

What's new with
PyNN?
Sumatra?

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What the *** is
PyNN?
Sumatra?



Simulator diversity: problem and opportunity

Cons

- Considerable difficulty in translating models from one simulator to another...
- ...or even in understanding someone else's code.
- This:
 - impedes communication between investigators,
 - makes it harder to reproduce other people's work,
 - makes it harder to build on other people's work.

Pros

- Each simulator has a different balance between efficiency, flexibility, scalability and user-friendliness → can choose the most appropriate for a given problem.
- Any given simulator is likely to have bugs and hidden assumptions, which will be revealed by cross-checking results between different simulators → greater confidence in correctness of results.



Find Models by Simulation Environment

Click on a link to show a list of models implemented in that simulation environment or programming language.

| Simulation Environment | Homepage | Number of models |
|---|----------|------------------|
| BioPAX (web link to model) | | 1 |
| Brian | | 4 |
| C or C++ program | | 34 |
| C or C++ program (web link to model) | | 19 |
| CONTENT | | 1 |
| CSIM | | 1 |
| CSIM (web link to model) | | 3 |
| CalC Calcium Calculator | | 1 |
| CalC Calcium Calculator (web link to model) | | 7 |
| Catacomb (web link to model) | | 1 |
| CellExcite (web link to model) | | 1 |
| CellML | | 0 |
| CellML (web link to model) | | 1 |
| Chemesis | | 2 |
| Dynamics Solver | | 1 |
| Emergent/PDP++ | | 3 |
| FORTRAN | | 4 |
| FORTRAN (web link to a model) | | 1 |
| GNUstep NeXTStep/OpenStep | | 1 |
| Genesis | | 13 |
| Genesis (web link to model) | | 7 |
| IChMASCOT | | 0 |
| IGOR Pro | | 3 |
| IonChannelLab | | 0 |
| Java | | 5 |
| Java (web link to model) | | 2 |

| | | |
|--|--|-----|
| KInNeSS (web link to model) | | 1 |
| L-Neuron | | 0 |
| MATLAB | | 67 |
| MATLAB (web link to model) | | 34 |
| MCell | | 1 |
| MOOSE/PyMOOSE (web link to method) | | 1 |
| MVASpike | | 1 |
| MadSim | | 1 |
| NCS | | 1 |
| NEST (formerly BLISS/SYNOD) | | 2 |
| NEURONPM (web link to tool) | | 2 |
| NSL | | 0 |
| Neosim | | 0 |
| Network | | 1 |
| NeuGen | | 0 |
| Neuron | | 261 |
| Neuron (web link to model) | | 14 |
| NeuronC | | 0 |
| NeuronetExperimenter (web link to model) | | 1 |
| Octave | | 1 |
| PCSIM | | 1 |
| PSpice | | 2 |
| Pascal (web link to model) | | 1 |
| Pascal/Delphi | | 2 |
| PyNN | | 2 |
| Python | | 5 |
| Python (web link to model) | | 1 |
| QBasic/QuickBasic/Turbo Basic | | 2 |
| QuB | | 1 |
| R (web link to model) | | 1 |
| SABER | | 1 |
| SBML (web link to model) | | 1 |
| SNNAP | | 21 |
| SciLab | | 1 |
| Scilab (web link to model) | | 2 |
| Simulink | | 6 |
| Sspice Symbolic SPICE | | 1 |
| Surf-Hippo | | 0 |
| Synthesis | | 0 |
| Topographica | | 0 |
| Topographica (web link to model) | | 1 |
| Virtual Cell (web link to model) | | 3 |
| XML (web link to model) | | 3 |
| XNBC | | 0 |
| XPP | | 50 |
| XPP (web link to model) | | 7 |
| neuroConstruct (web link to model) | | 1 |
| parplex | | 2 |



a common API for spiking
network simulators

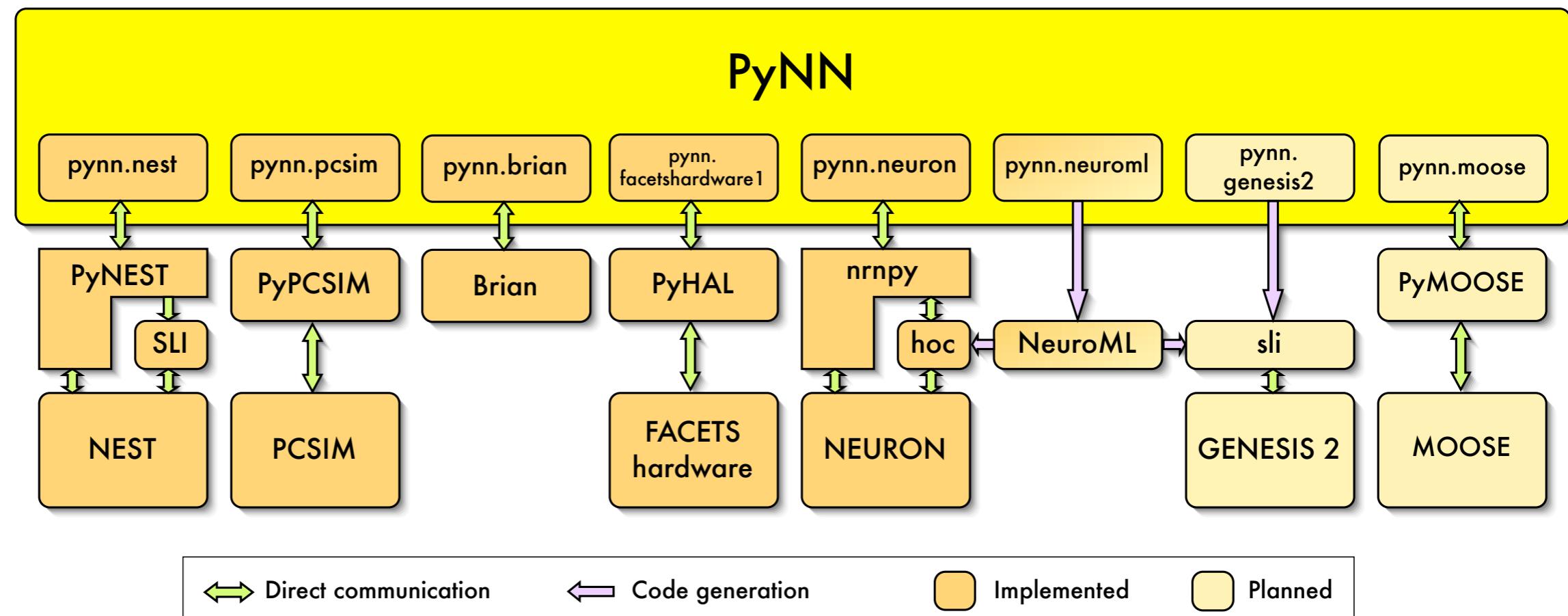
- Goal: write the code for a simulation once, run it on any supported simulator or hardware device *without modification.*
 - ◆ keep the advantages of having multiple simulators or hardware devices
 - ◆ but remove the translation barrier*.



a common API for spiking network simulators

- Goal: write the code for a simulation once, run it on any supported simulator or hardware device *without modification*.
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 - ◆ but remove the translation barrier*.





```

sim.setup(timestep=0.1)
cell_parameters = {"tau_m": 12.0, "cm": 0.8, "v_thresh": -50.0,
                   "v_reset": -65.0}
pE = sim.Population((100,100), sim.IF_cond_exp, cell_parameters,
                     label="excitatory neurons")
pI = sim.Population((50,50), sim.IF_cond_exp, cell_parameters,
                     label="inhibitory neurons")
input = sim.Population(100, sim.SpikeSourcePoisson)
rate_distr = random.RandomDistribution("normal", (10.0, 2.0))
input.rset("rate", rate_distr)
background = sim.NoisyCurrentSource(mean=0.1, stdev=0.01)
pE.inject(background)
pI.inject(background)
DDPC = sim.DistanceDependentProbabilityConnector
weight_distr = random.RandomDistribution("uniform", (0.0, 0.1))
connector = DDPC("exp(-d**2/400.0)", weights=weight_distr,
                  delays="0.5+0.01d")
TMM = sim.TsodyksMarkramMechanism
depressing = sim.DynamicSynapse(fast=TMM(U=0.5, tau_rec=800.0))
e2e = sim.Projection(pE, pE, connector, target="excitatory",
                      synapse_dynamics=plasticity)
e2i = sim.Projection(pE, pI, connector, target="excitatory")
i2e = sim.Projection(pI, pE, connector, target="inhibitory")

```

```
import pyNN.neuron as sim
sim.setup(timestep=0.1)
cell_parameters = {"tau_m": 12.0, "cm": 0.8, "v_thresh": -50.0,
                   "v_reset": -65.0}
pE = sim.Population(100, 100, sim.IF_cond_exp, cell_parameters,
                     label="excitatory neurons")
pI = sim.Population(50, 50, sim.IF_cond_exp, cell_parameters,
                     label="inhibitory neurons")
input = sim.Population(100, sim.SpikeSourcePoisson)
rate_distr = random.RandomDistribution("normal", (10.0, 2.0))
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e2e = sim.Projection(pE, pE, connector, target="excitatory",
                      synapse_dynamics=plasticity)
e2i = sim.Projection(pE, pI, connector, target="excitatory")
i2e = sim.Projection(pI, pE, connector, target="inhibitory")
```

```
import pyNN.nest as sim
sim.setup(timestep=0.1)
cell_parameters = {"tau_m": 12.0, "cm": 0.8, "v_thresh": -50.0,
                   "v_reset": -65.0}
pE = sim.Population(100, 100, sim.IF_cond_exp, cell_parameters,
                     label="excitatory neurons")
pI = sim.Population(50, 50, sim.IF_cond_exp, cell_parameters,
                     label="inhibitory neurons")
input = sim.Population(100, sim.SpikeSourcePoisson)
rate_distr = random.RandomDistribution("normal", (10.0, 2.0))
input.rset("rate", rate_distr)
background = sim.NoisyCurrentSource(mean=0.1, stdev=0.01)
pE.inject(background)
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DDPC = sim.DistanceDependentProbabilityConnector
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                  delays="0.5+0.01d")
TMM = sim.TsodyksMarkramMechanism
depressing = sim.DynamicSynapse(fast=TMM(U=0.5, tau_rec=800.0))
e2e = sim.Projection(pE, pE, connector, target="excitatory",
                      synapse_dynamics=plasticity)
e2i = sim.Projection(pE, pI, connector, target="excitatory")
i2e = sim.Projection(pI, pE, connector, target="inhibitory")
```

```
import pyNN.hardware.facets.stage1 as sim
sim.setup(timestep=0.1)
cell_parameters = {"tau_m": 12.0, "cm": 0.8, "v_thresh": -50.0,
                   "v_reset": -65.0}
pE = sim.Population(100, 100, sim.IF_cond_exp, cell_parameters,
                     label="excitatory neurons")
pI = sim.Population(50, 50, sim.IF_cond_exp, cell_parameters,
                     label="inhibitory neurons")
input = sim.Population(100, sim.SpikeSourcePoisson)
rate_distr = random.RandomDistribution("normal", (10.0, 2.0))
input.rset("rate", rate_distr)
background = sim.NoisyCurrentSource(mean=0.1, stdev=0.01)
pE.inject(background)
pI.inject(background)
DDPC = sim.DistanceDependentProbabilityConnector
weight_distr = random.RandomDistribution("uniform", (0.0, 0.1))
connector = DDPC("exp(-d**2/400.0)", weights=weight_distr,
                  delays="0.5+0.01d")
TMM = sim.TsodyksMarkramMechanism
depressing = sim.DynamicSynapse(fast=TMM(U=0.5, tau_rec=800.0))
e2e = sim.Projection(pE, pE, connector, target="excitatory",
                      synapse_dynamics=plasticity)
e2i = sim.Projection(pE, pI, connector, target="excitatory")
i2e = sim.Projection(pI, pE, connector, target="inhibitory")
```

Since CodeJam #3

0.6

1. **Spikes, membrane potential and synaptic conductances can now be saved to file in various binary formats.** To do this, pass a PyNN File object to Population.print_X(), instead of a filename. There are various types of PyNN File object, defined in the recording.files module, e.g., StandardTextFile, PickleFile, NumpyBinaryFile, HDF5ArrayFile.
2. **Added a reset() function and made the behaviour of setup() consistent across simulators.** reset() sets the simulation time to zero and sets membrane potentials to their initial values, but does not change the network structure. setup() destroys any previously defined network.
3. The possibility of expressing **distance-dependent weights and delays** was extended to the AllToAllConnector and FixedProbabilityConnector classes. To reduce the number of arguments to the constructors, the arguments affecting the spatial topology (periodic boundary conditions, etc.) were moved to a new Space class, so that only a single Space instance need be passed to the Connector constructor.
4. **Assorted speed-ups**
5. **Testing** that results are independent of number of processors added to regression tests.

Since CodeJam #3

trunk

1. internal sub-package reorganisation in preparation for multi-compartmental models
2. connection speed-ups
3. added SmallWorldConnector
4. removed `v_init` as a parameter, replaced with `Population.initialize()` method
5. Population structure no longer restricted to a grid
6. began implementing `PopulationView` (sub-populations) and `Assembly` (collection of Populations)

http://neuralensemble.org/PyNN

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{3} Active Tickets by Milestone (39 matches)

This report shows how to color results by priority, while grouping results by milestone.

Last modification time and description are included as hidden fields for useful RSS export.

0.7.0 Release

| Ticket | Summary | Component | Version | Type | Owner | Created | Reporter |
|--------|--|---------------|---------|-------------|-------------|----------|-------------|
| #155 | When using `Projection.set/getWeights()` with arrays, the case of multiple connections between source and target is not consistently handled or tested | all | trunk | defect | | 02/03/10 | apdavison |
| #160 | SpikeSourceArray ignores new spike_times | common | trunk | defect | apdavison * | 02/26/10 | mschmucker |
| #62 | Draw dynamic synapses parameters from RNG Distributions | common | trunk | enhancement | pierre | 04/03/08 | pierre |
| #102 | SubPopulation should be extracted from a Population object | all | trunk | enhancement | apdavison * | 06/21/08 | Pierre |
| #113 | Add `Projection.record_weights()` or something similar | all | trunk | enhancement | apdavison * | 08/27/08 | apdavison |
| #119 | Padding and cells labeling | all | trunk | enhancement | | 11/04/08 | pierre |
| #137 | Reimplement connectors in terms of arrays | common | trunk | enhancement | apdavison | 06/05/09 | apdavison |
| #138 | All issues of which connections are local should be dealt with within ConnectionManager, not in the Connectors | common | trunk | enhancement | apdavison | 06/05/09 | apdavison |
| #153 | A way to reset the list of things to record | common | trunk | enhancement | apdavison | 01/26/10 | apdavison |
| #154 | Implement `Population.record_gsyn()` method and `record_gsyn()` function in the `pcsim` module | pcsim | trunk | enhancement | apdavison | 02/02/10 | apdavison |
| #161 | Rethink the connectors as convergent_connect() and problems with set/getWeight | Documentation | trunk | enhancement | | 03/26/10 | pierre |
| #2 | Separate standard models into a membrane part and a synapse part | unspecified | trunk | task | somebody | 04/24/07 | apdavison |
| #4 | Any int or float cell or connection parameter should be replaceable by a RandomDistribution object | unspecified | trunk | task | Pierre | 04/24/07 | apdavison |
| #5 | More sophisticated parameter handling | unspecified | trunk | task | somebody | 04/24/07 | apdavison |
| #18 | Test multicompartmental models with `neuron` module | unspecified | trunk | task | apdavison * | 04/24/07 | apdavison |
| #125 | Update NMODL files in src/hoc to be thread-safe, where possible | hoc | trunk | task | apdavison * | 01/27/09 | apdavison |
| #157 | Split `common` into multiple files | common | trunk | task | apdavison * | 02/16/10 | apdavison |
| #51 | More sophisticated error handling for writing to file | common | trunk | defect | apdavison | 03/19/08 | apdavison |
| #124 | setup.py does not recompile .mod files | hoc | trunk | defect | apdavison | 01/01/09 | apdavison |
| #165 | Temporary files are not closed correctly by Recorder class | nest | trunk | defect | apdavison | 05/21/10 | brueederle |
| #24 | Implement user-specified output formats for spikes, etc | unspecified | trunk | enhancement | somebody | 05/16/07 | apdavison |
| #35 | Access to neuron variables via properties of the ID class | common | trunk | enhancement | apdavison * | 11/14/07 | apdavison |
| #65 | Add a `get_simulator()` function | common | trunk | enhancement | apdavison * | 04/09/08 | apdavison |
| #69 | Change `set(cells, params, val)` to `set(cells, **parameters)` | common | trunk | enhancement | apdavison | 04/09/08 | apdavison |
| #114 | `dummy` or `test` module to check argument types, etc in code before starting a time-consuming run | all | trunk | enhancement | apdavison * | 09/09/08 | apdavison |
| #132 | The selection of dynamic synapse models that is done in `Projection.__init__()` would be better done in the `SynapseDynamics` class | all | trunk | enhancement | | 06/01/09 | apdavison |
| #133 | Add functions `run_for()` and `run_until()`, with `run()` an alias for `run_for()` | all | trunk | enhancement | | 06/01/09 | apdavison |
| #139 | Add a FromArrayConnector class | common | trunk | enhancement | apdavison | 06/05/09 | apdavison |
| #142 | When creating a Projection it is not clear how to define if it is a excitatory or inhibitory synapse (in the case of conductance based synapses) | all | trunk | enhancement | | 06/12/09 | JensKremkow |
| #164 | In the `random` module, we should use mpi4py instead of relying on the correct rank, etc. being passed | random | trunk | enhancement | apdavison | 05/14/10 | apdavison |
| #1 | Combine print() and print_v() into a single write() that takes what-to-print as an argument | unspecified | trunk | task | apdavison * | 04/24/07 | apdavison |
| #8 | Create a NEURON equivalent of Izhikevich's adapting I&F model in NEST | hoc | trunk | task | apdavison * | 04/24/07 | apdavison |
| #9 | Add an Izhikevich standard model | unspecified | trunk | task | somebody | 04/24/07 | apdavison |
| #10 | Improve NEURON implementation of IF_curr_alpha, etc | hoc | trunk | task | apdavison | 04/24/07 | apdavison |
| #20 | Performance benchmarks | unspecified | trunk | task | somebody | 04/24/07 | apdavison |
| #54 | Thoroughly test with native models | unspecified | trunk | task | apdavison | 03/20/08 | apdavison |
| #67 | Move the `max_delay` argument of `setup()` into `extra_params`, since not all simulators use it | common | trunk | task | apdavison | 04/09/08 | apdavison |
| #73 | Compatible output should save times in voltage files | common | trunk | task | apdavison | 04/09/08 | apdavison |
| #151 | Additional information regarding pyNN installation with NEURON | Documentation | trunk | enhancement | apdavison * | 12/08/09 | bkaplan |

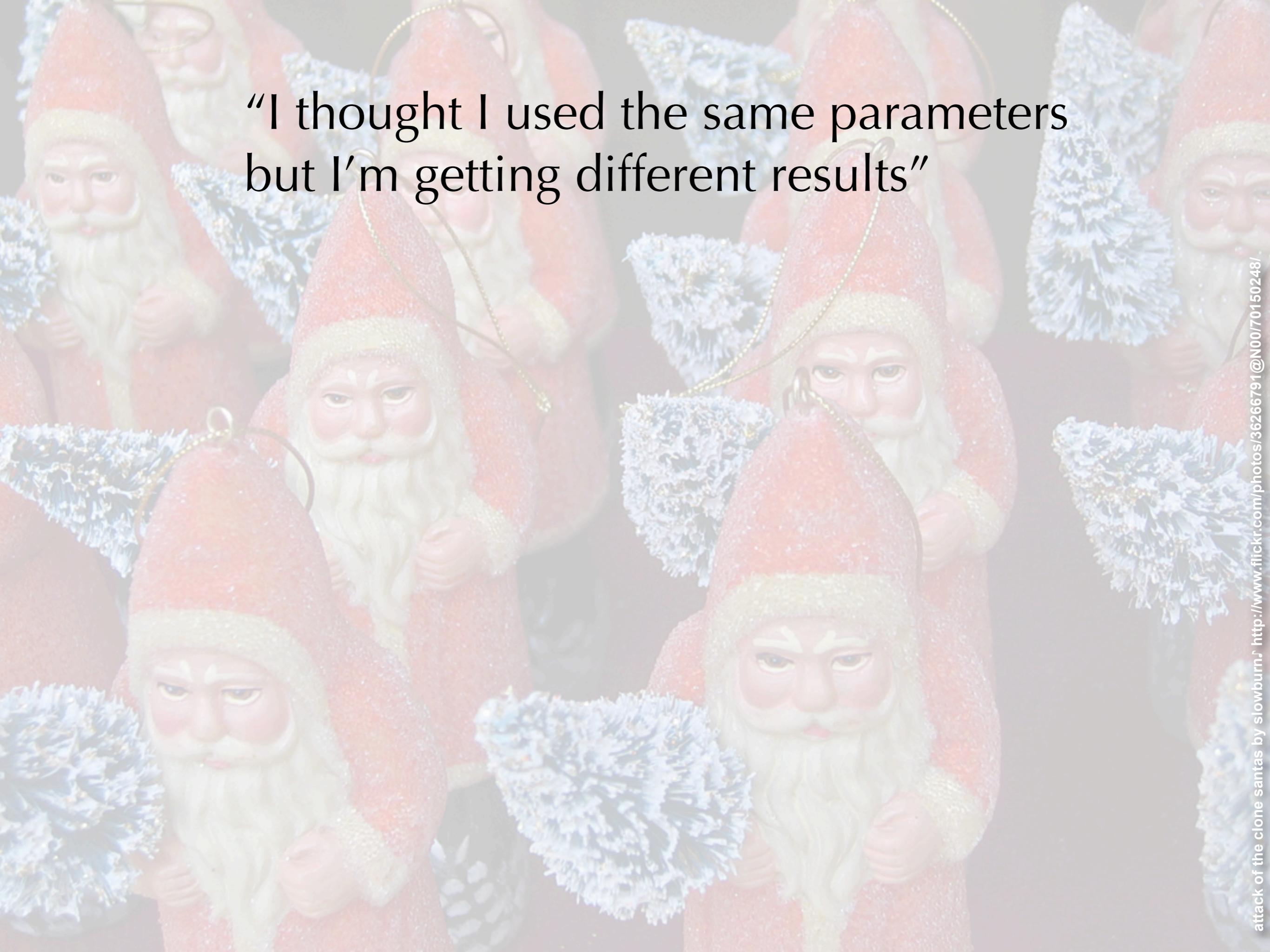
Note: See [TracReports](#) for help on using and creating reports.



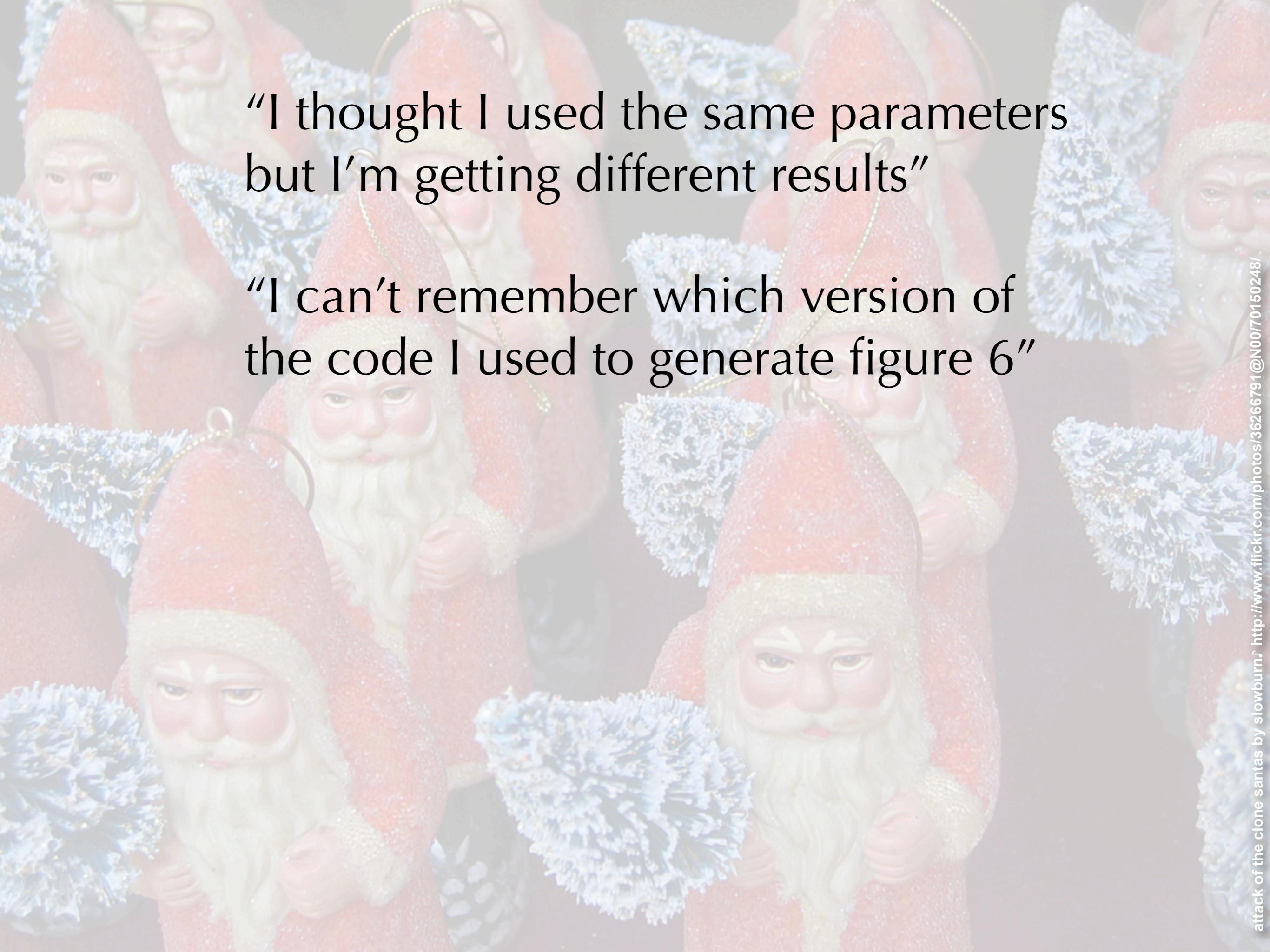
Sumatra

A cluster of identical Santa Claus figurines hanging from a string. The Santas are dressed in traditional red suits with white fur trim and hats, and have white beards. They are surrounded by blue, spiky Christmas trees.

Replicability

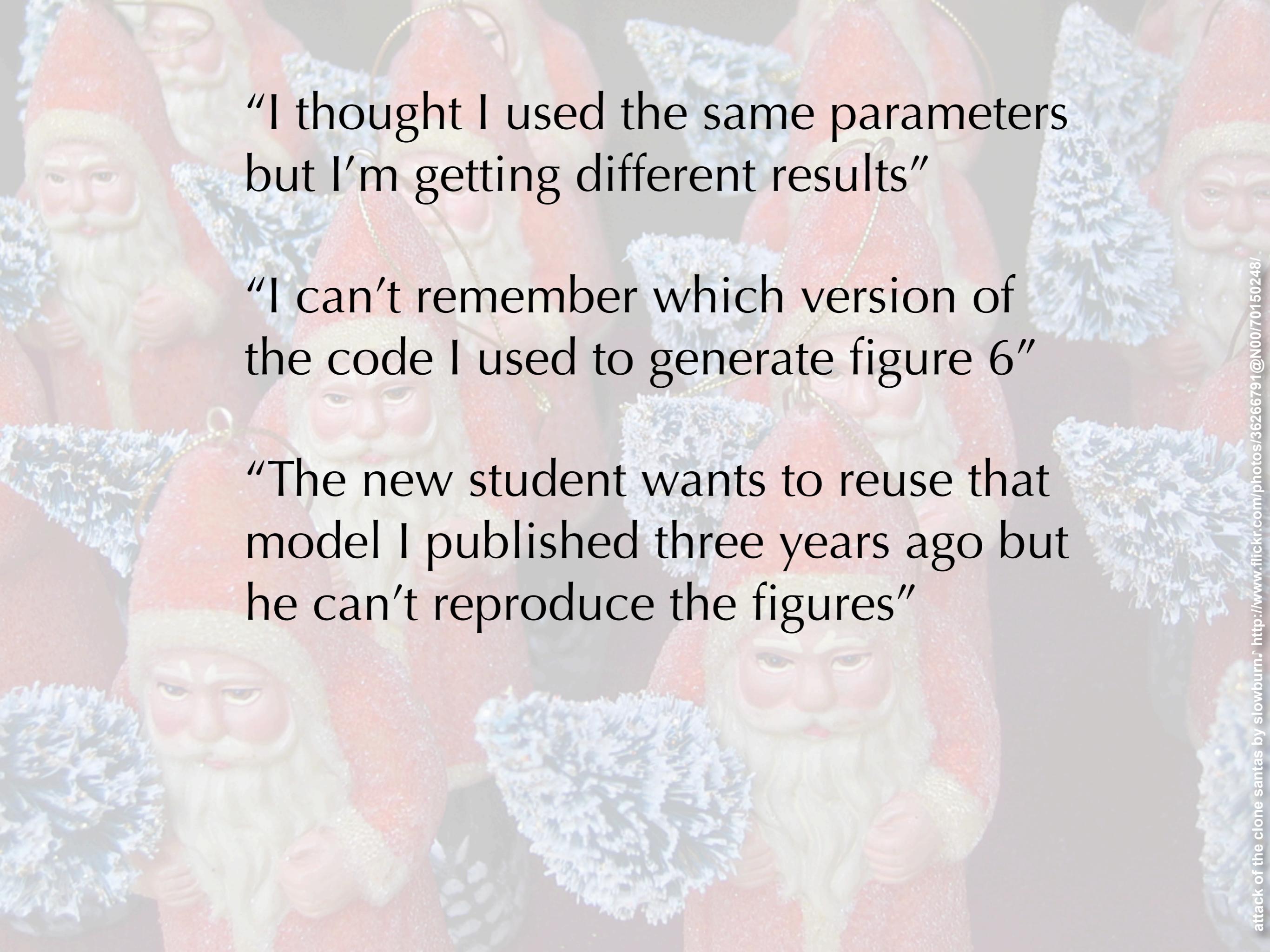
A cluster of Santa Claus figurines, possibly made of ceramic or plastic, arranged in a dense, overlapping group. They all feature the classic red suit with white trim, a white beard, and a pointed red hat with a white pom-pom. However, each figure has a unique and slightly distorted facial expression, ranging from wide-eyed surprise to a mischievous grin, illustrating the concept of 'different results' despite using the same parameters.

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



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

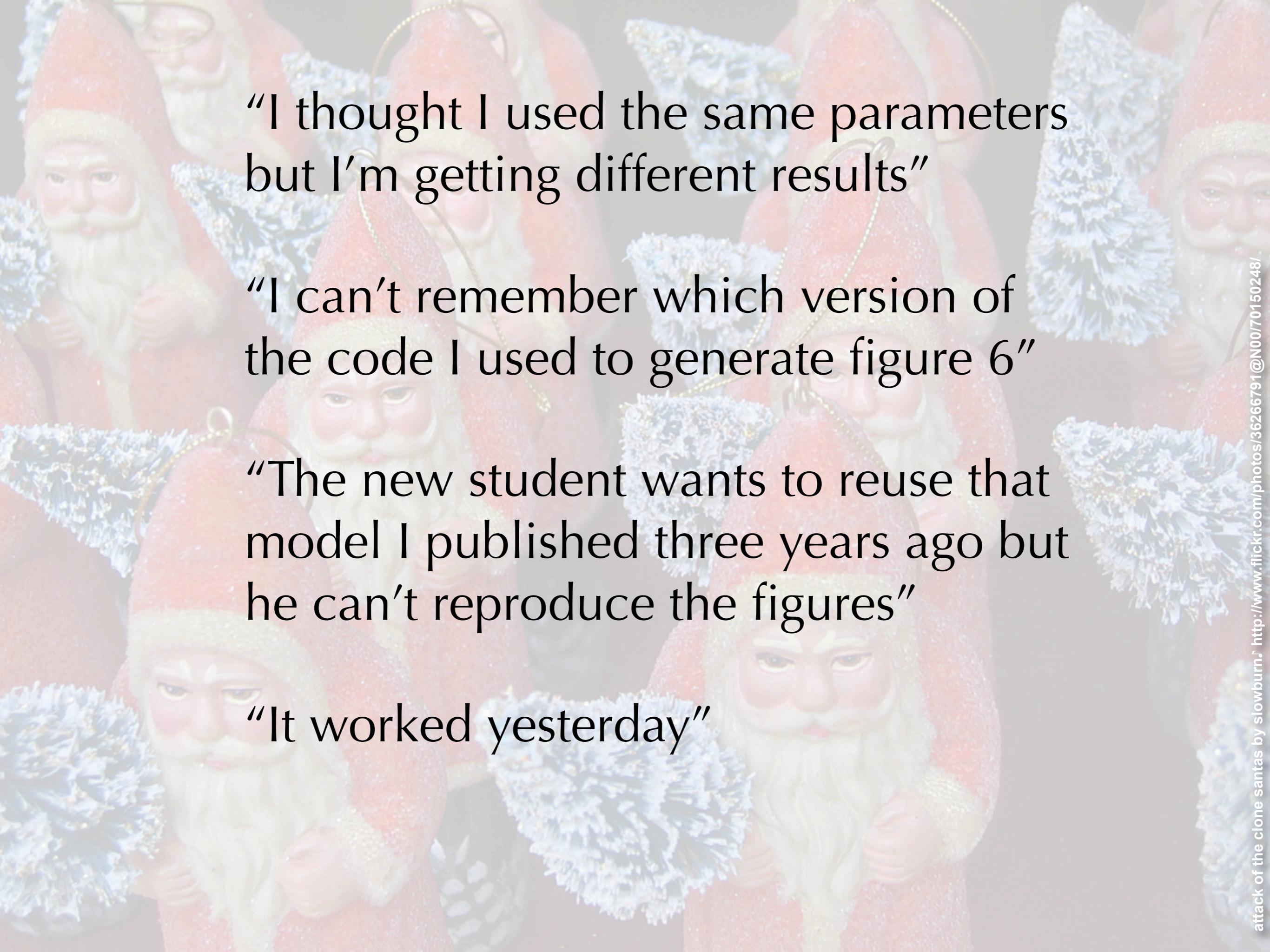
“I can’t remember which version of
the code I used to generate figure 6”



“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”

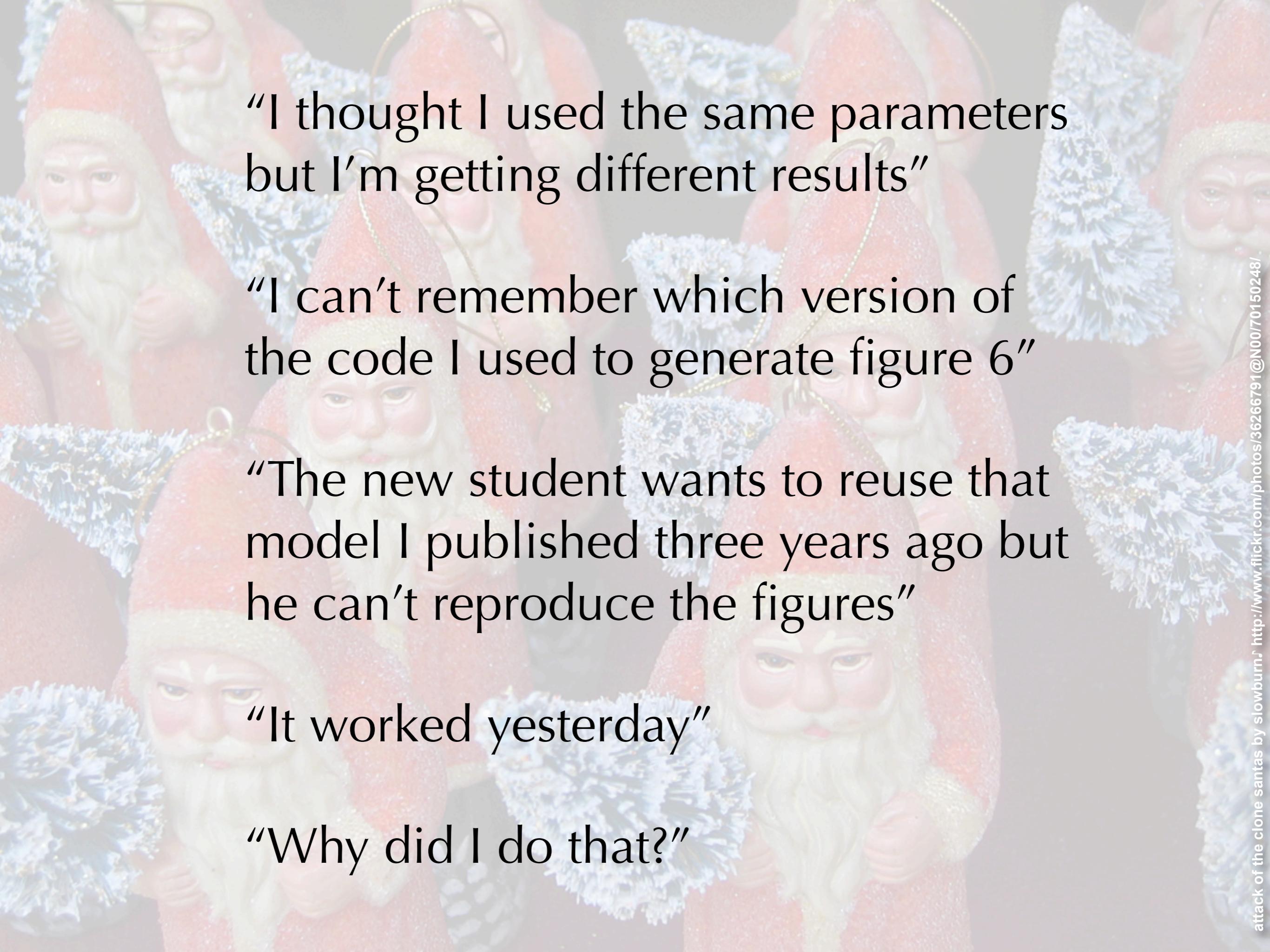


“I thought I used the same parameters
but I’m getting different results”

“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”



“I thought I used the same parameters
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“The new student wants to reuse that
model I published three years ago but
he can’t reproduce the figures”

“It worked yesterday”

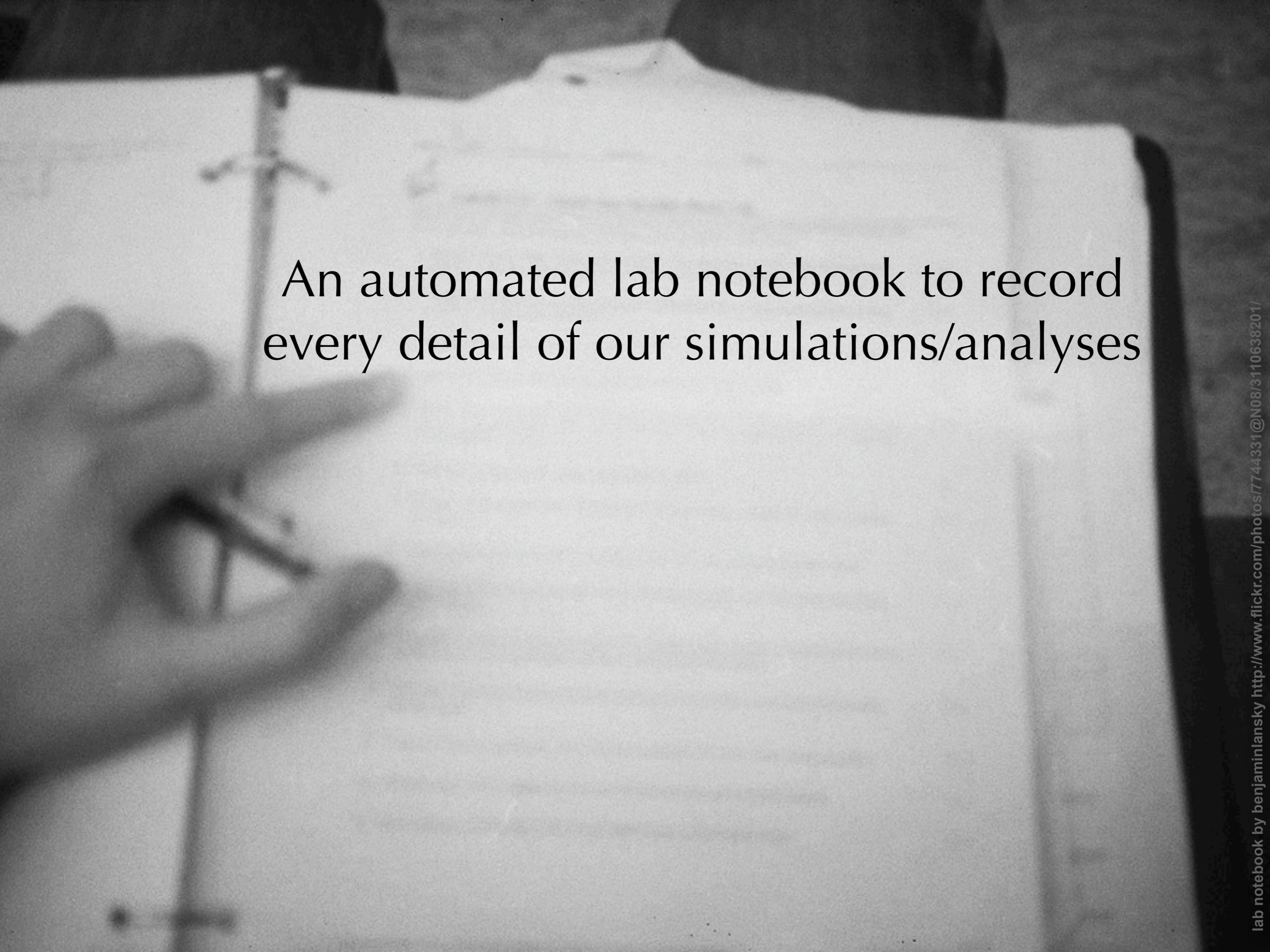
“Why did I do that?”

A close-up photograph of two dogs, likely Alaskan Malamutes or Huskies, standing on a tiled floor. They are both wearing leashes and looking directly at the camera with slightly weary expressions. The dog on the left has a black and tan coat, while the dog on the right is mostly white with some tan markings.

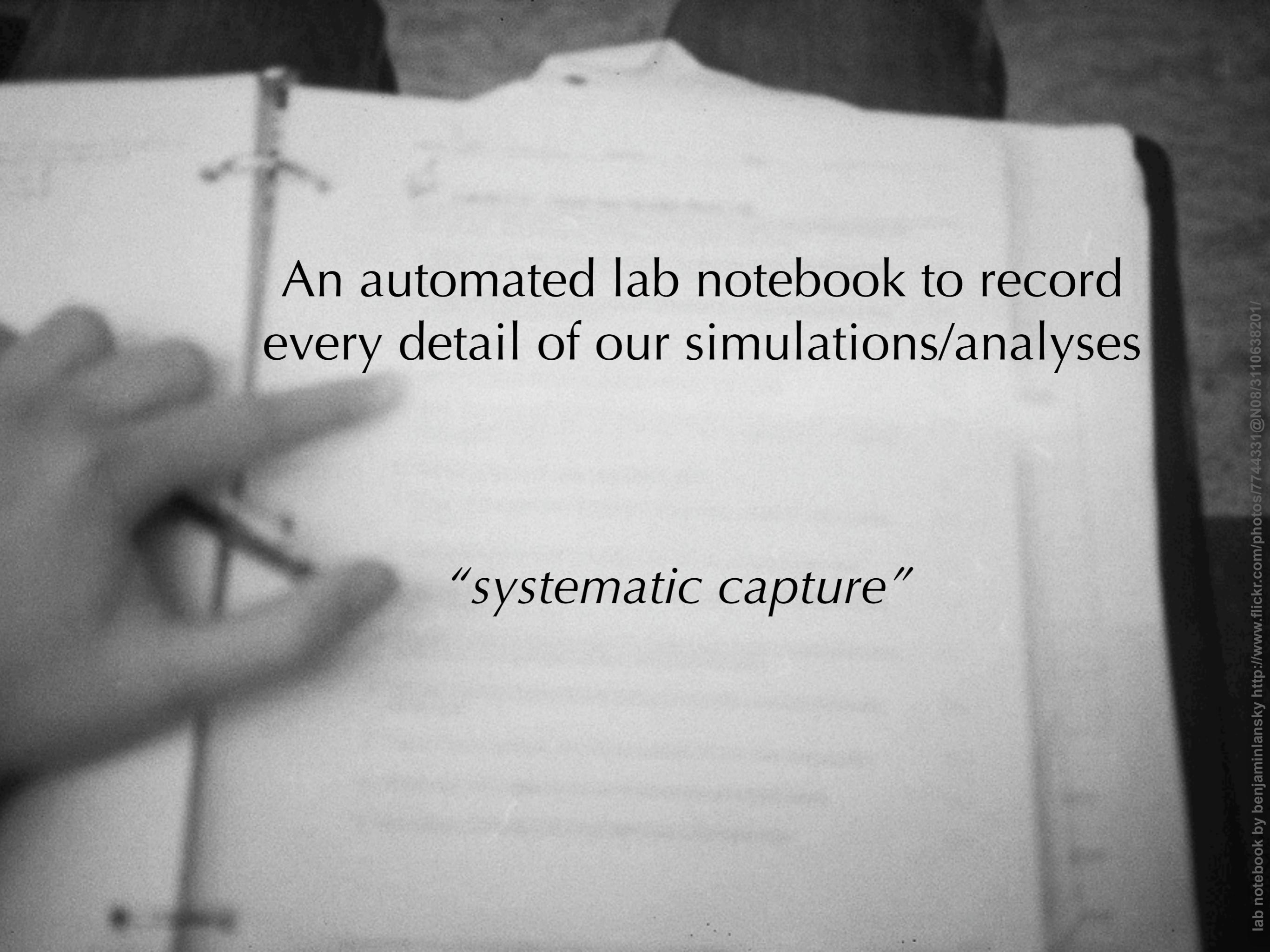
Why isn't it easy to reproduce a
computational experiment exactly?

A close-up photograph of two fluffy white dogs, possibly Border Collies or similar herding breeds, looking down at something on the floor. They are standing on a light-colored tiled floor. The dog on the left is wearing a green harness. The dog on the right has a pink bow in its hair. A black leash is attached to the dog on the left.

What can we do about it?

A black and white photograph of an open lab notebook. The left page contains handwritten notes, while the right page is blank. A pen lies across the top of the pages. The background is dark.

An automated lab notebook to record
every detail of our simulations/analyses

A grayscale photograph of an open lab notebook. The left page contains handwritten notes, while the right page is blank. A black pen lies diagonally across the top of the pages. The background is dark.

An automated lab notebook to record
every detail of our simulations/analyses

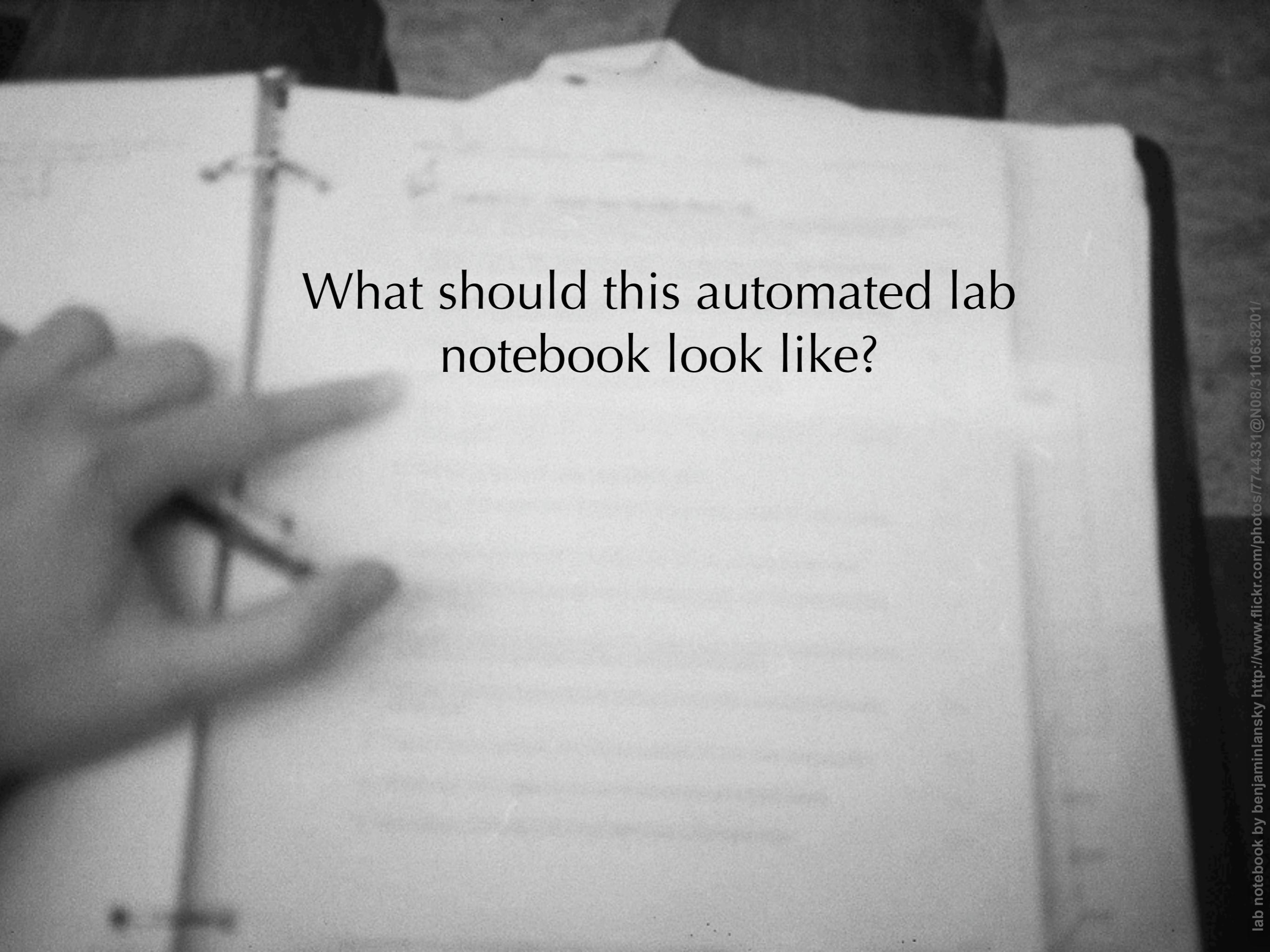
“systematic capture”

What do we need to record?



What do we need to record?

- > the code that was run
- > how it was run (parameter files, command-line options)
- > the platform on which it was run
- > why was it run?
- > what was the outcome?

A black and white photograph of an open lab notebook. The notebook is laid flat, showing two blank, off-white pages. The pages have a subtle texture and a few small dark spots. The edges of the notebook and its cover are visible in the background.

What should this automated lab
notebook look like?

Different researchers, different workflows

- > command-line
- > GUI
- > batch jobs
- > solo or collaborative
- > any combination of these for different components and phases of the project

Requirements

- > automate as much as possible, prompt the user for the rest
- > interact with version control systems (Subversion, Git, Mercurial, Bazaar, Perforce, ...)
- > support serial, distributed, batch simulations/analyses
- > link to data generated by the simulation/analysis
- > support all and any (command-line driven) simulation/analysis programs
- > support both local and networked storage of simulation/analysis records

SiO_2 : 0.2881 g

B_2O_3 : 0.3338 g

Cs_2O : 3.3781 g

aq wt. loss: 12%

Requirements

heated at 850°C for 10 minutes in

Be very easy to use, or only the very
conscientious will use it

crucible exploded

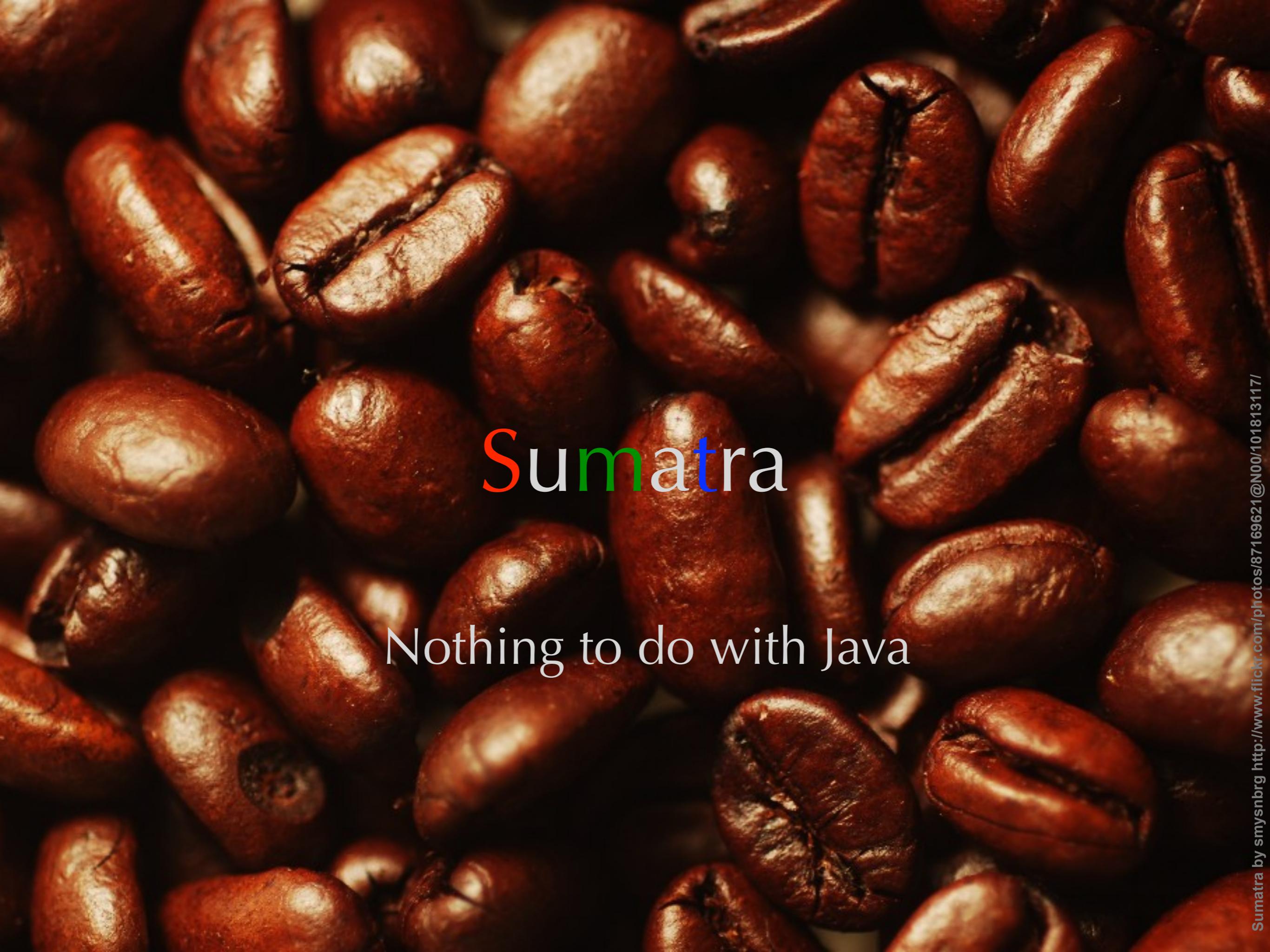
no sample



Sumatra

Simulation Management Tool

<http://neuralensemble.org/trac/sumatra>



Sumatra

Nothing to do with Java

- > a Python package, **sumatra**, to enable automated recording of provenance information
- > can be used directly in your own code
- > or as the basis for interfaces

Current

- > a command line interface, **smt**
- > a web interface, **smtweb**
- > integrated into **NeuronVisio**

Future

- > could be integrated into other existing GUIs
(neuroConstruct, Topographica, nrngui)
- > or new desktop/web-based GUIs written from scratch

Dependencies

- > Python bindings for your preferred version control system (`pysvn`, `mercurial`, `PyGit`)
- > Django (only needed for web interface)

Installation

```
> easy_install sumatra
```

Using sumatra within your own scripts

```
import numpy
import sys

parameter_file = sys.argv[1]
parameters = {}
execfile(parameter_file, parameters) # this way of reading parameters
# is not necessarily recommended
numpy.random.seed(parameters["seed"])
distr = getattr(numpy.random, parameters["distr"])
data = distr(size=parameters["n"])

output_file = "example.dat"
numpy.savetxt(output_file, data)
```

```
import numpy
import sys
import time
from sumatra.projects import load_simulation_project
from sumatra.parameters import build_parameters

project = load_simulation_project()
start_time = time.time()

parameter_file = sys.argv[1]
parameters = build_parameters(parameter_file)

sim_record = project.new_record(parameters=parameters,
                                main_file=__file__,
                                label="api_example",
                                reason="reason for running this simulation")

numpy.random.seed(parameters["seed"])
distr = getattr(numpy.random, parameters["distr"])
data = distr(size=parameters["n"])

output_file = "%s.dat" % sim_record.label
numpy.savetxt(output_file, data)

sim_record.duration = time.time() - start_time
sim_record.data_key = sim_record.datastore.find_new_files(sim_record.timestamp)
project.add_record(sim_record)

project.save()
```

smt

```
$ cd myproject  
$ smt init MyProject
```

```
$ python main.py default.param
```

```
$ python main.py default.param  
$ smt run --simulator=python --main=main.py default.param
```

```
$ python main.py default.param  
$ smt run --simulator=python --main=main.py default.param  
$ smt configure --simulator=python --main=main.py
```

```
$ python main.py default.param  
$ smt run --simulator=python --main=main.py default.param  
$ smt configure --simulator=python --main=main.py  
$ smt run default.param
```

```
$ smt list  
default_20090930-174949  
default_20090930-175111
```

```
$ smt list -l
```

```
-----  
Label      : default_20090930-174949  
Reason     :  
Outcome    :  
Duration   : 0.0548920631409  
Script     : MercurialRepository at /path/to/myproject  
              rf9ab74313efe (main file is main.py)  
Executable : Python (version: 2.6.2) at /usr/bin/python  
Timestamp  : 2009-09-30 17:49:49.235772  
Tags       :  
.  
.  
.
```

```
$ 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 comment default_20090930-174949 "Eureka! Nobel  
prize here we come."
```

\$ smt tag "Figure 6"

```
$ smt run --reason="test effect of a smaller time  
constant" default.param tau_m=10.0
```

```
$ smt repeat haggling_2009101002  
The simulation results match.
```

```
$ smt
```

```
Usage: smt <subcommand> [options] [args]
```

```
Simulation management tool, version 0.1
```

```
Available subcommands:
```

```
init
```

```
configure
```

```
info
```

```
run
```

```
list
```

```
delete
```

```
comment
```

```
tag
```

```
repeat
```

```
help
```

\$ smtweb 8002 &

SimProject

```
name
default_executable
default_repository
default_main_file
default_launch_mode
data_store
record_store
on_changed
save()
info()
new_record()
launch_simulation()
update_code()
add_record()
get_record()
delete_record()
delete_group()
delete_by_tag()
format_records()
most_recent()
add_comment()
add_tag()
remove_tag()
show_diff()
```

Executable

```
name
path
version
```

RecordStore

```
save()
get()
list()
delete()
delete_group()
delete_by_tag()
```

SimRecord

```
group
reason
duration
executable
repository
main_file
version
parameters
launch_mode
datastore
outcome
data_key
timestamp
dependencies
platforms
tags
diff
user
on_changed
run()
describe()
difference()
```

DataStore

```
find_new_files()
archive()
list_files()
get_content()
```

ParameterSet

```
save()
update()
__getitem__()
```

Dependency

```
name
path
version
diff
on_changed
```

Repository

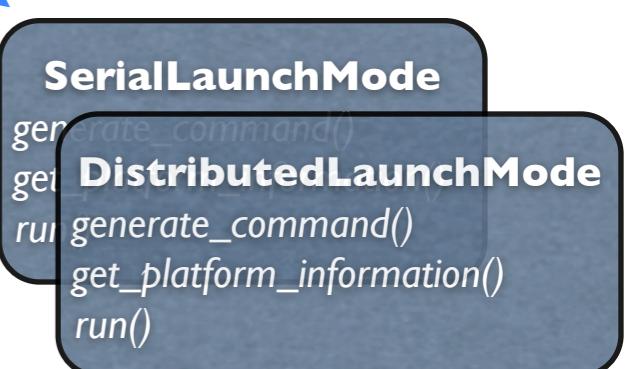
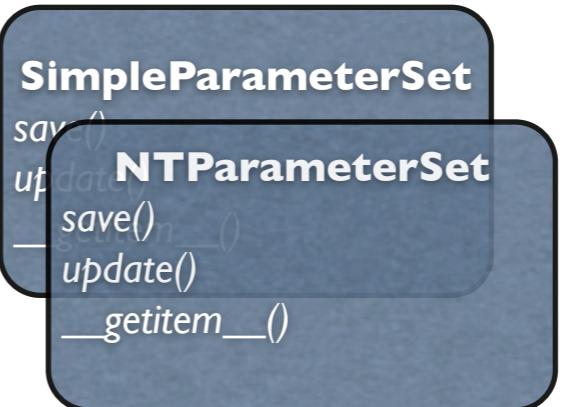
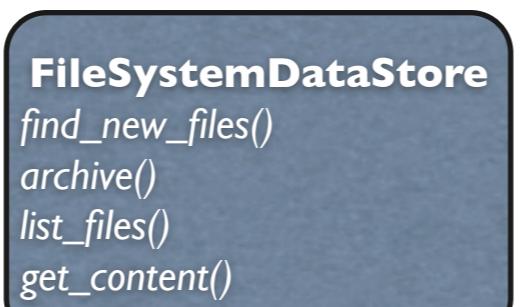
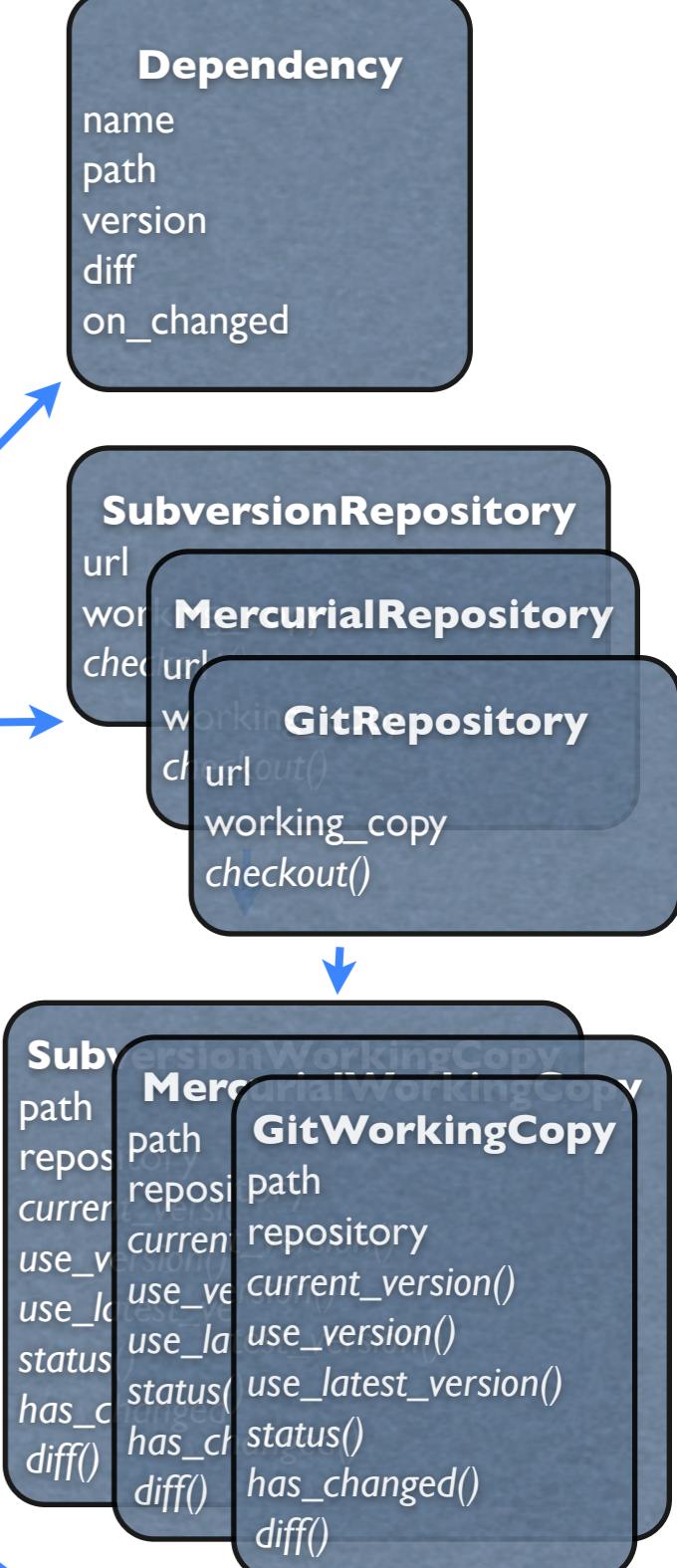
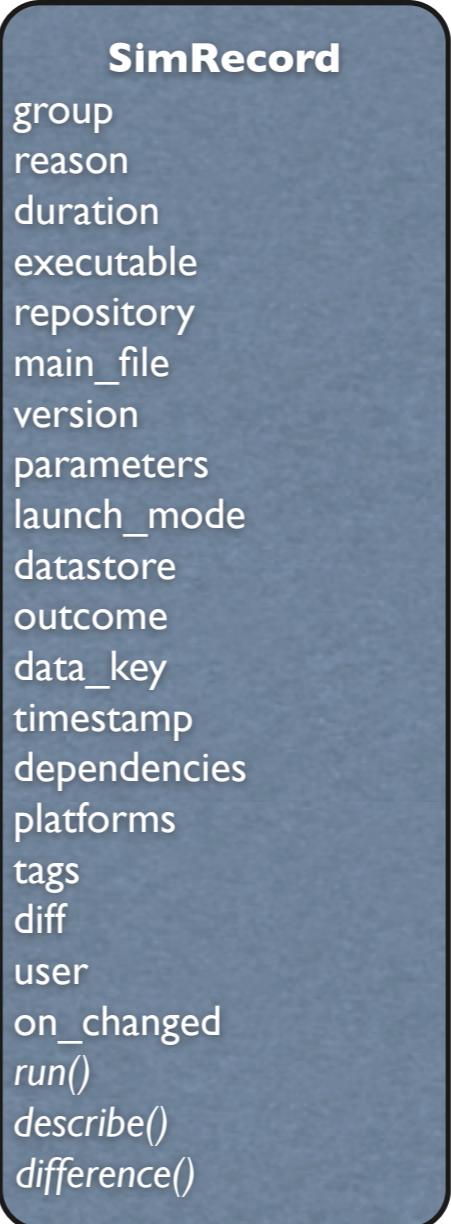
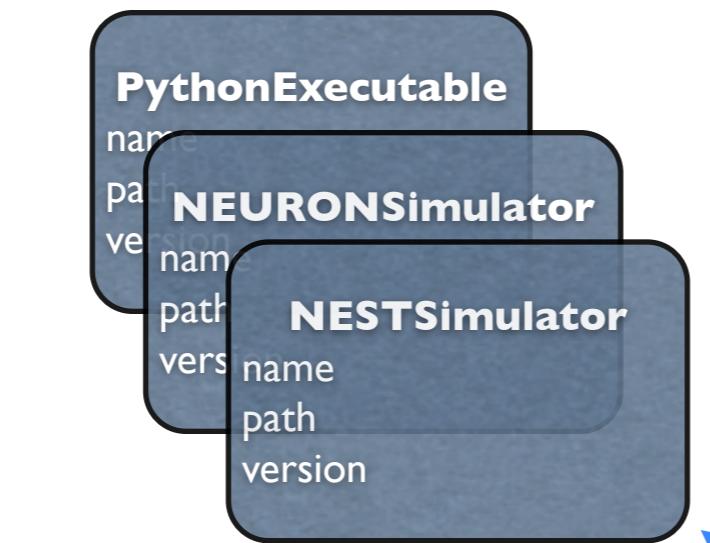
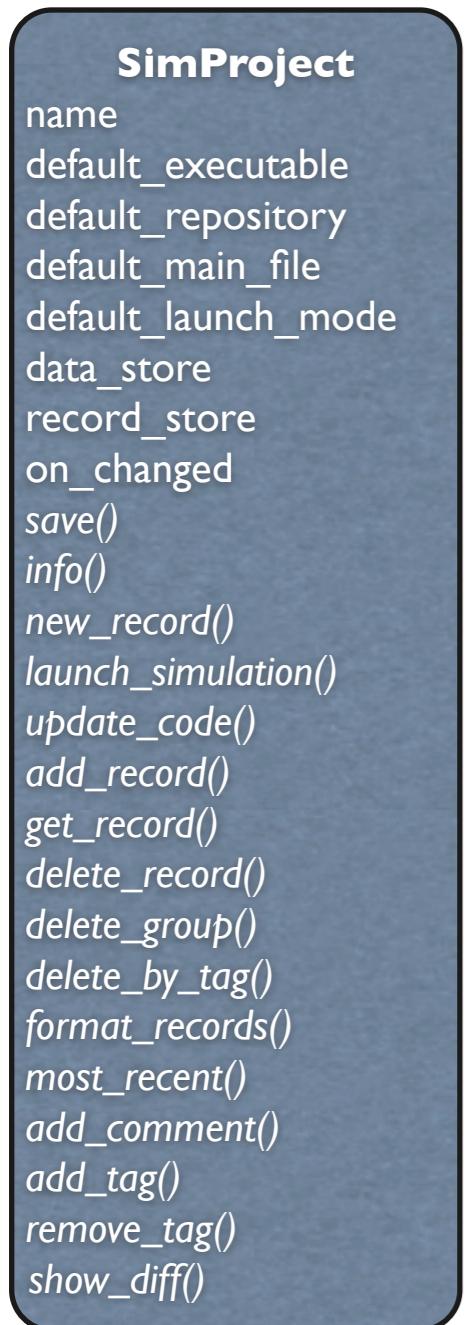
```
url
working_copy
checkout()
```

WorkingCopy

```
path
repository
current_version()
use_version()
use_latest_version()
status()
has_changed()
diff()
```

LaunchMode

```
generate_command()
get_platform_information()
run()
```



What's new since CodeJam #3

- Released version 0.1 (not vaporware anymore)
- Michele Mattioni added git support
- RecordStore can now contain records from multiple projects/users
- Added HttpRecordStore* enabling storing records on a remote server

*almost finished

A close-up photograph of a Sumatran orangutan's face. The orangutan has dark brown fur on its head and reddish-brown fur on its cheeks and chin. Its eyes are dark brown, and it has a large, expressive nose. The skin around the mouth is wrinkled and greyish-blue.

<http://neuralensemble.org/trac/sumatra>

@apdavison
<http://www.andrewdavison.info>

Sumatran orangutan

by BelalangJantan <http://www.flickr.com/photos/7164478@N07/3575735482/>



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