

16th Meeting of the Hamburg R-User-Group, 13th Feb 2019

Project „easystats“ Making R stats easier!

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<https://github.com/easystats>

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Dominique



Neuropsychologist,
psychotherapist, pizza lover 🍕

Postdoc at the Clinical Brain Lab
(Singapore) on the neuroscience
of deception

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Daniel



Gerontologist, kind of
sociologist, prefers burgers 🍔

Postdoc at the Department of
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Medical Center Hamburg)



Objectives

- Provide a set of packages that makes it easier to do statistical analysis and reporting with R.
 - Low-level (or „core“) packages
 - Target group: advanced users and developers
 - Aims (examples): accessor functions to access the internals of models, such as variables, formulas, model frame/data, random effects, their structure and so on...



Objectives

- Provide a set of packages that makes it easier to do statistical analysis and reporting with R.
 - Mid-level packages
 - Target group: end-user
 - Aims (examples): computation of model "performance" metrics (R^2 , ICC, CoD, AIC, BIC and whatnot), model comparison, Bayesian analysis, ...



Objectives

- Provide a set of packages that makes it easier to do statistical analysis and reporting with R.
- High-level packages
 - Target groups: non-experts/beginners who want fully-baked solutions to solve their problems and to experience the power of R
 - Aims: reporting, plotting



Objectives

- Provide a set of packages that makes it easier to do statistical analysis and reporting with R.



And most important!

- All packages, especially the low-level packages, should run with minimum dependencies!

```
Version: 0.1.0.0001
Date: 2019-01-29
Authors@R: c(person("Daniel", "Lüdecke", role = c("aut", "cre"), email = "d.luedecke@uke.de", comment =
c(ORCID = "0000-0002-8895-3206")),
            person("Dominique", "Makowski", role = c("ctb"), email = "dom.makowski@gmail.com", comment =
c(ORCID = "0000-0001-5375-9967")))
Maintainer: Daniel Lüdecke <d.luedecke@uke.de>
License: GPL-3
URL: https://github.com/easystats/insight
Depends: R (>= 3.2), stats and no imports!
Suggests: brms, GLMMadaptive, glmmTMB, knitr, lme4, nlme, splines,
          testthat
Encoding: UTF-8
LazyData: true
RoxygenNote: 6.1.1
VignetteBuilder: knitr
Author: Daniel Lüdecke [aut, cre] (<https://orcid.org/0000-0002-8895-3206>),
        Dominique Makowski [ctb] (<https://orcid.org/0000-0001-5375-9967>)
Built: R 3.5.2; ; 2019-02-04 08:08:22 UTC; windows
```


A first low-level package...

insight

Model objects are terrifying

```
# model frame?

library(nlme)

m <- gls(
  follicles ~ sin(2*pi*Time) +
  cos(2*pi*Time), Ovary,
  correlation = corAR1(form = ~ 1 | Mare)
)

model.frame(m)
#> corStruct parameters:
#> [1] 1.960656
```



Model objects are terrifying

```
# model family?

fm1 <- lme(
  distance ~ age, data = Orthodont
)

family(fm1)
#> Error in UseMethod("family") :
#>   no applicable method for 'family'
#>   applied to an object of class "lme"
```



Model objects are terrifying

```
# model terms?

library(MCMCglmm)
data(PlodiaPO)

m <- MCMCglmm(
  PO~1, random=~FSfamily, data=PlodiaPO,
  verbose=FALSE, nitt=1300, burnin=300,
  thin=1
)

all.vars(terms(m))
#> Error in terms.default(m) : no
#> terms component nor attribute
```





Gain insight into your models!

Gain insight into your models!

- Thanks to a stunning **x-ray-technology**, the *insight*-package allows to easily get insights into your model object!



Gain insight into your models!

- Simple, consistent API:
 - `get_*()` to retrieve data, `find_*()` to access model information.



Objectives

- The goal of this package is to provide tools that make it **easy** and **intuitive** to access information contained in various models.
- Although there are generic functions to get information and data from models, many modelling-functions from different packages do not provide such methods to access these information.
- *insight* aims at closing this gap by providing **consistent** functions that work for (almost) any models.

I'm afraid of no model

```
library(insight)
library(nlme)

m <- gls(
  follicles ~ sin(2*pi*Time) +
  cos(2*pi*Time), Ovary,
  correlation = corAR1(form = ~ 1 | Mare)
)

get_data(m)
#>      Mare      Time follicles
#> 1      1 -0.13636360      20
#> 2      1 -0.09090910      15
#> 3      1 -0.04545455      19
#> ... (truncated)
```



I'm afraid of no model

```
library(MCMCglmm)
data(PlodiaP0)
m <- MCMCglmm(
  P0~1, random=~FSfamily, data=PlodiaP0,
  verbose=FALSE, nitt=1300, burnin=300,
  thin=1
)

find_terms(m)
$response
[1] "P0"

$conditional
[1] 1

$random
[1] "FSfamily"
```



I'm afraid of no model

```
library(GLMMadaptive)

m <- mixed_model(
  count ~ child + camper,
  random = ~ 1 | persons,
  zi_fixed = ~ child + livebait,
  zi_random = ~ 1 | persons,
  data = fish,
  family = zi.poisson()
)

find_predictors(m, component = "zi")
#> $zero_inflated
#> [1] "child"      "livebait"
```





Tell others about your research!

Objectives

- Higher-level package.
- *report*'s primary goal is to fill the gap between R's output and the formatted result description of your manuscript, with the automated use of best practices guidelines.
- This ensures standardization and quality of reporting research results.

From R to Manuscript

■ Short form summary:

```
lm(Sepal.Length ~ Species, data=iris) %>%  
  report()
```

```
## We fitted a linear model to predict Sepal.Length with Species.  
## The model's explanatory power (R2) is of 0.62 (adj. R2 = 0.61).  
## The model's intercept is at 5.01.
```

```
## Within this model:  
## - Speciesversicolor is significant (beta = 0.93,  
##   95% CI [0.73, 1.13], p < .001) and large (Std. beta = 1.12).  
## - Speciesvirginica is significant (beta = 1.58,  
##   95% CI [1.38, 1.79], p < .001) and large (Std. beta = 1.91).
```

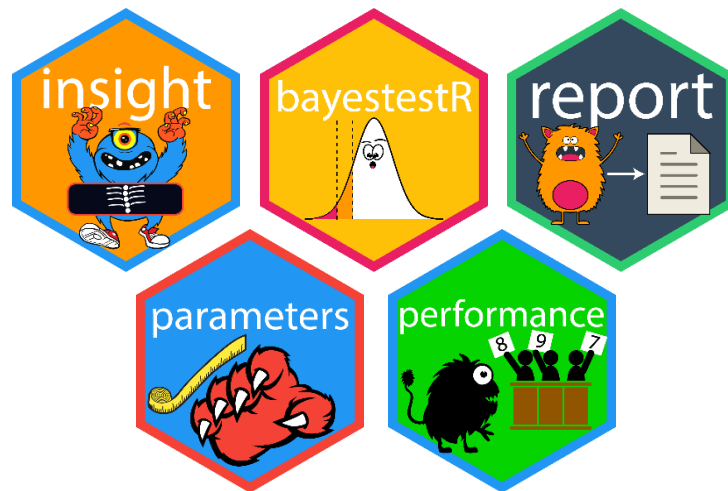


easystats



Want to join us?

<https://github.com/easystats>



And many more packages to come...

Dominique & Daniel





Want to join us?

<https://github.com/easystats>

We are...

- ✓ waiting for your feedback
- ✓ open to opinions and ideas
- ✓ beginning-developers friendly

Dominique & Daniel

