

Calibration Profiles

eX Modelo school

OpenMOLE

June 25, 2019

Context

Reminder You get one of the best parameter set to minimise a given fitness function



Reminder You get one of the best parameter set to minimise a given fitness function



Problem You only get one parameter set!

Reminder You get one of the best parameter set to minimise a given fitness function



Problem You only get one parameter set!

→ What is happening in the rest of the input space?

How does a small variation of one of the parameters affect the model output?

Objective Find outputs with a good fitness (but not the best) in different zones of the input space

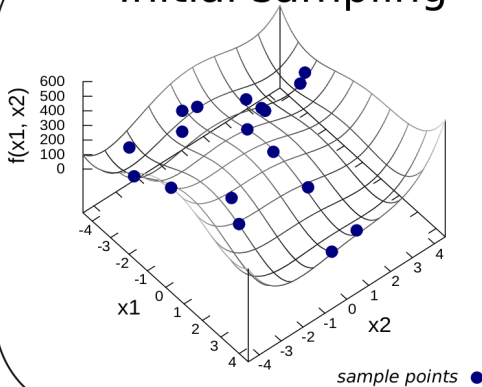
Method

Control the variations of one parameter x_1
and calibrate over the other parameters

→ **calibration profile of x_1**

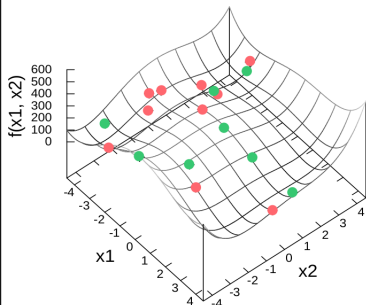
Initial sampling

1

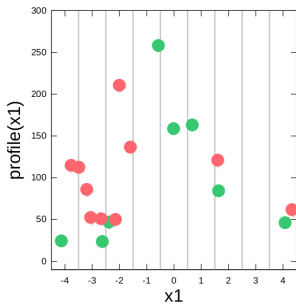


2

Elitism



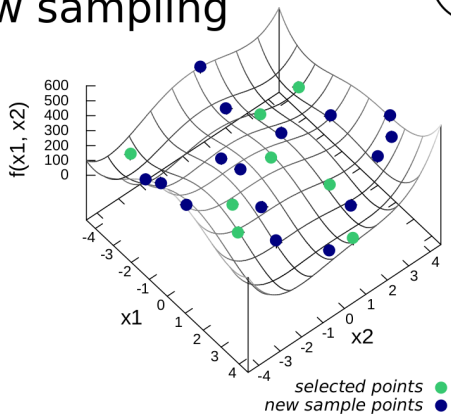
2D projection



selected points ●
excluded points ●

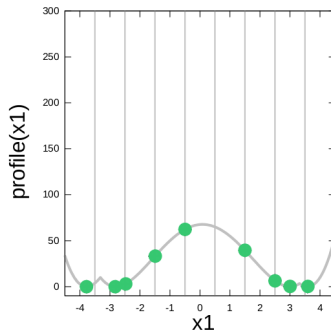
3

New sampling



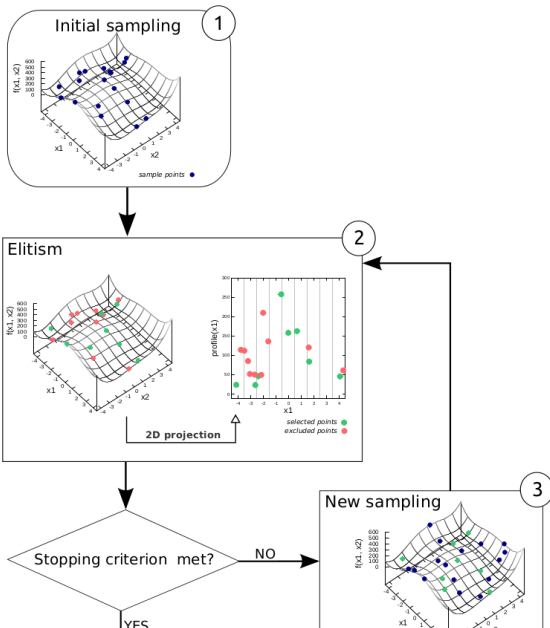
4

Profile approximation



points of the profile
theoretical continuous profile





Interpretation

We know how x_1 variations influence our model's fitness

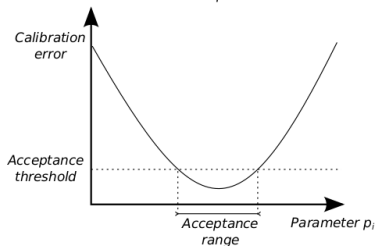
→ **solutions of an optimisation problem all along x_1 domain**

We know how x_1 variations influence our model's fitness

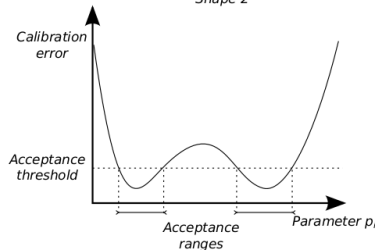
→ **solutions of an optimisation problem all along x_1 domain**

- ▶ Does the parameter impact the model's capacity to produce plausible outcomes?
- ▶ What is the variation interval of the parameter?
- ▶ Is the parameter useful to the model?

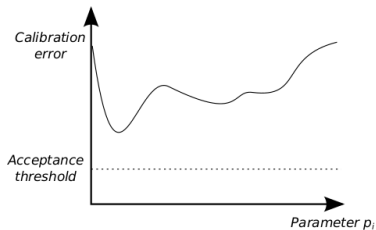
Shape 1



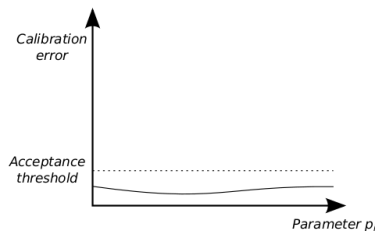
Shape 2

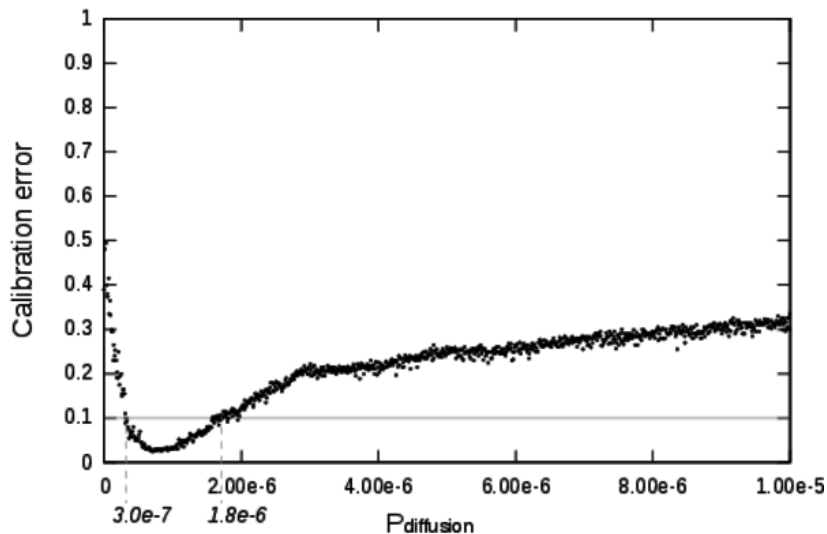


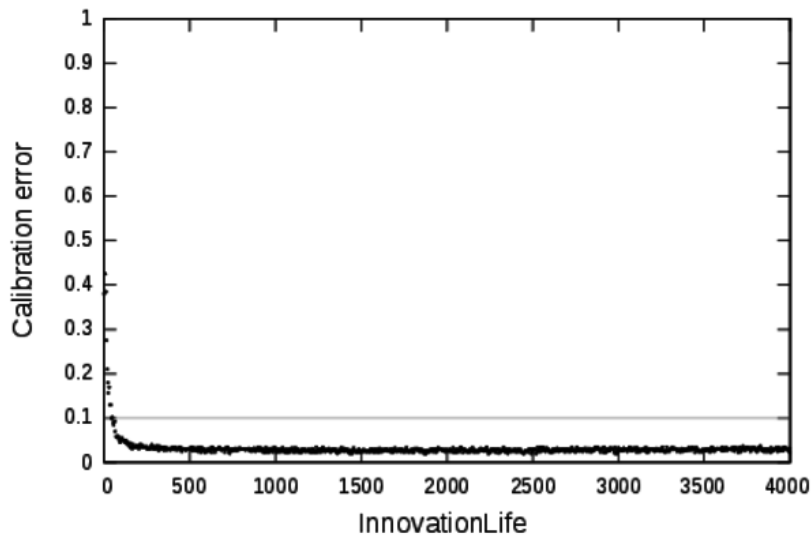
Shape 3



Shape 4







Profile in OpenMOLE

```
val param1 = Val[Double]
val param2 = Val[Double]
val fitness = Val[Double]

ProfileEvolution(
  evaluation = modelTask,
  objective = fitness,
  x = param1,
  nX = 20,
  genome = Seq(
    param1 in (0.0, 99.0),
    param2 in (0.0, 99.0)
  ),
  termination = 200000,
  parallelism = 500,
  stochastic = Stochastic(seed = seed, replications = 100),
  distribution = Island(10 minutes)
) hook(workDirectory / "path/to/a/directory")
```

```
val param1 = Val[Double]
val param2 = Val[Double]
val fitness = Val[Double]

ProfileEvolution(
  evaluation = modelTask,
  objective = fitness,
  x = param1,
  nX = 20,
  genome = Seq(
    param1 in (0.0, 99.0),
    param2 in (0.0, 99.0)
  ),
  termination = 200000,
  parallelism = 500,
  stochastic = Stochastic(seed = seed, replications = 100),
  distribution = Island(10 minutes)
) hook(workDirectory / "path/to/a/directory")
```

evaluation	the model task
objective	the fitness function to minimise
x	the parameter to profile
nX	the size of the subintervals in x domain
genome	a list of the model input parameters with their variation ranges