# Package 'infercnv'

October 16, 2019

**Type** Package

**Title** Infer Copy Number Variation from Single-Cell RNA-Seq Data

**Version** 1.0.4

**Date** 2019-09-16

**BugReports** https://github.com/broadinstitute/inferCNV/issues

**Description** Using single-cell RNA-Seq expression to visualize CNV in cells.

**biocViews** Software, CopyNumberVariation, VariantDetection, StructuralVariation, GenomicVariation, Genetics, Transcriptomics, StatisticalMethod, Bayesian, HiddenMarkovModel, SingleCell

**Depends** R(>= 3.6)

**License** BSD_3_clause + file LICENSE

**LazyData** TRUE

**VignetteBuilder** knitr

**Suggests** BiocStyle, knitr, rmarkdown, testthat

**RoxygenNote** 6.1.1

**NeedsCompilation** no

**SystemRequirements** JAGS 4.x.y

**Imports** graphics, grDevices, RColorBrewer, gplots, futile.logger, stats, utils, methods, ape, Matrix, fastcluster, dplyr, HiddenMarkov, ggplot2, edgeR, coin, caTools, reshape, rjags, fitdistrplus, future, foreach, doParallel, BiocGenerics, SummarizedExperiment, SingleCellExperiment, tidyr, parallel, coda, gridExtra, argparse

**URL** https://github.com/broadinstitute/inferCNV/wiki

**Collate** 'SplatterScrape.R' 'data.R' 'inferCNV.R' 'inferCNV_BayesNet.R' 'inferCNV_HMM.R' 'inferCNV_constants.R' 'inferCNV_heatmap.R' 'inferCNV_hidden_spike.R' 'inferCNV_i3HMM.R' 'inferCNV_mask_non_DE.R' 'inferCNV_meanVarSim.R' 'inferCNV_ops.R' 'inferCNV_simple_sim.R' 'inferCNV_tumor_subclusters.R' 'inferCNV_tumor_subclusters.random_smoothed_trees.R' 'noise_reduction.R'

**git_url** https://git.bioconductor.org/packages/infercnv

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**Author** Timothy Tickle [aut],
Itay Tirosh [aut],
Christophe Georgescu [aut, cre],
Maxwell Brown [aut],
Brian Haas [aut]

**Maintainer** Christophe Georgescu <cgeorges@broadinstitute.org>

# R topics documented:



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`infercnv-package` *infercnv: Infer Copy Number Variation from Single-Cell RNA-Seq Data*

---

## Description

Using single-cell RNA-Seq expression to visualize CNV in cells.

## Details

The main functions you will need to use are CreateInfercnvObject() and run(infercnv_object). For additional details on running the analysis step by step, please refer to the example vignette.

### Author(s)

**Maintainer**: Christophe Georgescu <cgeorges@broadinstitute.org>

Authors:

- Timothy Tickle <ttickle@broadinstitute.org>
- Itay Tirosh <tirosh@broadinstitute.org>
- Maxwell Brown <mbrown@broadinstitute.org>
- Brian Haas <bhaas@broadinstitute.org>

### See Also

Useful links:

- https://github.com/broadinstitute/inferCNV/wiki
- Report bugs at https://github.com/broadinstitute/inferCNV/issues

---

## annots *Generated classification for 10 normal cells and 10 tumor cells.*

---

### Description

Generated classification for 10 normal cells and 10 tumor cells.

### Usage

```
annots
```

### Format

A data frame with 20 rows (cells) and 1 columns (classification)

---

## apply_median_filtering *apply_median_filtering*

---

### Description

Apply a median filtering to the expression matrix within each tumor bounds

### Usage

```
apply_median_filtering(infercnv_obj, window_size = 7,
  on_observations = TRUE, on_references = TRUE)
```

### Arguments

| | |
|---|---|
| infercnv_obj | infercnv_object |
| window_size | Size of the window side centered on the data point to filter (default = 7). |
| on_observations | boolean (default=TRUE), run on observations data (tumor cells). |
| on_references | boolean (default=TRUE), run on references (normal cells). |

### Value

infercnv_obj with median filtering applied to observations

### Examples

```
# data(data)
# data(annots)
# data(genes)

# infercnv_obj <- infercnv::CreateInfercnvObject(raw_counts_matrix=data,
#                                                gene_order_file=genes,
#                                                annotations_file=annots,
#                                                ref_group_names=c("normal"))

# infercnv_obj <- infercnv::run(infercnv_obj,
#                               cutoff=1,
#                               out_dir=tempfile(),
#                               cluster_by_groups=TRUE,
#                               denoise=TRUE,
#                               HMM=FALSE,
#                               num_threads=2,
#                               no_plot=TRUE)

data(infercnv_object)

infercnv_obj <- infercnv::apply_median_filtering(infercnv_obj)
# plot result object
```

---

## CreateInfercnvObject *CreateInfercnvObject*

---

### Description

Creation of an infercnv object. This requires the following inputs: A more detailed description of each input is provided below:

The raw_counts_matrix:

MGH54_P16_F12 MGH53_P5_C12 MGH54_P12_C10 MGH54_P16_F02 MGH54_P11_C11 ... DDX11L1 0.0000000 0.000000 0.000000 0.000000 0.0000000 WASH7P 0.0000000 2.231939 7.186235 5.284944 0.9650009 FAM138A 0.1709991 0.000000 0.000000 0.000000 0.0000000 OR4F5 0.0000000 0.000000 0.000000 0.000000 0.0000000 OR4F29 0.0000000 0.000000 0.000000 0.000000 0.0000000 ...

The gene_order_file, contains chromosome, start, and stop position for each gene, tab-delimited:

chr start stop DDX11L1 chr1 11869 14412 WASH7P chr1 14363 29806 FAM138A chr1 34554 36081 OR4F5 chr1 69091 70008 OR4F29 chr1 367640 368634 OR4F16 chr1 621059 622053 ...

The annotations_file, containing the cell name and the cell type classification, tab-delimited.

V1 V2 1 MGH54_P2_C12 Microglia/Macrophage 2 MGH36_P6_F03 Microglia/Macrophage 3 MGH53_P4_H08 Microglia/Macrophage 4 MGH53_P2_E09 Microglia/Macrophage 5 MGH36_P5_E12 Oligodendrocytes (non-malignant) 6 MGH54_P2_H07 Oligodendrocytes (non-malignant) ... 179 93_P9_H03 malignant 180 93_P10_D04 malignant 181 93_P8_G09 malignant 182 93_P10_B10 malignant 183 93_P9_C07 malignant 184 93_P8_A12 malignant ...

and the ref_group_names vector might look like so: c("Microglia/Macrophage","Oligodendrocytes (non-malignant)")

## Usage

```
CreateInfercnvObject(raw_counts_matrix, gene_order_file, annotations_file,
  ref_group_names, delim = "\t", max_cells_per_group = NULL,
  min_max_counts_per_cell = NULL, chr_exclude = c("chrX", "chrY",
  "chrM"))
```

## Arguments

| | |
|---|---|
| raw_counts_matrix | the matrix of genes (rows) vs. cells (columns) containing the raw counts If a filename is given, it'll be read via read.table() otherwise, if matrix or Matrix, will use the data directly. |
| gene_order_file | data file containing the positions of each gene along each chromosome in the genome. |
| annotations_file | a description of the cells, indicating the cell type classifications |
| ref_group_names | a vector containing the classifications of the reference (normal) cells to use for infering cnv |
| delim | delimiter used in the input files |
| max_cells_per_group | maximun number of cells to use per group. Default=NULL, using all cells defined in the annotations_file. This option is useful for randomly subsetting the existing data for a quicker preview run, such as using 50 cells per group instead of hundreds. |
| min_max_counts_per_cell | minimum and maximum counts allowed per cell. Any cells outside this range will be removed from the counts matrix. default=NULL and uses all cells. If used, should be set as c(min_counts, max_counts) |
| chr_exclude | list of chromosomes in the reference genome annotations that should be excluded from analysis. Default = c('chrX', 'chrY', 'chrM') |

## Value

infercnv

## Examples

```
data(data)
data(annots)
data(genes)

infercnv_obj <- infercnv::CreateInfercnvObject(raw_counts_matrix=data,
                                               gene_order_file=genes,
                                               annotations_file=annots,
                                               ref_group_names=c("normal"))
```

---

`data` *Generated SmartSeq2 expression data with 10 normal cells and 10 tumor cells. This is only to demonstrate how to use methods, not actual data to be used in an analysis.*

---

## Description

Generated SmartSeq2 expression data with 10 normal cells and 10 tumor cells. This is only to demonstrate how to use methods, not actual data to be used in an analysis.

## Usage

```
data
```

## Format

A data frame with 8252 rows (genes) and 20 columns (cells)

---

`filterHighPNormals` *filterHighPNormals: Filter the HMM identified CNV's by the CNV's posterior probability of belonging to a normal state.*

---

## Description

The following function will filter the HMM identified CNV's by the CNV's posterior probability of belonging to a normal state identified by the function inferCNVBayesNet(). Will filter CNV's based on a user desired threshold probability. Any CNV with a probability of being normal above the threshold will be removed.

## Usage

```
filterHighPNormals(MCMC_inferCNV_obj, HMM_states, BayesMaxPNormal)
```

## Arguments

| | |
|---|---|
| `MCMC_inferCNV_obj` | MCMC infernCNV object. |
| `HMM_states` | InferCNV object with HMM states in expression data. |
| `BayesMaxPNormal` | Option to filter CNV or cell lines by some probability threshold. |

## Value

Returns a list of (MCMC_inferCNV_obj, HMM_states) With removed CNV's.

## Examples

```
data(mcmc_obj)

mcmc_obj_hmm_states_list <- infercnv::filterHighPNormals( MCMC_inferCNV_obj = mcmc_obj,
                                          HMM_states        = HMM_states,
                                          BayesMaxPNormal   = 0.5)
```

---

# genes *Downsampled gene coordinates file from GrCh37*

---

## Description

Downsampled gene coordinates file from GrCh37

## Usage

```
genes
```

## Format

A data frame with 10338 rows (genes) and 3 columns (chr, start, end)

---

# HMM_states *infercnv object result of the processing of run() in the HMM example, to be used for other examples.*

---

## Description

infercnv object result of the processing of run() in the HMM example, to be used for other examples.

## Usage

```
HMM_states
```

## Format

An infercnv object containing HMM predictions

`infercnv-class` *The infercnv Class*

## Description

An infercnv object encapsulates the expression data and gene chromosome ordering information that is leveraged by infercnv for data exploration. The infercnv object is passed among the infercnv data processing and plotting routines.

## Details

Slots in the infercnv object include:

## Slots

`expr.data` <matrix> the count or expression data matrix, manipulated throughout infercnv ops

`count.data` <matrix> retains the original count data, but shrinks along with expr.data when genes are removed.

`gene_order` <data.frame> chromosomal gene order

`reference_grouped_cell_indices` <list> mapping [['group_name']] to c(cell column indices) for reference (normal) cells

`observation_grouped_cell_indices` <list> mapping [['group_name']] to c(cell column indices) for observation (tumor) cells

`tumor_subclusters` <list> stores subclustering of tumors if requested

`.hspike` a hidden infercnv object populated with simulated spiked-in data

`inferCNVBayesNet` *inferCNVBayesNet: Run Bayesian Network Mixture Model To Obtain Posterior Probabilities For HMM Predicted States*

## Description

Uses Markov Chain Monte Carlo (MCMC) and Gibbs sampling to estimate the posterior probability of being in one of six Copy Number Variation states (states: 0, 0.5, 1, 1.5, 2, 3) for CNV's identified by inferCNV's HMM. Posterior probabilities are found for the entire CNV cluster and each individual cell line in the CNV.

## Usage

```
inferCNVBayesNet(file_dir, infercnv_obj, HMM_states, out_dir,
  model_file = NULL, CORES = 1, postMcmcMethod = NULL,
  plotingProbs = TRUE, quietly = TRUE, diagnostics = FALSE,
  HMM_type = HMM_type, k_obs_groups = k_obs_groups,
  cluster_by_groups = cluster_by_groups)
```

## Arguments

| | |
|---|---|
| file_dir | Location of the directory of the inferCNV outputs. |
| infercnv_obj | InferCNV object. |
| HMM_states | InferCNV object with HMM states in expression data. |
| out_dir | (string) Path to where the output file should be saved to. |
| model_file | Path to the BUGS Model file. |
| CORES | Option to run parallel by specifying the number of cores to be used. (Default: 1) |
| postMcmcMethod | What actions to take after finishing the MCMC. |
| plotingProbs | Option for adding plots of Cell and CNV probabilities. (Default: TRUE) |
| quietly | Option to print descriptions along each step. (Default: TRUE) |
| diagnostics | Option to plot Diagnostic plots and tables. (Default: FALSE) |
| HMM_type | The type of HMM that was ra, either 'i3' or 'i6'. Determines how many state were predicted by the HMM. |
| k_obs_groups | Number of groups in which to break the observations. (default: 1) |
| cluster_by_groups | If observations are defined according to groups (ie. patients), each group of cells will be clustered separately. (default=FALSE, instead will use k_obs_groups setting) |

## Value

Returns a MCMC_inferCNV_obj and posterior probability of being in one of six Copy Number Variation states (states: 0, 0.5, 1, 1.5, 2, 3) for CNV's identified by inferCNV's HMM.

## Examples

```
data(data)
data(annots)
data(genes)
data(HMM_states)

infercnv_obj <- infercnv::CreateInfercnvObject(raw_counts_matrix=data,
                                               gene_order_file=genes,
                                               annotations_file=annots,
                                               ref_group_names=c("normal"))

out_dir = tempfile()
infercnv_obj <- infercnv::run(infercnv_obj,
                              cutoff=1,
                              out_dir=out_dir,
                              cluster_by_groups=TRUE,
                              denoise=TRUE,
                              HMM=TRUE,
                              num_threads=2,
                              no_plot=TRUE)
mcmc_obj <- infercnv::inferCNVBayesNet( infercnv_obj   = infercnv_obj,
                              HMM_states         = HMM_states,
                              file_dir           = out_dir,
                              postMcmcMethod     = "removeCNV",
                              out_dir            = out_dir,
                              quietly            = TRUE,
```

```
CORES              = 2,
plotingProbs       = FALSE,
diagnostics        = FALSE,
HMM_type           = 'i6',
k_obs_groups       = 1,
cluster_by_groups  = FALSE)
```

---

`infercnv_obj` *infercnv object result of the processing of run() in the example, to be used for other examples.*

---

## Description

infercnv object result of the processing of run() in the example, to be used for other examples.

## Usage

```
infercnv_obj
```

## Format

An infercnv object

---

`MCMC_inferCNV-class` *MCMC_inferCNV class*

---

## Description

Uses Markov Chain Monte Carlo (MCMC) and Gibbs sampling to estimate the posterior probability of being in one of six Copy Number Variation states (states: 0, 0.5, 1, 1.5, 2, 3) for CNV's identified by inferCNV's HMM. Posterior probabilities are found for the entire CNV cluster and each individual cell line in the CNV.

## Slots

`bugs_model` BUGS model.

`sig` fitted values for cell lines, 1/standard deviation to be used for determining the distribution of each cell line

`mu` Mean values to be used for determining the distribution of each cell line

`group_id` ID's given to the cell clusters.

`cell_gene` List containing the Cells and Genes that make up each CNV.

`cnv_probabilities` Probabilities of each CNV belonging to a particular state from 0 (least likely)to 1 (most likely).

`cell_probabilities` Probabilities of each cell being in a particular state, from 0 (least likely)to 1 (most likely).

`args` Input arguments given by the user

`cnv_regions` ID for each CNV found by the HMM

`States` States that are identified and (depending on posterior MCMC input methods) modified.

## mcmc_obj

*infercnv object result of the processing of inferCNVBayesNet in the example, to be used for other examples.*

### Description

infercnv object result of the processing of inferCNVBayesNet in the example, to be used for other examples.

### Usage

```
mcmc_obj
```

### Format

An infercnv object containing posterior probability of CNV states

## plot_cnv

*Plot the matrix as a heatmap, with cells as rows and genes as columns, ordered according to chromosome*

### Description

Formats the data and sends it for plotting.

### Usage

```
plot_cnv(infercnv_obj, out_dir = ".", title = "inferCNV",
  obs_title = "Observations (Cells)", ref_title = "References (Cells)",
  cluster_by_groups = TRUE, cluster_references = TRUE,
  k_obs_groups = 3, contig_cex = 1,
  x.center = mean(infercnv_obj@expr.data), x.range = "auto",
  hclust_method = "ward.D", color_safe_pal = FALSE,
  output_filename = "infercnv", output_format = "png", png_res = 300,
  dynamic_resize = 0, ref_contig = NULL, write_expr_matrix = FALSE)
```

### Arguments

| | |
|---|---|
| infercnv_obj | infercnv object |
| out_dir | Directory in which to save pdf and other output. |
| title | Plot title. |
| obs_title | Title for the observations matrix. |
| ref_title | Title for the reference matrix. |
| cluster_by_groups | Whether to cluster observations by their annotations or not. Using this ignores k_obs_groups. |
| cluster_references | Whether to cluster references within their annotations or not. (dendrogram not displayed) |

| | |
|---|---|
| k_obs_groups | Number of groups to break observation into. |
| contig_cex | Contig text size. |
| x.center | Value on which to center expression. |
| x.range | vector containing the extreme values in the heatmap (ie. c(-3,4) ) |
| hclust_method | Clustering method to use for hclust. |
| color_safe_pal | Logical indication of using a color blindness safe palette. |
| output_filename | Filename to save the figure to. |
| output_format | format for heatmap image file (default: 'png'), options('png', 'pdf', NA) If set to NA, will print graphics natively |
| png_res | Resolution for png output. |
| dynamic_resize | Factor (>= 0) by which to scale the dynamic resize of the observation heatmap and the overall plot based on how many cells there are. Default is 0, which disables the scaling. Try 1 first if you want to enable. |
| ref_contig | If given, will focus cluster on only genes in this contig. |
| write_expr_matrix | Includes writing a matrix file containing the expression data that is plotted in the heatmap. |

## Value

A list of all relevent settings used for the plotting to be able to reuse them in another plot call while keeping consistant plotting settings, most importantly x.range.

## Examples

```
# data(data)
# data(annots)
# data(genes)

# infercnv_obj <- infercnv::CreateInfercnvObject(raw_counts_matrix=data,
#                                                gene_order_file=genes,
#                                                annotations_file=annots,
#                                                ref_group_names=c("normal"))

# infercnv_obj <- infercnv::run(infercnv_obj,
#                               cutoff=1,
#                               out_dir=tempfile(),
#                               cluster_by_groups=TRUE,
#                               denoise=TRUE,
#                               HMM=FALSE,
#                               num_threads=2,
#                               no_plot=TRUE)

data(infercnv_object)

plot_cnv(infercnv_obj,
         out_dir=tempfile(),
         obs_title="Observations (Cells)",
         ref_title="References (Cells)",
         cluster_by_groups=TRUE,
         x.center=1,
```

```
            x.range="auto",
            hclust_method='ward.D',
            color_safe_pal=FALSE,
            output_filename="infercnv",
            output_format="png",
            png_res=300,
            dynamic_resize=0
            )
```

---

run *run() : Invokes a routine inferCNV analysis to Infer CNV changes given a matrix of RNASeq counts.*

---

## Description

Function doing the actual analysis before calling the plotting functions.

## Usage

```
run(infercnv_obj, cutoff = 1, min_cells_per_gene = 3, out_dir = NULL,
  window_length = 101, smooth_method = c("pyramidinal", "runmeans"),
  num_ref_groups = NULL, ref_subtract_use_mean_bounds = TRUE,
  cluster_by_groups = FALSE, cluster_references = TRUE,
  k_obs_groups = 1, hclust_method = "ward.D2",
  max_centered_threshold = 3, scale_data = FALSE, HMM = FALSE,
  HMM_transition_prob = 1e-06, HMM_report_by = c("subcluster",
  "consensus", "cell"), HMM_type = c("i6", "i3"), HMM_i3_pval = 0.05,
  HMM_i3_use_KS = TRUE, BayesMaxPNormal = 0.5,
  sim_method = "meanvar", sim_foreground = FALSE,
  analysis_mode = c("samples", "subclusters", "cells"),
  tumor_subcluster_partition_method = c("random_trees", "qnorm",
  "pheight", "qgamma", "shc"), tumor_subcluster_pval = 0.1,
  denoise = FALSE, noise_filter = NA, sd_amplifier = 1.5,
  noise_logistic = FALSE, outlier_method_bound = "average_bound",
  outlier_lower_bound = NA, outlier_upper_bound = NA,
  final_scale_limits = NULL, final_center_val = NULL, debug = FALSE,
  num_threads = 4, plot_steps = FALSE, resume_mode = TRUE,
  png_res = 300, plot_probabilities = TRUE, diagnostics = FALSE,
  remove_genes_at_chr_ends = FALSE, prune_outliers = FALSE,
  mask_nonDE_genes = FALSE, mask_nonDE_pval = 0.05,
  test.use = "wilcoxon", require_DE_all_normals = "any",
  hspike_aggregate_normals = FALSE, no_plot = FALSE,
  no_prelim_plot = FALSE)
```

## Arguments

| | |
|---|---|
| infercnv_obj | An infercnv object populated with raw count data |
| cutoff | Cut-off for the min average read counts per gene among reference cells. (default: 1) |

min_cells_per_gene
: minimum number of reference cells requiring expression measurements to include the corresponding gene. default: 3

out_dir
: path to directory to deposit outputs (default: NULL, required to provide non NULL)
## Smoothing params

window_length
: Length of the window for the moving average (smoothing). Should be an odd integer. (default: 101)#'

smooth_method
: Method to use for smoothing: c(runmeans,pyramidinal) default: pyramidinal
#####

num_ref_groups
: The number of reference groups or a list of indices for each group of reference indices in relation to reference_obs. (default: NULL)

ref_subtract_use_mean_bounds
: Determine means separately for each ref group, then remove intensities within bounds of means (default: TRUE) Otherwise, uses mean of the means across groups.
##############################

cluster_by_groups
: If observations are defined according to groups (ie. patients), each group of cells will be clustered separately. (default=FALSE, instead will use k_obs_groups setting)

cluster_references
: Whether to cluster references within their annotations or not. (dendrogram not displayed) (default: TRUE)

k_obs_groups
: Number of groups in which to break the observations. (default: 1)

hclust_method
: Method used for hierarchical clustering of cells. Valid choices are: "ward.D", "ward.D2", "single", "complete", "average", "mcquitty", "median", "centroid". default("ward.D2")

max_centered_threshold
: The maximum value a value can have after centering. Also sets a lower bound of -1 * this value. (default: 3), can set to a numeric value or "auto" to bound by the mean bounds across cells. Set to NA to turn off.

scale_data
: perform Z-scaling of logtransformed data (default: FALSE). This may be turned on if you have very different kinds of data for your normal and tumor samples. For example, you need to use GTEx representative normal expression profiles rather than being able to leverage normal single cell data that goes with your experiment.
################################################################################
## Downstream Analyses (HMM or non-DE-masking) based on tumor subclusters

HMM
: when set to True, runs HMM to predict CNV level (default: FALSE)

HMM_transition_prob
: transition probability in HMM (default: 1e-6)

HMM_report_by
: cell, consensus, subcluster (default: subcluster) Note, reporting is performed entirely separately from the HMM prediction. So, you can predict on subclusters, but get per-cell level reporting (more voluminous output).

HMM_type
: HMM model type. Options: (i6 or i3): i6: infercnv 6-state model (0, 0.5, 1, 1.5, 2, >2) where state emissions are calibrated based on simulated CNV levels. i3: infercnv 3-state model (del, neutral, amp) configured based on normal cells and HMM_i3_pval

HMM_i3_pval p-value for HMM i3 state overlap (default: 0.05)

HMM_i3_use_KS boolean: use the KS test statistic to estimate mean of amp/del distributions (ala HoneyBadger). (default=TRUE)

## Filtering low-conf HMM preds via BayesNet P(Normal)

BayesMaxPNormal
maximum P(Normal) allowed for a CNV prediction according to BayesNet. (default=0.5, note zero turns it off)

####################### ## Tumor subclustering

sim_method method for calibrating CNV levels in the i6 HMM (default: 'meanvar')

sim_foreground don't use... for debugging, developer option.

analysis_mode options(samples|subclusters|cells), Grouping level for image filtering or HMM predictions. default: samples (fastest, but subclusters is ideal)

tumor_subcluster_partition_method
method for defining tumor subclusters. Options('random_trees', 'qnorm') random_trees: (default) slow but best. Uses permutation statistics w/ tree construction. qnorm: defines tree height based on the quantile defined by the tumor_subcluster_pval

tumor_subcluster_pval
max p-value for defining a significant tumor subcluster (default: 0.1)

############################## ## de-noising parameters ####

denoise If True, turns on denoising according to options below

noise_filter Values +- from the reference cell mean will be set to zero (whitening effect) default(NA, instead will use sd_amplifier below.

sd_amplifier Noise is defined as mean(reference_cells) +- sdev(reference_cells) * sd_amplifier default: 1.5

noise_logistic use the noise_filter or sd_amplifier based threshold (whichever is invoked) as the midpoint in a logistic model for downscaling values close to the mean. (default: FALSE)

################## ## Outlier pruning

outlier_method_bound
Method to use for bounding outlier values. (default: "average_bound") Will preferentially use outlier_lower_bounda and outlier_upper_bound if set.

outlier_lower_bound
Outliers below this lower bound will be set to this value.

outlier_upper_bound
Outliers above this upper bound will be set to this value.

########################## ## Misc options

final_scale_limits
The scale limits for the final heatmap output by the run() method. Default "auto". Alt, c(low,high)

final_center_val
Center value for final heatmap output by the run() method.

debug If true, output debug level logging.

num_threads (int) number of threads for parallel steps (default: 4)

plot_steps If true, saves infercnv objects and plots data at the intermediate steps.

resume_mode leverage pre-computed and stored infercnv objects where possible. (default=TRUE)

png_res Resolution for png output.

plot_probabilities
option to plot posterior probabilities (default: TRUE)

diagnostics option to create diagnostic plots after running the Bayesian model (default: FALSE)
########################## ## Experimental options

remove_genes_at_chr_ends
experimental option: If true, removes the window_length/2 genes at both ends of the chromosome.

prune_outliers Define outliers loosely as those that exceed the mean boundaries among all cells. These are set to the bounds.
## experimental opts involving DE analysis

mask_nonDE_genes
If true, sets genes not significantly differentially expressed between tumor/normal to the mean value for the complete data set (default: 0.05)

mask_nonDE_pval
p-value threshold for defining statistically significant DE genes between tumor/normal

test.use statistical test to use. (default: "wilcoxon") alternatives include 'perm' or 't'.'

require_DE_all_normals
If mask_nonDE_genes is set, those genes will be masked only if they are are found as DE according to test.use and mask_nonDE_pval in each of the comparisons to normal cells options: "any", "most", "all" (default: "any")
other experimental opts

hspike_aggregate_normals
instead of trying to model the different normal groupings individually, just merge them in the hspike.

no_plot don't make any of the images. Instead, generate all non-image outputs as part of the run. (default: FALSE)

no_prelim_plot don't make the preliminary infercnv image (default: FALSE)

## Value

infercnv_obj containing filtered and transformed data

## Examples

```
data(data)
data(annots)
data(genes)

infercnv_obj <- infercnv::CreateInfercnvObject(raw_counts_matrix=data,
                                               gene_order_file=genes,
                                               annotations_file=annots,
                                               ref_group_names=c("normal"))

infercnv_obj <- infercnv::run(infercnv_obj,
                              cutoff=1,
                              out_dir=tempfile(),
                              cluster_by_groups=TRUE,
                              denoise=TRUE,
```

```
                                HMM=FALSE,
                                num_threads=2,
                                no_plot=TRUE)
```

---

validate_infercnv_obj *validate_infercnv_obj()*

---

## Description

validate an infercnv_obj ensures that order of genes in the @gene_order slot match up perfectly with the gene rows in the @expr.data matrix. Otherwise, throws an error and stops execution.

## Usage

```
validate_infercnv_obj(infercnv_obj)
```

## Arguments

| | |
|---|---|
| infercnv_obj | infercnv_object |

## Value

none

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