Package 'CRUST'

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Title Multi-regional clonal deconvolution of tumor sequencing data

Version 1.0.1

Description Functions to deconvolute clones and sub-clones in multi-regional/temporal massive parallel DNA sequencing of solid tumor in presence of microarray based copy number profiles. Additional functions include estimation of said copy number profiles from exome sequencing.

Depends R (¿= 3.6.0)

URL https://github.com/Subhayan18/CRUST/

BugReports https://github.com/Subhayan18/CRUST/issues/

License GPL-3

Encoding UTF-8

LazyData TRUE

Imports factoextra,
FactoMineR,
bootcluster,
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fpc,
ggpubr,
mclust,
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readxl,
rlang,
scales,
sequenza,
tidyr,
vcfR,
dplyr,
ggplot2

Suggests copynumber, tidyverse

NeedsCompilation no

RoxygenNote 7.1.1

R topics documented:

`AlleleComp` *Copynumber estimation*

Description

Allelic segmentations are estimated for one sample at a time with unfiltered sequencing calls.

Usage

```
AlleleComp(data, AD, file.name, method, uniform.break)
```

Arguments

`data`	A `vcfR` object of the sequencing calls.
`AD`	a `character` deoning *ID* for depth of the reference allele. This is often separately present in the VCF file. Default is `NULL`.
`file.name`	an optional `character` to define output file name. Default is *tumor.sample*.
`method`	Algorithm to be used for copy number calculations. options include "apri-ori" wich uses `CopySeg_sequenza` and "naive" using `CopySeg_falcon`.
`uniform.break`	A numeric value signifying fixed length of the genomic window. Each window is considered as distinct chromosomal segment with edges being the break points for copy number estimation. A good window length is 1Mb (i.e. 1e6)

Details

The function writes a *.txt* data in working directory with the name defined in `file.name` used by *sequenza*. The output file written can be used in conjunction with post variants call sequence file. These can be merged and used for surther analysis with `cluster.doc` or `seqn.scale`

Value

A transformed `dataframe` usable in *CloneStrat* that represents data on all variants in the .vcf file. It returns summaries on the variants with the collumn *CN.profile* depicting the estimated allelic compositions.

See Also

`segment.plot`

Examples

```
#AlleleComp(data = x, AD = "AD", method = "naive")
```

`cluster.doc` *Clonal deconvolution*

Description

Clone / Sub-clone decomposition of DNA sequencing data. This is recommended to be used for more than one sample preferably collected from the same individual at different times. If the sample qualities vary, it is recommended to perform scaling first with `seqn.scale`.

Usage

```
cluster.doc(
  data = NULL,
  sample = NULL,
  vaf = NULL,
  allele.comp = NULL,
  n.clone = NULL,
  n.subclone = NULL,
  optimization.method = "GMM",
  clustering.method = "HKM",
  clonality = "Allelic composition",
  instruct = TRUE
)
```

Arguments

`data`	A `dataframe` containing summary from DNA sequencing. It must include a column of sample IDs and a corresponding column with the variant allele frequencies.
`sample`	`Integer or character` of the column name or column number of the sample IDs.
`vaf`	`Integer or character` of the column name or column number of the variant allele frequency.
`allele.comp`	`Character` string for allelic composition of the variants. example: '1+1' or '2+3' etc.
`n.clone`	Optional `integer` for number of suspected clones, default NULL.

`n.subclone` Optional `interger` for number of suspected subclones, default NULL.

`optimization.method`
Method to find optimal number of clusters; *GMM* or *bootstrap*. Default is *GMM*.

`clustering.method`
Clustering methods; *HKM*, *bootkm* or *hybrid*. Default is *hkm*.

`clonality` Method for determining clonality of the predicted clusters; *Allelic composition* (default) or *density*

`instruct` `Character` input for accepting program suggestion.

Details

`cluster.doc` is meant to do two things, first determine the optimum number of clusters that *should* be fitted and second, to infer what groups the clusters thus obtained should be assigned to.

The data inputs interactively requested from the user help obtain the following information

`chromosomal segmentation` helps in determining the number of clone/sub-clone cloud to be expected in the data. As variant alleles from different aberrant chromosomes may have similar relative frequencies but discordant clonal interpretation. On the contrary convergent clonal alleles may demonstrate divergent frequencies if arisen from dissimilar aneuploidy.

`clouds` give the program a visual feedback from the user that assume to carry some biological interpretation of the frequency distributions present in the data. This is a subjective estimate that the program later uses for cluster assignment.

Out of the two methods used for cluster optimization, *GMM* stands for *Gaussian Mixed Models* whereas *bootstrap*, as the name suggests perform *bootstrap* resampling of the VAFs in 50 repetitions with 20 runs each to find the most stable parameter for clustering. *GMM* outputs the optimization curve with `BIC` or *Bayesian Information Criterion* against number of clusters chosen in the `X-axis` where *bootstrap* shows the `Smin` statistics instead in the `Y-axis`. In both cases the statistics are to be interpreted as proxies for the *entropy* of the system. The maximum entropy is likely to indicate the most stable solution.

`clustering.method` gives the user three choices:

`HKM` is *Heierarchical K-means clustering* which uses heierarchical clustering first to determine the cluster centers that are subsequently used as the starting point for the K-means clustering. `bootkm` performs a *bootstrap* resampling of 20 fitted K-means clusters with 50 resamplings to out put the clusters. `hybrid` performs *hkm* on the principal component of the data.

`clonality` provides two choices for clonality assignment. The default is *Allelic composition* that measures expected clonality patterns according to the copy numbers. But in cases of unreliable allelic composition estimates this method may fail. In such situations the clonality can be assigned without apriori assumptions with the alternate *density* based method.

Value

A list of 12 objects is returned that includes all the summary statistics, diagnositics and the predictions as well as the mapping internally used for clonal deconvolution.

`predicted.data` is necessarily an extension to the input `data` with the addition of the predicted clone and sub-clone status of each variant for corresponding samples.

`density.map` is a distance matrix convoluted from cluster distances and desity departures.

`collapse` are clusters that are initially prredicted but later collapsed on each other dues to similarity between them.

`fitted.hkm`,`fitted bootkm` or `fitted.hybrid` is a vector of initial cluster assignment by the algorithm chosen. Only one of these will have an output and the rest will show `NA`.

`Number of unscaled clusters` gives umber of predicted clusters before collapsing with density estimates.

`Number of scaled clusters` gives number of predicted clusters after collapsing (if any).

`cluster.diagnostics` if the optimization method was chosen to be *GMM*, this is an object of `S3` class that includes clustering diagnostics from the model-based clustering. If the chosen method was *bootstrap* then this is a list.

`cluster centers` are the centroids of the predicted scaled clusters.

`cluster mapping` provides the map between scaled clusters and the clonal deconvolution assignments

`Dunn index` is the Dunn index for the fitted cluster.

See Also

`seqn.scale` `cluster.doubt`

Examples

```
#cluster.doc(test.dat, 1, 2, optimization.method = 'GMM', clustering.method = 'HKM')
```

`cluster.doubt` *User overriden clonal deconvolution*

Description

Sample specific user curated Clone / Sub-clone decomposition of DNA sequencing data

Usage

```
cluster.doubt(CD.obj, sample, vaf, sample.name, cluster.num)
```

Arguments

`CD.obj`	A `cluster.doc` object
`sample`	Collumn number of the *predicted.data* from the `cluster.doc` output that contain sample IDs
`vaf`	Collumn number of the *predicted.data* from the `cluster.doc` output that contain variant allele frequencies used for the analysis.
`sample.name`	a vector of sample IDs
`cluster.num`	a numeric vetor of clone/sub-clonal split of respective sample

Value

A list of 3 objects

`fitted.cluster` includes the clustering results from the final fit with user input

`predicted.data` A dataframe shows the changed clustering results due to the user defined clone / sub-clone smear for the selected samples

See Also

cluster.doc

Examples

```
#cd.res<-cluster.doc(test.dat)
#cd.new<-cluster.doubt(cd.res,sample,vaf,c("Sample_1","Sample_3"),c(2,2,3,2))
```

CopySeg_falcon *Copynumber estimation*

Description

NGS probes are extracted rom a vcfR object, scaled and bias corrected to optimize estimatio of allelelic composition. This function can handle only a combination of one tumor sample with a matched normal sample. Analysis is performed using the package falcon

Usage

```
CopySeg_falcon(data, AD, file.name, uniform.break)
```

Arguments

data	A vcfR object with one normal and one tumor sample. The *AD* element of the *FORMAT* field is a manadatory input
AD	a character denoting *ID* for depth of the reference allele.
file.name	A character string. this name will be used to save the scaled and unscaled relative coverage plot along with the final copy number estimate plot in the working directory
uniform.break	A numeric value signifying fixed length of the genomic window. Each window is considered as distinct chromosomal segment with edges being the break points for copy number estimation.

Details

This function uses falcon to estimate allele specific copy number of all sequeneced probes. Subsequently sliding window algorithm is used to generate chromosomal segments with precicted distinct copynumbers. The relative coverages are sclaed with GC content of the binned windows

Value

A list of two data frames that is further used to obtain the allelic segmentation plot

See Also

Benjamini *et al.*, 2012 with a loess regression loess.

`CopySeg_sequenza` *Copynumber estimation*

Description

Allelic segmentations are estimated for one sample at a time with unfiltered sequencing calls using the package `sequenza`. This function can handle only a combination of one tumor sample with a matched normal sample.

Usage

```
CopySeg_sequenza(x, AD, file.name)
```

Arguments

`x`	A `vcfR` object of the sequencing calls. The sample names can be queried from `x`.
`AD`	a `character` deoning *ID* for depth of the reference allele. This is often separately present in the VCF file. Default is `NULL`.
`file.name`	an optional `character` to define output file name. Default is *tumor.sample*.

Details

The function writes a *.txt* data in working directory with the name defined in `file.name` used by *sequenza*. The output file written can be used in conjunction with post variants call sequence file. These can be merged and used for surther analysis with `cluster.doc` or `seqn.scale`

Value

A transformed `dataframe` usable in *CloneStrat* that represents data on all variants in the .vcf file. It returns summaries on the variants with the collumn *CN.profile* depicting the estimated allelic segmentations.

`match.maker` *Summary estimate compiler*

Description

Combining `AlleleComp` outputs from different samples with the variant sequence data.

Usage

```
match.maker(x, y)
```

Arguments

`x`	A list object needs to be created by `split` from the sequencing data.
`y`	A character vector of sample names or IDs.

Details

The variant sequence data needs to be split by sample names or IDs for `x`. And the input of `y` has to be in the same order as that of the split object. See `example` for more details.

Value

A `dataframe` object identical to the original variant data with an additional column named `segment` signifying the allelic make up of each variant in the corresponding sample.

See Also

`AlleleComp`

Examples

```
#NB<-split(Neuroblastoma,Neuroblastoma$Sample)
#NB<-match.maker(x=NB,y=c("metastasis.1","metastasis.2","primary.1","primary.2"))
#View(NB)
```

---

metastasis_1 *Human neuroblastoma tumor sample*

Description

DNA sample collected from a metastatic site (different than that of *primary_1*) was sequenced. This is a pre-processing vcfR file used for variant calling.

Usage

```
metastasis_1
```

Format

An object of class `vcfR` of dimension 141095 x 8 x 3.

See Also

`Neuroblastoma` `primary_1` `primary_2` `metastasis_2`

Karlsson *et al.*, 2018

metastasis_2 *Human neuroblastoma tumor sample*

Description

DNA sample collected from a metastatic site (different than that of *primary_1*) was sequenced. This is a pre-processing vcfR file used for variant calling.

Usage

```
metastasis_2
```

Format

An object of class `vcfR` of dimension 152565 x 8 x 3.

See Also

`Neuroblastoma` `primary_1` `primary_2` `metastasis_1`

Karlsson *et al.*, 2018

mutect2.qc *Quality Control on Mutect2 output*

Description

A quality control (QC) and transformation on the WES output from the Mutect2 variant caller. This re-organizes the data in a way that is friendlier for using in *CloneStrat*

Usage

```
mutect2.qc(WES, sample.name)
```

Arguments

`WES`	A `dataframe` of the Mutect2 output
`sample.name`	a `vector` of sample names or IDs

Value

A transformed `dataframe` usable in *CloneStrat* that represents data on each variant of each sample in rows

Examples

```
#res<-mutect2.qc(WES,sample.name)
```

Neuroblastoma *Human neuroblastoma data*

Description

Exome sequencing data of human neuroblastoma tumor samples available in public library.

Usage

```
data(Neuroblastoma)
```

Format

An object of class `"dataframe"`

Value

`Sample` is column of IDs corresponding to 4 samples (2x primary and 2x metastasis).

`VAF` denotes the variant allele frequencies.

`RefseqID` annotates each of the variants.

See Also

`primary_1` `primary_2` `metastasis_1` `metastasis_2`

Karlsson *et al.*, 2018

Examples

```
data(Neuroblastoma)
```

primary_1 *Human neuroblastoma tumor sample*

Description

DNA sample collected from a primary tumor site (different than that of *primary_2*) was sequenced. This is a pre-processing vcfR file used for variant calling.

Usage

```
primary_1
```

Format

An object of class `vcfR` of dimension 150125 x 8 x 3.

See Also

`Neuroblastoma` `primary_2` `metastasis_1` `metastasis_2`

Karlsson *et al.*, 2018

primary_2 *Human neuroblastoma tumor sample*

Description

DNA sample collected from a primary tumor site (different than that of *primary_1*) was sequenced. This is a pre-processing vcfR file used for variant calling.

Usage

```
primary_2
```

Format

An object of class vcfR of dimension 149873 x 8 x 3.

See Also

Neuroblastoma primary_1 metastasis_1 metastasis_2

Karlsson *et al.*, 2018

segment.plot *Plot of allelic composition*

Description

Departure in clusters of different allelic composition are portrayed for tumor sample

Usage

```
segment.plot(data, base.copy)
```

Arguments

data	A match.maker or AlleleComp derived object.
base.copy	is the baseline balanced copynumber present in the sample usually "1 + 1" or "2 + 2".

Value

A plot of the allelic segmentation with average log-transformed coverage ratios in X-axis and average allelic-imbalances in the Y-axis. This plot can be interpreted in the similar fashion as described by Rasmussen *et al.*, 2011

See Also

match.maker, AlleleComp

Examples

```
#segment.plot(data = data, base.copy = "1 + 1")
```

`seqn.scale` *Probabilistic quotient normalization of DNA sequencing data*

Description

A normalization technique based on cancer / tumor cell fractions of the samples sequenced to infer homogeneity

Usage

```
seqn.scale(x, vaf, CCF)
```

Arguments

`x`	A `dataframe` containing summary from DNA sequencing with first column as sample IDs of corresponding variants.
`vaf`	The column number of `x` that includes VAFs.
`CCF`	The column number of `x` that includes CCFs.

Details

Probabilistic quotient normalization normalization technique described in *Dieterle, et al. (2006)* applied on the cancer cell fraction (CCF) of respective samples to rescale variant allele frequencies (VAF) accordingly. The general idea is to put most confidence in the sample with highest CCF and adjust the VAFs of other samples based on the departure in CCF of the other samples from that with the highest.

This method is particularly suggested if the CCFs accross samples vary more than 10

Value

A `dataframe` with all the elements of `x` with the new estimated VAFs in the column *scaled.vaf* and an additional column *unscaled.vaf* that includes the original VAFs.

See Also

`cluster.doc`

Examples

```
#pqn.dat<-seqn.scale(test.dat,vaf=2,CCF=3)
#hist(pqn.dat$scaled.vaf)
```

`T.goodness.test` *Test of fit of clonal deconvolution*

Description

A chi square test to assess the *goodness of fit* of the clonal : sub-clonal clouds. This test can be used to obtain outliers that do not fit into the proposed clonal deconvolution space.

Usage

```
T.goodness.test(x)
```

Arguments

`x`	A `dataframe` with the first three columns in the specific order: sample name or ID of a variant, variant allele frquencies (VAF) and cancer cell fraction (CCF)

Value

A list of two objects. *x* is same as the input `dataframe` with addede columns named *expected VAF_*, *chi_sq_* and *P value_* corresponding to each cloud of clone : Sub-clone combination. *rej* is a subset of `x` containing variants that fail the test for at least one cloud.

*expected VAF_* represents estimated variant allele frequencies for a given cloud.

*chi_sq_* is the Chi square test statistic for the cloud.

*P value_* is the P value corresponding to the *chi_sq_* statistic.

Examples

```
#test<-T.goodness.test(test.dat)
#head(test)
```

`test.dat` *Random number generated WES data for eight hypothetical samples*

Description

Data generated with varying random normal probabilities. Ideal llelic composition is assumed resulting in two separate distinct clouds of clones and sub-clones.

Usage

```
data(test.dat)
```

Format

An object of class `"dataframe"`

Value

`sample` is column of IDs corresponding to 8 distinct samples.

`vaf` denotes the variant allele frequencies of each variant (see `annotation`).

`CCF` are the cancer cell fractions of each sample.

`annotation` indicates corresponding variants for which observations are notes in each row. Variants can be shared among several samples as well as be private mutation.

Examples

```
data(test.dat)
table(test.dat$CCF)
table(test.dat$annotation)
hist(test.dat$vaf)
```

---

variant.auto.plot *Automated Multi-sample plot*

Description

Automated plotting of all variants present in the WES data

Usage

```
variant.auto.plot(CD.obj, annotation.col)
```

Arguments

`CD.obj`	A `cluster.doc object`
`annotation.col`	name of the column containing annotations of the variants in original WES `dataframe` used in the clonal deconvolution using `cluster.doc`

Value

Plot objects with the relevant annotation highlighted.

This function plots all variants present in the sample. Depending on the number of variants this can generate a *lot* of plots. All of these plots will be saved under a new directory named `img` inside the working directory. Hence, it is important to check that there are no directory named `img` inside the working directory

Examples

```
#cd.res<-cluster.doc(test.dat,1,2)
#variant.auto.plot(cd.res,'annotation')
```

variant.plot *Multi-sample variant plot*

Description

Plotting a specific variant present in more than one WES sample

Usage

```
variant.plot(CD.obj, annotation.col, variant)
```

Arguments

CD.obj	A cluster.doc object
annotation.col	name of the column containing annotations of the variants in original WES dataframe used in the clonal deconvolution using cluster.doc
variant	a character string specifying *only one* annotation which is to be displayed

Value

A plot object with the relevant annotation highlighted

Examples

```
#cd.res<-cluster.doc(test.dat,1,2)
#variant.plot(cd.res,'annotation','variant_74')
```

View_summary *Copynumber plots*

Description

Summaries of copynumber estimations and allelic segmentations described in four plots

Usage

```
View_summary(data, filename = NULL)
```

Arguments

data	An AlleleComp object of the sequencing calls.
filename	a character denominating sample name.

Value

A pdf file with plots on twenty two autosomes. The left panel of each plot shows allelic imbalance against average segmental log ratios. In the right panel from top to bottom three plots describes chromosomal relative coverage, allele frequency and estimated copynumber.

Examples

```
#met1<-AlleleComp(data = metastasis_1, AD = "AD", method = "naive", file = "TEMP");
#View_summary(data = met1, filename = "NB_met1")
```

Index