

# Package: rsocsim (via r-universe)

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**Type** Package

**Title** SOCSIM

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**Description** Tools for preparing inputs, running SOCSIM (SOCial SIMulator) demographic kinship microsimulations, and reading simulation outputs from R. The package includes helpers for creating simulation folders, downloading demographic rate schedules, starting simulations, and loading population and marriage result files.

**License** GPL-3

**Imports** Rcpp (>= 1.0.5), magrittr, dplyr, tidyr, utils

**LinkingTo** Rcpp

**Suggests** future, parallel, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**URL** <https://github.com/MPIDR/rsocsim>, <https://mpidr.github.io/rsocsim/>

**BugReports** <https://github.com/MPIDR/rsocsim/issues>

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create\_simulation\_folder

*Create a directory structure for the simulation*

---

### Description

Create a two-level directory structure. If the first-level argument is NULL, we look for and, if needed, create the directory 'socsim' in the current temporary directory. If the second-level argument is NULL, we create a directory named like 'socsim\_sim\_' followed by a random component in the first-level directory.

### Usage

```
create_simulation_folder(basedir = NULL, simdir = NULL)
```

### Arguments

basedir	A string. Optional. First-level directory where the simulation-specific directory will be created. Defaults to <code>file.path(tempdir(), "socsim")</code> .
simdir	A string. Optional. Simulation-specific directory which will be created within 'basedir'. Defaults to 'socsim_sim_' plus a random component created with <code>tempfile()</code> .

### Value

A string. The full path to the simulation-specific directory.

---

create_sup_file	<i>Create a basic .sup file for a simulation</i>
-----------------	--

---

**Description**

The simulation is only a simple one. The file will be saved into the directory 'simdir'.

**Usage**

```
create_sup_file(simdir, simname = "socsim")
```

**Arguments**

simdir	A string. The directory where the .sup file will be saved.
simname	A string. The base name of the simulation. Defaults to "socsim".

**Value**

A string. The basename of the created supervisory file, for example "socsim.sup". The file is written to simdir, and the function also copies the bundled rate and initial-population input files into simdir.

---

estimate_fertility_rates	<i>Estimate yearly age-specific fertility rates (ASFR) from a SOCSIM-generated population file</i>
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---

**Description**

Given a population file ('opop') generated by rsocsim, the function estimates age-specific fertility rates.

**Usage**

```
estimate_fertility_rates(  
  opop,  
  final_sim_year,  
  year_min,  
  year_max,  
  year_group = 5,  
  age_min_fert = 15,  
  age_max_fert = 50,  
  age_group = 5  
)
```

**Arguments**

opop	An R object from SOCSIM microsimulation output (population file).
final_sim_year	numeric. Final simulated year in 'real world' time ( used to convert 'SOCSIM time' to 'real world' time.)
year_min	numeric. Lower-bound year for which rate should be estimated.
year_max	numeric. Upper-bound year for which rate should be estimated.
year_group	numeric. Size of year groups to estimate rate (year_group=1 will produce single-year estimates)
age_min_fert	numeric. Lower-bound age of female reproductive period
age_max_fert	numeric. Upper-bound age of female reproductive period
age_group	numeric. Size of age groups to estimate rate (age_group=1 will produce single-age estimates)

**Details**

The final\_sim\_year can be obtained from the .sup file and must refer to to a real-world year.

Grouped year and age ranges (i.e., if year\_group > 1 or age\_group > 1) are created as [year;year+year\_group).

**Value**

A data frame with columns year, age, and socsim. year is a factor describing the grouped calendar-year interval, age is a factor describing the maternal-age interval, and socsim is the estimated fertility rate for that cell.

**Examples**

```

opop <- data.frame(
  pid = 1:6,
  fem = c(1, 0, 1, 0, 1, 1),
  group = 1,
  nev = 0,
  dob = c(120, 120, 336, 348, 180, 360),
  mom = c(0, 0, 1, 1, 0, 5),
  pop = c(0, 0, 2, 2, 0, 2),
  nesibm = 0,
  nesibp = 0,
  lborn = 0,
  marid = 0,
  mstat = 0,
  dod = c(0, 300, 0, 0, 0, 0),
  fmult = 0
)

asfr <- estimate_fertility_rates(opop = opop,
                                final_sim_year = 2021,
                                year_min = 1998,
                                year_max = 2000,
                                year_group = 5,

```

```

                                age_min_fert = 15,
                                age_max_fert = 50,
                                age_group = 5)
head(asfr)

```

---

```
estimate_mortality_rates
```

*Estimate yearly age-specific mortality rates (ASMR) from a SOCSIM-generated population file*

---

### Description

Given a population file ('opop') generated by rsocsim, the function estimates (yearly) age-specific mortality rates.

### Usage

```

estimate_mortality_rates(
  opop,
  final_sim_year,
  year_min,
  year_max,
  year_group,
  age_max_mort,
  age_group
)

```

### Arguments

opop	An R object from SOCSIM microsimulation output (population file).
final_sim_year	numeric. Final simulated year in 'real world' time ( used to convert 'SOCSIM time' to 'real world' time.)
year_min	numeric. Lower-bound year for which rate should be estimated.
year_max	numeric. Upper-bound year for which rate should be estimated.
year_group	numeric. Size of year groups to estimate rate (year_group=1 will produce single-year estimates)
age_max_mort	numeric. Maximum age for estimating mortality.
age_group	numeric. Size of age groups to estimate rate (age_group=1 will produce single-age estimates)

### Details

The final\_sim\_year can be obtained from the .sup file and must refer to to a real-world year.

Grouped year and age ranges (i.e., if year\_group > 1 or age\_group > 1) are created as [year;year+year\_group). For age\_group > 1, mortality rates are split into an infant group [0,1) and then grouped ages [1, age\_group), [age\_group, age\_group + age\_group), and so on.

**Value**

A data frame with columns year, sex, age, and socsim. year is a factor describing the grouped calendar-year interval, sex is "male" or "female", age is a factor describing the age interval, and socsim is the estimated mortality rate for that cell.

**Examples**

```

opop <- data.frame(
  pid = 1:6,
  fem = c(1, 0, 1, 0, 1, 1),
  group = 1,
  nev = 0,
  dob = c(120, 120, 336, 348, 180, 360),
  mom = c(0, 0, 1, 1, 0, 5),
  pop = c(0, 0, 2, 2, 0, 2),
  nesibm = 0,
  nesibp = 0,
  lborn = 0,
  marid = 0,
  mstat = 0,
  dod = c(0, 300, 0, 0, 0, 0),
  fmult = 0
)

asmr <- estimate_mortality_rates(opop = opop,
                                final_sim_year = 2021,
                                year_min = 1995,
                                year_max = 2000,
                                year_group = 5,
                                age_max_mort = 100,
                                age_group = 5)

head(asmr)

```

---

read\_omar

*Read output marriage file into a data frame*


---

**Description**

When fn contains multiple file paths, or when seed contains multiple values and fn is NULL, the matching result files are read and row-bound into a single data frame. To keep identifiers unique across simulations, positive ID columns are offset by  $(\text{index} - 1) * \text{id\_offset}$ , while sentinel zeros remain unchanged.

**Usage**

```

read_omar(
  folder = NULL,
  supfile = "socsim.sup",
  seed = 42,

```

```

    suffix = "",
    fn = NULL,
    id_offset = 10000000L,
    quiet = FALSE
  )

```

### Arguments

folder	simulation base folder ("~/socsim/simulation_235/")
supfile	name of supervisory-file ("socsim.sup")
seed	random number seed (42)
suffix	optional suffix for the results-directory (default="")
fn	complete path to the file. If not provided, it will be created from the other arguments
id_offset	positive integer stride used to offset IDs when combining multiple files. Ignored for single-file reads. Default is 10 million, which allows combining up to 214 files with a total population of 10 million each.
quiet	logical. If FALSE, emit a message with the file path being read.

### Details

1	mid	Marriage id number (unique sequential integer)
2	wpid	Wife's person id
3	hpid	Husband's person id
4	dstart	Date marriage began
5	dend	Date marriage ended or zero if still in force at end of simulation
6	rend	Reason marriage ended 2 = divorce; 3 = death of one partner
7	wprior	Marriage id of wife's next most recent prior marriage
8	hprior	Marriage id of husband's next most recent prior marriage

you can either provide the complete path to the file or the folder, supfilename, seed and suffix with which you started the simulation

### Value

A data frame with columns mid, wpid, hpid, dstart, dend, rend, wprior, and hprior, matching the SOCSIM result.omar file. If the file is missing or empty, a zero-row data frame with these columns is returned.

---

read_opop	<i>Read output population file into a data frame</i>
-----------	--

---

### Description

When `fn` contains multiple file paths, or when `seed` contains multiple values and `fn` is `NULL`, the matching result files are read and row-bound into a single data frame. To keep identifiers unique across simulations, positive ID columns are offset by  $(\text{index} - 1) * \text{id\_offset}$ , while sentinel zeros remain unchanged.

### Usage

```
read_opop(
  folder = NULL,
  supfile = "socsim.sup",
  seed = 42,
  suffix = "",
  fn = NULL,
  id_offset = 10000000L,
  quiet = FALSE
)
```

### Arguments

<code>folder</code>	simulation base folder (" <code>~/socsim/simulation_235/</code> ")
<code>supfile</code>	name of supervisory-file (" <code>socsim.sup</code> ")
<code>seed</code>	random number seed (42)
<code>suffix</code>	optional suffix for the results-directory (default="")
<code>fn</code>	complete path to the file. If not provided, it will be created from the other arguments
<code>id_offset</code>	positive integer stride used to offset IDs when combining multiple files. Ignored for single-file reads. Default is 10 million, which allows combining up to 214 files with a total population of 10 million each.
<code>quiet</code>	logical. If <code>FALSE</code> , emit a message with the file path being read.

### Details

after the end of the simulation, `socsim` writes every person of the simulation into a file called `result.opop.l`

1	<code>pid</code>	Person id unique identifier assigned as integer in birth order
2	<code>fem</code>	1 if female 0 if male
3	<code>group</code>	Group identifier 1..60 current group membership of individual
4	<code>nev</code>	Next scheduled event
5	<code>dob</code>	Date of birth integer month number

6	mom	Person id of mother
7	pop	Person id of father
8	nesibm	Person id of next eldest sibling through mother
9	nesibp	Person id of next eldest sibling through father
10	lborn	Person id of last born child
11	marid	Id of marriage in .omar file
12	mstat	Marital status at end of simulation integer 1=single;2=divorced; 3=widowed; 4=married
13	dod	Date of death or 0 if alive at end of simulation
14	fmult	Fertility multiplier

This table explains the columns of the opop file and the columns of the output data frame. You can either provide the complete path to the file or the folder, supfilename, seed and suffix with which you started the simulation

### Value

A data frame with columns pid, fem, group, nev, dob, mom, pop, nesibm, nesibp, lborn, marid, mstat, dod, and fmult, matching the SOCSIM result.opop file. If the file is missing or empty, a zero-row data frame with these columns is returned.

---

retrieve_kin	<i>Identify members of a kin network for an individual or individuals of interest.</i>
--------------	--

---

### Description

Identify members of a kin network for an individual or individuals of interest.

### Usage

```
retrieve_kin(
  opop,
  omar,
  pid,
  extra_kintypes = character(),
  kin_by_sex = FALSE,
  KidsOf = NULL
)
```

### Arguments

opop	An R object from SOCSIM microsimulation output (population file). Create this object with the function read_opop().
omar	An R object from SOCSIM microsimulation output (marriage file). Create this object with the function read_omar().

pid	A vector of person IDs, indicating persons of interest for whom these kin networks should be identified.
extra_kintypes	A vector of character values indicating which additional types of kin should be obtained. For reasons of computational efficiency, the function will by default only identify an individual's great-grandparents ("ggparents" in function output), grandparents ("gparents"), parents, siblings, spouse, children, and grandchildren ("gchildren"). However, by selecting one or more of the following kin types, the kin network generated will also include these individuals: <ul style="list-style-type: none"> <li>• "gunclesaunts": Great-uncles and great-aunts</li> <li>• "unclesaunts": Uncles and aunts</li> <li>• "firstcousins": First cousins (Children of uncles and aunts)</li> <li>• "niblings": Nieces and nephews (Children of siblings)</li> <li>• "inlaws": Parents-in-law (parents of spouse) and brothers and sisters in law (siblings of spouse and spouse of siblings)</li> </ul>
kin_by_sex	A logical value indicating whether output should include kin relations additionally disaggregated by the sex of the relative. Setting this value to TRUE will result in additional objects being generated to identify individuals' relatives by sex.
KidsOf	An optional precomputed list object containing the children of each person in the population. If NULL, it is built from opop.

### Value

A named list whose components are kinship categories such as parents, siblings, or children. Each component is itself a named list of integer person IDs, organized by relationship. These person ID values will be named based on the person of interest with whom they are associated. For example, for a list named "parents", the values will be person IDs of the parents of individuals of interest. These values will be named according to their children's IDs (given that their children are, in this case, the persons of interest provided to the function input). With `kin_by_sex` set to TRUE and `extra_kintypes` set to `c("gunclesaunts", "unclesaunts", "firstcousins", "niblings", "inlaws")`, the full list of kin relations identified are:

- "ggparents": great-grandparents
- "ggmothers": great-grandmothers
- "ggfathers": great-grandfathers
- "gparents": grandparents
- "gmothers": grandmothers
- "gfathers": grandfathers
- "gunclesaunts": great-uncles and great-aunts
- "guncles": great-uncles
- "gaunts": great-aunts
- "parents": parents
- "mother": mother
- "father": father

- "unclesaunts": uncles and aunts (siblings of parents)
- "uncles": uncles
- "aunts": aunts
- "siblings": siblings
- "sisters": sisters
- "brothers": brothers
- "firstcousins": first cousins
- "firstcousinsfemale": female first cousins
- "firstcousinsmale": male first cousins
- "children": children
- "daughters": daughters
- "sons": sons
- "gchildren": grandchildren
- "gdaughters": granddaughters
- "gsons": grandsons
- "niblings": nephews and nieces
- "nieces": nieces
- "nephews": nephews
- "spouse": spouse (based on final marriage, in the case of multiple marriages)
- "parentsinlaw": parents-in-law
- "motherinlaw": mother-in-law
- "fatherinlaw": father-in-law
- "siblingsinlaw": brothers and sisters in law
- "sistersinlaw": sisters-in-law
- "brothersinlaw": brothers-in-law

### Examples

```
opop <- data.frame(  
  pid = 1:4,  
  fem = c(1, 0, 1, 0),  
  group = 1,  
  nev = 0,  
  dob = c(120, 120, 300, 300),  
  mom = c(0, 0, 1, 1),  
  pop = c(0, 0, 2, 2),  
  nesibm = 0,  
  nesibp = 0,  
  lborn = 0,  
  marid = c(1, 1, 0, 0),  
  mstat = c(4, 4, 1, 1),  
  dod = 0,  
  fmult = 0
```

```

)
omar <- data.frame(
  mid = 1,
  wpid = 1,
  hpid = 2,
  dstart = 0,
  dend = 0,
  rend = 0,
  wprior = 0,
  hprior = 0
)

kin_network <- retrieve_kin(
  opop = opop,
  omar = omar,
  pid = 3,
  extra_kintypes = c("niblings", "inlaws"),
  kin_by_sex = TRUE
)
kin_network$parents[[1]]

```

---

simulation\_time\_to\_years

*Calculate for how many years the simulation ran*

---

### Description

Calculate for how many years the simulation ran

### Usage

```
simulation_time_to_years(simulation_time, pre_simulation_time, start_year)
```

### Arguments

simulation\_time

An integer. The number of periods (months) the simulation ran.

pre\_simulation\_time

An integer. The number of periods (months) the simulation ran before getting to a stable population. This is subtracted from 'simulation\_time' in order to arrive at the "real" simulation time

start\_year

An integer. The year the simulation started.

### Value

A numeric scalar giving the calendar year reached at the end of the simulated period after subtracting `pre_simulation_time / 12`. The value can include a fractional year.

---

socsim	<i>Run a single Socsim simulation with a given supervisory file and directory</i>
--------	---

---

## Description

Run a single Socsim simulation with a given supervisory file and directory

## Usage

```
socsim(
  folder,
  supfile,
  seed = "42",
  process_method = "inprocess",
  compatibility_mode = "1",
  suffix = ""
)
```

## Arguments

folder	A string. This is the base directory of the simulation. Every .sup and rate file should be named relative to this directory.
supfile	A string. The name of the .sup file to start the simulation, relative to the directory.
seed	A string. The seed for the RNG, so expects an integer. Defaults to "42".
process_method	A string. Whether and how SOCSIM should be started in its own process or in the running R process. Defaults to "inprocess". Use one of: <ul style="list-style-type: none"> <li>• "future" - the safest option. A new process will be started via the "future" package</li> <li>• "inprocess" - SOCSIM runs in the R-process. Beware if you run several different simulations, they may affect later simulations.</li> <li>• "clustercall" - if the future package is not available, try this method instead.</li> </ul>
compatibility_mode	A string.
suffix	A string.

## Value

Returns 1L when the simulation finishes successfully. If the simulation errors before completion, the function returns NULL after issuing warnings. Result files are written to the directory `sim_results_<basename(supfile)>_<seed>_<suffix>` inside folder.

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