

# Implementing open science

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**MAX PLANCK INSTITUTE**  
FOR DEMOGRAPHIC RESEARCH

# **Benefits of reproducibility and open science**

## Some personal experiences

Together with



**Roland Rau**  
@Demographie

CRAN Task View: Survival Analysis

**Maintainer:** Arthur Allignol, Aurelien Latouche  
**Contact:** arthur.allignol at gmail.com  
**Version:** 2022-03-07  
**URL:** <https://CRAN.R-project.org/view=Survival>  
**Source:** <https://github.com/cran-task-views/Survival/>

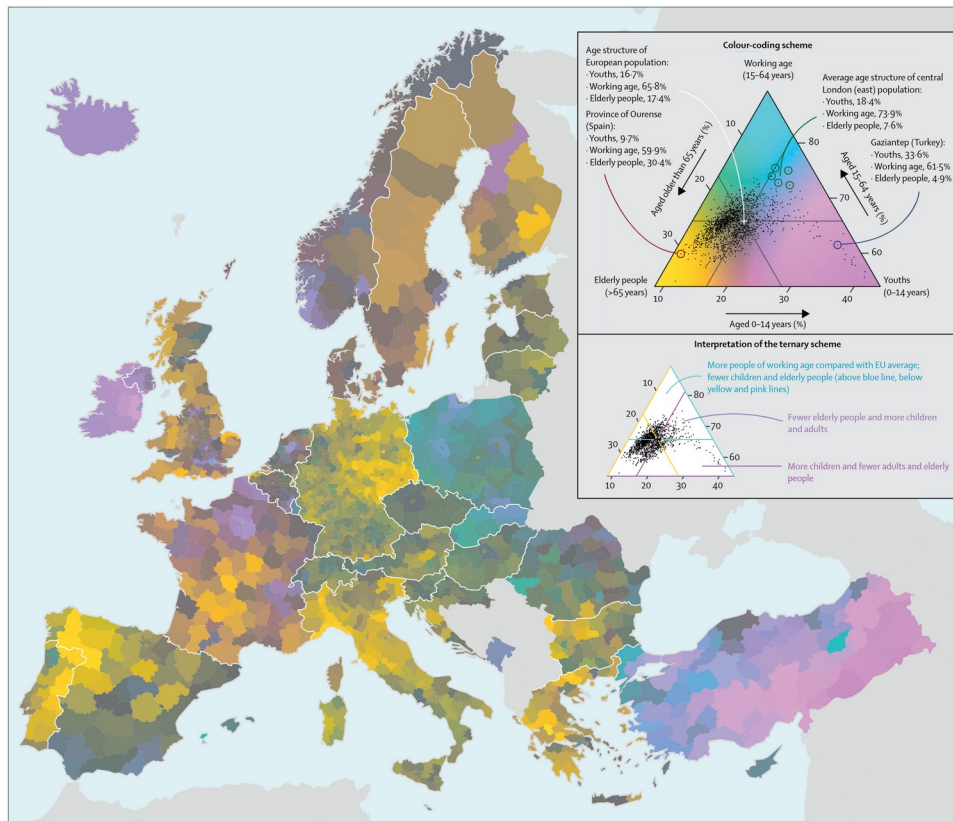
## Testing

- The `survdif` function in [survival](#) compares survival curves using the Fleming-Harrington G-rho family of test. [NADA](#) implements this class of tests for left-censored data.
- The [maxcombo](#) package compares survival curves using the max-combo test, which is often based on the Fleming-Harrington G-rho family of tests and is designed to have higher power than the logrank test in the scenario of non-proportional hazards such as those resulting from delayed treatment effects.
- [clinfun](#) implements a permutation version of the logrank test and a version of the logrank that adjusts for covariates.
- The [exactRankTests](#) implements the shift-algorithm by Streitberg and Roehmel for computing exact conditional p-values and quantiles, possibly for censored data.
- `SurvTest` in the [coin](#) package implements the logrank test reformulated as a linear rank test.
- The [maxstat](#) package performs tests using maximally selected rank statistics.
- The [interval](#) package implements logrank and Wilcoxon type tests for interval-censored data.
- Three generalised logrank tests and a score test for interval-censored data are implemented in the [glrt \(archived\)](#) package.
- [survcomp](#) compares 2 hazard ratios.
- The [TSHRC](#) implements a two stage procedure for comparing hazard functions.
- The [FHtest](#) package offers several tests based on the Fleming-Harrington class for comparing survival curves with right- and interval censored data.
- The [LogrankA \(archived\)](#) package provides a logrank test for which aggregated data can be used as input.
- The short term and long term hazard ratio model for two samples survival data can be found in the [YPmodel](#) package.
- The [controlTest](#) implements a nonparametric two-sample procedure for comparing the median survival time.
- The [survRM2](#) package performs two-sample comparison of the restricted mean survival time
- The [emplik2](#) package permits to compare two samples with censored data using empirical likelihood ratio tests.
- The [KONPsurv](#) package provides powerful nonparametric K-sample tests for right-censored data. The tests are consistent against any differences between the hazard functions of the groups.

Together with



**Ilya Kashnitsky**  
@ikashnitsky



**Figure: Colour-coded map of population structures in European Nomenclature of Territorial Units for Statistics 3 regions in 2015**  
Each population composition in the European Nomenclature of Territorial Units for Statistics 3 regions is uniquely colour coded. Colours show direction and magnitude of deviations from the centrepiece, which represents the average age of the European population, and is dark grey. The hue component of a colour encodes the direction of deviation: yellow indicates an elderly population (>65 years), cyan indicates people of working age (15-64 years), and magenta indicates children (0-14 years). Chroma and lightness components signify the distance from the centre ranging from desaturated and dark colours near the centre to vivid and bright colours at the corners. We provide R code to fully reproduce this map.<sup>20</sup>

Kashnitsky & Schöley (2018). Regional population structures at a glance. [10.1016/S0140-6736\(18\)31194-2](https://doi.org/10.1016/S0140-6736(18)31194-2)

Together with



Ilya Kashnitsky  
@ikashnitsky

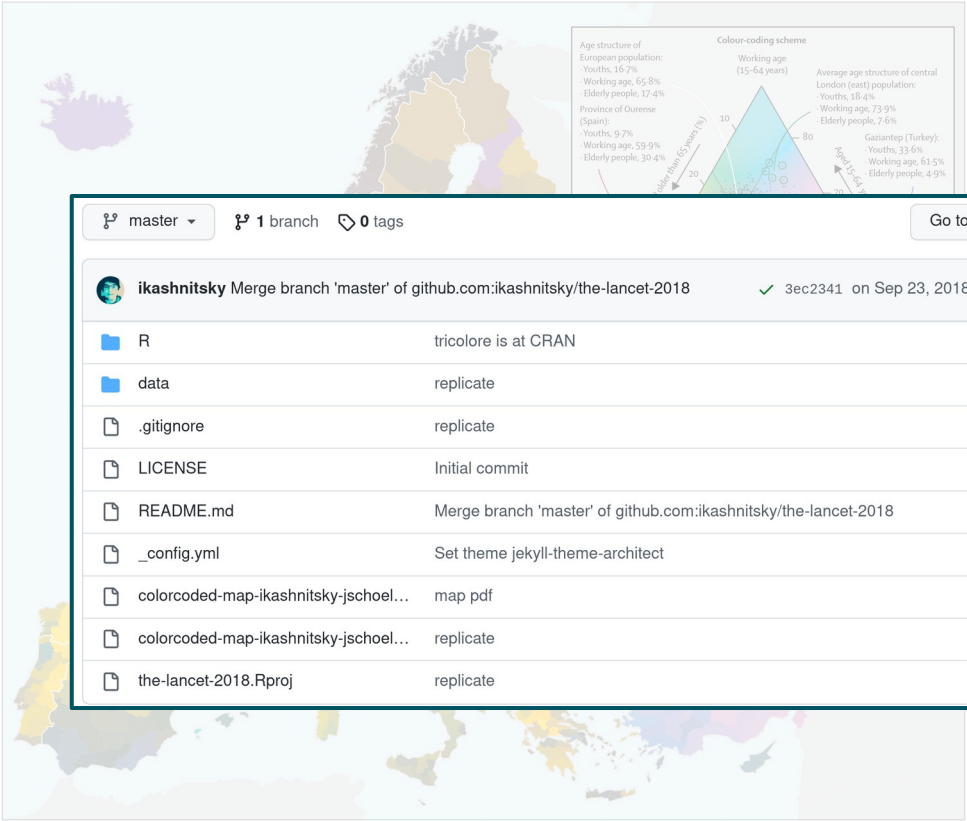


Figure: Colour-coded map of population structures in European Nomenclature of Territorial Units for Statistics 3 regions in 2015  
Each population composition in the European Nomenclature of Territorial Units for Statistics 3 regions is uniquely colour coded. Colours show direction and magnitude of deviations from the centrepoint, which represents the average age of the European population, and is dark grey. The hue component of a colour encodes the direction of deviation: yellow indicates an elderly population (>65 years), cyan indicates people of working age (15–64 years), and magenta indicates children (0–14 years). Chroma and lightness components signify the distance from the centre ranging from desaturated and dark colours near the centre to vivid and bright colours at the corners. We provide R code to fully reproduce this map.<sup>26</sup>

master 1 branch 0 tags Go to file Code

ikashnitsky Merge branch 'master' of github.com:ikashnitsky/the-lancet-2018 3ec2341 on Sep 23, 2018 15 commits

R	tricolore is at CRAN	4 years ago
data	replicate	4 years ago
.gitignore	replicate	4 years ago
LICENSE	Initial commit	4 years ago
README.md	Merge branch 'master' of github.com:ikashnitsky/the-lancet-2018	4 years ago
_config.yml	Set theme jekyll-theme-architect	4 years ago
colorcoded-map-ikashnitsky-jschoel...	map pdf	4 years ago
colorcoded-map-ikashnitsky-jschoel...	replicate	4 years ago
the-lancet-2018.Rproj	replicate	4 years ago

About

Reproduce "Regional population structures at a glance"

[doi.org/10.1016/S0140-6736\(18\)31194-2](https://doi.org/10.1016/S0140-6736(18)31194-2)

Readme

MIT license

74 stars

7 watching

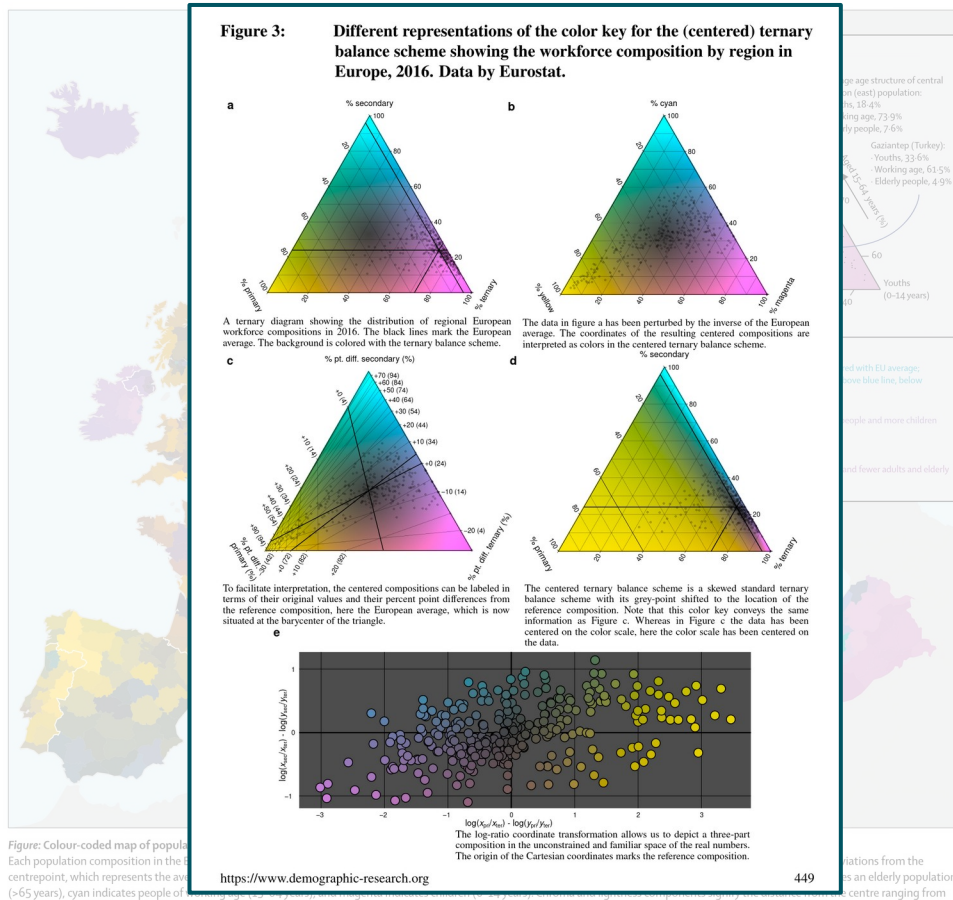
18 forks

Releases

No releases published



Ilya Kashnitsky  
@ikashnitsky





## Together with



Ilya Kashnitsky  
@ikashnitsky

### tricolore. A flexible color scale for ternary compositions

Jonas Schöley & Ilya Kashnitsky

CRAN 1.2.0 build: passing License: GPL v3



#### What is tricolore?

`tricolore` is an R library providing a flexible color scale for the visualization of three-part (ternary) compositions. Its main functionality is to color-code any ternary composition as a mixture of three primary colours and to draw a suitable color-key. `tricolore` flexibly adapts to different visualization challenges via

- *discrete* and *continuous* color support,
- support for unbalanced compositional data via *centering*,
- support for data with very narrow range via *scaling*,
- *hue*, *chroma* and *lightness* options.

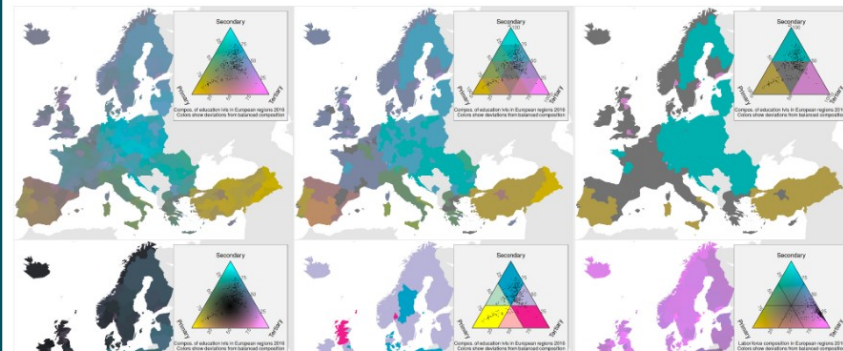
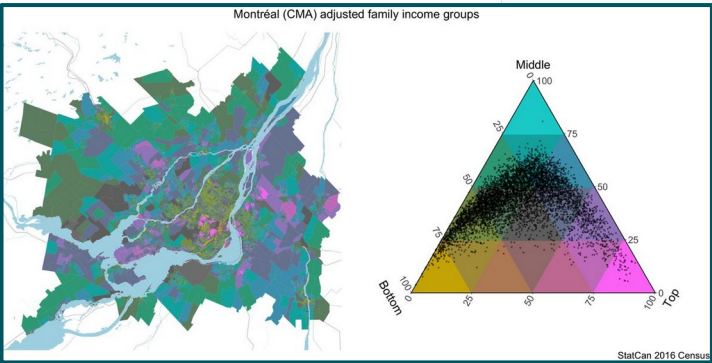


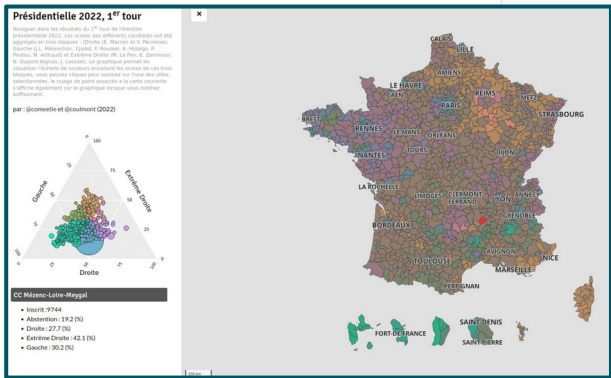
Figure: Colours of population composition in the European Nomenclature of territorial units for statistics regions (NUTS-3 regions) is uniquely colour coded. Colours show direction and magnitude of deviations from the centrepoint, which represents the average age of the European population, and is dark grey. The hue component of a colour encodes the direction of deviation: yellow indicates an elderly population (>65 years), cyan indicates people of working age (15-64 years), and magenta indicates children (0-14 years). Chroma and lightness components signify the distance from the centre ranging from desaturated and dark colours near the centre to vivid and bright colours at the corners. We provide R code to fully reproduce this map.<sup>16</sup>



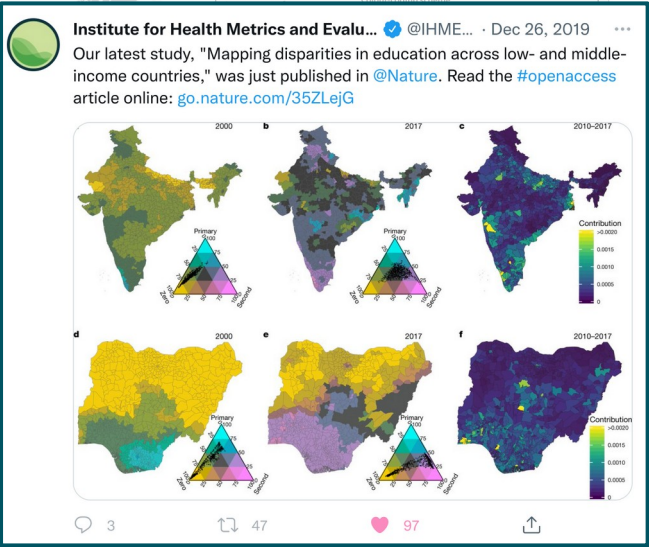
Income distribution in Canadian cities



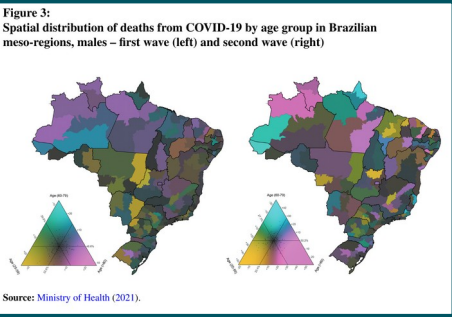
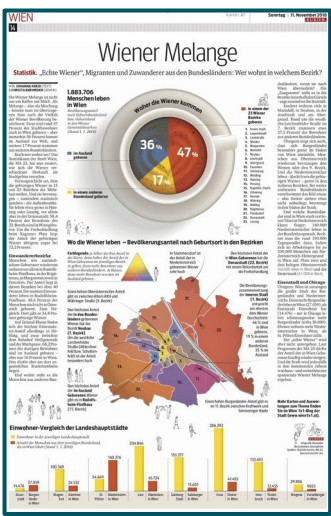
French election results



LMIC education disparity



Vienna's population by origin



Regional age distribution of COVID deaths In Brazil

Kashnitsky & Schöley (2018). Regional population structures at a glance. [10.1016/S0140-6736\(18\)31194-2](https://doi.org/10.1016/S0140-6736(18)31194-2)



## Agricultural and Forest Meteorology

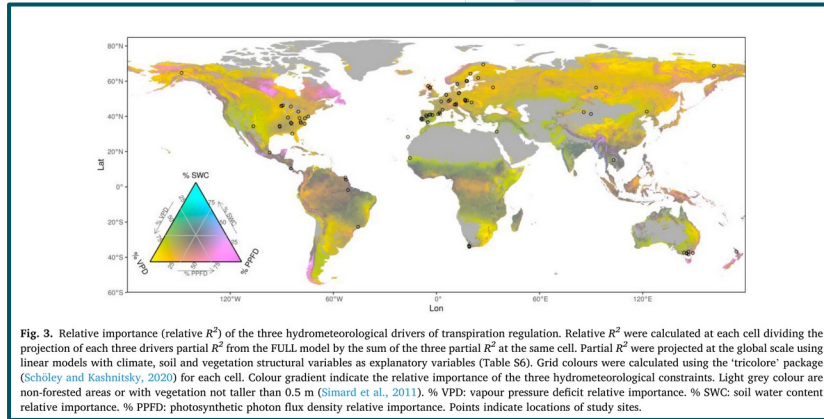
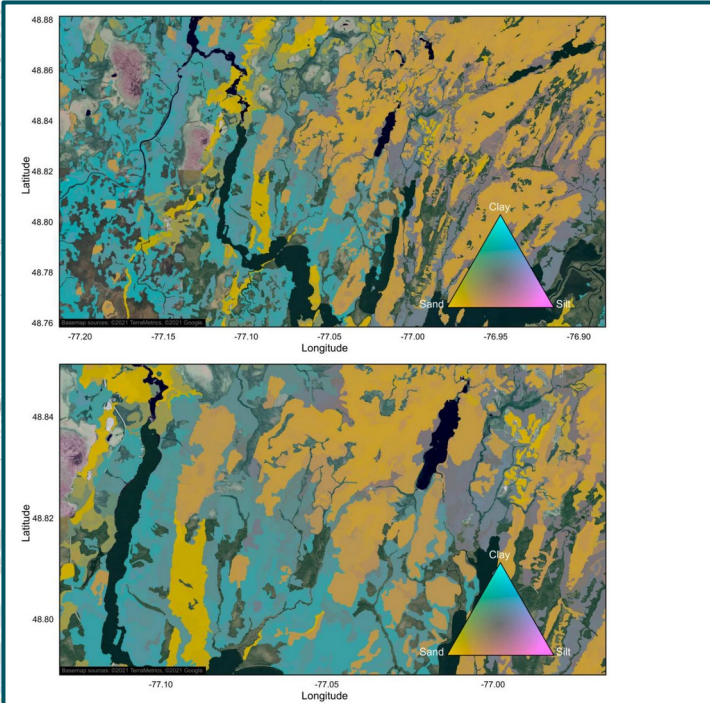


Figure: Colour-coded map of population structures in European Nomenclature of Territorial Units for Statistics 3 regions in 2018. Each population composition in the European Nomenclature of Territorial Units for Statistics 3 regions is uniquely colour coded. Colours represent the average age of the European population, and is dark grey. The hue component of a colour encode (>65 years), cyan indicates people of working age (15–64 years), and magenta indicates children (0–14 years). Chroma and lightness desaturated and dark colours near the centre to vivid and bright colours at the corners. We provide R code to fully reproduce this map.

## Soil composition



**Figure 8** Maps of soil texture composition at two zoom levels, for a region at the southern edge of the Abitibi and James Bay Lowlands soil province. Only productive forest land characterized by mineral soils was mapped. Agricultural and unproductive forest land, organic soils, anthropogenic infrastructures, and water areas were excluded. Maps were produced with QGIS software, version 3.4 (QGIS, 2020). Basemap credit: ©2021 TerraMetrics, ©2021 Google.

Full-size [DOI: 10.7717/peerj.11685/fig-8](https://doi.org/10.7717/peerj.11685/fig-8)

# Reproducible Demographers

Tim **Riffe** @timriffe1 & Enrique **Acosta** @Acosta\_Kike\_ &  
Manal **Elzalabany** & Maxi **Kniffka** @MaxiKniffka & Jessica **Donzowa** @jdonzowa

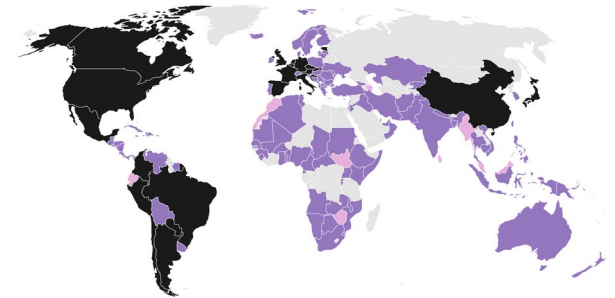


Created a fully reproducible data base of  
age specific COVID-19 statistics.

## Data availability

You can get the most up-to-date data at the [OSF](https://osf.io/mpwjq/) site that we mirror to: <https://osf.io/mpwjq/>.

Here's an overview of global coverage as of now. A country marked as *forthcoming* means we've identified a source, but that collection is pending for one reason or another. Are you from one of the countries not yet in the collection and want to pitch in? Are you interested in adopting collection for one of our time series that has fallen behind? We're in need of more support. Please reach out, if so by emailing us at [coverage-db@demogr.mpg.de](mailto:coverage-db@demogr.mpg.de).



■ National and subnational ■ National ■ Forthcoming ■ Not included yet

# Reproducible Demographers

Christina **Bohk**



Method00_FreezeRates
Method01_Hadwiger1940
Method02_CoaleMcNeil1972
Method03_CoaleTrussell1974
Method04_Brass1974
Method05_Evans1986
Method06_Chandola1999
Method07_Schmertmann2003
Method08_PeristeraKostaki2007M1
Method09_PeristeraKostaki2007M2
Method10_MyrskyläGoldstein2013
Method11_Saboia1977
Method12_WillekensBaydar1984
Method13_deBeer1985and1989
Method14_Lee1993Log
Method16_HyndmanUllah2007
Method17_ChengLin2010
Method18_Myrskylä2013
Method22_LiWu2003

Bohk et al. (2018). Forecast accuracy hardly improves with methods complexity when completing cohort fertility. [10.1109/5.771073](https://doi.org/10.1109/5.771073)

Implemented, shared and compared 22 fertility forecasting methods

[github.com/fertility-forecasting/validate-forecast-methods/tree/master/basic-scripts-forecast-methods](https://github.com/fertility-forecasting/validate-forecast-methods/tree/master/basic-scripts-forecast-methods)

# Reproducible Demographers

Rob Hyndman



Author of countless R packages widely applied in demography.



demography: Forecasting Mortality, Fertility, Migration and Population Data


Functions for demographic analysis including lifetable calculations; Lee-Carter modelling; functional data analysis of mortality rates, fertility rates, net migration numbers; and stochastic population forecasting.

Version: 1.22  
Depends: R ( $\geq 3.4$ ), [forecast](#) ( $\geq 8.5$ )  
Imports: [ftsa](#) ( $\geq 4.8$ ), [rainbow](#), [cobs](#), [mgcv](#), [strucchange](#), [RCurl](#)  
Published: 2019-04-22  
Author: Rob J Hyndman with contributions from Heather Booth, Leonie Tickle and John Maindonald.  
Maintainer: Rob J Hyndman <Rob.Hyndman@monash.edu>  
BugReports: <https://github.com/robjhyndman/demography/issues>  
License: [GPL-2](#) | [GPL-3](#) [expanded from: GPL ( $\geq 2$ )]  
URL: <https://github.com/robjhyndman/demography>  
NeedsCompilation: no  
Materials: [README](#) [ChangeLog](#)  
CRAN checks: [demography results](#)

[github.com/robjhyndman](https://github.com/robjhyndman)

# Consuming open science

🔑 main ▾    🔑 1 branch    🏷️ 0 tags    [Go to file](#)    [Code ▾](#)

 **akarlinsky** Local Mortality Update    d3a6d38 11 hours ago    ⌚ 579 commits

📁 local_mortality	Local Mortality Update	11 hours ago
📁 preliminary_mortality	Preliminary Mortality update	15 days ago
📄 .gitignore	Update .gitignore	5 months ago
📄 LICENSE	Create LICENSE	11 months ago
📄 README.md	2022-06-07 Update	9 days ago
📄 coverage_map_title.png	Update coverage_map_title.png	2 months ago
📄 world_mort_plot_all.png	2022-06-10 Update	6 days ago
📄 world_mortality.csv	2022-06-10 Update	6 days ago

Karlinsky & Kobak (2022). World Mortality Database. [github.com/akarlinsky/world\\_mortality](https://github.com/akarlinsky/world_mortality)



# Consuming open science

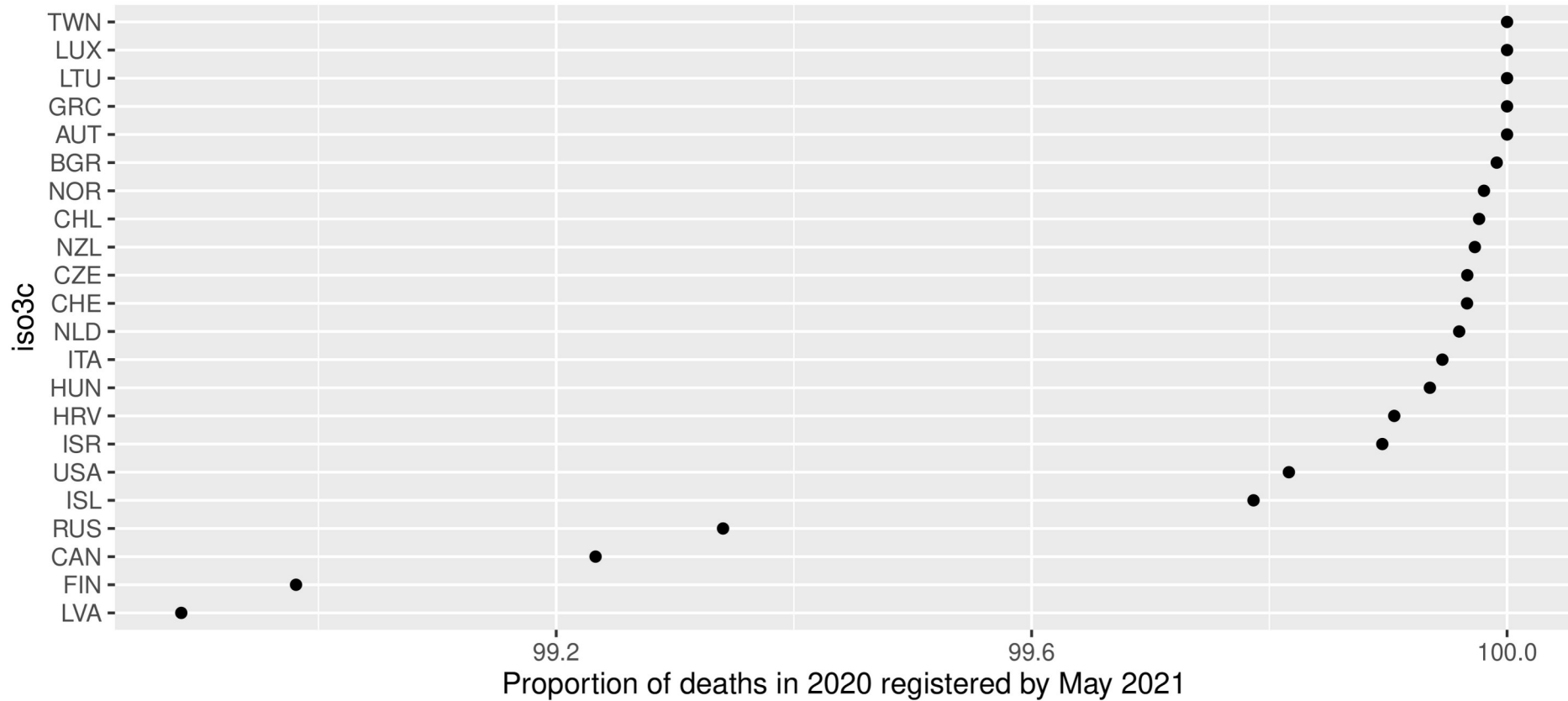
The screenshot shows the GitHub repository page for 'akarlinsky Local Mortality Update'. The repository has 1 branch and 0 tags. The file list on the left includes:

- local\_mortality (Local Mortality Update)
- preliminary\_mortality (Preliminary Mortality update)
- .gitignore (Update .gitignore)
- LICENSE (Create LICENSE)
- README.md (2022-06-07 Update)
- coverage\_map\_title.png (Update coverage\_map\_title.p)
- world\_mort\_plot\_all.png (2022-06-10 Update)
- world\_mortality.csv (2022-06-10 Update)

The commit history on the right shows a series of updates by 'akarlinsky' committed 22 days ago, 24 days ago, and 29 days ago. A red box highlights the commit history, and a red line connects it to a '579 commits' badge on the right.

Karlinsky & Kobak (2022). World Mortality Database. [github.com/akarlinsky/world\\_mortality](https://github.com/akarlinsky/world_mortality)

# Consuming open science



Derived from Karlinsky & Kobak (2022). World Mortality Database.  
[github.com/akarlinsky/world\\_mortality](https://github.com/akarlinsky/world_mortality)

Given **your data** and **your analysis**  
I arrive at **your results**

---

Given **your research question**,  
**my data** and **my analysis**  
I arrive at **your results**

# Implementing reproducibility & replicability

**Ensure everyone  
can run your  
analysis**



**Share and version  
your analysis**



**Share your data  
Archive your data  
Get DOIs**



# The computational reproducibility stack

Ensure everyone  
can run your  
analysis



**Scripts & Data**

**R Libraries**

**System dependencies**

**Hardware**





# The computational reproducibility stack

Ensure everyone  
can run your  
analysis



Scripts & Data

R Libraries

System dependencies

Hardware



# The computational reproducibility stack

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analysis

## Scripts & Data



```
Warning message:
“`funs()` was deprecated in dplyr 0.8.0.
i Please use a list of either functions or lambdas:

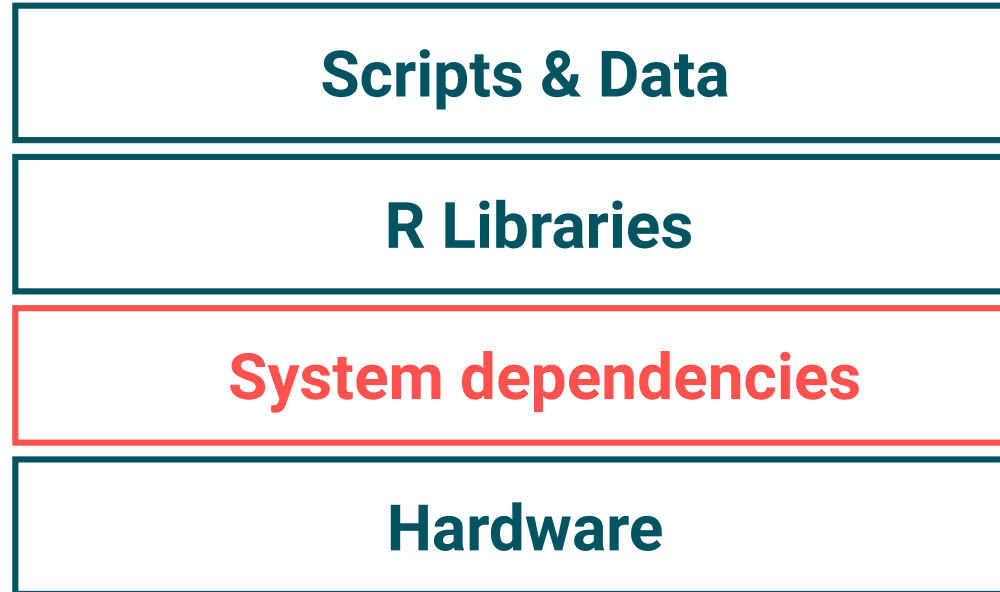
# Simple named list: list(mean = mean, median = median)

# Auto named with `tibble::lst()`: tibble::lst(mean, median)

# Using lambdas list(~ mean(., trim = .2), ~ median(., na.rm = TRUE)
i The deprecated feature was likely used in the dataiku package.
Please report the issue to the authors.”
```

# The computational reproducibility stack

Ensure everyone  
can run your  
analysis



# The computational reproducibility stack

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can run your  
analysis

## Scripts & Data



```
Error in stop_no_virtualenv_starter(version = version, python =  
python) :  
  Suitable Python installation for creating a venv not found.  
  Requested Python: /usr/bin/python3.10  
  Requested version constraint: 3.10  
Please install Python with one of following methods:  
- https://github.com/rstudio/python-builds/  
- reticulate::install_python(version = '<version>')  
- Install python3-venv and python3-pip using the system package  
anager
```



# The computational reproducibility stack

Ensure everyone  
can run your  
analysis



Scripts & Data

R Libraries

System dependencies

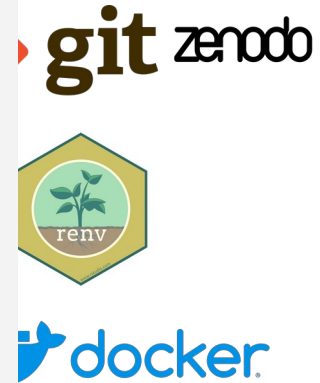
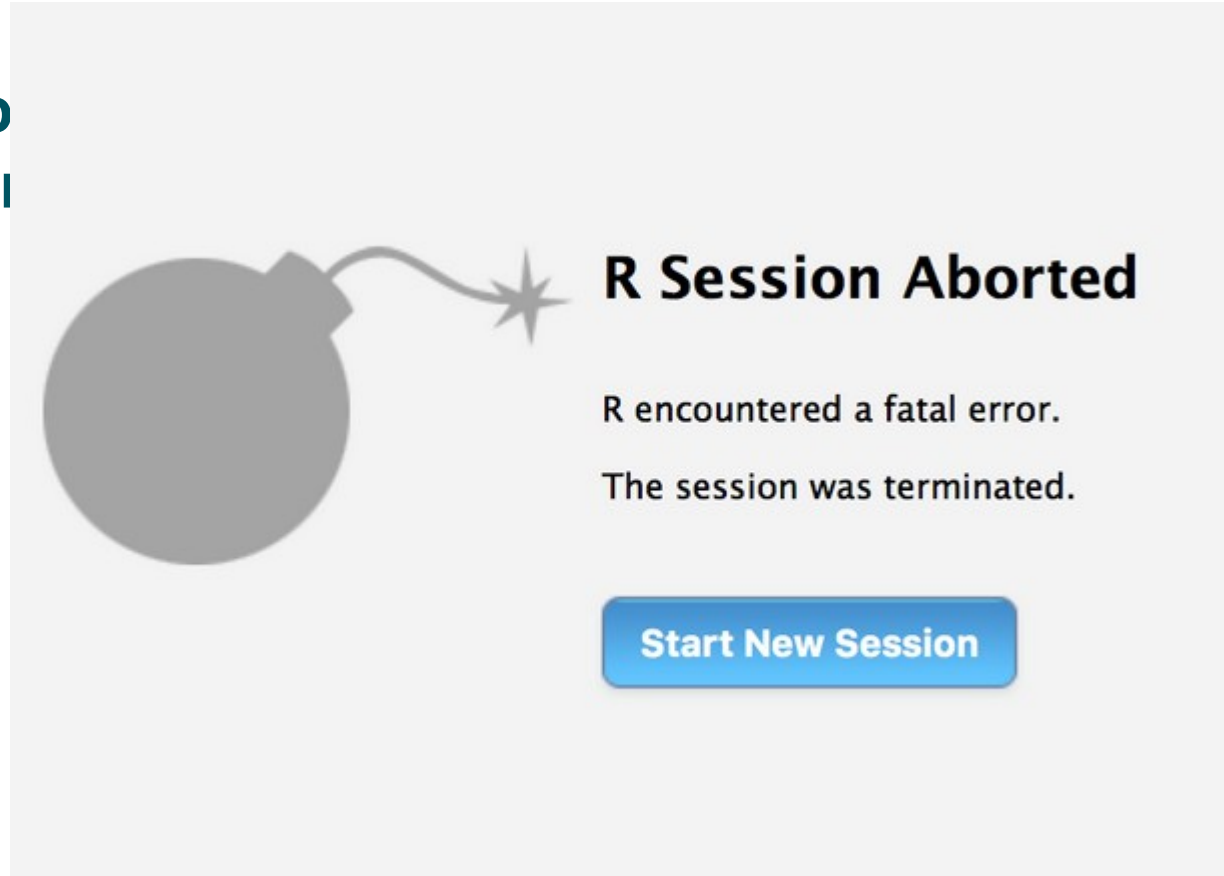
Hardware





# The computational reproducibility stack

Ensure everyone  
can run your  
analysis



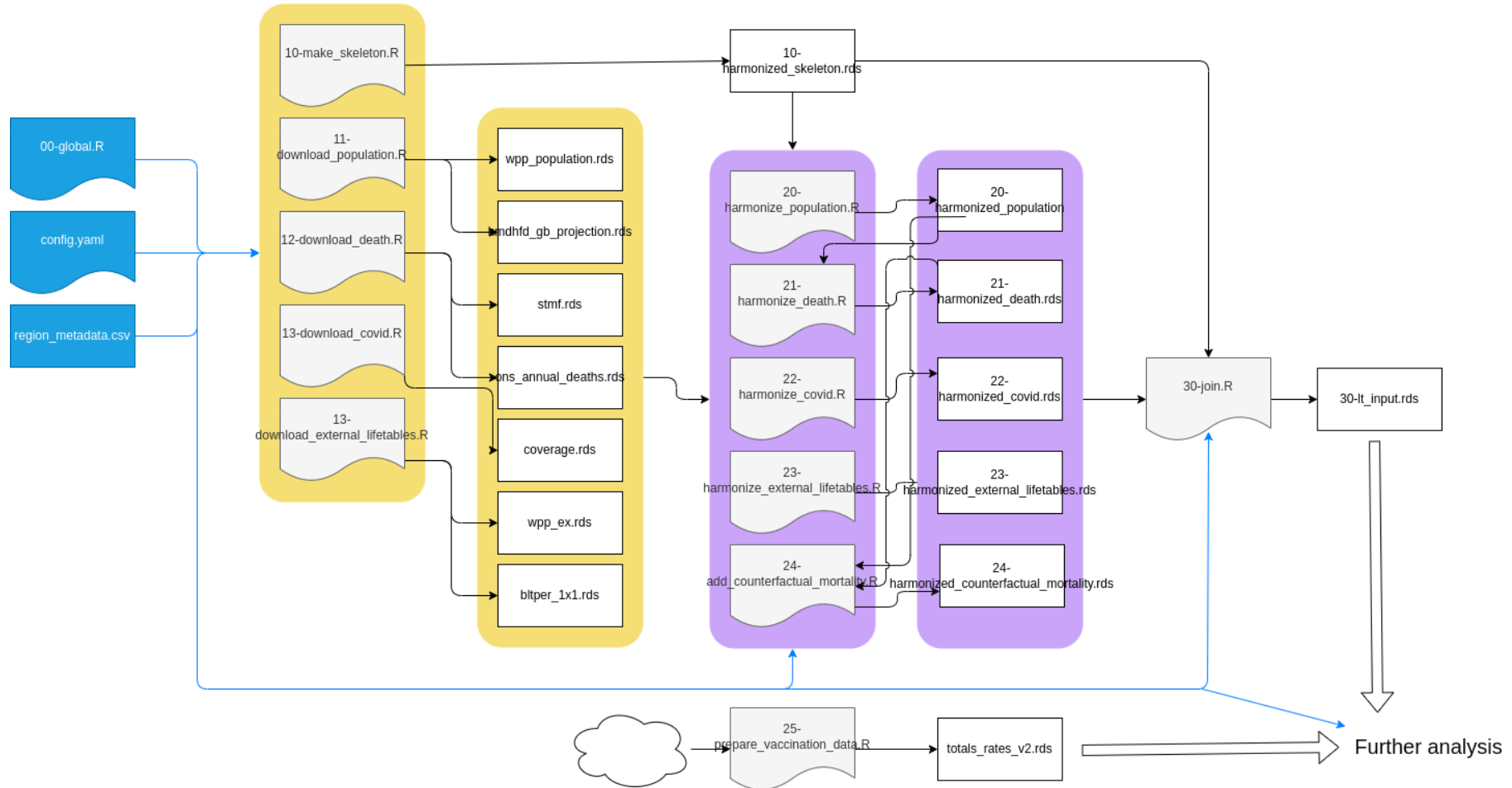
# **Demonstrating the reproducible workflow**

## Sharing a statistical model

# **Demonstrating the reproducible workflow**

## Life expectancy changes in 2021

# The dependency graph



**Roadblocks to open science**  
I can't share my data



# **Roadblocks to open science**

## My code sucks

**Roadblocks to open science**  
Others will copy my stuff

**Roadblocks to open science**  
My co-authors are not on-board

# Reproducible analysis

[github.com/jschoeley](https://github.com/jschoeley)

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