pfasbiomon

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Type Package

Title What the Package Does (Title Case)

Version 0.1.0

Author Who wrote it

Maintainer The package maintainer <yourself@somewhere.net>

Description More about what it does (maybe more than one line)
Use four spaces when indenting paragraphs within the Description.

License What license is it under?

Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

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

`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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