VoI book code: Case study and guidelines for estimating EVPPI using regression in R

Change this path to reflect where you downloaded the Chemotherapy_Book repository

This block of code is only needed if you want to compile this Rmd source file into a document.

Draw a sample from probabilistic analysis of the model.

```
source("04_analysis/01_model_run.R")
nb <- as.data.frame(m_costs_effects[,1,]*20000 - m_costs_effects[,2,])</pre>
```

Calculating single-parameter EVPPI.

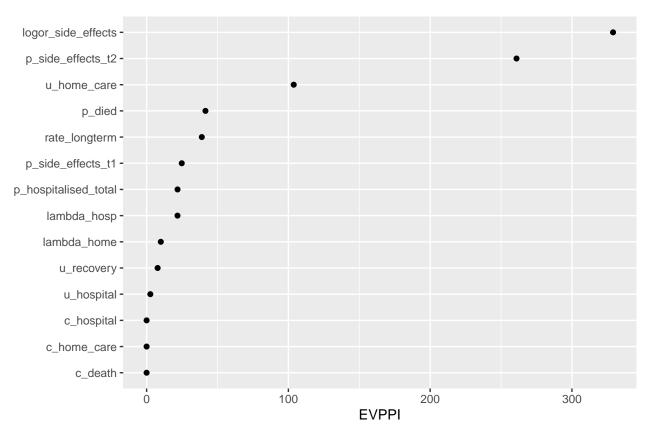
Calculate the single-parameter EVPPI for all the parameters in the model. This returns a data frame containing the EVPPI estimates.

```
library(voi)
pars_all <- as.list(names(m_params))
ev_single <- evppi(outputs=nb, inputs=m_params, pars=pars_all)
ev_single</pre>
```

```
##
                              evppi
                      pars
## 1
         p_side_effects_t1 24.7915
## 2
         p_side_effects_t2 260.9055
## 3
                             0.0000
               c_home_care
## 4
                c_hospital
                             0.0032
## 5
                   c_death
                             0.0000
## 6
                u recovery
                             7.7910
## 7
               u_home_care 103.7762
## 8
                u hospital
                             2.6355
        logor_side_effects 329.0098
## 9
## 10 p_hospitalised_total 21.8343
## 11
                    p_died 41.5116
## 12
               lambda home 10.0146
## 13
               lambda_hosp
                            21.7919
             rate_longterm 38.9335
```

Dot-plot of the estimates, sorted with the highest values at the top.

```
plot(ev_single, order = TRUE)
```



Single-parameter EVPPIs for a specified subset of parameters.

Multi-parameter EVPPI for four groups of parameters: those associated with side effects, transition probabilites, costs and utilities respectively.

```
par_groups <- list(
    "side_effects" = c("p_side_effects_t1","logor_side_effects"),
    "trans_probs" = c("p_hospitalised_total","p_died","lambda_home","lambda_hosp"),
    "costs" = c("c_home_care","c_hospital","c_death"),
    "utilities" = c("u_recovery","u_home_care","u_hospital")
)
ev_grouped <- evppi(outputs=nb, inputs=m_params, pars=par_groups)
ev_grouped</pre>
```

```
## pars evppi
## 1 side_effects 330.62
## 2 trans_probs 63.14
## 3 costs 7.01
## 4 utilities 105.27
```

In this example, it is clear that the parameters associated with the risk of side effects have the greatest EVPPI.

Checking regression models for EVPPI calculation

Figure shown in the book

```
ev_single <- evppi(outputs=nb, inputs=m_params, pars=pars_all, check=TRUE)</pre>
check_regression(ev_single, pars = "logor_side_effects")
  400 -
                                                   3000 -
                                                   2000 -
  300 -
Frequency
                                               Residuals
                                                   1000 -
  200 -
  100 -
                                                  -1000 -
    -2000
           -1000
                          1000
                                 2000
                                        3000
                                                                -2000
                                                                                     2000
                                                                            0
                     Residuals
                                                                     Fitted values
Additional analysis with standard errors:
evppi(outputs=nb, inputs=m_params, pars=list("p_side_effects_t2","u_hospital"), se=TRUE)
Alternative regression models:
evppi(outputs=nb, inputs=m_params, pars=list("p_side_effects_t2","u_hospital"))
evppi(outputs=nb, inputs=m_params, pars=list("p_side_effects_t2","u_hospital"), method="earth")
Comparing different regression specifications: single-parameter EVPPI
(e1 <- evppi(outputs=nb, inputs=m_params, pars=par_groups[1], check=TRUE))</pre>
##
             pars evppi
## 1 side_effects
                     331
(e2 <- evppi(outputs=nb, inputs=m_params, pars=par_groups[1],</pre>
             gam_formula="s(p_side_effects_t1) + s(logor_side_effects)", check=TRUE))
##
             pars evppi
## 1 side_effects
                     332
check_regression(e1, plot=FALSE)
## $AIC
## [1] 74754
check_regression(e2, plot=FALSE)
```

(e1 <- evppi(outputs=nb, inputs=m_params, pars=par_groups[1], method = "earth", check=TRUE))</pre>

\$AIC ## [1] 74838

##

earth models with two-way versus three-way interactions

pars evppi

Comparing different regression specifications: multi-parameter EVPPI