Supplement to "Improving the Transparency of Meta Analyses with Interactive Web Applications"

This resource serves as a guide for replicating a selection of the meta-analyses reported in Table 2 of our paper using the web application available at:

http://galaxy.med.uvm.edu:3838/thomasahern/2d6meta/

or

https://tpahern.shinyapps.io/2d6meta

A conventional (frequentist) random-effects meta-analysis

In Table 2 of our paper, we report the conventional meta-analysis of studies reporting associations between CYP2D6 impairment and disease-free survival with RR≤2. To replicate this analysis, open the web application and verify that "Conventional (frequentist)" is selected for the type of meta-analysis. Then, under the "Select model" heading, select "Random effects" by clicking the circle next to it:
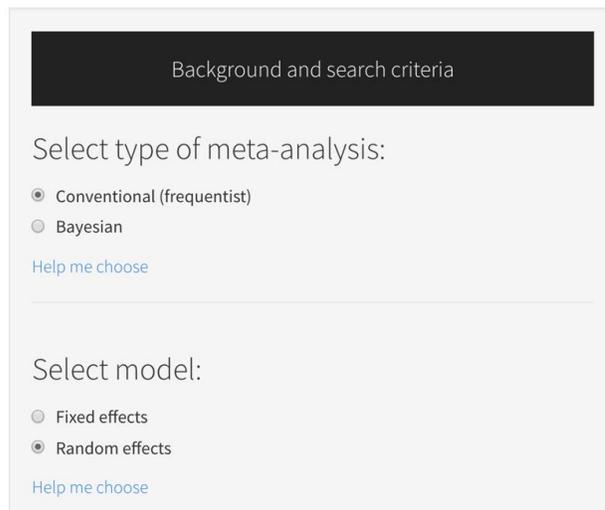
Next, scroll down to the "Select studies to include" heading, click inside the dialog box, and click on "Studies with RR<=2".
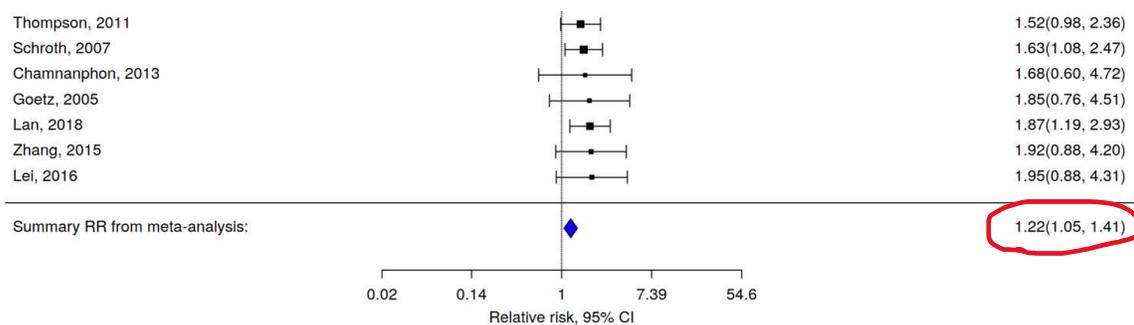
Select studies to include:

All studies ▲

All studies

Studies with RR<=2

Studies of CYP2D6*4 among Caucasians

Studies of CYP2D6*10 among Asians

Studies genotyping non-neoplastic DNA

Studies genotyping tumor DNA

☑ Bijl, 2009

☑ Chamnanphon, 2013

☑ Damodaran, 2012

☑ De Ameida Melo, 2016

☑ Dezentje, 2013

☑ Goetz, 2005

The list of individual studies will change, and only those that reported a RR≤2 will have their boxes checked. Now scroll all the way down and click the "Run analysis" button:
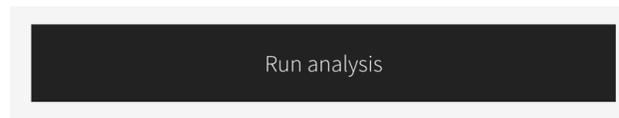
Run analysis

Scroll back up to the top of the application to view the various results tabs. Select the "Forest plot" tab (it should already be selected for you) and take a look at the plot. At the bottom of the plot, look at the "Summary RR from meta-analysis" row. This gives the association reported in Table 2 (1.22, 95% CI: 1.05, 1.41), which is circled in red below.

Thompson, 2011	1.52(0.98, 2.36)
Schroth, 2007	1.63(1.08, 2.47)
Chamnanphon, 2013	1.68(0.60, 4.72)
Goetz, 2005	1.85(0.76, 4.51)
Lan, 2018	1.87(1.19, 2.93)
Zhang, 2015	1.92(0.88, 4.20)
Lei, 2016	1.95(0.88, 4.31)
Summary RR from meta-analysis:	1.22(1.05, 1.41)

0.02   0.14   1   7.39   54.6

Relative risk, 95% CI

A Bayesian meta-analysis

Now let's walk through the Bayesian meta-analysis of studies that genotyped from tumour-derived DNA, and using a vague prior for the association between CYP2D6 impairment and disease-free survival. Recall from the paper that we defined a vague prior as a normally distributed prior with 95% of its density between 0.25 and 4.0.

Make sure you're at the top of the application. Select "Bayesian" for the type of meta-analysis. To specify the vague prior, first enter "0.25" for the lower 95% limit of the relative risk, then enter "4" for the upper 95% limit of the relative risk:

Next, choose one of the options for the form of the prior for the heterogeneity parameter (tau). The default (Jeffreys) is what we used in our example, so we'll keep that. If you're interested in learning more about these options, go ahead a click the "Help me choose" link beneath the options.

Now, select the subset of studies that genotyped with tumour-derived DNA:

Select studies to include:

Studies with RR<=2

All studies
Studies with RR<=2
Studies of CYP2D6*4 among Caucasians
Studies of CYP2D6*10 among Asians
Studies genotyping non-neoplastic DNA
Studies genotyping tumor DNA

Scroll all the way down, and click the "Run analysis" button. Be a little patient with the Bayesian models—they take several seconds to run.
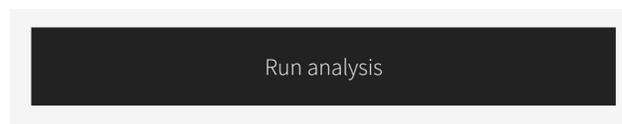
Run analysis

When the run is complete, you will see summary statistics and a plot for the vague prior just beneath the "Run analysis" button. The vague prior has a mean of 1 and a variance of 0.5. From the plot we see that the prior puts most credence in their being no effect (relative risk of 1), but leaves open the possibility that the association could be negative or positive.

Summary of specified prior:
Prior mean RR = 1
Prior variance = 0.5
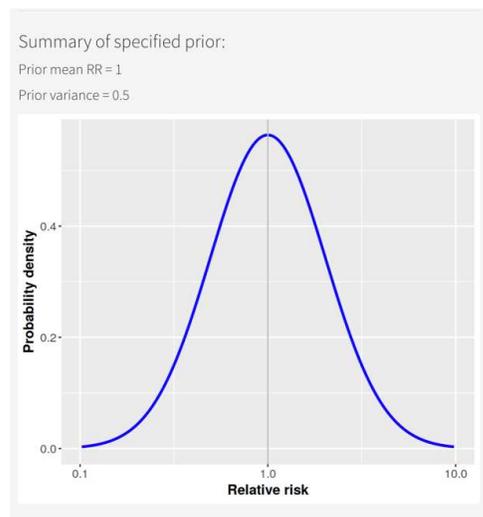
Scrolling up the "Forest plot" output, we can see the meta-analytic summary estimate of effect, which is labeled as "mean" in the Bayesian analysis. We find the estimate reported in Table 2 (1.18, 95% CI: 0.88, 1.55):
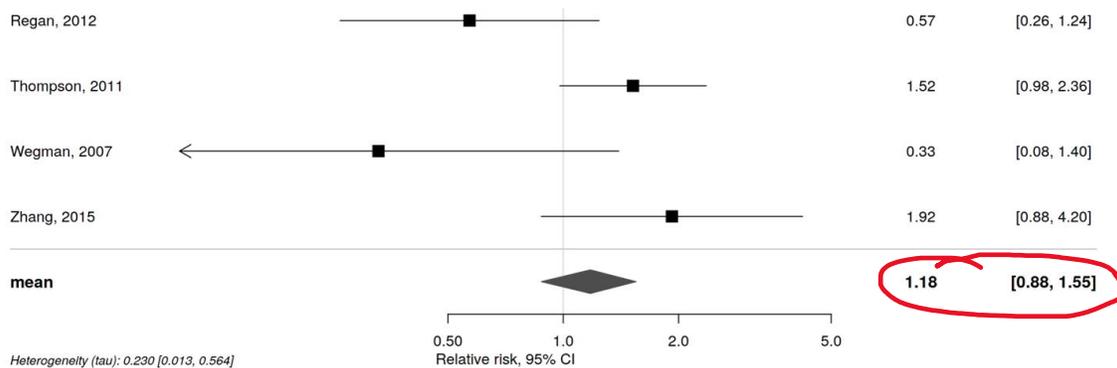
If you have any questions about replicating any of the other results from Table 2, or have any other comments or suggestions for the application, please get in touch!
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