Package 'tbdiag'

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Type Package

Title Functions for tuberculosis diagnostics research

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Description This package provides functions to assist researchers
working in the field of tuberculosis diagnostics. Functions
for the interpretation of two popular interferon-gamma release
assays are provided, and additional functionality is planned.

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URL <https://github.com/mmparker/tbdiag>

LazyLoad yes

LazyData true

Suggests testthat

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'qft.criteria.070.r' 'qft.criteria.cellestis.nomito.r'
'qft.criteria.cellestis.usa.r' 'trim.output.r'
'tbdiag-package.r' 'tspot.cens.r' 'tspot.criteria.10spot.r'
'tspot.criteria.oxford.global.r' 'tspot.criteria.oxford.usa.r'
'qft.interp.R' 'tspot.interp.R'

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tbdiag-package   *tbdiag: utilities for tuberculosis diagnostics research*

Description

This package provides functions to assist researchers working in the field of tuberculosis diagnostics. Functions for the interpretation of two popular interferon-gamma release assays are provided, and additional functionality is planned.

Author(s)

Matt Parker <mattmparker@gmail.com>

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equal.lengths   *Confirm that all input vectors are the same length.*

Description

Confirm that all input vectors are the same length.

Usage

```
equal.lengths(...)
```

Arguments

...   Two or more vectors to be compared.

Value

Returns an error if the vectors are of unequal length, returns a warning if only one vector is supplied, and returns nothing if the vectors are of equal length.

Examples

```
## Not run: equal.lengths(rnorm(10), rnorm(10), rnorm(9))
## Not run: equal.lengths(rnorm(10))
## Not run: equal.lengths(rnorm(10), rnorm(10), rnorm(10))
```

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qft.interp	*Interpret the results of the Cellestis Quantiferon Gold In-Tube assay for latent tuberculosis infection.*

Description

Given vectors of nil, TB antigen, and mitogen results in IU/mL, this function computes QFT qualitative interpretations. The function uses the Cellestis USA criterion by default; other criteria sets can be created as methods for the qft.criteria function.

Usage

```
qft.interp(nil, tb, mito, criteria = "cellestis.usa",
    verbosity = "terse", ...)
```

Arguments

nil	A vector of nil results (in IU/mL)
tb	A vector of TB antigen results (in IU/mL)
mito	A vector of mitogen results (in IU/mL)
criteria	The name of the desired result criteria (defaults to the Cellestis criteria for the United States).
verbosity	The level of verbosity ("onechar", "terse", "verbose") of the output.
...	Other arguments passed to the crtieria evaluation function chosen by the "criteria" argument.

Details

All IU/mL results greater than 10 are automatically censored to 10 for the purposes of calculating qualitative results, following Cellestis's interpretation instructions.

Value

The function returns a vector of qualitative assay results according to the criteria chosen using the "criteria" argument. The verbosity of the results depends on the value passed to the "verbosity" argument:

onechar	Returns a single character indicating the result (N for Negative, P for Positive, I for Indeterminate).
terse	Returns a single word indicating the result (Negative, Positive, Indeterminate).
verbose	Returns the same results as "terse", with the addition of a short comment indicating the reason for an "Indeterminate" result.

Multiple criteria sets are available. The function defaults to the standard Cellestis criteria for the United States of America (criteria = "cellestis.usa"), but other currently available options include:

criteria = "cellestis.nomito"

>The Cellestis criteria for many regions outside of North America, in which indeterminate results are indicated for tests with high nil results, but not for tests with a `Mitogen - Nil` difference of less than 0.50 (as is the case in the US);

criteria = "070"

>A criteria set in which the threshold for positivity is raised from `Antigen - Nil = 0.35` to `Antigen - Nil =   0.70`, as has been suggested by some studies.

Note

This function is provided purely as a convenience and is not a replacement for manual interpretation, manufacturer-provided software, or common sense. Absolutely not for clinical use.

References

Cellestis <http://www.cellestis.com/>

See Also

tspot.interp for TSPOT.TB interpretation.

Examples

```
# Calculate results
test.qfts$result.check <- with(test.qfts,
                               qft.interp(nil = nil,
                                          tb = tb,
                                          mito = mito))

# Compare lab and calculated results
with(test.qfts, table(lab.result, result.check, exclude = NULL))

# Compare different levels of verbosity
test.qfts$verbose.check <- with(test.qfts,
                                qft.interp(nil = nil,
                                           tb = tb,
                                           mito = mito,
                                           verbosity = "verbose"))

test.qfts$onechar.check <- with(test.qfts,
                                qft.interp(nil = nil,
                                           tb = tb,
                                           mito = mito,
                                           verbosity = "onechar"))

unique(test.qfts[ , c("lab.result", "result.check",
                      "verbose.check", "onechar.check")])
```

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test.qfts	*A sample of 6,833 real QFT results.*

Description

A sample of 6,833 real QFT results.

Author(s)

Matt Parker <mattmparker@gmail.com>

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test.tspots	*A sample of 6,434 real TSPOT results.*

Description

A sample of 6,434 real TSPOT results.

Author(s)

Matt Parker <mattmparker@gmail.com>

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tspot.interp	*Interpret the results of the Oxford Immunotec TSPOT.TB assay for latent tuberculosis infection.*

Description

Given vectors of nil, TB antigen (panels A and B), and mitogen results in spots, this function computes TSPOT qualitative interpretations. The function uses the Oxford Immunotec North America criterion by default; alternative criteria sets can be created as methods for the tspots.criteria function

Usage

```
tspot.interp(nil, panel.a, panel.b, mito,
  criteria = "oxford.usa", verbosity = "terse", ...)
```

Arguments

`nil`	A vector of nil results (in spots)
`panel.a`	A vector of Panel A TB antigen (ESAT-6) results (in spots)
`panel.b`	A vector of Panel B TB antigen (CFP10) results (in spots)
`mito`	A vector of mitogen results (in spots)
`criteria`	The name of the desired result criteria (defaults to the Oxford Immunotec criteria for North America).
`verbosity`	The level of verbosity ("onechar", "terse", "verbose") of the output.
`...`	Other arguments passed to the crtieria evaluation function chosen by the "criteria" argument.

Details

All spot counts greater than 20 are automatically censored to 20 for the purposes of calculating qualitative results, following Oxford's interpretation instructions.

Value

The function returns a vector of qualitative results. The verbosity of results depends on the argument passed to "verbosity":

onechar	Returns a single character indicating the result (N for Negative, B for Borderline, P for Positive, I for Indeterminate).
terse	Returns a single word indicating the result (Negative, Borderline, Positive, Indeterminate).
verbose	Returns the same results as "terse", with the addition of a short comment indicating the reason for an "Indeterminate" result.

Multiple criteria sets are available. The function defaults to the standard Oxford North American criteria (`criteria = "oxford.usa"`), but other currently available options include:

`criteria = "oxford.global"`
> The Oxford global criteria, for which the criterion for positivity is lowered from an 8-spot difference between the antigen and nil panels and which does not include the borderline qualitative result;

`criteria = "10spot"`
> A criteria set in which the borderline result is extended to include differences of 5 to 9 spots and only differences of 10 or more spots indicate a positive result.

Note

This function is provided purely as a convenience and is not a replacement for manual interpretation, manufacturer-provided software, or common sense. Absolutely not for clinical use.

References

Oxford Immunotec <http://www.oxfordimmunotec.com/>

See Also

qft.interp for Quantiferon interpretation.

Examples

```
# Calculate results
test.tspots$result.check <- with(test.tspots,
                                 tspot.interp(nil = nil,
                                              panel.a = panel.a,
                                              panel.b = panel.b,
                                              mito = mito))

# Compare lab and calculated results
with(test.tspots, table(lab.result, result.check, exclude = NULL))

# Compare different levels of verbosity
test.tspots$verbose.check <- with(test.tspots,
                                  tspot.interp(nil = nil,
                                               panel.a = panel.a,
                                               panel.b = panel.b,
                                               mito = mito,
                                               verbosity = "verbose"))

test.tspots$onechar.check <- with(test.tspots,
                                  tspot.interp(nil = nil,
                                               panel.a = panel.a,
                                               panel.b = panel.b,
                                               mito = mito,
                                               verbosity = "onechar"))

unique(test.tspots[ , c("lab.result", "result.check",
                        "verbose.check", "onechar.check")])
```

Index