Leptin SDS

```
library(childsds)
library(dplyr)
#>
#> Attaching package: 'dplyr'
#> The following objects are masked from 'package:stats':
#>
#>     filter, lag
#> The following objects are masked from 'package:base':
#>
#>     intersect, setdiff, setequal, union
data(leptin.ref)
```

Children: Age- and BMI-SDS-adjusted Leptin-SDS

For children and adolescents up to an age of 18.5 years, leptin standard deviation scores will be calclated based on age on years and BMI-SDS. BMI-SDS via the `x2=` argument to the `sds_2d()` function.

Besides, the `sds_2d()` function takes the leptin value (`value=`), sex (`sex=`) and age (`age=`) as arguments. These values have to be given as vectors of the same length. In addition, it needs a reference object (in our case `ref=leptin.ref`) and the item (`item=`). For children younger than 6, the item is 'leptin_until6', for children between 6 and 18, it is 'leptin_6to18'. The function returns a numeric vector of the same length containing leptin-SDS (`type="SDS"`) or leptin percentiles (`type="perc"`).

A single value

```
sds_2d(value = 20, age = 10, x2 = 1, sex = "male", item = "leptin_until6", ref = leptin.ref)
#> [1] 2.037242
```

Within a data set

Create a sample data set

```
df <- data.frame(age = seq(0.5, 6.5, by = 1),
                 sex = sample(c("m","f"),7, replace = T),
                 bmisds = rnorm(7),
                 leptin = runif(7, min = 0.01, max = 5))
df
#>   age sex     bmisds    leptin
#> 1 0.5   f -1.0895943 0.2355327
#> 2 1.5   f  0.7299258 1.8850280
#> 3 2.5   m  0.9581745 4.0191557
#> 4 3.5   m -1.7654899 1.6050032
#> 5 4.5   f -0.8113261 1.4233996
#> 6 5.5   m  1.0022442 2.3258233
#> 7 6.5   f  0.5802546 1.7829597
```

Calculate Leptin-SDS

```
df$leptin_sds <- sds_2d(value = df$leptin,
                        age = df$age,
                        x2 = df$bmisds,
                        sex = df$sex, male = "m", female = "f",
                        item = "leptin_until6",
                        ref = leptin.ref)
df
#>   age sex     bmisds    leptin leptin_sds
#> 1 0.5   f -1.0895943 0.2355327 -1.9583470
#> 2 1.5   f  0.7299258 1.8850280  0.3970873
#> 3 2.5   m  0.9581745 4.0191557  1.4295320
#> 4 3.5   m -1.7654899 1.6050032  1.3185698
#> 5 4.5   f -0.8113261 1.4233996  0.4436076
#> 6 5.5   m  1.0022442 2.3258233  0.1168205
#> 7 6.5   f  0.5802546 1.7829597 -0.6464500
```

Children: Tanner Stage and BMI-SDS dependent SDS values

For SDS adjusted for pubertal stage, you have to use the function `sds_pub2d()`. Again, the leptin value (`value=`), the Tanner stage (1-5, `pubstat=`), the BMI-SDS (`x2=`) and the sex (`sex=`) has to be given to the function as vectors of the same length. The `ref` object is still `leptin.ref` and the `item=lep_pub`. The reference values are valid for the age range 6-18.

A single value

```
sds_pub2d(value = 20,
          pubstat = 2,
          x2 = 1,
          sex = "male",
          item = "lep_pub", ref = leptin.ref)
#> [1] 1.946403
```

Create a sample data set

```
df <- data.frame(age = seq(0.5, 6.5, by = 1),
                 sex = sample(c("m","f"),7, replace = T),
                 bmisds = rnorm(7),
                 leptin = runif(7, min = 0.01, max = 5))
df
#>   age sex     bmisds   leptin
#> 1 0.5   f -1.0966543 3.658449
#> 2 1.5   f  0.3265145 1.486408
#> 3 2.5   m -1.1754974 3.715782
#> 4 3.5   f  0.3847249 1.547960
#> 5 4.5   m  1.0466260 3.405525
#> 6 5.5   m -0.5566505 4.941369
#> 7 6.5   f  0.5239635 3.749811
```

Calculate Leptin-SDS

```
df$leptin_sds <- sds_2d(value = df$leptin,
                        age = df$age,
                        x2 = df$bmisds,
                        sex = df$sex, male = "m", female = "f",
                        item = "leptin_until6",
                        ref = leptin.ref)
df
#>   age sex     bmisds   leptin leptin_sds
#> 1 0.5   f -1.0966543 3.658449  1.1218338
#> 2 1.5   f  0.3265145 1.486408  0.1974877
#> 3 2.5   m -1.1754974 3.715782  2.0973924
#> 4 3.5   f  0.3847249 1.547960 -0.2388123
#> 5 4.5   m  1.0466260 3.405525  0.8168908
#> 6 5.5   m -0.5566505 4.941369  2.0211629
#> 7 6.5   f  0.5239635 3.749811  0.7620845
```

Calculate Leptin-percentiles

```
df$leptin_perc <- sds_2d(value = df$leptin,
                        age = df$age,
                        x2 = df$bmisds,
                        sex = df$sex, male = "m", female = "f",
                        item = "leptin_until6",
                        type = "perc",
                        ref = leptin.ref)
df
#>   age sex     bmisds   leptin leptin_sds leptin_perc
#> 1 0.5   f -1.0966543 3.658449  1.1218338       86.90
#> 2 1.5   f  0.3265145 1.486408  0.1974877       57.83
#> 3 2.5   m -1.1754974 3.715782  2.0973924       98.20
#> 4 3.5   f  0.3847249 1.547960 -0.2388123       40.56
#> 5 4.5   m  1.0466260 3.405525  0.8168908       79.30
#> 6 5.5   m -0.5566505 4.941369  2.0211629       97.84
#> 7 6.5   f  0.5239635 3.749811  0.7620845       77.70
```

Adults: Age- and BMI-adjusted Leptin-SDS

For adults until 80 years, leptin standard deviation scores will be calclated based on age on years and BMI. BMI is passed to the `sds_2d()` function via the `x2=` argument.

Besides, the `sds_2d()` function takes the leptin value (`value=`), sex (`sex=`) and age (`age=`) as arguments. These values have to be given as vectors of the same length. In addition, it needs a reference object (in our case `ref=leptin.ref`) and the item (`item=`). For adults, it is 'lep_bmi'. The function returns a numeric vector of the same length containing leptin-SDS (`type="SDS"`) or leptin percentiles (`type="perc"`).

A single value

```
sds_2d(value = 20, age = 20, x2 = 25, sex = "male", item = "lep_bmi", ref = leptin.ref)
#> [1] 1.632996
```

Within a data set

Create a sample data set

```
df <- data.frame(age = seq(20, 80, by = 10),
                 sex = sample(c("M","F"),7, replace = T),
                 bmi = runif(7, 20, 40),
                 leptin = runif(7, min = 0.01, max = 20))
df
#>   age sex      bmi    leptin
#> 1  20   F 33.92015  7.550841
#> 2  30   M 21.74785  5.103679
#> 3  40   F 39.88167 13.246594
#> 4  50   M 39.42778  9.556688
#> 5  60   F 35.40523 11.457431
#> 6  70   F 33.29527 10.807725
#> 7  80   M 39.44476 19.014750
```

Calculate Leptin-SDS

```
df$leptin_sds <- sds_2d(value = df$leptin,
                        age = df$age,
                        x2 = df$bmi,
                        sex = df$sex, male = "M", female = "F",
                        item = "lep_bmi",
                        ref = leptin.ref)
df
#>   age sex      bmi    leptin leptin_sds
#> 1  20   F 33.92015  7.550841  -1.735157
#> 2  30   M 21.74785  5.103679   1.411136
#> 3  40   F 39.88167 13.246594  -1.478756
#> 4  50   M 39.42778  9.556688  -1.105775
#> 5  60   F 35.40523 11.457431  -1.380689
#> 6  70   F 33.29527 10.807725  -1.429440
#> 7  80   M 39.44476 19.014750  -0.494738
```