BayesCombo: A Quick Guide

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Introduction

Scientists often evaluate theories or draw conclusions by combining results from multiple experiments. The experiments and the measured outcomes are usually diverse, making a meta-analyses inappropriate, and researchers therefore base conclusions on the number of p-values that are are in line with hypotheses. P-values, however, are a poor way of integrating results, and since statistical power is often low, "conflicting results" are common. Informal methods of evaluating a series of experiments makes inefficient use of the data and can lead to incorrect conclusions and poor decisions. Here we show how to combine diverse evidence across diverse experiments based on a method developed by Kuiper et al.[1].

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Usage

The required inputs are coefficients and their standard errors obtained from the output of `lm()` and `glm()` functions (e.g. from ANOVAs, t-tests, or regressions with Gaussian, Poisson, or binomial outcomes). It's up to the user to ensure that the data being combined are testing the same overall hypothesis or theory. In addition, the direction of the effects should be aligned; for example, if a positive effect size in one study is interpreted as supporting a theory, but a negative effect size in another study also supports the theory, then the negative effect should be multiplied by -1 to change its direction.

The Bayes factors are not used directly but only as an intermediate step to calculate the probability that the true effect size is less than zero, greater than zero, or exactly zero. These three probabilities are called the posterior model probabilities (PMPs), where a model corresponds to one of the three effects.

Posterior probability for a single study

The figure below plots the raw data for an experiment where 20 rats were randomised to one of four treatment groups (dose of the antidepressant fluoxetine given in the drinking water).

```
library(labstats)
lattice::xyplot(time.immob ~ dose, data=fluoxetine, type=c("g","p","r"))
```
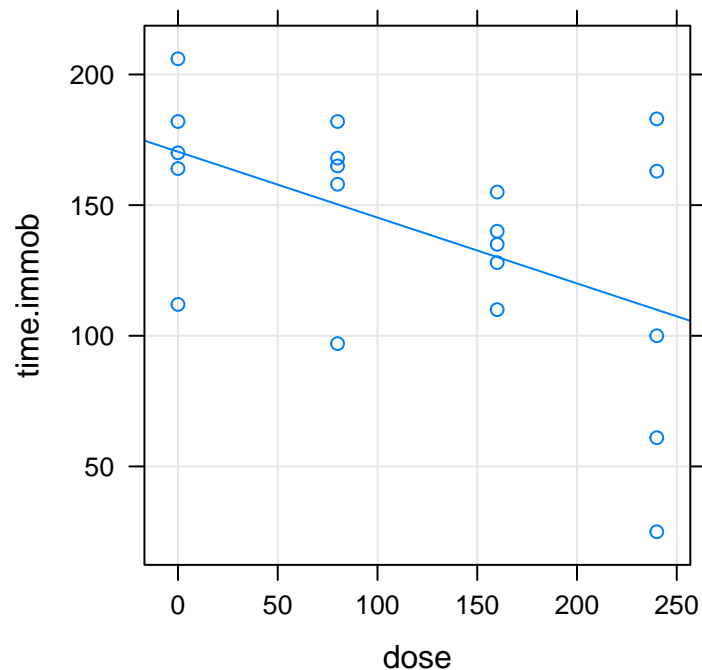
Suppose we conduct a simple experiment with a difference between groups of -0.252 and a standard error of 0.099. We can calculate the probability that this difference is negative, positive, or zero, using the `pmp()` function. Below, the default settings are used and the output shows that the probability that the difference is negative (`H<`) is 0.92, that it is positive (`H>`) is 0.01, and that it is exactly zero (`H0`) is 0.08.

```
summary(lm(time.immob ~ dose, data=fluoxetine))$coef
```

```
##              Estimate Std. Error  t value     Pr(>|t|)
## (Intercept)  170.440 14.8368131 11.48764 1.01541e-09
## dose          -0.252  0.0991326 -2.54205 2.04365e-02
```

```
x <- pmp(beta = -0.252, se.beta = 0.099, percent=95)
summary(x)
```

```
##     H<     H0     H>
## 0.915 0.076 0.009
```

The plot below shows the data, the default prior, and the posterior distributions. The mean of the data (dotted line) is centred on -0.252 and the standard error determines the width of this distribution. The `pmp()` function calculates a default prior with a mean of zero and variance such that the 99% confidence interval (CI) of the prior matchs the 99% CI of the data distribution. The PMPs are then calculated from these prior and posterior distributions.

```
par(las=1)
plot(x, leg.loc = "topright")
```
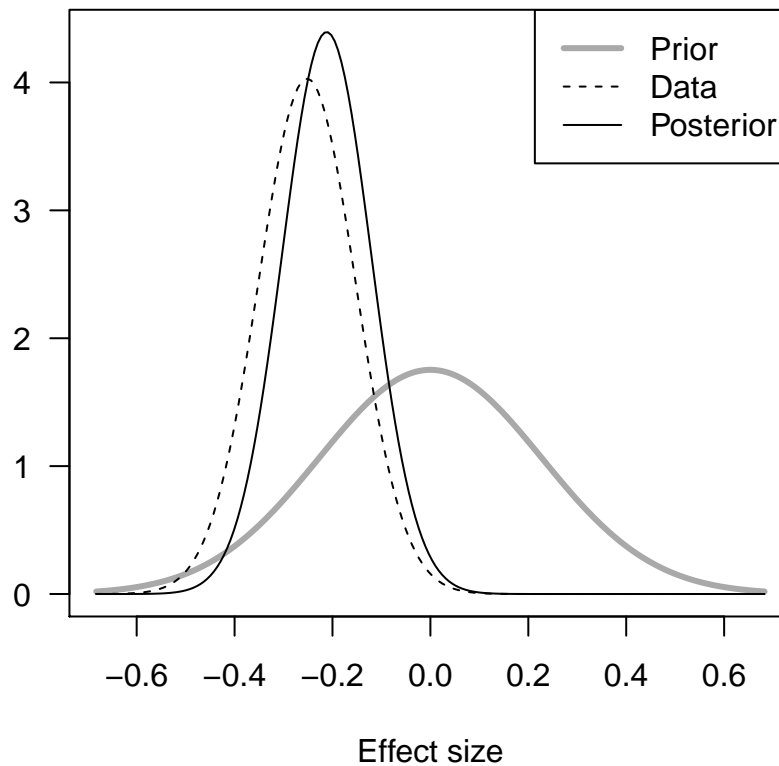
The above default prior may be more informative than desired (note how the posterior is pulled towards the prior) and the easiest way to decrease the influence of the prior is to make it wider by specifying a variance multiplier. The code below doubles the previous variance (`var.mult = 2`), and the posterior is now much closer to the data distribution. However, the PMPs have not changed much, rounded to two decimal places the probability that the difference is negative is still 0.92.

```
x2 <- pmp(beta = -0.252, se.beta = 0.099, var.mult = 2)
summary(x2)
```

```
##     H<     H0     H>
## 0.9051 0.0887 0.0062
```

```
par(las=1)
plot(x2, leg.loc = "topright")
```
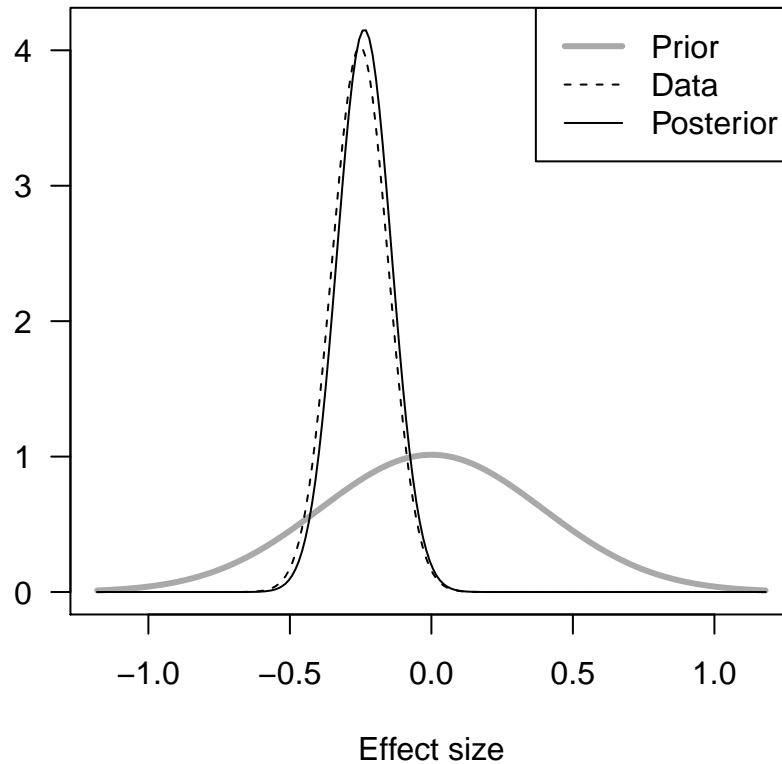
Posterior probability for multiple studies

PMPs from several studies can be combined to `pmp.combo()` is the main analysis function and only requires the effect sizes (`beta`) and their standard errors (`se.beta`) as input. The default prior mean (`beta0 = 0`) is suitable for most analyses, as is the equal prior model probabilities (`mod.priors = c(1/3, 1/3, 1/3)`) for each model (positive, negative, or zero difference). In the example below, assume we have four clinical trials where positive effect sizes indicate a beneficial effect of a treatment.

```
x <- pmp.combo(beta = c(2.3, 1.2, 0.2, 0.44),
               se.beta = c(1.03, 0.75, 0.16, 0.28))
```

Plotting a `PMPlist` object generates a graph resembling a forest plot, with the observed effect sizes and their 99% CI (black)[CHECK] and the prior effect sizes (usually zero) and their variances (red). All four studies have positive effect sizes but only the first study is significant at the usual 0.05 level.

```
par(las=1)
forestplot(x)
abline(v=0, lty=2)
```
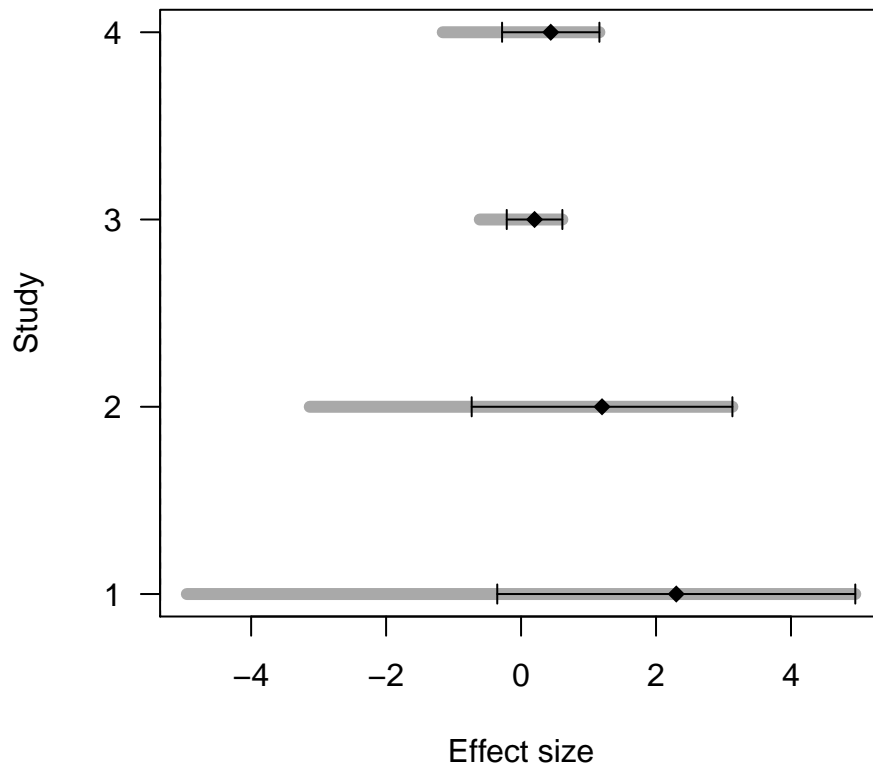
A summary of the results shows how the support for the three hypothesis changes as each study is added. For example, in the output below we see that when only the first study is included (first column) the probability that the effect size is greater than zero (`H:>`) is about 85%. As more studies are included, the probability increases to 98%, and the null has only 1.8% support.
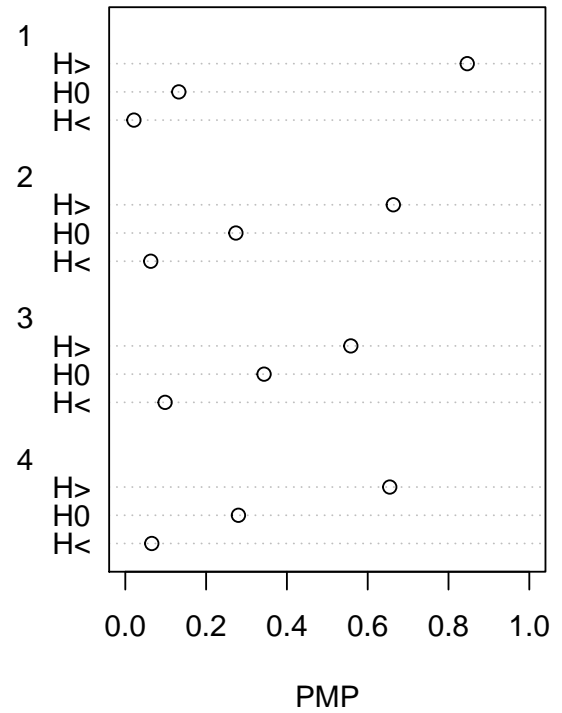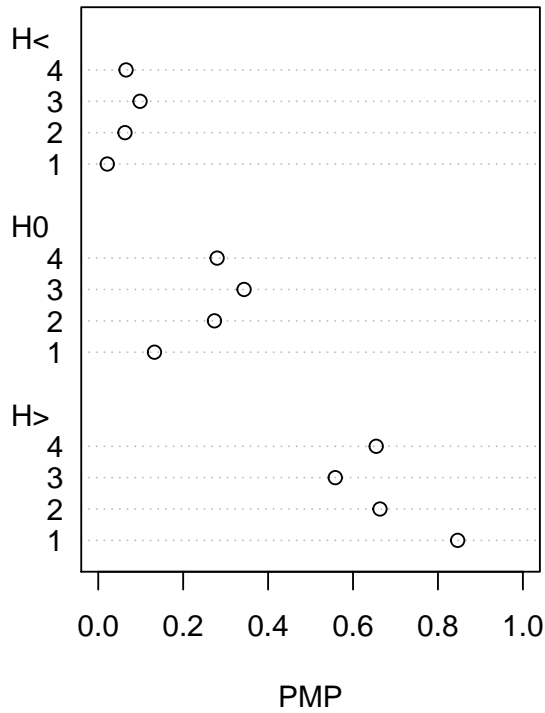
```
summary(x)
```

```
##           H<      H0      H>
## [1,] 0.3333 0.3333 0.3333
## [2,] 0.0213 0.1324 0.8464
## [3,] 0.0022 0.0605 0.9373
## [4,] 0.0004 0.0382 0.9614
## [5,] 0.0000 0.0167 0.9833
```

It is easier to see how these probabilities change as studies are added with a graph.

```
par(las=1)
plot(x)
```
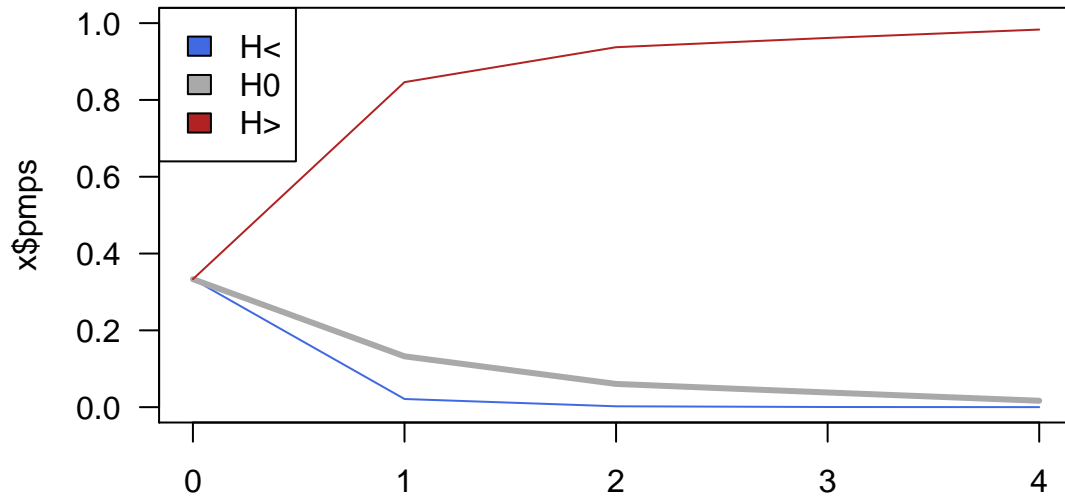
```
par(mfrow=c(1,2))
dotchart(x$pmp.uniform, xlim=c(0,1), xlab="PMP")
dotchart(t(x$pmp.uniform), xlim=c(0,1), xlab="PMP")
```


References

[1] Kuiper RM, Buskens V, Raub W, Hoijtink H (2012). Combining statistical evidence from several studies: A method using Bayesian updating and an example from research on trust problems in social and economic exchange. **Sociological Methods and Research** 42(1) 60-81.