Brainlab:

A toolkit to aid in the design, simulation, and analysis of spiking neural networks with the NCS environment

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Thesis defense

Outline

NCS, the NeoCortical Simulator

- Powerful batch processing spiking neural network simulator
- Parallel (MPI)
- Biologically realistic neuron and synapse models
- Accepts model and simulation parameters in text file

.in file: the BRAIN block

```
BRAIN
    TYPE                          AREA-BRAIN
    FSV                           10000.00
    JOB                           E0_332
    SEED                         -333
    DURATION                      80.0
    COLUMN_TYPE                   col
    COLUMN_TYPE                   datain0
    COLUMN_TYPE                   keyin0
    CONNECT                       datain0 datain0_1CELL ER SOMA
                                  col layER ES SOMA E 1.000 10.000
    CONNECT                       keyin0 keyin0_1CELL ER SOMA
                                  col layL1 ES SOMA E 1.000 10.000
    STIMULUS_INJECT               stimdatain0_0-inj-0
    REPORT                        EMRep
    OUTPUT_CELLS                  YES
    OUTPUT_CONNECT_MAP            YES
    DISTANCE                      YES
END_BRAIN
```

.in file: a COLUMN block

```
COLUMN
    TYPE                          col
    COLUMN_SHELL                  col_sh
    LAYER_TYPE                    layL1
    LAYER_TYPE                    layEM
    LAYER_TYPE                    layER
    LAYER_TYPE                    layES
    LAYER_TYPE                    layI1
    CONNECT                       layL1 ES SOMA layEM ES SOMA
                                  E 0.600 10.000
    CONNECT                       layER ES SOMA layEM ES SOMA
                                  E 1.000 10.000
    CONNECT                       layER ES SOMA layES ES SOMA
                                  E 0.600 10.000
    CONNECT                       layI1 I1 SOMA layES ES SOMA
                                  I 0.600 10.000
END_COLUMN
```

Typical MATLAB-NCS usage

```
fprintf(fid3,'\tAMP_START\t\t'); fprintf(fid3,'%g\n',AmpStart);
fprintf(fid3,'\tAMP_END\t\t\t'); fprintf(fid3,'%g\n',AmpEnd);
fprintf(fid3,'\tWIDTH\t\t\t'); fprintf(fid3,'%g\n',PulseWidth);
fprintf(fid3,'\tTIME_START\t\t'); fprintf(fid3,'%s\n',StimStart);
fprintf(fid3,'\tTIME_END\t\t'); fprintf(fid3,'%s\n',StimEnd);
fprintf(fid3,'\tFREQ_START\t\t'); fprintf(fid3,'%g\n',FreqStart);
```

My MATLAB-NCS experience

- "printf" style model building is limited
    - Easy to make errors
    - Small changes to model can require many changes
- Saving models and then executing them is limiting
    - Prevents strategies like GA search for models
    - Prevents encapsulation of an "experiment as a script"
- There is typically very little code reuse
- MATLAB is not a particularly elegant text processing language
- MATLAB support for general purpose libraries is weak

Design goals for a new approach to using NCS

- Allow very complex experiments with maximum clarity and minimum effort
- Allow very simple experiments with minimum overhead
- A model is a script (there is no other reasonable way)
- Object oriented neural model design
- Integrated modeling, experimentation, analysis
- Container for standard, reusable component libraries.
- Free, and open source, from top to bottom
- Based on a language that is clean, good at text processing as well as math, with extensive general purpose libraries
- Remote or local operation; make remote operation transparent
- Possible interactive use

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Hello, world

```
from brainlab import *

brain=BRAIN()
c1=brain.Standard1CellColumn()
c2=brain.Standard1CellColumn()
brain.AddConnect(c1, c2, prob=1.0)
brain.Run()
```

Paramaterized experiments

```
brain=BRAIN({'DURATION': .3})
c1=brain.Standard1CellColumn()
c2=brain.Standard1CellColumn()
syn=brain.syntypes['C.strong']
brain.AddConnect(c1, c2, syn, prob=1.0)
brain.AddSpikeStim(c1, [0.0, .01, .02, .03, .04, .05])
rep=brain.AddSimpleReport('test', c2, 'v', dur=(0, .3))

for maxcond in [0, .1, .2, .3, .4, .5, .6, .7, .8, .9]:
    syn.parms['MAX_CONDUCT']=maxcond

    job='tj%f' % maxcond
    brain.Run({'JOB': job})

    # analyze the results
    res=LoadSpikeData(brain, rep)
    print "G:", maxcond, "spikes:" len(res[0])
```

Algorithmic model building

```
b=BRAIN()

cols={}
for i in range(0, 10):
    for j in range(0, 10):
        cols[i,j]=b.Standard1CellColumn()

# make 1000 random connections, with probability
# proportional to distance
for i in range(0, 1000):
    x1,y1=randrange(0,10), randrange(0,10)
    x2,y2=randrange(0,10), randrange(0,10)
    p=1.0 - ((x1-x2)**2 + (y1-y2)**2) / 200.0
    b.AddConnect(cols[x1,y1], cols[x2,y2], prob=p)

print b     # a 5000 line .in file
b.Run()
```

Why Python?

- Open source, free
- Widely used and growing, active scientific community
- Competitive array math package and plotting packages
- Clean language design
- Object oriented, dynamically typed, garbage collected, bytecode compiled
- Efficient
- Enforced indentation!

Brainlab implementation

- `COLUMN`, `LAYER`, `CELL`, `SYNAPSE` are Python object classes
- These are *nested* classes of `BRAIN` class
- `__repr__()` is overridden to output the `.in` file representation
- NCS parameter names are dictionary keys
- Three modules:
  - brainlab.py: simulation environment, data analysis, graphing
  - brain.py: model construction
  - netplot.py: three dimensional display

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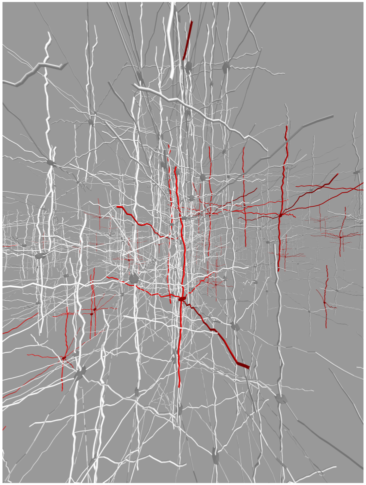
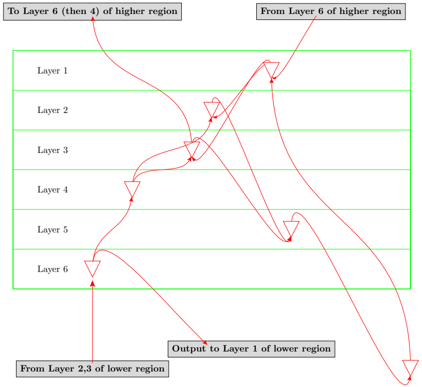
netplot 3D module



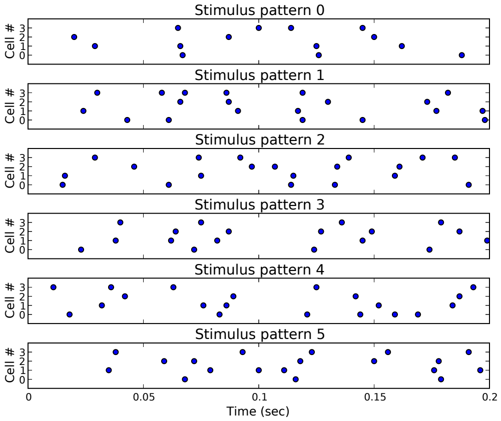
My Ph.D. research

Could a cortical microcircuit act as a functional unit for the memorization of correlations of spatio-temporal spike trains?

- Layer structured cortical microcircuit model
- Two input cell groups
    - Key
    - Data
- Output cell group
- Spatio-temporal spike trains as fundamental unit of information


To Layer 6 (then 4) of higher region
From Layer 6 of higher region
Layer 1
Layer 2
Layer 3
Layer 4
Layer 5
Layer 6
Output to Layer 1 of lower region
From Layer 2,3 of lower region

Stimulus patterns



My Ph.D. research: genetic model search

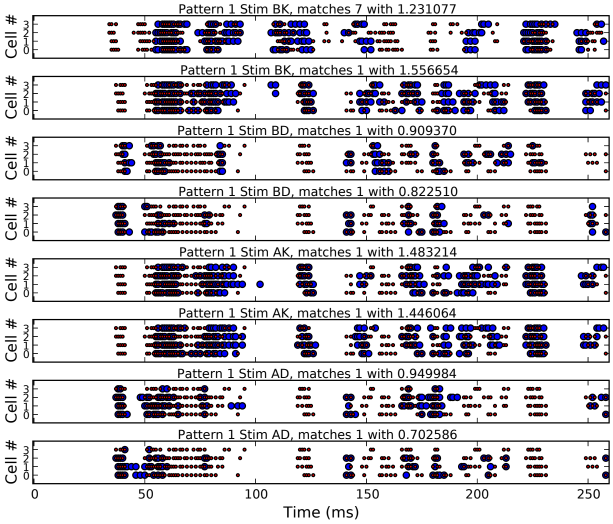
```
genelist=[]
genelist.append((ga.gene.list_gene([2,3,4,5,6,7,8]), 'ntapecells'))
genelist.append((ga.gene.float_gene((.005, .05)), 'allmaxcond'))
genelist.append((ga.gene.float_gene((.005,.3)), 'allF'))
genelist.append((ga.gene.float_gene((.005,.3)), 'allD'))
genelist.append((ga.gene.float_gene((.005,.3)), 'poshebbdeltause'))
genelist.append((ga.gene.float_gene((.005,.3)), 'neghebbdeltause'))
genelist.append((ga.gene.list_gene([(float(x)/1000.0) \
                    for x in range(200, 801, 100)]), 'stimdur'))
genelist.append((ga.gene.list_gene(range(20, 120, 10)), 'interspike'))
genelist.append((ga.gene.float_gene((.05, 1.0)), 'eresprob'))
genelist.append((ga.gene.float_gene((.05, 1.0)), 'eremprob'))
genelist.append((ga.gene.float_gene((.05, 1.0)), 'l1emprob'))
genelist.append((ga.gene.float_gene((.05, 1.0)), 'esthalprob'))
genelist.append((ga.gene.float_gene((0.0, 1.0)), 'L1L5prob'))
genelist.append((ga.gene.float_gene((0.0, 1.0)), 'L6L4prob'))

all_genes=[]
for (g, parmname) in genelist:
    all_genes+=g.replicate(1)
    mychrom.append(parmname)
```

My Ph.D. research: genetic model search

```
this_genome.performance=EOFitness
gnm=this_genome(all_genes)
pop=ga.population.population(gnm)
pop.evaluator=my_pop_evaluator()
galg=ga.algorithm.galg(pop)
settings={'pop_size':16,'p_replace':.8,'p_cross': .8, \
          'p_mutate':'gene', 'p_deviation': 0.,'gens':64,\
          'rand_seed':0,'rand_alg':'CMRG'}
galg.settings.update(settings)
galg.evolve()
print "best:", galg.pop.best()
```

My Ph.D. research: automated pattern matching



Phase space transitions in a recurrent network

Dr. Doursat:

"My goal is to explore bistability and other firing modes of the network through a survey of parameter space (especially E/I to E/I connections) and, from there, reveal what difference synaptic augmentation (SA) and/or reciprocal connections can make (changes in phase space landscape; easiness of phase transitions) when they are added to the model."

Setting up the experiment in Brainlab

- Convert plain .in file into a script
- Create experiment script
- Create data analysis/graphing

Tighter integration with NCS

Idea: eliminate NCS parsing module, and most of NCS' biological knowledge

- Simpler code; just a "flat" simulation engine that accepts GCList
- Less redundancy of code and documentation
- NCS would be more easily used with unstructured networks
- Easier to add new features

Short-term enhancements to Brainlab

- Some BRAIN.methods become brainlab functions
- Data loading and report plotting standardized, expanded
- Subdirectories for job execution (at least as an option)
- Support for new queueing environments
- Convenience functions for executing multiple jobs
- Automated installation, configuration, testing
- Expanded examples library

Use, so far

- A colleague in our lab used an earlier version of Brainlab
- I have made very extensive use of Brainlab in my own experiments
- A colleague in our lab has recently begun using Brainlab in his experiments
- Another lab is beginning to use NCS, and expressed interest in Brainlab

Acknowledgements

Thanks to:

- My committee
- Dr. Harris, chair
- Dr. Goodman, for the Brain Lab
- Brain Lab colleagues