*Introductory Statistics for the Life and Biomedical Sciences*R
R
LEAP
Description:
Usage:
Format:
Details:
Source
indices

```
##   participant.ID    treatment.group age.months
## 1    LEAP_100522 Peanut Consumption     6.0780
## 2    LEAP_103358 Peanut Consumption     7.5893
## 3    LEAP_105069   Peanut Avoidance     5.9795
## 4    LEAP_105328 Peanut Consumption     7.0308
## 5    LEAP_106377   Peanut Avoidance     6.4066
```

dataset[rows,columns]

```
##   participant.ID    treatment.group age.months    sex primary.ethnicity
## 1    LEAP_100522 Peanut Consumption     6.0780 Female             Black
## 2    LEAP_103358 Peanut Consumption     7.5893 Female             White
## 3    LEAP_105069   Peanut Avoidance     5.9795   Male             White
## 4    LEAP_105328 Peanut Consumption     7.0308 Female             White
## 5    LEAP_106377   Peanut Avoidance     6.4066   Male             White
##   overall.V60.outcome
## 1            PASS OFC
## 2            PASS OFC
## 3            PASS OFC
## 4            PASS OFC
## 5            PASS OFC
```

LEAP[1:5,1:6]R
*OI Biostat*c()

```
##     participant.ID    treatment.group overall.V60.outcome
## 1      LEAP_100522 Peanut Consumption            PASS OFC
## 2      LEAP_103358 Peanut Consumption            PASS OFC
## 3      LEAP_105069   Peanut Avoidance            PASS OFC
## 639    LEAP_994047   Peanut Avoidance            PASS OFC
## 640    LEAP_997608 Peanut Consumption            PASS OFC
```

*OI Biostat*table()addmargins()
treatment.group, *LEAP*

```
##
##                       FAIL OFC PASS OFC
##   Peanut Avoidance         36      227
##   Peanut Consumption        5      262
```

treatment.group, *LEAP*

```
##
##                       FAIL OFC PASS OFC Sum
##   Peanut Avoidance         36      227 263
##   Peanut Consumption        5      262 267
##   Sum                      41      489 530
```

*OI Biostat*frog.altitudefrog.df

```
##     altitude latitude clutch.size body.size clutch.volume egg.size
## 1   3,462.00    34.82    181.9701  3.630781      177.8279 1.949845
## 2   3,462.00    34.82    269.1535  3.630781      257.0396 1.949845
## 3   3,462.00    34.82    158.4893  3.715352      151.3561 1.949845
## 150 2,597.00    34.05    537.0318        NA      776.2471 2.238721
```

OI Biostat

```
##         sex age      race height weight actn3.r577x ndrm.ch
## 1    Female  27 Caucasian   65.0    199          CC    40.0
## 2      Male  36 Caucasian   71.7    189          CT    25.0
## 3    Female  24 Caucasian   65.0    134          CT    40.0
## 1348 Female  30 Caucasian   64.0    134          CC    43.8
```

Rsummary()*clutch.volume*)

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   151.4   609.6   831.8   882.5  1096.0  2630.0
```

mean$x_1, x_2, \ldots, x_n n$
$\overline{x} = \frac{x_1+x_2+\cdots+x_n}{n}$
R*clutch.volume*)n

```
## [1] 431
```

clutch.volume)/n

```
## [1] 882.474
```

Rmean()*clutch.volume*)$x.bar$

```
## [1] 882.474
## [1] 882.5
```

median
clutch.volume)

```
## [1] 831.7638
```

deviation$1^{st}2^{nd}3^{rd}431^{th}$clutch.volume
clutch.volume[c(1,2,3,431)]$-x.bar$

segmented bar plot*OI Biostat*`actn3.r577xc()`
`legend`
race, *famuss*

standardized segmented bar plot`ylim`
race, $famuss$
OI Biostat`racecounts.table`
$actn3.r577x$, $famuss$
side-by-side*OI Biostatyx*
$ndrm.ch famuss$
OI Biostat
$clutch.volume frog.altitude.data$
hollow histogram`add = T`
$ndrm.ch[famussndrm.ch[famussndrm.ch[famuss$
`errorcolor## Error in boxplot(golub.exprs.pheno[, 7:9]):  object 'golub.exprs.pheno' not found`