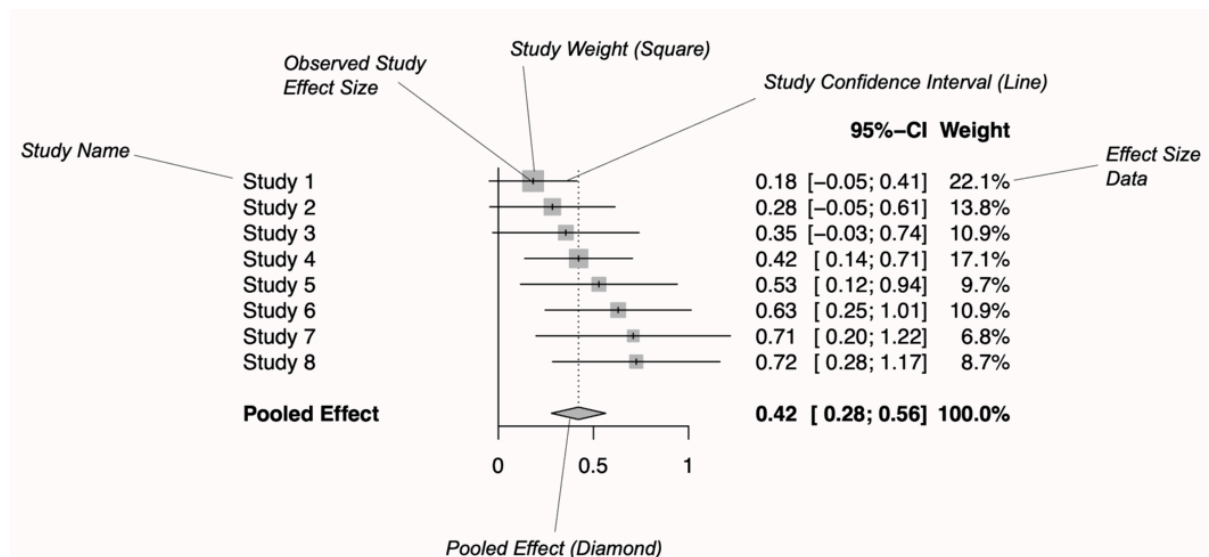


6 Forest Plots



▼ Intro

We already learn how to 1) Pool effect sizes in R , and how to 2) assess the heterogeneity in a meta-analysis.

NOW: We come to visualize the results we obtained in previous steps.

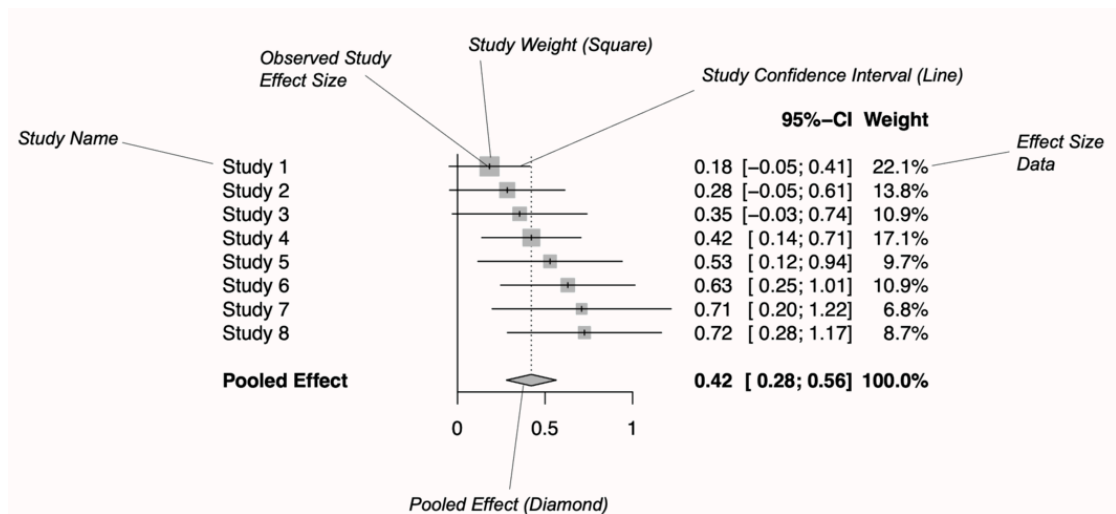
- 常用的可视化方法是使用 Forest plot ，其可以展示：
 - Observed effect sizes in each study
 - Confidence interval (observed effect size and pooled effect size)
 - The weight of each study
 - Pooled effect size
- The {meta} package has an in-built function which makes it very easy to produce beautiful forest plots directly in R .

本节主要关注：

1. `{meta}` 森林图函数 `meta::forest()`，以及我们如何在实践中使用它。
2. 一种meta分析结果可视化的替代方法：`Drapery plot` (Rücker and Schwarzer 2021)。

▼ 6.1 What Is a Forest Plot?

下图展示了森林图所包含的主要元素：



- forest plots can be `enhanced` by also displaying, for example, a `heterogeneity measure` such as I^2 or τ^2 .

▼ 6.2 Forest Plots in R

We can produce a forest plot for any type of `{meta}` meta-analysis object (e.g. results of `metagen`, `metacont`, or `metabin`) using the `meta::forest` function.

- 使用 `{meta}` 包的 `forest()` 函数的default 的输出已经不错，但有些参数还可调整，请运行 `?meta::forest` 查看 该函数的 `R documentation`。以下是常见的参数设置：
 1. `sortvar`. The variable in the meta-analysis data set by which studies are sorted in the forest plot. If we want to `order the results by effect size`, for example, we can use the code `sortvar = TE`.

2. `comb.fixed` . Logical, indicating if the fixed-effect model estimate should be included in the plot .
3. `comb.random` . Logical, indicating if the random-effects model estimate should be included in the plot .
4. `text.fixed` . The **label** for the pooled effect according to the fixed-effect model. By default, "Fixed effect model" is printed.
5. `text.random` . The label for the pooled effect according to the random-effects model. By default, "Random effects model" is printed.
6. `prediction` . Logical, indicating if the prediction interval should be added to the plot.
7. `label.left` and `label.right` . Label added to the left and right side of the forest plot. This can be used to specify that, for example, effects on this side favor the treatment (e.g. `label.left = "Favors treatment"`).
8. `smlab` . A label displayed on top of the plot. This can be used to show which effect size metric was used .
9. `xlim` . The limits of the x-axis , or the character "s" to produce symmetric forest plots. This is argument particularly relevant when your results deviate substantially from zero, or if you also want to have outliers depicted. If we want that the x-axis ranges from 0 to 2, for example, the code is `xlim = c(0,2)` .
10. `ref` . The reference line in the plot. Depending on the summary measure we used, this is either 0 or 1 by default.
11. `leftcols` and `rightcols` . Here, you can specify which variables should be displayed on the left and right side of the forest plot . There are a few in-built elements that the function uses by default. For example, "studlab" stands for the study label, "effect" for the observed effect size, and `effect.ci` for both the effect size and its confidence interval. It is also possible to add user-defined columns, as long as these were included in the `data.frame` we initially provided to the `{meta}` function. **In this case, we only have to add the name of the column as a character string.**

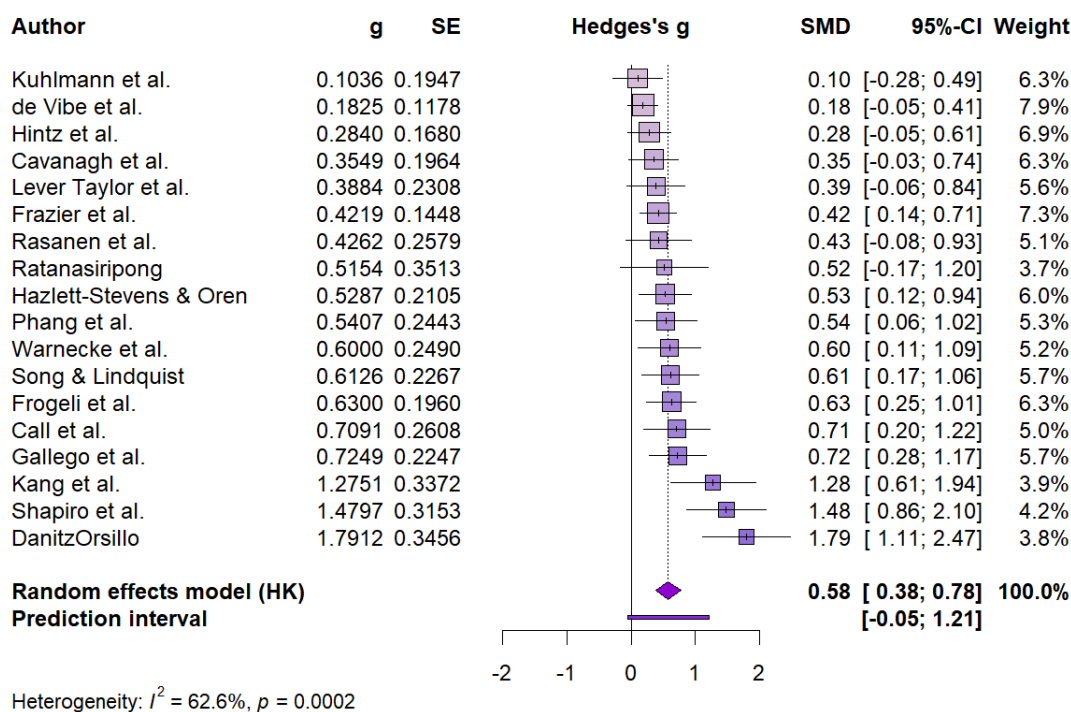
```
#1
forest(m, leftcols = c("studlab", "country"))
#2
```

```
meta::forest(m.gen,
             sortvar = TE,
             prediction = TRUE,
             print.tau2 = FALSE,
             leftcols = c("studlab", "TE", "seTE", "RiskOfBias"),
             leftlabs = c("Author", "g", "SE", "Risk of Bias"))
```

12. `leftlabs` and `rightlabs`. The labels that should be used for the columns displayed to the left and right of the forest plot.
 13. `print.I2` and `print.I2.ci`. Logical, indicating if the I^2 value and its confidence interval should be printed. This is `TRUE` by default.
 14. `print.tau2` and `print.tau`. Logical, indicating if the τ^2 and τ value should be printed. The value of τ^2 is printed by default.
 15. `col.square`, `col.diamond` and `col.predict`. The color (e.g. `"blue"`) of the square, diamond and prediction interval, respectively.
- Time to generate our first forest plot. In this example, we plot the `m.gen` object. We sort the studies in the forest plot **by effect size**, add a prediction interval, and **user-defined labels** to the left. The `meta::forest` function prints the `$\tau^2$` value by default, which we do not want here, so we set `print.tau2` to `FALSE`.

This is how our code looks in the end:

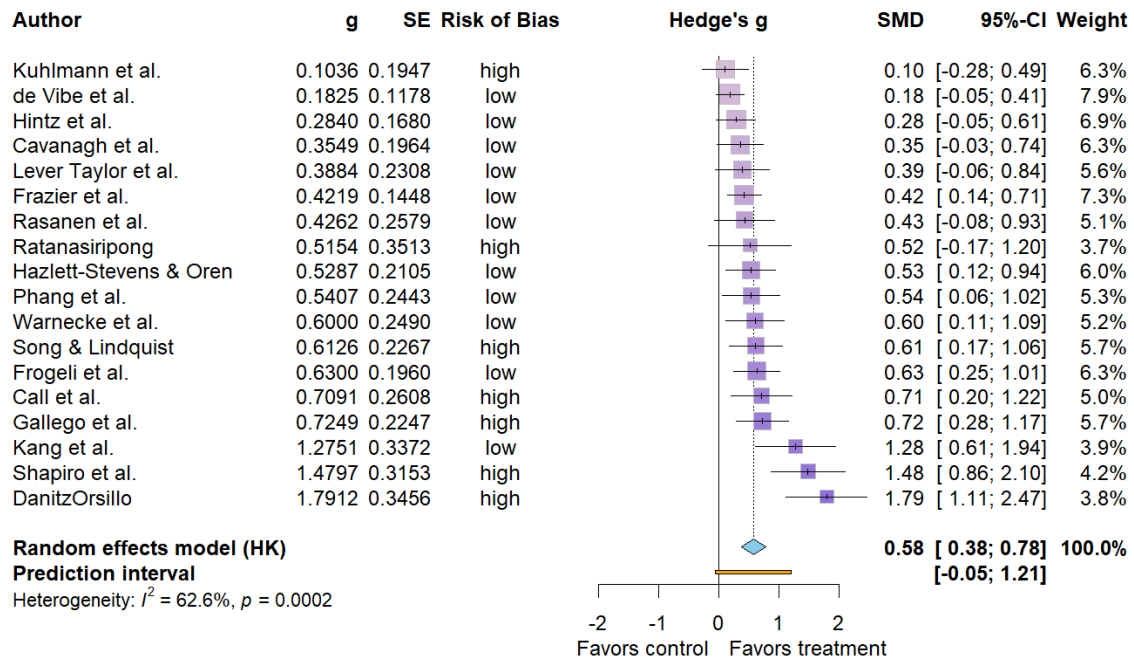
```
meta::forest(m.gen,
             sortvar = TE,
             prediction = TRUE,
             print.tau2 = FALSE,
             leftlabs = c("Author", "g", "SE"))
```



进一步增强信息的可视化：添加“Risk of bias”列：

```
meta::forest(m.gen,
  sortvar = TE,
  prediction = TRUE,
  print.tau2 = FALSE,
  leftcols = c("studlab", "TE", "seTE", "RiskOfBias"),
  leftlabs = c("Author", "g", "SE", "Risk of Bias"))
```

1. 导入R的 `Data set` 需包括 “RiskOfBias” 列，可视化时只需要以 `字符串` 的形式引入 `leftcols =` 即可。
2. 当我们对导入的 `Data set` 进行计算时，`Data set` 内的列会出现在计算后的结果模型中。



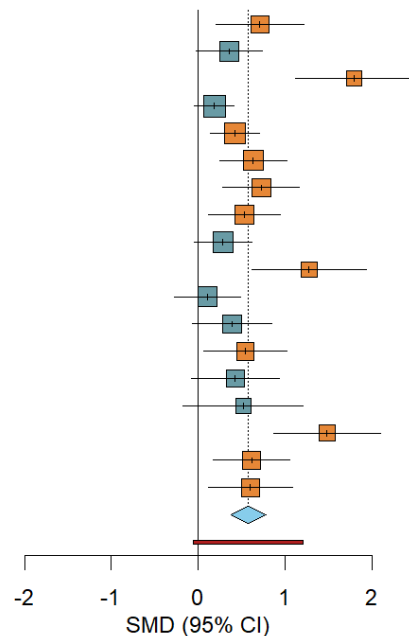
We see that now, the **risk of bias** information of each study has been **added** to the forest plot.

▼ 6.2.1 Layout Types

1. **"JAMA"** layout

```
meta::forest(m.gen, layout = "JAMA")
```

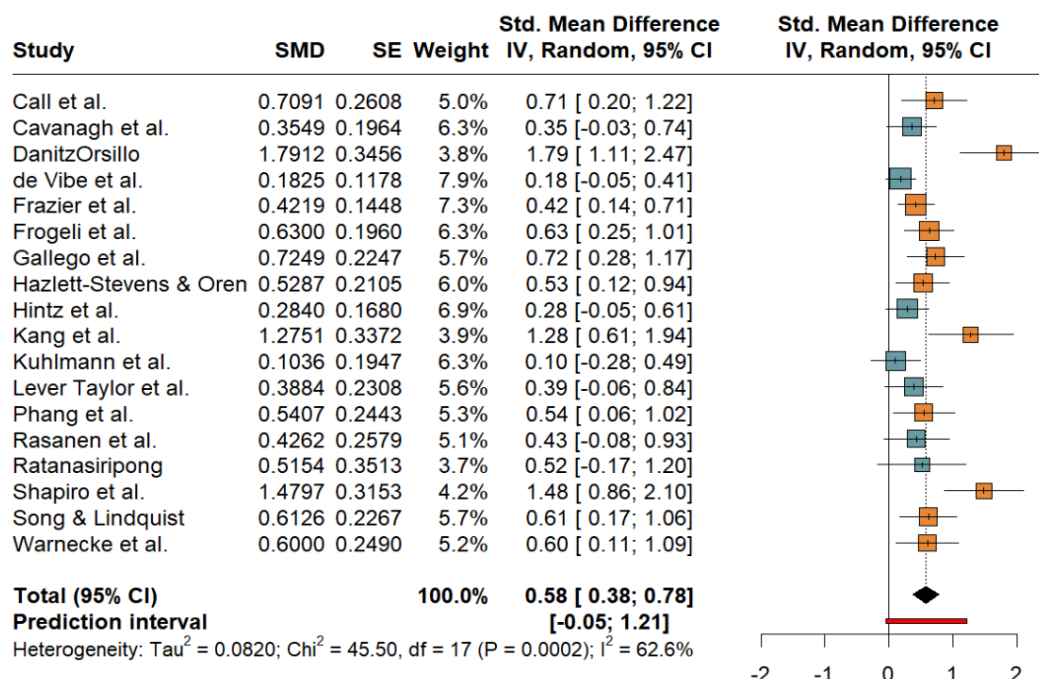
Source	SMD (95% CI)
Call et al.	0.71 [0.20; 1.22]
Cavanagh et al.	0.35 [-0.03; 0.74]
DanitzOrsillo	1.79 [1.11; 2.47]
de Vibe et al.	0.18 [-0.05; 0.41]
Frazier et al.	0.42 [0.14; 0.71]
Frogeli et al.	0.63 [0.25; 1.01]
Gallego et al.	0.72 [0.28; 1.17]
Hazlett-Stevens & Oren	0.53 [0.12; 0.94]
Hintz et al.	0.28 [-0.05; 0.61]
Kang et al.	1.28 [0.61; 1.94]
Kuhlmann et al.	0.10 [-0.28; 0.49]
Lever Taylor et al.	0.39 [-0.06; 0.84]
Phang et al.	0.54 [0.06; 1.02]
Rasanen et al.	0.43 [-0.08; 0.93]
Ratanasiripong	0.52 [-0.17; 1.20]
Shapiro et al.	1.48 [0.86; 2.10]
Song & Lindquist	0.61 [0.17; 1.06]
Warnecke et al.	0.60 [0.11; 1.09]
Random effects model	0.58 [0.38; 0.78]
Prediction interval	[-0.05; 1.21]



Heterogeneity: $\chi^2_{17} = 45.50$ ($P < .001$), $I^2 = 62.6\%$

2. "RevMan5" layout (which produces a forest plot similar to the ones generated by Cochrane's **Review Manager 5**).

```
meta::forest(m.gen, layout = "RevMan5")
```



▼ 6.2.2 Saving the Forest Plots

在R中，我们可以将森林图 保存 为 PDF, PNG 和 SVG 。

1. PDF

```
pdf(file = "forestplot.pdf", width = 8, height = 7)

meta::forest(m.gen,
              sortvar = TE,
              prediction = TRUE,
              print.tau2 = FALSE,
              leftlabs = c("Author", "g", "SE"))

dev.off()
```

2. PNG

```
png(file = "forestplot.png", width = 2800, height = 2400, res = 300)

meta::forest(m.gen,
              sortvar = TE,
              prediction = TRUE,
              print.tau2 = FALSE,
              leftlabs = c("Author", "g", "SE"))

dev.off()
```

3. SVG

```
svg(file = "forestplot.svg", width = 8, height = 7)

meta::forest(m.gen,
              sortvar = TE,
              prediction = TRUE,
              print.tau2 = FALSE,
              leftlabs = c("Author", "g", "SE"))

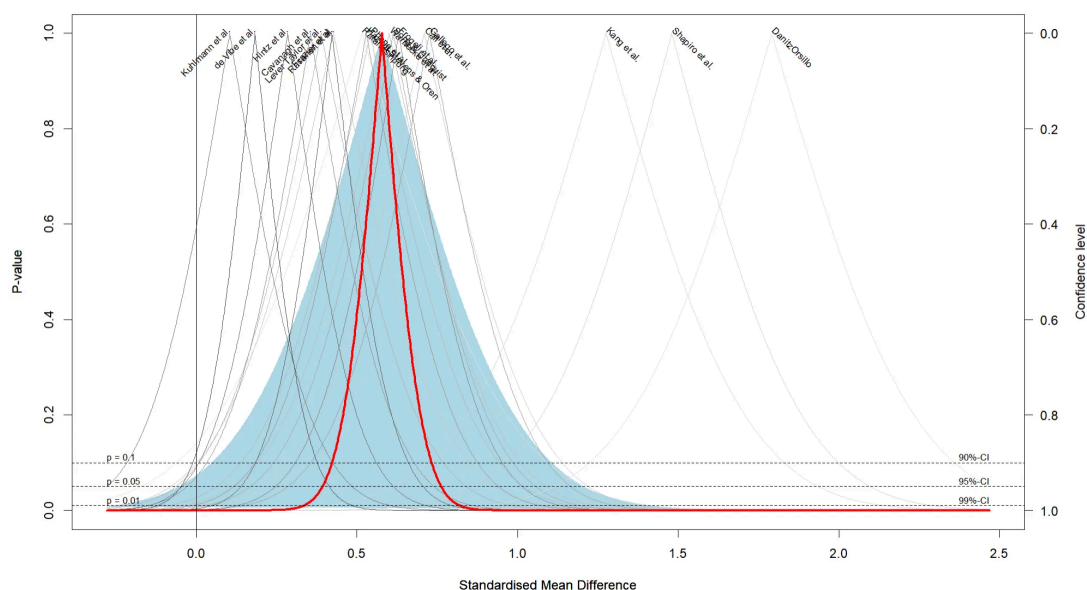
dev.off()
```


▼ 6.3 Drapery Plots

Drapery plot (帷幕图) 可用于meta分析的可视化。

2021. "Beyond the Forest Plot: The Drapery Plot." *Research Synthesis Methods* 12 (1): 13–19.

森林图的一个不足之处是：只能显示假设一个固定的显著性阈值（通常 $p < 0.05$ ）的置信区间（即95%CI）。研究人员正是基于这些置信区间来决定一个效应是否显著。



- 在我们的元分析中， p 值函数的“**峰值**”代表了效应量的确切值。当我们沿着 y 轴向下移动时， p 值变得越来越小，置信区间越来越宽，直到我们达到传统的显著性阈值，用虚线表示。
- 森林图只能显示假设一个固定的显著性阈值（通常 $\alpha = 0.05$ ）。帷幕图可以用来显示不同 p 值下效应大小的置信区间（以及显著性）。
- Rücker 等人（2021）建议，除森林图外，还应主要使用帷幕图。简单地将森林图替换为帷幕图可能不是一个好主意，因为后者不包含其他研究者可能需要的效应大小信息来复制我们的结果。

▼ 6.4 Summary

- It is conventional to **visualize the results** of meta-analyses **through forest plots**.

- **Forest plots** contain a graphical representation of **each study's effect size and confidence interval**, and also show the calculated **overall effect**. Furthermore, they contain the **effect size data** that was used for pooling.
- It is also possible to **add other kinds of information to a forest plot**, for example the quality rating that each study received.
- Forest plots can only display results assuming a fixed significance threshold, usually $p < 0.05$. **To visualize how results change for varying significance thresholds, drapery plots can be generated in addition.**