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 <- m_net_benefit[ , , wtp_seq == 20000]
```

Calculating single-parameter EVPPI.

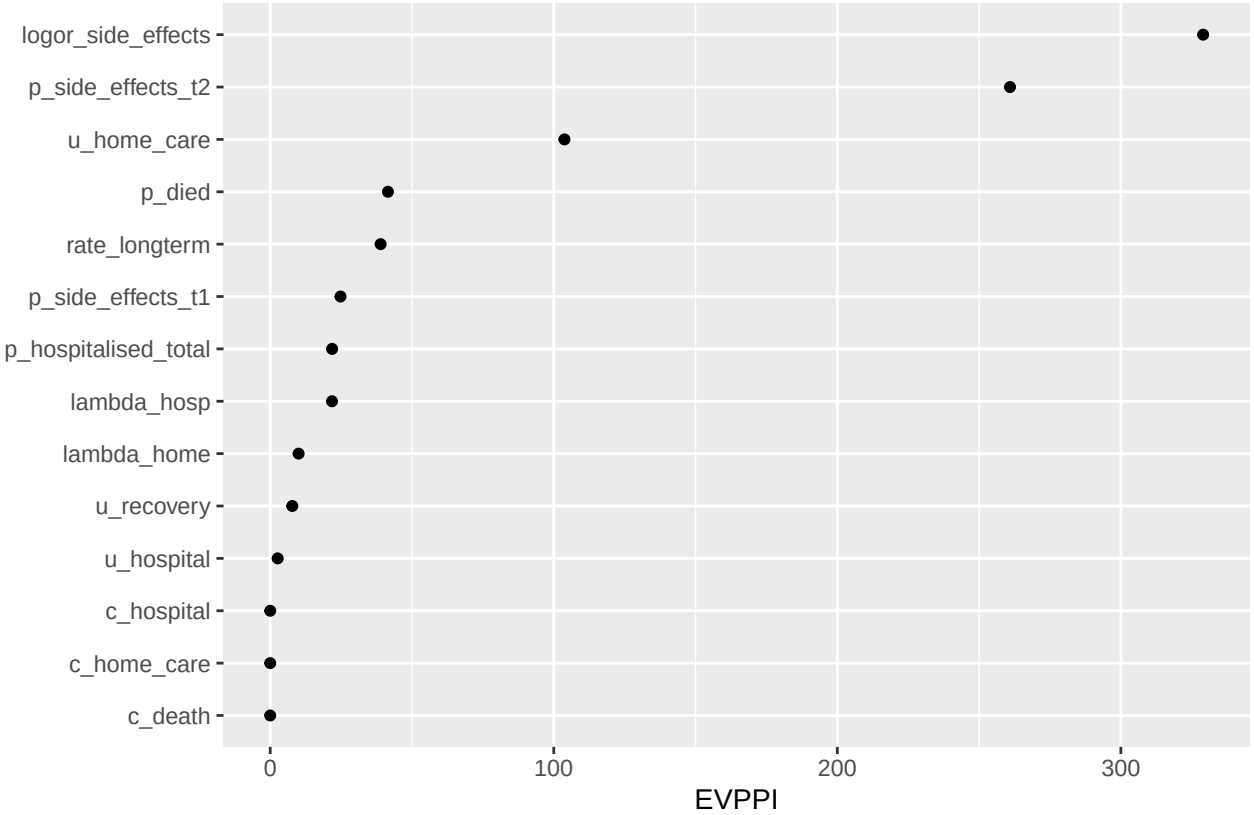
Calculate the single-parameter EVPPI for all the parameters in the model. This returns a data frame containing the EVPPI estimates.

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

```
##                    pars    evppi
## 1     p_side_effects_t1  24.7915
## 2     p_side_effects_t2 260.9055
## 3           c_home_care   0.0000
## 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
## 9    logor_side_effects 329.0098
## 10 p_hospitalised_total  21.8343
## 11               p_died  41.5116
## 12         lambda_home  10.0146
## 13         lambda_hosp  21.7919
## 14       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.

```
evppi(outputs=nb, inputs=m_params,
      pars=list("logor_side_effects", "p_side_effects_t1", "u_hospital"))
```

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
```

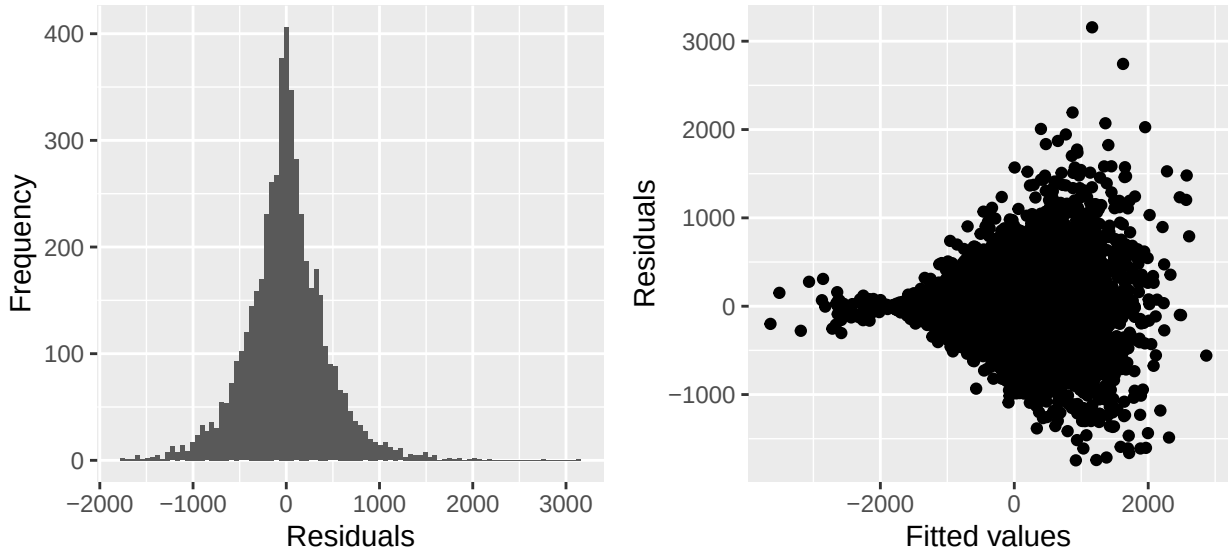
```
##           pars  evppi
## 1 side_effects 330.62
## 2  trans_probs  63.14
## 3        costs   7.01
## 4    utilities 105.22
```

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)
check_regression(ev_single, pars = "logor_side_effects")
```



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"))
```

```
##                pars  evppi
## 1 p_side_effects_t2 260.91
## 2        u_hospital   2.64
```

```
evppi(outputs=nb, inputs=m_params,
      pars = list("p_side_effects_t2","u_hospital"),
      method="earth")
```

```
##                pars evppi
## 1 p_side_effects_t2   262
## 2        u_hospital     0
```

Comparing different regression specifications: single-parameter EVPPI

```
(e1 <- evppi(outputs=nb, inputs=m_params, pars=par_groups[1], check=TRUE))
```

```
##           pars evppi
## 1 side_effects   331
```

```
(e2 <- evppi(outputs=nb, inputs=m_params, pars=par_groups[1],
             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)
```

```
## $AIC
## [1] 74838
```

`earth` models with two-way versus three-way interactions

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

```
##           pars evppi
## 1 side_effects   334
```

```
(e2 <- evppi(outputs=nb, inputs=m_params, pars=par_groups[1], method = "earth",
             degree=3, check=TRUE))
```

```
##           pars evppi
## 1 side_effects   333
```

```
check_regression(e1,plot=FALSE)
```

```
## $gcv
## [1] 185678
```

```
check_regression(e2,plot=FALSE)
```

```
## $gcv
## [1] 183384
```

Comparing different regression specifications: multi-parameter EVPPI

```
costs_utilities <- c(par_groups$costs, par_groups$utilities)
ev1 <- evppi(outputs=nb, inputs=m_params, pars=costs_utilities, method="gam",
             gam_formula = "s(c_home_care) + s(c_hospital) + s(c_death) +
                            s(u_recovery) + s(u_home_care) + s(u_hospital)",
             check=TRUE)
ev2 <- evppi(outputs=nb, inputs=m_params, pars=costs_utilities, method="gam",
             gam_formula = all_interactions(costs_utilities, 2), check=TRUE)
ev3 <- evppi(outputs=nb, inputs=m_params, pars=costs_utilities, method="earth", check=TRUE)
ev4 <- evppi(outputs=nb, inputs=m_params, pars=costs_utilities, method="earth",
             degree=2, check=TRUE)
ev5 <- evppi(outputs=nb, inputs=m_params, pars=costs_utilities, method="gp")
ev6 <- evppi(outputs=nb, inputs=m_params, pars=costs_utilities, method="inla")
```