Bayesian meta-analysis in Stan with \textit{baggr}
baggr

*baggr* (Bayesian aggregator): Bayesian meta-analysis in R with Stan

Overall goals:

1. Implement all basic meta-analysis models and tools
2. Focus on accessibility, model criticism and comparison
3. Help people avoid basic mistakes
4. Keep the framework flexible and extend to more models

(Probably) *not* our goal:

5. Build a package for people who already build their models in Stan

*baggr* v0.7 beta is on CRAN and GitHub
Features

- Continuous and categorical data
- “Hand-holding” approach (don’t assume users know what they’re doing)
- Meta-analytic workflow (data preparation, p.p. checking, LOO CV)
- Allows summary and individual-level data
- Meta-regression
- Plain language prior definitions (like rstanarm)
Development

Next (?):

Driven largely by suggestions from users.

- Port to command-line Stan
- More flexible (formula-driven?) definition of REs
- Modeling more parameters (mixtures, variances, quantiles)
- Working with counts and (parameteric/Cox) survival
  - Survival models already programmed by RAs at UChicago
- BYO? (part of the wider workflow effortit)

Some health-specific applications for m-a:

- Dealing with small samples (e.g. chemical risk assessment)
- “Model-based” meta-analysis (PK/PD modeling drug development)
- Network meta-analysis / ITC (health technology assessment)
Example (8 schools!)

We use a familiar summary-level dataset from Rubin (1981). Individual-level data works just as well.

```
library(baggr)
schools
```

<table>
<thead>
<tr>
<th>group</th>
<th>tau</th>
<th>se</th>
</tr>
</thead>
<tbody>
<tr>
<td>School A</td>
<td>28</td>
<td>15</td>
</tr>
<tr>
<td>School B</td>
<td>8</td>
<td>10</td>
</tr>
<tr>
<td>School C</td>
<td>-3</td>
<td>16</td>
</tr>
<tr>
<td>School D</td>
<td>7</td>
<td>11</td>
</tr>
<tr>
<td>School E</td>
<td>-1</td>
<td>9</td>
</tr>
<tr>
<td>School F</td>
<td>1</td>
<td>11</td>
</tr>
<tr>
<td>School G</td>
<td>18</td>
<td>10</td>
</tr>
<tr>
<td>School H</td>
<td>12</td>
<td>18</td>
</tr>
</tbody>
</table>
baggr syntax example: simple model workflow

```r
# Fitting function is baggr()
fitted_model <- baggr(schools, model = "rubin", pooling = "partial",
                   prior_hypermean = normal(0, 25), prior_hypersd = uniform(0, 100))

# Semi-automatic prior choice, automatic model choice (with prompts):
eff_lab <- "mean SAT improvement"
fitted_model_c <- baggr(schools, prior_hypersd = cauchy(0, 50), effect = eff_lab)
fitted_model_n <- baggr(schools, prior_hypersd = normal(0, 10), effect = eff_lab)
fitted_model_u <- baggr(schools, prior_hypersd = uniform(0, 100),
                        prior_hypermean = normal(-5, 10), effect = eff_lab)

# Plot results for one model, making use of bayesplot
baggr_theme_update(text = element_text(family = "mono"))
plot(fitted_model_c, style = "areas", hyper = TRUE, order = TRUE)

# Compare fit to data
baggr_compare(what = "pooling")
plot(bgc)

# Compare posterior predictive distribution (note ggplot)
effect_plot("Cauchy" = fitted_model_c, "Normal" = fitted_model_n, "Uniform" = fitted_model_u) + xlim(-10, 30)

# Compare the impact of different prior choices
baggr_compare(what = "pooling")
plot(bgc)

# Use LOO cross-validation to choose between partial & full pooling
loo_partial <- loocv(schools, pooling = "partial")
loo_full <- loocv(schools, pooling = "full")
loo_compare(loo_partial, loo_full)
```

Bayesian meta-analysis in Stan with baggr
## Model type: Rubin model with aggregate data
## Pooling of effects: partial
##
## Aggregate treatment effect (on mean SAT improvement):
## Hypermean (tau) = 7.9 with 95% interval -1.8 to 17.8
## Hyper-SD (sigma_tau) = 6.28 with 95% interval 0.22 to 19.58
## Total pooling (1 - I^2) = 0.8 with 95% interval 0.3 to 1.0
##
## Treatment effects on mean SAT improvement:
##
<table>
<thead>
<tr>
<th>School</th>
<th>mean</th>
<th>sd</th>
<th>2.5%</th>
<th>50%</th>
<th>97.5%</th>
<th>pooling</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>11.2</td>
<td>8.2</td>
<td>-2.26</td>
<td>10.1</td>
<td>31</td>
<td>0.83</td>
</tr>
<tr>
<td>B</td>
<td>7.9</td>
<td>6.2</td>
<td>-4.34</td>
<td>7.8</td>
<td>21</td>
<td>0.73</td>
</tr>
<tr>
<td>C</td>
<td>6.1</td>
<td>7.6</td>
<td>-11.2</td>
<td>6.6</td>
<td>20</td>
<td>0.85</td>
</tr>
<tr>
<td>D</td>
<td>7.6</td>
<td>6.4</td>
<td>-5.57</td>
<td>7.6</td>
<td>21</td>
<td>0.76</td>
</tr>
<tr>
<td>E</td>
<td>5.2</td>
<td>6.3</td>
<td>-9.09</td>
<td>5.7</td>
<td>16</td>
<td>0.70</td>
</tr>
<tr>
<td>F</td>
<td>6.2</td>
<td>6.7</td>
<td>-8.67</td>
<td>6.6</td>
<td>18</td>
<td>0.76</td>
</tr>
<tr>
<td>G</td>
<td>10.6</td>
<td>6.7</td>
<td>-0.87</td>
<td>10.0</td>
<td>26</td>
<td>0.73</td>
</tr>
<tr>
<td>H</td>
<td>8.4</td>
<td>7.7</td>
<td>-6.79</td>
<td>8.2</td>
<td>25</td>
<td>0.87</td>
</tr>
</tbody>
</table>
plot(fit_c, style = "areas", hyper = TRUE, order = TRUE)

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mean SAT improvement

model Cauchy Normal Uniform

mean SAT improvement

Treatment effect (95% interval)
effect_plot("Cauchy" = fit_c, "Normal" = fit_n, "Uniform" = fit_u) +
coord_cartesian(xlim = c(-10, 30)) +
ggtitle("Posterior predictive", "Treatment effect in a new school")
bgc_pooling <- baggr_compare(schools, prior_hypersd = normal(0, 10),
what = "pooling")
plot(bgc_pooling)
loo_p <- loocv(schools, pooling = "partial")
loo_f <- loocv(schools, pooling = "full")
loo_compare(loo_p, loo_f)

## Comparison of cross-validation
##
## ELPD ELPD SE
## Model 1 - Model 2 -0.754 0.33

Additional commands:

treatment_effect(fit)
group_effects(fit)
effect_draw(fit)
forest_plot(fit)
pooling(fit)