brms: An R Package for Bayesian Multilevel Models using Stan

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Agenda

- 1 Short introduction to Stan
- 2 The brms package
 - Model Specification
 - Model Fitting
 - Post-Processing
- 3 Discussion



Stan Overview

- Probabilistic programming language...
- ... to fit open-ended Bayesian Models
- Powerful sampling algorithms: HMC and NUTS
- Automatic differentiation library
- Runs on all major platforms (Windows, OS X, Linux)
- Can be called from R, Python, Julia, Stata, and Matlab

Stan code for simple linear regression

```
1 data {
    int<lower=1> N; // number of observations
2
   vector[N] Y; // response variable
   int<lower=1> K; // number of fixed effects
    matrix[N, K] X; // FE design matrix
5 l
6
  parameters {
8
   vector[K] b; // fixed effects
    real<lower=0> sigma; // residual SD
10 }
11 transformed parameters {
    vector[N] eta; // linear predictor
12
    eta <- X * b;
13
14 }
15 model {
16
    // prior specifications
   sigma ~ student_t(3, 0, 100);
17
18 // likelihood contribution
    Y ~ normal(eta, sigma);
19
20 }
```

The idea of brms

Make Stan usable for a wider range of audience

- use R formula syntax
- internally write Stan code that is readable yet fast
- provide an easy interface for defining priors
- facilitate post-processing

Some features of brms

Basic model types:

- (Robust multivariate) linear models
- Count data models
- Categorical and ordinal models
- Survival models
- Zero-inflated and hurdle models
- Non-linear models

Other modeling options:

- Group specific terms (random effects) using Ime4 syntax
- Residual autocorrelation
- censored / truncated data



Example: Censored survival regression

```
brm(time | cens(censored) ~ age * sex + (1 + age|patient),
data = kidney, family = exponential())
```

Let's add some priors:

```
brm(time | cens(censored) ~ age * sex + (1 + age|patient),

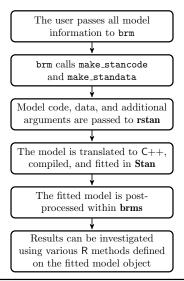
data = kidney, family = exponential(),

prior = c(set_prior("normal(0,5)", class = "b"),

set_prior("cauchy(0,2)", class = "sd"),

set_prior("lkj(2)", class = "cor")))
```

Flow chart of the model fitting procedure

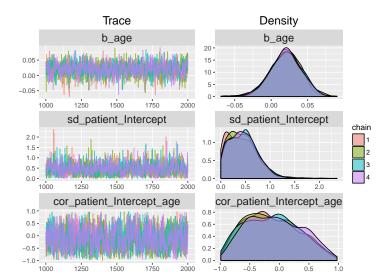


Example: Summary

```
Family: exponential (log)
2 Formula: time | cens(censored) ~ age * sex + (1 + age | patient)
    Data: kidney (Number of observations: 76)
  Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup samples = 4000
5
   WATC: 668.22
6
7
8 Random Effects:
9 ~patient (Number of levels: 38)
                  Estimate Est.Error 1-95% CI u-95% CI Eff.Sample Rhat
10
11 sd(Intercept)
                   0.45 0.30 0.02 1.07 1172 1.00
12 sd (age)
                   0.01 0.01 0.00 0.03 450 1.01
13 cor(Intercept, age) -0.12 0.45 -0.87 0.77 1133 1.00
14
15 Fixed Effects:
16
             Estimate Est.Error 1-95% CI u-95% CI Eff.Sample Rhat
17 Intercept 2.91
                         0.93
                             1.22
                                        4.85
                                                  1636
18 age
              0.02
                        0.02 -0.02 0.06
                                                 1527
19 sexfemale 2.76
                        1.07 0.59 4.77
                                                 1578
20 age:sexfemale -0.03 0.02 -0.08 0.02
                                                  1478
```

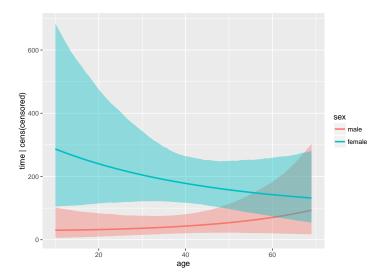


Example: Trace and density plots



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Example: Marginal plots

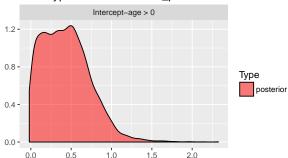


Post-Processing



Example: Hypothesis Testing

Hypothesis for class sd_patient



Plans for the future

- Full support for multivariate models
- Spatial correlation structures
- Generalized additive multilevel models
- Mixture distributions

Your ideas are always welcome!



Learn more about brms and Stan

- Help within R: vignette("brms") or help("brms")
- List of all applicable methods: methods (class = "brmsfit")
- Website of brms: https://github.com/paul-buerkner/brms
- Website of Stan: http://mc-stan.org/
- Contact me: paul.buerkner@gmail.com

Thank you for your attention! Questions?