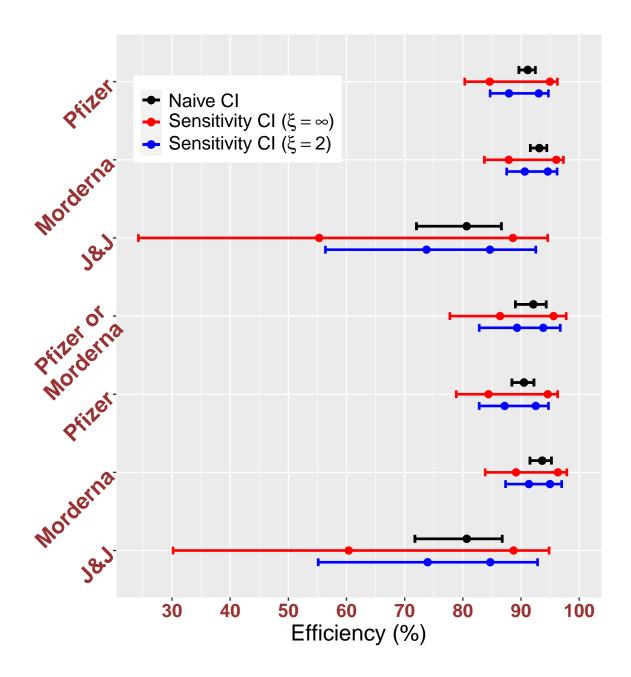
## Plots

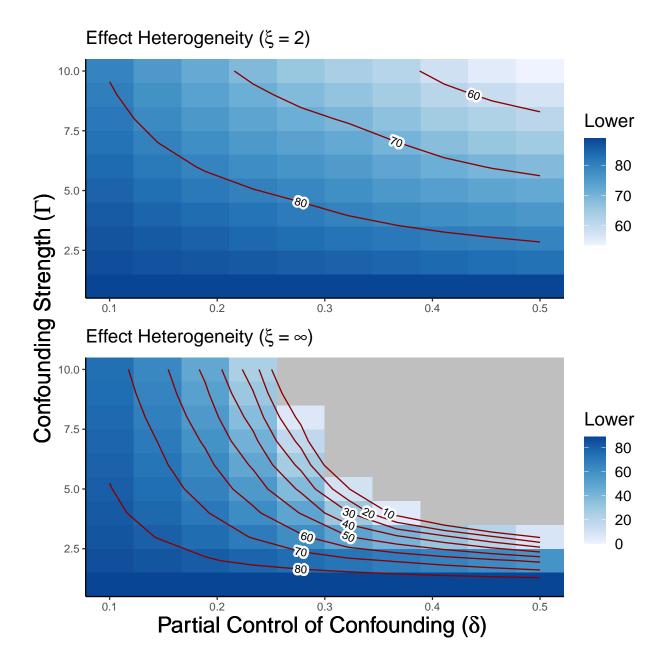
#### Real Data Plots

#### New England Journal Plot

```
library(grid)
library(pBrackets)
source('./scripts/datasets.R')
source('./scripts/real_data_plots.R')
#### Data from New England Journal of Medicine
#### The last column is indicator of non-vaccinated referent group
data_vaccine = data.frame(matrix(c()))
                           20406, 3695, 1,
                            8500, 163, 0,
                            6374, 95, 0,
                           10761, 2006, 1,
                             707,
                                   30, 0,
                           4024,
                                 692, 1,
                           2359,
                                    38, 0,
                           11812, 2847, 1,
                            3589, 105, 0,
                            2476,
                                   49, 0,
                            8461, 2200, 1,
                                    29, 0), ncol = 3, byrow = TRUE))
                             456,
colnames(data_vaccine) = c("All", "Control", "non-vaccinated")
#### Plot
new_england_data = new_england(data_vaccine)
real_data_graphs(new_england(data_vaccine),
                     delta = 0.1, gamma = 5, xi = c(2, Inf), alpha = 0.95, conf.type = 'normal',
                     title = "Vaccine Efficiency for Different Vaccines",
                     labs = c("Pfizer", "Morderna", "J&J", "Pfizer or\nMorderna",
                                     "Pfizer", "Morderna", "J&J"))
```



#### Contour Plot for Pfizer

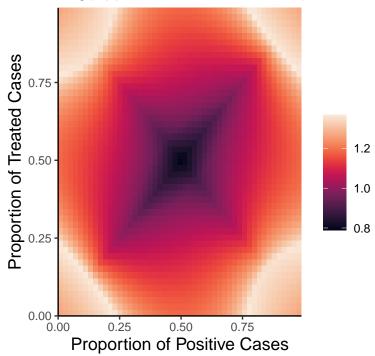


### **Numerical Simulations**

#### Heatmap for same Odds Ratio

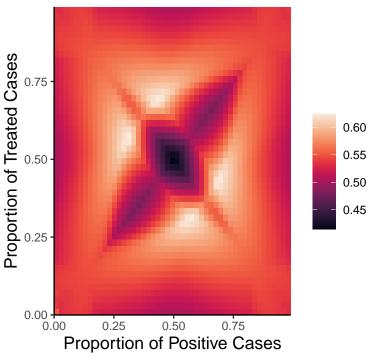
```
source('./scripts/heatmap_same_odds_ratio.R')
heatmap_same_odds_ratio(0.5, 0.1, 5, xi = Inf, choice = 1, grid = 50, log.transform = TRUE)
```

## Log(Upper Bound/Lower Bound)



heatmap\_same\_odds\_ratio(0.5, 0.1, 5, xi = 2, choice = 1, grid = 50, log.transform = TRUE)

# Log(Upper Bound/Lower Bound)



### Compare Confidence Interval

```
source('./scripts/CI_compare.R')
set.seed(123)
o = c(0.1, 0.2, 0.3, 0.4)
CI_comparison(o, delta=0.1, gamma=5, xi=2, alpha=0.95, n.population=1000, n.sim=20)
```

