Package ‘allMT’

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Type Package

Title Acute Lymphoblastic Leukemia Maintenance Therapy Analysis

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Description
Evaluates acute lymphoblastic leukemia maintenance therapy practice at patient and cohort level.

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Encoding UTF-8

RoxygenNote 7.3.3

Imports dplyr (>= 1.0.10), ggplot2 (>= 3.3.6), htmlTable (>= 2.2.1), plyr (>= 1.8.6), readxl (>= 1.3.1), reshape2 (>= 1.4.4), rio (>= 0.5.29), scales (>= 1.2.1), stringr (>= 1.4.1), survival (>= 3.2.11), survminer (>= 0.4.9), tibble (>= 3.1.8), tools (>= 3.6.1), utils (>= 3.6.1)

Suggests bibtex (>= 0.5.0), bookdown (>= 0.30), knitr (>= 1.39), rmarkdown (>= 2.18)

Collate 'UPN_914.R' 'UPN_915.R' 'UPN_916.R' 'rounding_off.R' 'assess_anemia.R' 'assess_increased_doses.R' 'assess_neutropenia.R' 'assess_reduced_doses.R' 'assess_stop_doses.R' 'assess_thrombocytopenia.R' 'compare_cohorts.R' 'convert_external_format.R' 'convert_tmc_format.R' 'plot_progression.R' 'summarize_cohortMT.R' 'summarize_cycle_progression.R' 'time_to_first_dose_increase.R'

VignetteBuilder knitr

URL `https://github.com/tmungle/allMT`, `https://tmungle.github.io/allMT/`

BugReports `https://github.com/tmungle/allMT/issues`

Depends R (>= 2.10)

LazyData true

NeedsCompilation no

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Contents

`assess_anemia` *Assess hematological toxicities: Anemia*

Description

Evaluate number of anemia episodes and their duration for a given patient or cohort

Usage

```
assess_anemia(input_files_path, hb_range, duration_hb = NA)
```

Arguments

`input_files_path`	path to a file or a folder with MT csv files (in quotes).
`hb_range`	Hemoglobin (HB) value range of c(Anemic HB threshold, recovered HB threshold). NOTE: Ensure that units are the same as unit of HB in the input data.
`duration_hb`	numeric duration (in weeks) that is used to categorize event as "long duration anemia" (optional)

Value

Returns a list with (1) the anemia information for each patient as listed below, (2) analysis summary as dataframe (3) analysis summary as HTML table.

1. Pat ID
2. Number of particular toxicity episodes
3. Duration of particular toxicity (in weeks)
4. Number of long duration toxicity episodes
5. Duration of long duration toxicity (in weeks)

Note

1. If the function is used for cohort analysis then values are represented as median and interquartile range (IQR) (25%-75%). The median and IQR is rounded off to upper integer value if decimal value is greater or equal to 0.5, else to lower integer value. Example 1.4->1 and 3.75->4
2. Long duration toxicity is only analyzed if "duration_hb" is included in provided arguments
3. User may save the result as a list, if required, to analyze each patient seperatly please use 1st element of list

See Also

`assess_neutropenia()`, `assess_thrombocytopenia()`

Examples

```
pat_data = system.file("extdata/processed_data/", "UPN_915.csv", package = "allMT")
assess_anemia(input_files_path = pat_data,
                      hb_range = c(7, 8), duration_hb = 3)



cohort_path = paste0(system.file("extdata/processed_data/", package = "allMT"), "/")
assess_anemia(input_files_path = cohort_path,
                      hb_range = c(7, 8), duration_hb = 3)

result <- assess_anemia(input_files_path = pat_data,
                      hb_range = c(7, 8), duration_hb = 3)
print(result[[1]])
print(result[[2]])
print(result[[3]])
```

`assess_increased_doses` *Analyze physicians' compliance to dosing guidelines: INCREASE DOSE*

Description

Evaluate number of times blood counts did not support physicians' INCREASE DOSE decision

Usage

```
assess_increased_doses(
  input_files_path,
  anc_threshold = NA,
  plt_threshold = NA,
  hb_threshold = NA,
  escalation_factor,
  tolerated_dose_duration
)
```

Arguments

`input_files_path`	path to a file or a folder with MT csv files (in quotes).
`anc_threshold`	Absolute neutrophil count (ANC) value threshold above which doses should be increased. NOTE: Ensure that the threshold value is represented with same unit as of the input ANC data.
`plt_threshold`	Platelet (PLT) value threshold above which doses should be increased. NOTE: Ensure that the threshold value is represented with same unit as of the input PLT data.
`hb_threshold`	Hemoglobin (HB) value threshold below which doses should be increased. NOTE: Ensure that the threshold value is represented with same unit as of the input Hb data.
`escalation_factor`	Percentage of increase from previous tolerated dose to be considered as "increased" dose.
`tolerated_dose_duration`	Number of weeks with ANC, PLT, and Hb values consistently above threshold with same dose prescription, following which dose should be increased.

Value

Returns a list with (1) the 'INCREASE DOSE' analysis for each patient as listed below, (2) analysis summary as dataframe (3) analysis summary as HTML table in viewer.

1. Pat ID

2. Number of decisions where the physician increased dose (a)
3. Number of times blood counts did not support dose suspension (b)
4. Discordance (%) = $(1 - (b/a) * 100)$

Note

1. Atleast one of the threshold parameters (anc_threshold, plt_threshold, hb_threshold) must be provided to carry out analysis. Missing threshold parameter will not be considered.
2. If the function is used for cohort analysis then a and b will be represented as median and interquartile range (IQR) (25%-75%). The median and IQR is rounded off to upper integer value if decimal value is greater or equal to 0.5, else to lower integer value Example 1.4->1 and 3.75->4
3. User may save the result as a list, if required, to analyze each patient separately - use 1st element of list. Please refer to examples from assess_anemia

See Also

`time_to_first_dose_increase()`, `assess_reduced_doses()`, `assess_stop_doses()`

Examples

```
cohort_path = paste0(system.file("extdata/processed_data/", package = "allMT"), "/")
assess_increased_doses(input_files_path = cohort_path, anc_threshold = 0.75,
                      plt_threshold = 75, hb_threshold = 8,
                      escalation_factor = 25, tolerated_dose_duration = 8)


pat_data = system.file("extdata/processed_data/", "UPN_914.csv", package = "allMT")
assess_increased_doses (input_files_path = pat_data, anc_threshold = 0.75,
                      plt_threshold = 75, hb_threshold = 8,
                      escalation_factor = 15, tolerated_dose_duration = 6)

assess_increased_doses(input_files_path = cohort_path,
                      anc_threshold = 0.7, plt_threshold = 60)
```

`assess_neutropenia` *Assess hematological toxicities: Neutropenia*

Description

Evaluate number of neutropenia episodes and their duration for a given patient or cohort

Usage

```
assess_neutropenia(input_files_path, anc_range, duration_anc = NA)
```

Arguments

`input_files_path`	path to a file or a folder with MT csv files (in quotes).
`anc_range`	Absolute neutrophil count (ANC) value range of c(Neutropenic ANC threshold, recovered ANC threshold). NOTE: Ensure that units are the same as unit of ANC in the input data.
`duration_anc`	numeric duration (in weeks) that is used to categorize event as "long duration neutropenia" (optional)

Value

Returns a list with (1) the neutropenia information for each patient as listed below, (2) analysis summary as dataframe (3) analysis summary as HTML table.

1. Pat ID
2. Number of particular toxicity episodes
3. Duration of particular toxicity (in weeks)
4. Number of long duration toxicity episodes
5. Duration of long duration toxicity (in weeks)

Note

1. If the function is used for cohort analysis then values are represented as median and interquartile range (IQR) (25%-75%). The median and IQR is rounded off to upper integer value if decimal value is greater or equal to 0.5, else to lower integer value. Example 1.4->1 and 3.75->4
2. Long duration toxicity is only analyzed if "duration_anc" is included in provided arguments
3. User may save the result as a list, if required, to analyze each patient neutropenia analysis by analyzing 1st element of list

See Also

`assess_anemia()`, `assess_thrombocytopenia()`

Examples

```
pat_data = system.file("extdata/processed_data/", "UPN_915.csv", package = "allMT")
assess_neutropenia(input_files_path = pat_data,
                      anc_range = c(0.5, 0.75), duration_anc = 3)



cohort_path = paste0(system.file("extdata/processed_data/", package = "allMT"), "/")
assess_neutropenia(input_files_path = cohort_path,
                      anc_range = c(0.5, 0.75), duration_anc = 3)


result <- assess_neutropenia(input_files_path = pat_data,
```

```
                    anc_range = c(0.5, 0.75), duration_anc = 3)
print(result[[1]])
print(result[[2]])
print(result[[3]])
```

`assess_reduced_doses` *Analyze physicians' compliance to dosing guidelines: REDUCE DOSE*

Description

Evaluate number of times blood counts did not support physicians' REDUCE DOSE decision

Usage

```
assess_reduced_doses(
  input_files_path,
  anc_range = NA,
  plt_range = NA,
  hb_range = NA,
  reduction_factor
)
```

Arguments

`input_files_path`	path to a file or a folder with MT csv files (in quotes).
`anc_range`	Absolute neutrophil count (ANC) range between which doses should be reduce. NOTE: Ensure that values are represented with same unit as of the input ANC data.
`plt_range`	Platelet (PLT) range between which doses should be reduce. NOTE: Ensure that values are represented with same unit as of the input PLT data.
`hb_range`	Hemoglobin (HB) range between which doses should be stopped. NOTE: Ensure that values are represented with same unit as of the input Hb data.
`reduction_factor`	Percentage of 6MP starting dose (first visit dose) dose that will be called as "reduced" dose. Default = 50% of starting dose.

Value

Returns a list with (1) the 'REDUCE DOSE' analysis for each patient as listed below, (2) analysis summary as dataframe (3) analysis summary as HTML table in viewer.

1. Pat ID
2. Number of decisions where the physician reduced dose (a)

3. Number of times blood counts did not support dose reduction (b)
4. Discordance (%) = $((b/a) * 100)$

#' @note

1. Atleast one of the threshold parameters (anc_threshold, plt_threshold, hb_threshold) must be provided to carry out analysis. Missing threshold parameter will not be considered.
2. If the function is used for cohort analysis then a and b will be represented as median and interquartile range (IQR) (25%-75%). The median and IQR is rounded off to upper integer value if decimal value is greater or equal to 0.5, else to lower integer value Example 1.4->1 and 3.75->4
3. User may save the result as a list, if required, to analyze each patient separately - use 1st element of list. Please refer to examples from assess_anemia

See Also

`assess_stop_doses()`, `assess_increased_doses()`

Examples

```
pat_data <- system.file("extdata/processed_data/", "UPN_915.csv", package = "allMT")
assess_reduced_doses(input_files_path = pat_data,
                     anc_range = c(0.5,0.75), plt_range = c(50,75),
                     hb_range = c(7,8), reduction_factor = 50)


cohort_path = paste0(system.file("extdata/processed_data/", package = "allMT"), "/")
assess_reduced_doses(input_files_path = cohort_path,
                     anc_range = c(0.5,0.75), plt_range = c(50,75),
                     hb_range = c(7,8), reduction_factor = 50)
```

`assess_stop_doses` *Analyze physicians' compliance to dosing guidelines: STOP DOSE*

Description

Evaluate number of times blood counts did not support physicians' STOP DOSE decision

Usage

```
assess_stop_doses(
  input_files_path,
  anc_threshold = NA,
  plt_threshold = NA,
  hb_threshold = NA
)
```

Arguments

`input_files_path`	path to a file or a folder with MT csv files (in quotes).
`anc_threshold`	Absolute neutrophil count (ANC) value threshold below which doses should be stopped. NOTE: Ensure that the threshold value is represented with same unit as of the input ANC data.
`plt_threshold`	Platelet (PLT) value threshold below which doses should be stopped. NOTE: Ensure that the threshold value is represented with same unit as of the input PLT data.
`hb_threshold`	Hemoglobin (HB) value threshold below which doses should be stopped. NOTE: Ensure that the threshold value is represented with same unit as of the input Hb data.

Value

Returns a list with (1) the 'STOP DOSE' analysis for each patient as listed below, (2) analysis summary as dataframe (3) analysis summary as HTML table in viewer.

1. Pat ID
2. Number of decisions where the physician stopped dose (a)
3. Number of times blood counts did not support dose suspension (b)
4. Discordance (%) = $((b/a) * 100)$

Note

1. Atleast one of the threshold parameters (anc_threshold, plt_threshold, hb_threshold) must be provided to carry out analysis. Missing threshold parameter will not be considered.
2. If the function is used for cohort analysis then a and b will be represented as median and interquartile range (IQR) (25%-75%). The median and IQR is rounded off to upper integer value if decimal value is greater or equal to 0.5, else to lower integer value Example 1.4->1 and 3.75->4
3. User may save the result as a list, if required, to analyze each patient separately - use 1st element of list. Please refer to examples from assess_anemia

See Also

`assess_reduced_doses()`, `assess_increased_doses()`

Examples

```
pat_data <- system.file("extdata/processed_data/", "UPN_915.csv", package = "allMT")
assess_stop_doses(input_files_path = pat_data,
                  anc_threshold = 0.5, plt_threshold = 50, hb_threshold = 7)


assess_stop_doses(input_files_path = pat_data,
                  anc_threshold = 0.5)
```

```
cohort_path = paste0(system.file("extdata/processed_data/", package = "allMT"), "/")
assess_stop_doses(input_files_path = cohort_path,
                  anc_threshold = 0.5,plt_threshold = 50, hb_threshold = 7)
```

---

assess_thrombocytopenia

Assess hematological toxicities : Thrombocytopenia

Description

Evaluate number of thrombocytopenia episodes and their duration for a given patient or cohort

Usage

```
assess_thrombocytopenia(input_files_path, plt_range, duration_plt = NA)
```

Arguments

`input_files_path`	path to a file or a folder with MT csv files (in quotes).
`plt_range`	Platelet (PLT) value range of c(thrombocytopenic PLT threshold, recovered PLT threshold). NOTE: Ensure that units are the same as unit of PLT in the input data.
`duration_plt`	numeric duration (in weeks) that is used to categorize event as "long duration thrombocytopenia" (optional)

Value

Returns a list with (1) the thrombocytopenia information for each patient as listed below, (2) analysis summary as dataframe (3) analysis summary as HTML table.

1. Pat ID
2. Number of particular toxicity episodes
3. Duration of particular toxicity (in weeks)
4. Number of long duration toxicity episodes
5. Duration of long duration toxicity (in weeks)

Note

1. If the function is used for cohort analysis then values are represented as median and interquartile range (IQR) (25%-75%). The median and IQR is rounded off to upper integer value if decimal value is greater or equal to 0.5, else to lower integer value. Example 1.4->1 and 3.75->4
2. Long duration toxicity is only analyzed if "duration_plt" is included in provided arguments
3. User may save the result as a list, if required, to analyze each patient thrombocytopenia analysis by analyzing 1st element of list

See Also

`assess_neutropenia()`, `assess_anemia()`

Examples

```
pat_data = system.file("extdata/processed_data/", "UPN_914.csv", package = "allMT")
assess_thrombocytopenia(input_files_path = pat_data,
                        plt_range = c(50, 75), duration_plt = 3)


cohort_path = paste0(system.file("extdata/processed_data/", package = "allMT"), "/")
assess_thrombocytopenia(input_files_path = cohort_path,
                        plt_range = c(50, 75), duration_plt = 3)


result <- assess_thrombocytopenia(input_files_path = pat_data,
                        plt_range = c(0.5, 0.75), duration_plt = 3)
print(result[[1]])
print(result[[2]])
print(result[[3]])
```

`compare_cohorts` *Plot summarized maintenance therapy (MT) data to compare two or more cohorts*

Description

Create an integrated summary graph facetted (by cohort). Graph illustrates weighted mean absolute neutrophil count (ANC) and dose information for each patient.

Usage

```
compare_cohorts(
  input_files_path,
  unit,
  anc_range,
  dose_intensity_threshold,
  method,
  intervention_date,
  group_data_path
)
```

Arguments

`input_files_path`
Path to folder with MT csv files (in quotes)

`unit`	Choose either "million" or "billion". **million** Million cells/L (x10^6 cells/L or cells/μl) **billion** Billion cells/L (x10^9 cells/L or x10^3 cells/μl)
`anc_range`	Vector with lower and upper thresholds of absolute neutrophil count target range: (c(lower threshold, upper threshold)) **Note** Ensure units of anc_range and patient data (unit) match.
`dose_intensity_threshold`	numeric value of reference drug dose intensity (%).
`method`	Choose from "M1" or "M2". **M1** Comparison of cohorts that started MT therapy before or after a particular date of intervention (intervention_date). **M2** Comparison of MT therapy between pre-determined groups.
`intervention_date`	Only applicable if method = "M1". Provide date in yyyy-mm-dd format (in quotes)
`group_data_path`	Only applicable for method = "M2". Path to EXCEL FILE containing "group" information. Ensure "ID" and "Group" columns are present.

Value

Comparative summary graph

Note

Note If more than one chort need to be compared then only "M2" method is applicable

See Also

`summarize_cohortMT()`

Examples

```
cohort_path = paste0(system.file("extdata/processed_data/", package = "allMT"), "/")
compare_cohorts(input_files_path = cohort_path,
        method = "M1", intervention_date = "2020-12-01",
        unit = "billion", anc_range = c(0.75, 1.5), dose_intensity_threshold = 100)


group_path = system.file("extdata/grouped_data/group_data.xlsx", package = "allMT")
compare_cohorts(input_files_path = cohort_path,
       method = "M2", group_data_path = group_path,
       unit = "billion", anc_range = c(0.75, 1.5), dose_intensity_threshold = 80)
```

`convert_external_format`

Get standard data structure

Description

Convert a maintenance therapy excel sheet created by user into a standard format for analysis

Usage

```
convert_external_format(
  inputpath_to_excelfolder,
  exportpath_to_csvfolder,
  pat_data_file_path,
  daily_mp_dose = 60,
  weekly_mtx_dose = 20
)
```

Arguments

`inputpath_to_excelfolder`	Path to folder containing input excel files (in quotes)
`exportpath_to_csvfolder`	Path to folder in which to save final output csv files (in quotes)
`pat_data_file_path`	Path to excel file with patient IDs and corresponding BSA (body surface area) values. Column names - "ID", "BSA".
`daily_mp_dose`	numeric value of DAILY 6-Mercaptopurine dose per $1m^2$ (mg/m^2) as per the MT dosing protocol. Default = $60mg/m^2$ (as per ICiCLe-ALL-14 protocol)
`weekly_mtx_dose`	numeric value of WEEKLY absolute Methotrexate dose per $1m^2$ (mg/m^2) as per the MT dosing protocol. Default = $20mg/m^2$ (as per ICiCLe-ALL-14 protocol)

Value

Folder with converted csv files

Note

If MT excel files are missing in the input folder for any patient IDs provided in the pat_data_file ID column, the function will show a message of missing IDs but will continue to convert the available files.

See Also

`convert_tmc_format()`

Examples

```
# As per ICiCLe-ALL-14 protocol (Reference PMID - 35101099):
path_to_excel = paste0(system.file("extdata/external_data/", package = "allMT"), "/")
save_path = paste0(tempdir(),"/")
path_to_bsa = system.file("extdata/external_data/", "BSA.xlsx", package = "allMT")
convert_external_format(inputpath_to_excelfolder = path_to_excel,
                   exportpath_to_csvfolder = save_path,
                   pat_data_file_path = path_to_bsa,
                   daily_mp_dose = 60,
                   weekly_mtx_dose = 20)

# As per ICiCLe-ALL-14 protocol (Reference PMID - 35101099):
convert_external_format(inputpath_to_excelfolder = "../csv_trial/",
                   exportpath_to_csvfolder = save_path,
                   pat_data_file_path = "BSAFile.xlsx")

# As per BFM protocol (Reference PMID - 15902295):
convert_external_format(inputpath_to_excelfolder = "../csv_trial/",
                   exportpath_to_csvfolder = save_path,
                   pat_data_file_path = "BSAFile.xlsx",
                   daily_mp_dose = 50,
                   weekly_mtx_dose = 20)

# As per St Jude protocol (Reference PMID - 15902295):
convert_external_format(inputpath_to_excelfolder = "../csv_trial/",
                   exportpath_to_csvfolder = save_path,
                   pat_data_file_path = "BSAFile.xlsx",
                   daily_mp_dose = 75,
                   weekly_mtx_dose = 40)
```

`convert_tmc_format` *Get standard data structure*

Description

Convert a Tata Medical Center Kolkata India (TMC) based excel workbook into a standard format for analysis

Convert a maintenance therapy excel workbook (with individual sheets per cycle) into a single csv file with longitudinal data of blood count parameters, absolute doses and dose intensities of administered drugs.

Usage

```
convert_tmc_format(
  inputpath_to_excelfolder,
  exportpath_to_csvfolder,
  daily_mp_dose = 60,
```

```
  weekly_mtx_dose = 20
)
```

Arguments

`inputpath_to_excelfolder`
Path to folder containing input excel files (in quotes)

`exportpath_to_csvfolder`
Path to folder in which to save final output csv files (in quotes)

`daily_mp_dose` numeric value of DAILY 6-Mercaptopurine dose per $1m^2$ (mg/m^2) as per the MT dosing protocol. Default = $60mg/m^2$ (as per ICiCLe-ALL-14 protocol)

`weekly_mtx_dose`
numeric value of WEEKLY absolute Methotrexate dose per $1m^2$ (mg/m^2) as per the MT dosing protocol. Default = $20mg/m^2$ (as per ICiCLe-ALL-14 protocol)

Value

Folder with converted csv files

See Also

`convert_external_format()`

Examples

```
# As per ICiCLe-ALL-14 protocol (Reference PMID - 35101099):
path_to_excel = paste0(system.file("extdata/tmc_data/", package = "allMT"), "/")
save_path = paste0(tempdir(),"/")
convert_tmc_format(inputpath_to_excelfolder = path_to_excel,
                   exportpath_to_csvfolder = save_path,
                   daily_mp_dose = 60,
                   weekly_mtx_dose = 20)


# As per ICiCLe-ALL-14 protocol (Reference PMID - 35101099):
convert_tmc_format(inputpath_to_excelfolder = path_to_excel,
                   exportpath_to_csvfolder = save_path)

# As per BFM protocol (Reference PMID - 15902295):
convert_tmc_format(inputpath_to_excelfolder = path_to_excel,
                   exportpath_to_csvfolder = save_path,
                   daily_mp_dose = 50,
                   weekly_mtx_dose = 20)

# As per St Jude protocol (Reference PMID - 15902295):
convert_tmc_format(inputpath_to_excelfolder = path_to_excel,
                   exportpath_to_csvfolder = save_path,
                   daily_mp_dose = 75,
                   weekly_mtx_dose = 40)
```

`plot_progression` *Graphical representation of maintenance therapy data for single patient*

Description

Creates a line graph (trends) for absolute neutrophil count (ANC), 6-Mercaptopurine (6MP) and Methotrexate (MTX) doses across all visits for the given patient

Usage

```
plot_progression(input_file_path, anc_range, unit)
```

Arguments

`input_file_path`	Path to input csv file for the patient (in quotes)
`anc_range`	ANC target range as per the protocol: (c(lower threshold, upper threshold)). NOTE: Ensure that units are the same as unit of ANC in the input data.
`unit`	Choose either "million" or "billion". • "million" = million cells/L (x10^6 cells/L or cells/μl) • "billion" = billion cells/L (x10^9 cells/L or x10^3 cells/μl)

Value

plot image

Note

- If there is only one threshold for anc_range parameter, please specify the respective value and keep the other threshold as NA. eg : c(2000, NA)
- Horizontal dotted lines on the graph indicate anc_range thresholds and starting doses for 6MP and MTX as a reference (colour coded to corresponding parameter)

See Also

`summarize_cycle_progression()`

Examples

```
pat_data = system.file("extdata/processed_data/", "UPN_915.csv", package = "allMT")
plot_progression(input_file_path = pat_data, anc_range = c(0.75,1.5), unit = "billion")


# As per BFM protocol (Reference PMID - 15902295):
plot_progression(input_file_path = "../UPN1.csv", anc_range = c(2, NA), unit = "billion")
```

```
# As per St Jude protocol (Reference PMID - 15902295):
plot_progression(input_file_path = "../../UPN1.csv", anc_range = c(0.3, 1), unit = "billion")
```

`summarize_cohortMT` *Plot summarized maintenance therapy (MT) data for a cohort*

Description

Create an integrated summary graph illustrating weighted mean absolute neutrophil count (ANC) and dose information for each patient in the cohort.

Usage

```
summarize_cohortMT(input_files_path, anc_range, unit, dose_intensity_threshold)
```

Arguments

`input_files_path`	Path to folder with MT csv files (in quotes)
`anc_range`	ANC target range as per the protocol: (c(lower threshold, upper threshold)). NOTE: Ensure that units are the same as unit of ANC in the input data.
`unit`	Choose either "million" or "billion". • "million" = million cells/L (x10^6 cells/L or cells/μl) • "billion" = billion cells/L (x10^9 cells/L or x10^3 cells/μl)
`dose_intensity_threshold`	numeric value of reference drug dose intensity (%). (optional)

Value

Summary graph

Note

- If there is only one threshold for anc_range or dose_intensity_range parameters, please specify the respective value and keep the other threshold as NA. eg : c(2000, NA), c(100, NA)
- Horizontal dotted lines on the graph indicate anc_range thresholds.Red dot represents summarized overall MT data.

See Also

`compare_cohorts()`

Examples

```
cohort_path = paste0(system.file("extdata/processed_data/", package = "allMT"), "/")
summarize_cohortMT (input_files_path = cohort_path, unit = "billion",
                    anc_range = c(0.75, 1.5), dose_intensity_threshold = c(80, 100))


summarize_cohortMT(input_files_path = cohort_path,
                unit = "billion", anc_range = c(0.8, 2), dose_intensity_threshold = 150)

# As per BFM protocol (Reference PMID - 15902295):
summarize_cohortMT (input_files_path = cohort_path,
                 unit = "billion", anc_range = c(2, NA), dose_intensity_threshold = 150)

# As per St Jude protocol (Reference PMID - 15902295):
summarize_cohortMT (input_files_path = cohort_path,
                unit = "billion", anc_range = c(0.8, 2), dose_intensity_threshold = 100)
```

`summarize_cycle_progression` *Plot a cycle-specific summary graph of maintenance therapy (MT) data for single patient*

Description

Create summary graph with maintenance therapy data. Weighted mean absolute neutrophil count (ANC) and dose information is calculated and plotted for each cycle.

Usage

```
summarize_cycle_progression(input_file_path, anc_range, unit)
```

Arguments

`input_file_path`	Path to input csv file for the patient (in quotes)
`anc_range`	ANC target range as per the protocol: (c(lower threshold, upper threshold)). NOTE: Ensure that units are the same as unit of ANC in the input data.
`unit`	Choose either "million" or "billion". • "million" = million cells/L (x10^6 cells/L or cells/μl) • "billion" = billion cells/L (x10^9 cells/L or x10^3 cells/μl)

Value

Plot image

Note

- If there is only one threshold for anc_range parameter, please specify the respective value and keep the other threshold as NA. eg : c(2000, NA)
- Horizontal dotted lines on the graph indicate anc_range thresholds.Red dot represents summarized overall MT data.

See Also

`plot_progression()`

Examples

```
pat_data = system.file("extdata/processed_data/", "UPN_916.csv", package = "allMT")
summarize_cycle_progression(input_file_path = pat_data, anc_range = c(0.75, 1.5),
                 unit = "billion")

summarize_cycle_progression(input_file_path = pat_data,
                 anc_range = c(0.8, 2), unit = "billion")

# As per BFM protocol (Reference PMID - 15902295):
summarize_cycle_progression(input_file_path = pat_data,
                 anc_range = c(2, NA),
                 unit = "billion")

# As per St Jude protocol (Reference PMID - 15902295):
summarize_cycle_progression(input_file_path = pat_data,
                 anc_range = c(0.8, 2),
                 unit = "billion")
```

`time_to_first_dose_increase` *Plot the time taken for FIRST 6-Mercaptopurine (6MP) dose increase in cohort*

Description

Evaluate median time (in weeks) to first 6MP dose increase for the cohort using Kaplan-Meier cumulative incidence estimator using ggsurvplot package

Usage

```
time_to_first_dose_increase(input_files_path, escalation_factor)
```

Arguments

`input_files_path`
: Path to folder with MT csv files (in quotes)

`escalation_factor`
: Percentage of increase from first dose to be considered as an "increased" dose.

Value

Median time (in weeks) to first 6MP dose increase plot

See Also

`assess_increased_doses()`

Examples

```
cohort_path = paste0(system.file("extdata/processed_data/", package = "allMT"), "/")
time_to_first_dose_increase(input_files_path = cohort_path,
                escalation_factor = 10)
```

UPN_914 *Sample data for a patient with unique patient number (UPN) 914*

Description

Data for the patient consists of a `dataframe` that is used for viewing data

Usage

```
UPN_914
```

Format

A `dataframe` with 10 columns

1. Cycle: 96 weeks of maintenance therapy (MT) is divided into 8 cycles. The column represents the cycles number for the patient with new assessment
2. Date: Patient's new assessment date when doses were prescribed
3. Weeks: MT consist of 96 weeks. Column represent week number for new assessment
4. ANC: Absolute neutrophil count (ANC) values for new assessment
5. PLT: Platelet count (PLT) values for new assessment
6. Hb: Hemoglobin (Hb) values for new assessment
7. MP: 6-mercaptopurine (MP or 6MP) doses for new assessment
8. MTX: Methotraxate (MTX) doses for new assessment
9. MP_adj: MP dose intensity (%). See note for dose intensity calculation
10. MTX_adj: MTX dose intensity (%). See note for dose intensity calculation

Note

1. For running examples you need to read the patient data as csv. The data (rda) is for viewing only
2. Dose intensity (%) = $(a * 100)/b$; where a = MP dose prescribed on new assessment and b = Protocol based MP dose adjusted to patient's body surface area

---

`UPN_915` *Sample data for a patient with unique patient number (UPN) 915*

Description

Data for the patient consists of a `dataframe` that is used for viewing data

Usage

```
UPN_915
```

Format

A `dataframe` with 10 columns

1. Cycle: 96 weeks of maintenance therapy (MT) is divided into 8 cycles. The column represents the cycles number for the patient with new assessment
2. Date: Patient's new assessment date when doses were prescribed
3. Weeks: MT consist of 96 weeks. Column represent week number for new assessment
4. ANC: Absolute neutrophil count (ANC) values for new assessment
5. PLT: Platelet count (PLT) values for new assessment
6. Hb: Hemoglobin (Hb) values for new assessment
7. MP: 6-mercaptopurine (MP or 6MP) doses for new assessment
8. MTX: Methotraxate (MTX) doses for new assessment
9. MP_adj: MP dose intensity (%). See note for dose intensity calculation
10. MTX_adj: MTX dose intensity (%). See note for dose intensity calculation

Note

1. For running examples you need to read the patient data as csv. The data (rda) is for viewing only
2. Dose intensity (%) = $(a * 100)/b$; where a = MP dose prescribed on new assessment and b = Protocol based MP dose adjusted to patient's body surface area

---

`UPN_916` *Sample data for a patient with unique patient number (UPN) 916*

Description

Data for the patient consists of a `dataframe` that is used for viewing data

Usage

```
UPN_916
```

Format

A `dataframe` with 10 columns

1. Cycle: 96 weeks of maintenance therapy (MT) is divided into 8 cycles. The column represents the cycles number for the patient with new assessment
2. Date: Patient's new assessment date when doses were prescribed
3. Weeks: MT consist of 96 weeks. Column represent week number for new assessment
4. ANC: Absolute neutrophil count (ANC) values for new assessment
5. PLT: Platelet count (PLT) values for new assessment
6. Hb: Hemoglobin (Hb) values for new assessment
7. MP: 6-mercaptopurine (MP or 6MP) doses for new assessment
8. MTX: Methotraxate (MTX) doses for new assessment
9. MP_adj: MP dose intensity (%). See note for dose intensity calculation
10. MTX_adj: MTX dose intensity (%). See note for dose intensity calculation

Note

1. For running examples you need to read the patient data as csv. The data (rda) is for viewing only
2. Dose intensity (%) = $(a * 100)/b$; where a = MP dose prescribed on new assessment and b = Protocol based MP dose adjusted to patient's body surface area

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