

Cost-effectiveness acceptability curve plots

Introduction

The intention of this vignette is to show how to plot different styles of cost-effectiveness acceptability curves using the BCEA package.

Two interventions only

This is the simplest case, usually an alternative intervention ($i = 1$) versus status-quo ($i = 0$).

The plot show the probability that the alternative intervention is cost-effective for each willingness to pay, k ,

$$p(NB_1 \geq NB_0 | k) \text{ where } NB_i = ke - c$$

Using the set of N posterior samples, this is approximated by

$$\frac{1}{N} \sum_j^N \mathbb{I}(k\Delta e^j - \Delta c^j)$$

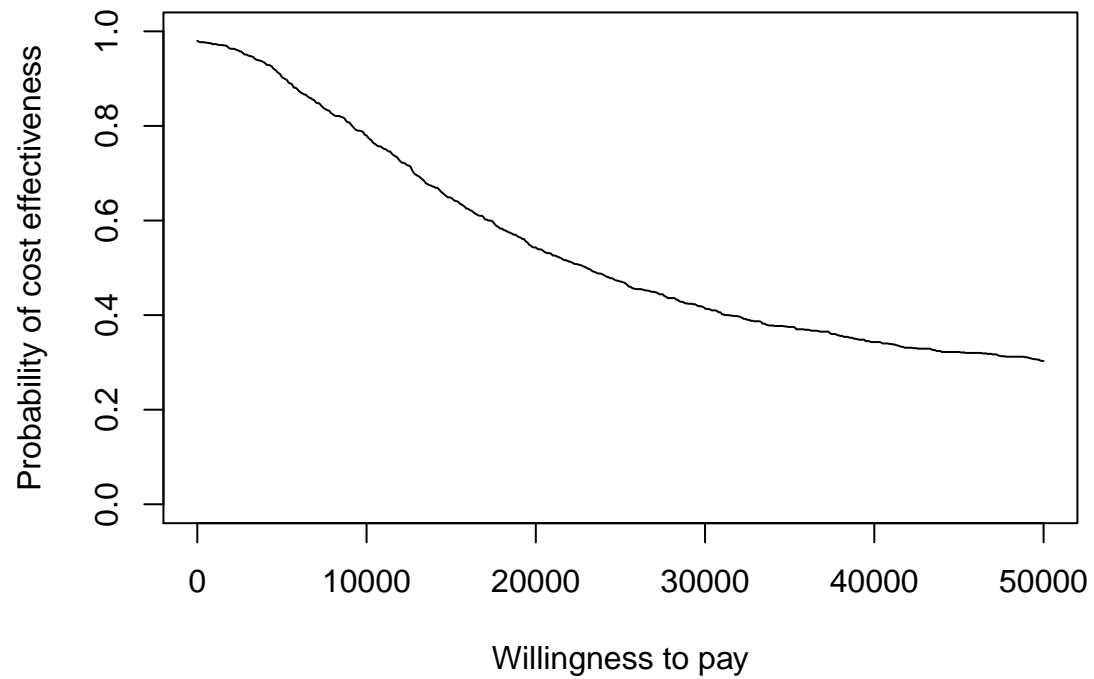
R code To calculate these in BCEA we use the `bcea()` function.

```
data("Vaccine")

he <- bcea(e, c)
# str(he)

ceac.plot(he)
```

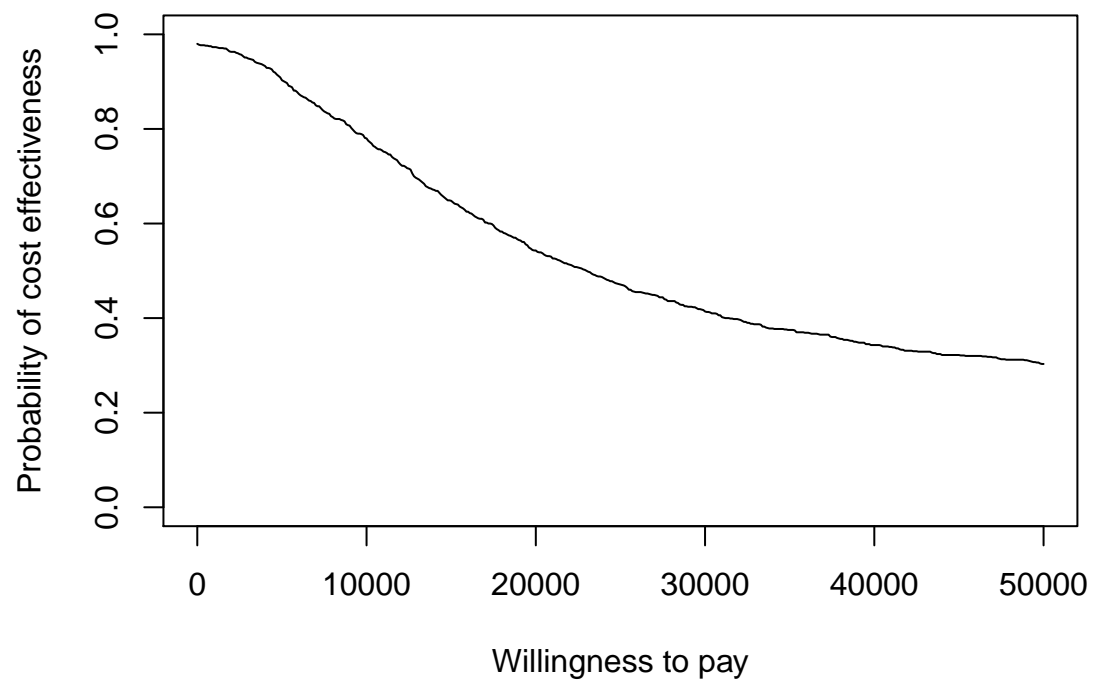
Cost Effectiveness Acceptability Curve



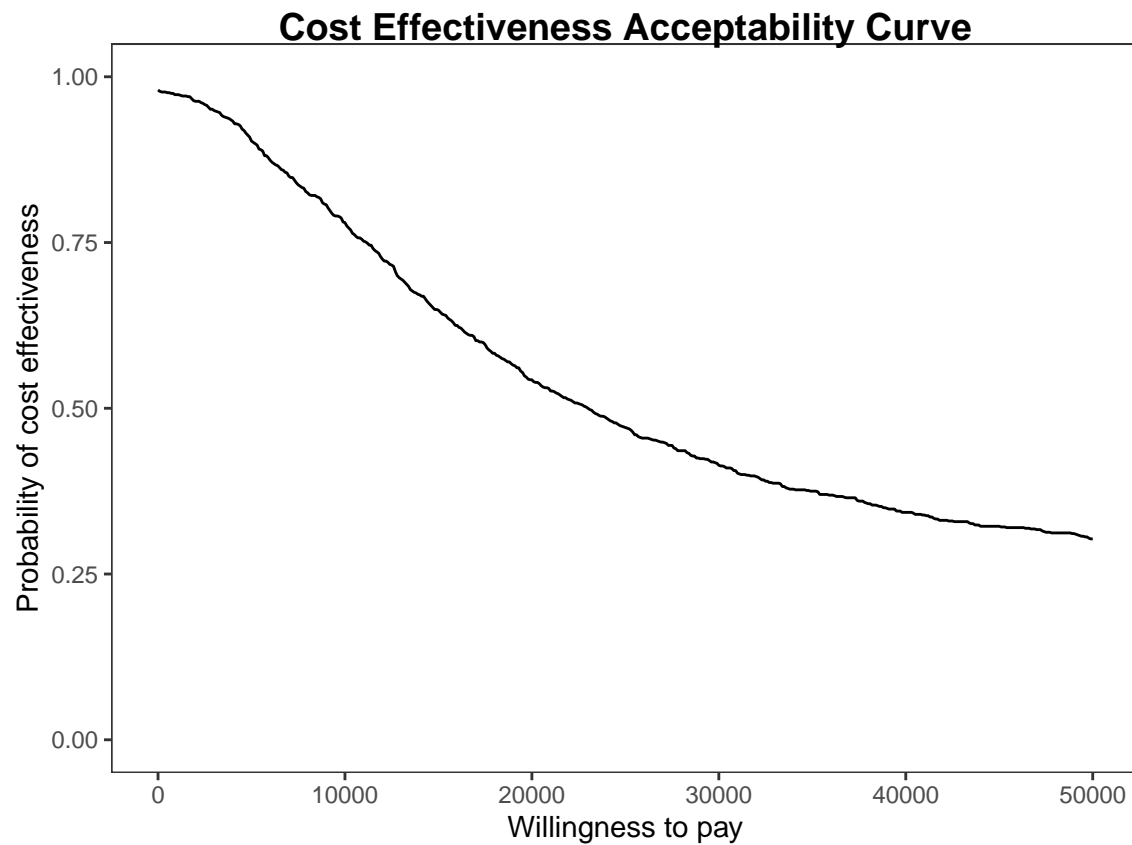
The plot defaults to base R plotting. Type of plot can be set explicitly using the `graph` argument.

```
ceac.plot(he, graph = "base")
```

Cost Effectiveness Acceptability Curve



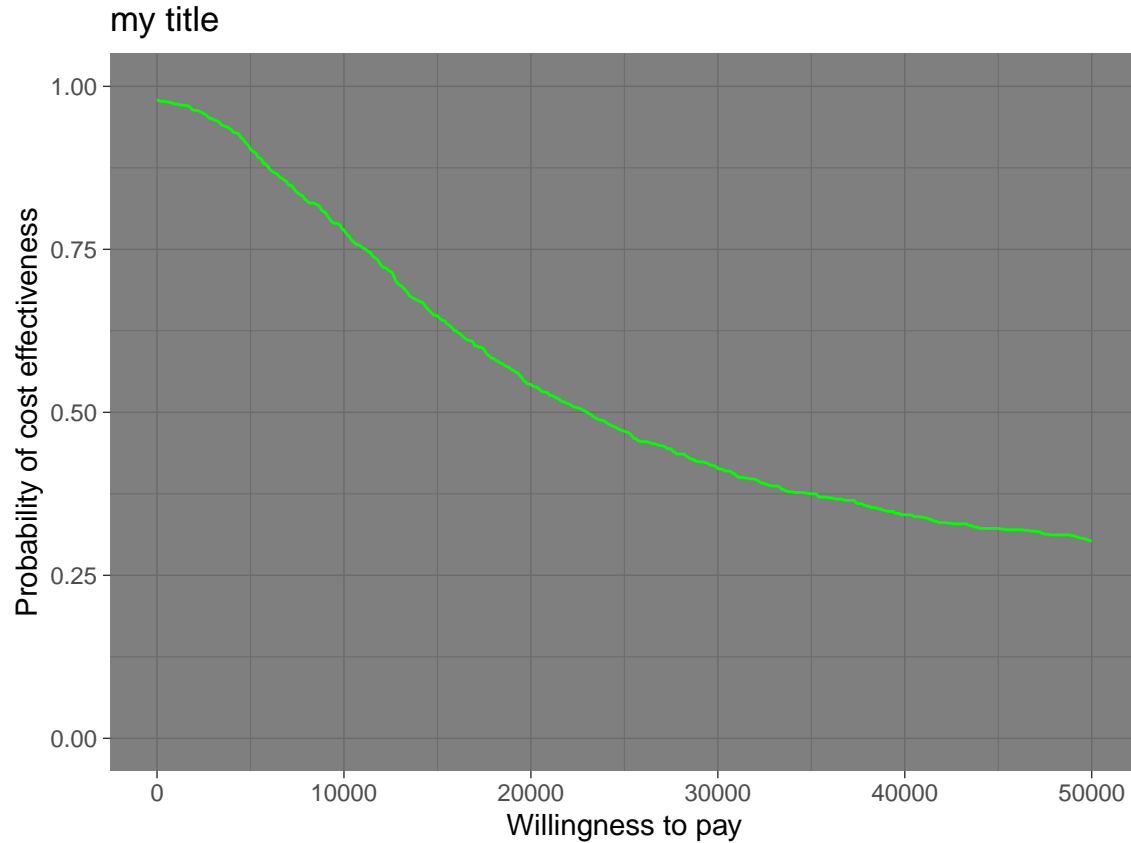
```
ceac.plot(he, graph = "ggplot2")
```



```
# ceac.plot(he, graph = "plotly")
```

Other plotting arguments can be specified such as title, line colours and theme.

```
ceac.plot(he,  
  graph = "ggplot2",  
  title = "my title",  
  line = list(colors = "green"),  
  theme = theme_dark())
```



Multiple interventions

This situation is when there are more than two interventions to consider. Incremental values can be obtained either always against a fixed reference intervention, such as status-quo, or for all pair-wise comparisons.

Against a fixed reference intervention

Without loss of generality, if we assume that we are interested in intervention $i = 1$, then we wish to calculate

$$p(NB_1 \geq NB_s | k) \quad \exists s \in S$$

Using the set of N posterior samples, this is approximated by

$$\frac{1}{N} \sum_j^N \mathbb{I}(k\Delta e_{1,s}^j - \Delta c_{1,s}^j)$$

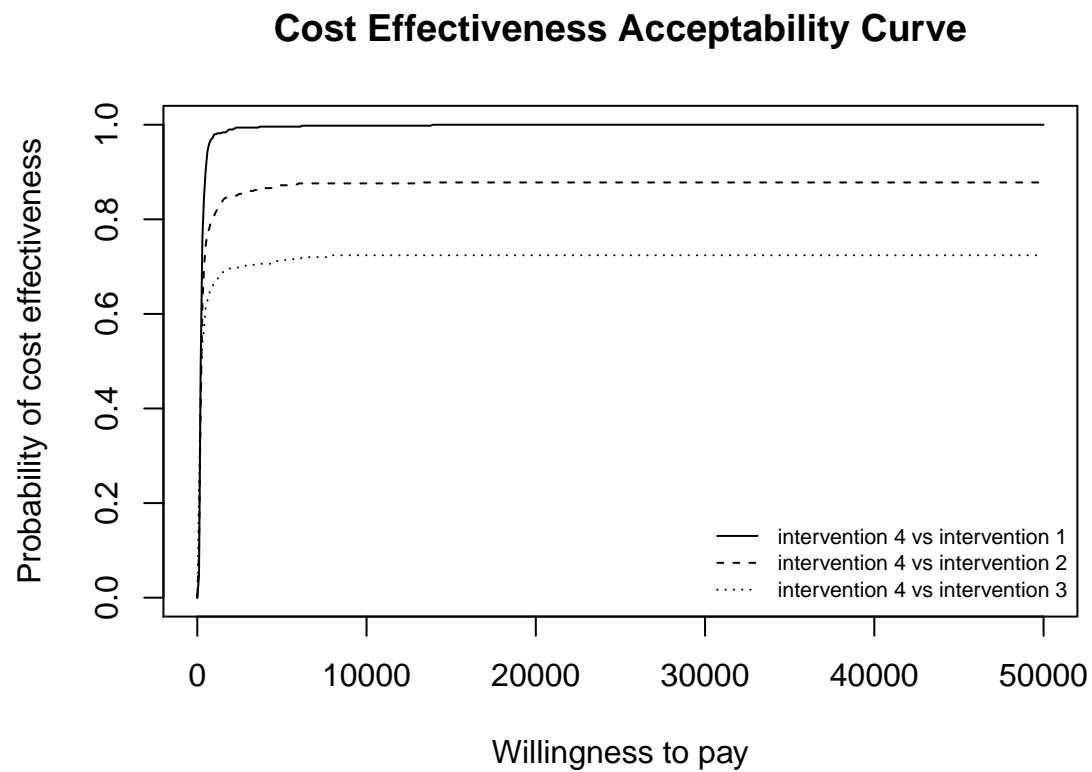
R code This is the default plot for `ceac.plot()` so we simply follow the same steps as above with the new data set.

```
data("Smoking")
```

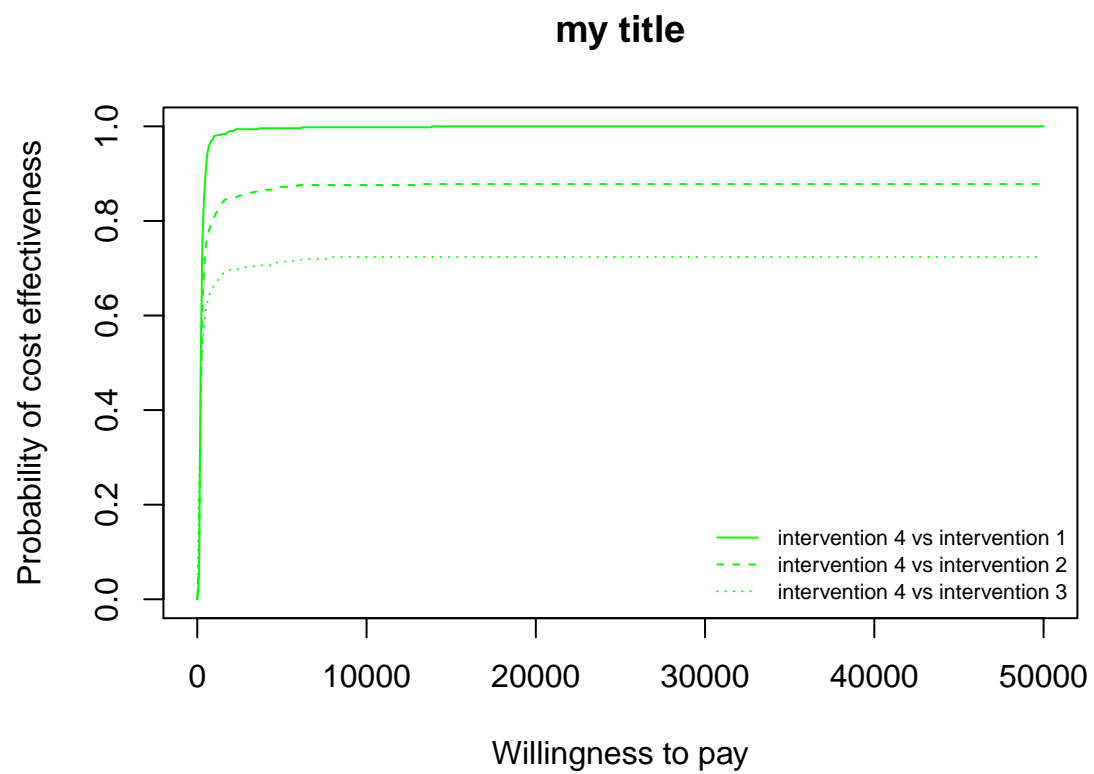
```
he <- bcea(e, c, ref = 4)
```

```
# str(he)
```

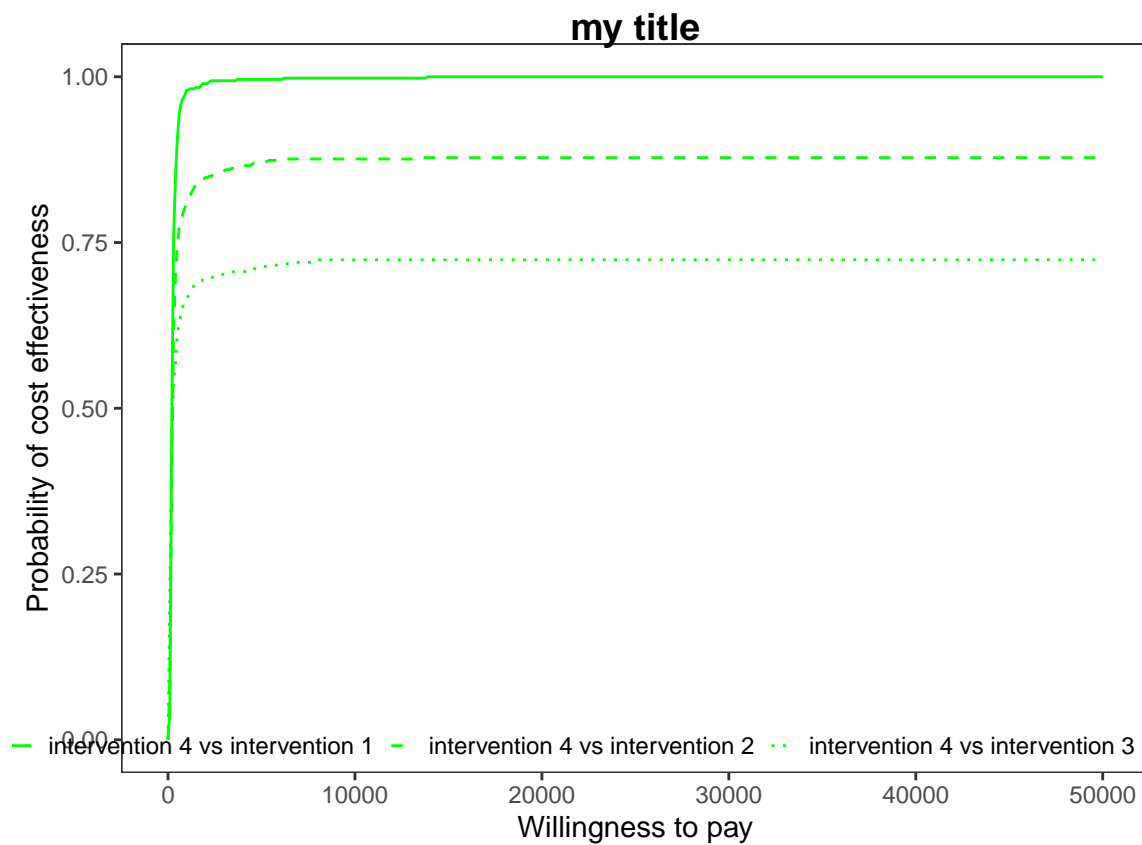
```
ceac.plot(he)
#> Wrong number of colours provided. Falling back to default
```



```
ceac.plot(he,
  graph = "base",
  title = "my title",
  line = list(colors = "green"))
#> Wrong number of colours provided. Falling back to default
```



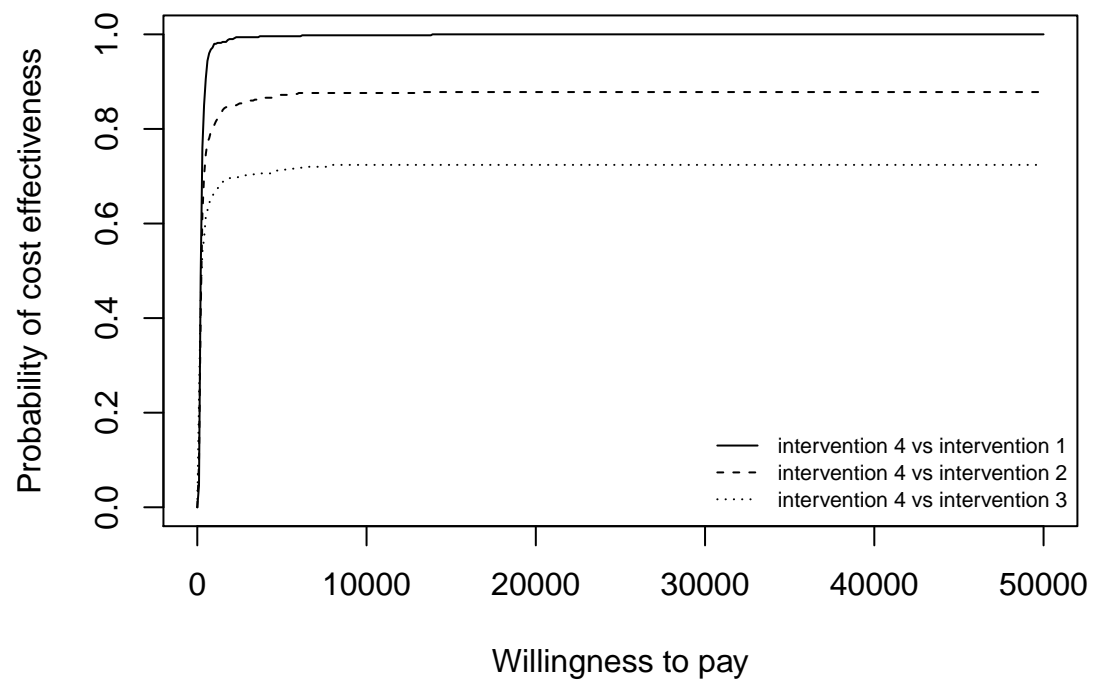
```
ceac.plot(he,  
  graph = "ggplot2",  
  title = "my title",  
  line = list(colors = "green"))
```



Reposition legend.

```
ceac.plot(he, pos = FALSE) # bottom right
#> Wrong number of colours provided. Falling back to default
```

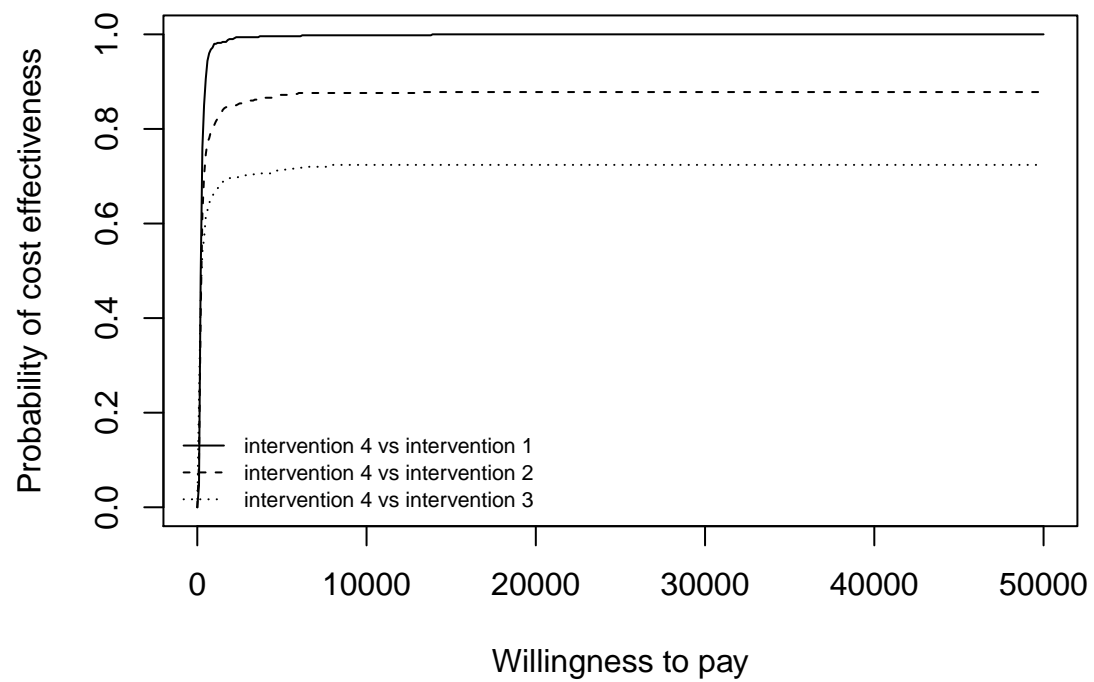

Cost Effectiveness Acceptability Curve



```
ceac.plot(he, pos = c(0, 0))
```

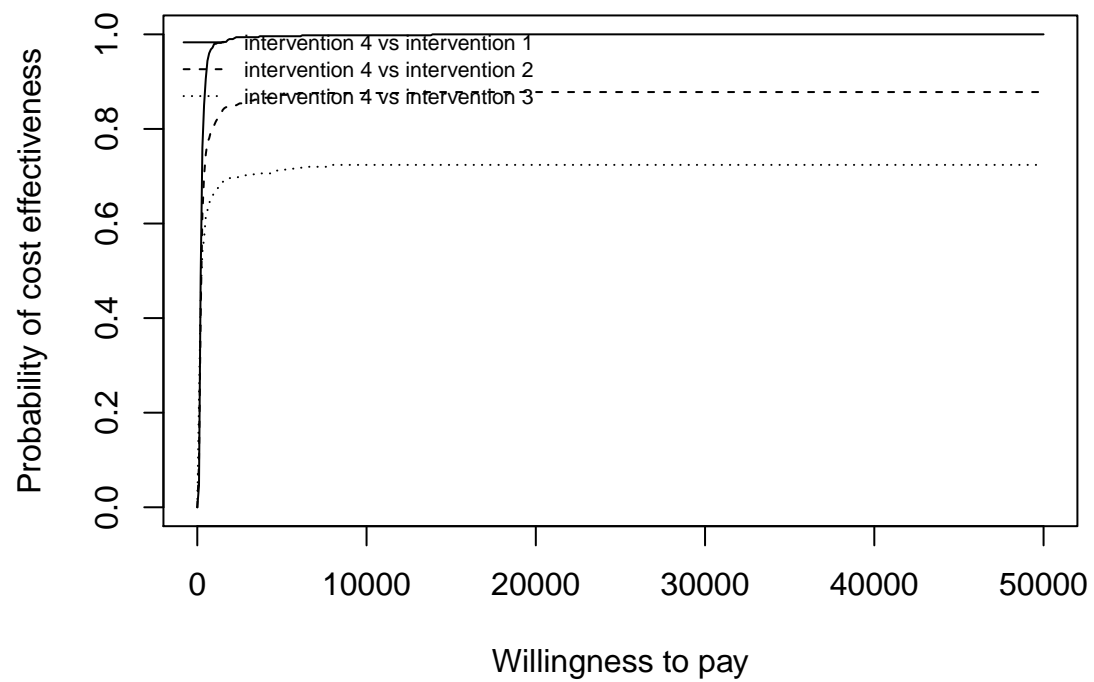
```
#> Wrong number of colours provided. Falling back to default
```

Cost Effectiveness Acceptability Curve



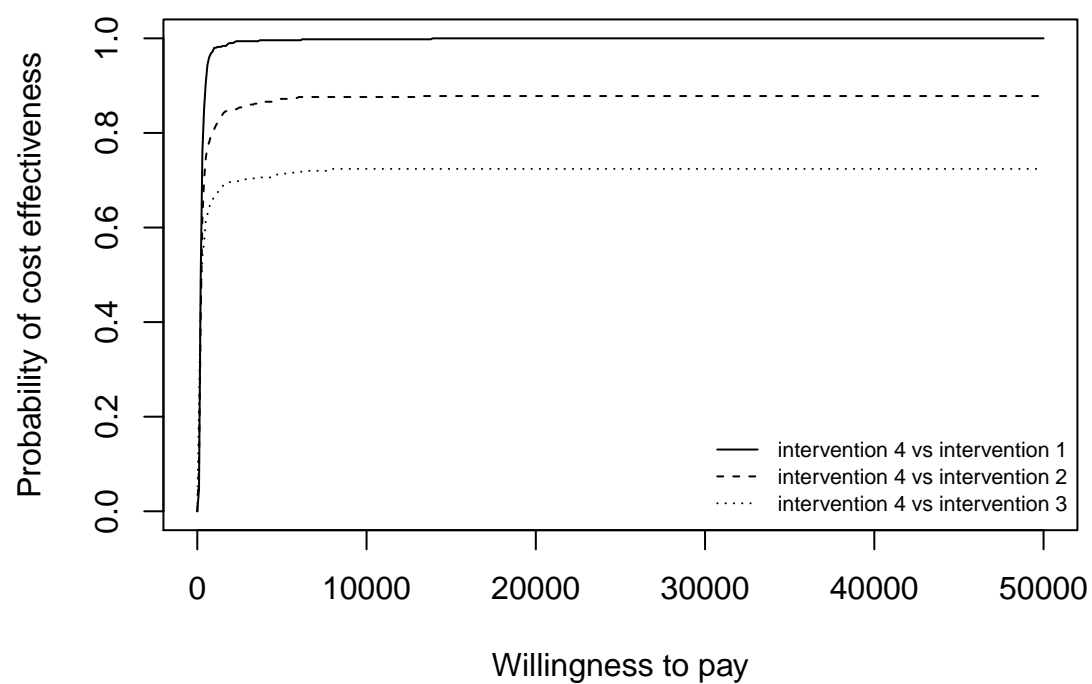
```
ceac.plot(he, pos = c(0, 1))  
#> Wrong number of colours provided. Falling back to default
```

Cost Effectiveness Acceptability Curve



```
ceac.plot(he, pos = c(1, 0))  
#> Wrong number of colours provided. Falling back to default
```

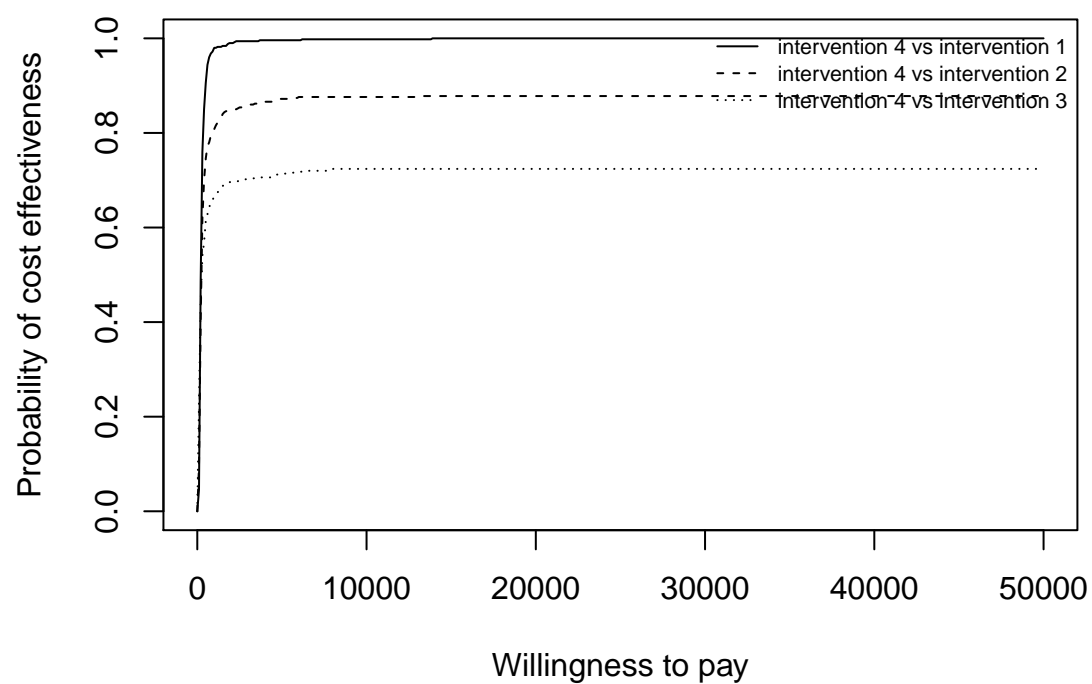
Cost Effectiveness Acceptability Curve



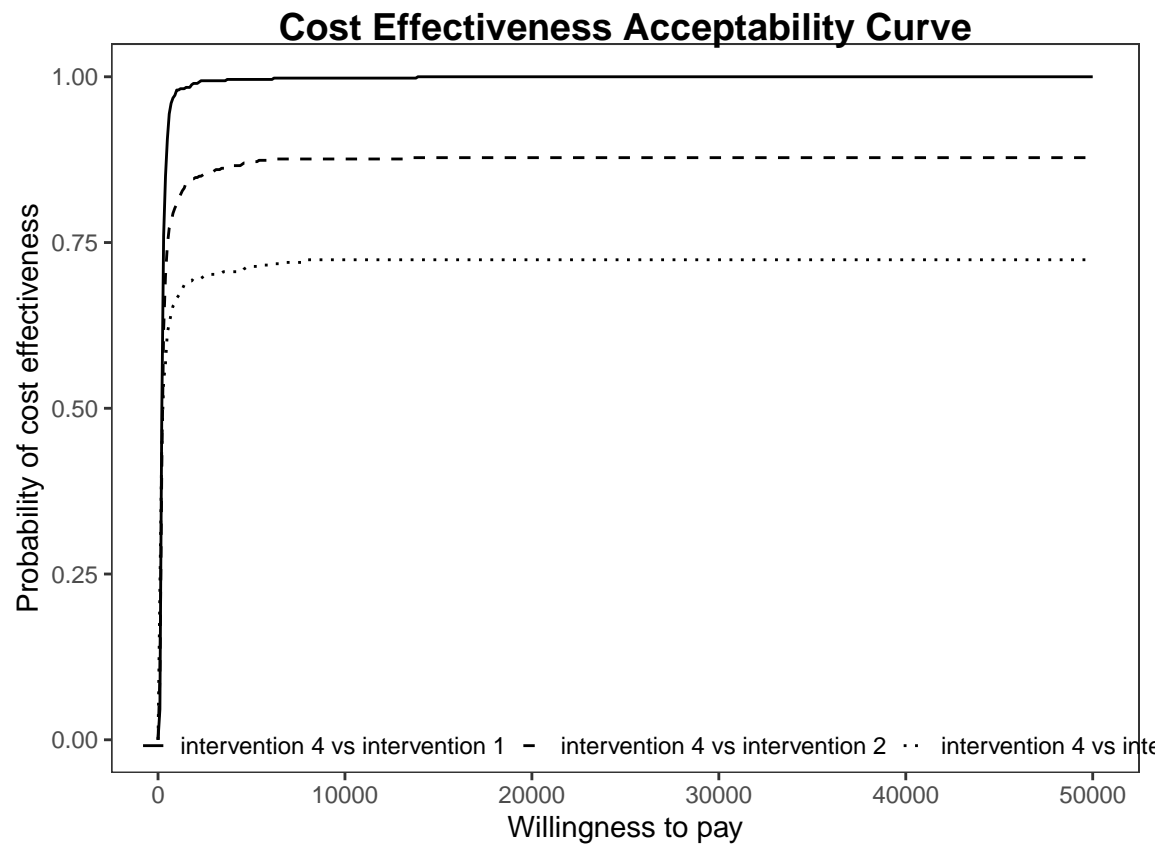
```
ceac.plot(he, pos = c(1, 1))
```

```
#> Wrong number of colours provided. Falling back to default
```

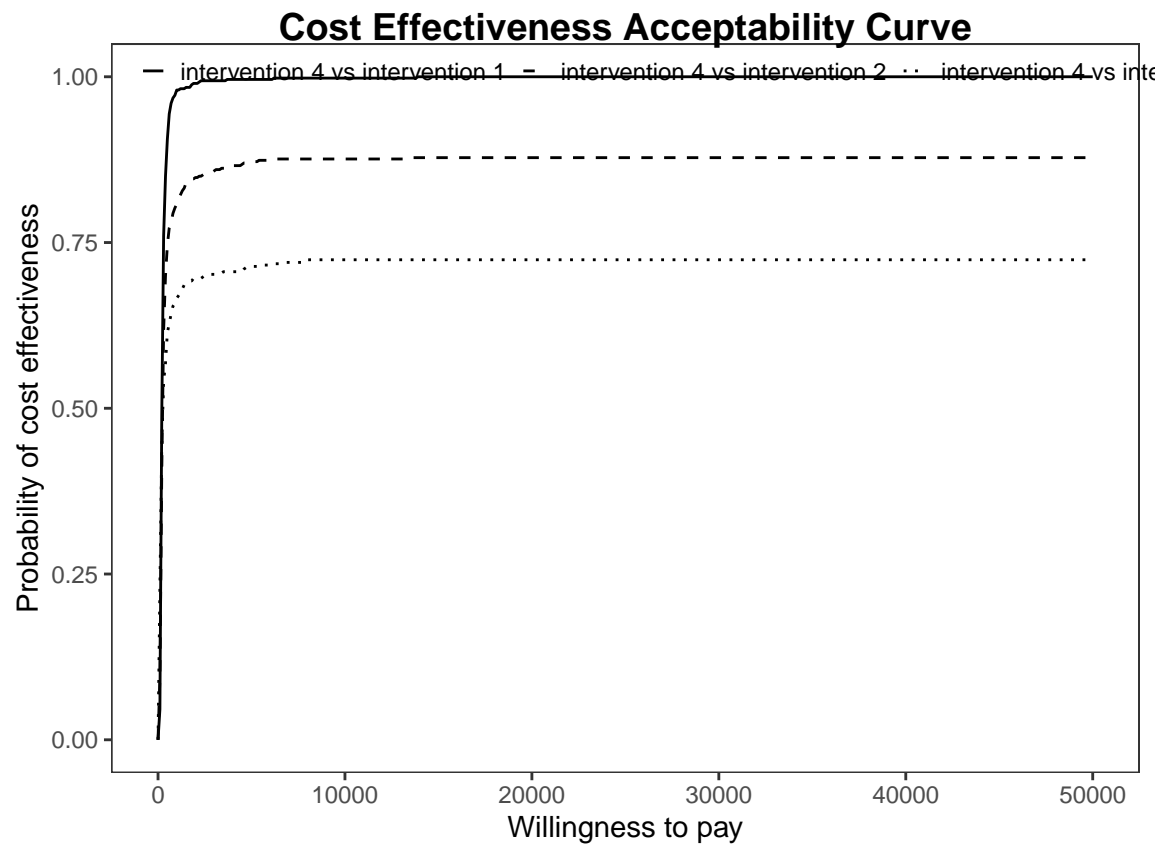
Cost Effectiveness Acceptability Curve



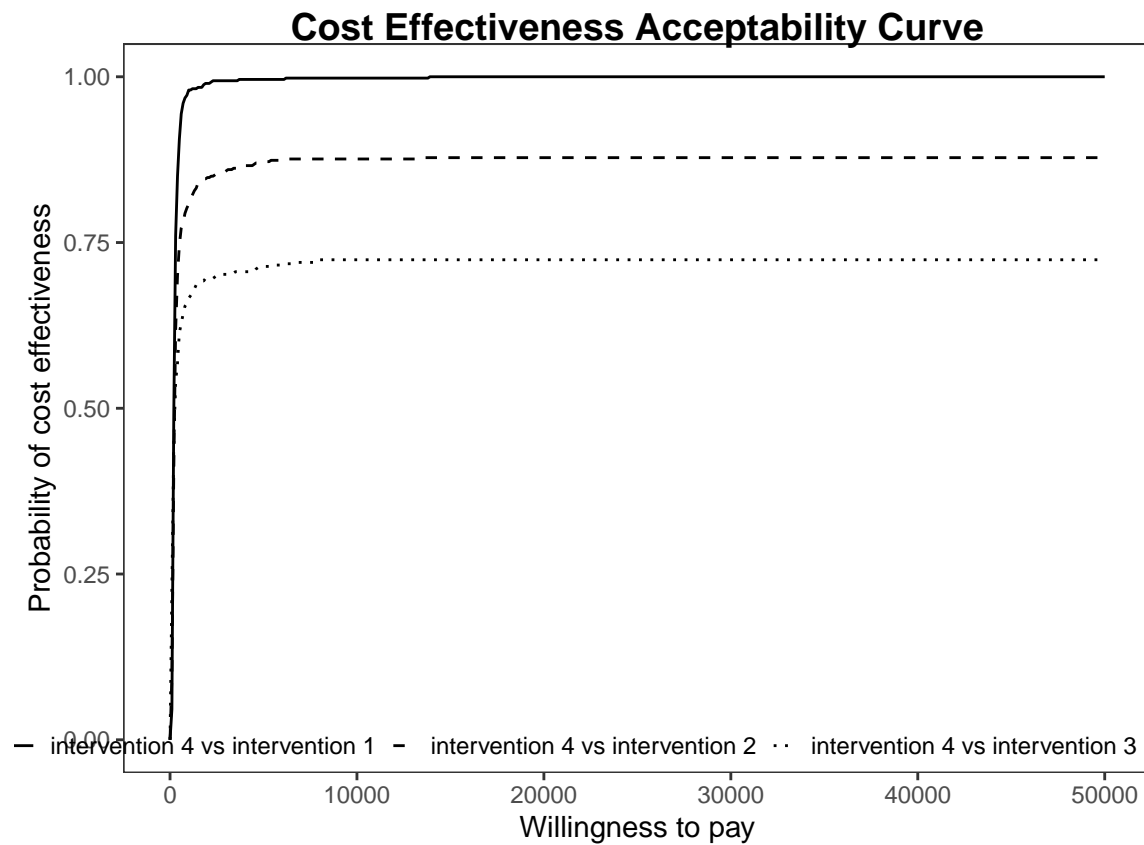
```
ceac.plot(he, graph = "ggplot2", pos = c(0, 0))
```



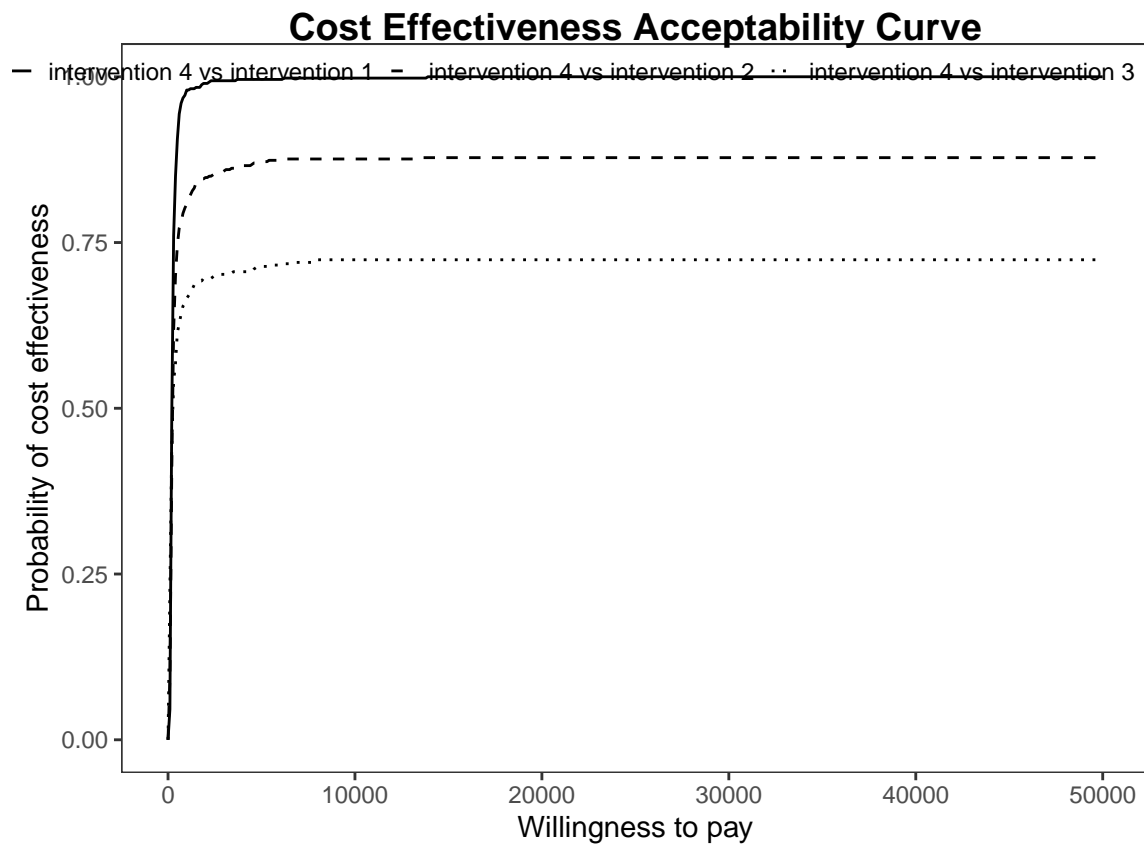
```
ceac.plot(he, graph = "ggplot2", pos = c(0, 1))
```



```
ceac.plot(he, graph = "ggplot2", pos = c(1, 0))
```



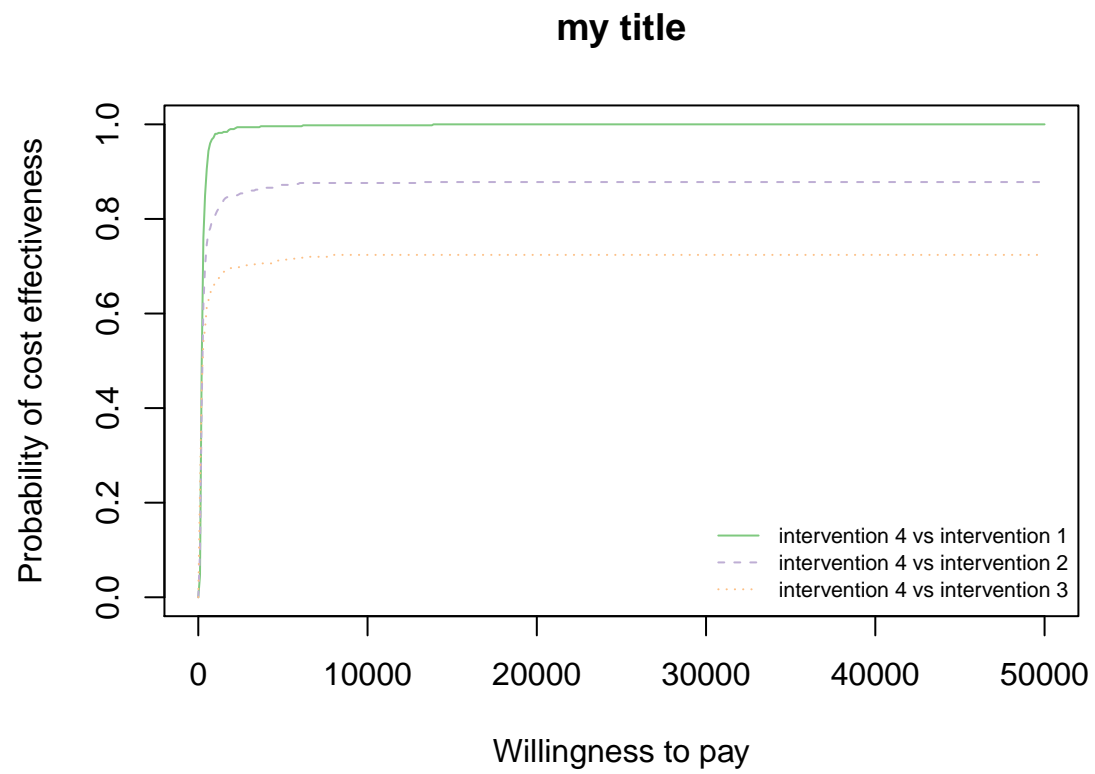
```
ceac.plot(he, graph = "ggplot2", pos = c(1, 1))
```

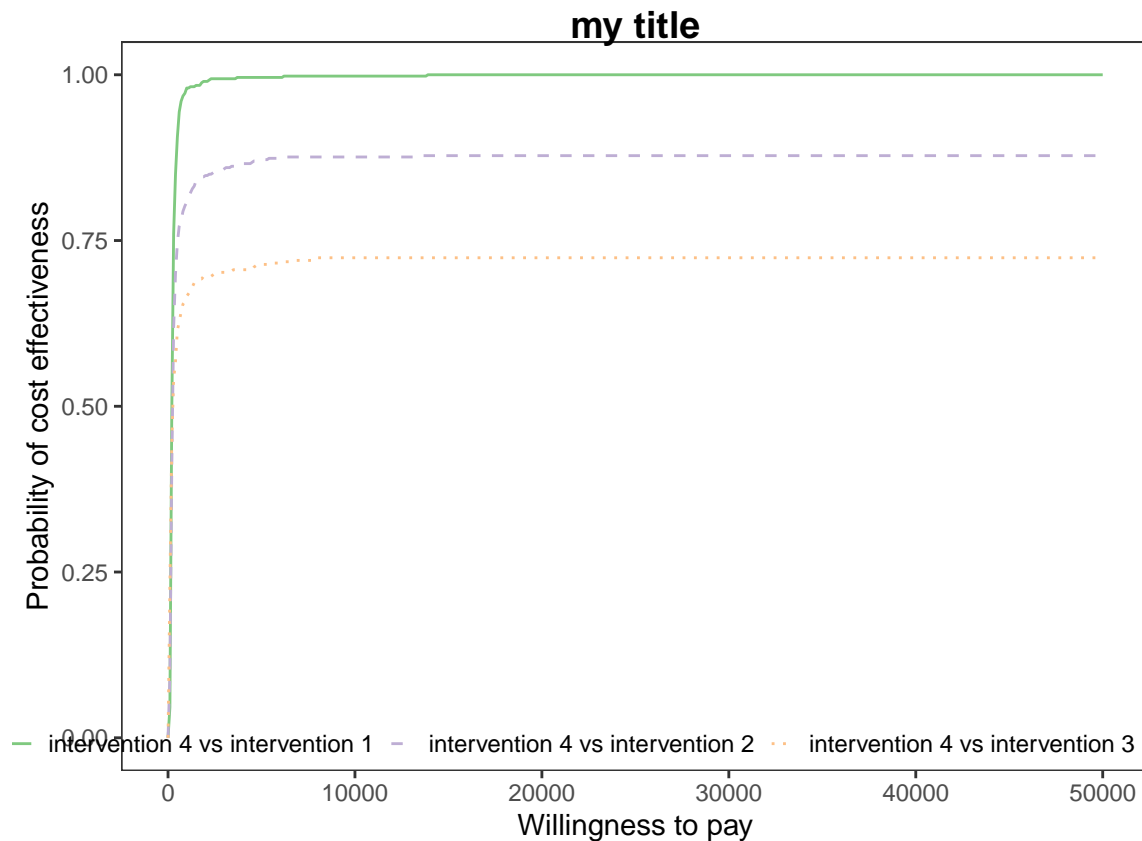
Define colour palette.

```
mypalette <- RColorBrewer::brewer.pal(3, "Accent")
```

```
ceac.plot(he,
  graph = "base",
  title = "my title",
  line = list(colors = mypalette),
  pos = FALSE)
```



```
ceac.plot(he,  
  graph = "ggplot2",  
  title = "my title",  
  line = list(colors = mypalette),  
  pos = FALSE)
```



Pair-wise comparisons

Again, without loss of generality, if we assume that we are interested in intervention $i = 1$, then we wish to calculate

$$p(NB_1 = \max\{NB_i : i \in S\} | k)$$

This can be approximated by the following.

$$\frac{1}{N} \sum_j^N \prod_{i \in S} \mathbb{I}(k \Delta e_{1,i}^j - \Delta c_{1,i}^j)$$

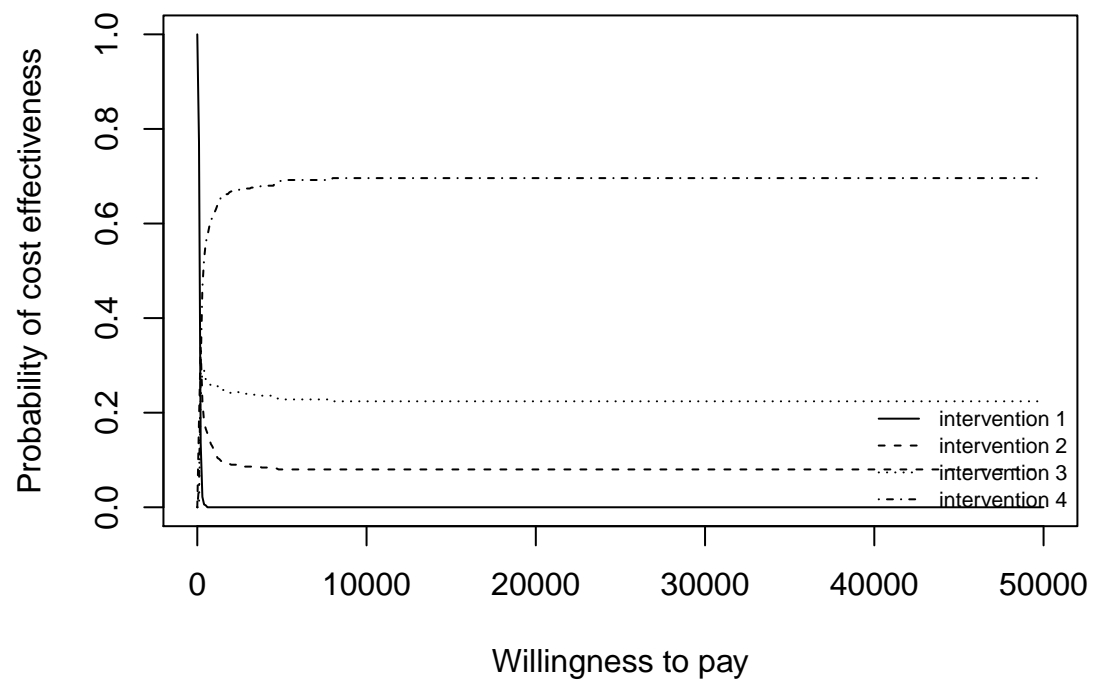
R code In BCEA we first we must determine all combinations of paired interventions using the `multi.ce()` function.

```
he <- multi.ce(he)
```

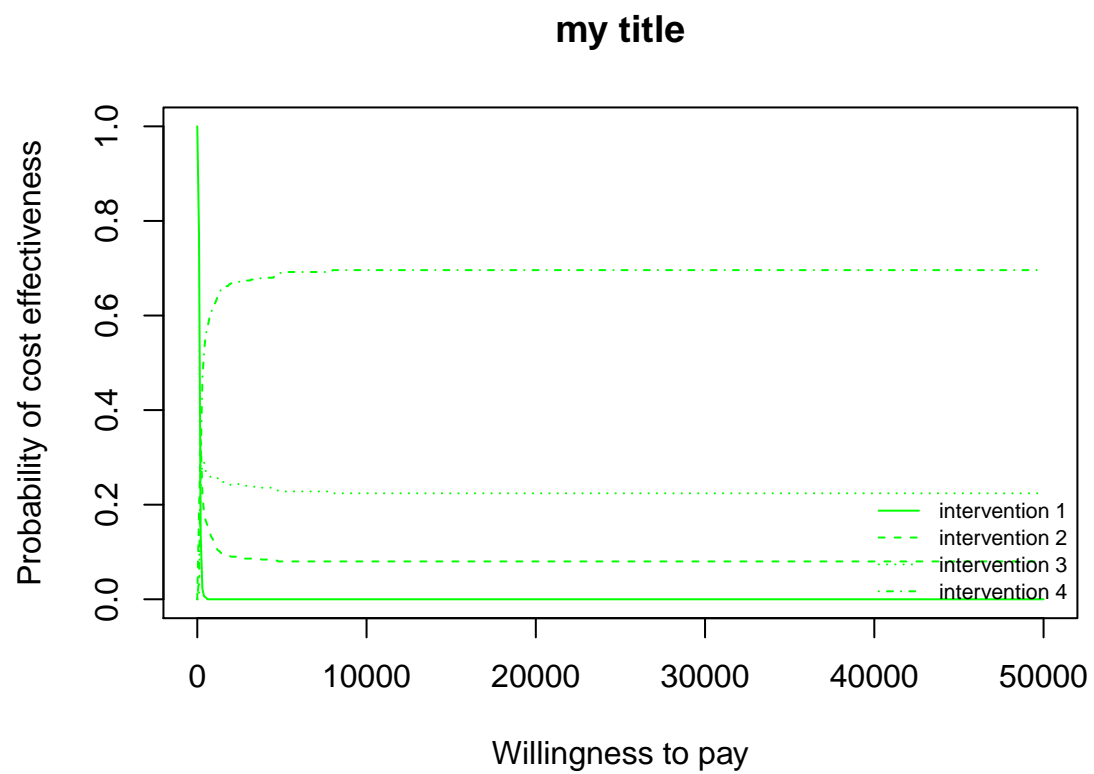
We can use the same plotting calls as before i.e. `ceac.plot()` and BCEA will deal with the pairwise situation appropriately. Note that in this case the probabilities at a given willingness to pay sum to 1.

```
ceac.plot(he, graph = "base")
#> Wrong number of colours provided. Falling back to default
```

Cost Effectiveness Acceptability Curve

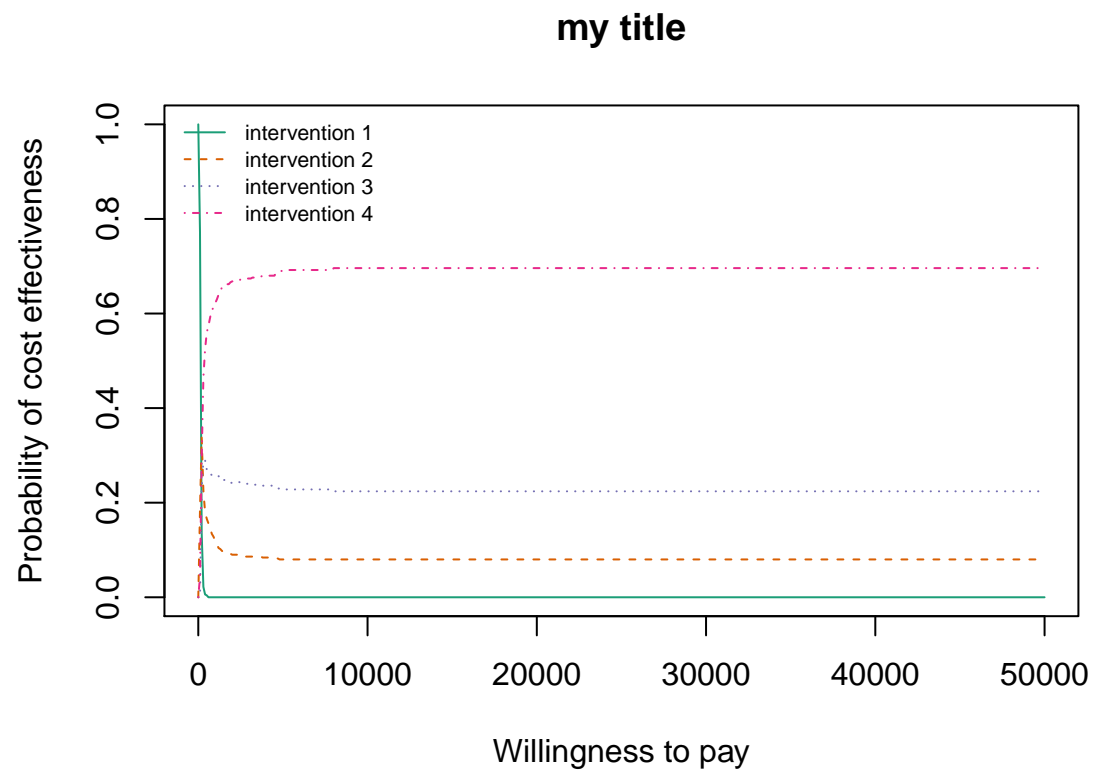


```
ceac.plot(he,  
  graph = "base",  
  title = "my title",  
  line = list(colors = "green"),  
  pos = FALSE)  
#> Wrong number of colours provided. Falling back to default
```



```
mypalette <- RColorBrewer::brewer.pal(4, "Dark2")

ceac.plot(he,
  graph = "base",
  title = "my title",
  line = list(colors = mypalette),
  pos = c(0,1))
```



```
ceac.plot(he,  
  graph = "ggplot2",  
  title = "my title",  
  line = list(colors = mypalette),  
  pos = c(0,1))
```

