Package 'Neoantimon'

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Type Package

Title Neoantimon: An R package for automatic identification of tumor-specific neoantigens from sequencing data

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Description This Package is develped to calculate candidates neoantigens from Mutation Data (.vcf) requiring netMHCpan3.0, netMHCIIpan3.1, human refMrna, and, refFlat. If you do not have some of these files, see README.md.

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VignetteBuilder knitr

Suggests knitr, rmarkdown

LazyData TRUE

Imports utils

RoxygenNote 6.0.1

R topics documented:

MainINDELClass1 *Calculate Neoantigen Candidates on Indels for MHC Class1*

Description

Calculate Neoantigen Candidates on Indels for MHC Class1

Usage

```
MainINDELClass1(input_file, HLA_file, file_name_in_HLA_table = input_file,
  hmdir = getwd(), job_ID = "NO_JOB_ID", RNAseq_file = NA, RNA_bam = NA,
  CNV = NA, ccfp_dir = paste(hmdir, "lib/ccfp.jar", sep = ""),
  Purity = NA, netMHCpan_dir = paste(hmdir,
  "lib/netMHCIIpan-3.1/netMHCIIpan", sep = ""), refDNA = paste(hmdir,
  "lib/GRCh37.fa", sep = ""), refFlat_file = paste(hmdir, "/data/refFlat.txt",
  sep = ""), refMrna_1 = paste(hmdir, "/data/refMrna.cut1.fa", sep = ""),
  refMrna_3 = paste(hmdir, "/data/refMrna.cut3.fa", sep = ""),
  samtools_dir = "samtools", bcftools_dir = "bcftools", Chr_Column = 1,
  Mutation_Start_Column = 2, Mutation_End_Column = 3,
  Mutation_Ref_Column = 4, Mutation_Alt_Column = 5, NM_ID_Column = 10,
  Depth_Normal_Column = NA, Depth_Tumor_Column = NA,
  ambiguous_between_exon = 0, ambiguous_codon = 0, peptide_length = c(8,
  9, 10, 11, 12, 13))
```

Arguments

input_file	(Required) An input vcf file annotated by, e.g., ANNOVAR (http://annovar.openbioinformatics.org/en or other softwares. See by data(sample_vcf); sample_vcf;
HLA_file	(Required) A tab separated file indicating HLA types . The 1st column is input_file name, and the following columns indicate HLA types. See by data(sample_hla_table_c2); sample_hla_table_c2;
file_name_in_HLA_table	If the name (1st column) in HLA table is not input_file, indicate the corresponding name (Default=input_file).
hmdir	Home directory for the analysis (Default=getwd()).
job_ID	Job-Id to be attached in output files (Default="NO_JOB_ID").
RNAseq_file	(Default=NA) A file including RNA expressions. The 1st, 2nd and 3rd columns are "GeneSymbol Chr:ExonStart-ExonEnd(locus) Expression Amount", respectively. The 1st row should be any header. See by data(sample_rna_exp); sample_rna_exp;
RNA_bam	RNA bam file to calculate variant allele frequency of RNA at each mutation (Default=NA).
CNV	A file including copy number variation to calculate cancer cell fraction probability (CCFP) (Default=NA). The format is according to ASCAT (https://www.crick.ac.uk/peter-van-loo/software/ASCAT) output files. The columns are "Chromosome Position Log R segmented LogR BAF segmented BAF Copy number Minor allele Raw copy number" The 1st row should be the above header. See data(sample_copynum); sample_copynum;
ccfp_dir	The file directory to CCFP.pl (Default="lib/ccfp.jar").

`Purity` Tumor purity or tumor contents ratio required to calculate CCFP (Default=NA).

`netMHCpan_dir` The file directory to netMHCpan (Default="lib/netMHCpan-3.0/netMHCpan").

`refDNA` refDNA information to be used to calculate RNA VAF (Default="ib/GRCh37.fa").

`refFlat_file` refFlat file to be used in constructing peptide. (Default=paste(hmdir,"lib/refFlat.txt",sep="")

`refMrna_1` refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut1.fa",sep= This file is automaticalluy generated through the command in README, but includes NM_IDs.

`refMrna_3` refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut3.fa",sep= This file is automaticalluy generated through the command in README, but includes the amino acid sequence.

`samtools_dir` The file directory to samtools (Default="samtools"). It shouled be indicated when you indicate RNA-bam and try to calculate RNA VAF .

`bcftools_dir` The file directory to netMHCpan (Default="bcftools"). It shouled be indicated when you indicate RNA-bam and try to calculate RNA VAF . samtools 0_x_x includes bcftools in the directory.

`Chr_Column` The column number describing Chromosome number in input_file (Default=1).

`Mutation_Start_Column`
The column number describing Mutation Start Position in input_file (Default=2) .

`Mutation_End_Column`
The column number describing Mutation End Position in input_file (Default=3).

`Mutation_Ref_Column`
The column number describing Mutation Ref in input_file (Default=4).

`Mutation_Alt_Column`
The column number describing Mutation Alt in input_file (Default=5).

`NM_ID_Column` The column number describing NM IDs in input_file (Default=10).

`Depth_Normal_Column`
The column number describing the read count from normal cells (Default = NA)

`Depth_Tumor_Column`
The column number describing the read count from tumor cells (Default = NA)

`ambiguous_between_exon`
The maximum number to permit the differences between Exon-Lengths from refFlat and refMrna (Default=0).

`ambiguous_codon`
The maximum number to permit the differences between inputfile- and refMrna-oriented translation START/END position (Default=0).

`peptide_length` Peptide Length to be generated (Default=8,9,10,11,12,13).

Value

void (Calculated Neoantigen Files will be generated as .tsv files.)

MainINDELClass2 *Calculate Neoantigen Candidates on Indels for MHC Class2*

Description

Calculate Neoantigen Candidates on Indels for MHC Class2

Usage

```
MainINDELClass2(input_file, HLA_file, file_name_in_HLA_table = input_file,
  hmdir = getwd(), job_ID = "NO_JOB_ID", RNAseq_file = NA, RNA_bam = NA,
  CNV = NA, ccfp_dir = paste(hmdir, "lib/ccfp.jar", sep = ""),
  Purity = NA, netMHCpan_dir = paste(hmdir,
  "lib/netMHCIIpan-3.1/netMHCIIpan", sep = ""), refDNA = paste(hmdir,
  "lib/GRCh37.fa", sep = ""), refFlat_file = paste(hmdir, "/data/refFlat.txt",
  sep = ""), refMrna_1 = paste(hmdir, "/data/refMrna.cut1.fa", sep = ""),
  refMrna_3 = paste(hmdir, "/data/refMrna.cut3.fa", sep = ""),
  samtools_dir = "samtools", bcftools_dir = "bcftools", Chr_Column = 1,
  Mutation_Start_Column = 2, Mutation_End_Column = 3,
  Mutation_Ref_Column = 4, Mutation_Alt_Column = 5, NM_ID_Column = 10,
  Depth_Normal_Column = NA, Depth_Tumor_Column = NA,
  ambiguous_between_exon = 0, ambiguous_codon = 0, peptide_length = c(15))
```

Arguments

input_file	(Required) An input vcf file annotated by, e.g., ANNOVAR (http://annovar.openbioinformatics.org/en or other softwares. See by data(sample_vcf); sample_vcf;
HLA_file	(Required) A tab separated file indicating HLA types . The 1st column is input_file name, and the following columns indicate HLA types. See by data(sample_hla_table_c2); sample_hla_table_c2;
file_name_in_HLA_table	If the name (1st column) in HLA table is not input_file, indicate the corresponding name (Default=input_file).
hmdir	Home directory for the analysis (Default=getwd()).
job_ID	Job-Id to be attached in output files (Default="NO_JOB_ID").
RNAseq_file	(Default=NA) A file including RNA expressions. The 1st, 2nd and 3rd columns are "GeneSymbol Chr:ExonStart-ExonEnd(locus) Expression Amount", respectively. The 1st row should be any header. See by data(sample_rna_exp); sample_rna_exp;
RNA_bam	RNA bam file to calculate variant allele frequency of RNA at each mutation (Default=NA).
CNV	A file including copy number variation to calculate cancer cell fraction probability (CCFP) (Default=NA). The format is according to ASCAT (https://www.crick.ac.uk/peter-van-loo/software/ASCAT) output files. The columns are "Chromosome Position Log R segmented LogR BAF segmented BAF Copy number Minor allele Raw copy number" The 1st row should be the above header. See data(sample_copynum); sample_copynum;
ccfp_dir	The file directory to CCFP.pl (Default="lib/ccfp.jar").

Purity	Tumor purity or tumor contents ratio required to calculate CCFP (Default=NA).
netMHCpan_dir	The file directory to netMHCpan (Default="lib/netMHCIIpan-3.1/netMHCpan").
refDNA	refDNA information to be used to calculate RNA VAF (Default="lib/GRCh37.fa").
refFlat_file	refFlat file to be used in constructing peptide. (Default=paste(hmdir,"lib/refFlat.txt",sep="")
refMrna_1	refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut1.fa",sep= This file is automaticalluy generated through the command in README, but includes NM_IDs.
refMrna_3	refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut3.fa",sep= This file is automaticalluy generated through the command in README, but includes the amino acid sequence.
samtools_dir	The file directory to samtools (Default="samtools"). It shouled be indicated when you indicate RNA-bam and try to calculate RNA VAF .
bcftools_dir	The file directory to netMHCpan (Default="bcftools"). It shouled be indicated when you indicate RNA-bam and try to calculate RNA VAF . samtools 0_x_x includes bcftools in the directory.
Chr_Column	The column number describing Chromosome number in input_file (Default=1).
Mutation_Start_Column	The column number describing Mutation Start Position in input_file (Default=2) .
Mutation_End_Column	The column number describing Mutation End Position in input_file (Default=3).
Mutation_Ref_Column	The column number describing Mutation Ref in input_file (Default=4).
Mutation_Alt_Column	The column number describing Mutation Alt in input_file (Default=5).
NM_ID_Column	The column number describing NM IDs in input_file (Default=10).
Depth_Normal_Column	The column number describing the read count from normal cells (Default = NA)
Depth_Tumor_Column	The column number describing the read count from tumor cells (Default = NA)
ambiguous_between_exon	The maximum number to permit the differences between Exon-Lengths from refFlat and refMrna (Default=0).
ambiguous_codon	The maximum number to permit the differences between inputfile- and refMrna-oriented translation START/END position (Default=0).
peptide_length	Peptide Length to be generated (Default=15 in HLA Class2).

Value

void (Calculated Neoantigen Files will be generated as .tsv files.)

`MainMergeClass1` *Merge Results from MainSnvClass1.R*

Description

Merge Results from MainSnvClass1.R

Usage

```
MainMergeClass1(hmdir = getwd(), input_dir, input_file_prefix,
  Tumor_RNA_BASED_ON_DNA = TRUE, INDEL = FALSE)
```

Arguments

`hmdir`	Home directory for the analysis (Default=getwd()).
`input_dir`	Directory storing netMHCpan Results (Required).
`input_file_prefix`	File prefix of netMHCpan Results (Required). If you have "sample_annovar.txt.NO_JOB_ID.HLACL please set "sample_annovar", "sample_annovar.txt" or "sample_annovar.txt.NO_JOB_ID".
`Tumor_RNA_BASED_ON_DNA`	In calculating tumor specific RNA expression, TRUE uses variant allele frequency on DNA. Otherwise, use VAF on RNA (Default=TRUE).
`INDEL`	If the targeting results are generated from Indels, Please check TRUE.

Value

void (Calculated Neoantigen Files will be generated as .tsv files.):

Pos: The position of the fraction of peptide used to be evaluated from the full-length peptide.

Gene: Gene symbol used to be evaluated in NetMHCpan.

MutatedPeptide: The mutant peptide to be evaluated.

Mut_IC50: IC50 value for evaluated mutant peptide.

Mut_Rank: Rank value for evaluated mutanat peptide.

Norm_Peptide: The wild-type peptide to be evaluated.

Norm_IC50: IC50 value for evaluated wild-type peptide.

Norm_Rank: Rank value for evaluated wild-type peptide.

Gene ID: Gene symbol for the peptide.

Chr: Chromosome Number of the mutation.

NM_ID: NM_ID used to construct peptides from the mutation.

Change: The annotation to be described in .vcf file.

ref: reference type nucleic acid base.

alt: alternative type nucleic acid base.

Prob: A probability of reference nucleic acid base described in .vcf file.

MutationProb: A probability of alternative nucleic acid base described in .vcf file.

ExonStart: The exon start position of the corrsponding NM_ID.

ExonEnd: The exon end position of the corrsponding NM_ID.

MutationPosition: The mutation position of the corrsponding NM_ID.

Depth: The depth of the reference nucleic acid base.

TumorDepth: The depth of the alternative nucleic acid base.

PeptideNormal: The full-length of the wild-type peptide.

PeptideMutation: The full-length of the mutant peptide.

TotalRNA: The expression amount of the corresponding RNA.

TumorRNARatio: The variant allele frequency of the corresponding RNA.

TumorRNA: The modified amount of the corresponding RNA level based on (RNA/DNA) VCF.

nA: The total number of A allele copies.

nB: The total number of B allele copies.

Checker: CheckSum

MutRatio: The mean value of the cancer cell fraction probability.

MutRatioMin: The 1% percentile of the cancer cell fraction probability.

MutRatioMax: The 99% percentile of the cancer cell fraction probability.

`MainMergeClass2` *Merge Results from MainSnvClass2.R*

Description

Merge Results from MainSnvClass2.R

Usage

```
MainMergeClass2(hmdir = getwd(), input_dir, input_file_prefix,
  Tumor_RNA_BASED_ON_DNA = TRUE, INDEL = FALSE)
```

Arguments

`hmdir`	Home directory for the analysis (Default=getwd()).
`input_dir`	Directory storing netMHCpan Results (Required).
`input_file_prefix`	File prefix of netMHCpan Results (Required). If you have "sample_annovar.txt.NO_JOB_ID.HLACL please set "sample_annovar", "sample_annovar.txt" or "sample_annovar.txt.NO_JOB_ID".
`Tumor_RNA_BASED_ON_DNA`	In calculating tumor specific RNA expression, TRUE uses variant allele frequency on DNA. Otherwise, use VAF on RNA (Default=TRUE).
`INDEL`	If the targeting results are generated from Indels, Please check TRUE.

Value

void (Calculated Neoantigen Files will be generated as .tsv files.):

Pos: The position of the fraction of peptide used to be evaluated from the full-length peptide.

Gene: Gene symbol used to be evaluated in NetMHCpan.

MutatedPeptide: The mutant peptide to be evaluated.

Mut_IC50: IC50 value for evaluated mutant peptide.

Mut_Rank: Rank value for evaluated mutanat peptide.

Norm_Peptide: The wild-type peptide to be evaluated.

Norm_IC50: IC50 value for evaluated wild-type peptide.

Norm_Rank: Rank value for evaluated wild-type peptide.

Gene ID: Gene symbol for the peptide.

Chr: Chromosome Number of the mutation.

NM_ID: NM_ID used to construct peptides from the mutation.

Change: The annotation to be described in .vcf file.

ref: reference type nucleic acid base.

alt: alternative type nucleic acid base.

Prob: A probability of reference nucleic acid base described in .vcf file.

MutationProb: A probability of alternative nucleic acid base described in .vcf file.

ExonStart: The exon start position of the corrsponding NM_ID.

ExonEnd: The exon end position of the corrsponding NM_ID.

MutationPosition: The mutation position of the corrsponding NM_ID.

Depth: The depth of the reference nucleic acid base.

TumorDepth: The depth of the alternative nucleic acid base.

PeptideNormal: The full-length of the wild-type peptide.

PeptideMutation: The full-length of the mutant peptide.

TotalRNA: The expression amount of the corresponding RNA.

TumorRNARatio: The variant allele frequency of the corresponding RNA.

TumorRNA: The modified amount of the corresponding RNA level based on (RNA/DNA) VCF.

nA: The total number of A allele copies.

nB: The total number of B allele copies.

Checker: CheckSum

MutRatio: The mean value of the cancer cell fraction probability.

MutRatioMin: The 1% percentile of the cancer cell fraction probability.

MutRatioMax: The 99% percentile of the cancer cell fraction probability.

MainSNVClass1 *Calculate Neoantigen Candidates on SNVs for MHC Class1*

Description

Calculate Neoantigen Candidates on SNVs for MHC Class1

Usage

```
MainSNVClass1(input_file, HLA_file, file_name_in_HLA_table = input_file,
  hmdir = getwd(), job_ID = "NO_JOB_ID", RNAseq_file = NA, RNA_bam = NA,
  CNV = NA, ccfp_dir = paste(hmdir, "lib/ccfp.jar", sep = ""),
  Purity = NA, netMHCpan_dir = paste(hmdir,
  "lib/netMHCIIpan-3.1/netMHCIIpan", sep = ""), refDNA = paste(hmdir,
  "lib/GRCh37.fa", sep = ""), refFlat_file = paste(hmdir, "/data/refFlat.txt",
  sep = ""), refMrna_1 = paste(hmdir, "/data/refMrna.cut1.fa", sep = ""),
  refMrna_3 = paste(hmdir, "/data/refMrna.cut3.fa", sep = ""),
  samtools_dir = "samtools", bcftools_dir = "bcftools", Chr_Column = 1,
  Mutation_Start_Column = 2, Mutation_End_Column = 3,
  Mutation_Ref_Column = 4, Mutation_Alt_Column = 5, NM_ID_Column = 10,
  Depth_Normal_Column = NA, Depth_Tumor_Column = NA,
  ambiguous_between_exon = 0, ambiguous_codon = 0, peptide_length = c(8,
  9, 10, 11, 12, 13))
```

Arguments

input_file	(Required) An input vcf file annotated by, e.g., ANNOVAR (http://annovar.openbioinformatics.org/en or other softwares. See by data(sample_vcf); sample_vcf;
HLA_file	(Required) A tab separated file indicating HLA types . The 1st column is input_file name, and the following columns indicate HLA types. See by data(sample_hla_table_c1); sample_hla_table_c1;
file_name_in_HLA_table	If the name (1st column) in HLA table is not input_file, indicate the corresponding name (Default=input_file).
hmdir	Home directory for the analysis (Default=getwd()).
job_ID	Job-Id to be attached in output files (Default="NO_JOB_ID").
RNAseq_file	(Default=NA) A file including RNA expressions. The 1st, 2nd and 3rd columns are "GeneSymbol Chr:ExonStart-ExonEnd(locus) Expression Amount", respectively. The 1st row should be any header. See by data(sample_rna_exp); sample_rna_exp;
RNA_bam	RNA bam file to calculate variant allele frequency of RNA at each mutation (Default=NA).
CNV	A file including copy number variation to calculate cancer cell fraction probability (CCFP) (Default=NA). The format is according to ASCAT (https://www.crick.ac.uk/peter-van-loo/software/ASCAT) output files. The columns are "Chromosome Position Log R segmented LogR BAF segmented BAF Copy number Minor allele Raw copy number" The 1st row should be the above header. See data(sample_copynum); sample_copynum;
ccfp_dir	The file directory to CCFP.pl (Default="lib/ccfp.jar").

`Purity` Tumor purity or tumor contents ratio required to calculate CCFP (Default=NA).

`netMHCpan_dir` The file directory to netMHCpan (Default="lib/netMHCpan-3.0/netMHCpan").

`refDNA` refDNA information to be used to calculate RNA VAF (Default="lib/GRCh37.fa").

`refFlat_file` refFlat file to be used in constructing peptide. (Default=paste(hmdir,"lib/refFlat.txt",sep="")

`refMrna_1` refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut1.fa",sep= This file is automaticalluy generated through the command in README, but includes NM_IDs.

`refMrna_3` refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut3.fa",sep= This file is automaticalluy generated through the command in README, but includes the amino acid sequence.

`samtools_dir` The file directory to samtools (Default="samtools"). It shouled be indicated when you indicate RNA-bam and try to calculate RNA VAF .

`bcftools_dir` The file directory to netMHCpan (Default="bcftools"). It shouled be indicated when you indicate RNA-bam and try to calculate RNA VAF . samtools 0_x_x includes bcftools in the directory.

`Chr_Column` The column number describing Chromosome number in input_file (Default=1).

`Mutation_Start_Column`
The column number describing Mutation Start Position in input_file (Default=2) .

`Mutation_End_Column`
The column number describing Mutation End Position in input_file (Default=3).

`Mutation_Ref_Column`
The column number describing Mutation Ref in input_file (Default=4).

`Mutation_Alt_Column`
The column number describing Mutation Alt in input_file (Default=5).

`NM_ID_Column` The column number describing NM IDs in input_file (Default=10).

`Depth_Normal_Column`
The column number describing the read count from normal cells (Default = NA)

`Depth_Tumor_Column`
The column number describing the read count from tumor cells (Default = NA)

`ambiguous_between_exon`
The maximum number to permit the differences between Exon-Lengths from refFlat and refMrna (Default=0).

`ambiguous_codon`
The maximum number to permit the differences between inputfile- and refMrna-oriented translation START/END position (Default=0).

`peptide_length` Peptide Length to be generated (Default=8,9,10,11,12,13).

Value

void (Calculated Neoantigen Files will be generated as .tsv files.)

MainSNVClass2 *Calculate Neoantigen Candidates on SNVs for MHC Class2*

Description

Calculate Neoantigen Candidates on SNVs for MHC Class2

Usage

```
MainSNVClass2(input_file, HLA_file, file_name_in_HLA_table = input_file,
  hmdir = getwd(), job_ID = "NO_JOB_ID", RNAseq_file = NA, RNA_bam = NA,
  CNV = NA, ccfp_dir = paste(hmdir, "lib/ccfp.jar", sep = ""),
  Purity = NA, netMHCpan_dir = paste(hmdir,
  "lib/netMHCIIpan-3.1/netMHCIIpan", sep = ""), refDNA = paste(hmdir,
  "lib/GRCh37.fa", sep = ""), refFlat_file = paste(hmdir, "/data/refFlat.txt",
  sep = ""), refMrna_1 = paste(hmdir, "/data/refMrna.cut1.fa", sep = ""),
  refMrna_3 = paste(hmdir, "/data/refMrna.cut3.fa", sep = ""),
  samtools_dir = "samtools", bcftools_dir = "bcftools", Chr_Column = 1,
  Mutation_Start_Column = 2, Mutation_End_Column = 3,
  Mutation_Ref_Column = 4, Mutation_Alt_Column = 5, NM_ID_Column = 10,
  Depth_Normal_Column = NA, Depth_Tumor_Column = NA,
  ambiguous_between_exon = 0, ambiguous_codon = 0, peptide_length = c(15))
```

Arguments

input_file	(Required) An input vcf file annotated by, e.g., ANNOVAR (http://annovar.openbioinformatics.org/en or other softwares. See by data(sample_vcf); sample_vcf;
HLA_file	(Required) A tab separated file indicating HLA types . The 1st column is input_file name, and the following columns indicate HLA types. See by data(sample_hla_table_c2); sample_hla_table_c2;
file_name_in_HLA_table	If the name (1st column) in HLA table is not input_file, indicate the corresponding name (Default=input_file).
hmdir	Home directory for the analysis (Default=getwd()).
job_ID	Job-Id to be attached in output files (Default="NO_JOB_ID").
RNAseq_file	(Default=NA) A file including RNA expressions. The 1st, 2nd and 3rd columns are "GeneSymbol Chr:ExonStart-ExonEnd(locus) Expression Amount", respectively. The 1st row should be any header. See by data(sample_rna_exp); sample_rna_exp;
RNA_bam	RNA bam file to calculate variant allele frequency of RNA at each mutation (Default=NA).
CNV	A file including copy number variation to calculate cancer cell fraction probability (CCFP) (Default=NA). The format is according to ASCAT (https://www.crick.ac.uk/peter-van-loo/software/ASCAT) output files. The columns are "Chromosome Position Log R segmented LogR BAF segmented BAF Copy number Minor allele Raw copy number" The 1st row should be the above header. See data(sample_copynum); sample_copynum;
ccfp_dir	The file directory to CCFP.pl (Default="lib/ccfp.jar").

Purity	Tumor purity or tumor contents ratio required to calculate CCFP (Default=NA).
netMHCpan_dir	The file directory to netMHCpan (Default="lib/netMHCIIpan-3.1/netMHCpan").
refDNA	refDNA information to be used to calculate RNA VAF (Default="lib/GRCh37.fa").
refFlat_file	refFlat file to be used in constructing peptide. (Default=paste(hmdir,"lib/refFlat.txt",sep="")
refMrna_1	refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut1.fa",sep= This file is automaticalluy generated through the command in README, but includes NM_IDs.
refMrna_3	refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut3.fa",sep= This file is automaticalluy generated through the command in README, but includes the amino acid sequence.
samtools_dir	The file directory to samtools (Default="samtools"). It shouled be indicated when you indicate RNA-bam and try to calculate RNA VAF .
bcftools_dir	The file directory to netMHCpan (Default="bcftools"). It shouled be indicated when you indicate RNA-bam and try to calculate RNA VAF . samtools 0_x_x includes bcftools in the directory.
Chr_Column	The column number describing Chromosome number in input_file (Default=1).
Mutation_Start_Column	The column number describing Mutation Start Position in input_file (Default=2) .
Mutation_End_Column	The column number describing Mutation End Position in input_file (Default=3).
Mutation_Ref_Column	The column number describing Mutation Ref in input_file (Default=4).
Mutation_Alt_Column	The column number describing Mutation Alt in input_file (Default=5).
NM_ID_Column	The column number describing NM IDs in input_file (Default=10).
Depth_Normal_Column	The column number describing the read count from normal cells (Default = NA)
Depth_Tumor_Column	The column number describing the read count from tumor cells (Default = NA)
ambiguous_between_exon	The maximum number to permit the differences between Exon-Lengths from refFlat and refMrna (Default=0).
ambiguous_codon	The maximum number to permit the differences between inputfile- and refMrna-oriented translation START/END position (Default=0).
peptide_length	Peptide Length to be generated (Default=15 in HLA Class2).

Value

void (Calculated Neoantigen Files will be generated as .tsv files.)

Neoantimon *Neoantimon*

Description

Calculate Lists of Candidate Neoantingens on SNVs and Indels to MHC Class1 and Class2. First use MainSNVClass1, MainSNVClass2, MainINDELClass1, and MainINDELClass2.

sample_copynum *A Format / Sample file for Copy Number Information*

Description

A dataset containing the copy number information obtained by, e.g., ASCAT.

Usage

```
data(sample_copynum)
```

Format

A data frame with 7 rows and 9 variables

sample_hla_table_c1 *A Format / Sample file for HLA CLASS1 Table*

Description

A dataset containing the HLA types of patients in each row.

Usage

```
data(sample_hla_table_c1)
```

Format

A data frame with 3 rows and at most 7 variables

sample_hla_table_c2 *A Format / Sample file for HLA CLASS2 Table*

Description

A dataset containing the HLA types of patients in each row.

Usage

```
data(sample_hla_table_c2)
```

Format

A data frame with at least 3 row and at most 10 variables

sample_rna_exp *A Format / Sample file for RNA Expression Information*

Description

A dataset containing the RNA expression amount of patient for each gene.

Usage

```
data(sample_rna_exp)
```

Format

A data frame with 22 rows and 3 variables

sample_vcf *A Format / Sample file for Analyzed vcf file.*

Description

A dataset containing the variant information of a patient.

Usage

```
data(sample_vcf)
```

Format

A data frame with 9 rows and 38 variables

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