Bysd: System Dynamics Models in Python

purpose, capabilities, examples, structure, development plan

Motivation

- More powerful analysis tools
- Better ways to structure multi-part models
- Tighter integration with "big data" (including nontimeseries data)
- Integration with other simulation and analysis methods
- Better communication of analysis method and results (replicability!)

Traditional: Bring analysis capabilities into SD software

Timeseries Data

SD Model Building and Simulation Engine:

- Interface for CLD's, Stock and Flow Diagrams
- Equation editing
- Simulation
- Result plotting

Monte Carlo Simulation

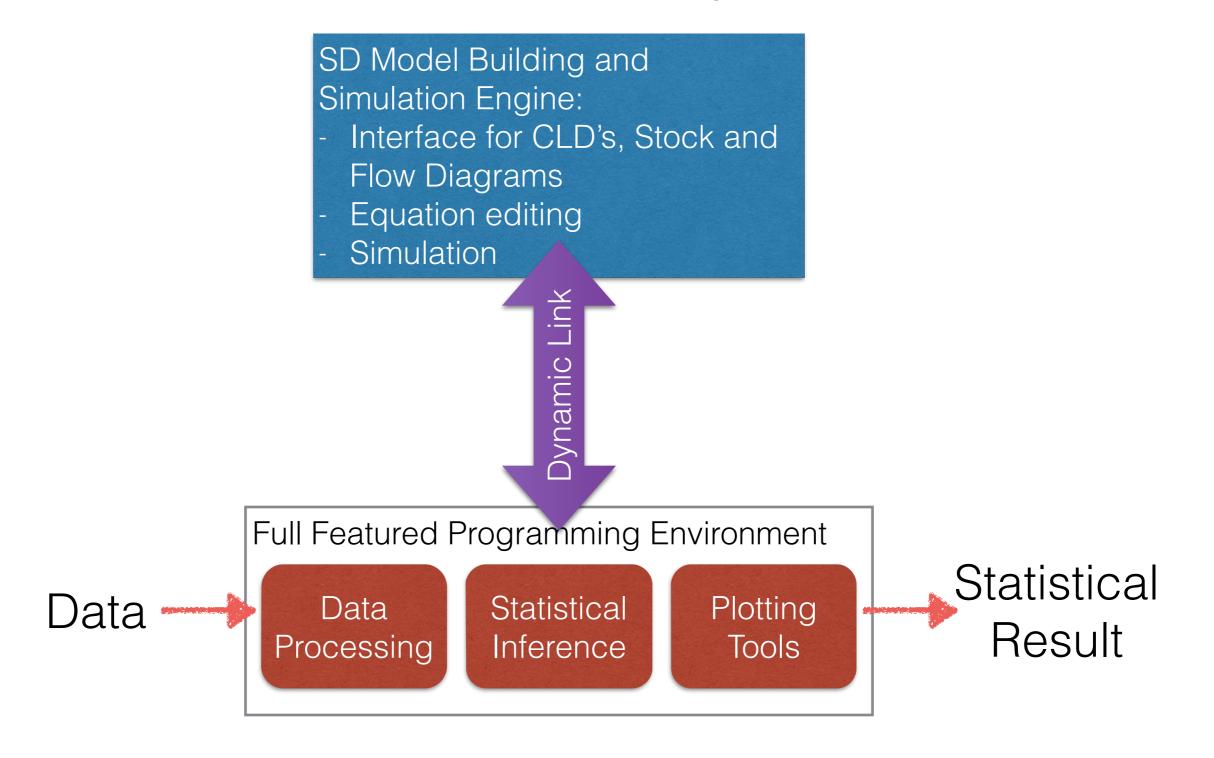
Subscripted Models

Optimization

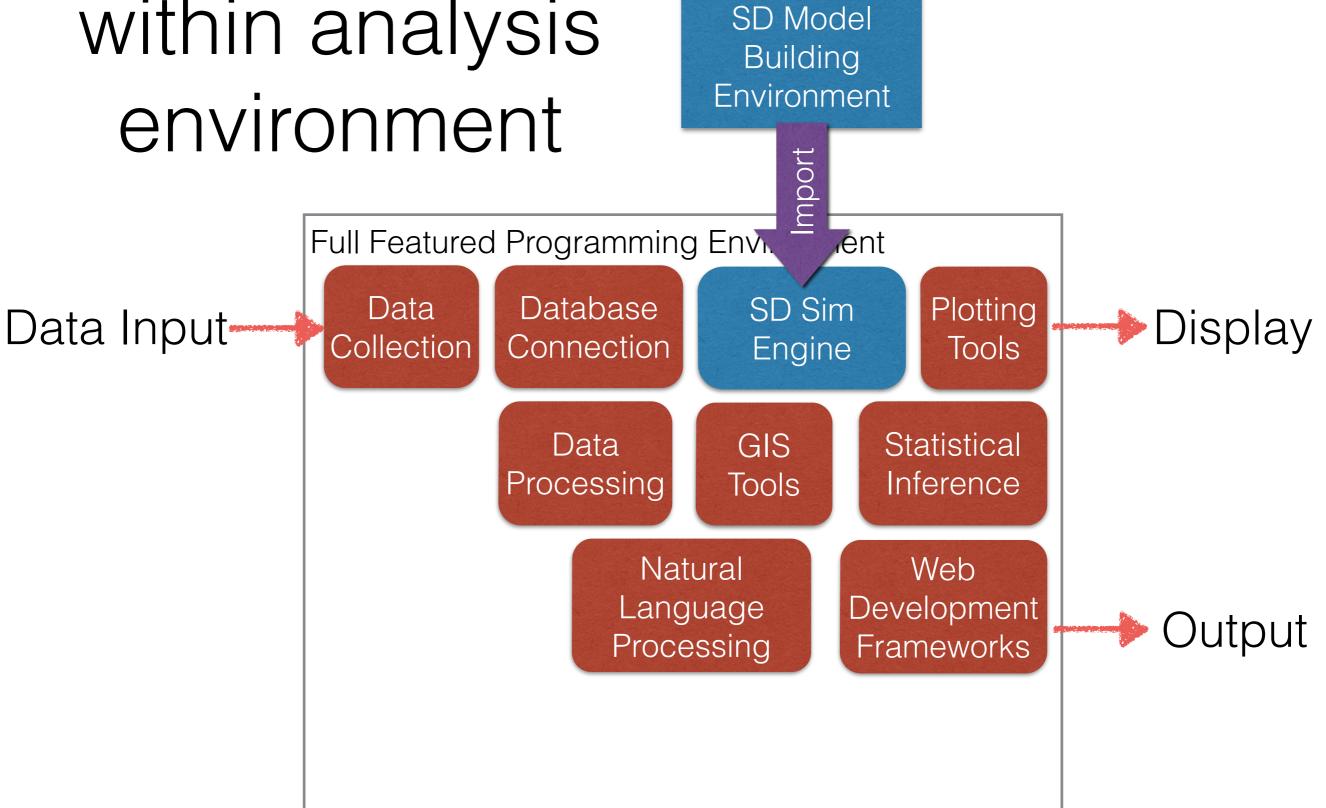
Timeseries Plots



State of the art: Interface SD software with external analysis tools



pysd: Simulate within analysis environment



pysd: Simulate within analysis environment

SD Model Building Environment

Display

Live-Result

Interactive

Web-Based

Output

Management

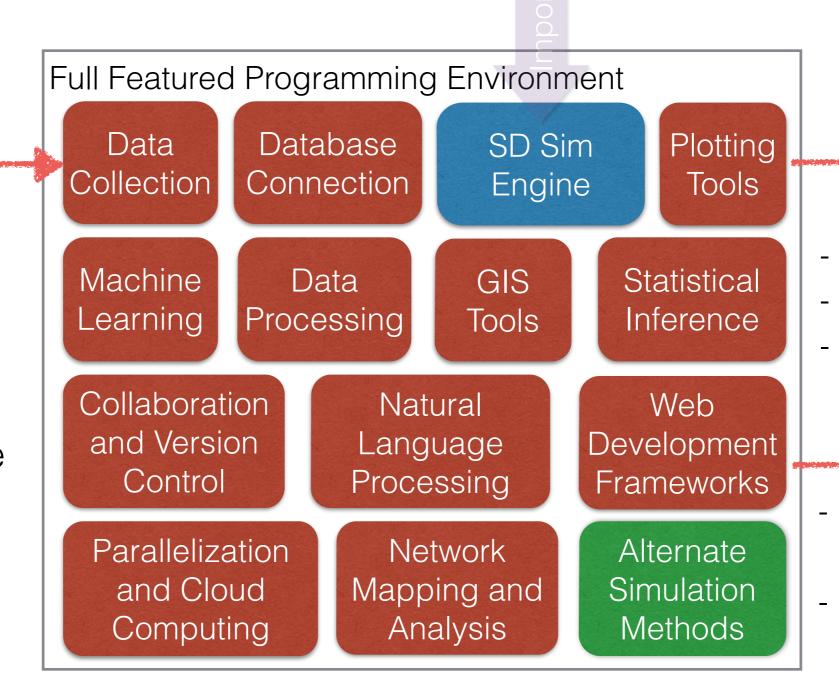
Decision-

Support

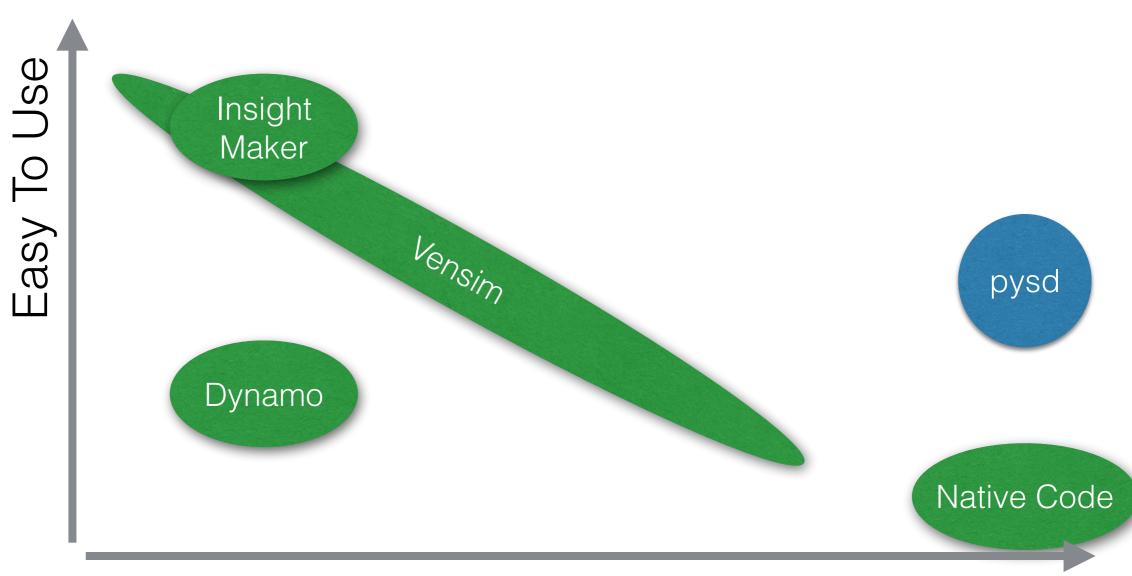
Project

Data Input

- Statistical
- Geographic
- Web-Based
- Streaming
- Textual
- Raw Sample



An incomplete map of the SD software space



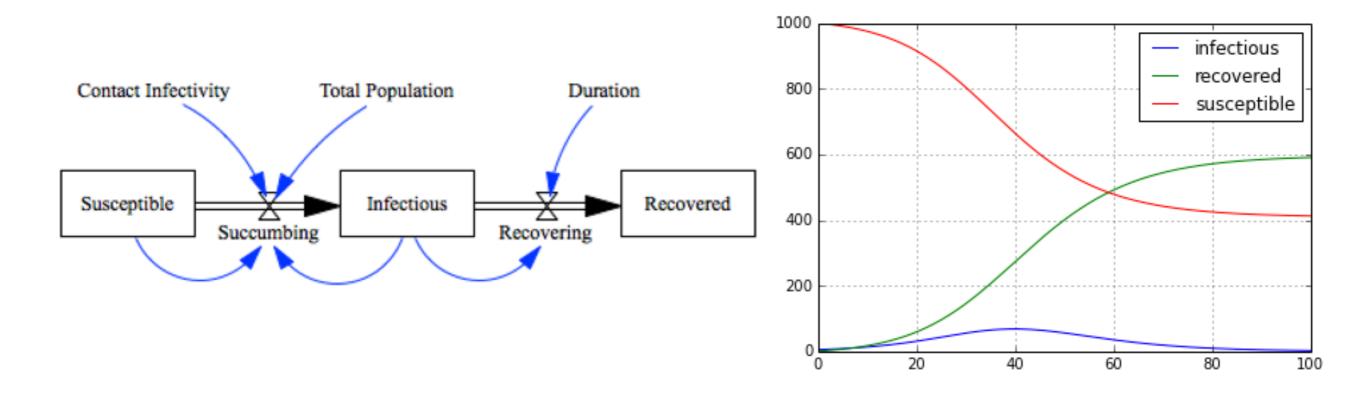
Powerful Analysis

Status

- Functioning prototype available at: https://github.com/JamesPHoughton/pysd
- Supports subset of XMILE, Vensim commands
- Install through python package exchange:
 >> pip install pysd

Basic Usage

```
import pysd
model = pysd.read_vensim('SIR.mdl')
model.run().plot()
```



Mechanics of Importing

Import

```
SIR.mdl:
Contact Infectivity=
     0.3
          Persons/Persons/Day
Duration=
     5
          Days
Infectious= INTEG (
     Succumbing-Recovering,
          Persons
Recovered = INTEG (
     Recovering,
          Persons
Recovering=
     Infectious/Duration
          Persons/Day
```

```
def model_function(stocks, t):
  infectious, recovered, susceptible, = stocks
  total_population = 1000
  duration = 5
  recovering = infectious/duration
  contact_infectivity = 0.3
  succumbing = susceptible*infectious/
                  total_population*
                  contact_infectivity
  dinfectious_dt = succumbing-recovering
  dsusceptible_dt = -succumbing
  drecovered_dt = recovering
  return [dinfectious_dt, drecovered_dt,
         dsusceptible_dt]
```

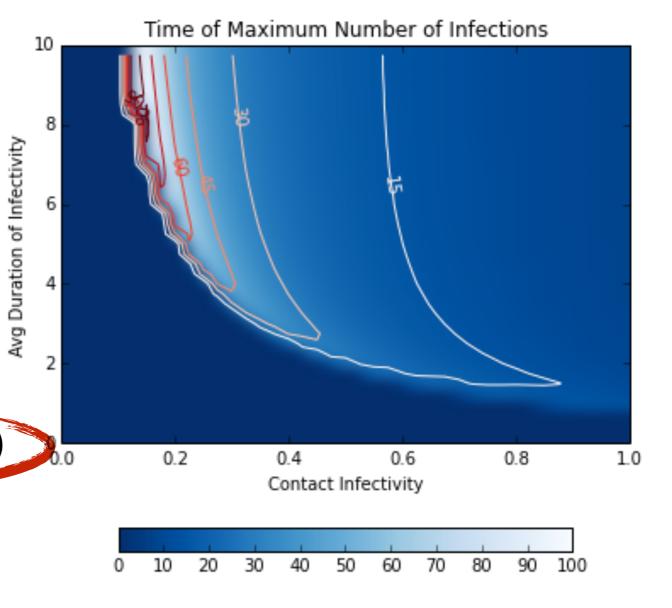
odeint(model_function, initial_values, tseries)

Model Exploration

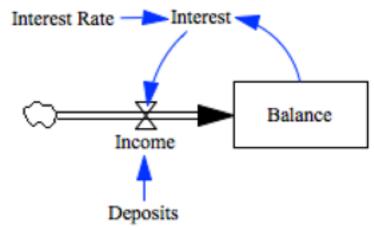
```
ci = np.arange(0,1,.025)
d = np.arange(.5,10,.25)
ci_grid, d_grid = np.meshgrid(ci, d)

def tmax(ci, d):
    ps = {'contact_infectivity':ci,
        'duration':d}
    stocks = model.run(params=ps)
    return stocks['infectious'].idxmax()
```

vtmax = np.vectorize(tmax) tmax_grid = vtmax(ci_grid, d_grid)

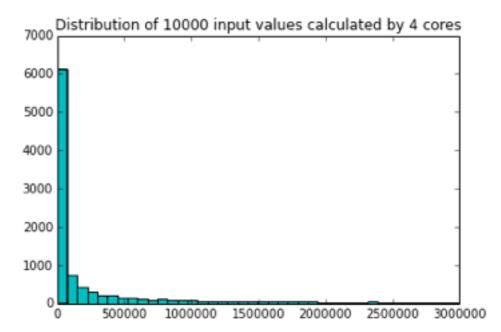


Parallelization



model = pysd.read_vensim('bank_balance.mdl') interest_rate = np.random.uniform(high=.1, size=10000)

```
def final(rate):
    ps={'interest_rate':rate}
    stocks = model.run(params=ps)
    return stocks['balance'].iloc[-1]
```



Series Monte Carlo:

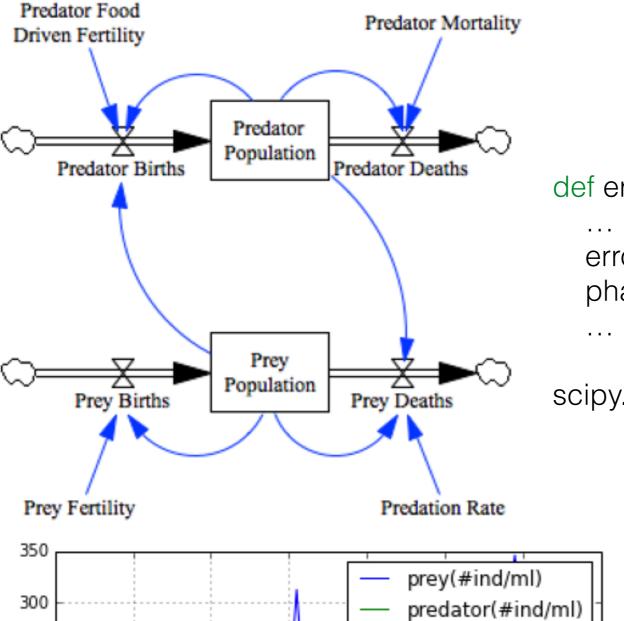
Parallel Monte Carlo:

[final(rate) for rate in interest_rate]

from IPython.parallel import Client dview = Client().cli[:] dview.push(model) dview.map(final, interest_rate)

Execution Time: 11s

Execution Time: 2.9s



20

25

30

35

10

15

time(d)

250

200

150

100

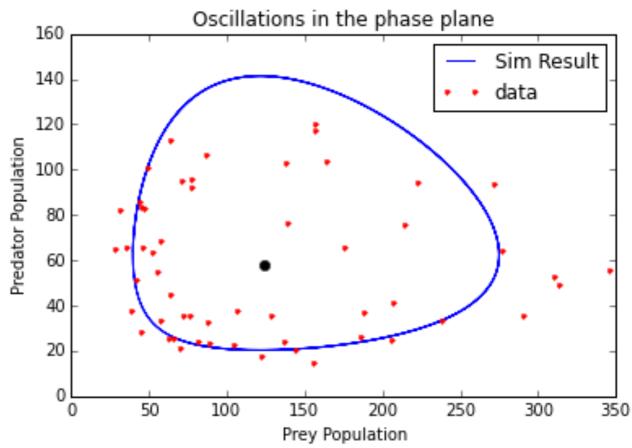
50

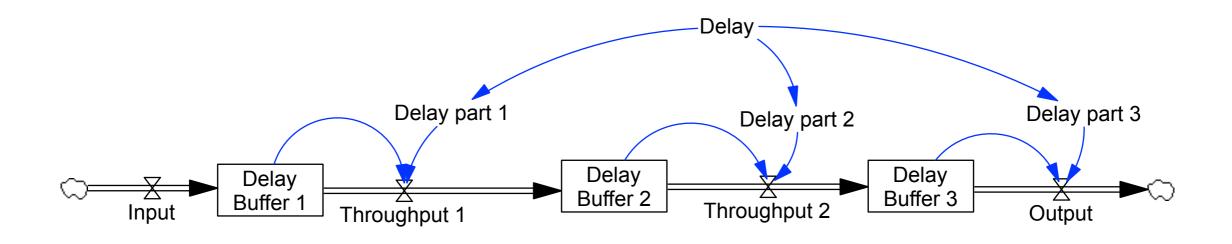
Non-Timeseries Optimization

def error(parameter_list):

errors = sim_result - data_transform phase_plot_error = (errors**2).sum()

scipy.optimize.minimize(error, x0=[.005, 1, 1, .002], method='L-BFGS-B', bounds=[(0,10), (0,None), (0,10), (0,None)])





Realtime Interaction

Maybe a demo?

```
def animate(t):
  #draw a live result
  #run the simulation forward
  global stocks
  model.tstart = x[-1]
  model.tstop = x[-1]+1./fps
  model.initial_values = stocks
  ps={'input':input_val,
       'delay':adjustment_delay})
  stocks = model.run(params=ps).iloc[-1]
  #collect user input
```

anim = animation.FuncAnimation(fig, animate, frames=seconds*fps)

Network/Patch Models

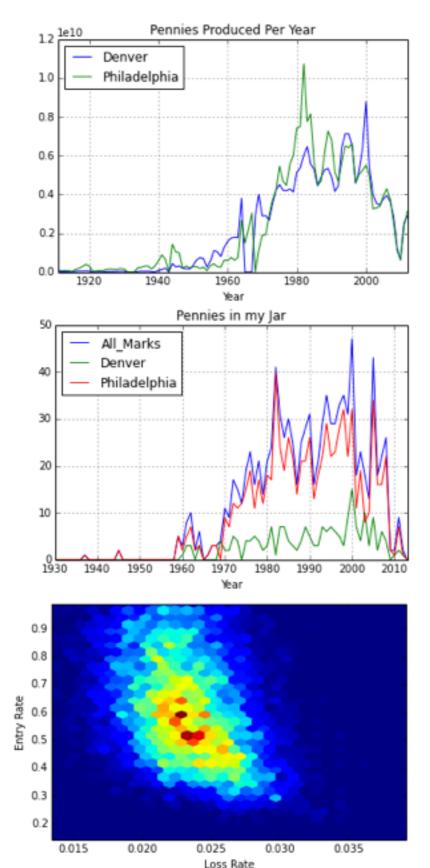
```
import networkx as nx
g = nx.graph(...)

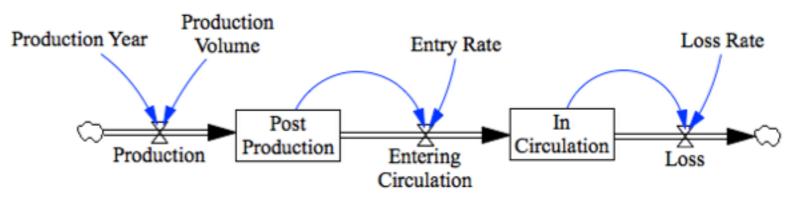
for node in g.nodes_iter():
    g[node]['model'] = pysd.read_vensim('Patch SIR.mdl')

for t in np.arange(model.tstart, model.tstop, model.dt):
    for node in g.nodes_iter():
        ps = {'cross_infectivity': nx.edgelist(node)...}
        g[node]['model'].run(params=ps)
```

import geopandas as gpd
towns = gpd.read_file("TOWNSSURVEY_POLY.shp")

Subscripted MCMC





models = [[year, pysd.read_vensim('penny_jar.mdl')] for year in range(1930,2014)]

```
entry_rate = mc.Uniform('entry_rate', lower=0,
upper=.99, value=.08)
loss_rate = mc.Uniform('loss_rate', lower=0,
upper=.3, value=.025)
```

```
@mc.stochastic(trace=True, observed=True)
def circulation(...)
    population = models['model'].run(...)...
    return log_prob
```

mcmc = mc.MCMC(...) mcmc.sample(20000)

To be demonstrated:

- Fitting models to streaming data
- Machine learning regressions in place of lookups
- Reversible jump MCMC for model selection
- Web-based interactive result display
- Runtime connection to ABM, etc...
- Adaptive sampling of parameter spaces
- Integration with decision models

• ...

To be Developed:

- cython/theano speedups
- Step function with memory
- Smart parameter modification
- Additional XMILE/Vensim translation ability