

# Package ‘NRMSampling’

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**Type** Package

**Title** Sampling Design and Estimation Methods for Natural Resource Management

**Version** 0.2.2

**Description** Provides functions for probability and non-probability sampling design, sample selection, and population estimation tailored to natural resource management. Probability methods include simple random sampling, stratified sampling, systematic sampling, cluster sampling, and probability-proportional-to-size sampling. Non-probability methods include convenience, judgement-based, and quota sampling. Estimation functions cover means, totals, ratio estimators, regression estimators, and the unequal-probability estimator of Horvitz and Thompson (1952, <doi:10.2307/2280784>) for unequal-probability designs. Utilities support biomass, soil-loss, and carbon-stock estimation from field plots. Spatial extensions provide random, systematic, stratified, and raster-weighted sampling within geographic polygons using the 'sf' and 'terra' packages, with extraction of remote-sensing covariates at sample locations. Applications include forest inventory, soil erosion monitoring, watershed studies, and ecological field surveys.

**License** GPL (>= 3)

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NRMSampling-package    *NRMSampling: Sampling Design and Estimation for Natural Resource Management*

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## Description

Provides functions for probability and non-probability sampling design, sample selection, and estimation tailored to natural resource management.

## Probability Sampling

`srs_sample`, `stratified_sample`, `systematic_sample`, `cluster_sample`, `pps_sample`

## Non-Probability Sampling

`convenience_sample`, `purposive_sample`, `quota_sample`

## Estimation

`estimate_mean`, `estimate_total`, `estimate_variance`, `estimate_se`, `estimate_ci`, `ratio_estimator`, `regression_estimator`, `ht_estimator`, `ht_variance`, `stratified_estimator`

## NRM Utilities

`biomass_estimate`, `soil_loss_estimate`, `carbon_stock_estimate`, `plot_summary`, `sampling_efficiency`

## Spatial Sampling

`to_sf_points`, `spatial_random_sample`, `spatial_systematic_sample`, `spatial_stratified_sample`, `spatial_cluster_sample`, `raster_stratified_sample`, `raster_pps_sample`, `extract_raster_values`, `spatial_biomass_estimate`, `plot_sampling`, `plot_sampling_gg`

## Datasets

`sample_nrm`, `sample_spatial`

## Note

`sample()`, `runif()`, `setNames()`, and `mean()` are `base::` functions and must NOT be listed in `importFrom(stats, ...)`. They are always available without any import declaration.

## Author(s)

**Maintainer:** Sadikul Islam <sadikul.islamiasri@gmail.com> ([ORCID](#))

## References

Cochran, W.G. (1977). *Sampling Techniques*, 3rd ed. Wiley. Lohr, S.L. (2022). *Sampling: Design and Analysis*, 3rd ed. CRC Press.

---

biomass\_estimate      *Biomass Estimation from Field Plots*

---

### Description

Estimates total standing biomass over a landscape or management unit from plot-level measurements.

### Usage

```
biomass_estimate(df, biomass_var, area)
```

### Arguments

df	A data frame of sampled plots.
biomass_var	Character. Name of the column containing plot-level biomass density (e.g., Mg/ha or kg/plot).
area	Numeric. Total area of the management unit (same units as the denominator of biomass_var). E.g., if biomass_var is in Mg/ha, area should be in ha.

### Value

A named list with elements:

mean\_biomass Mean biomass density across sampled plots.  
total\_biomass Estimated total biomass over the study area.  
se Standard error of the mean biomass density.  
n Number of plots used.

### References

Avery, T.E. and Burkhart, H.E. (2002). *Forest Measurements*, 5th ed. McGraw-Hill, New York.

### Examples

```
data(sample_nrm)
srs <- srs_sample(sample_nrm, n = 30)
biomass_estimate(srs, biomass_var = "biomass", area = 1000)
```

---

carbon\_stock\_estimate *Carbon Stock Estimation*

---

**Description**

Converts a biomass estimate to carbon stock using a biomass-to-carbon conversion factor.

**Usage**

```
carbon_stock_estimate(df, biomass_var, area, carbon_fraction = 0.47)
```

**Arguments**

df	A data frame of sampled plots.
biomass_var	Character. Name of the biomass density column.
area	Numeric. Total study area.
carbon_fraction	Numeric. Fraction of biomass that is carbon. Default 0.47 (IPCC default for tropical forests).

**Value**

A named list with elements total\_biomass, total\_carbon, carbon\_fraction, and n.

**References**

IPCC (2006). *IPCC Guidelines for National Greenhouse Gas Inventories, Volume 4: Agriculture, Forestry and Other Land Use*. IGES, Hayama, Japan.

**Examples**

```
data(sample_nrm)
srs <- srs_sample(sample_nrm, n = 30)
carbon_stock_estimate(srs, biomass_var = "biomass", area = 1000)
```

---

cluster\_sample *Cluster Sampling*

---

**Description**

Performs single-stage cluster sampling.

**Usage**

```
cluster_sample(data, cluster_var, n_clusters)
```

**Arguments**

data	A data frame.
cluster_var	Character. Cluster column.
n_clusters	Integer. Number of clusters.

**Value**

A data frame of sampled clusters.

---

convenience_sample	<i>Convenience Sampling</i>
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---

**Description**

Returns the first  $n$  rows of a data frame as a convenience sample. This is the simplest non-probability method; results are generally not representative of the population.

**Usage**

```
convenience_sample(data, n)
```

**Arguments**

data	A data frame.
n	Integer. Number of units to select.

**Details**

Convenience sampling is fast but prone to selection bias. It may be appropriate for pilot studies or logistical constraints, but population inference requires strong assumptions. See Lohr (2022) for discussion.

**Value**

A data frame containing the first  $n$  rows.

**References**

Lohr, S.L. (2022). *Sampling: Design and Analysis*, 3rd ed. CRC Press, Boca Raton, FL.

**Examples**

```
data(sample_nrm)
cs <- convenience_sample(sample_nrm, n = 10)
nrow(cs)
```

---

estimate_ci	<i>Confidence Interval for the Population Mean</i>
-------------	--

---

**Description**

Computes a confidence interval for the population mean based on a simple random sample, using the t-distribution.

**Usage**

```
estimate_ci(y, N = NULL, conf_level = 0.95)
```

**Arguments**

y	Numeric vector. Sample observations.
N	Integer. Population size. Used for the finite-population correction. Set to NULL to omit.
conf_level	Numeric. Confidence level in (0, 1). Default 0.95.

**Value**

A named numeric vector with elements mean, lower, and upper.

**Examples**

```
data(sample_nrm)
srs <- srs_sample(sample_nrm, n = 30)
estimate_ci(srs$biomass, N = nrow(sample_nrm))
```

---

estimate_mean	<i>Sample Mean</i>
---------------	--------------------

---

**Description**

Computes the sample mean of a numeric vector, ignoring missing values.

**Usage**

```
estimate_mean(y)
```

**Arguments**

y	Numeric vector. Sample observations.
---	--------------------------------------

**Value**

Numeric scalar. The sample mean.

**Examples**

```
data(sample_nrm)
srs <- srs_sample(sample_nrm, n = 30)
estimate_mean(srs$biomass)
```

---

estimate\_se

*Standard Error of the Sample Mean*

---

**Description**

Computes the estimated standard error of the sample mean under simple random sampling without replacement (SRSWOR).

**Usage**

```
estimate_se(y, N = NULL)
```

**Arguments**

**y** Numeric vector. Sample observations.  
**N** Integer. Population size. If NULL (default), the finite-population correction (fpc) is omitted.

**Details**

With fpc:

$$SE(\bar{y}) = \sqrt{\frac{s^2}{n} \left(1 - \frac{n}{N}\right)}$$

Without fpc:

$$SE(\bar{y}) = \sqrt{\frac{s^2}{n}}$$

**Value**

Numeric scalar. Estimated standard error.

**Examples**

```
data(sample_nrm)
srs <- srs_sample(sample_nrm, n = 30)
estimate_se(srs$biomass, N = nrow(sample_nrm))
```

---

estimate_total	<i>Population Total Estimator</i>
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---

**Description**

Estimates the population total by expanding the sample mean to the full population size.

**Usage**

```
estimate_total(y, N)
```

**Arguments**

y	Numeric vector. Sample observations.
N	Integer. Known population size (number of units).

**Details**

$$\hat{Y} = N\bar{y}$$

**Value**

Numeric scalar. Estimated population total.

**References**

Cochran, W.G. (1977). *Sampling Techniques*, 3rd ed. John Wiley & Sons, New York.

**Examples**

```
data(sample_nrm)
srs <- srs_sample(sample_nrm, n = 30)
estimate_total(srs$biomass, N = nrow(sample_nrm))
```

---

estimate\_variance      *Sample Variance*

---

### Description

Computes the unbiased sample variance of a numeric vector.

### Usage

```
estimate_variance(y)
```

### Arguments

y                      Numeric vector. Sample observations.

### Value

Numeric scalar. The unbiased sample variance  $s^2$ .

### Examples

```
data(sample_nrm)
estimate_variance(sample_nrm$biomass)
```

---

extract\_raster\_values      *Extract Raster Values at Sample Points*

---

### Description

Extracts cell values from a SpatRaster at the locations of sf point features, returning the results as a data frame.

### Usage

```
extract_raster_values(raster, points_sf)
```

### Arguments

raster                  A SpatRaster object.  
points\_sf                An sf POINT object. Must have a compatible CRS with raster.

### Details

Requires both the **terra** and **sf** packages. The CRS of points\_sf is reprojected to match raster if needed.

**Value**

A data frame with one row per point and one column per raster layer.

**Examples**

```
if (requireNamespace("terra", quietly = TRUE) &&
    requireNamespace("sf", quietly = TRUE)) {
  r <- terra::rast(nrows=20, ncols=20, vals=runif(400))
  bbox <- sf::st_as_sfc(sf::st_bbox(terra::ext(r)))
  pts <- spatial_random_sample(bbox, n = 10)
  sf::st_crs(pts) <- sf::st_crs(terra::crs(r))
  extract_raster_values(r, pts)
}
```

---

ht\_estimator

*Horvitz-Thompson (HT) Estimator*


---

**Description**

Provides a design-unbiased estimate of the population total for unequal-probability sampling designs.

**Usage**

```
ht_estimator(y, pi)
```

**Arguments**

**y** Numeric vector. Sample values of the study variable.

**pi** Numeric vector. First-order inclusion probabilities (same length as y). All values must be in (0, 1].

**Details**

$$\hat{Y}_{HT} = \sum_{i \in s} \frac{y_i}{\pi_i}$$

**Value**

Numeric scalar. HT estimate of the population total.

**References**

Horvitz, D.G. and Thompson, D.J. (1952). A generalization of sampling without replacement from a finite universe. *Journal of the American Statistical Association*, 47(260), 663–685.

### Examples

```
data(sample_nrm)
pps <- pps_sample(sample_nrm, size_var = "size", n = 20)
pi_i <- pps$.inclusion_prob
ht_estimator(pps$biomass, pi = pi_i)
```

---

ht\_variance

*Variance of the Horvitz-Thompson Estimator*

---

### Description

Estimates the variance of the Horvitz-Thompson total estimator using the Sen-Yates-Grundy approximation for with-replacement PPS designs.

### Usage

```
ht_variance(y, pi)
```

### Arguments

**y** Numeric vector. Sample values of the study variable.  
**pi** Numeric vector. First-order inclusion probabilities.

### Value

Numeric scalar. Estimated variance of the HT total.

### References

Yates, F. and Grundy, P.M. (1953). Selection without replacement from within strata with probability proportional to size. *Journal of the Royal Statistical Society B*, 15, 253–261.

### Examples

```
data(sample_nrm)
pps <- pps_sample(sample_nrm, size_var = "size", n = 20)
ht_variance(pps$biomass, pps$.inclusion_prob)
```

---

plot_sampling	<i>Plot Sample Points (Base Graphics)</i>
---------------	---

---

### Description

Produces a simple plot of sample point locations using base graphics.

### Usage

```
plot_sampling(  
  sf_points,  
  col = "steelblue",  
  pch = 16,  
  main = "Sample Locations"  
)
```

### Arguments

sf_points	An sf POINT object.
col	Character. Point colour. Default "steelblue".
pch	Integer. Point character. Default 16.
main	Character. Plot title. Default "Sample Locations".

### Details

Requires the `sf` package.

### Value

NULL invisibly. Called for its side effect (a plot).

### Examples

```
if (requireNamespace("sf", quietly = TRUE)) {  
  bbox <- sf::st_as_sfc(sf::st_bbox(c(xmin=77, xmax=78,  
                                     ymin=30, ymax=31),  
                                crs = sf::st_crs(4326)))  
  pts <- spatial_random_sample(bbox, n = 20)  
  plot_sampling(pts)  
}
```

---

plot\_sampling\_gg      *Plot Sample Points with ggplot2*

---

## Description

Produces a publication-quality map of sample point locations using **ggplot2**.

## Usage

```
plot_sampling_gg(  
  sf_points,  
  colour = "tomato",  
  size = 2,  
  title = "Spatial Sample Locations"  
)
```

## Arguments

sf_points	An sf POINT object.
colour	Character. Point colour. Default "tomato".
size	Numeric. Point size. Default 2.
title	Character. Plot title.

## Details

Requires the **sf** and **ggplot2** packages.

## Value

A ggplot object.

## Examples

```
if (requireNamespace("sf", quietly = TRUE) &&  
    requireNamespace("ggplot2", quietly = TRUE)) {  
  bbox <- sf::st_as_sfc(sf::st_bbox(c(xmin=77, xmax=78,  
                                     ymin=30, ymax=31),  
                               crs = sf::st_crs(4326)))  
  pts <- spatial_random_sample(bbox, n = 25)  
  plot_sampling_gg(pts)  
}
```

---

`plot_summary`*Summary Statistics for a Sampled NRM Plot Dataset*

---

**Description**

Returns a concise summary table of key variables from a sample, including means, standard deviations, and sample sizes.

**Usage**

```
plot_summary(df, vars = NULL)
```

**Arguments**

`df` A data frame (sample or population).  
`vars` Character vector. Names of numeric columns to summarise. If NULL (default), all numeric columns are included.

**Value**

A data frame with columns `variable`, `n`, `mean`, `sd`, `min`, and `max`.

**Examples**

```
data(sample_nrm)
srs <- srs_sample(sample_nrm, n = 30)
plot_summary(srs, vars = c("biomass", "soil_loss"))
```

---

`pps_sample`*PPS Sampling*

---

**Description**

Performs probability proportional to size sampling.

**Usage**

```
pps_sample(data, size_var, n)
```

**Arguments**

`data` A data frame.  
`size_var` Character. Size variable.  
`n` Integer. Sample size.

**Value**

A data frame with inclusion probabilities.

---

purposive_sample	<i>Purposive (Judgement) Sampling</i>
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---

**Description**

Selects units from a data frame that satisfy a logical condition supplied as a character string. This is a non-probability method in which units are selected based on expert judgement or predetermined criteria.

**Usage**

```
purposive_sample(data, condition)
```

**Arguments**

data	A data frame.
condition	Character string. A valid R logical expression referring to column names in data. Example: "biomass > 30 & strata == 'forest'".

**Details**

The condition is parsed and evaluated in the context of data using `with()`. Only columns present in data may be referenced.

**Value**

A data frame of rows satisfying condition.

**Examples**

```
data(sample_nrm)
# Select high-biomass forest plots
ps <- purposive_sample(sample_nrm,
                       condition = "biomass > 30 & strata == 'forest'")
nrow(ps)
```

---

quota_sample	<i>Quota Sampling</i>
--------------	-----------------------

---

### Description

Selects a fixed number of units from the top of each stratum. This non-probability method resembles stratified sampling but does not use random selection within strata.

### Usage

```
quota_sample(data, strata_var, quota)
```

### Arguments

data	A data frame.
strata_var	Character. Name of the column defining quota groups.
quota	Integer or named integer vector. <ul style="list-style-type: none"><li>• A single integer: the same quota applied to every stratum.</li><li>• A named integer vector: stratum-specific quotas; names must match unique values of strata_var.</li></ul>

### Value

A data frame containing the selected rows from each stratum.

### References

Lohr, S.L. (2022). *Sampling: Design and Analysis*, 3rd ed. CRC Press, Boca Raton, FL.

### Examples

```
data(sample_nrm)
qs <- quota_sample(sample_nrm, strata_var = "strata", quota = 5)
table(qs$strata)

# Variable quotas
q <- c(forest = 6, agriculture = 3, grassland = 4)
qs2 <- quota_sample(sample_nrm, "strata", quota = q)
```

---

raster_pps_sample	<i>Raster-Weighted PPS Spatial Sampling</i>
-------------------	---

---

### Description

Selects sample points from a `SpatRaster` with probability proportional to cell values (e.g., vegetation density, erosion risk).

### Usage

```
raster_pps_sample(raster, n)
```

### Arguments

raster	A <code>SpatRaster</code> object.
n	Integer. Number of sample points.

### Details

Requires both the **terra** and **sf** packages. Identical in behaviour to `raster_stratified_sample`; exposed as a separate function to match PPS nomenclature.

### Value

An `sf POINT` object.

### Examples

```
if (requireNamespace("terra", quietly = TRUE) &&
    requireNamespace("sf", quietly = TRUE)) {
  r <- terra::rast(nrows = 20, ncols = 20, vals = runif(400, 0, 1))
  pts <- raster_pps_sample(r, n = 10)
}
```

---

raster_stratified_sample	<i>Raster-Stratified Spatial Sampling</i>
--------------------------	---

---

### Description

Samples a specified number of cells from a `SpatRaster` with probability proportional to cell values, and returns their coordinates as an `sf point` object.

**Usage**

```
raster_stratified_sample(raster, n)
```

**Arguments**

**raster**            A SpatRaster object (from the **terra** package).  
**n**                    Integer. Number of sample points.

**Details**

Requires both the **terra** and **sf** packages. Cells with NA values are excluded from sampling.

**Value**

An sf POINT object with CRS taken from raster.

**Examples**

```
if (requireNamespace("terra", quietly = TRUE) &&
    requireNamespace("sf", quietly = TRUE)) {
  r <- terra::rast(nrows = 20, ncols = 20, vals = runif(400, 1, 100))
  pts <- raster_stratified_sample(r, n = 15)
  plot(sf::st_geometry(pts))
}
```

---

ratio_estimator	<i>Ratio Estimator</i>
-----------------	------------------------

---

**Description**

Estimates the population total or mean of a study variable  $y$  using a correlated auxiliary variable  $x$  with a known population total  $X$ .

**Usage**

```
ratio_estimator(y, x, X_total)
```

**Arguments**

**y**                    Numeric vector. Sample values of the study variable.  
**x**                    Numeric vector. Sample values of the auxiliary variable (same length as  $y$ ).  
**X\_total**            Numeric. Known population total of the auxiliary variable.

**Details**

$$\hat{R} = \frac{\sum y_i}{\sum x_i}, \quad \hat{Y}_R = \hat{R} \cdot X$$

**Value**

Numeric scalar. Ratio estimate of the population total of  $y$ .

**References**

Cochran, W.G. (1977). *Sampling Techniques*, 3rd ed. John Wiley & Sons, New York.

**Examples**

```
data(sample_nrm)
srs <- srs_sample(sample_nrm, n = 30)
X_total <- sum(sample_nrm$size)
ratio_estimator(y = srs$biomass, x = srs$size, X_total = X_total)
```

---

regression\_estimator    *Regression Estimator*

---

**Description**

Provides a model-assisted estimate of the population mean of  $y$  using a known population mean of the auxiliary variable  $x$ .

**Usage**

```
regression_estimator(y, x, X_mean)
```

**Arguments**

$y$	Numeric vector. Sample values of the study variable.
$x$	Numeric vector. Sample values of the auxiliary variable.
$X_{\text{mean}}$	Numeric. Known population mean of $x$ .

**Details**

$$\hat{Y}_{\text{reg}} = \bar{y} + \hat{\beta}(\bar{X} - \bar{x})$$

where  $\hat{\beta}$  is the ordinary least-squares slope from regressing  $y$  on  $x$ .

**Value**

Numeric scalar. Regression estimate of the population mean.

## References

Sarndal, C.E., Swensson, B., and Wretman, J. (2003). *Model Assisted Survey Sampling*. Springer, New York.

## Examples

```
data(sample_nrm)
srs <- srs_sample(sample_nrm, n = 30)
X_mean <- mean(sample_nrm$size)
regression_estimator(y = srs$biomass, x = srs$size, X_mean = X_mean)
```

---

sample\_nrm

*Simulated NRM Plot Dataset*

---

## Description

A synthetic dataset of 100 field plots representing a heterogeneous natural resource management landscape with three strata and ten spatial clusters.

## Format

A data frame with 100 rows and 7 variables:

`plot_id` Integer. Unique plot identifier (1–100).

`biomass` Numeric. Aboveground biomass density (Mg/ha), drawn from Uniform(5, 50).

`soil_loss` Numeric. Annual soil loss (Mg/ha/yr), drawn from Uniform(0.1, 10).

`strata` Character. Land-use stratum: one of "forest", "agriculture", or "grassland".

`cluster` Integer. Spatial cluster identifier (1–10).

`size` Numeric. Plot size measure used for PPS sampling (e.g., stand basal area), drawn from Uniform(1, 100).

`carbon` Numeric. Estimated carbon stock (Mg C/ha), derived as  $0.47 * \text{biomass}$ .

## Source

Synthetic data generated in `data-raw/generate_datasets.R`.

## Examples

```
data(sample_nrm)
head(sample_nrm)
table(sample_nrm$strata)
summary(sample_nrm[, c("biomass", "soil_loss")])
```

---

sample_spatial	<i>Simulated Spatial NRM Dataset</i>
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---

### Description

A synthetic dataset of 100 geo-referenced field observations within a one-degree tile (77–78 degrees E, 30–31 degrees N) representing a Himalayan watershed zone.

### Format

A data frame with 100 rows and 8 variables:

`id` Integer. Observation identifier.

`lon` Numeric. Longitude (decimal degrees, WGS 84).

`lat` Numeric. Latitude (decimal degrees, WGS 84).

`biomass` Numeric. Aboveground biomass (Mg/ha).

`soil_loss` Numeric. Annual soil loss (Mg/ha/yr).

`strata` Character. Land-use class: "forest" or "agriculture".

`cluster` Integer. Spatial cluster (1–5).

`ndvi` Numeric. Synthetic NDVI value (0–1), correlated with biomass.

### Source

Synthetic data generated in `data-raw/generate_datasets.R`.

### Examples

```
data(sample_spatial)
head(sample_spatial)

if (requireNamespace("sf", quietly = TRUE)) {
  pts <- to_sf_points(sample_spatial, lon = "lon", lat = "lat")
  plot(sf::st_geometry(pts))
}
```

---

sampling\_efficiency     *Sampling Efficiency Comparison*

---

**Description**

Computes the relative efficiency (RE) of two sampling designs by comparing their estimated variances of the mean.  $RE > 1$  indicates Design 2 is more efficient than Design 1.

**Usage**

```
sampling_efficiency(y1, y2, N = NULL)
```

**Arguments**

y1                    Numeric vector. Sample from Design 1.  
y2                    Numeric vector. Sample from Design 2.  
N                     Integer. Population size (for fpc). Set NULL to omit.

**Value**

A named numeric vector with var\_design1, var\_design2, and relative\_efficiency (var1 / var2).

**Examples**

```
data(sample_nrm)
srs1 <- srs_sample(sample_nrm, n = 20)
srs2 <- srs_sample(sample_nrm, n = 30)
sampling_efficiency(srs1$biomass, srs2$biomass, N = 100)
```

---

soil\_loss\_estimate     *Soil Loss Estimation from Sample Plots*

---

**Description**

Estimates mean and total soil loss from a set of erosion measurement plots, with a standard error.

**Usage**

```
soil_loss_estimate(df, loss_var, area)
```

**Arguments**

df	A data frame of sampled erosion plots.
loss_var	Character. Name of the column containing plot-level soil loss measurements (e.g., Mg/ha/year).
area	Numeric. Total catchment or management area.

**Value**

A named list with elements mean\_loss, total\_loss, se, and n.

**References**

Wischmeier, W.H. and Smith, D.D. (1978). *Predicting Rainfall Erosion Losses*. USDA Agriculture Handbook 537.

**Examples**

```
data(sample_nrm)
srs <- srs_sample(sample_nrm, n = 25)
soil_loss_estimate(srs, loss_var = "soil_loss", area = 500)
```

---

spatial\_biomass\_estimate

*Spatial Biomass Estimation from sf Points*

---

**Description**

Estimates total biomass over a study area from field measurements stored in an `sf` point object.

**Usage**

```
spatial_biomass_estimate(sf_data, biomass_var, area)
```

**Arguments**

sf_data	An <code>sf</code> object with a biomass attribute column.
biomass_var	Character. Name of the biomass density column.
area	Numeric. Total study area (in consistent units).

**Details**

Requires the `sf` package.

**Value**

A named list with mean\_biomass, total\_biomass, se, and n.

## Examples

```
if (requireNamespace("sf", quietly = TRUE)) {  
  data(sample_spatial)  
  pts_sf <- to_sf_points(sample_spatial, lon = "lon", lat = "lat")  
  spatial_biomass_estimate(pts_sf, biomass_var = "biomass", area = 1000)  
}
```

---

spatial\_cluster\_sample

*Spatial Cluster Sampling*

---

## Description

Randomly selects a number of spatial clusters (e.g., sub-watersheds, administrative units) and returns all features within selected clusters.

## Usage

```
spatial_cluster_sample(sf_data, cluster_var, n_clusters)
```

## Arguments

sf_data	An sf object.
cluster_var	Character. Name of the column identifying clusters.
n_clusters	Integer. Number of clusters to select.

## Details

Requires the **sf** package.

## Value

An sf object containing features from the selected clusters.

## Examples

```
if (requireNamespace("sf", quietly = TRUE)) {  
  data(sample_spatial)  
  pts_sf <- to_sf_points(sample_spatial, lon = "lon", lat = "lat")  
  cl_sp <- spatial_cluster_sample(pts_sf, "cluster", n_clusters = 3)  
  length(unique(cl_sp$cluster))  
}
```

---

spatial\_random\_sample *Spatial Random Sampling within a Polygon*

---

### Description

Draws a random sample of points uniformly distributed within an sf polygon or multipolygon geometry.

### Usage

```
spatial_random_sample(polygon, n)
```

### Arguments

polygon	An sf or sfc object representing the sampling frame (polygon boundary).
n	Integer. Number of random points to generate.

### Details

Requires the **sf** package. Points are drawn using `sf::st_sample(..., type = "random")`.

### Value

An sf object of POINT geometries within polygon.

### Examples

```
if (requireNamespace("sf", quietly = TRUE)) {  
  # Create a simple rectangular polygon for illustration  
  bbox <- sf::st_as_sfc(sf::st_bbox(c(xmin=77, xmax=78,  
                                     ymin=30, ymax=31),  
                                crs = sf::st_crs(4326)))  
  pts <- spatial_random_sample(bbox, n = 20)  
  plot(sf::st_geometry(pts))  
}
```

---

`spatial_stratified_sample`*Stratified Spatial Sampling*

---

### Description

Selects a random sample of `n_per_stratum` features from each stratum of an `sf` object.

### Usage

```
spatial_stratified_sample(sf_data, strata_var, n_per_stratum)
```

### Arguments

<code>sf_data</code>	An <code>sf</code> object with a <code>stratum</code> attribute column.
<code>strata_var</code>	Character. Name of the column defining strata.
<code>n_per_stratum</code>	Integer or named integer vector. Sample size per stratum (see <a href="#">stratified_sample</a> for details).

### Details

Requires the `sf` package.

### Value

An `sf` object with the selected features.

### Examples

```
if (requireNamespace("sf", quietly = TRUE)) {  
  data(sample_spatial)  
  pts_sf <- to_sf_points(sample_spatial, lon = "lon", lat = "lat")  
  st_sp <- spatial_stratified_sample(pts_sf, "strata", n_per_stratum = 5)  
  table(st_sp$strata)  
}
```

---

`spatial_systematic_sample`*Systematic Grid Sampling within a Polygon*

---

### Description

Generates a systematic grid of points at a specified spacing within an `sf` polygon, retaining only points that fall inside the boundary.

### Usage

```
spatial_systematic_sample(polygon, spacing)
```

### Arguments

<code>polygon</code>	An <code>sf</code> or <code>sfc</code> polygon object.
<code>spacing</code>	Numeric. Grid cell size in the units of the CRS (degrees for EPSG:4326, metres for projected CRS).

### Details

Requires the `sf` package.

### Value

An `sf` object of POINT geometries inside polygon.

### Examples

```
if (requireNamespace("sf", quietly = TRUE)) {  
  bbox <- sf::st_as_sfc(sf::st_bbox(c(xmin=77, xmax=78,  
                                     ymin=30, ymax=31),  
                                   crs = sf::st_crs(4326)))  
  grid_pts <- spatial_systematic_sample(bbox, spacing = 0.1)  
  plot(sf::st_geometry(grid_pts))  
}
```

---

srs_sample	<i>Simple Random Sampling</i>
------------	-------------------------------

---

**Description**

Draws a simple random sample from a data frame.

**Usage**

```
srs_sample(data, n, replace = FALSE)
```

**Arguments**

data	A data frame representing the population.
n	Integer. Number of units to sample.
replace	Logical. Sample with replacement? Default FALSE.

**Value**

A data frame with sampled rows and a ".sample\_id" column.

---

stratified_estimator	<i>Stratified Mean Estimator</i>
----------------------	----------------------------------

---

**Description**

Estimates the population mean from a stratified sample using stratum weights (proportional to stratum size).

**Usage**

```
stratified_estimator(y, strata, N_h)
```

**Arguments**

y	Numeric vector. Sample values of the study variable.
strata	Character or factor vector. Stratum labels (same length as y).
N_h	Named numeric vector. Population stratum sizes; names must match unique values of strata.

**Details**

$$\hat{Y}_{st} = \sum_h W_h \bar{y}_h, \quad W_h = N_h/N$$

**Value**

Numeric scalar. Estimated population mean.

**References**

Cochran, W.G. (1977). *Sampling Techniques*, 3rd ed. John Wiley & Sons, New York.

**Examples**

```
data(sample_nrm)
st <- stratified_sample(sample_nrm, "strata", n_per_stratum = 5)
N_h <- table(sample_nrm$strata)
stratified_estimator(st$biomass, st$strata, N_h)
```

---

stratified\_sample      *Stratified Sampling*

---

**Description**

Performs stratified random sampling.

**Usage**

```
stratified_sample(data, strata_var, n_per_stratum, replace = FALSE)
```

**Arguments**

data	A data frame.
strata_var	Character. Column defining strata.
n_per_stratum	Integer or named vector.
replace	Logical. Sample with replacement?

**Value**

A data frame with sampled rows.

---

systematic_sample	<i>Systematic Sampling</i>
-------------------	----------------------------

---

**Description**

Performs systematic sampling using interval k.

**Usage**

```
systematic_sample(data, k)
```

**Arguments**

data	A data frame.
k	Integer. Sampling interval.

**Value**

A data frame of sampled rows.

---

to_sf_points	<i>Convert a Data Frame to an sf Point Object</i>
--------------	---

---

**Description**

Creates an sf simple-features point object from longitude and latitude columns in a data frame.

**Usage**

```
to_sf_points(data, lon, lat, crs = 4326)
```

**Arguments**

data	A data frame containing coordinate columns.
lon	Character. Name of the longitude column.
lat	Character. Name of the latitude column.
crs	Integer or character. Coordinate reference system as an EPSG code or PROJ string. Default 4326 (WGS 84 geographic).

**Details**

Requires the **sf** package.

**Value**

An sf object with a POINT geometry column.

**Examples**

```
if (requireNamespace("sf", quietly = TRUE)) {  
  data(sample_spatial)  
  pts <- to_sf_points(sample_spatial, lon = "lon", lat = "lat")  
  print(pts)  
}
```

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