grp.seq.mix	*Calculate critical values and arm size for a mixture alternative*

Description

grp.seq.mix() is used for the design of one-sided group sequential clinical trials with mixture alternative using the Sequential Average Rank (SAR) test statistic. Error spending functions are implemented such that the test may reject early for efficacy or accept early for futility. The function can handle a fixed sample (single stage) design as well as a pure shift (theta=1). Requires packages rmutil if f = "laplace" and mvtnorm if norm.approx = TRUE.

Usage

```
grp.seq.mix(num.stages, alpha, beta, rho, theta, K,
    f = c("normal", "logistic", "laplace", "t3"),
    mu = 0, sigma = 1, method = c("sar","sr"),
    B = 1e5, norm.approx = TRUE)
```

Arguments

num.stages	Maximum number of planned stages.
alpha	Overall Type I error for the design.
beta	Overall Type II error for the design.
rho	Exponent in the error spending functions.
theta	Specified proportion of nonresponders in the treatment distribution.
K	Size of the location-shift in terms of standard deviations.
f	Distribution of the data.
mu	Mean of f.
sigma	Standard deviation of f.
method	Choice of test statistic.
B	Number of simulations used for approximating the exact distribution.
norm.approx	If TRUE, the normal approximation of the distribution of the test statistic is used instead of simulation.

Values

Design Alternative	Prints the number of stages, f, theta, and K values inputted for the design alternative.
Arm Size	Arm size per stage per group needed to detect the alternative.
Upper Critical Values	Vector of the upper critical values. In the case of a single stage trial, this is replaced with Critical Value showing the only critical value used in that case.
Lower Critical Values	Vector of the lower critical values. Omitted if the trial is only a single stage.
Type I Error	Vector of the realized Type I error per stage and overall.
Type II Error	Vector of the realized Type II error per stage and overall.

Example

```
grp.seq.mix(num.stages=3, alpha=0.05, beta=0.2, rho=2, theta=0.8, K=0.5, sigma=1,
f="logistic", B=10000, method="sar", norm.approx=TRUE)
```

Example Output

```
$'Design Alternative'
 Stages          f  theta    K
      3  logistic    0.8  0.5
$'Arm Size'
[1] 27
$'Upper Critical Values'
[1] 2.5392 2.0680 1.6965
$'Lower Critical Values'
[1] -0.4587 0.7480 1.6965
$'Type I Error'
 Stage 1  Stage 2  Stage 3  Overall
  0.0056   0.0167   0.0278   0.0500
$'Type II Error'
 Stage 1  Stage 2  Stage 3  Overall
  0.0222   0.0667   0.1042   0.1931
```