

## Calibration Profiles

eX Modelo school

**OpenMOLE**

June 25, 2019

# Context

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



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**Problem** You only get one parameter set!

**Reminder** You get 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

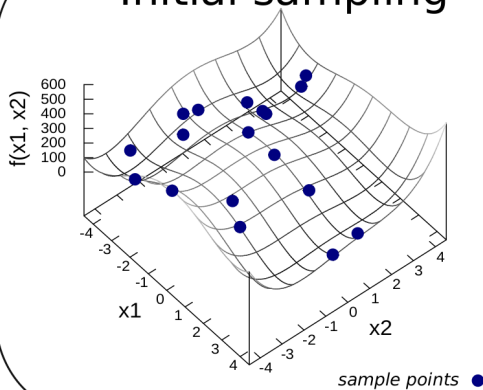
Control the variations of one parameter  $x_1$   
and calibrate over the other parameters

→ **calibration profile of  $x_1$**



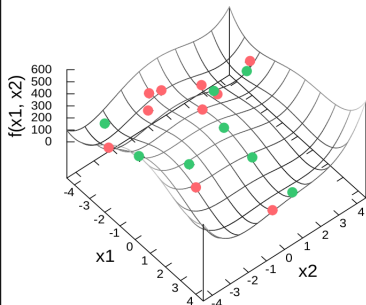
## Initial sampling

1

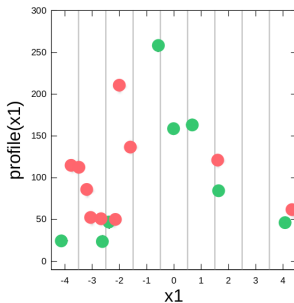


2

## Elitism



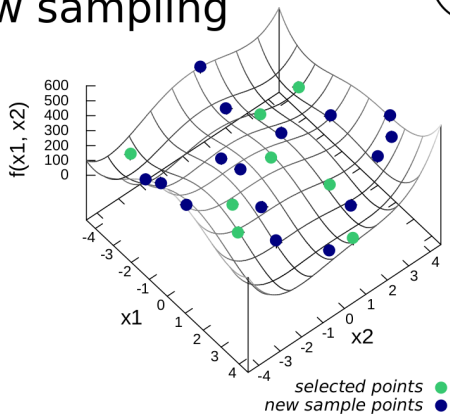
2D projection



selected points ●  
excluded points ●

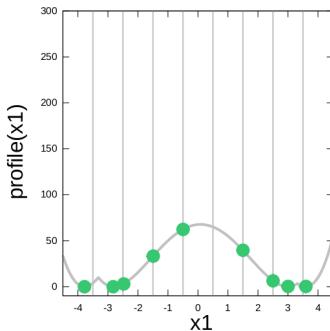
3

## New sampling



4

## Profile approximation



*points of the profile*  
*theoretical continuous profile*



# Interpretation

We know how  $x_1$  variations influence our model's fitness

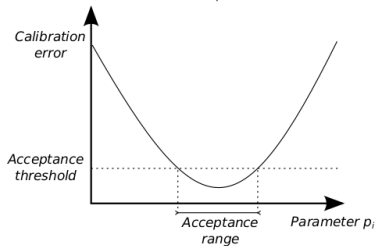
→ **solutions of an optimisation problem all along  $x_1$  domain**

We know how  $x_1$  variations influence our model's fitness

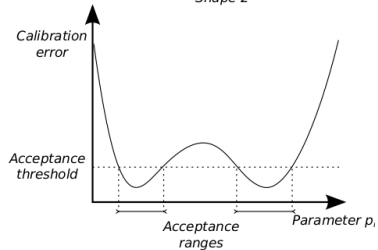
→ **solutions of an optimisation problem all along  $x_1$  domain**

- ▶ 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?

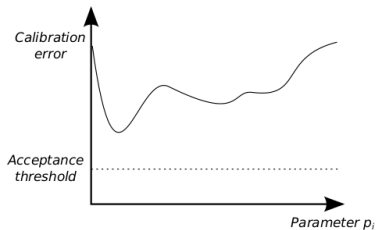
Shape 1



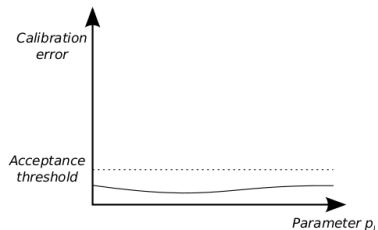
Shape 2



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")
```

```
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```

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