-axis label)
axis.font.size	An integer value (axis font size)
label.font.size	An integer value (label font size)
title.font.size	An integer value (title font size)

Value

A ggboxplot

PlotVCFStatsHistograms

PlotVCFStatsHistograms

Description

Plots multiple VCF stats histograms into one figure

Usage

```
PlotVCFStatsHistograms(plot.values, x.axis.labels, stat.y.max.vals,
  stat.x.max.vals, sample.id, save.file, title, cutoff.values,
  plot.boxplot = F, plot.cutoff.line.color = "#D4012E",
  plot.cutoff.value.lines = F, bin.width = 1, ncol = 4, nrow = 3,
  font.size.med = 10, font.size.large = 12, plot.margin = unit(c(0.5,
  0.5, 0.5, 0.5), "cm"))
```

Arguments

plot.values	A list of multiple numeric vectors
x.axis.labels	A character vector of x axis labels
stat.y.max.vals	A numeric vector of max y-axis values

`stat.x.max.vals`
: A numeric vector of max x-axis values

`sample.id`
: A string value of sample ID

`save.file`
: A string value of file to which the resulting plot will be saved

`title`
: A string value of plot title

`cutoff.values`
: A numeric vector of cutoff values

`plot.boxplot`
: A boolean value (default = False)

`plot.cutoff.line.color`
: A hex string value (default = "#D4012E")

`plot.cutoff.value.lines`
: A boolean value (default = False)

`bin.width`
: An integer value (default = 1; histogram bin width)

`ncol`
: An integer value (default = 4; ggarrange ncol)

`nrow`
: An integer value (default = 3; ggarrange nrow)

`font.size.med`
: An integer value (default = 10)

`font.size.large`
: An integer value (default = 12)

`plot.margin`
: A list (default = unit(c(0.5, 0.5, 0.5, 0.5), "cm"))

Value

A list with the following elements

- f = A ggarrange object
- graphs = A list of length 3; each element is a ggplot histogram

---

`PrepareAnnotationDB` *PrepareAnnotationDB*

Description

Prepares df.genes.of.interest from a vcf.obj (`ReadVCF`) of COSMIC or ClinVar vcf for `AnnotateVCFObj`

Usage

```
PrepareAnnotationDB(annotation.vcf.obj)
```

Arguments

`annotation.vcf.obj`
: vcf.obj of COSMIC or ClinVar vcf file

Value

A data.frame of annotation.vcf.obj

`PrepareArtifactAnnotationTable` *PrepareArtifactAnnotationTable*

Description

Prepares artifactual mutations annotation (filtered, queried) table

Usage

```
PrepareArtifactAnnotationTable(data)
```

Arguments

`data`	A list of elements returned from `RunFIREVAT`

Value

A data.frame

`PrepareArtifactStrandBiasTable` *PrepareArtifactStrandBiasTable*

Description

Prepares artifactual mutations strand biased variants table

Usage

```
PrepareArtifactStrandBiasTable(data)
```

Arguments

`data`	A list of elements returned from `RunFIREVAT`

Value

A data.frame

PrepareArtifactualMutsOptimizationIterationsPlot

PrepareArtifactualMutsOptimizationIterationsPlot

Description

Prepares artifactual mutations optimization iterations plot

Usage

```
PrepareArtifactualMutsOptimizationIterationsPlot(data)
```

Arguments

data	A list of elements returned from RunFIREVAT

Value

A ggplot object

PrepareFilterCutoffsTable

PrepareFilterCutoffsTable

Description

Prepares filter cutoffs table for reporting

Usage

```
PrepareFilterCutoffsTable(data)
```

Arguments

data	A list of elements returned from RunFIREVAT

Value

A data.frame

`PrepareGeneticAlgorithmParametersTable` *PrepareGeneticAlgorithmParametersTable*

Description

Prepares Genetic Algorithm parameters table

Usage

```
PrepareGeneticAlgorithmParametersTable(data)
```

Arguments

`data`	A list of elements returned from `RunFIREVAT`

Value

A data.frame

`PrepareIdentifiedSignaturesPlot` *PrepareIdentifiedSignaturesPlot*

Description

Prepares identified signatures plot for reporting

Usage

```
PrepareIdentifiedSignaturesPlot(data)
```

Arguments

`data`	A list of elements returned from `RunFIREVAT`

Value

A ggarrange object

PrepareMLEReconstructedSpectrumsPlot
PrepareMLEReconstructedSpectrumsPlot

Description

Prepares MLE reconstructed spectrums plot

Usage

```
PrepareMLEReconstructedSpectrumsPlot(data)
```

Arguments

data	A list of elements returned from RunFIREVAT

Value

A ggarrange object

PrepareNucleotideSubstitutionTypesPlot
PrepareNucleotideSubstitutionTypesPlot

Description

Prepares nucleotide substitution types plot

Usage

```
PrepareNucleotideSubstitutionTypesPlot(data)
```

Arguments

data	A list of elements returned from RunFIREVAT

Value

A ggarrange object

PrepareObservedSpectrumsPlot
PrepareObservedSpectrumsPlot

Description

Prepares observed spectrums plot

Usage

```
PrepareObservedSpectrumsPlot(data)
```

Arguments

data	A list of elements returned from RunFIREVAT

Value

A ggarrange object

PrepareOptimizationResultsTable
PrepareOptimizationResultsTable

Description

Prepares optimization results table

Usage

```
PrepareOptimizationResultsTable(data)
```

Arguments

data	A list of elements returned from RunFIREVAT

Value

A data.frame

PrepareOptimizedVCFStatisticsPlot
PrepareOptimizedVCFStatisticsPlot

Description

Prepares optimized VCF statistics plot

Usage

```
PrepareOptimizedVCFStatisticsPlot(data)
```

Arguments

data	A list of elements returned from RunFIREVAT

Value

A ggarrange object

PrepareRefinedAnnotationTable
PrepareRefinedAnnotationTable

Description

Prepares refined mutations annotation (filtered, queried) table

Usage

```
PrepareRefinedAnnotationTable(data)
```

Arguments

data	A list of elements returned from RunFIREVAT

Value

A data.frame

`PrepareRefinedMutsOptimizationIterationsPlot`
PrepareRefinedMutsOptimizationIterationsPlot

Description

Prepares refined mutations optimization iterations plot

Usage

```
PrepareRefinedMutsOptimizationIterationsPlot(data)
```

Arguments

`data`	A list of elements returned from `RunFIREVAT`

Value

A ggplot object

`PrepareRefinedStrandBiasTable`
PrepareRefinedStrandBiasTable

Description

Prepares refined mutations strand biased variants table

Usage

```
PrepareRefinedStrandBiasTable(data)
```

Arguments

`data`	A list of elements returned from `RunFIREVAT`

Value

A data.frame

PrepareResidualSpectrumsPlot
PrepareResidualSpectrumsPlot

Description

Prepares residual spectrums plot

Usage

```
PrepareResidualSpectrumsPlot(data)
```

Arguments

data	A list of elements returned from RunFIREVAT

Value

A ggarrange object

PrepareTrinucleotideSpectrumsTable
PrepareTrinucleotideSpectrumsTable

Description

Prepares trinucleotide spectrums table

Usage

```
PrepareTrinucleotideSpectrumsTable(data)
```

Arguments

data	A list of elements returned from RunFIREVAT

Value

A data.frame

QueryAnnotatedVCF *FilterAnnotatedVCF*

Description

Annotates a vcf.obj using df.variants.of.interest (from (PrepareAnnotationDB)

Usage

```
QueryAnnotatedVCF(vcf.obj.annotated, filter.key.value.pairs,
  filter.condition = "AND")
```

Arguments

vcf.obj.annotated	AnnotateVCFObj
filter.key.value.pairs	A list with the key as the column name and value as the filtering values. E.g. list("CLNSIG" = c("Pathogenic", "Pathogenic/Likely_pathogenic"))
filter.condition	'AND' or 'OR'.

Value

A vcf.obj

ReadOptimizationIterationReport *ReadOptimizationIterationReport*

Description

Read optimization iteration report

Usage

```
ReadOptimizationIterationReport(data)
```

Arguments

data	A list of elements returned from RunFIREVAT

Value

A data.frame of FIREVAT optimization logs

ReadVCF *ReadVCF*

Description

Reads a .vcf file

Usage

```
ReadVCF(vcf.file, genome = "hg19", split.info = FALSE,
  check.chromosome.name = TRUE)
```

Arguments

vcf.file	(full path of a .vcf file)
genome	('hg19' or 'hg38')
split.info	A boolean value. If TRUE, then makes the INFO column in the vcf as a separate column. Default value is FALSE.
check.chromosome.name	A boolean value. If TRUE, then check whether converts 'MT' to 'M' and adds 'chr' to the CHROM column. Default value is TRUE.

Value

A list with elements 'data', 'header', 'genome'

ReportFIREVATResults *ReportFIREVATResults*

Description

Reports FIREVAT results in html format (generated from Rmd)

Usage

```
ReportFIREVATResults(data)
```

Arguments

data	A list of main data from RunFIREVAT

Value

An updated data list

RunFIREVAT *RunFIREVAT*

Description

Runs FIREVAT using configuration data. Filters point mutations in the user-specified vcf file based on mutational signature identification and outputs the refined and artifact vcf files as well as metadata related to the refinement process.

Usage

```
RunFIREVAT(vcf.file, vcf.file.genome, config.file, df.ref.mut.sigs,
  target.mut.sigs, sequencing.artifact.mut.sigs, num.cores, output.dir,
  mode = "ga", init.artifact.stop = 0.05,
  objective.fn = Default.Obj.Fn, use.suggested.soln = TRUE,
  ga.type = "real-valued", ga.pop.size = 200, ga.max.iter = 200,
  ga.run = 50, ga.pmutation = 0.25, mutalisk = TRUE,
  mutalisk.method = "all", mutalisk.random.sampling.count = 20,
  mutalisk.random.sampling.max.iter = 10,
  perform.strand.bias.analysis = TRUE,
  strand.bias.perform.fdr.correction = TRUE,
  strand.bias.fdr.correction.method = "BH",
  ref.forward.strand.var = NULL, ref.reverse.strand.var = NULL,
  alt.forward.strand.var = NULL, alt.reverse.strand.var = NULL,
  annotate = TRUE, df.annotation.db = NULL,
  annotated.columns.to.display = NULL,
  annotation.filter.key.value.pairs = NULL,
  annotation.filter.condition = "AND", write.vcf = TRUE,
  report = TRUE, save.rdata = TRUE, save.tsv = TRUE,
  report.format = "html", verbose = TRUE)
```

Arguments

`vcf.file`	String value corresponding to input .vcf file. Please provide the full path.
`vcf.file.genome`	Genome assembly of the input .vcf file. The value should be eitehr 'hg19' or 'hg38'.
`config.file`	String value corresponding to input configuration file. For more details please refer to ...
`df.ref.mut.sigs`	A data.frame of the reference mutational signatures
`target.mut.sigs`	A character vector of the target mutational signatures from reference mutational signatures.
`sequencing.artifact.mut.sigs`	A character vector of the sequencing artifact mutational signatures from reference mutational signatures.

num.cores Number of cores to allocate

output.dir String value of the desired output directory

mode String value. The value should be either 'ga' or 'manual'.

init.artifact.stop
Numeric value less than 1. If the sum of sequencing artifact weights in the user-specified original VCF file (i.e. vcf.file) is less than or equal to this value then FIREVAT does not perform variant refinement. Default value is 0.05. Note that this option does not apply if 'mode' is 'manual'.

objective.fn Objective value derivation function. Default: Default.Obj.Fn.

use.suggested.soln
Boolean value. If TRUE, then FIREVAT passes the default values of filter variables declared as 'use_in_filter' in the config file to the 'suggestions' parameter of the Genetic Algorithm package. If FALSE, then FIREVAT supplies NULL to the GA package 'suggestions' parameter. FIREVAT also computes baseline performance of each filter variable and uses fittest population from each variable as a suggested solution.

ga.type String value. The value should be either 'binray' or 'real-valued'.

ga.pop.size Integer value of the Genetic Algorithm 'population size' parameter. Default: 200. This value should be set based on the number of filter parameters. Recommendation: 40 per filter parameter.

ga.max.iter Integer value of the Genetic Algorithm 'maximum iterations' parameter. Ddefault: 200. This value should be set based on the number of filter parameters. Recommendation: same as 'ga.pop.size'.

ga.run Integer value of the Genetic Algorithm 'run' parameter. Default: 50. This value should be set based on the 'ga.max.iter' parameter. Recommendation: 25 percent of 'ga.max.iter'.

ga.pmutation Float value of the Genetic Algorithm 'mutation probability' parameter. Default: 0.25.

mutalisk If TRUE, confirm mutational signature analysis with Mutalisk. Default: TRUE.

mutalisk.method
Mutalisk signature identification method. Default: 'random.sampling'. The value can be either 'all' or 'random.sampling'. 'all' uses all target.mut.sigs to identify mutational signatures. 'random.sampling' randomly samples from target.mut.sigs to identify mutational signatures.

mutalisk.random.sampling.count
Mutalisk random sampling count. Default: 20. The number of signatures to sample from target.mut.sigs

mutalisk.random.sampling.max.iter
Mutalisk random sampling maximum iteration. Default: 10. The number of times Mutalisk randomly samples from target.mut.sigs before determining the candidate signatures.

perform.strand.bias.analysis
If TRUE, then performs strand bias analysis.

strand.bias.perform.fdr.correction
If TRUE, then performs false discovery rate correction for strand bias analysis.

`strand.bias.fdr.correction.method`
: A string value. Default value is 'BH'. Refer to 'p.adjust()' function method.

`ref.forward.strand.var`
: A string value.

`ref.reverse.strand.var`
: A string value,

`alt.forward.strand.var`
: A string value,

`alt.reverse.strand.var`
: A string value,

`annotate`
: A boolean value. Default value is TRUE.

`df.annotation.db`
: A data.frame. Please refer to `PrepareAnnotationDB`

`annotated.columns.to.display`
: A character vector.

`annotation.filter.key.value.pairs`
: A list.

`annotation.filter.condition`
: 'AND' or 'OR'.

`write.vcf`
: If TRUE, write original/refined/artifact vcfs. Default: TRUE.

`report`
: If TRUE, generate report. Default: TRUE.

`save.rdata`
: If TRUE, save rdata. Default: TRUE.

`save.tsv`
: If TRUE, save tsv. Default: TRUE.

`report.format`
: The format of FIREVAT report. We currently only support 'html'.

`verbose`
: If TRUE, provides process detail. Default: TRUE.

Value

A list with the following elements

- f = A ggarrange object
- graphs = A list of length 3; each element is a ggplot histogram

---

`RunMutalisk` *RunMutalisk*

Description

Identifies mutational signatures using Mutalisk

Usage

```
RunMutalisk(vcf.obj, df.ref.mut.sigs, target.mut.sigs,
  random.sampling.candidate.mut.sigs = c(), method = "random.sampling",
  n.sample = 20, n.iter = 10, verbose = TRUE)
```

Arguments

vcf.obj	A list (from firevat_vcf::ReadVCF)
df.ref.mut.sigs	A data.frame of reference mutational signatures
target.mut.sigs	A character vector of target mutational signatures names to identify from
random.sampling.candidate.mut.sigs	A character vector of mutational signatures names that gets appended to the list of candidate mutational signatures so that these are always considered.
method	A string value (must be either 'random.sampling' or 'all'). The method 'random.sampling' samples (without replacement) 'n.sample' number of signatures 'n.iter' number of times and runs the candidate signatures one last time. The method 'all' uses all target.mut.sigs
n.sample	An integer value ('random.sampling' method parameter) Number of signatures to choose for each iteration of random sampling).
n.iter	An integer value ('random.sampling' method parameter). Number of iterations to perform random sampling.
verbose	If true, provides process details

Value

A list with the following elements

- num.point.mutationsAn integer value - count of total point mutations
- sub.typesA character vector of length 96
- sub.types.spectrumA numeric vector of length 96
- num.mut.sigsAn integer value (count of unique mutational signatures identified)
- identified.mut.sigsA character vector where each element is a mutational signature identified
- identified.mut.sigs.probsA numeric vector where each element is the weight of mutational signature identified. The ordering follows identified.mut.sigs
- identified.mut.sigs.spectrumA numeric vector of length 96
- residualsA numeric vector of length 96
- rssA numeric value (residual sum of squares)
- cos.sim.scoreA numeric value (cosine similarity score between observed mutational spectrum and reconstructed mutational signatures)
- all.models.sigsA list where each element is a model; a model is a list of signatures identified)
- all.models.sigs.probsA list where each element is a model; a model is a list of contribution probabilities
- all.models.cos.sim.scoresA list where each element is a model; a model is a list of cosine similarity socres

RunMutaliskHelper *RunMutaliskHelper*

Description

Helper function for RunMutalisk

Usage

```
RunMutaliskHelper(vcf.trinucleotide.data, df.ref.mut.sigs, target.mut.sigs)
```

Arguments

vcf.trinucleotide.data	A data.frame (from firevat_mutalisk::MutaliskParseVCFObj)
df.ref.mut.sigs	A data.frame of reference mutational signatures
target.mut.sigs	A character vector of target mutational signatures names

Value

A list with the following elements

- num.point.mutationsAn integer value - count of total point mutations
- sub.typesA character vector of length 96
- sub.types.spectrumA numeric vector of length 96
- num.mut.sigsAn integer value (count of unique mutational signatures identified)
- identified.mut.sigsA character vector where each element is a mutational signature identified
- identified.mut.sigs.probsA numeric vector where each element is the weight of mutational signature identified. The ordering follows identified.mut.sigs
- identified.mut.sigs.spectrumA numeric vector of length 96
- residualsA numeric vector of length 96
- rssA numeric value (residual sum of squares)
- cos.sim.scoreA numeric value (cosine similarity score between observed mutational spectrum and reconstructed mutational signatures)
- all.models.sigsA list where each element is a model; a model is a list of signatures identified)
- all.models.sigs.probsA list where each element is a model; a model is a list of contribution probabilities
- all.models.cos.sim.scoresA list where each element is a model; a model is a list of cosine similarity socres

RunMutPat *RunMutPat*

Description

Identifies mutational signatures using Mutational Patterns

Usage

```
RunMutPat(mut.pat.input, df.mut.pat.ref.sigs, target.mut.sigs,
  verbose = TRUE)
```

Arguments

mut.pat.input	A list from MutPatParseVCFObj
df.mut.pat.ref.sigs	A data.frame returned by MutPatParseRefMutSigs
target.mut.sigs	A character vector of target mutational signatures names
verbose	If true, provides process details

Value

A list with the following elements

- tumor.mutation.types.spectrumA numeric vector of length 96 - 'observed' spectrum
- identified.mutation.types.spectrumA numeric vector of length 96 - 'identified' spectrum
- residualsA numeric vector of length 96 - residuals
- mutation.typesA character vector of length 96
- identified.mut.sigsA character vector where each element is a mutational signature identified
- identified.mut.sigs.contribution.weightsA numeric vector where each element is the weight of mutational signature identified. The ordering follows identified.mut.sigs
- cosine.similarity.scoreA numeric value

Examples

```
## Not run:
vcf.obj <- ReadVCF(vcf.file = "../data/sample/HNT-082-BT.final.call.vcf", genome = "hg19")
df.ref.mut.sigs <- GetPCAWGMutSigs()
target.mut.sigs <- GetPCAWGMutSigsNames()
RunMutPat(vcf.obj = vcf.obj,
df.ref.mut.sigs = df.ref.mut.sigs,
target.mut.sigs = target.mut.sigs)

## End(Not run)
```

TriNuc.Mutation.Type.Hex.Colors *Constant*

Description

Hex codes for the mutation types (for plotting purposes)

Usage

```
TriNuc.Mutation.Type.Hex.Colors
```

Format

An object of class `character` of length 6.

UpdateFilter *UpdateFilter*

Description

Update filter based on optim parameter values

Usage

```
UpdateFilter(vcf.filter, param.values)
```

Arguments

`vcf.filter`	A list from MakeFilterFromConfig
`param.values`	A numeric vector contains filtering value (same length with length(vcf.config.filter))

Value

Updated vcf.filter (list)

`WriteFIREVATResultsToTSV` *WriteFIREVATResultsToTSV*

Description

Writes FIREVAT results to a csv file

Usage

```
WriteFIREVATResultsToTSV(firevat.results)
```

Arguments

`firevat.results`	List returned from RunFIREVAT

`WriteVCF` *WriteVCF*

Description

Writes a vcf.obj to a .vcf file

Usage

```
WriteVCF(vcf.obj, save.file)
```

Arguments

`vcf.obj`	(from the function ReadVCF)
`save.file`	(full path including filename)

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