

Package ‘SeqExpMatch’

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Type Package

Title Sequential Experimental Design via Matching on-the-Fly with Estimation and Testing

Version 0.1.1.1

Description DEPRECATED. This package is deprecated and no longer maintained; all of its functionality has been superseded by the 'EDI' package, which provides faster, more general, and actively maintained implementations of the same sequential designs and inference procedures. Please migrate to 'EDI'. This package previously generated the following sequential two-arm experimental designs:

- (1) completely randomized (Bernoulli)
- (2) balanced completely randomized
- (3) Efron's (1971) Biased Coin
- (4) Atkinson's (1982) Covariate-Adjusted Biased Coin
- (5) Kapelner and Krieger's (2014) Covariate-Adjusted Matching on the Fly
- (6) Kapelner and Krieger's (2021) CARA Matching on the Fly with Differential Covariate Weights
- (7) Kapelner and Krieger's (2021) CARA Matching on the Fly with Differential Covariate Weights (Stepwise)

and also provides the following types of inference:

- (1) estimation (with both Z-style estimators and OLS estimators),
- (2) frequentist testing (via asymptotic distribution results and via employing the nonparametric randomization test) and
- (3) frequentist confidence intervals (only under the superpopulation sampling assumption currently).

Details can be found in Kapelner and Krieger (2021) <[doi:10.1111/biom.13561](https://doi.org/10.1111/biom.13561)>.
The 'EDI' package is on CRAN at <<https://CRAN.R-project.org/package=EDI>> and on GitHub at <<https://github.com/kapelner/EDI>>.

URL https://github.com/kapelner/matching_on_the_fly_designs_R_package_and_paper_repr

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NeedsCompilation no
Author Adam Kapelner [aut, cre],
Abba Krieger [aut]
Maintainer Adam Kapelner <kapelner@qc.cuny.edu>
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SeqDesign	<i>A Sequential Design</i>
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Description

An R6 Class encapsulating the data and functionality for a sequential experimental design. This class takes care of data intialization and sequential assignments. The class object should be saved securely after each assignment e.g. on an encrypted cloud server.

Deprecated

This class is deprecated. All of its functionality (the "CRD", "BCRD", "Efron", "Atkinson", "KK14", "KK21", and "KK21stepwise" designs) is provided by the actively maintained EDI package's sequential one-by-one design classes: DesignSeqOneByOneBernoulli, DesignSeqOneByOneEfron, DesignSeqOneByOneAtkinson, DesignSeqOneByOneKK14, DesignSeqOneByOneKK21, and DesignSeqOneByOneKK21stepwise (balanced completely randomized designs are available via EDI's fixed designs). See each method below for the specific EDI code that reproduces its behavior.

Use the EDI package instead. The design argument maps to an EDI class as follows: "CRD" to DesignSeqOneByOneBernoulli, "Efron" to DesignSeqOneByOneEfron, "Atkinson" to DesignSeqOneByOneAtkinson, "KK14" to DesignSeqOneByOneKK14, "KK21" to DesignSeqOneByOneKK21, and "KK21stepwise" to DesignSeqOneByOneKK21stepwise. For example:

```
# library(SeqExpMatch):
seq_des = SeqDesign$new(n = 100, p = 10, design = "KK21stepwise")

# library(EDI) equivalent:
seq_des = EDI::DesignSeqOneByOneKK21stepwise$new(n = 100, response_type = "continuous")
```

```

# library(SeqExpMatch):
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))

# library(EDI) equivalent (covariates passed as a one-row data.frame):
seq_des$add_one_subject_to_experiment_and_assign(
  data.frame(x1 = 1, x2 = 38, x3 = 142, x4 = 71, x5 = 5.3, x6 = 0, x7 = 0, x8 = 0, x9 = 1, x10 = 0)
)

# library(EDI) equivalent:
seq_des$print_current_subject_assignment() # same method name in EDI::DesignSeqOneByOne*

# library(EDI) equivalent (t is the subject's index, dead defaults to 1 for non-survival):
seq_des$add_one_subject_response(t = seq_des$t, y = 4.71)

# library(EDI) equivalent, using the convenience wrapper for already-assigned designs:
add_all_subject_responses_seq(seq_des, c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))

# library(EDI) equivalent (KK14/KK21/KK21stepwise designs expose matching structure
# as cluster IDs, one per subject: 0/NA values are unmatched reservoir subjects and
# equal positive values denote a matched pair):
cluster_ids = seq_des$get_matching_cluster_ids()
num_matches = length(unique(cluster_ids[cluster_ids > 0])) / 1 # groups of size 2
prop_subjects_matched = mean(cluster_ids > 0)

# library(EDI) equivalent:
seq_des$assert_experiment_completed() # same method name in EDI::DesignSeqOneByOne*

# library(EDI) equivalent:
seq_des$check_experiment_completed() # same method name in EDI::DesignSeqOneByOne*

```

Public fields

- t** The current number of subjects in this sequential experiment (begins at zero).
- design** The type of sequential experimental design (see constructor's documentation).
- X** A numeric matrix of subject data with number of rows *n* (the number of subjects) and number of columns *p* (the number of characteristics measured for each subject). This matrix is filled in sequentially and thus will have data present for rows 1...*t* (i.e. the number of subjects in the experiment currently) but otherwise will be missing.
- y** A numeric vector of subject responses with number of entries *n* (the number of subjects). During the KK21 designs this must be filled in sequentially (similar to **X**) and will have data present for entries 1...*t* (i.e. the number of subjects in the experiment currently) but otherwise will be missing. For non-KK21 designs, this vector can be set at anytime (but must be set before inference is desired).
- w** A binary vector of subject assignments with number of entries *n* (the number of subjects). This vector is filled in sequentially (similar to **X**) and will have assignments present for entries 1...*t* (i.e. the number of subjects in the experiment currently) but otherwise will be missing.
- verbose** A flag that indicates whether messages should be displayed to the user

Methods

Public methods:

- `SeqDesign$new()`
- `SeqDesign$add_subject_to_experiment()`
- `SeqDesign$print_current_subject_assignment()`
- `SeqDesign$add_current_subject_response()`
- `SeqDesign$add_all_subject_responses()`
- `SeqDesign$matching_statistics()`
- `SeqDesign$sassert_experiment_completed()`
- `SeqDesign$check_experiment_completed()`
- `SeqDesign$clone()`

`SeqDesign$new()`: Initialize a sequential experimental design

Usage:

```
SeqDesign$new(n, p, design, verbose = TRUE, ...)
```

Arguments:

`n` Number of subjects fixed beforehand. A future version of this software will allow for sequential stopping and thus `n` will not need to be prespecified.

`p` Number of characteristics measured for each subject. If measurement `j` are categorical with `Lj` levels, you must select a reference level and convert this information to `Lj-1` dummies. Thus `p := # of numeric variables + sumj (Lj - 1)`.

`design` The type of sequential experimental design. This must be one of the following "CRD" for the completely randomized design / Bernoulli design, "BCRD" for the balanced completely randomized design with `n/2` T's and `n/2` C's, "Efron" for Efron's (1971) Biased Coin Design "Atkinson" for Atkinson's (1982) Covariate-Adjusted Biased Coin Design "KK14" for Kapelner and Krieger's (2014) Covariate-Adjusted Matching on the Fly Design "KK21" for Kapelner and Krieger's (2021) CARA Matching on the Fly with Differential Covariate Weights Design "KK21stepwise" for Kapelner and Krieger's (2021) CARA Matching on the Fly with Differential Covariate Weights Stepwise Design

`verbose` A flag indicating whether messages should be displayed to the user. Default is TRUE.

`...` Design-specific parameters: "Efron" requires "weighted_coin_prob" which is the probability of the weighted coin for assignment. If unspecified, default is 2/3. All "KK" designs require "lambda", the quantile cutoff of the subject distance distribution for determining matches. If unspecified, default is 10 All "KK" designs require "t_0_pct", the percentage of total sample size `n` where matching begins. If unspecified, default is 35 All "KK21" designs further require "num_boot" which is the number of bootstrap samples taken to approximate the subject-distance distribution. If unspecified, default is 500.

Returns: A new 'SeqDesign' object.

Examples:

```
seq_des = SeqDesign$new(n = 100, p = 10, design = "KK21stepwise")
```

`SeqDesign$add_subject_to_experiment()`: Add subject-specific measurements for the next subject entrant

Usage:

```
SeqDesign$add_subject_to_experiment(x_vec)
```

Arguments:

`x_vec` A p-length numeric vector

Examples:

```
seq_des = SeqDesign$new(n = 100, p = 10, design = "CRD")
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
```

`SeqDesign$print_current_subject_assignment()`: Prints the current assignment to screen. Should be called after `add_subject_to_experiment`.

Usage:

```
SeqDesign$print_current_subject_assignment()
```

Examples:

```
seq_des = SeqDesign$new(n = 100, p = 10, design = "CRD")

seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$print_current_subject_assignment()
```

`SeqDesign$add_current_subject_response()`: For CARA designs, add subject response for the current subject entrant

Usage:

```
SeqDesign$add_current_subject_response(y)
```

Arguments:

`y` The response as a numeric scalar

Examples:

```
seq_des = SeqDesign$new(n = 100, p = 10, design = "KK21")

seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))

seq_des$add_current_subject_response(4.71)
```

`SeqDesign$add_all_subject_responses()`: For non-CARA designs, add all subject responses

Usage:

```
SeqDesign$add_all_subject_responses(y)
```

Arguments:

`y` The responses as a numeric vector of length n

Examples:

```
seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")

seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))

seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))
```

`SeqDesign$matching_statistics()`: For KK designs only, this returns a list with useful matching statistics.

Usage:

```
SeqDesign$matching_statistics()
```

Returns: A list with the following data: `num_matches`, `prop_subjects_matched`, `num_subjects_remaining_in_reservoir`, `prop_subjects_remaining_in_reservoir`.

Examples:

```
seq_des = SeqDesign$new(n = 6, p = 10, design = "KK14")
```

```
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))
```

```
seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))
```

```
seq_des$matching_statistics()
```

`SeqDesign$assert_experiment_completed()`: Asserts if the experiment is completed (all n assignments are assigned in the w vector and all n responses in the y vector are recorded), i.e. throws descriptive error if the experiment is incomplete.

Usage:

```
SeqDesign$assert_experiment_completed()
```

Examples:

```
seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")
```

```
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
```

```
#if run, it would throw an error since all of the covariate vectors are not yet recorded
#seq_des$assert_experiment_completed()
```

```
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))
```

```
#if run, it would throw an error since the responses are not yet recorded
#seq_des$assert_experiment_completed()
```

```
seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))
```

```
seq_des$assert_experiment_completed() #no response means the assert is true
```

`SeqDesign$check_experiment_completed()`: Checks if the experiment is completed (all n assignments are assigned in the w vector and all n responses in the y vector are recorded).

Usage:

```
SeqDesign$check_experiment_completed()
```

Returns: TRUE if experiment is complete, FALSE otherwise.

Examples:

```
seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
```

```
#returns FALSE since all of the covariate vectors are not yet recorded
seq_des$check_experiment_completed()
```

```
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))
```

```
#returns FALSE since the responses are not yet recorded
seq_des$check_experiment_completed()
```

```
seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))
```

```
seq_des$check_experiment_completed() #returns TRUE
```

`SeqDesign$clone()`: The objects of this class are cloneable with this method.

Usage:

```
SeqDesign$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
## -----
## Method `SeqDesign$new()`
## -----

seq_des = SeqDesign$new(n = 100, p = 10, design = "KK21stepwise")

## -----
## Method `SeqDesign$add_subject_to_experiment()`
## -----

seq_des = SeqDesign$new(n = 100, p = 10, design = "CRD")
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))

## -----
## Method `SeqDesign$print_current_subject_assignment()`
```

```
## -----

seq_des = SeqDesign$new(n = 100, p = 10, design = "CRD")

seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$print_current_subject_assignment()

## -----
## Method `SeqDesign$add_current_subject_response()`
## -----

seq_des = SeqDesign$new(n = 100, p = 10, design = "KK21")

seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))

seq_des$add_current_subject_response(4.71)

## -----
## Method `SeqDesign$add_all_subject_responses()`
## -----

seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")

seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))

seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))

## -----
## Method `SeqDesign$matching_statistics()`
## -----

seq_des = SeqDesign$new(n = 6, p = 10, design = "KK14")

seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))

seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))

seq_des$matching_statistics()
```

```
## -----
## Method `SeqDesign$assert_experiment_completed()`
## -----

seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))

#if run, it would throw an error since all of the covariate vectors are not yet recorded
#seq_des$assert_experiment_completed()

seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))

#if run, it would throw an error since the responses are not yet recorded
#seq_des$assert_experiment_completed()

seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))

seq_des$assert_experiment_completed() #no response means the assert is true

## -----
## Method `SeqDesign$check_experiment_completed()`
## -----

seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))

#returns FALSE since all of the covariate vectors are not yet recorded
seq_des$check_experiment_completed()

seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))

#returns FALSE since the responses are not yet recorded
seq_des$check_experiment_completed()

seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))

seq_des$check_experiment_completed() #returns TRUE
```

Description

An R6 Class that estimates, tests and provides intervals for a treatment effect in a sequential design. This class takes a SeqDesign object as an input where this object contains data for a fully completed sequential experiment (i.e. all treatment assignments were allocated and all responses were collected). Then the user specifies the type of estimation (difference-in-means or OLS) and the type of sampling assumption (i.e. the superpopulation assumption leading to normal-based inference or the finite population assumption implying randomization-exact-based inference) and then can query the estimate and pval for the test. If the test is normal-theory based it is testing the population $H_0: \beta_T = 0$ and if the test is a randomization test, it is testing the sharp null that $H_0: Y_{T_i} = Y_{C_i}$ for all subjects. Confidence interval construction is available for normal-theory based test type as well.

Deprecated

This class is deprecated. Its estimation, testing, and confidence interval functionality is provided by the actively maintained EDI package's inference classes (e.g. InferenceAllSimpleMeanDiff, InferenceContinOLS, InferenceContinKKOLSIVWC, and many others registered per response type and design). See each method below for the specific EDI code that reproduces its behavior.

```
# library(SeqExpMatch):
seq_des_inf = SeqDesignInference$new(seq_des, estimate_type = "OLS", test_type = "randomization-exact")

# library(EDI) equivalent (choose the class matching your design/response and estimator;
# e.g. for a completed continuous-response design with OLS estimation):
inf = EDI::InferenceContinOLS$new(seq_des, verbose = FALSE)
# or, for a difference-in-means estimator:
inf = EDI::InferenceAllSimpleMeanDiff$new(seq_des, verbose = FALSE)
# for KK designs (KK14/KK21/KK21stepwise), use the corresponding KK-specific class, e.g.:
inf = EDI::InferenceContinKKOLSIVWC$new(seq_des, verbose = FALSE)

# library(EDI) equivalent (method name is compute_estimate() in EDI inference classes):
inf$compute_estimate()

# library(EDI) equivalent:
inf$compute_asymp_two_sided_pval() # for test_type = "normal-based"
inf$compute_rand_two_sided_pval(r = 501) # for test_type = "randomization-exact"

# library(EDI) equivalent (draw the randomization distribution directly):
samps = inf$approximate_randomization_distribution_beta_hat_T(r = 501)

# library(EDI) equivalent:
inf$compute_asymp_confidence_interval(alpha = 0.05) # for test_type = "normal-based"
inf$compute_rand_confidence_interval(alpha = 0.05, r = 501) # for test_type = "randomization-exact"
```

Public fields

`estimate_type` The type of estimate to compute (either "difference-in-means" or "OLS").
`test_type` The type of test to run (either "normal-based" or "randomization-exact").
`num_cores` The number of CPU cores to employr during sampling within randomization inference
`verbose` A flag that indicates whether messages should be displayed to the user

Methods

Public methods:

- `SeqDesignInference$new()`
- `SeqDesignInference$compute_treatment_estimate()`
- `SeqDesignInference$compute_pval_for_no_treatment_effect()`
- `SeqDesignInference$randomization_inference_samples_for_no_treatment_effect()`
- `SeqDesignInference$compute_confidence_interval()`
- `SeqDesignInference$clone()`

`SeqDesignInference$new()`: Initialize a sequential experimental design estimation and test object after the sequential design is completed.

Usage:

```
SeqDesignInference$new(
  seq_des_obj,
  estimate_type = "OLS",
  test_type = "randomization-exact",
  num_cores = 1,
  verbose = TRUE
)
```

Arguments:

`seq_des_obj` A `SeqDesign` object whose entire `n` subjects are assigned and response `y` is recorded within.

`estimate_type` The type of estimate to compute (either "difference-in-means" or "OLS"). Default is "OLS" as this provided higher power in our simulations.

`test_type` The type of test to run (either "normal-based" implying your subject entrant sampling assumption is from a superpopulation or "randomization-exact" implying a finite sampling assumption). The default option is "randomization-exact" as it provided properly-sized tests in our simulations.

`num_cores` The number of CPU cores to use to parallelize the sampling during randomization-based inference (which is very slow). The default is 1 for serial computation. This parameter is ignored for `test_type = "normal-based"`.

`verbose` A flag indicating whether messages should be displayed to the user. Default is TRUE

Returns: A new 'SeqDesignTest' object.

Examples:

```
seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))
seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))

seq_des_inf = SeqDesignInference$new(seq_des)
```

`SeqDesignInference$compute_treatment_estimate()`: Computes either the classic different-in-means estimate of the additive treatment effect, i.e. $\bar{y}_T - \bar{y}_C$ or the OLS estimate of the additive treatment effect linearly i.e. the treatment different adjusted linearly for the p covariates.

Usage:

```
SeqDesignInference$compute_treatment_estimate()
```

Returns: The numeric estimate of the treatment effect

Examples:

```
seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))
seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))

seq_des_inf = SeqDesignInference$new(seq_des)
seq_des_inf$compute_treatment_estimate()
```

`SeqDesignInference$compute_pval_for_no_treatment_effect()`: Computes either the classic different-in-means estimate of the additive treatment effect, i.e. $\bar{y}_T - \bar{y}_C$ or the OLS estimate of the additive treatment effect linearly i.e. the treatment different adjusted linearly for the p covariates.

Usage:

```
SeqDesignInference$compute_pval_for_no_treatment_effect(nsim_exact_test = 501)
```

Arguments:

`nsim_exact_test` The number of randomization vectors to use in the randomization test (ignored if `test_type` is not "randomization-exact"). The default is 501 providing pvalue resolution to a fifth of a percent.

Returns: The frequentist p-val for the test of nonzero treatment effect

Examples:

```
seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))
seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))

seq_des_inf = SeqDesignInference$new(seq_des)
seq_des_inf$compute_pval_for_no_treatment_effect()
```

`SeqDesignInference$randomization_inference_samples_for_no_treatment_effect()`: Computes many randomization samples of either the classic different-in-means estimate of the additive treatment effect, i.e. $\bar{y}_T - \bar{y}_C$ or the OLS estimate of the additive treatment effect linearly i.e. the treatment different adjusted linearly for the p covariates. This function is useful if you wish to run your own, custom hypothesis tests.

Usage:

```
SeqDesignInference$randomization_inference_samples_for_no_treatment_effect(
  nsim_exact_test = 501
)
```

Arguments:

`nsim_exact_test` The number of randomization vectors. The default is 501 providing pvalue resolution to a fifth of a percent.

Returns: The `nsim_exact_test` samples of the treatment effect under the null hypothesis of no treatment effect where each sample is estimated from a different assignment vector for the prespecified design

Examples:

```
seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))
seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))

seq_des_inf = SeqDesignInference$new(seq_des)
samps = seq_des_inf$randomization_inference_samples_for_no_treatment_effect()
summary(samps)
```

`SeqDesignInference$compute_confidence_interval()`: Computes either a:

1. classic frequentist confidence interval (CI) of the additive treatment effect employing the normal theory approximation for both the (a) difference in means estimator i.e. $[\bar{y}_T - \bar{y}_C \pm t_{\{\alpha/2, n_T + n_C - 2\}} s_{\{\bar{y}_T - \bar{y}_C\}}]$ or (b) the OLS estimator i.e. $[\hat{\beta}_T \pm t_{\{\alpha/2, n + p - 2\}} s_{\{\hat{\beta}_T\}}]$ where the z approximation is employed in lieu of the t if the design is a KK design or
2. a randomization-based CI of an additive shift effect of the potential outcomes under treatment and control by an inversion of the randomization test at level α (this feature is incomplete).

Usage:

```
SeqDesignInference$compute_confidence_interval(
  alpha = 0.05,
  nsim_exact_test = 501
)
```

Arguments:

`alpha` The confidence level in the computed confidence interval is $1 - \alpha$. The default is 0.05.

`nsim_exact_test` The number of randomization vectors. The default is 1000 providing good resolutions to confidence intervals.

Returns: A 1 - alpha sized frequentist confidence interval for the treatment effect

Examples:

```
seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))
seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))

seq_des_inf = SeqDesignInference$new(seq_des, test_type = "normal-based")
seq_des_inf$compute_confidence_interval()
```

`SeqDesignInference$clone()`: The objects of this class are cloneable with this method.

Usage:

```
SeqDesignInference$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
## -----
## Method `SeqDesignInference$new()`
## -----

seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))
seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))

seq_des_inf = SeqDesignInference$new(seq_des)

## -----
## Method `SeqDesignInference$compute_treatment_estimate()`
## -----

seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
```

```

seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))
seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))

seq_des_inf = SeqDesignInference$new(seq_des)
seq_des_inf$compute_treatment_estimate()

## -----
## Method `SeqDesignInference$compute_pval_for_no_treatment_effect()`
## -----

seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))
seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))

seq_des_inf = SeqDesignInference$new(seq_des)
seq_des_inf$compute_pval_for_no_treatment_effect()

## -----
## Method `SeqDesignInference$randomization_inference_samples_for_no_treatment_effect()`
## -----

seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))
seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))

seq_des_inf = SeqDesignInference$new(seq_des)
samps = seq_des_inf$randomization_inference_samples_for_no_treatment_effect()
summary(samps)

## -----
## Method `SeqDesignInference$compute_confidence_interval()`
## -----

seq_des = SeqDesign$new(n = 6, p = 10, design = "CRD")
seq_des$add_subject_to_experiment(c(1, 38, 142, 71, 5.3, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(0, 27, 127, 60, 5.5, 0, 0, 0, 1, 0))
seq_des$add_subject_to_experiment(c(1, 42, 169, 74, 5.1, 0, 1, 0, 0, 0))
seq_des$add_subject_to_experiment(c(0, 59, 105, 62, 5.9, 0, 0, 0, 1, 0))

```

```
seq_des$add_subject_to_experiment(c(1, 32, 186, 66, 5.6, 1, 0, 0, 0, 0))
seq_des$add_subject_to_experiment(c(1, 37, 178, 75, 6.5, 0, 0, 0, 0, 1))
seq_des$add_all_subject_responses(c(4.71, 1.23, 4.78, 6.11, 5.95, 8.43))

seq_des_inf = SeqDesignInference$new(seq_des, test_type = "normal-based")
seq_des_inf$compute_confidence_interval()
```

SeqExpMatch

*Sequential Experimental Designs via Matching On-the-Fly***Description**

SeqExpMatch

Details

Generates the following sequential two-arm experimental designs (1) completely randomized (Bernoulli) (2) balanced completely randomized (3) Efron's (1971) Biased Coin (4) Atkinson's (1982) Covariate-Adjusted Biased Coin (5) Kapelner and Krieger's (2014) Covariate-Adjusted Matching on the Fly (6) Kapelner and Krieger's (2021) CARA Matching on the Fly with Weighted Covariates (7) Kapelner and Krieger's (2021) CARA Matching on the Fly with Weighted Covariates Stepwise

Deprecated

This package is deprecated and no longer maintained. All of its designs and inference procedures have been superseded by the EDI package, available on CRAN at <https://CRAN.R-project.org/package=EDI> and on GitHub at <https://github.com/kapelner/EDI>. Please migrate to EDI; see ?SeqDesign and ?SeqDesignInference for the specific migration code.

Author(s)

Adam Kapelner <kapelner@qc.cuny.edu>

References

Adam Kapelner and Abba Krieger, A Matching Procedure for Sequential Experiments that Iteratively Learns which Covariates Improve Power, Biometrics (2021), [doi:10.1111/biom.13561](https://doi.org/10.1111/biom.13561)

See Also

Useful links:

- https://github.com/kapelner/matching_on_the_fly_designs_R_package_and_paper_repr

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