Calibration Profiles

eX Modelo school

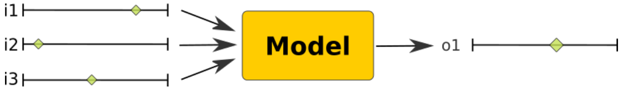
OpenMOLE

June 25, 2019

Context

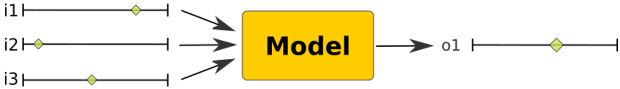
Calibration

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



Calibration

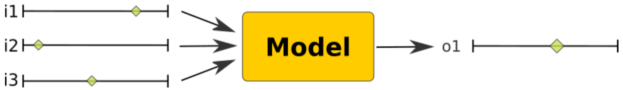
Reminder You get one of the best parameter set to minimise a given fitness function



Problem You only get one parameter set!

Calibration

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?

Explore 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

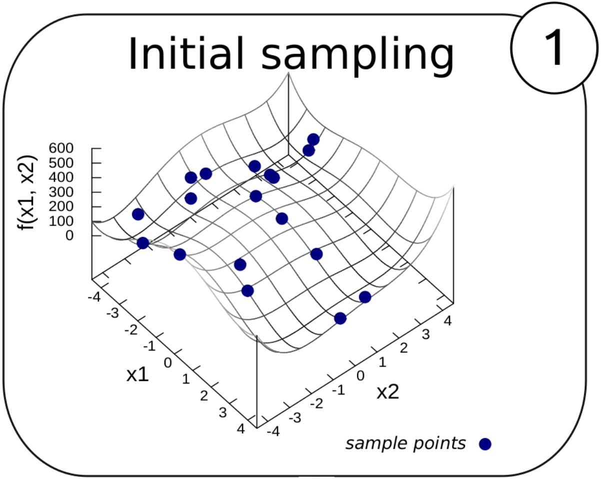
Method

Process

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

→ **calibration profile of** x_1

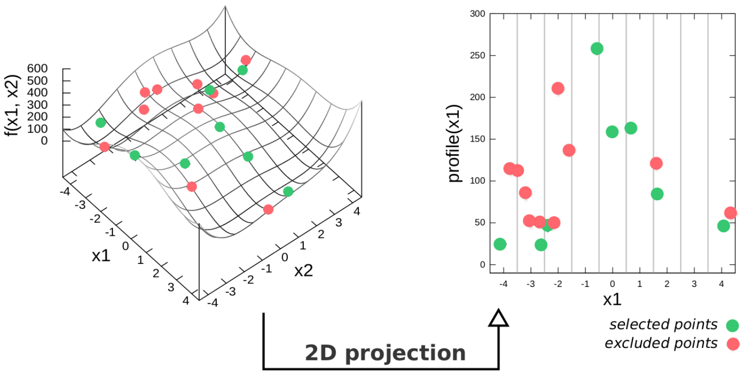
The algorithm



The algorithm

2

Elitism

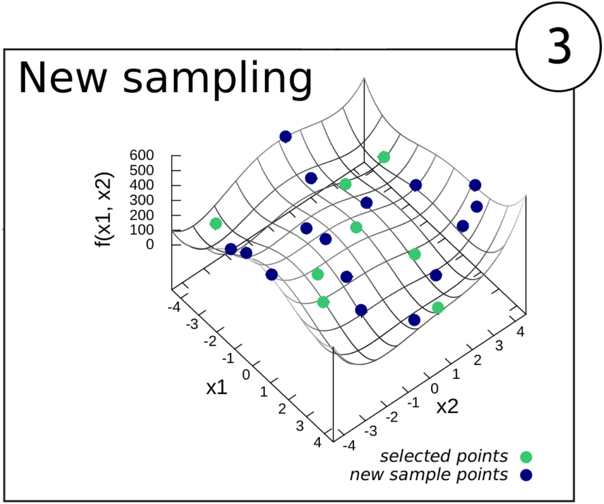


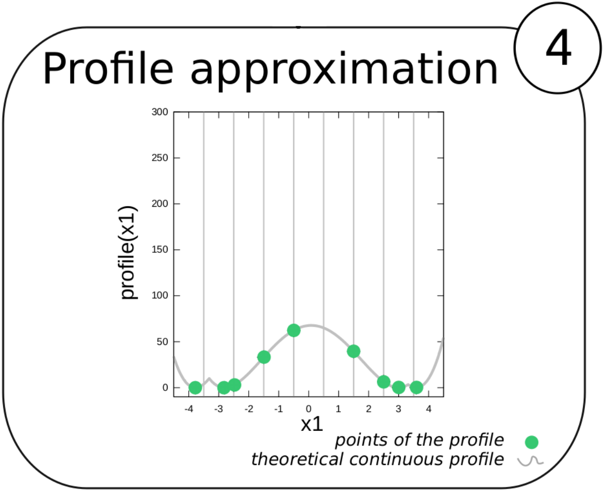
2D projection

selected points ●

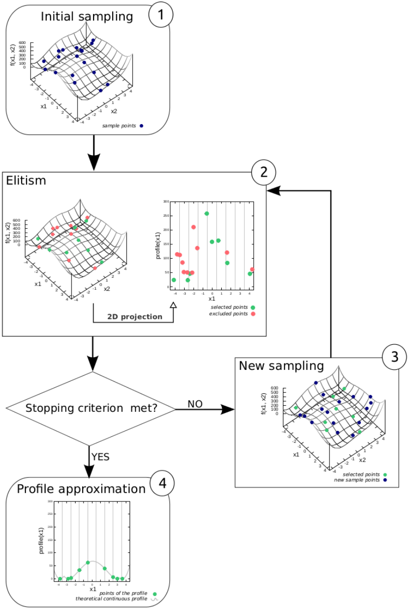
excluded points ●

The algorithm




Profile approximation
4
300
250
200
150
100
50
0
profile(x1)
-4
-3
-2
-1
0
1
2
3
4
x1
points of the profile ●
theoretical continuous profile

The algorithm



Interpretation

New information

We know how x_1 variations influence our model's fitness

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

New information

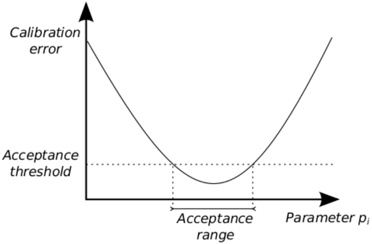
We know how x_1 variations influence our model's fitness

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

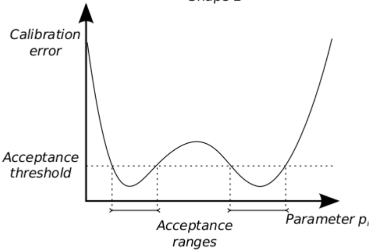
- Does the parameter impact the model's capacity to produce plausible outcomes?
- What is the variation interval of the parameter?
- Is the parameter useful to the model?

Typical shapes

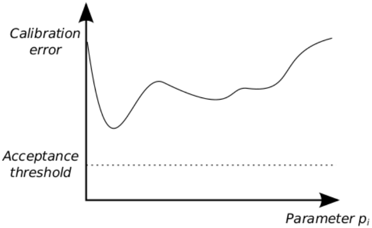
Shape 1



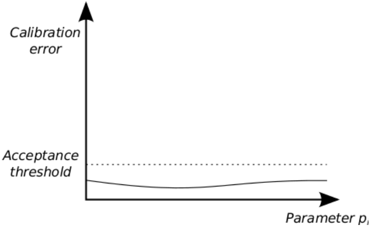
Shape 2



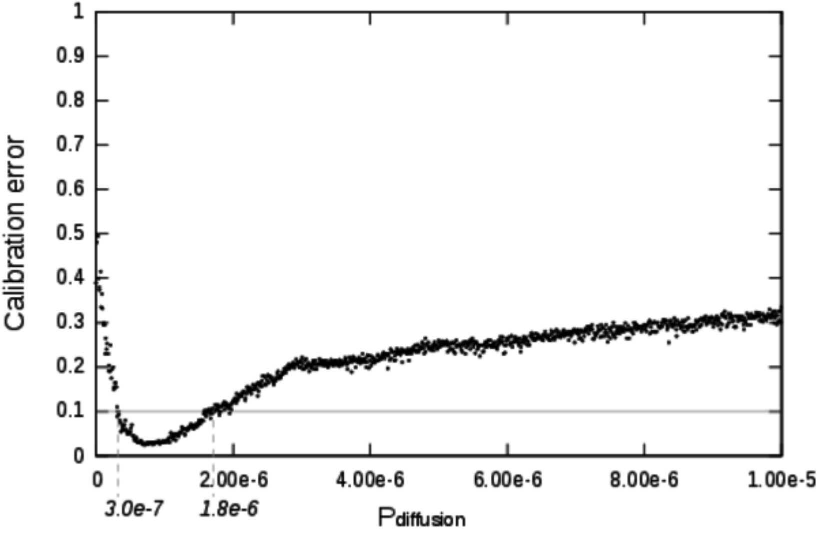
Shape 3



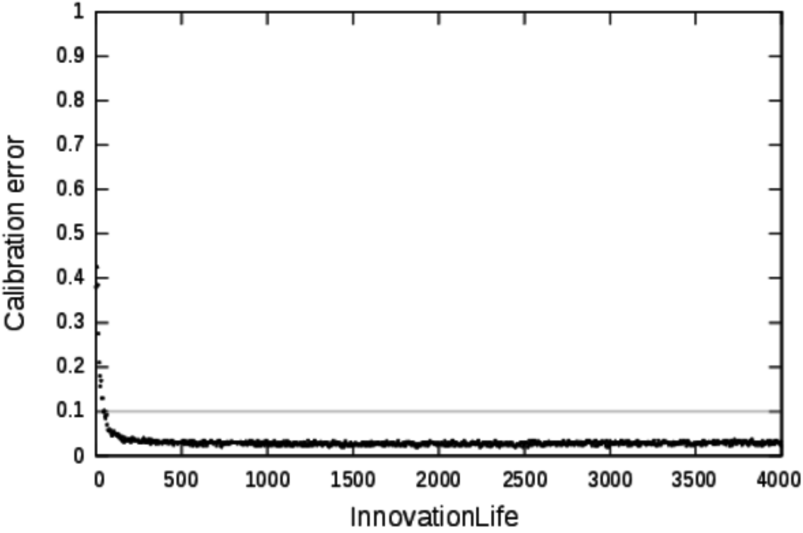
Shape 4



Use case

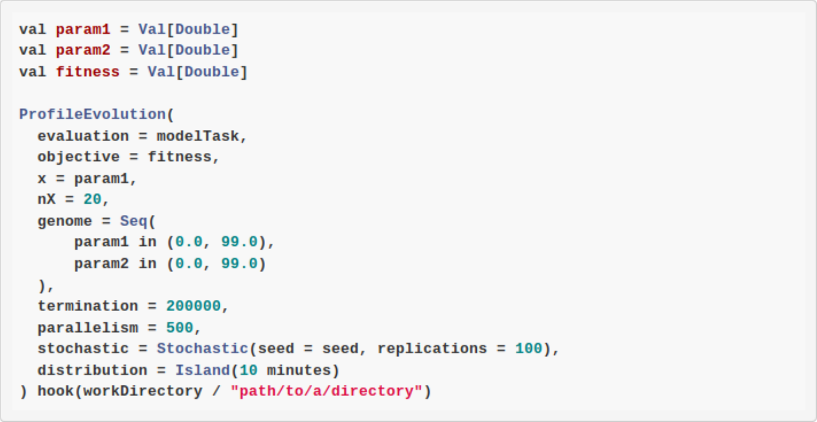

Calibration error
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
2.00e-6
4.00e-6
6.00e-6
8.00e-6
1.00e-5
3.0e-7
1.8e-6
Pdiffusion

Use case


Calibration error
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
500
1000
1500
2000
2500
3000
3500
4000
InnovationLife

Profile in OpenMOLE

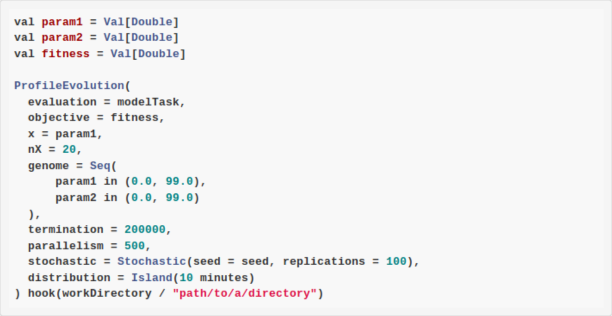
The ProfileEvolution constructor



```
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")
```

The ProfileEvolution constructor



```
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 functio 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

What about our Zombie situation?

Questions

- How can profiles help us better understand the model?

Questions

- How can profiles help us better understand the model?
- What can we profile?

Questions

- How can profiles help us better understand the model?
- What can we profile?
- With what objective function?