Challenges and solutions in replicability and provenance tracking for simulation projects

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Why is reproducing a simulation exactly so hard?

- complexity of code
- complexity of computing environment
- rapid change (in own code and in dependencies)
- difficulty in capturing every piece of information necessary to reproduce a simulation

What can we do about it?

- reduce the complexity of our code through good software engineering practices
- use version control (Subversion, Mercurial, Git, etc.)
- develop tools to automatically and systematically capture every detail of our simulations and their environment: an automated lab notebook

What do we need to capture?

- the code that was run
  - the executable (version, library versions, compiler, compilation options)
  - the script (repository URL, version, imported modules/packages and their versions)
- how it was run: parameter files, command-line options
- the platform on which it was run: processor architecture, operating system, cluster architecture
- why was it run?
- what was the outcome?

Requirements

- support many different workflows: command-line, GUI, batch jobs, solo or collaborative
- automate as much as possible, prompt the user for the rest
- interact with version control systems
- link to data generated by the simulation
- support all and any command-line driven simulators
- support both local and networked storage of data
- be easily extensible and configurable to different workflows
- **be very easy to use, or only the very conscientious will use it**

Background

Reproducibility of experiments is one of the foundation stones of science. A related concept is provenance, being able to track a given scientific result, such as a figure in an article, back through all the analysis steps (verifying the correctness of each) to the original raw data, and the experimental protocol used to obtain it. In computational, simulation-based science, reproduction of previous experiments, and establishing the provenance of results, ought to be easy, given that computers are deterministic, not suffering from the problems of inter-subject and trial-to-trial variability that make reproduction of biological experiments more challenging. In general, however, it is not at all easy.

It is useful to distinguish between independent reproduction of an experiment by an independent researcher, and replication of an experiment, using the same code, perhaps some months or years later. Independent reproducibility is the gold standard, and difficulties in achieving it arise mainly from the challenges in describing complex models and simulation experiments in sufficient detail (Nordlie et al., 2009). Replicability is also important, however, not least in determining whether the failure of others to reproduce a result is due to errors in the original code, and is not necessarily any more frequently achieved. The difficulties of replicability are an underappreciated problem in computational neuroscience, one that will only become more important as the ambition of computational neuroscience and the scrutiny placed upon science in general (*cf* the recent media attention to problems of replicability in climate science simulations) grow.

The failure to routinely achieve replicability in computational science in general (Donoho et al., 2009) is probably due to the complexity and rapidity of change of our code and our computing environments, and the difficulty of capturing every essential piece of information needed to reproduce a computational experiment using existing tools (spreadsheets, version control systems and paper notebooks). In other areas of science, particularly in applied science laboratories with high-throughput, highly-standardised procedures, electronic lab notebooks and laboratory information management systems (LIMS) are in widespread use, but none of these tools seem to be well suited for tracking simulation experiments. VisTrails (http://www.vistrails.org/) is a promising tool for visually creating and running computational workflows with provenance tracking, but its use requires totally recreating your current workflow within the VisTrails environment.

In developing a tool for tracking simulation experiments, something like an electronic lab notebook for computational science, there are a number of challenges: (i) different researchers have very different ways of working and different workflows: command line, GUI, batch-jobs (e.g. in supercomputer environments), or any combination of these for different components (simulation, analysis, graphing, etc.) and phases of a project; (ii) some projects are essentially solo endeavours, others collaborative projects, possibly distributed geographically; (iii) as much as possible should be recorded automatically; if it is left to the researcher to record critical details there is a risk that some details will be missed or left out, particularly under pressure of deadlines.

Here I present a proposed solution to the problems of ensuring reproducibility and tracking the provenance of results, that addresses the challenges outlined above. This solution consists of a core library, implemented as a Python package, Sumatra, together with a series of interfaces that build on top of this: a command-line interface and web interface are provided; it could also be incorporated in existing graphical environments such as neuroConstruct or nrngui. Each of these interfaces enables (i) launching simulations with automated recording of provenance information; and (ii) managing a simulation project: browsing, viewing, deleting simulations. Alternatively, modellers using Python can use the Sumatra package directly in their own code then simply launch simulations in their usual way. Sumatra is distributed as open-source software (http://neuralensemble.org/sumatra/) and is developed using a community model: anyone is welcome to get involved with its development.

References

Nordlie E., Gewaltig M-O, Plesser HE (2009): Towards Reproducible Descriptions of Neuronal Network Models. PLoS Computational Biology. 5:e1000456. http://dx.doi.org/10.1371/journal.pcbi.1000456

Donoho DL, Maleki A, Rahman IU, Shahram M, and Stodden V (2009). 15 years of reproducible research in computational harmonic analysis. Computing in Science & Engineering, 11:8–18. http://dx.doi.org/10.1109/MCSE.2009.15

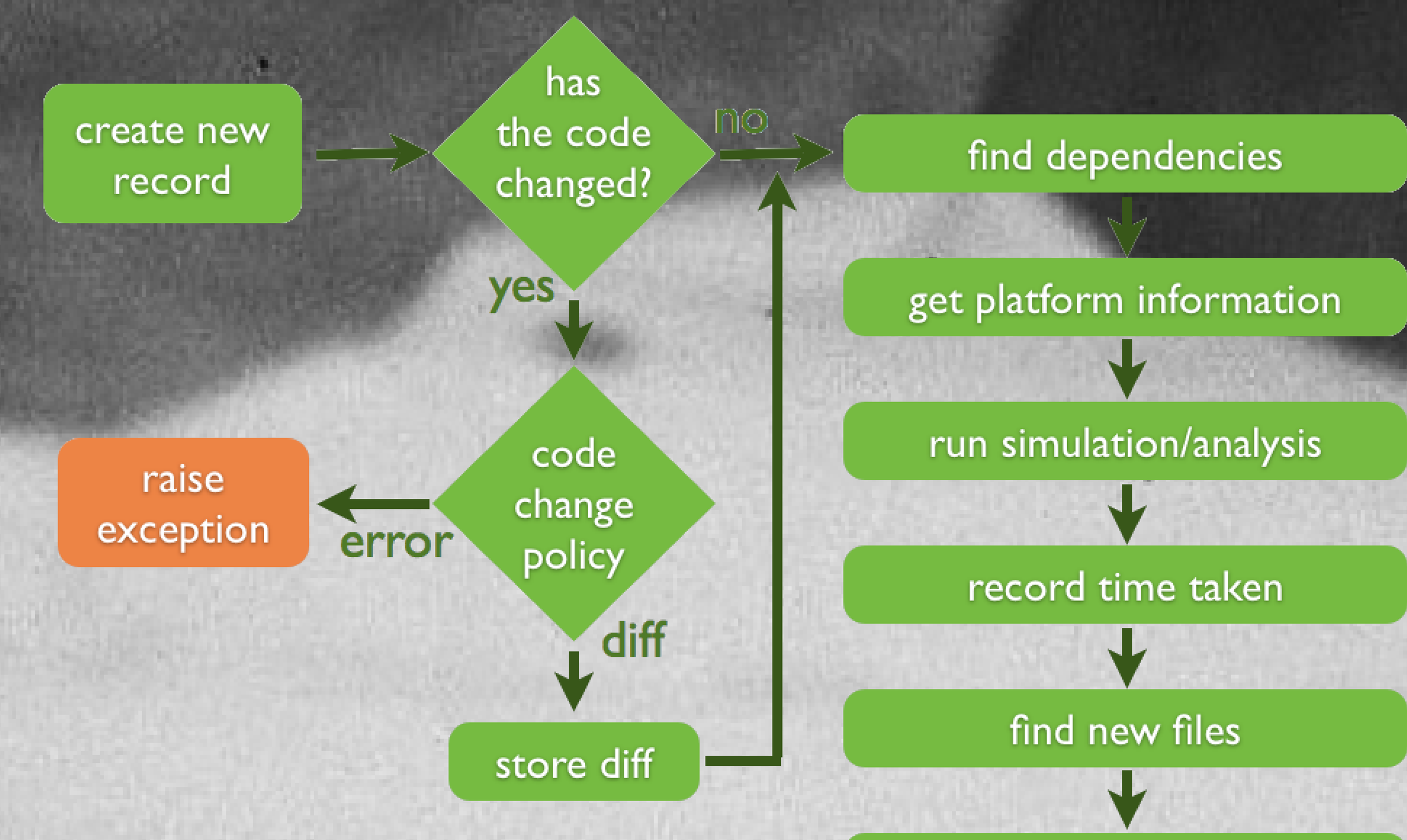
“I thought I used the same parameters but I'm getting different results”

“I can't remember which version of the code I used to generate figure 6”

“The new student wants to reuse that model I published three years ago but he can't reproduce the figures”

“It worked yesterday”

“Why did I do that?”

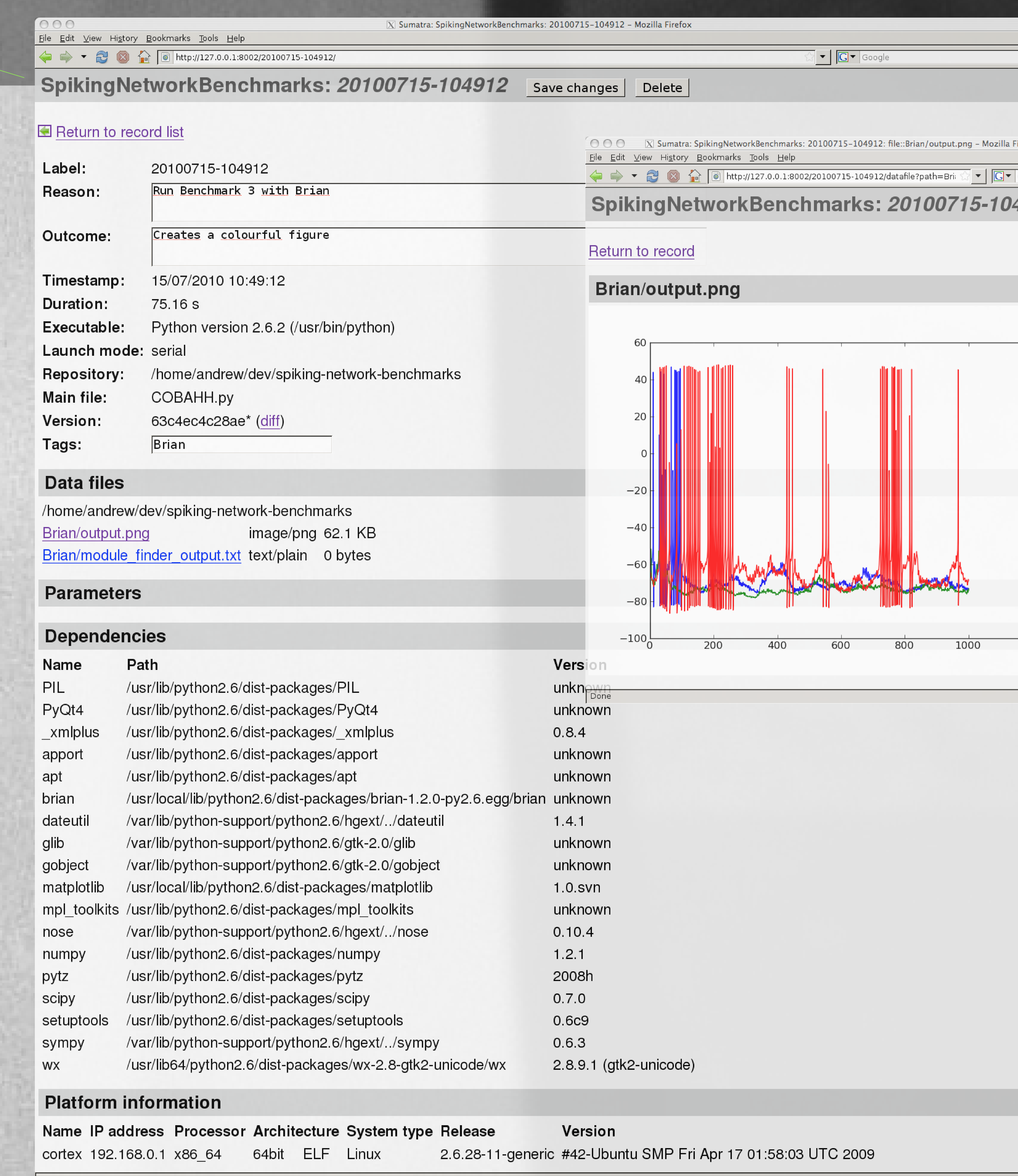


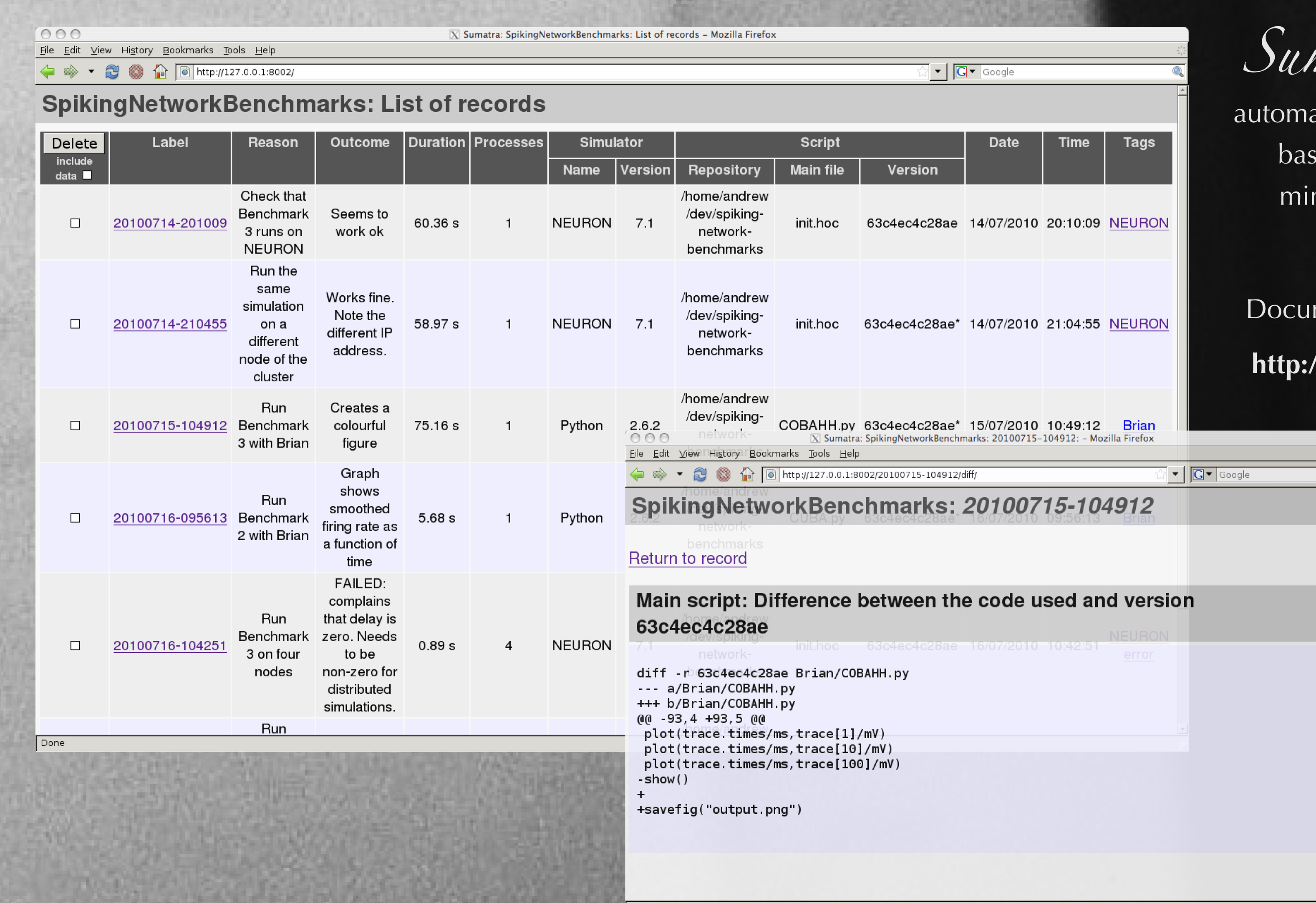
Control flow when running a simulation with Sumatra

Running simulations using Sumatra

```
$ cd myproject
$ smt init MyProject
$ nrniv main.hoc default.param
$ smt run --executable=nrniv --main=main.hoc default.param
$ smt configure --simulator=nrniv --main=main.hoc
$ smt run default.param
$ smt run -n 10 default.param
$ smt list
20100715-174949
20100715-175111
$ smt run --label=haggling --reason="determine whether the
gourd is worth 3 or 4 shekels" romans.param
$ smt comment "apparently, it is worth NaN shekels."
$ smt tag “Figure 6”
$ smt run --reason="test effect of a smaller time constant"
default.param tau_m=10.0
$ smt repeat haggling
The simulation results match.
$ smtweb 8000 &
```

how you run your simulation normally · *how to run it with Sumatra* · *set defaults so you don't have to do so much typing* · *that's better* · *run a distributed simulation with MPI* · *use smt list -l for more details* · *Sumatra generates labels automatically based on the timestamp* · *or you can specify your own label* · *tell Sumatra why you did the simulation (invaluable 6 months later when you're writing the paper)* · *and summarize the outcome* · *add tags to help you find it later* · *change parameters on the command line* · *just to check. If they don't match, Sumatra will show you exactly what changed* · *start a local webserver for the web interface*

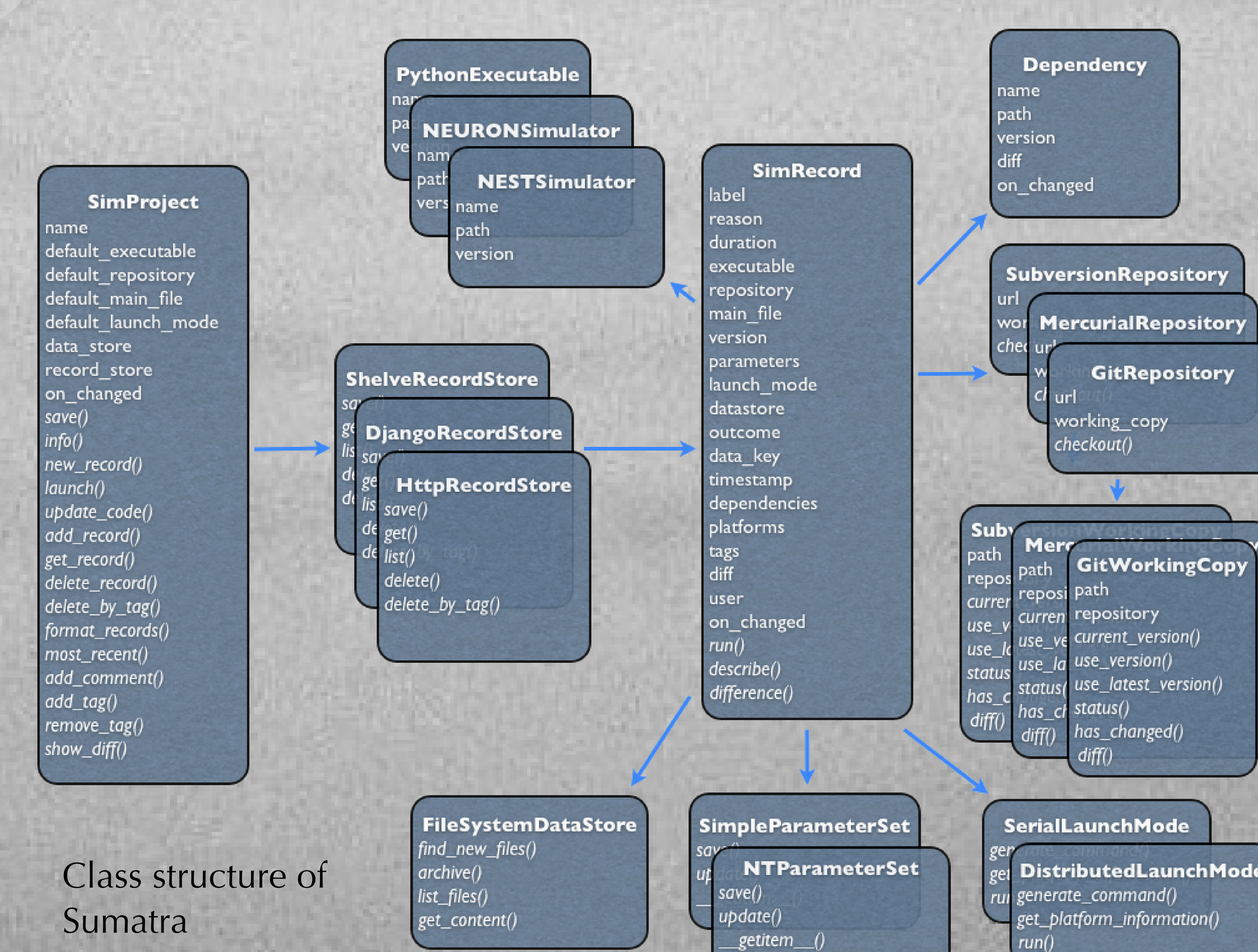




Sumatra is something like an automated lab notebook for simulation-based science, designed to have minimal impact on your current workflow.

Documentation and downloads from:

http://neuralensemble.org/sumatra/



Class structure of Sumatra