

# Package ‘FIREVAT’

March 11, 2019

**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.

**Version** 0.1.9

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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

---

Chromosome.Names	<i>Constant</i>
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---

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	<i>ComputeZScore</i>
---------------	----------------------

---

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	<i>Default.Obj.Fn</i>
----------------	-----------------------

---

### 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	<i>Transform default filtering parameters to a binary vector</i>
-----------------------	--

---

### 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 <a href="#">MakeFilter</a>
params.bit.len	A list with bit lengths of filtering parameters which is generated from <a href="#">ParameterToBits</a>

### 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	<i>Euc.Obj.Fn</i>
------------	-------------------

---

**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	<i>Exp.Weighted.Obj.Fn.1</i>
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---

**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**

<code>vcf.obj</code>	A list from <a href="#">ReadVCF</a>
<code>save.config</code>	If true, save config.obj to config.path
<code>config.path</code>	File path to write config.obj (json or yaml)

**Value**

`config.obj`

---

GetCOSMICMutSigs	<i>GetCOSMICMutSigs</i>
------------------	-------------------------

---

**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
<i>GetCOSMICMutSigsNames</i>

---

**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

---

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'

---

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	<i>MutaliskParseVCFObj</i>
---------------------	----------------------------

---

**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	<i>MutPatParseRefMutSigs</i>
-----------------------	------------------------------

---

**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	<i>MutPatParseVCFObj</i>
-------------------	--------------------------

---

**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	<i>ParameterToBits</i>
-----------------	------------------------

---

**Description**

Calculate the number of bits needed to conduct FIREVAT GA 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  $\max(\text{vcf.obj\$data}[[\text{param}]]) < 1$ , then multiply multiplier to the vector

**Value**

A list with the elements 'params.bit.len' containing the bit lengths of each parameter 'vcf.obj' 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	<i>PlotMutaliskResults</i>
---------------------	----------------------------

---

**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 <a href="#">RunMutalisk</a>
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	<i>PlotMutationTypes</i>
-------------------	--------------------------

---

## 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

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

<code>df.identified.mut.sigs</code>	A data.frame of identified mutational signatures
<code>df.ref.sigs.groups.colors</code>	A data.frame with 'signature', 'group', and 'color' columns
<code>title</code>	Plot title
<code>convert.to.percentage</code>	If true, convert y values to percentage (x 100); Default = T,
<code>font.size.small</code>	Small font size; Default = 8,
<code>font.size.med</code>	Medium font size; Default = 14,
<code>plot.margin</code>	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	<i>PlotTable</i>
-----------	------------------

---

**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	<i>PlotTriNucSpectrum</i>
--------------------	---------------------------

---

**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**

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

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

<code>stat.x.max.vals</code>	A numeric vector of max x-axis values
<code>sample.id</code>	A string value of sample ID
<code>save.file</code>	A string value of file to which the resulting plot will be saved
<code>title</code>	A string value of plot title
<code>cutoff.values</code>	A numeric vector of cutoff values
<code>plot.boxplot</code>	A boolean value (default = False)
<code>plot.cutoff.line.color</code>	A hex string value (default = "#D4012E")
<code>plot.cutoff.value.lines</code>	A boolean value (default = False)
<code>bin.width</code>	An integer value (default = 1; histogram bin width)
<code>ncol</code>	An integer value (default = 4; ggarrange ncol)
<code>nrow</code>	An integer value (default = 3; ggarrange nrow)
<code>font.size.med</code>	An integer value (default = 10)
<code>font.size.large</code>	An integer value (default = 12)
<code>plot.margin</code>	A list (default = <code>unit(c(0.5, 0.5, 0.5, 0.5), "cm")</code> )

**Value**

A list with the following elements

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

---

PrepareAnnotationDB	<i>PrepareAnnotationDB</i>
---------------------	----------------------------

---

**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 with the columns specified in `columns.to.include`

---

PrepareArtifactAnnotationTable
<i>PrepareArtifactAnnotationTable</i>

---

**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
<i>PrepareArtifactStrandBiasTable</i>

---

**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
<i>PrepareGeneticAlgorithmParametersTable</i>

---

**Description**

Prepares Genetic Algorithm parameters table

**Usage**

PrepareGeneticAlgorithmParametersTable(data)

**Arguments**

data                    A list of elements returned from [RunFIREVAT](#)

**Value**

A data.frame

---

PrepareIdentifiedSignaturesPlot
<i>PrepareIdentifiedSignaturesPlot</i>

---

**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
<i>PrepareObservedSpectrumsPlot</i>

---

**Description**

Prepares observed spectrums plot

**Usage**

PrepareObservedSpectrumsPlot(data)

**Arguments**

data                   A list of elements returned from [RunFIREVAT](#)

**Value**

A ggarrange object

---

PrepareOptimizationResultsTable
<i>PrepareOptimizationResultsTable</i>

---

**Description**

Prepares optimization results table

**Usage**

PrepareOptimizationResultsTable(data)

**Arguments**

data                   A list of elements returned from [RunFIREVAT](#)

**Value**

A data.frame

---

PrepareOptimizedVCFStatisticsPlot
<i>PrepareOptimizedVCFStatisticsPlot</i>

---

**Description**

Prepares optimized VCF statistics plot

**Usage**

PrepareOptimizedVCFStatisticsPlot(data)

**Arguments**

data                    A list of elements returned from [RunFIREVAT](#)

**Value**

A ggarrange object

---

PrepareRefinedAnnotationTable
<i>PrepareRefinedAnnotationTable</i>

---

**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
<i>PrepareResidualSpectrumsPlot</i>

---

**Description**

Prepares residual spectrums plot

**Usage**

PrepareResidualSpectrumsPlot(data)

**Arguments**

data                    A list of elements returned from [RunFIREVAT](#)

**Value**

A ggarrange object

---

PrepareTrinucleotideSpectrumsTable
<i>PrepareTrinucleotideSpectrumsTable</i>

---

**Description**

Prepares trinucleotide spectrums table

**Usage**

PrepareTrinucleotideSpectrumsTable(data)

**Arguments**

data                    A list of elements returned from [RunFIREVAT](#)

**Value**

A data.frame

---

QueryAnnotatedVCF	<i>FilterAnnotatedVCF</i>
-------------------	---------------------------

---

**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	<i>ReadOptimizationIterationReport</i>
---------------------------------	--

---

**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	<i>ReadVCF</i>
---------	----------------

---

**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	<i>ReportFIREVATResults</i>
----------------------	-----------------------------

---

**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 specified vcf file based on mutational signature decomposition and outputs the refined and artifact vcf 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", objective.fn = Default.Obj.Fn,
            use.suggested.soln = TRUE, ga.pop.size = 200, ga.max.iter = 200,
            ga.run = 50, ga.pmutation = 0.25, 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,
            report.format = "html", annotate = TRUE, df.annotation.db = NULL,
            annotated.columns.to.display = NULL,
            annotation.filter.key.value.pairs = NULL,
            annotation.filter.condition = "AND", 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 either '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'.
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.
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. Default: 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.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,



`report.format` The format of FIREVAT report. We currently only support 'html'.  
`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'.  
`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.mutations An integer value - count of total point mutations
- sub.types A character vector of length 96
- sub.types.spectrum A numeric vector of length 96
- num.mut.sigs An integer value (count of unique mutational signatures identified)
- identified.mut.sigs A character vector where each element is a mutational signature identified
- identified.mut.sigs.probs A numeric vector where each element is the weight of mutational signature identified. The ordering follows identified.mut.sigs
- identified.mut.sigs.spectrum A numeric vector of length 96
- residuals A numeric vector of length 96
- rss A numeric value (residual sum of squares)
- cos.sim.score A numeric value (cosine similarity score between observed mutational spectrum and reconstructed mutational signatures)
- all.models.sigs A list where each element is a model; a model is a list of signatures identified
- all.models.sigs.probs A list where each element is a model; a model is a list of contribution probabilities
- all.models.cos.sim.scores A list where each element is a model; a model is a list of cosine similarity scores

---

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.mutations` An integer value - count of total point mutations
- `sub.types` A character vector of length 96
- `sub.types.spectrum` A numeric vector of length 96
- `num.mut.sigs` An integer value (count of unique mutational signatures identified)
- `identified.mut.sigs` A character vector where each element is a mutational signature identified
- `identified.mut.sigs.probs` A numeric vector where each element is the weight of mutational signature identified. The ordering follows `identified.mut.sigs`
- `identified.mut.sigs.spectrum` A numeric vector of length 96
- `residuals` A numeric vector of length 96
- `rss` A numeric value (residual sum of squares)
- `cos.sim.score` A numeric value (cosine similarity score between observed mutational spectrum and reconstructed mutational signatures)
- `all.models.sigs` A list where each element is a model; a model is a list of signatures identified
- `all.models.sigs.probs` A list where each element is a model; a model is a list of contribution probabilities
- `all.models.cos.sim.scores` A list where each element is a model; a model is a list of cosine similarity scores

---

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.spectrum` A numeric vector of length 96 - 'observed' spectrum
- `identified.mutation.types.spectrum` A numeric vector of length 96 - 'identified' spectrum
- `residuals` A numeric vector of length 96 - residuals
- `mutation.types` A character vector of length 96
- `identified.mut.sigs` A character vector where each element is a mutational signature identified
- `identified.mut.sigs.contribution.weights` A numeric vector where each element is the weight of mutational signature identified. The ordering follows `identified.mut.sigs`
- `cosine.similarity.score` A 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	<i>UpdateFilter</i>
--------------	---------------------

---

**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)

---

WriteVCF	<i>WriteVCF</i>
----------	-----------------

---

**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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