

Creating a simple emulator case study from scratch: a cookbook

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Abstract

This document constructs a minimal working example of a simple application of the **emulator** package, step by step. Datasets and functions have a `.vig` suffix, representing “vignette”.

Keywords: emulator, BACCO, R.

1. Introduction

Package **emulator** of bundle **BACCO** performs Bayesian emulation of computer models. This document constructs a minimal working example of a simple problem, step by step. Datasets and functions have a `.vig` suffix, representing “vignette”.

This document is not a substitute for [Kennedy and O’Hagan \(2001a\)](#) or [Kennedy and O’Hagan \(2001b\)](#) or [Hankin \(2005\)](#) or the online help files in **BACCO**. It is not intended to stand alone: for example, the notation used here is that of [Kennedy and O’Hagan \(2001a,b\)](#), and the user is expected to consult the online help in the **BACCO** package when appropriate.

This document is primarily didactic, although it is informal.

Nevertheless, many of the points raised here are duplicated in the **BACCO** helpfiles.

The author would be delighted to know of any improvements or suggestions. Email me at hankin.robin@gmail.com.

2. List of objects that the user needs to supply

The user needs to supply three objects:

- A design matrix, here `val.vig` (rows of this show where the code has been evaluated)
- Basis functions. Here `basis.vig()`. This shows the basis functions used for fitting the prior
- Data, here `z.vig`. This shows the data obtained from evaluating the various levels of code at the points given by the design matrix and the subsets object.

Each of these is discussed in a separate subsection below.

But the first thing we need to do is install the library:

2.1. Design matrix: USER TO SUPPLY

In these sections I show the objects that the user needs to supply, under a heading like the one above. In the case of the `emulator` we need a design matrix and a vector of outputs.

The first thing needed is the design matrix `val.vig`, ie the points in parameter space at which the lowest-level code is executed. The example here has just two parameters, `a` and `b`:

```
> head(val.vig)

      [,1]      [,2]
[1,] 0.1833333 0.31666667
[2,] 0.5833333 0.78333333
[3,] 0.4500000 0.01666667
[4,] 0.9500000 0.88333333
[5,] 0.2166667 0.95000000
[6,] 0.7500000 0.11666667
```

```
> nrow(val.vig)
```

```
[1] 30
```

Notes

- Each row is a point in parameter space, here two dimensional.
- The parameters are labelled `a` and `b`

2.2. Basis functions: USER TO SUPPLY

Now we need to choose a basis function. Do this by copying `basis.toy()` but fiddling with it:

```
> basis.vig <-
+ function (x)
+ {
+   out <- c(1, x , x[1]*x[2])
+   names(out) <- c("const", LETTERS[1:2], "interaction")
+   return(out)
+ }
```

Notes

- This is shamelessly ripped off from `basis.toy()`, except that I've changed the basis to be `c(1,a,b,ab)`.
- in the function, `out` is a vector of length four: `c(1,x[1],x[2], x[1]*x[2])`.

2.3. Data: USER TO SUPPLY

The data we have for the `.vig` example is a vector whose elements are the output of the code at the points specified in `val.vig`:

```
> head(z.vig)
```

```
[1] 2.665212 5.669395 1.982193 9.058192 4.184136 2.703376
```

```
> summary(z.vig)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
1.982   2.651   3.275   4.126   5.361   9.058
```

3. Data analysis

The previous section showed what data and functions the user needs to supply. These all have a `.vig` suffix. This section shows the data being analyzed.

First we will estimate the scales to use:

```
> os <- optimal.scales(val=val.vig, scales.start=c(10,10), d=z.vig, func=basis.vig)
> os
```

```
[1] 2.756270 6.585481
```

So we can estimate the coefficients. But first we have to calculate the variance matrix and invert it:

```
> A.os <- corr.matrix(xold=val.vig, scales=REAL.SCALES)
> Ainv.os <- solve(A)
```

Given this, use `betahat.fun()` to get the coeffs:

```
> betahat.fun(xold=val.vig, d=z.vig, Ainv=solve(A), func=basis.vig)
```

```
      const          A          B interaction
1.192844  1.505521  2.370638  4.991648
```

The central function is interpolant:

```
> interpolant(x=c(0.5,0.5), d=z.vig, Ainv=Ainv.os, scales=os,
+ xold=val.vig, func=basis.vig, give.full.list=TRUE)
```

```

$betahat
      const          A          B interaction
1.192844  1.505521  2.370638  4.991648

$prior
      [,1]
[1,] 4.378835

$beta.var
      const          A          B interaction
const  0.1598272 -0.1575722 -0.1692980  0.1833158
A      -0.1575722  0.3098934  0.1718790 -0.3557060
B      -0.1692980  0.1718790  0.2931635 -0.2870850
interaction 0.1833158 -0.3557060 -0.2870850  0.6113408

$beta.marginal.sd
      const          A          B interaction
0.3997839  0.5566807  0.5414457  0.7818828

$sigma.hat.square
[1] 0.1944991

$mstar.star
      [,1]
[1,] 4.033889

$cstar
[1] -0.007999019

$cstar.star
[1] -0.007991267

$Z
[1] 0.03942454

```

And that's it, really.

References

- Hankin RKS (2005). “Introducing **BACCO**, an R bundle for Bayesian analysis of computer code output.” *Journal of Statistical Software*, **14**(16).
- Kennedy MC, O’Hagan A (2001a). “Bayesian calibration of computer models.” *Journal of the Royal Statistical Society, Series B*, **63**(3), 425–464.
- Kennedy MC, O’Hagan A (2001b). “Supplementary details on Bayesian calibration of computer models.” Internal Report. URL <http://www.shef.ac.uk/~st1ao/ps/calsup.ps>.

A. Data generation

The data used in this study were created by directly sampling from the appropriate multivariate Gaussian:

```
> REAL.BETA <- 1:4
> REAL.SCALES <- c(3,6)
> REAL.SIGMASQUARED <- 0.3
> A <- corr.matrix(xold=val.vig,scales=REAL.SCALES)
> z.vig <-
+ as.vector(rmvnorm(n=1,mean=crossprod(REAL.BETA,apply(val.vig,1,basis.vig)),sigma=A*REAL.
```

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