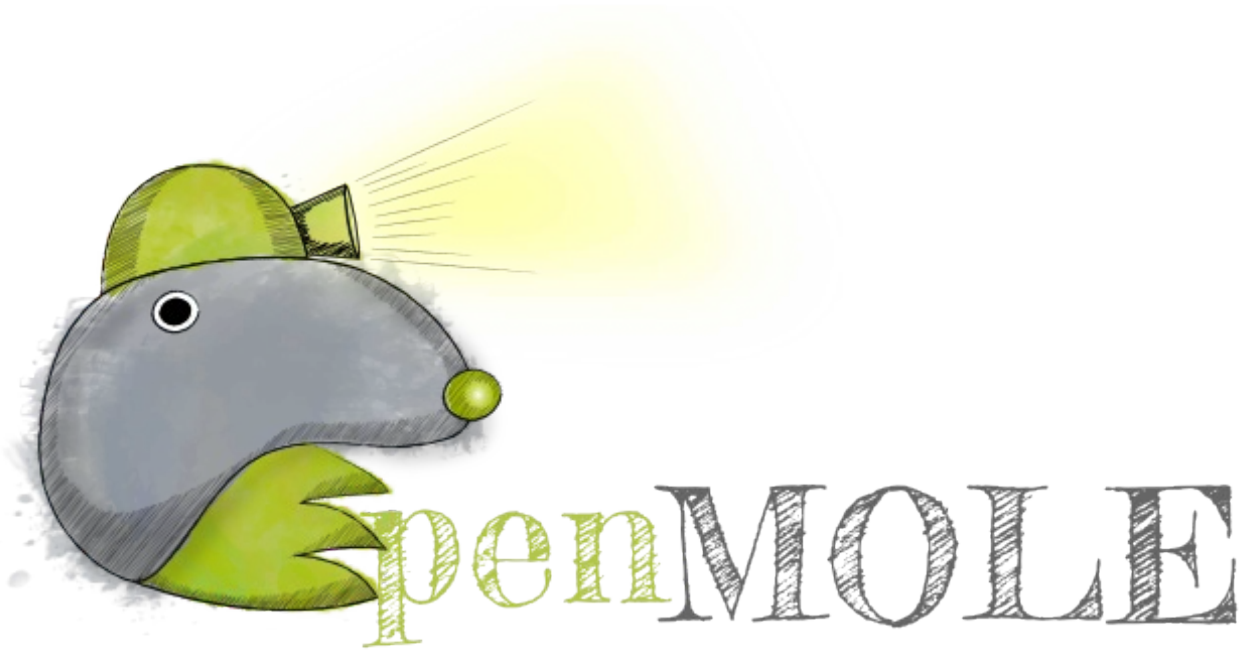
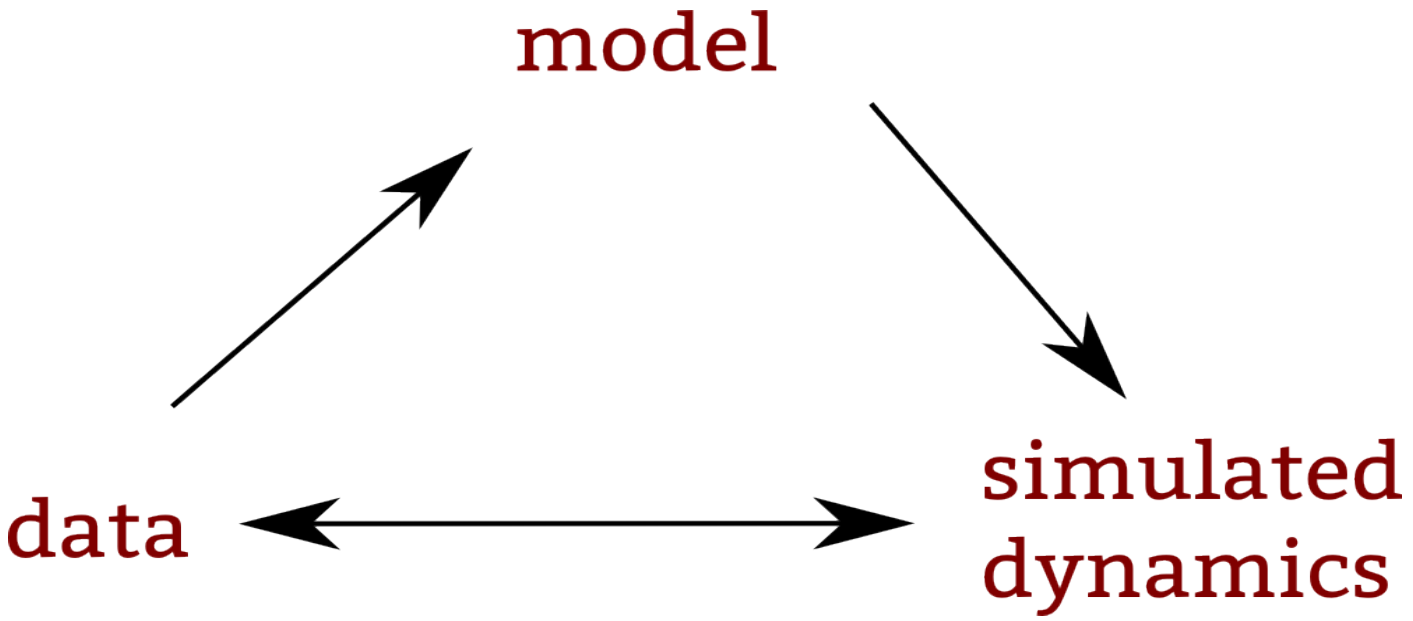


Open MOdeL Experiment

Institut des Systèmes Complexes Paris Ile de France

GÉOGRAPHIE-CITÉS UMR 8504

ERC GeoDiverCity

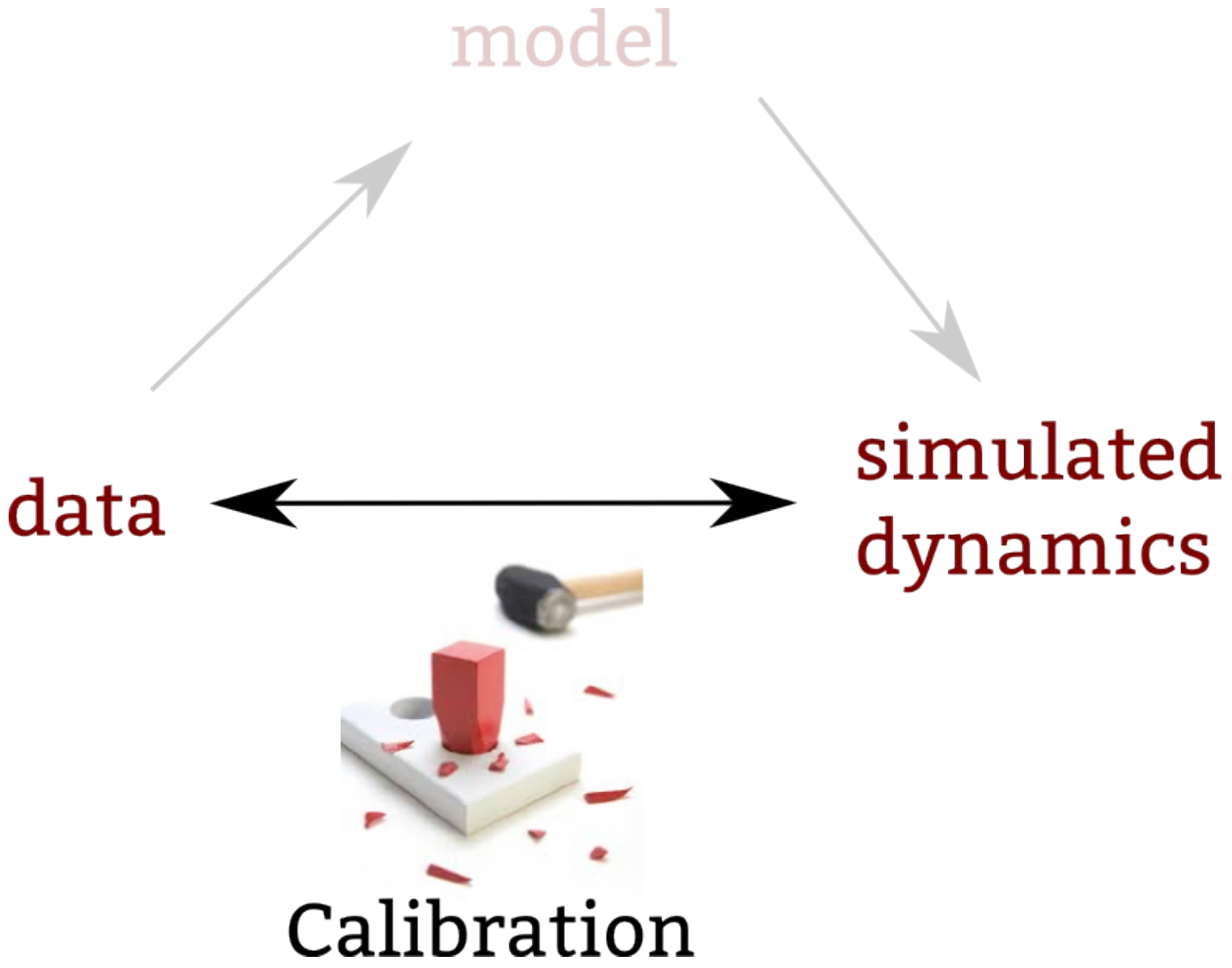

model
data
simulated
dynamics

Data processing

model

data

simulated
dynamics


model
data
simulated
dynamics
Calibration

model

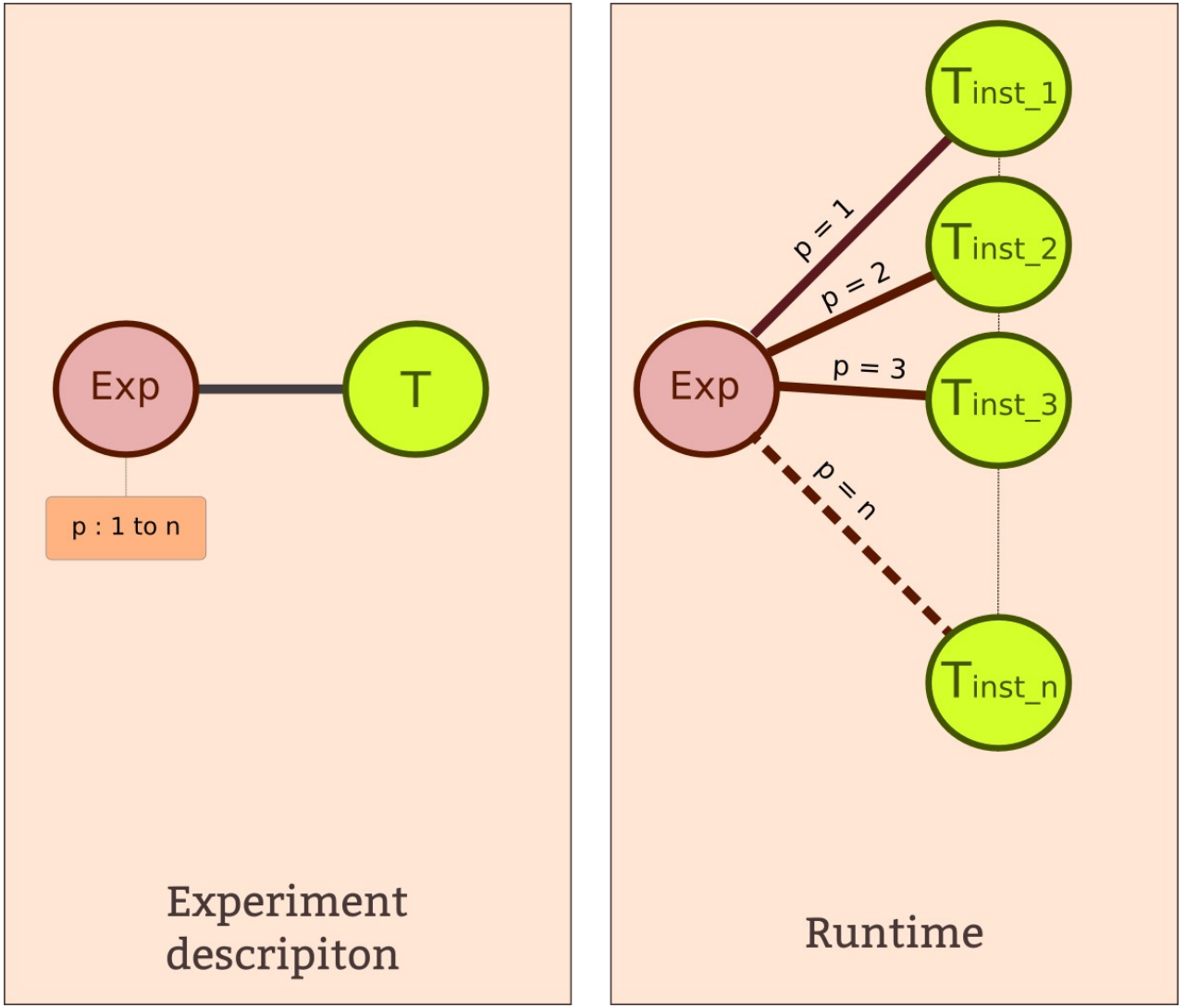
Sensitivity analysis
Design of Experiments

data

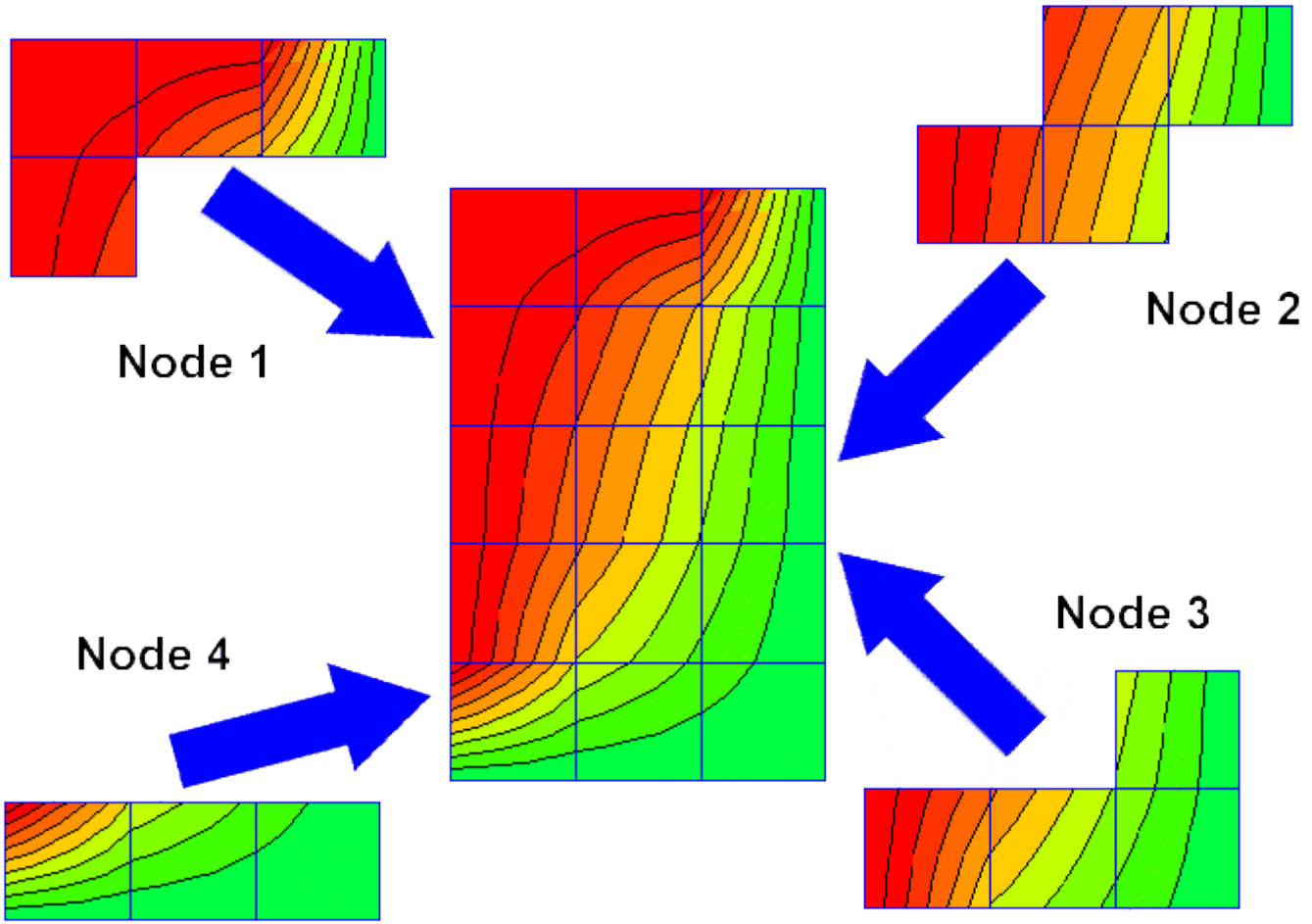
simulated dynamics

These methods are **time consuming**

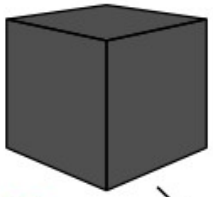
Naturally parallel algorithms permit to leverage parallelism



Data parallelism



The parallelisation by message

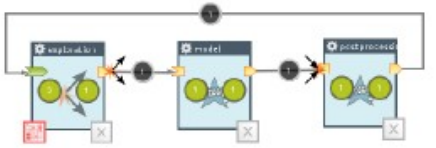


1 Models as blackboxes

C
R
C++
Java
Scala
Scilab
Octave
Python
Netlogo
...

embeds

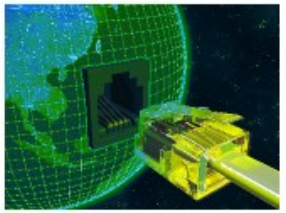
provides



2 Methods

Data processing
Design of Experiments
Sensitivity analysis
Calibration

runs on



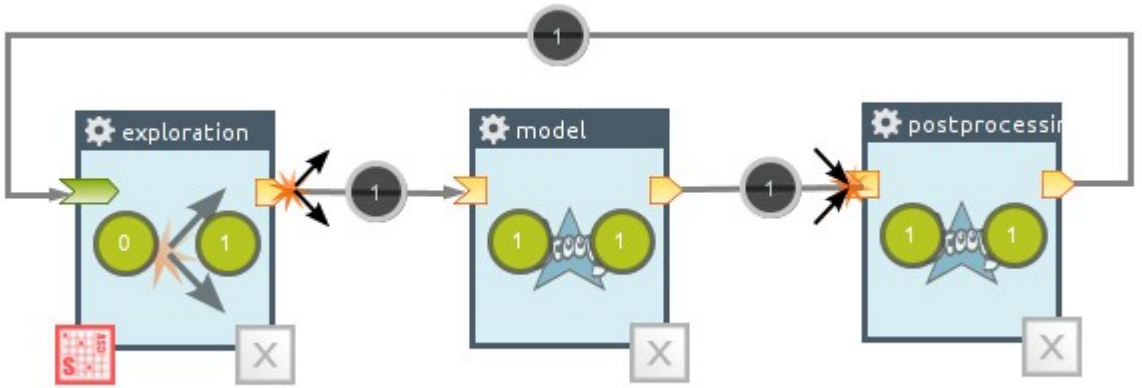
3 Massively parallel environments

Multicore
Server
Cluster
The Grid

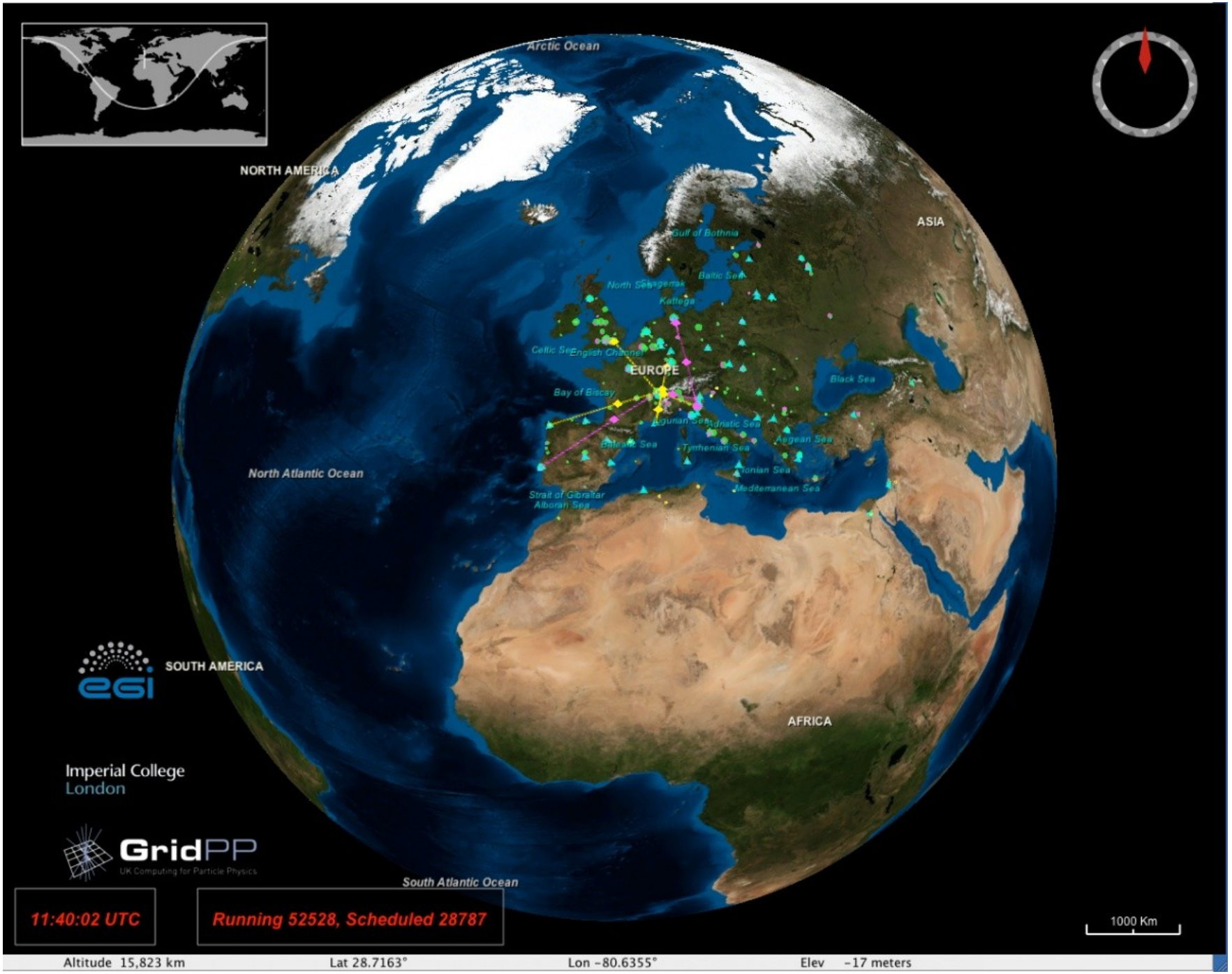
2008
Scientific knowledge producer since

OpenMOLE

Embed your model as a **black box**



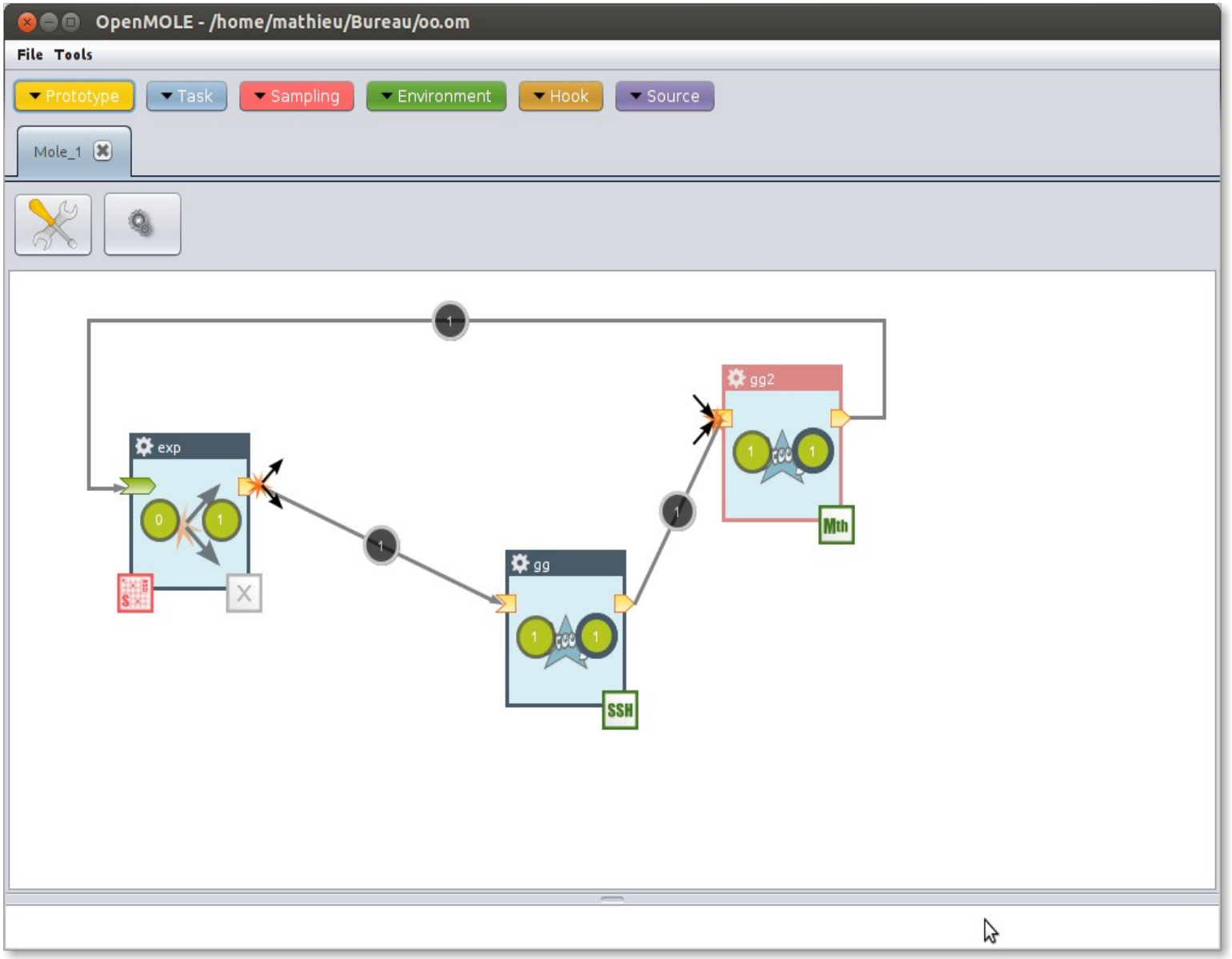
A **naturally parallel formalism** to design experiments


Arctic Ocean
NORTH AMERICA
ASIA
Gulf of Bothnia
Baltic Sea
North Sea
Skagerrak
Kattegat
Celtic Sea
English Channel
EUROPE
Black Sea
Bay of Biscay
Ligurian Sea
Adriatic Sea
Aegean Sea
Balearic Sea
Tyrrhenian Sea
Ionian Sea
Mediterranean Sea
North Atlantic Ocean
Strait of Gibraltar
Alboran Sea
SOUTH AMERICA
AFRICA
Imperial College
London
GridPP
UK Computing for Particle Physics
South Atlantic Ocean
11:40:02 UTC
Running 52528, Scheduled 28787
1000 Km
Altitude 15,823 km
Lat 28.7163°
Lon -80.6355°
Elev -17 meters

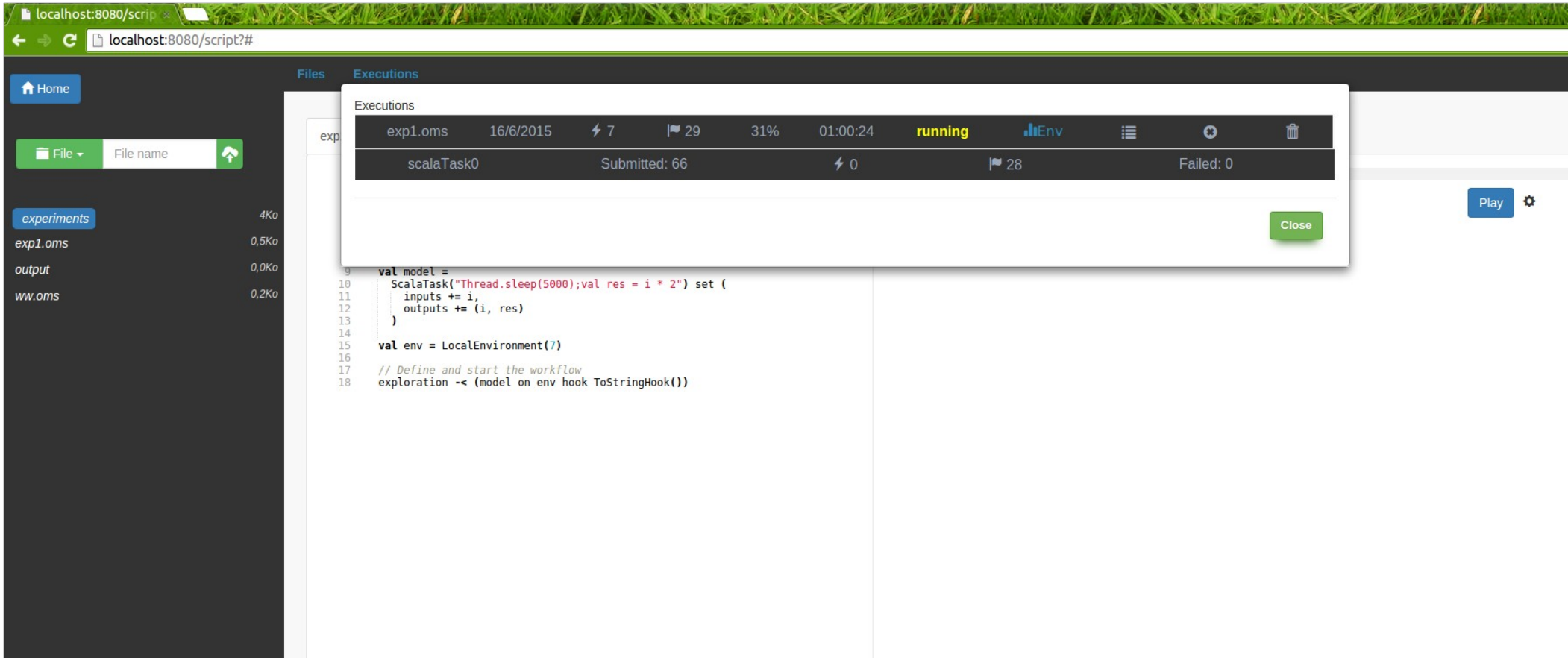
The Grid

```
val i1 = Prototype[Int]("i1")
val i2 = Prototype[Int]("i2")
val j = Prototype[Int]("j")

val hello = GroovyTask("hello", "j = Model.compute(i1, i2)")

hello addInput i1
hello addInput i2
hello addOutput j
hello addLib "/path/to/model.jar"

val exploration = ExplorationTask(
  "exploration",
  Factor(i1, 0 to 100 by 2 toDomain) x
  Factor(i2, new UniformIntDistribution take 10)
 )

val ex = exploration -< (hello by 10 on biomed) toExecution
ex.start
```

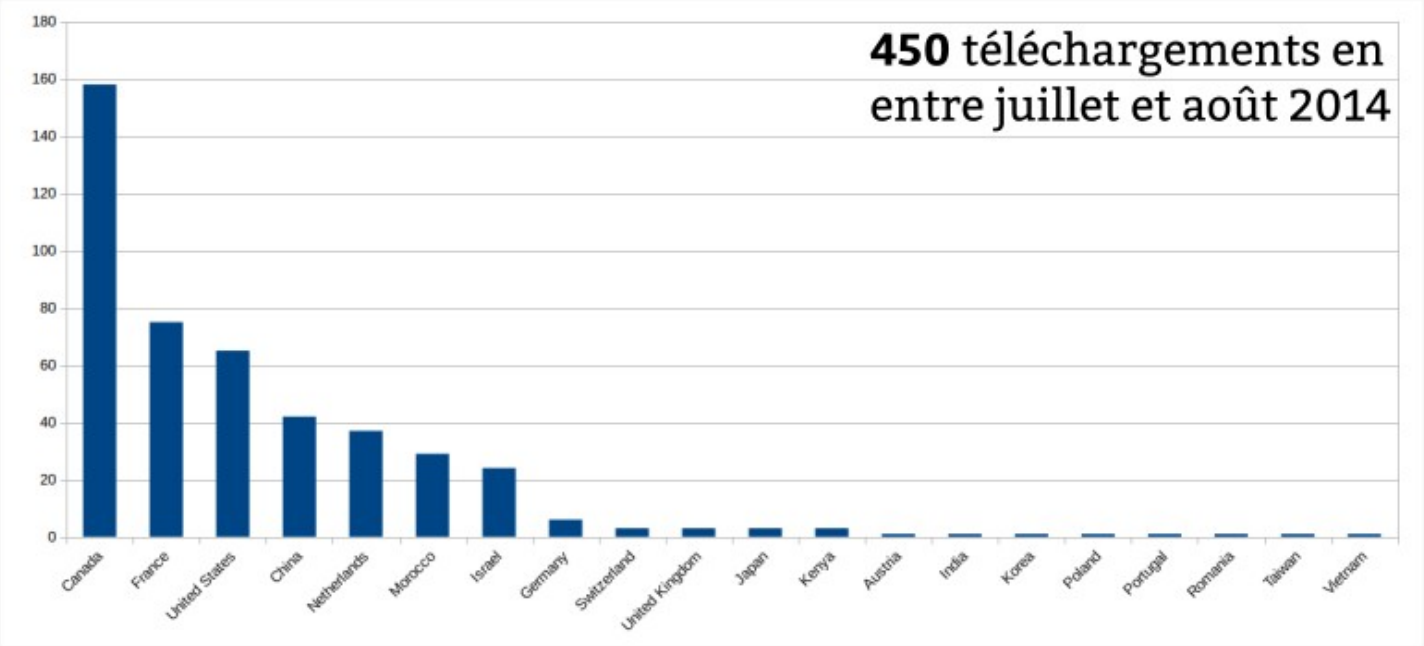
OpenMOLE from a **DSL**



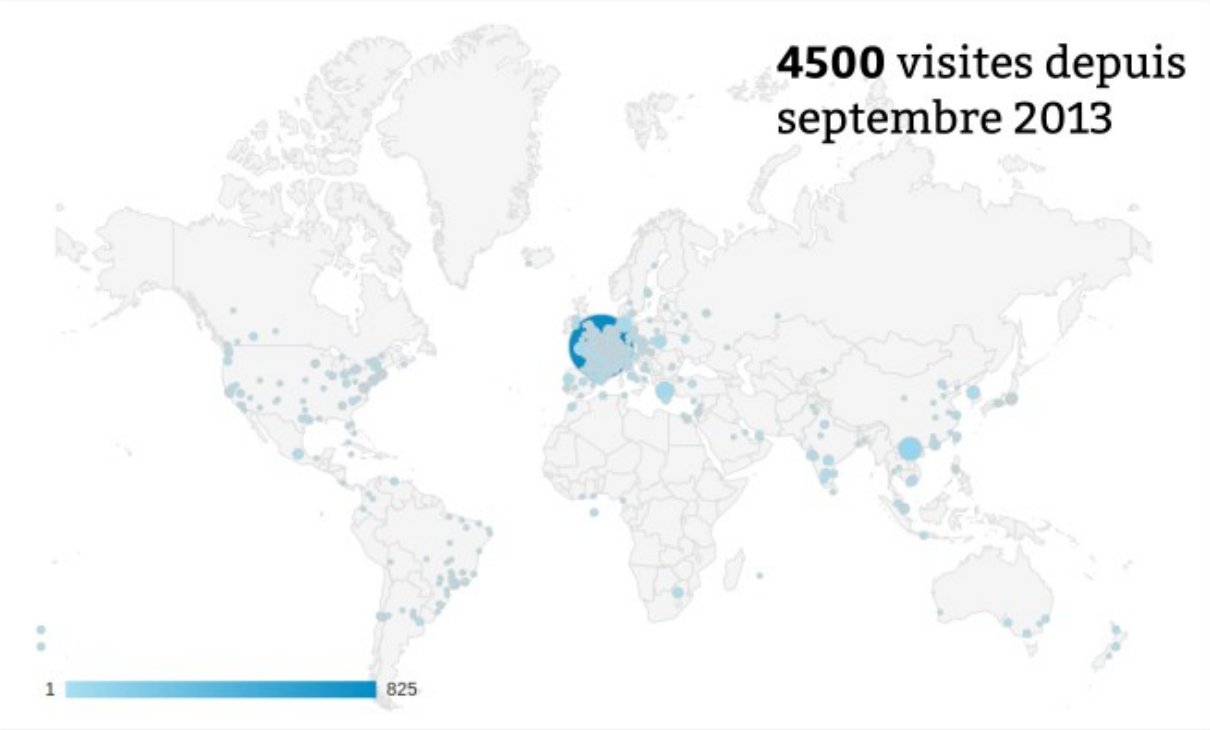
OpenMOLE from a **GUI**



OpenMOLE **online**

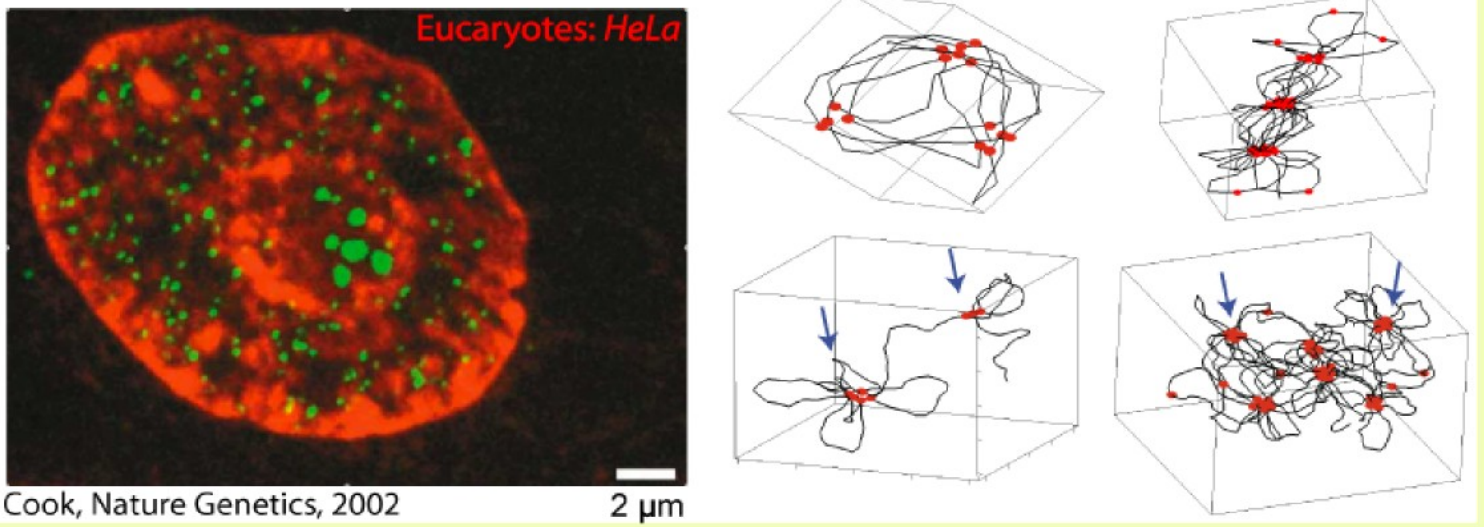


14 Formations et 10 communications orales depuis Mai 2012



Adoption dans au moins 10 laboratoires en **France** et à **l'étranger**
(Imperial College - Londres) dans des disciplines variées: Écologie, SHS, Sciences de l'environnment, Neurosciences, Embryogénèse, Morphogénèse, Géographie, Économie, ...

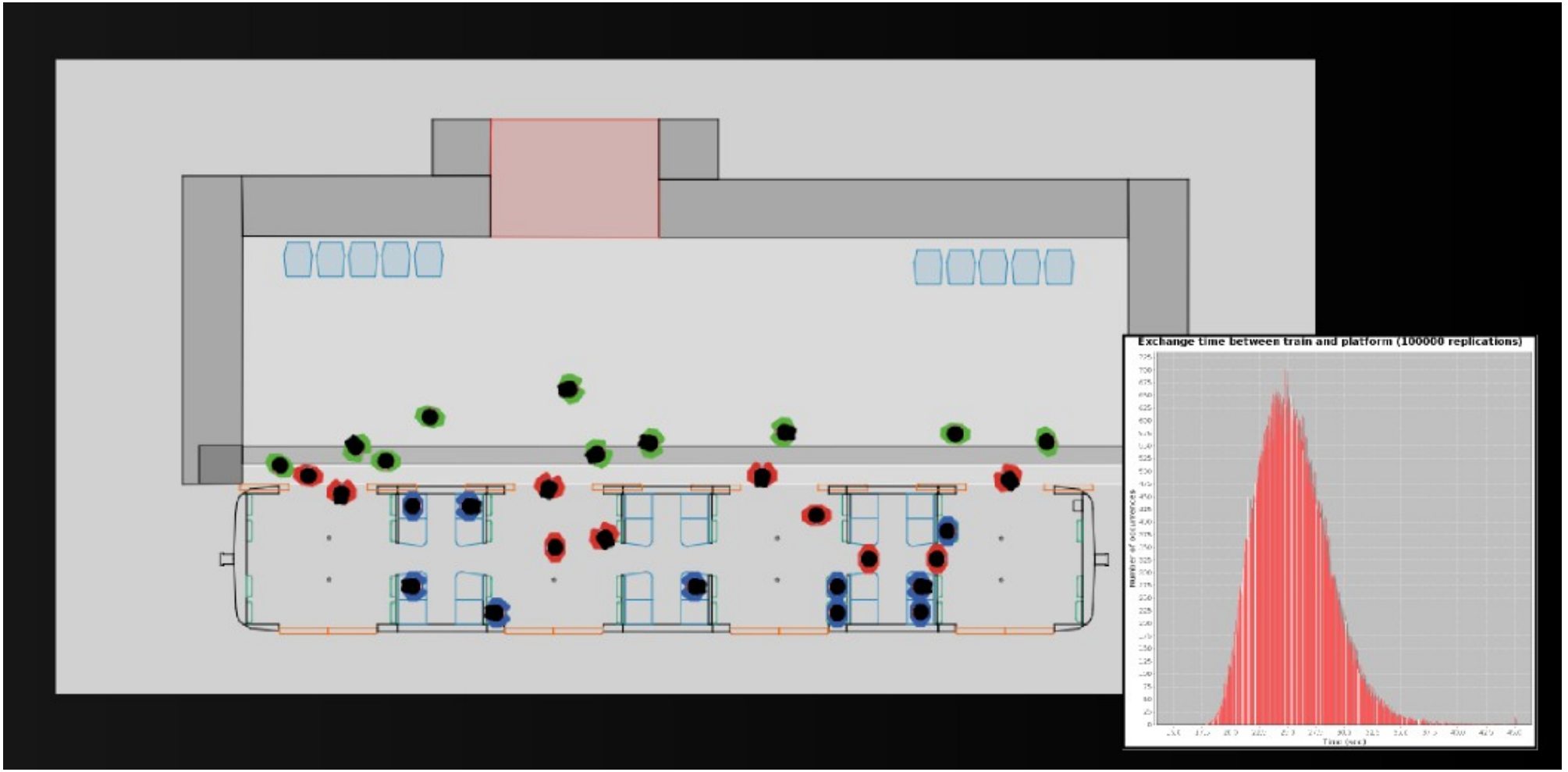
Chromosome structuring



C++ model

2 days per simulation for 1600 simulations: 8.5 years CPU time

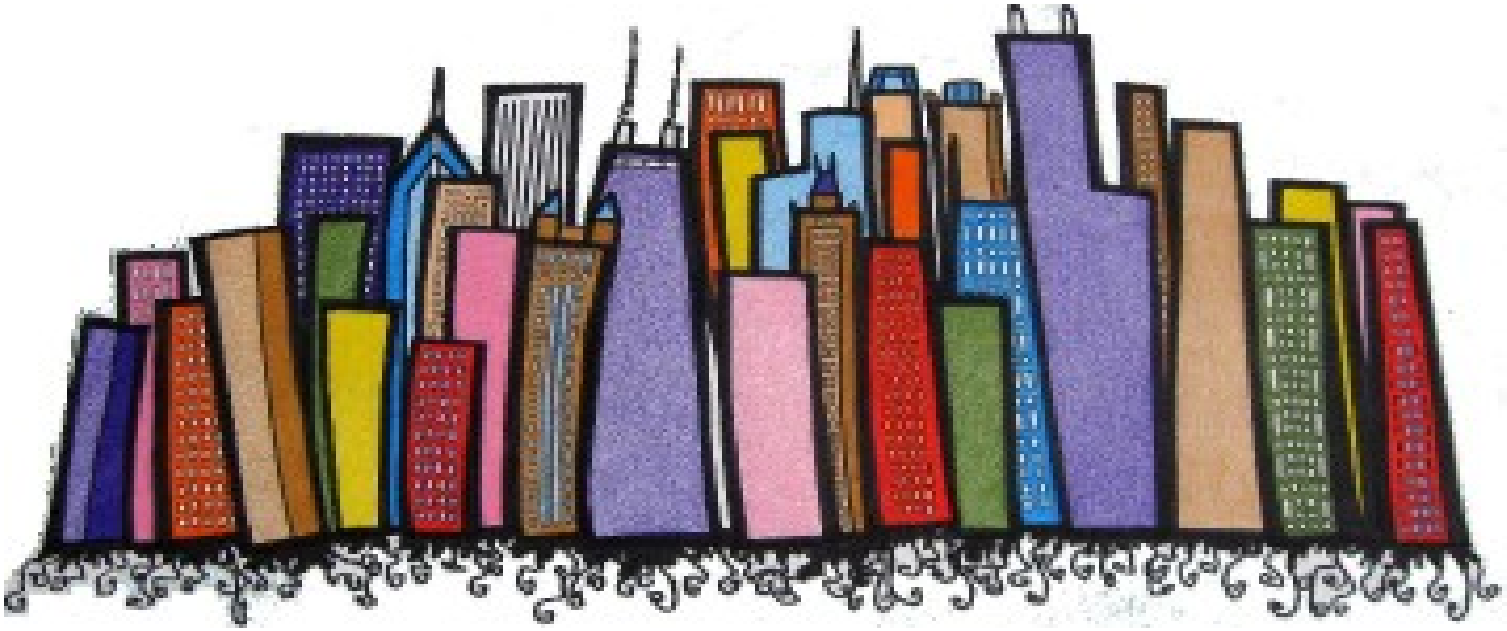
SimTrap



Netlogo model

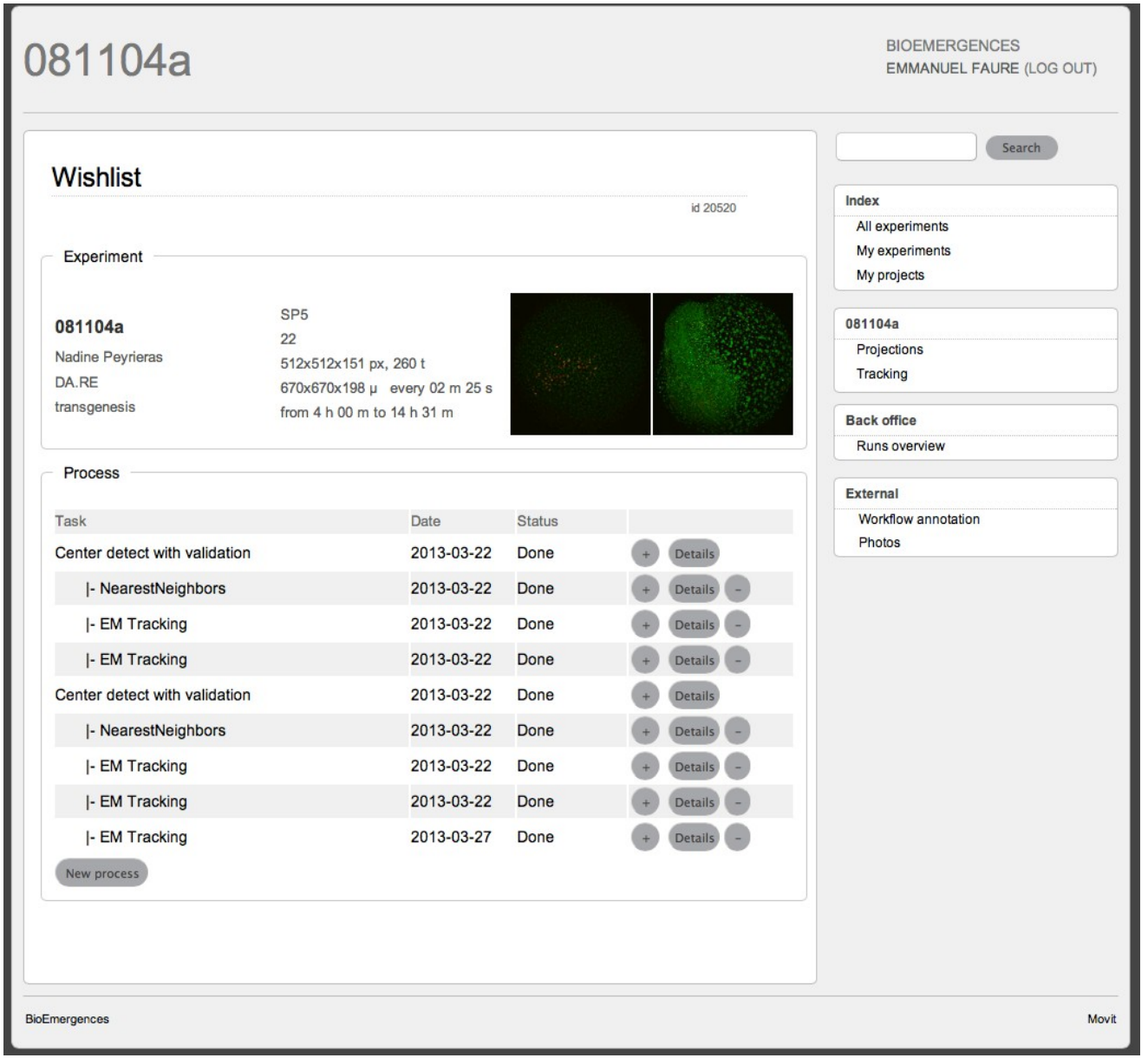
5 min per simulation for 100000 simulations : 1 year CPU time

Simpop

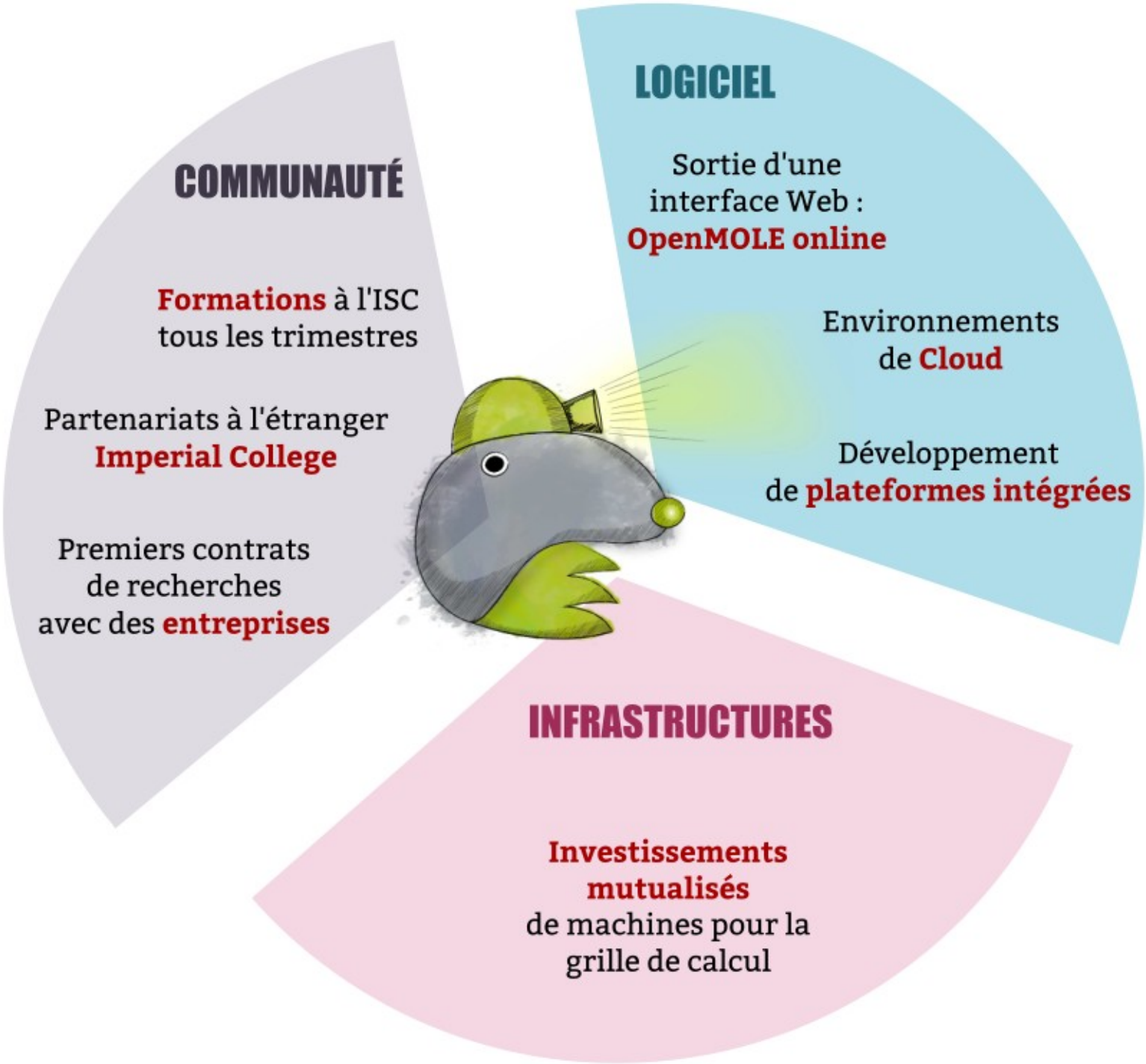


Scala model // 5 min per simulation
for 500 000 000 simulations : 30 years CPU time

Bioemergences



C models // daily productions (10000 jobs / day)



Développement et pérennisation d'OpenMOLE - 2015