

# Supplementary Information

## GeNN: a code generation framework for accelerated brain simulations

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### Appendix S1: Izhikevich model definition in GeNN

This is the source code for defining the network used in Benchmark 1.

It can also be accessed online at [https://github.com/genn-team/genn/blob/v2.0\\_benchmark/userproject/lzh\\_sparse\\_project/model/lzh\\_sparse.cc](https://github.com/genn-team/genn/blob/v2.0_benchmark/userproject/lzh_sparse_project/model/lzh_sparse.cc).

```
#define DT 1.0

#include "modelSpec.h"
#include "modelSpec.cc"
#include <vector>
#include "sizes.h"

std::vector<unsigned int> neuronPSize;
std::vector<unsigned int> neuronVSize;
std::vector<unsigned int> synapsePSize;

scalar meanInpExc = 5.0; //5.0 for balanced regime, 7.5 for irregular, 2.5 for
quiet
scalar meanInpInh = 2.0; //2.0 for balanced regime, 3.0 for irregular, 1.0 for
quiet

double *excIzh_p = NULL;
double *inhIzh_p = NULL;

double IzhExc_ini[6]={
//Izhikevich model initial conditions - excitatory population
    -65.0,    //0 - V
    0.0,    //1 - U
    0.02,    // 0 - a
    0.2,    // 1 - b
    -65.0,    // 2 - c
    8.0    // 3 - d
};

double IzhInh_ini[6]={
```

```

//Izhikevich model initial conditions - inhibitory population
    -65, //0 - V
    0.0, //1 - U
    0.02, // 0 - a
    0.25, // 1 - b
    -65.0, // 2 - c
    2.0 // 3 - d
};

double *SynIzh_p= NULL;

double postExpP[2]={
    0.0, // 0 - tau_S: decay time constant for S [ms]
    0.0 // 1 - Erev: Reversal potential
};

double *postSynV = NULL;

double SynIzh_ini[1]= {
    0.0 // default synaptic conductance
};

void modelDefinition(NNmodel &model)

{
    initGeNN();

    model.setGPUDevice(0); //force using device 0 for benchmarking

    model.setName("Izh_sparse");

    model.addNeuronPopulation("PExc", _NExc, IZHIKEVICH_V, excIzh_p, IzhExc_ini);
    model.addNeuronPopulation("PInh", _NInh, IZHIKEVICH_V, inhIzh_p, IzhInh_ini);

    model.addSynapsePopulation("Exc_Exc", NSYNAPSE, SPARSE, INDIVIDUALG, NO_DELAY,
    IZHIKEVICH_PS, "PExc", "PExc", SynIzh_ini, SynIzh_p, postSynV, postExpP);
    model.addSynapsePopulation("Exc_Inh", NSYNAPSE, SPARSE, INDIVIDUALG, NO_DELAY,
    IZHIKEVICH_PS, "PExc", "PInh", SynIzh_ini, SynIzh_p, postSynV, postExpP);
    model.addSynapsePopulation("Inh_Exc", NSYNAPSE, SPARSE, INDIVIDUALG, NO_DELAY,
    IZHIKEVICH_PS, "PInh", "PExc", SynIzh_ini, SynIzh_p, postSynV, postExpP);
    model.addSynapsePopulation("Inh_Inh", NSYNAPSE, SPARSE, INDIVIDUALG, NO_DELAY,
    IZHIKEVICH_PS, "PInh", "PInh", SynIzh_ini, SynIzh_p, postSynV, postExpP);

    fprintf(stderr, "#model created.\n");

    model.activateDirectInput("PExc", INPRULE);
    model.activateDirectInput("PInh", INPRULE);
    model.setMaxConn("Exc_Exc", _NMaxConnP0);
    model.setMaxConn("Exc_Inh", _NMaxConnP1);

```

```

model.setMaxConn("Inh_Exc", _NMaxConnP2);
model.setMaxConn("Inh_Inh", _NMaxConnP3);

#ifdef nGPU
    cerr << "nGPU: " << nGPU << endl;
    model.setGPUDevice(nGPU);
#endif
model.setPrecision(_FTYPE);
model.finalize();
}

```

## Appendix S2: Insect olfaction model definition in GeNN

This is the source code for defining the network used in Benchmark 2.

It can also be accessed online at [https://github.com/genn-](https://github.com/genn-team/genn/blob/v2.0_benchmark/userproject/MBody1_benchmark_project/model/MBody1.cc)

[team/genn/blob/v2.0\\_benchmark/userproject/MBody1\\_benchmark\\_project/model/MBody1.cc](https://github.com/genn-team/genn/blob/v2.0_benchmark/userproject/MBody1_benchmark_project/model/MBody1.cc).

Equivalent code using sparse connectivity and user-defined neuron and synapse models can be accessed at [https://github.com/genn-](https://github.com/genn-team/genn/blob/v2.0_benchmark/userproject/MBody_userdef_benchmark_project/model/MBody_u)

[team/genn/blob/v2.0\\_benchmark/userproject/MBody\\_userdef\\_benchmark\\_project/model/MBody\\_u](https://github.com/genn-team/genn/blob/v2.0_benchmark/userproject/MBody_userdef_benchmark_project/model/MBody_u)  
[serdef.cc](https://github.com/genn-team/genn/blob/v2.0_benchmark/userproject/MBody_userdef_benchmark_project/model/MBody_u).

```

#define DT 0.2 //!< This defines the global time step at which the simulation
will run

#include "modelSpec.h"
#include "modelSpec.cc"
#include "sizes.h"

double myPOI_p[4]= {
    0.1,          // 0 - firing rate
    2.5,          // 1 - refractory period
    20.0,         // 2 - Vspike
    -60.0         // 3 - Vrest
};

double myPOI_ini[3]= {
    -60.0,        // 0 - V
    0,            // 1 - seed
    -10.0         // 2 - SpikeTime
};

double stdTM_p[8]= {
    7.15,          // 0 - gNa: Na conductance in 1/(mOhms * cm^2)
    50.0,          // 1 - ENa: Na equi potential in mV
    1.43,          // 2 - gK: K conductance in 1/(mOhms * cm^2)
    -95.0,         // 3 - EK: K equi potential in mV
    0.02672,       // 4 - gl: leak conductance in 1/(mOhms * cm^2)
    -63.563,       // 5 - El: leak equi potential in mV
    0.143,         // 6 - Cmem: membr. capacity density in muF/cm^2

```

```

5          // 7 - ntimes: number of inner iterations for better precision
};

double stdTM_ini[4]= {
    -60.0,          // 0 - membrane potential E
    0.0529324,     // 1 - prob. for Na channel activation m
    0.3176767,     // 2 - prob. for not Na channel blocking h
    0.5961207      // 3 - prob. for K channel activation n
};

double *myPNKC_p= NULL;

double myPNKC_ini[1]= {
    0.01           // 0 - g: initial synaptic conductance
};

double postExpPNKC[2]={
    1.0,           // 0 - tau_S: decay time constant for S [ms]
    0.0            // 1 - Erev: Reversal potential
};

double *myPNLHI_p= NULL;

double myPNLHI_ini[1]= {
    0.0            // 0 - g: initial synaptic conductance
};

double postExpPNLHI[2]={
    1.0,           // 0 - tau_S: decay time constant for S [ms]
    0.0            // 1 - Erev: Reversal potential
};

double myLHIKC_p[2]= {
    -40.0,         // 0 - Epre: Presynaptic threshold potential
    50.0           // 1 - Vslope: Activation slope of graded release
};

double myLHIKC_ini[1] = {
    1.0/_NLHI     // 0 - g: initial synaptic conductance
};

double postExpLHIKC[2]={
    1.5, //3.0,     // 0 - tau_S: decay time constant for S [ms]
    -92.0           // 1 - Erev: Reversal potential
};

double myKCDN_p[11]= {
    -20.0,         // 0 - Epre: Presynaptic threshold potential
    50.0, //25.0,   // 1 - TLRN: time scale of learning changes
    50.0, //100.0   // 2 - TCHNG: width of learning window
};

```

```

50000.0,      // 3 - TDECAY: time scale of synaptic strength decay
100000.0,    // 4 - TPUNISH10: Time window of suppression in response to 1/0
200.0, //100.0, // 5 - TPUNISH01: Time window of suppression in response to
0/1
0.015, // 0.06,      // 6 - GMAX: Maximal conductance achievable
0.0075, // 0.03,     // 7 - GMID: Midpoint of sigmoid g filter curve
33.33,      // 8 - GSLOPE: slope of sigmoid g filter curve
10.0,      // 9 - TAUSHIFT: shift of learning curve
0.00006 // 0.006 // 10 - GSYN0: value of syn conductance g decays to
};

double myKCDN_ini[2]={
    0.01,      // 0 - g: synaptic conductance
    0.01,      // 1 - graw: raw synaptic conductance
};

double postExpKCDN[2]={
    5.0,      // 0 - tau_S: decay time constant for S [ms]
    0.0      // 1 - Erev: Reversal potential
};

double myDNDN_p[2]= {
    -30.0,    // 0 - Epre: Presynaptic threshold potential
    50.0      // 1 - Vslope: Activation slope of graded release
};

double myDNDN_ini[1]={
    5.0/_NLB      // 0 - g: synaptic conductance
};

double postExpDNDN[2]={
    2.5,      // 0 - tau_S: decay time constant for S [ms]
    -92.0     // 1 - Erev: Reversal potential
};

double *postSynV = NULL;

void modelDefinition(INNmodel &model)
{
    initGeNN();

    model.setName("MBody1");
    model.addNeuronPopulation("PN", _NAL, POISSONNEURON, myPOI_p, myPOI_ini);
    model.addNeuronPopulation("KC", _NMB, TRAUBMILES_PSTEP, stdTM_p, stdTM_ini);
    model.addNeuronPopulation("LHI", _NLHI, TRAUBMILES_PSTEP, stdTM_p,
stdTM_ini);
    model.addNeuronPopulation("DN", _NLB, TRAUBMILES_PSTEP, stdTM_p, stdTM_ini);

    model.addSynapsePopulation("PNKC", NSYNAPSE, DENSE, INDIVIDUALG, NO_DELAY,
EXPDECAY, "PN", "KC", myPNKC_ini, myPNKC_p, postSynV, postExpPNKC);

```

```
    model.addSynapsePopulation("PNLHI", NSYNAPSE, ALLTOALL, INDIVIDUALG,  
NO_DELAY, EXPDECAY, "PN", "LHI", myPNLHI_ini, myPNLHI_p, postSynV,  
postExpPNLHI);  
    model.addSynapsePopulation("LHIKC", NGRADSYNAPSE, ALLTOALL, GLOBALG,  
NO_DELAY, EXPDECAY, "LHI", "KC", myLHIKC_ini, myLHIKC_p, postSynV,  
postExpLHIKC);  
    model.addSynapsePopulation("KCDN", LEARN1SYNAPSE, ALLTOALL, INDIVIDUALG,  
NO_DELAY, EXPDECAY, "KC", "DN", myKCDN_ini, myKCDN_p, postSynV, postExpKCDN);  
    model.addSynapsePopulation("DNDN", NGRADSYNAPSE, ALLTOALL, GLOBALG,  
NO_DELAY, EXPDECAY, "DN", "DN", myDNDN_ini, myDNDN_p, postSynV, postExpDNDN);  
  
#ifdef nGPU  
    cerr << "nGPU: " << nGPU << endl;  
    model.setGPUDevice(nGPU);  
#endif  
  
model.setSeed(1234);  
model.setPrecision(_FTYPE);  
model.setTiming(FALSE);  
model.finalize();  
}
```