# 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** 7.2.3

## R topics documented:

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

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## 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 |

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

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## 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 |

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

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## 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 |

`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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