BCEA: a R package to run Bayesian cost-effectiveness analysis

Gianluca Baio

Department of Statistical Science, University College London (UK)
Department of Statistics, University of Milano Bicocca (Italy)

gianluca@stats.ucl.ac.uk

European Conference on Health Economics
Zürich University Centre

20 July 2012

What is BCEA not?

- BCEA is **not** a package to automatically run a Bayesian analysis
  - It cannot build the health economic model for you
  - It does not prepare the data to be used in the model
  - It does not automatically run the MCMC simulations from the posterior distributions of the Bayesian model
  - It does not choose the prior distributions for you

BCEA: a package for Bayesian health economics

What is BCEA not?

- BCEA is **not** a package to automatically run a Bayesian analysis
  - It cannot build the health economic model for you
  - It does not prepare the data to be used in the model
  - It does not automatically run the MCMC simulations from the posterior distributions of the Bayesian model
  - It does not choose the prior distributions for you

So what *is* it, then?

- BCEA is a package that provides a set of specific functions to systematically post-process the output of a Bayesian health economic model
- Uses R (http://cran.r-project.org/) to achieve this
  - R is particularly good at interacting with standard MCMC software
    - WinBUGS (http://www.mrc-bsu.cam.ac.uk/bugs/winbugs/contents.shtml)
    - JAGS (http://mcmc-jags.sourceforge.net/)
  - R is **free** and there is a very large community of contributors
  - R is specifically designed for statistical analysis and has very good graphical capabilities

How does BCEA work?

1. Pre-process the data
   - Create, aggregate, modify original variables

How does BCEA work?

1. Pre-process the data
   - Create, aggregate, modify original variables
2. Code the Bayesian model to describe the distributional assumptions
   - In BUGS/JAGS this is usually done in a txt file

How does BCEA work?

1. Pre-process the data
   - Create, aggregate, modify original variables
2. Code the Bayesian model to describe the distributional assumptions
   - In BUGS/JAGS this is usually done in a txt file
3. Interface R with BUGS/JAGS
   - Runs the model
   - Produces the MCMC estimation of the posterior distributions of interest

How does BCEA work?

1. Pre-process the data
   - Create, aggregate, modify original variables
2. Code the Bayesian model to describe the distributional assumptions
   - In BUGS/JAGS this is usually done in a txt file
3. Interface R with BUGS/JAGS
   - Runs the model
   - Produces the MCMC estimation of the posterior distributions of interest
4. Post-process the results
   - Create suitable variables of cost and/or effectiveness

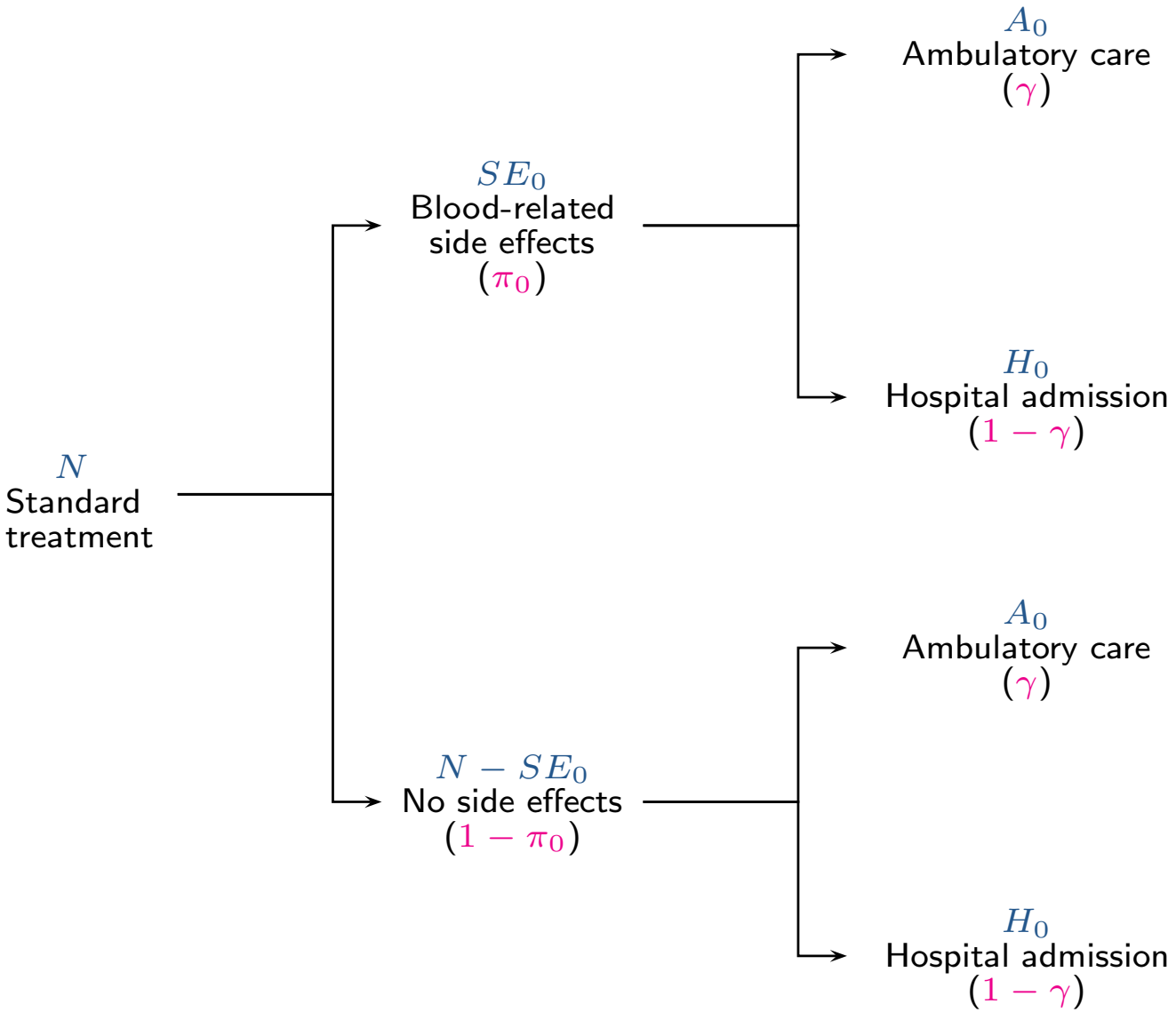
How does BCEA work?

1. Pre-process the data
   - Create, aggregate, modify original variables
2. Code the Bayesian model to describe the distributional assumptions
   - In BUGS/JAGS this is usually done in a txt file
3. Interface R with BUGS/JAGS
   - Runs the model
   - Produces the MCMC estimation of the posterior distributions of interest
4. Post-process the results
   - Create suitable variables of cost and/or effectiveness
5. Run the economic analysis
   - Compute expected utilities and identify the most cost-effective intervention
   - Compute EIB, ICER, CEAC, EVPI, ...
   - Cost-effectiveness plot and other graphical summaries

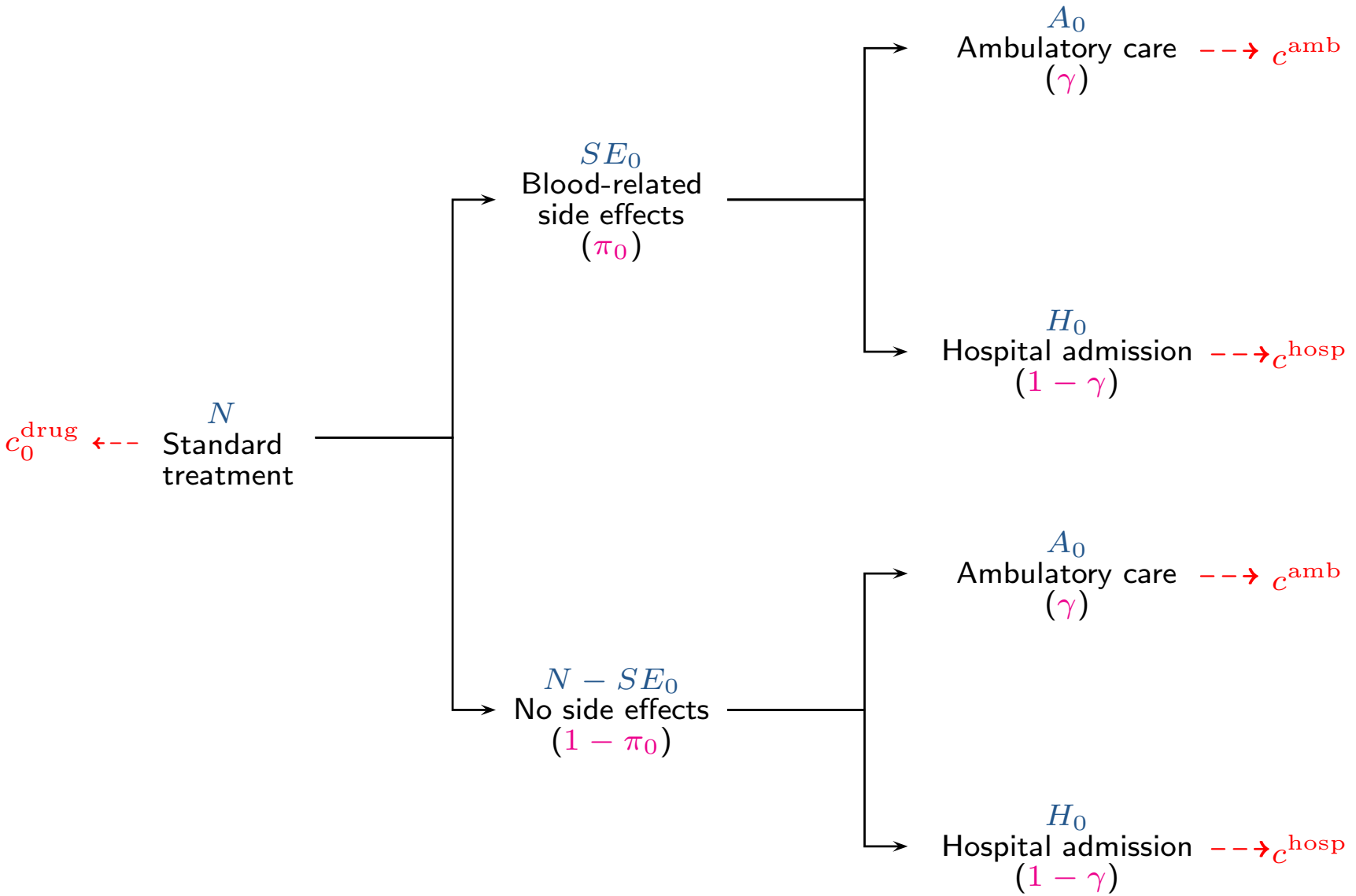
How does BCEA work?

1. Pre-process the data
   - Create, aggregate, modify original variables
2. Code the Bayesian model to describe the distributional assumptions
   - In BUGS/JAGS this is usually done in a txt file
3. Interface R with BUGS/JAGS
   - Runs the model
   - Produces the MCMC estimation of the posterior distributions of interest
4. Post-process the results
   - Create suitable variables of cost and/or effectiveness
5. Run the economic analysis
   - Compute expected utilities and identify the most cost-effective intervention
   - Compute EIB, ICER, CEAC, EVPI, ...
   - Cost-effectiveness plot and other graphical summaries

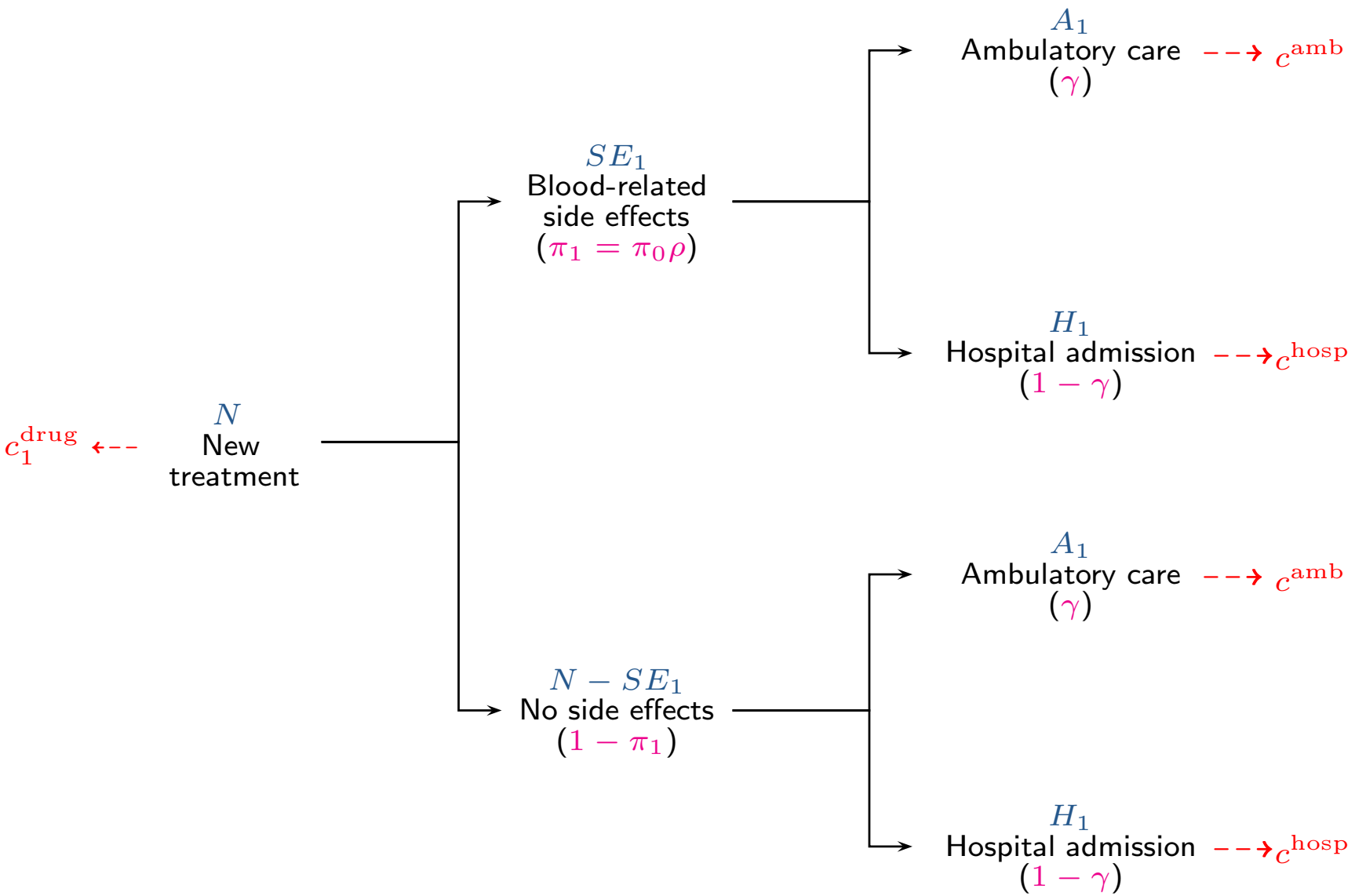
Example: Chemotherapy



Example: Chemotherapy



Example: Chemotherapy



Working with BCEA

- The model can be coded in BUGS/JAGS

```
model {
    pi[1] ~ dbeta(a.pi,b.pi)          # Baseline probability of side effects (t=0)
    pi[2] <- pi[1]*rho                # Decreased probability of side effects (t=1)
    rho ~ dnorm(m.rho,tau.rho)        # Decrement rate in side effects for t=1
    gamma ~ dbeta(a.gamma,b.gamma)    # Probability of ambulatory care
    c.amb ~ dlnorm(m.amb,tau.amb)     # Unit cost of ambulatory care
    c.hosp ~ dlnorm(m.hosp,tau.hosp)  # Unit cost of hospitalisation
    for (t in 1:2) {
        SE[t] ~ dbin(pi[t],N)         # Predicted no. patients with side effects
        A[t] ~ dbin(gamma,SE[t])      # Predicted no. patients needing ambulatory care
        H[t] <- SE[t] - A[t]          # Predicted no. patients needing hospitalisation
    }
}
```

and then run from R to perform the MCMC estimation using suitable libraries (eg R2WinBUGS or R2jags)

Working with BCEA

- The model can be coded in BUGS/JAGS

```
model {
    pi[1] ~ dbeta(a.pi,b.pi)          # Baseline probability of side effects (t=0)
    pi[2] <- pi[1]*rho                # Decreased probability of side effects (t=1)
    rho ~ dnorm(m.rho,tau.rho)        # Decrement rate in side effects for t=1
    gamma ~ dbeta(a.gamma,b.gamma)    # Probability of ambulatory care
    c.amb ~ dlnorm(m.amb,tau.amb)     # Unit cost of ambulatory care
    c.hosp ~ dlnorm(m.hosp,tau.hosp)  # Unit cost of hospitalisation
    for (t in 1:2) {
        SE[t] ~ dbin(pi[t],N)         # Predicted no. patients with side effects
        A[t] ~ dbin(gamma,SE[t])      # Predicted no. patients needing ambulatory care
        H[t] <- SE[t] - A[t]          # Predicted no. patients needing hospitalisation
    }
}
```

  and then run from R to perform the MCMC estimation using suitable libraries (eg R2WinBUGS or R2jags)

- This will generate samples from the posterior distributions of the relevant quantities, eg: $\boldsymbol{\theta}_t = (\pi_t, \gamma, \rho, SE_t, A_t, H_t)$

Working with BCEA

- The model can be coded in BUGS/JAGS

```
model {
    pi[1] ~ dbeta(a.pi,b.pi)          # Baseline probability of side effects (t=0)
    pi[2] <- pi[1]*rho                # Decreased probability of side effects (t=1)
    rho ~ dnorm(m.rho,tau.rho)        # Decrement rate in side effects for t=1
    gamma ~ dbeta(a.gamma,b.gamma)    # Probability of ambulatory care
    c.amb ~ dlnorm(m.amb,tau.amb)     # Unit cost of ambulatory care
    c.hosp ~ dlnorm(m.hosp,tau.hosp)  # Unit cost of hospitalisation
    for (t in 1:2) {
        SE[t] ~ dbin(pi[t],N)         # Predicted no. patients with side effects
        A[t] ~ dbin(gamma,SE[t])      # Predicted no. patients needing ambulatory care
        H[t] <- SE[t] - A[t]          # Predicted no. patients needing hospitalisation
    }
}
```

  and then run from R to perform the MCMC estimation using suitable libraries (eg R2WinBUGS or R2jags)

- This will generate samples from the posterior distributions of the relevant quantities, eg: $\boldsymbol{\theta}_t = (\pi_t, \gamma, \rho, SE_t, A_t, H_t)$

- Using one of the libraries above, the simulations will be available in the R workspace and can be used to post-process the results of the Bayesian model to run the health economic evaluation

Working with BCEA

- First, need to install the package [*only the first time/needs web connection*]

```
install.packages("BCEA")
```

Working with BCEA

- First, need to install the package [*only the first time/needs web connection*]
  ```
  install.packages("BCEA")
  ```
- Then need to load the library, which in R is done with
  ```
  library(BCEA)
  ```

Working with BCEA

- First, need to install the package [*only the first time/needs web connection*]
  ```
  install.packages("BCEA")
  ```
- Then need to load the library, which in R is done with
  ```
  library(BCEA)
  ```
- [*Optional*] We can define a vector of labels to be associated with the interventions being compared
  ```
  treats <- c("Old Chemotherapy","New Chemotherapy")
  ```

Working with BCEA

- First, need to install the package [*only the first time/needs web connection*]
```
install.packages("BCEA")
```
- Then need to load the library, which in R is done with
```
library(BCEA)
```
- [*Optional*] We can define a vector of labels to be associated with the interventions being compared
```
treats <- c("Old Chemotherapy","New Chemotherapy")
```
- Then, need to define the variables of cost and effectiveness in suitable matrices [*if not already available from the model*]
```
e <- c <- matrix(NA,1000,2)
e <- N - SE
for (t in 1:2) {
   c[,t] <- c.drug[t]*(N-SE[,t]) +
            (c.amb+c.drug[t])*A[,t] +
            (c.hosp+c.drug[t])*H[,t]
}
```

Working with BCEA

- Finally, we are ready to call the function bcea that runs the economic analysis

```
m <- bcea(e=e,c=c,ref=2,interventions=treats,Kmax=50000)
```

Working with BCEA

- Finally, we are ready to call the function bcea that runs the economic analysis

```
m <- bcea(e=e,c=c,ref=2,interventions=treats,Kmax=50000)
```

- The inputs of the function are
  - e: the matrix containing the simulations from the posterior distributions of the variable of clinical effectiveness ($n_{\text{sim}} \times n_{\text{int}}$ values)
  - c: the matrix containing the simulations from the posterior distributions of the variable of cost ($n_{\text{sim}} \times n_{\text{int}}$ values)
  - ref: an indication of which intervention is to be taken as reference (default: the intervention in the first column of e or c)
  - interventions: a vector of labels for the interventions being compared
  - Kmax: the maximum value of k, the parameter of willingness to pay

Working with BCEA

- Finally, we are ready to call the function bcea that runs the economic analysis

```
m <- bcea(e=e,c=c,ref=2,interventions=treats,Kmax=50000)
```

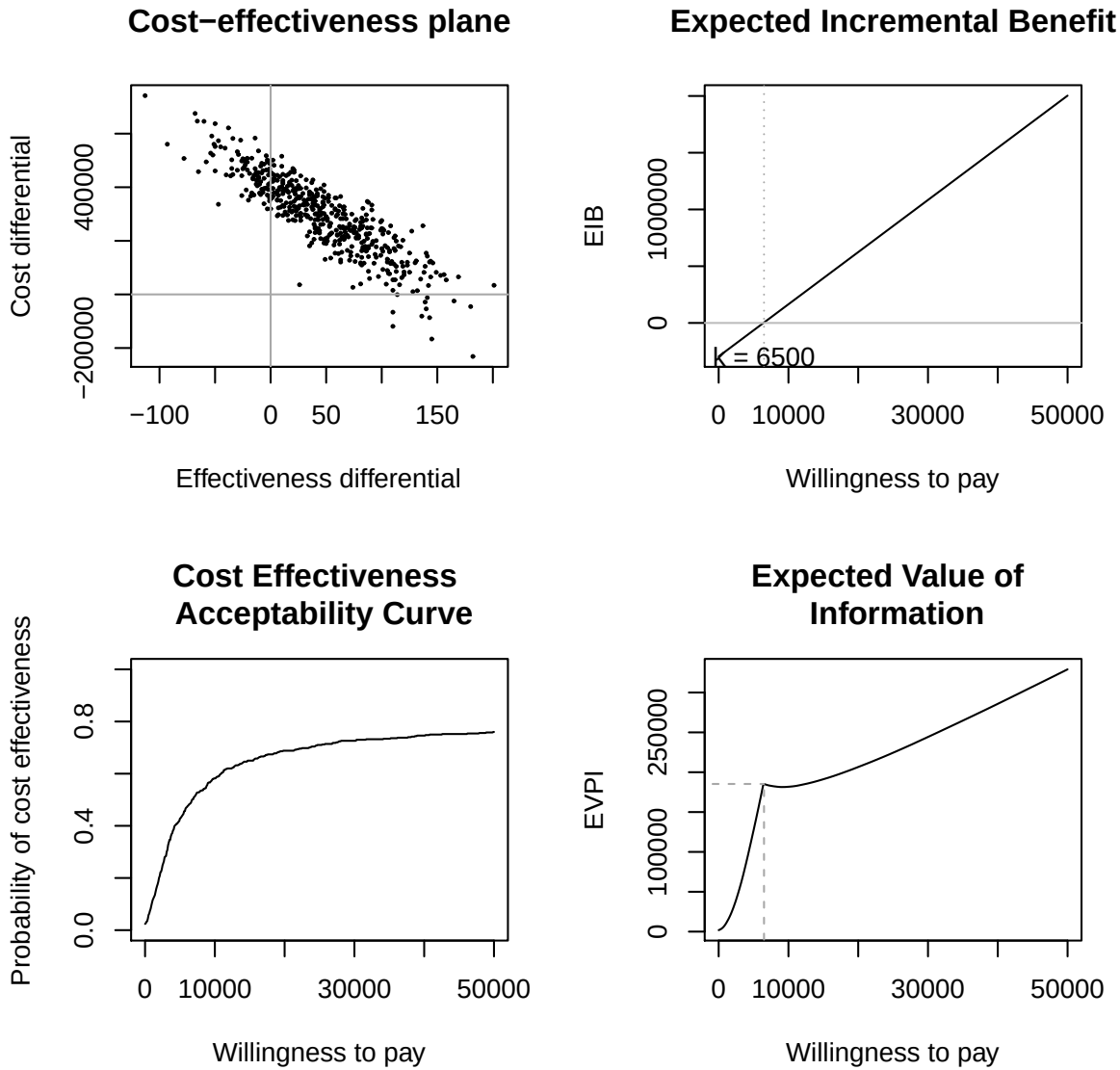
- The inputs of the function are
  - e: the matrix containing the simulations from the posterior distributions of the variable of clinical effectiveness ($n_{\text{sim}} \times n_{\text{int}}$ values)
  - c: the matrix containing the simulations from the posterior distributions of the variable of cost ($n_{\text{sim}} \times n_{\text{int}}$ values)
  - ref: an indication of which intervention is to be taken as reference (default: the intervention in the first column of e or c)
  - interventions: a vector of labels for the interventions being compared
  - Kmax: the maximum value of k, the parameter of willingness to pay

- The output is an object m, containing several elements

m$n.sim	m$delta.c	m$ceac	m$best	m$ol	m$comp
m$n.comparators	m$ICER	m$ib	m$U	m$evi	m$step
m$n.comparisons	m$Kmax	m$eib	m$vi	m$interventions	
m$delta.e	m$k	m$kstar	m$Ustar	m$ref	

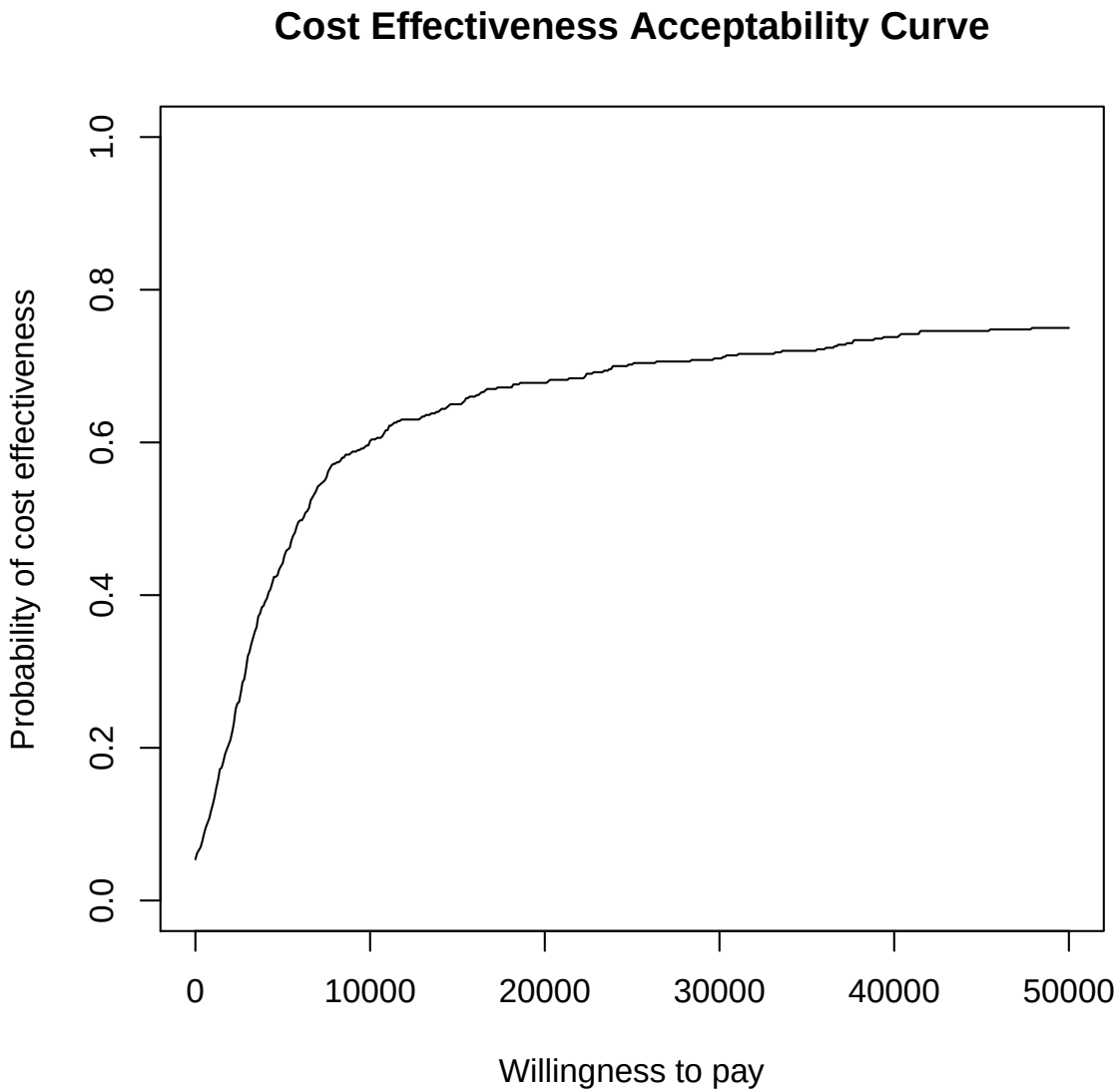
Working with BCEA

- These elements are processed to produce relevant summaries and graphs
- For example, the code `plot(m)` generates



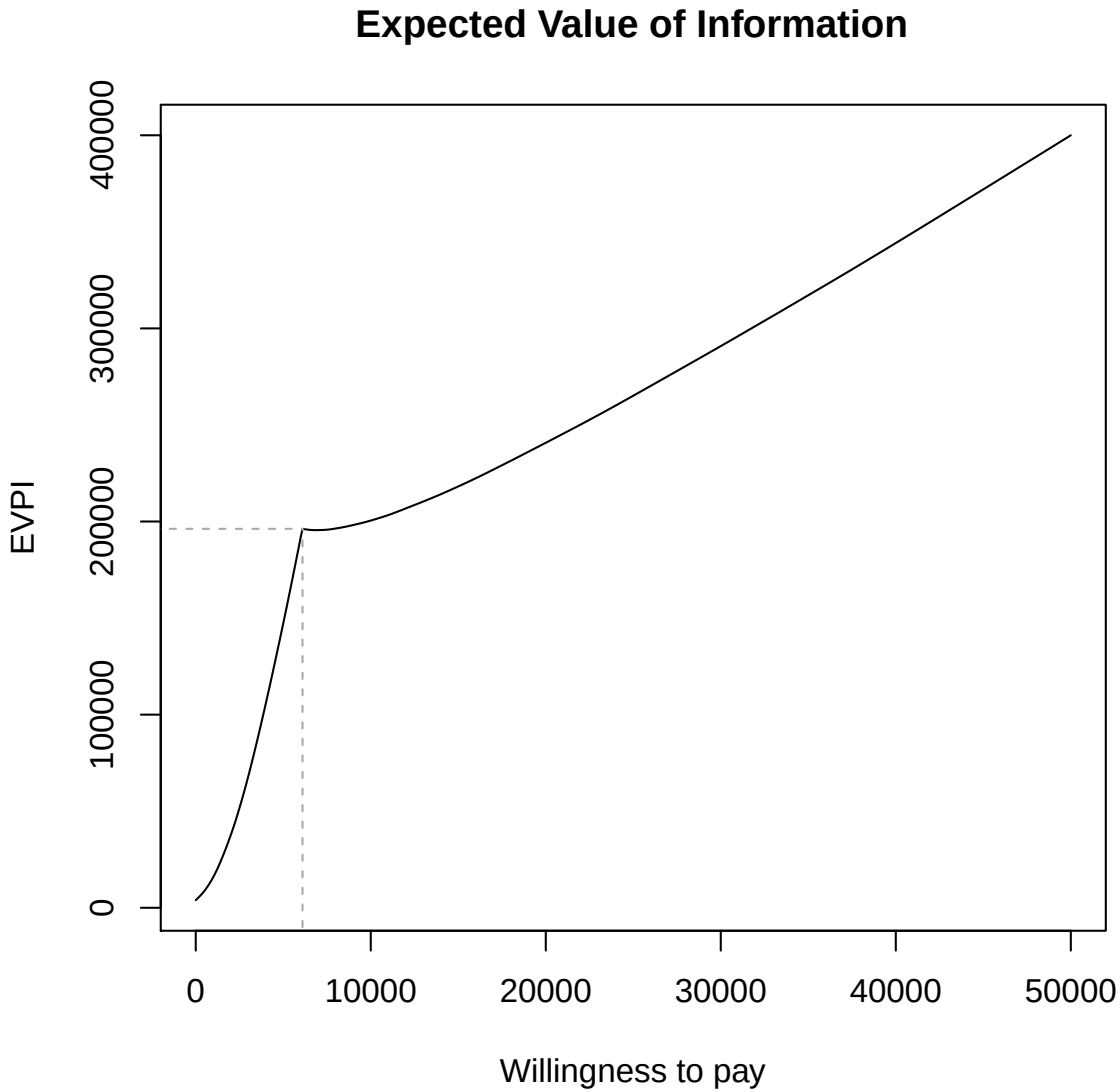
Working with BCEA

- The plots can be obtained separately
- For example: `ceac.plot(m)`



Working with BCEA

- The plots can be obtained separately
- For example: `evi.plot(m)`



Post-processing with BCEA

- Similarly, the code `summary(m)` produces a synthesis of the main results

```
Cost-effectiveness analysis summary

Reference intervention: New Chemotherapy
Comparator intervention: Old Chemotherapy

Optimal decision: choose Old Chemotherapy for k<6500 and
                         New Chemotherapy for k>=6500


Analysis for willingness to pay parameter k = 25000

                  Expected utility
Old Chemotherapy          18608376
New Chemotherapy          19410840

                                          EIB  CEAC   ICER
New Chemotherapy vs Old Chemotherapy 802465 0.728 6497.1

Optimal intervention (max expected utility) for k=25000: New Chemotherapy

EVPI 237560
```

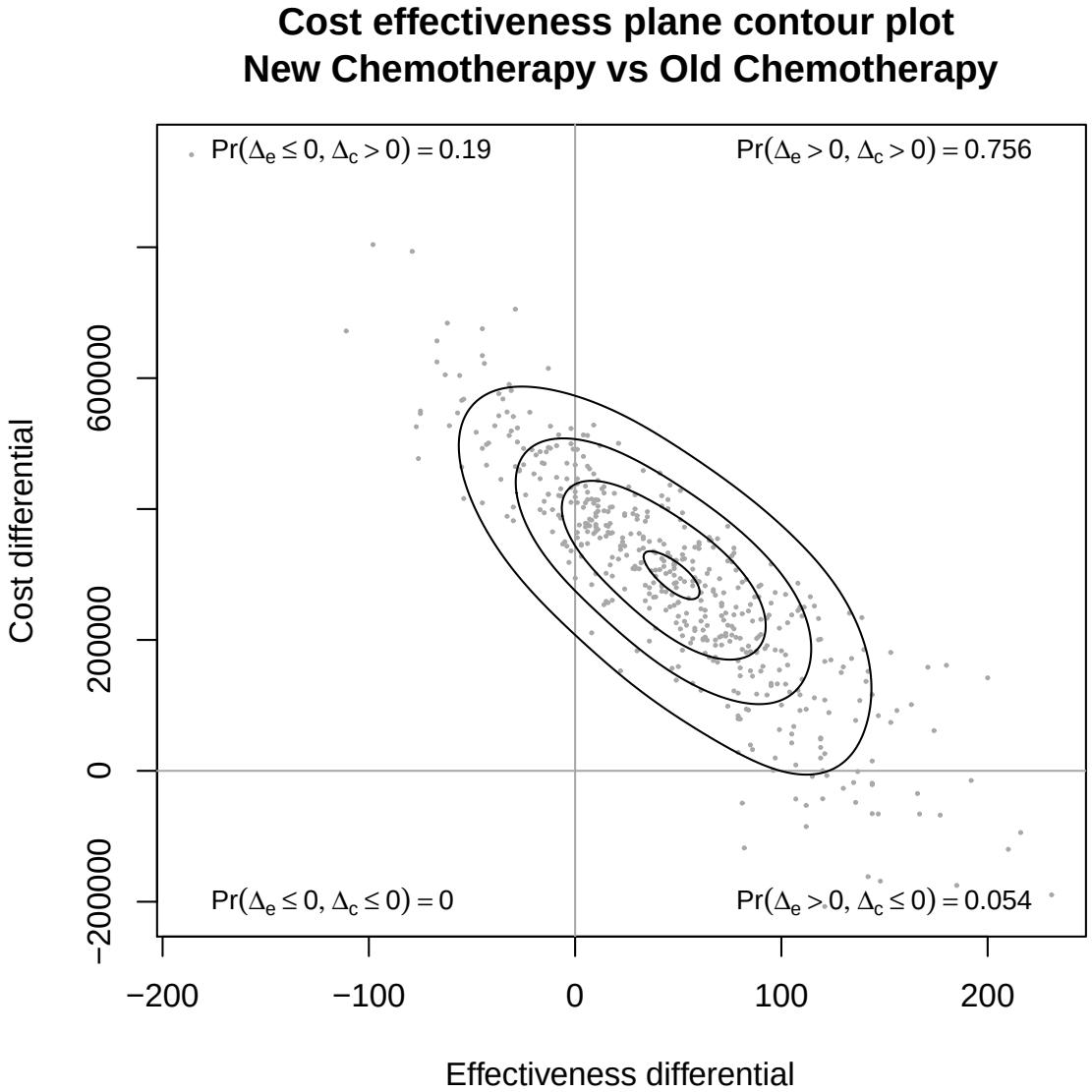
Post-processing with BCEA

- It is possible to specify additional options, eg `summary(m,wtp=1000)`

```
Cost-effectiveness analysis summary

Reference intervention: New Chemotherapy
Comparator intervention: Old Chemotherapy

Optimal decision: choose Old Chemotherapy for k<6500 and
                         New Chemotherapy for k>=6500


Analysis for willingness to pay parameter k = 1000

                  Expected utility
Old Chemotherapy           -44691
New Chemotherapy          -288267

                                          EIB  CEAC   ICER
New Chemotherapy vs Old Chemotherapy -243576 0.126 6497.1

Optimal intervention (max expected utility) for k=1000: Old Chemotherapy

EVPI 15877
```

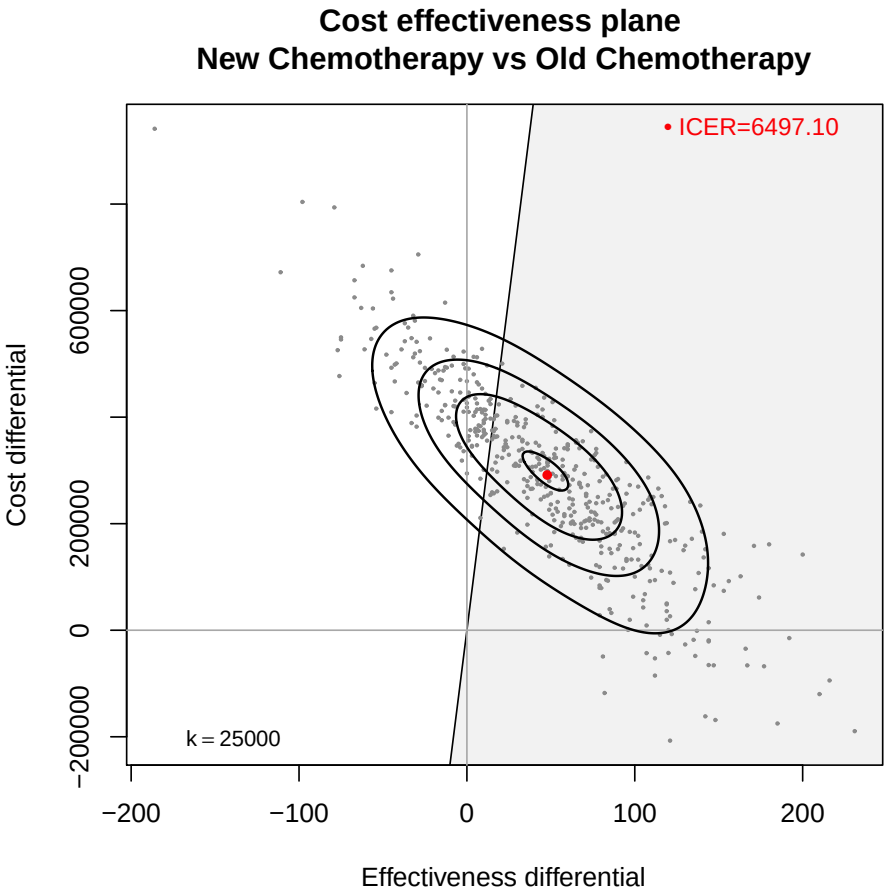
Working with BCEA

- The code `contour(m)` generates a contourplot of the cost-effectiveness plane and also estimates the proportion of points lying in each quadrant



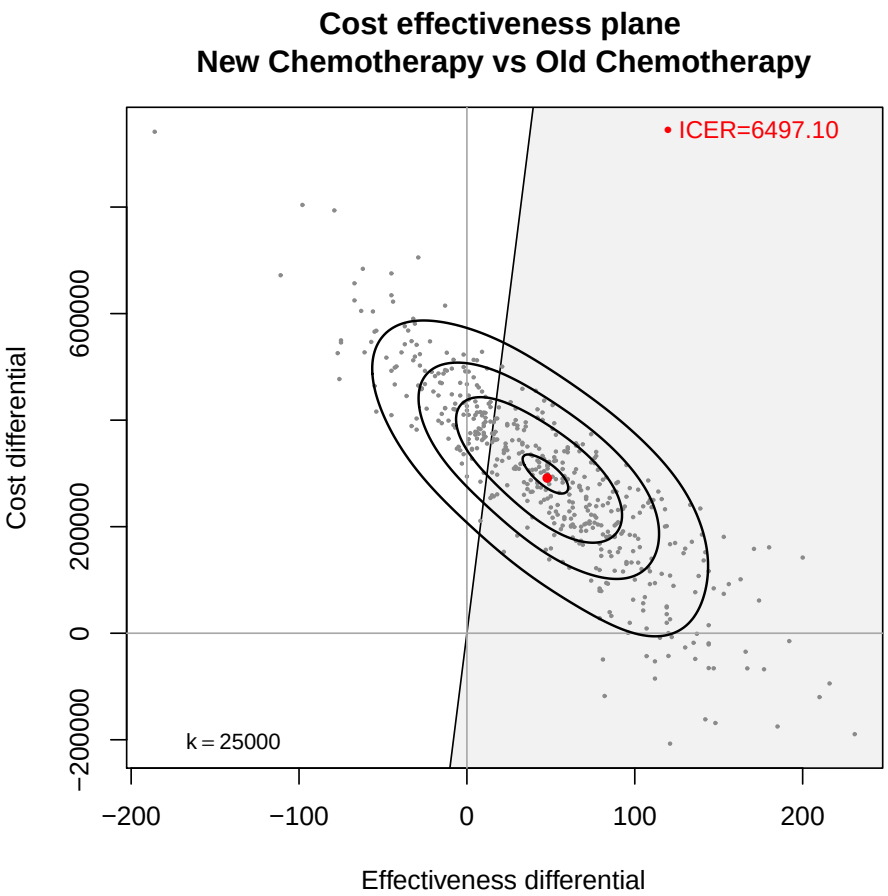
The specialised function `contour2` also shows the **sustainability area**

- `contour2(m)`

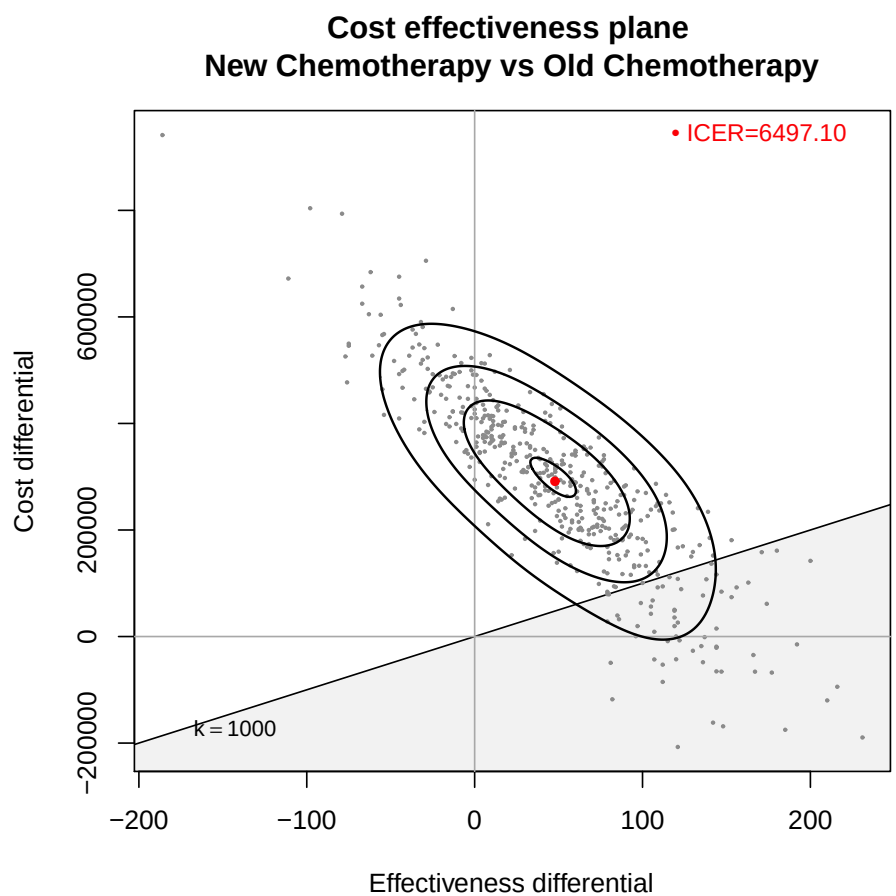


The specialised function `contour2` also shows the **sustainability area**

- `contour2(m)`

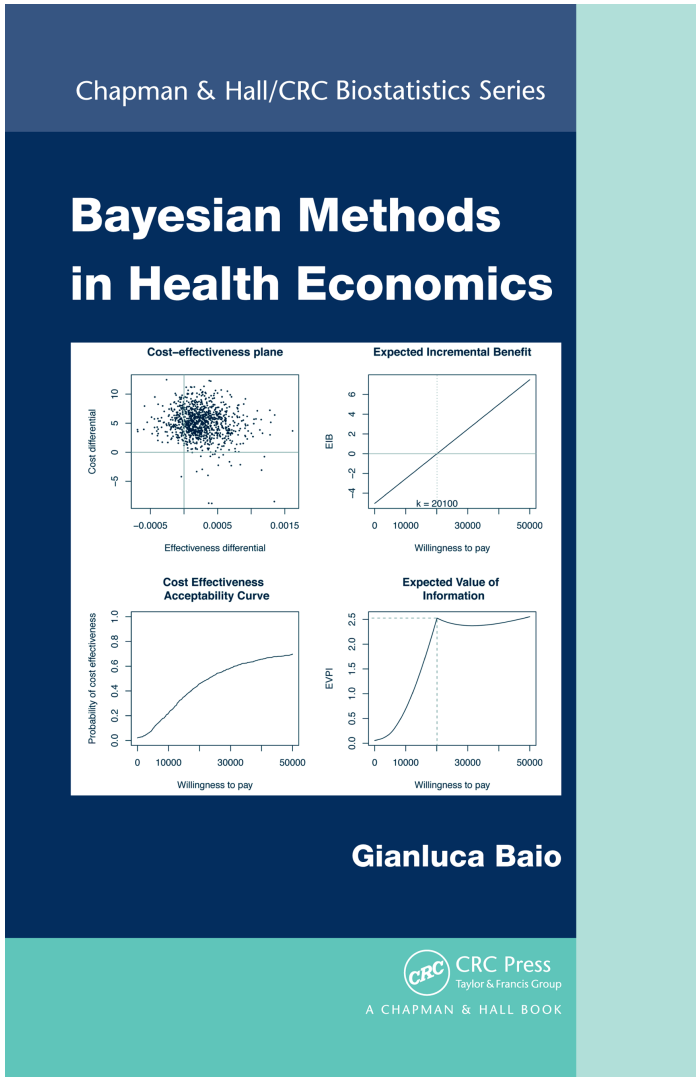


- `contour2(m,wtp=1000)`



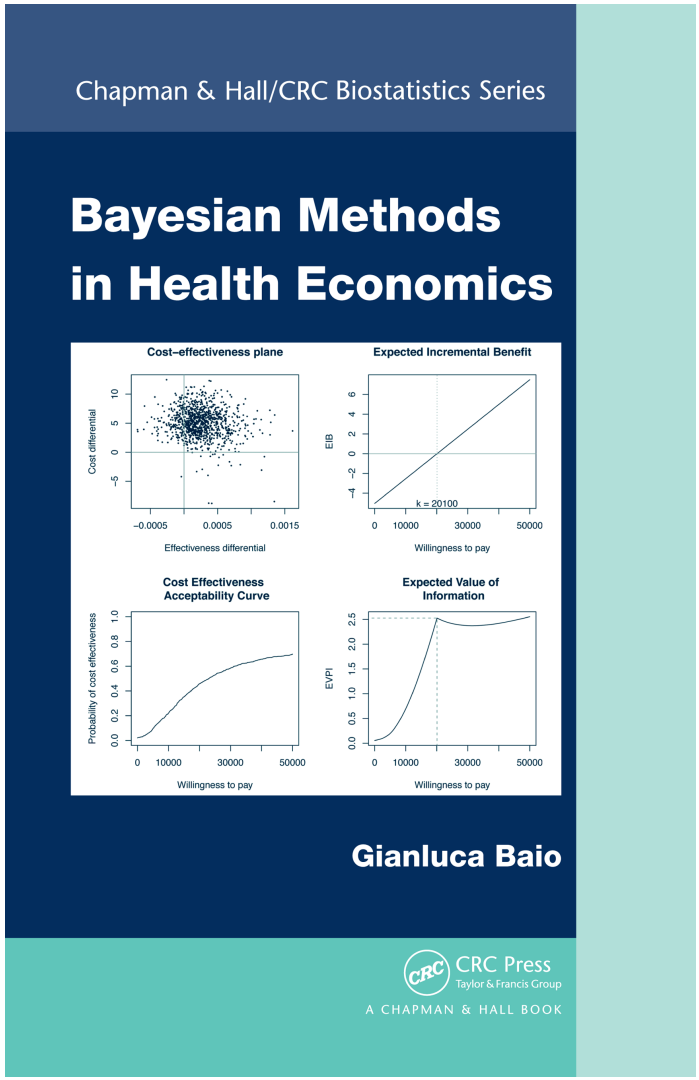
More info (and shameless marketing)

- `BCEA` features heavily in the brilliant, forthcoming book on Bayesian methods in health economics (written by me 😉)
- In the book, I describe the entire process of *making* Bayesian analysis in health economics, including pre-processing of the data and running the model



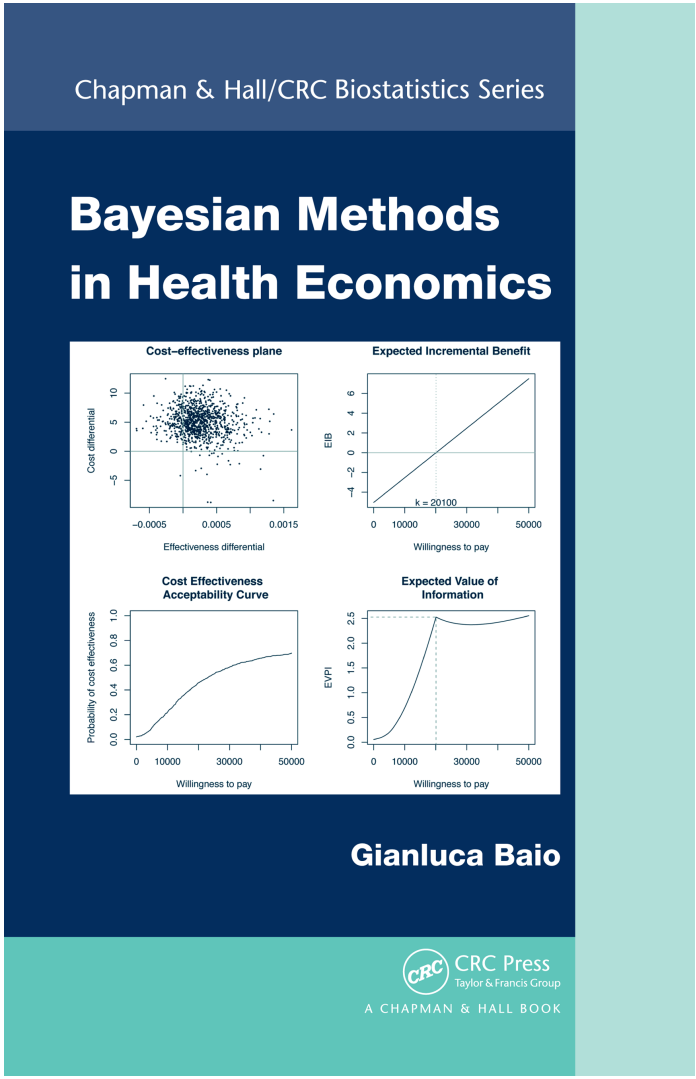
More info (and shameless marketing)

- BCEA features heavily in the brilliant, forthcoming book on Bayesian methods in health economics (written by me 😉)
- In the book, I describe the entire process of *making* Bayesian analysis in health economics, including pre-processing of the data and running the model
- Other analyses are available through BCEA and described in the book
  - Inclusion of risk aversion parameters
  - Mixed strategies
  - Possible extensions to compute the expected value of partial information



More info (and shameless marketing)

- BCEA features heavily in the brilliant, forthcoming book on Bayesian methods in health economics (written by me 😉)
- In the book, I describe the entire process of *making* Bayesian analysis in health economics, including pre-processing of the data and running the model
- Other analyses are available through BCEA and described in the book
  - Inclusion of risk aversion parameters
  - Mixed strategies
  - Possible extensions to compute the expected value of partial information
- More info is available at the webpages www.statistica.it/gianluca/BMHE and www.statistica.it/gianluca/BCEA
- Also, some discussion (and more to come) in a few posts on gianlubaio.blogspot.co.uk
- And you can even ask me for the promo code!



Thank you!