

# Package ‘fastpos’

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**Type** Package

**Title** Finds the Critical Sequential Point of Stability for a Pearson Correlation

**Version** 0.3.0

**Date** 2020-02-12

**Description** Finds the critical sample size (“critical point of stability”) for a correlation to stabilize in Schoenbrodt and Perugini’s definition of sequential stability (see <doi:10.1016/j.jrp.2013.05.009>).

**License** GPL-3

**Imports** Rcpp (>= 1.0.1), plyr, MASS

**LinkingTo** Rcpp, RcppArmadillo, RcppProgress

**URL** <https://github.com/johannes-titz/fastpos>

**BugReports** <https://github.com/johannes-titz/fastpos/issues>

**Encoding** UTF-8

**RoxygenNote** 7.0.2

**Suggests** knitr, rmarkdown, testthat (>= 2.1.0), covr

**VignetteBuilder** knitr

**NeedsCompilation** yes

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**Repository** CRAN

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create_pop	<i>Creates a population with a specified correlation.</i>
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**Description**

The correlation will be exactly the one specified. The used method is described here: <https://stats.stackexchange.com/question/a-random-variable-with-a-defined-correlation-to-an-existing-variables/15040#15040>

**Usage**

```
create_pop(rho, size)
```

**Arguments**

rho	Population correlation.
size	Population size.

**Value**

Two-dimensional population matrix with a specific correlation.

**Examples**

```
pop <- create_pop(0.5, 100000)
cor(pop)
```

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find_critical_pos	<i>Find the critical point of stability</i>
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**Description**

Run simulations for one or several population correlations and return the critical points of stability (POS). The critical point of stability is the sample size at which a certain percentage of studies will fall into an a priori specified interval and stay in this interval if the sample size is increased further.

**Usage**

```
find_critical_pos(
  rhos,
  precision = 0.1,
  precision_rel = FALSE,
  sample_size_min = 20,
  sample_size_max = 1000,
  n_studies = 10000,
  confidence_levels = c(0.8, 0.9, 0.95),
  pop_size = 1e+06
)
```

**Arguments**

rhos	Vector of population correlations (can also be a single correlation).
precision	Precision around the correlation which is acceptable (defaults to 0.1). The precision will determine the corridor of stability which is just rho+precision.
precision_rel	Whether the precision is absolute (rho+precision or relative rho+-rho*precision), boolean (defaults to FALSE).
sample_size_min	Minimum sample size for each study (defaults to 20).
sample_size_max	Maximum sample size for each study (defaults to 1e3).
n_studies	Number of studies to run for each rho (defaults to 10e3).
confidence_levels	Confidence levels for point of stability. This corresponds to the quantile of the distribution of all found critical sample sizes (defaults to c(.8, .9, .95)).
pop_size	Population size (defaults to 1e6).

**Value**

A data frame containing all the above information, as well as the points of stability.

**Examples**

```
find_critical_pos(rhos = 0.5)
find_critical_pos(rhos = c(0.4, 0.5), n_studies = 1e3)
```

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simulate_pos	<i>Simulate several points of stability</i>
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**Description**

Runs several simulations and returns the points of stability, which can then be further processed to calculate the critical point of stability.

**Usage**

```
simulate_pos(
  x_pop,
  y_pop,
  n_studies,
  sample_size_min,
  sample_size_max,
  replace,
  lower_limit,
  upper_limit
)
```

**Arguments**

<code>x_pop</code>	First vector of population.
<code>y_pop</code>	Second vector of population.
<code>n_studies</code>	How many studies to conduct.
<code>sample_size_min</code>	Minimum sample size to start in corridor of stability.
<code>sample_size_max</code>	How many participants to draw at maximum.
<code>replace</code>	Whether drawing samples is with replacement or not.
<code>lower_limit</code>	Lower limit of corridor of stability.
<code>upper_limit</code>	Upper limit of corridor of stability.

**Value**

Vector of sample sizes at which corridor of stability was reached.

**Examples**

```
pop <- fastpos::create_pop(0.5, 1000000)
simulate_pos(pop[,1], pop[,2], 100, 20, 1000, TRUE, 0.4, 0.6)
```

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