pfasbiomon

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Type Package

Title PFAS Biomonitoring and In Vitro PODs to generate Margins of Exposure

Version 0.1.0

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Description The package takes data from PFAS biomonitoring studies (blood, plasma) and in vitro bioactivity data and calculates margins of exposure (MoEs). This supports the manuscript titled ``A Comparison of In Vitro and In Vivo Points of Departure with Human Biomonitoring Levels for Per- and Polyfluoroalkyl Substances (PFAS)". In the manuscript, the term MoE is replaced by Bioactive Concentration to Blood Concentration Ratio (BCBCR)

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

R topics documented:

`ACToR.parse` *Parse the ACToR files and fill in the remaining missed data*

Description

Parse the ACToR files and fill in the remaining missed data

Usage

```
ACToR.parse(dataset = "PFAS_3M")
```

Arguments

`dir`	The directory where the lists are stored

`ACToR.parse.fillin` *Parse the ACToR files*

Description

Parse the ACToR files

Usage

```
ACToR.parse.fillin(
  datasets = c("Denmark", "Germany", "HealthCanada", "Japan", "Michigan",
    "Norway_Nordic", "Ohio", "Sweden")
)
```

Arguments

`dir`	The directory where the lists are stored

`dnt.check` *check the processing for the DNT PODs*

Description

check the processing for the DNT PODs

Usage

```
dnt.check(to.file = F)
```

driver — *Run all of the analyzes starting with the hand-edited data file*

Description

Run all of the analyzes starting with the hand-edited data file

Usage

```
driver()
```

extract_NHANES — *Code to format the NHANES data Note that this will only run under R 4.x*

Description

Code to format the NHANES data Note that this will only run under R 4.x

Usage

```
extract_NHANES(dir = "../data/", dataset = "PFAS_J")
```

Arguments

dir	The directory to look for data
dataset	The name of the NHANES dataset

hello — *Hello, World!*

Description

Prints 'Hello, world!'.

Usage

```
hello()
```

Examples

```
hello()
```

`pfas.for.mdh` *Pull the PFAS data fro MDH*

Description

Pull the PFAS data fro MDH

Usage

```
pfas.for.mdh(to.file = F)
```

`pfasBiomonitoringMerge` *Merge the ACToR data with NHANES and put in a common format*

Description

Merge the ACToR data with NHANES and put in a common format

Usage

```
pfasBiomonitoringMerge()
```

`pfasBiomonitoringOldNewMergeForFiltering` *Setup the new filtered input file using the latest assays from Doris*

Description

Setup the new filtered input file using the latest assays from Doris

Usage

```
pfasBiomonitoringOldNewMergeForFiltering()
```

`pfasBiomonitoringOutliers` *Find outliers*

Description

Find outliers

Usage

```
pfasBiomonitoringOutliers()
```

pfasBloodLevelxChainLength *Plotthe blood levels by chain length*

Description

Plotthe blood levels by chain length

Usage

```
pfasBloodLevelxChainLength(to.file = F)
```

Arguments

to.file	If TRUE, write graphs to a file
data.version	Label of folder where input data sits

pfasBloodLevelxChainLengthGG *Plotthe blood levels by chain length*

Description

Plotthe blood levels by chain length

Usage

```
pfasBloodLevelxChainLengthGG(to.file = F)
```

Arguments

to.file	If TRUE, write graphs to a file
data.version	Label of folder where input data sits

pfasChemicalTable *Generate a table of the chemicals and the data we have for them*

Description

Generate a table of the chemicals and the data we have for them

Usage

```
pfasChemicalTable()
```

pfasCorrrectedMOE *Calculate the TK-corrected MOE values*

Description

Calculate the TK-corrected MOE values

Usage

```
pfasCorrrectedMOE()
```

pfasCorrrectedMOE.noTK *Calculate the TK-corrected MOE values*

Description

Calculate the TK-corrected MOE values

Usage

```
pfasCorrrectedMOE.noTK()
```

pfasHalfLife *Extract the half-life information from Dawson et al. supplemental file*

Description

Extract the half-life information from Dawson et al. supplemental file

Usage

```
pfasHalfLife(species = "Human", route = "Oral")
```

Arguments

species	The species to use
route	The exposre route

pfasInVitroVsRat *Compare the in vitro PODs vs the Rat POD concentration*

Description

Compare the in vitro PODs vs the Rat POD concentration

Usage

```
pfasInVitroVsRat(to.file = F)
```

Arguments

to.file	If TRUE, write graphs to a file
data.version	Label of folder where input data sits

pfasMoeBoxplot *Plot the distribution of PODs*

Description

Plot the distribution of PODs

Usage

```
pfasMoeBoxplot(to.file = F)
```

Arguments

dir	The directory where the lists are stored

pfasMoeBoxplotOPPT *Plot the distribution of PODs*

Description

Plot the distribution of PODs

Usage

```
pfasMoeBoxplotOPPT(to.file = F)
```

Arguments

dir	The directory where the lists are stored

`pfasPartitionCoefficients` *Get the partition coefficients*

Description

Get the partition coefficients

Usage

```
pfasPartitionCoefficients(species = "Human")
```

Arguments

`to.file`	If TRUE, write graphs to a file
`data.version`	Label of folder where input data sits

`pfasPerChemicalMoeBoxplot` *Build the raw MoE Boxplots*

Description

Build the raw MoE Boxplots

Usage

```
pfasPerChemicalMoeBoxplot(to.file = F)
```

Arguments

`to.file`	If TRUE, write graphs to a file

`pfasRawMoeBoxplotsGG` *Build the raw MoE Boxplots*

Description

Build the raw MoE Boxplots

Usage

```
pfasRawMoeBoxplotsGG(to.file = F)
```

Arguments

`to.file`	If TRUE, write graphs to a file

printCurrentFunction *Print the name of the current function*

Description

Print the name of the current function

Usage

```
printCurrentFunction(comment.string = NA)
```

Arguments

comment.string	An optinal string to be printed

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