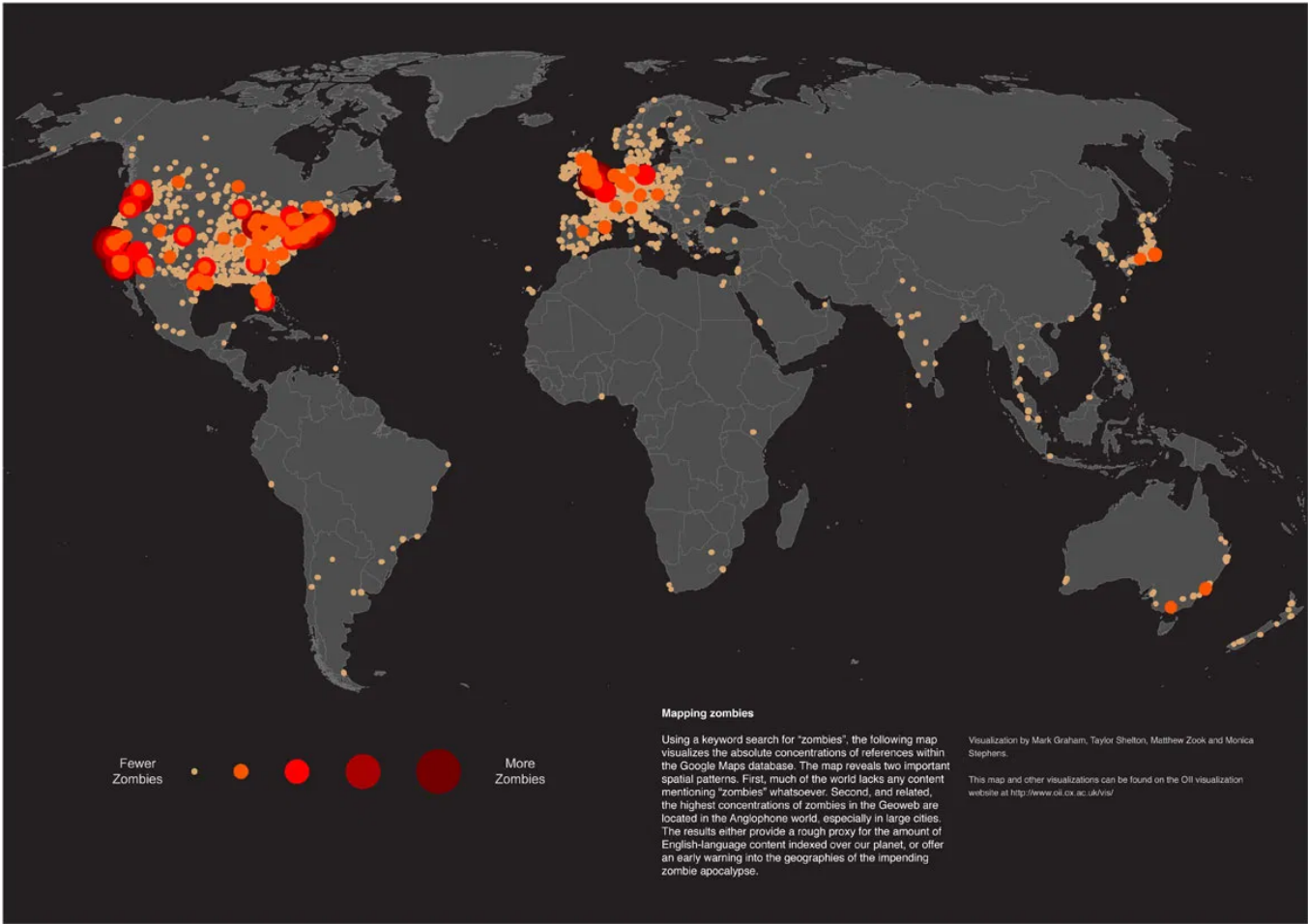


# OpenMOLE an essential software to face Zombie outbreaks



**22/11/2021**  
**Romain Reuillon**

# Zombies infections



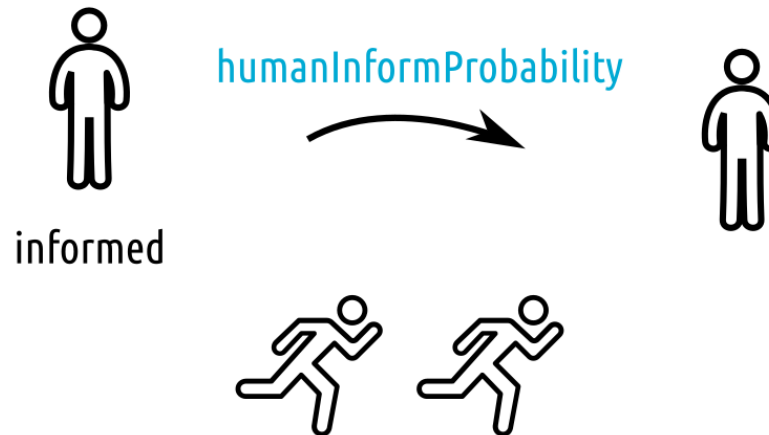
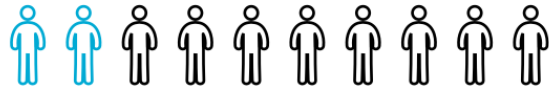
# A Zombie model

<https://zombieland.openmole.org/>

# Human communication is unknown

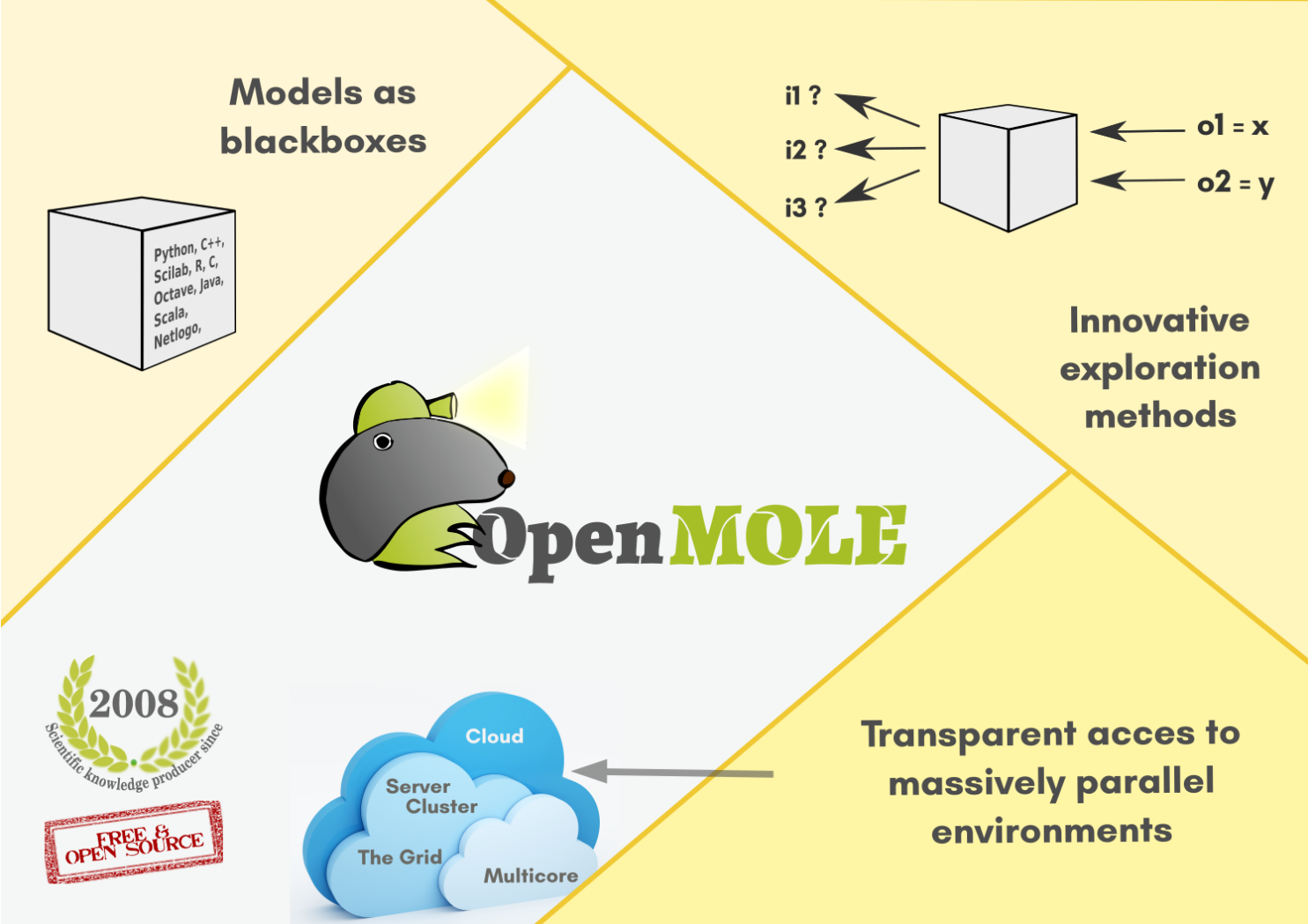
During a simulation, the humans can communicate about the *location of rescue zones*. Zombies do not communicate.

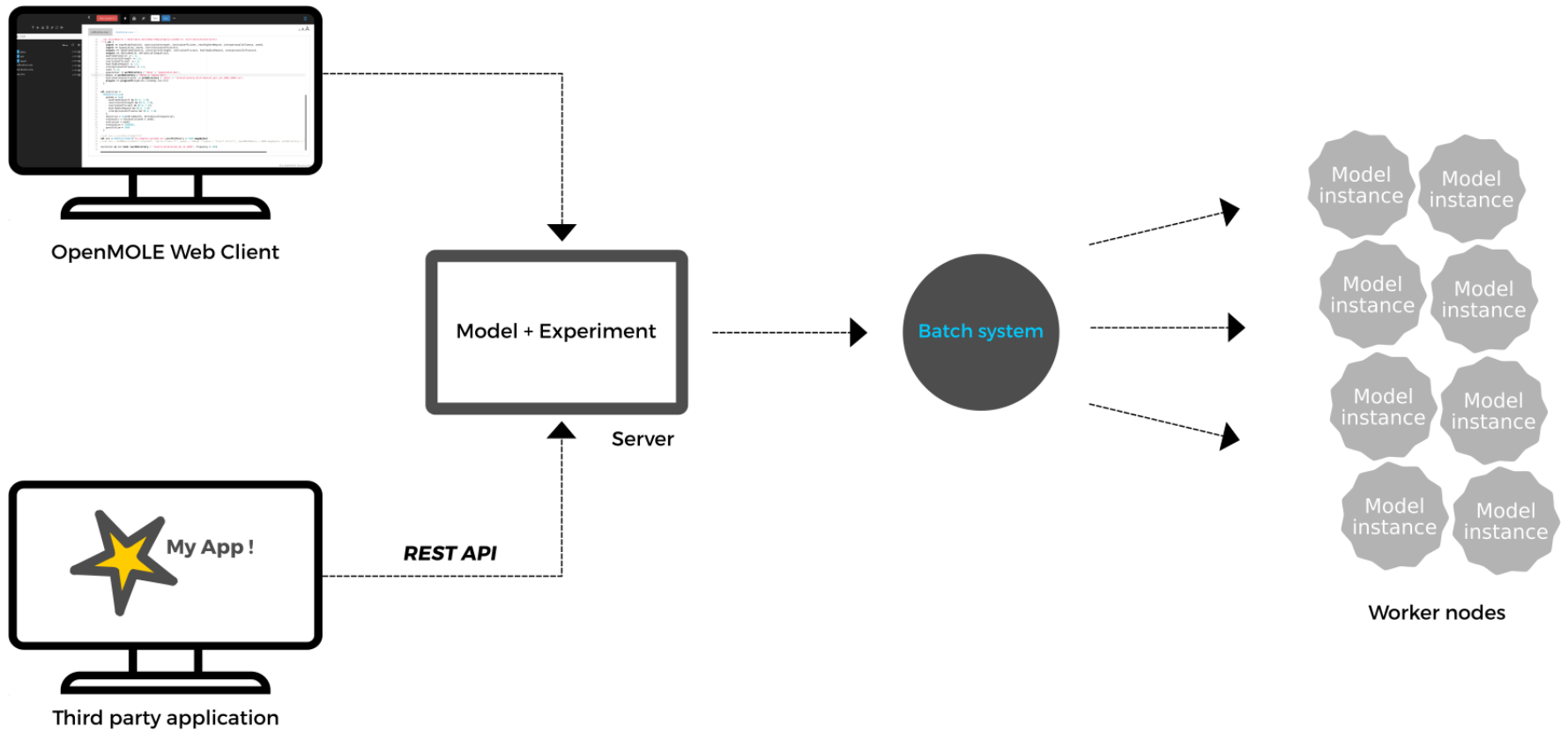
At the beginning of the simulation, `informedRatio` of the human population is informed.



Humans can follow a running human with a `humanFollowProbability`

# OpenMOLE to the rescue





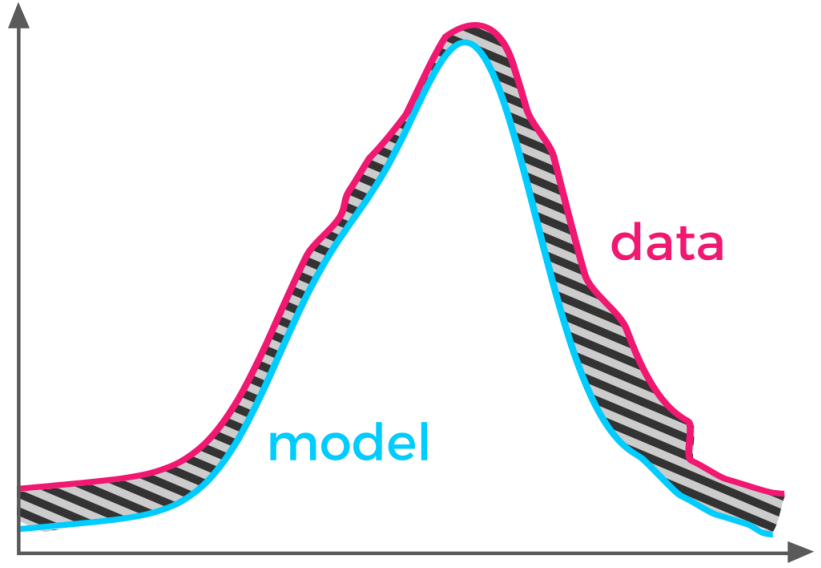
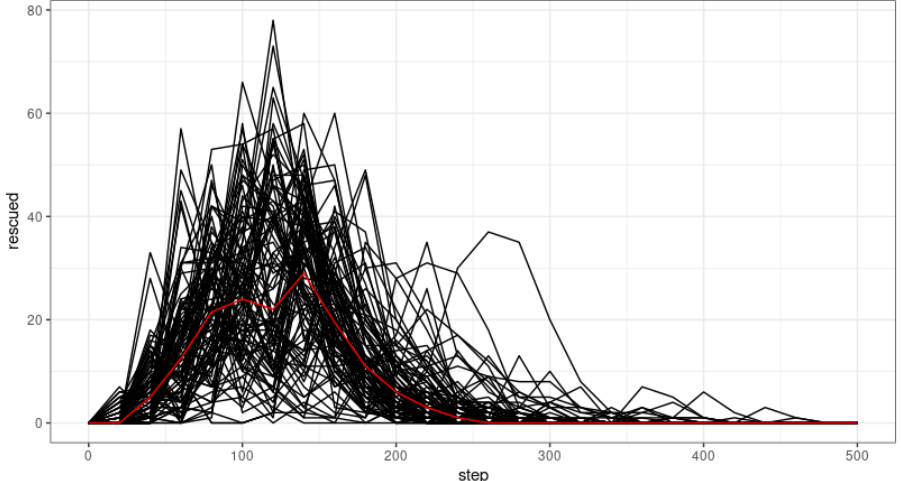
# OpenMOLE for real

The screenshot displays the OpenMOLE web interface in a browser. The address bar shows 'localhost:46857/app'. The interface includes a top navigation bar with 'New project', 'Test', and 'Run' buttons. A sidebar on the left lists various models, including 'army', 'coop', 'helene', 'netlogo', 'redcross', 'results', 'results\_test', 'trap', 'vigilance', 'calibrate.oms', 'explore.oms', 'model.oms', and 'replicate.oms'. The main area shows a code editor for 'model.oms' with the following Scala code:

```
1 import zombies._
2
3 // Model inputs
4 val humanFollowProbability = Val[Double]
5 val humanInformedRatio = Val[Double]
6 val humanInformProbability = Val[Double]
7
8 val seed = Val[Long]
9
10 // Model outputs
11 val totalRescued = Val[Int]
12 val halfRescued = Val[Int]
13 val rescuedDynamic = Val[Array[Int]]
14
15 val model =
16   ScalaTask("""
17     import zombies._
18
19     val rng = Random(seed)
20
21     val result = zombieInvasion(
22       humanFollowProbability = humanFollowProbability,
23       humanInformedRatio = humanInformedRatio,
24       humanInformProbability = humanInformProbability,
25       zombies = 4,
26       humans = 250,
27       steps = 500,
28       random = rng)
29
30     val totalRescued = result.totalRescued
31     val halfRescued = result.halfRescued
32     val rescuedDynamic = result.rescuedDynamic()
33   """) set (
34     inputs += (seed, humanFollowProbability, humanInformedRatio, humanInformProbability),
35     outputs += (rescuedDynamic, halfRescued, totalRescued),
36
```

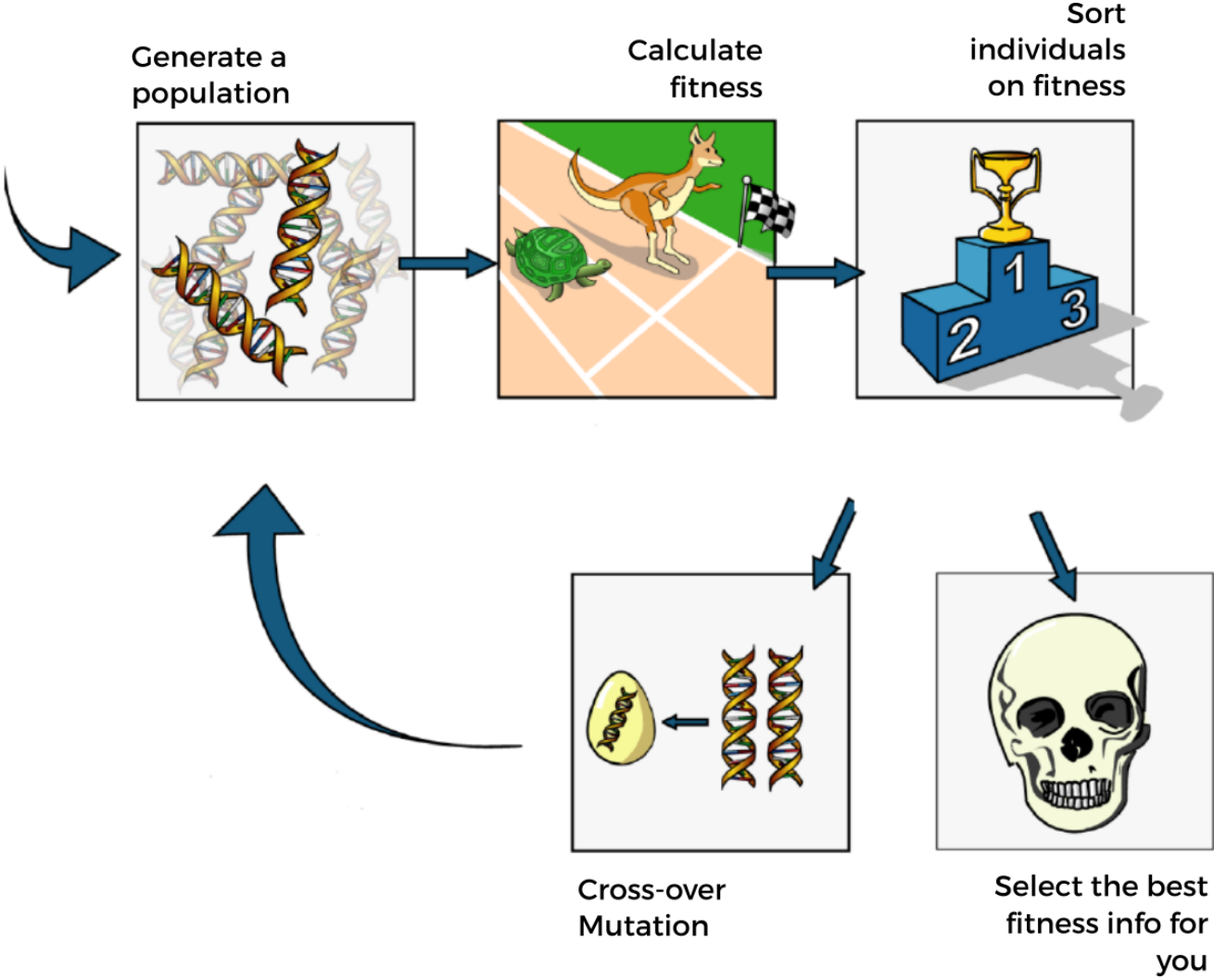
At the bottom right, there is a footer: '10.0-SNAPSHOT P... P... built the 11/10/2019 18:13:47'.

# Calibration





# Seek for the fittest parameter sets



## Some OpenMOLE code

```
NSGA2Evolution(  
  evaluation = model,  
  genome = Seq(  
    humanInformedRatio in (0.0, 1.0),  
    humanInformProbability in (0.0, 1.0),  
    humanFollowProbability in (0.0, 1.0)  
  ),  
  objective = Seq(rescuedDynamic aggregate distanceMedian),  
  stochastic = Stochastic(seed = mySeed, sample = 100),  
  ...  
)
```

# Result

population13000.csv

Raw Table Plot First 100 Last 100 All

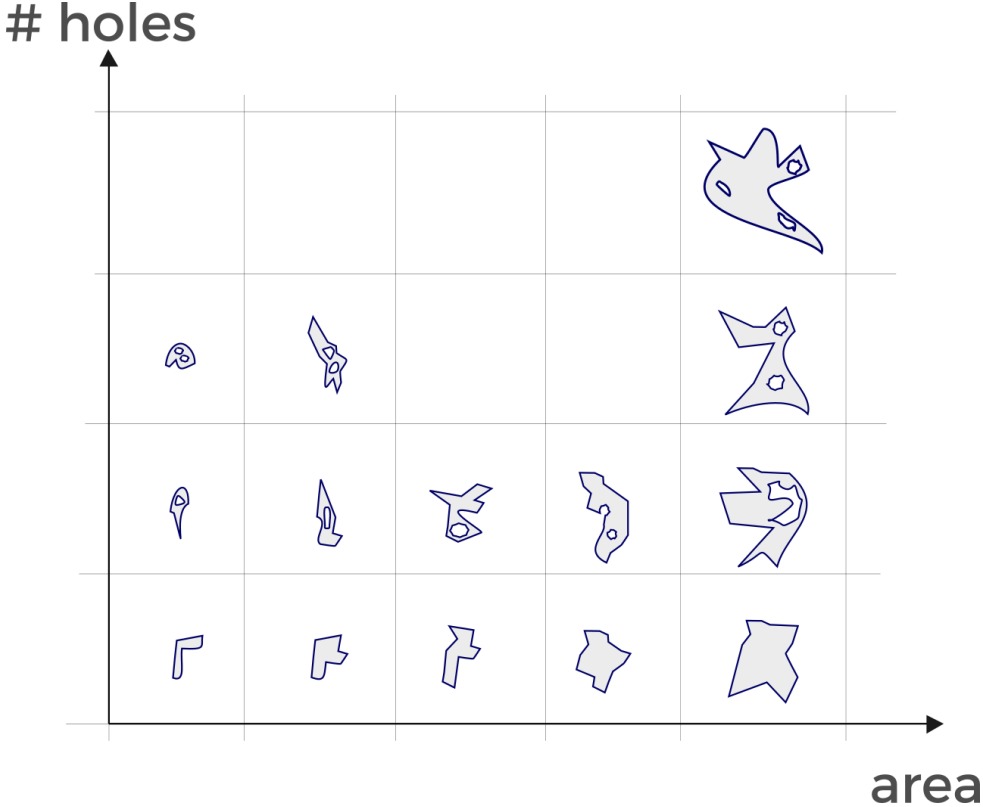
evolution\$generation	humanInformedRatio	humanInformProbability	humanFollowProbability	rescuedDynamic	evolution\$samples
13000	0.08806635922765362	0.09248903420070739	0.17051186535157378	4.5	100

10.0-SNAPSHOT P... P...  
built the 11/10/2019 10:25:50

# PSE: seek for diversity

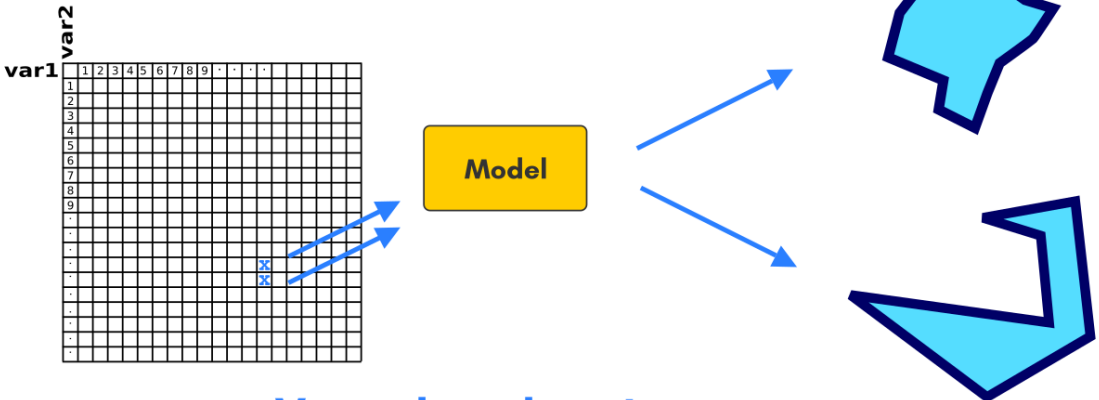
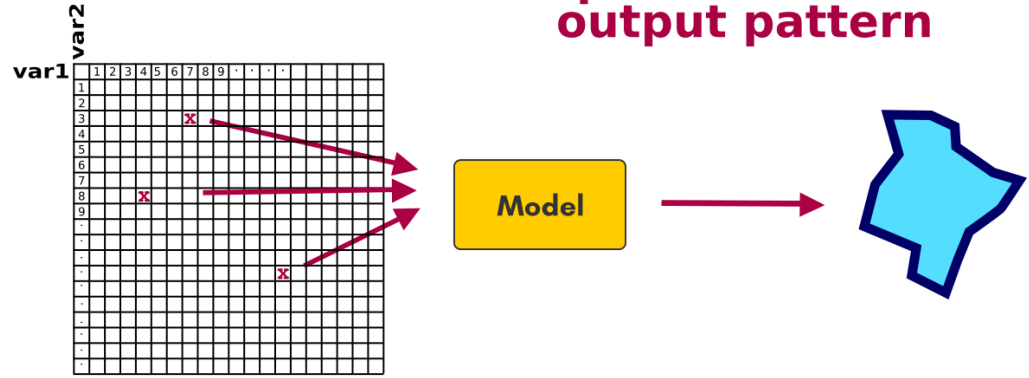


# Deversity metrics



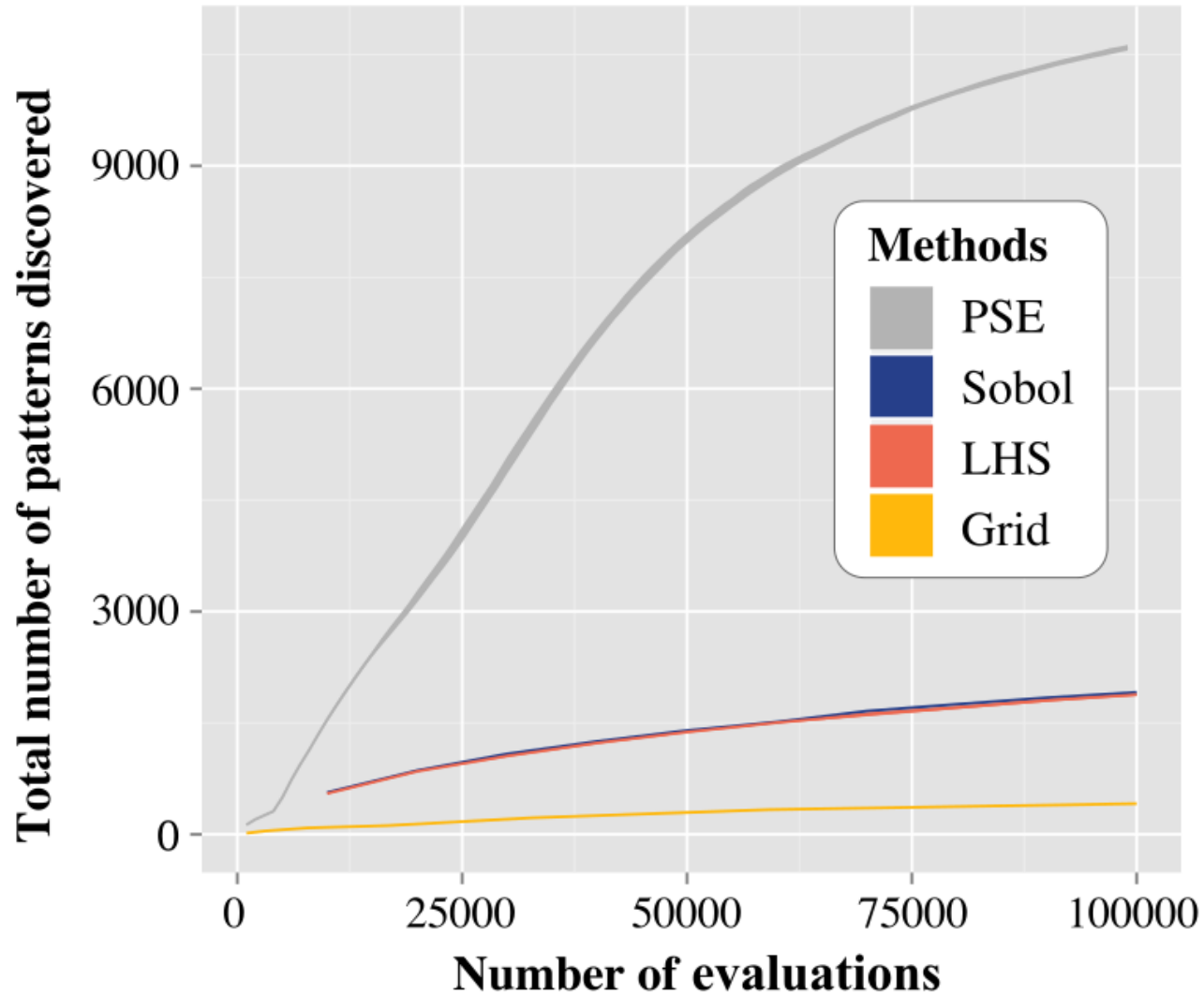
# Sampling for diversity search

**Very different inputs can produce a similar output pattern**



**Very close inputs can produce very different output patterns**

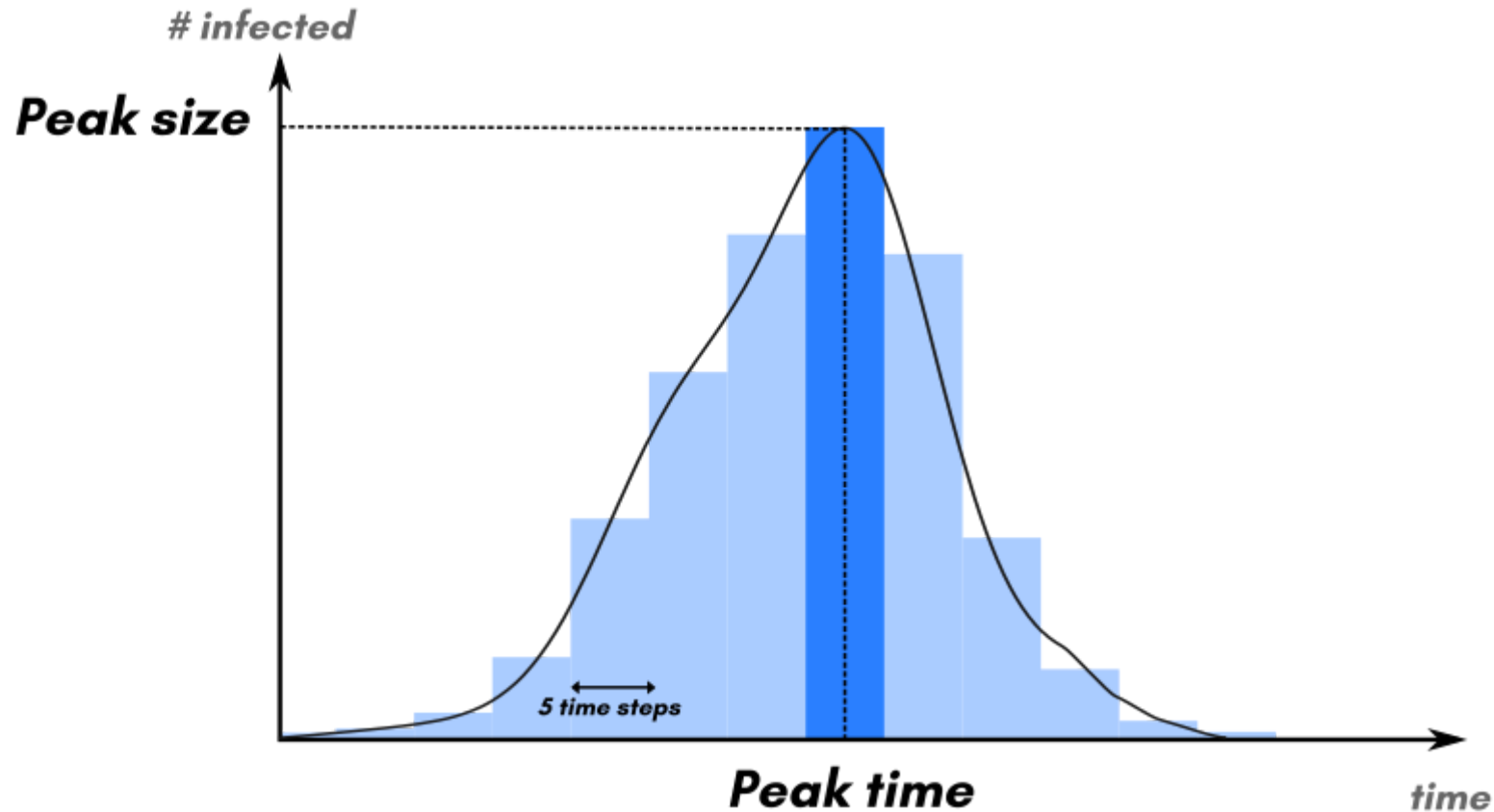
# PSE performances



# PSE for Zombies

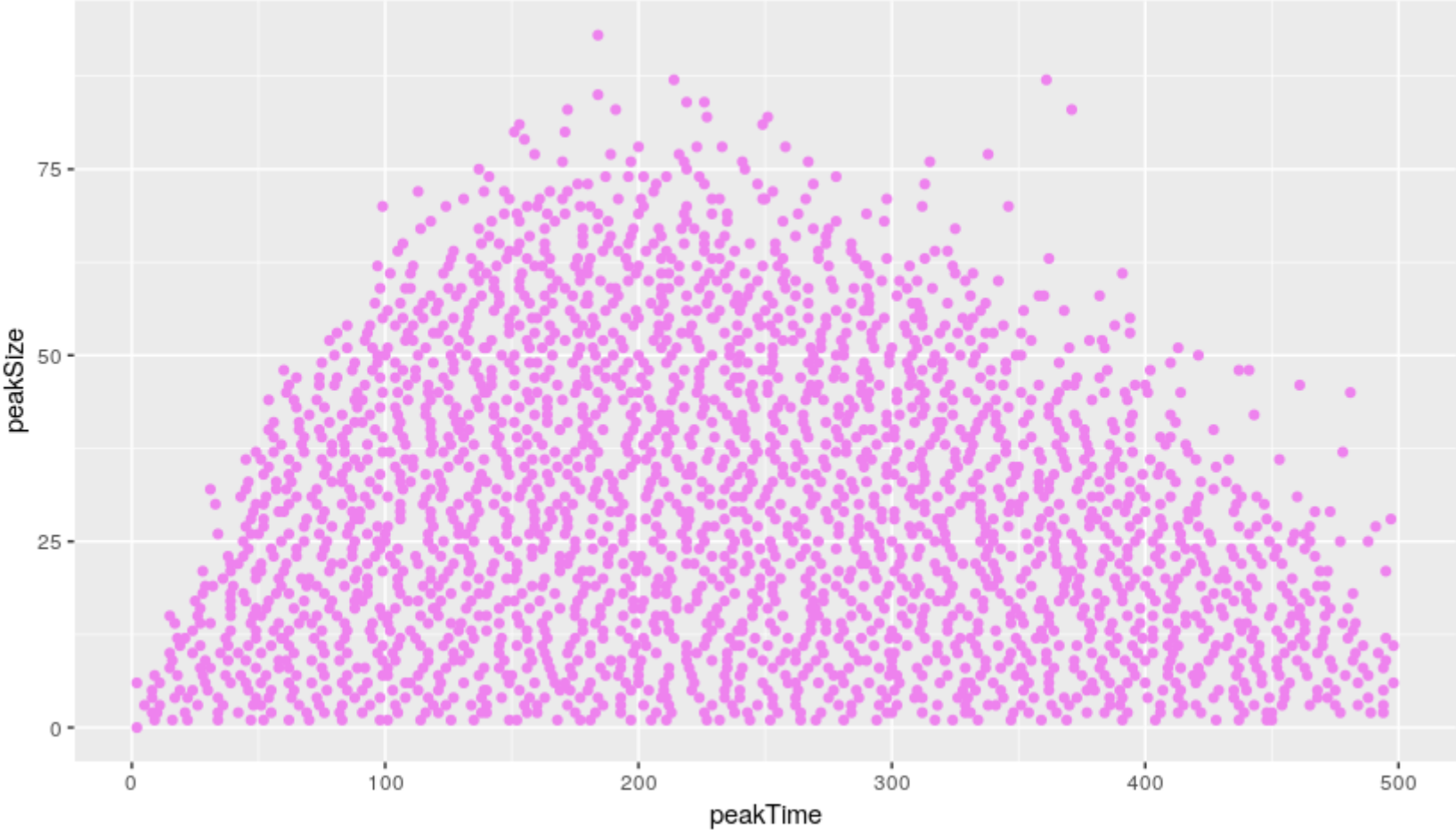
Looking for possible:

- Peak size of infected humans over 5 time steps
- Peak time of infected humans over 5 time steps





# Possible patterns

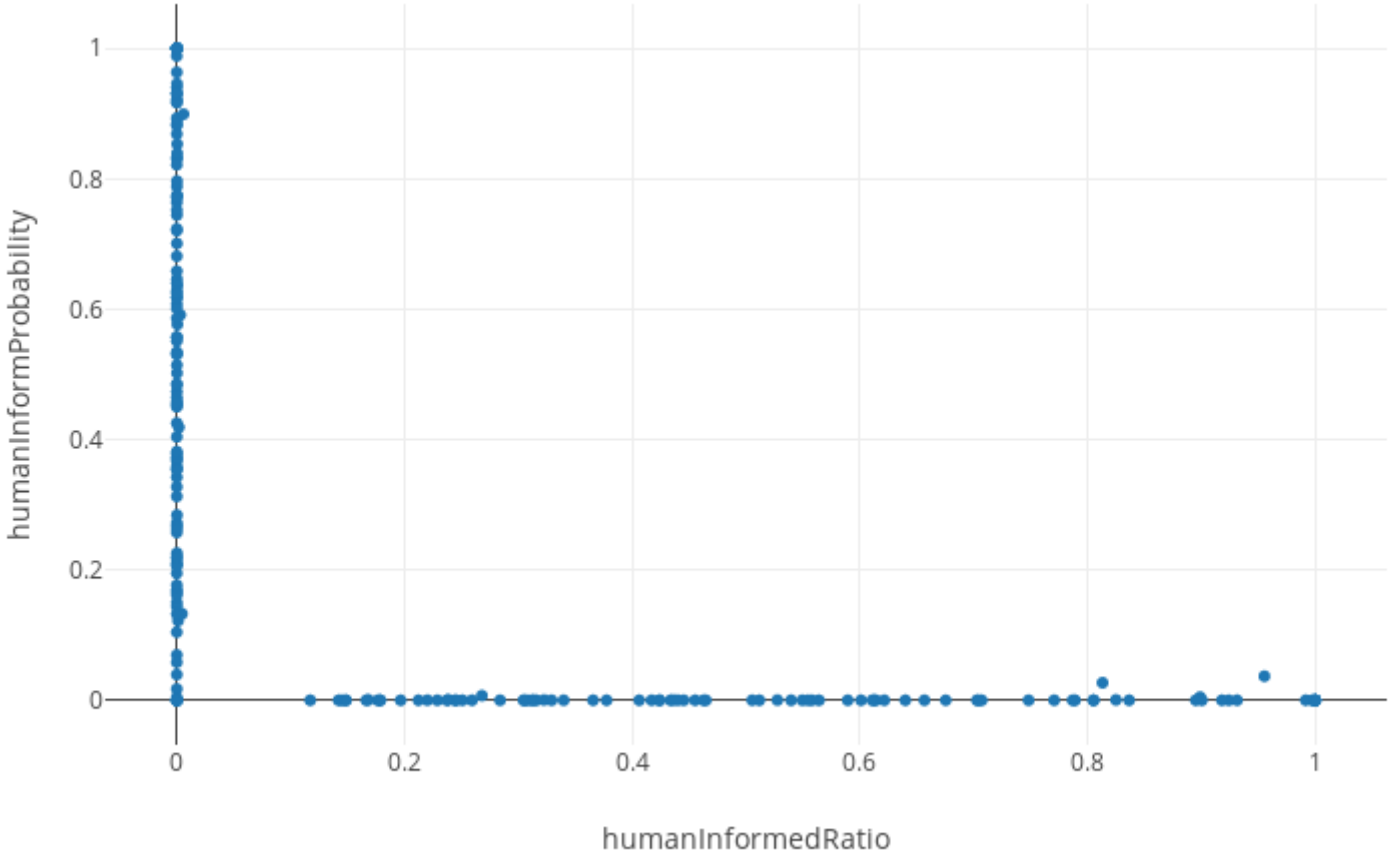


# OSE (Ancestor search)



Which input values may lead to a rare but terrible Zombie attack ( $\text{peakSize} > 50$ ) ?

# OSE Results



*At least 1 informed human or a very (non-zero) low informProbability permit to avoid a terrible attack.*

## Is it all?

- *Direct sampling*: Grid, Sobol, LHS, One Factor at A Time, Random, CSV, Spatial
- *Sensitivity*: Morris, Saltelli
- *Evolution*: NSGA2, Profiles, PSE, OSE, NicheNSGA2
- *Bayesian*: ABC
- And more to come: NSGA3, PPSE

Is OpenMOLE crafted for Zombies only?



# Of course not !

## DOCUMENTATION

### Plug Your Model

1. [Scala](#)
2. [Java](#)
3. [Python](#)
4. [R](#)
5. [NetLogo](#)
6. [GAMA](#)
7. [Scilab](#)
8. [Julia](#)
9. [Any Other Executable](#)

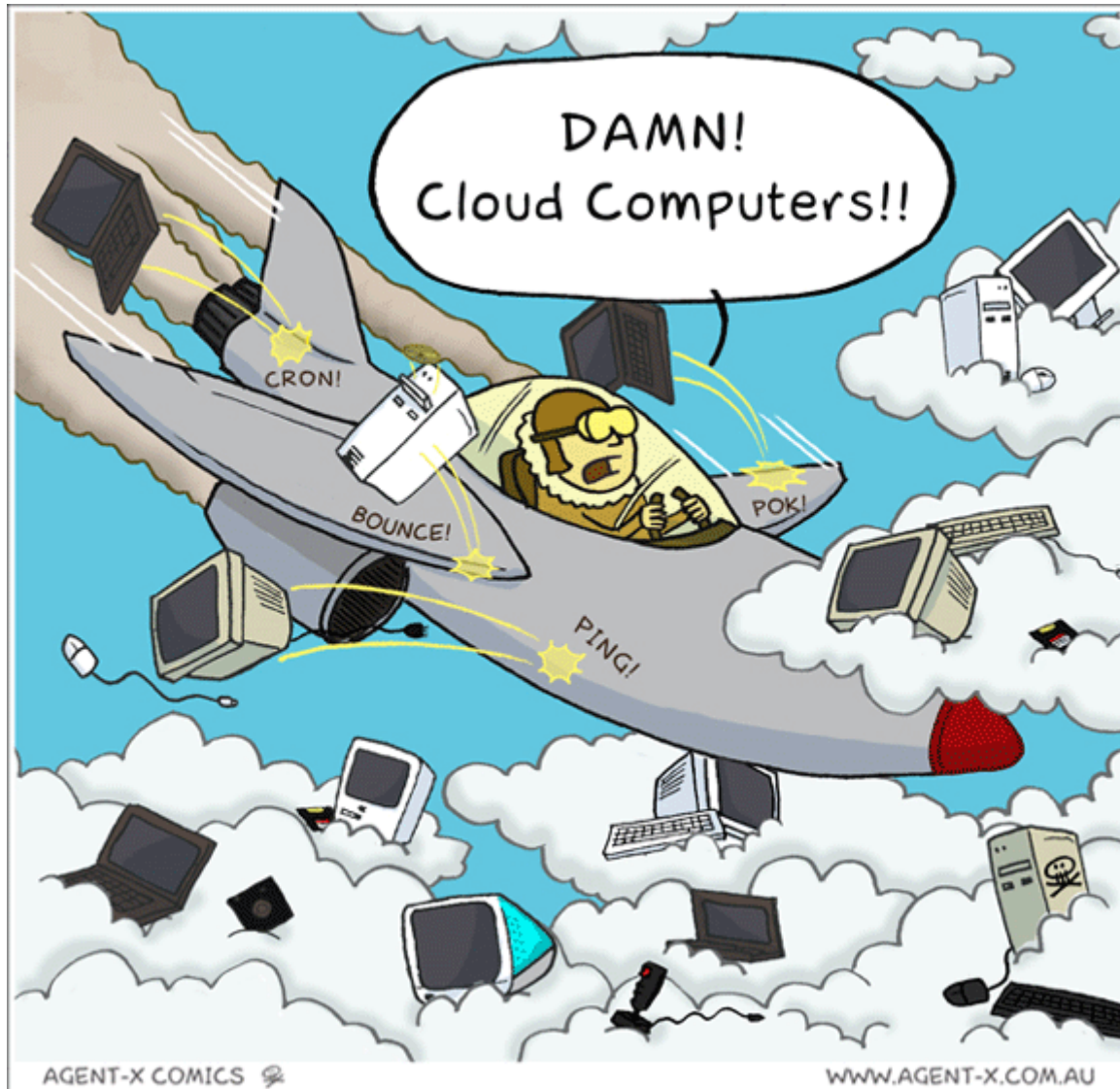
### Explore Your Model

1. [Samplings](#)
  - a. [Elementary Samplings](#)
  - b. [Samplings for High Dimension Spaces](#)
  - c. [Uniform Sampling](#)
  - d. [Sampling Over Files](#)

# Scaling



# Execute anywhere





# Zero deployment approach

- User code is automatically deployed at runtime
- No prior knowledge of remote environment needed
- No installation required on any machine

Distribute on your laptop ors cluster:

- PBS, Torque, Condor, SLURM, SGE, OAR, DIRAC...

# Useful links

- OpenMOLE site: [openmole.org](https://openmole.org)
- OpenMOLE chat: [chat.openmole.org](https://chat.openmole.org)
  
- OpenMOLE next version: [next.openmole.org](https://next.openmole.org)
- OpenMOLE github: [github.com/openmole/openmole](https://github.com/openmole/openmole)
- OpenMOLE gitlab: [gitlab.openmole.org/openmole/openmole](https://gitlab.openmole.org/openmole/openmole)

# Trempline



<https://trempline.io>