Appendix A
Acquiring and Installing GENESIS

A.1 System Requirements

GENESIS and its graphical front-end XODUS are written in C and run on SUN (SunOS 4 or Solaris 2), DECstation (Ultrix), Silicon Graphics (Irix 4.0.1 and up) or x86 PC (Linux or FreeBSD) machines with X-windows (versions X11R4, X11R5, and X11R6). IBM RS6000s (AIX), HPs (HPUX), DEC Alphas (OSF v2 and v3) and the Cray T3D have been successful in compiling and running, although our experience is limited. We welcome feedback on experiences with these platforms. Other platforms may be capable of running GENESIS, but the software has not been tested by Caltech outside of these environments. Although GENESIS may be ported to the Windows95 and NT operating systems at some time in the future, we currently recommend using the freely available Linux operating system for running GENESIS on a PC.

A.2 Using the CD-ROM

The CD-ROM included with this book contains the complete GENESIS version 2.1 distribution, which includes full source code and documentation for both GENESIS and XODUS, as well as the tutorial simulations described in this book. The CD-ROM also contains parallel GENESIS (PGENESIS) and a number of additional packages related to GENESIS that are usually available separately or via the World Wide Web. In addition to containing the GENESIS source code, the CD-ROM has precompiled binaries for the most common UNIX platforms. You may run these binaries directly from the CD-ROM. This will be useful if you are interested in trying the tutorials described in the book, or in evaluating the

GENESIS simulator. For regular use and best performance, the binaries can be installed on a hard disk.

Complete instructions for the use of the CD-ROM and the installation and running of GENESIS are given in the file *A-ReadMe.txt*. This information is also available in the hypertext file *A-ReadMe.html*, which may be viewed with a web browser, and which provides a convenient link to the hypertext GENESIS Reference Manual and other useful information.

A.3 Obtaining GENESIS over the Internet

GENESIS is continually evolving, and there will undoubtedly be new features incorporated into future versions. To be sure that you have the latest GENESIS distribution, and to learn about new developments, please check the GENESIS World Wide Web site (*http://www.bbb.caltech.edu/GENESIS*) or anonymous ftp site (*genesis.bbb.caltech.edu*). You may use these sites to download the latest versions of the software and documentation at no cost.

When using ftp to to connect to *genesis.bbb.caltech.edu*, log in as the user "anonymous" and give your full email address as the password. You can then type "`cd /pub/genesis`" and download the software. Your first step should be to download the files *README* and *LATEST.NEWS*, with the commands "`get README`" and "`get LATEST.NEWS`". These files will give further information about the current GENESIS version, and alert you to any new developments since the publication of this book. The *README* file will give further information on downloading and installing the files that are available. Typically, you will give the command "`binary`", followed by the command "`get genesis.tar.Z`". The file may take a while to transfer if you do this at a time when networks are busy. Finally, give the "`quit`" command.

The files mentioned above are directly accessible via hypertext links at the GENESIS web site. Information will also be available concerning "mirror" sites outside of the United States.

A.4 Installation and Documentation

GENESIS may be easily installed from the CD-ROM by using the installation script and instructions that are provided. To install GENESIS from a distribution that was obtained over the Internet, or to compile and install GENESIS on a platform for which there are no suitable precompiled binaries, you or your system administrator should change to the directory in which you wish the GENESIS directory tree to reside, and copy *genesis.tar.Z* to this directory. */usr* or */usr/local* would be a good location for this directory, although you may use your home directory or any other directory.

Then, give the UNIX command "`zcat genesis.tar.Z | tar xvf -`". This will create the directory *genesis* and a number of subdirectories. Begin by reading the *README* file in the *genesis* directory. Directions for compiling and installing the software may be found in the *README* file contained in the *src* subdirectory. Directions for printing the GENESIS Reference Manual and installing the hypertext documentation may be found in *Doc/README*. The *Scripts/README* file describes the demonstration and tutorial simulations that are included with this distribution. Further inquiries concerning GENESIS or its installation may be addressed to *genesis@bbb.caltech.edu* by email.

Individuals or research groups who are considering using GENESIS as a research tool are strongly encouraged to join the GENESIS Users Group, BABEL. Information regarding BABEL membership may be obtained by email from *babel@bbb.caltech.edu*.

A.5 Copyright Notice

Appendix B
GENESIS Script Listings

B.1 tutorial2.g

```
//genesis  -  tutorial2.g - GENESIS Version 2.0
/*==========================================================================
  A sample script to create a soma-like compartment. SI units are used.
  ==========================================================================*/

float   PI = 3.14159

// soma parameters - chosen to be the same as in SQUID (but in SI units)
float RM = 0.33333         // specific membrane resistance (ohms m^2)
float CM = 0.01            // specific membrane capacitance (farads/m^2)
float RA = 0.3             // specific axial resistance (ohms m)
float EREST_ACT = -0.07    // resting membrane potential (volts)
float Eleak = EREST_ACT + 0.0106  // membrane leakage potential (volts)
float ENA   = 0.045        // sodium equilibrium potential
float EK    = -0.082       // potassium equilibrium potential

// cell dimensions (meters)
float soma_l = 30e-6       // cylinder equivalent to 30 micron sphere
float soma_d = 30e-6

float dt = 0.00005         // simulation time step in sec
setclock  0  {dt}          // set the simulation clock

//==============================
//      Function Definitions
//==============================
```

```
function makecompartment(path, length, dia, Erest)
    str path
    float length, dia, Erest
    float area = length*PI*dia
    float xarea = PI*dia*dia/4

    create      compartment     {path}
    setfield   {path}               \
                Em      { Erest }   \           // volts
                Rm      { RM/area } \           // Ohms
                Cm      { CM*area } \           // Farads
                Ra      { RA*length/xarea }     // Ohms
end

function make_Vmgraph
    float vmin = -0.100
    float vmax = 0.05
    float tmax = 0.100 // default simulation time = 100 msec
    create xform /data
    create xgraph /data/voltage
    setfield ^ xmax {tmax} ymin {vmin} ymax {vmax}
    create xbutton /data/RESET  -script reset
    create xbutton /data/RUN  -script "step "{tmax}" -time"
    create xbutton /data/QUIT -script quit
    xshow /data
end

//================================
//         Main Script
//================================

create neutral /cell
// create the soma compartment "/cell/soma"
makecompartment /cell/soma {soma_l} {soma_d} {Eleak}

// provide current injection to the soma
setfield /cell/soma inject  0.3e-9      // 0.3 nA injection current

// make the graph to display soma Vm and pass messages to the graph
make_Vmgraph
addmsg /cell/soma /data/voltage PLOT Vm *volts *red

check
reset
```

B.2 tutorial3.g

```
//genesis  -  tutorial3.g - GENESIS Version 2.0
/*==========================================================================
  A sample script to create a compartment containing channels taken from
  hhchan.g in the neurokit prototypes library.  SI units are used.
  ==========================================================================*/

include hhchan // functions to create Hodgkin-Huxley channels
/* hhchan.g assigns values to the global variables EREST_ACT, ENA, EK,
   and SOMA_A.  These will be superseded by values defined below.      */

float   PI = 3.14159

// soma parameters - chosen to be the same as in SQUID (but in SI units)
float RM = 0.33333           // specific membrane resistance (ohms m^2)
float CM = 0.01              // specific membrane capacitance (farads/m^2)
float RA = 0.3               // specific axial resistance (ohms m)
float EREST_ACT = -0.07      // resting membrane potential (volts)
float Eleak = EREST_ACT + 0.0106  // membrane leakage potential (volts)
float ENA   = 0.045          // sodium equilibrium potential
float EK    = -0.082         // potassium equilibrium potential

// cell dimensions (meters)
float soma_l = 30e-6            // cylinder equivalent to 30 micron sphere
float soma_d = 30e-6
float SOMA_A = soma_l*PI*soma_d // variable used by hhchan.g for soma area

float tmax = 0.1                // simulation time in sec
float dt = 0.00005              // simulation time step in sec
setclock  0  {dt}               // set the simulation clock

//==============================
//      Function Definitions
//==============================

function makecompartment(path, length, dia, Erest)
    str path
    float length, dia, Erest
    float area = length*PI*dia
    float xarea = PI*dia*dia/4

    create      compartment     {path}
    setfield    {path}              \
                Em      { Erest }   \           // volts
                Rm      { RM/area } \           // Ohms
                Cm      { CM*area } \           // Farads
                Ra      { RA*length/xarea }     // Ohms
end
```

```
function step_tmax
    step {tmax} -time
end

//================================
//    Graphics Functions
//================================

function make_control
    create xform /control [10,50,250,145]
    create xlabel /control/label -hgeom 50 -bg cyan -label "CONTROL PANEL"
    create xbutton /control/RESET -wgeom 33%       -script reset
    create xbutton /control/RUN  -xgeom 0:RESET -ygeom 0:label -wgeom 33% \
         -script step_tmax
    create xbutton /control/QUIT -xgeom 0:RUN -ygeom 0:label -wgeom 34% \
         -script quit
    create xdialog /control/Injection -label "Injection (amperes)" \
         -value 0.3e-9 -script "set_inject <widget>"
    xshow /control
end

function make_Vmgraph
    float vmin = -0.100
    float vmax = 0.05
    create xform /data [265,50,350,350]
    create xlabel /data/label -hgeom 10% -label "Soma with Na and K Channels"
    create xgraph /data/voltage  -hgeom 90%  -title "Membrane Potential"
    setfield ^ XUnits sec YUnits Volts
    setfield ^ xmax {tmax} ymin {vmin} ymax {vmax}
    xshow /data
end

function set_inject(dialog)
    str dialog
    setfield /cell/soma inject {getfield {dialog} value}
end

//================================
//         Main Script
//================================

create neutral /cell
// create the soma compartment "/cell/soma"
makecompartment /cell/soma {soma_l} {soma_d} {Eleak}
setfield /cell/soma initVm {EREST_ACT} // initialize Vm to rest potential

// provide current injection to the soma
setfield /cell/soma inject  0.3e-9      // 0.3 nA injection current
```

```
// Create two channels, "/cell/soma/Na_squid_hh" and "/cell/soma/K_squid_hh"
pushe /cell/soma
make_Na_squid_hh
make_K_squid_hh
pope

// The soma needs to know the value of the channel conductance
// and equilibrium potential in order to calculate the current
// through the channel.  The channel calculates its conductance
// using the current value of the soma membrane potential.

addmsg /cell/soma/Na_squid_hh /cell/soma CHANNEL Gk Ek
addmsg /cell/soma /cell/soma/Na_squid_hh VOLTAGE Vm
addmsg /cell/soma/K_squid_hh /cell/soma CHANNEL Gk Ek
addmsg /cell/soma /cell/soma/K_squid_hh VOLTAGE Vm

// make the control panel
make_control

// make the graph to display soma Vm and pass messages to the graph
make_Vmgraph
addmsg /cell/soma /data/voltage PLOT Vm *volts *red

check
reset
```

B.3 tutorial4.g

```
//genesis  -  tutorial4.g - GENESIS Version 2.0

/*=====================================================================
  A sample script to create a multicompartmental neuron with synaptic
  input.  SI units are used.
  =====================================================================*/

include hhchan          // functions to create Hodgkin-Huxley channels
/* hhchan.g assigns values to the global variables EREST_ACT, ENA, EK,
   and SOMA_A.  These will be superseded by values defined below.      */

float PI = 3.14159

// soma parameters - chosen to be the same as in SQUID (but in SI units)
float RM = 0.33333            // specific membrane resistance (ohms m^2)
float CM = 0.01               // specific membrane capacitance (farads/m^2)
float RA = 0.3                // specific axial resistance (ohms m)
float EREST_ACT = -0.07       // resting membrane potential (volts)
float Eleak = EREST_ACT + 0.0106  // membrane leakage potential (volts)
```

```
float ENA   = 0.045           // sodium equilibrium potential
float EK    = -0.082          // potassium equilibrium potential

// cell dimensions (meters)
float soma_l = 30e-6            // cylinder equivalent to 30 micron sphere
float soma_d = 30e-6
float dend_l =100e-6            // we will add a 100 micron long dendrite
float dend_d =  2e-6            // give it a 2 micron diameter
float SOMA_A = soma_l*PI*soma_d // variable used by hhchan.g for soma area

float gmax = 5e-10              // maximum synaptic conductance (Siemen)

float tmax = 0.1                // simulation time in sec
float dt = 0.00005              // simulation time step in sec
setclock  0  {dt}               // set the simulation clock

//==============================
//      Function Definitions
//==============================

function makecompartment(path, length, dia, Erest)
    str path
    float length, dia, Erest
    float area = length*PI*dia
    float xarea = PI*dia*dia/4

    create      compartment     {path}
    setfield    {path}              \
                Em      { Erest }   \           // volts
                Rm      { RM/area } \           // Ohms
                Cm      { CM*area } \           // Farads
                Ra      { RA*length/xarea }     // Ohms
end

function makechannel(compartment,channel,Ek,tau1,tau2,gmax)
    str compartment
    str channel
    float Ek                            // Volts
    float tau1,tau2                     // sec
    float gmax                          // Siemens (1/ohms)

    create      synchan               {compartment}/{channel}
    setfield    ^ \
                Ek                      {Ek}   \
                tau1                    {tau1} \
                tau2                    {tau2} \
                gmax                    {gmax}
    addmsg   {compartment}/{channel}   {compartment} CHANNEL Gk Ek
    addmsg   {compartment}   {compartment}/{channel} VOLTAGE Vm
```

```
end

function makeneuron(path, soma_l, soma_d, dend_l, dend_d)
    str path
    float soma_l, soma_d, dend_l, dend_d

    create neutral {path}
    makecompartment {path}/soma {soma_l} {soma_d} {Eleak}
    setfield /cell/soma initVm {EREST_ACT}

// Create two channels, "{path}/soma/Na_squid_hh" and "{path}/soma/K_squid_hh"
    pushe {path}/soma
    make_Na_squid_hh
    make_K_squid_hh
    pope

    // The soma needs to know the value of the channel conductance
    // and equilibrium potential in order to calculate the current
    // through the channel.  The channel calculates its conductance
    // using the current value of the soma membrane potential.
    addmsg {path}/soma/Na_squid_hh {path}/soma CHANNEL Gk Ek
    addmsg {path}/soma {path}/soma/Na_squid_hh VOLTAGE Vm
    addmsg {path}/soma/K_squid_hh {path}/soma CHANNEL Gk Ek
    addmsg {path}/soma {path}/soma/K_squid_hh VOLTAGE Vm

    // make the dendrite compartment and link it to the soma
    makecompartment {path}/dend {dend_l} {dend_d} {EREST_ACT}
    makechannel {path}/dend Ex_channel {ENA} 0.003 0.003 {gmax}
    addmsg {path}/dend {path}/soma RAXIAL Ra previous_state
    addmsg {path}/soma {path}/dend AXIAL  previous_state

// add a spike generator to the soma
    create spikegen {path}/soma/spike
    setfield {path}/soma/spike  thresh 0  abs_refract 0.010  output_amp 1
    /* use the soma membrane potential to drive the spike generator */
    addmsg  {path}/soma  {path}/soma/spike  INPUT Vm
end  // makeneuron

function step_tmax
    step {tmax} -time
end

function makeinput(path)
    str path
    int msgnum
    create randomspike /randomspike
    setfield ^ min_amp 1.0 max_amp 1.0 rate 200 reset 1 reset_value 0
    addmsg /randomspike {path} SPIKE
    msgnum = {getfield {path} nsynapses} - 1
```

```
    setfield {path} \
        synapse[{msgnum}].weight 1 synapse[{msgnum}].delay 0
    addmsg /randomspike /data/voltage \
        PLOTSCALE state  *input *blue  0.01     0
//                       title  color  scale  offset
end

//==============================
//    Graphics Functions
//==============================

function make_control
    create xform /control [10,50,250,145]
    create xlabel /control/label -hgeom 50 -bg cyan -label "CONTROL PANEL"
    create xbutton /control/RESET -wgeom 33%       -script reset
    create xbutton /control/RUN  -xgeom 0:RESET -ygeom 0:label -wgeom 33% \
        -script step_tmax
    create xbutton /control/QUIT -xgeom 0:RUN -ygeom 0:label -wgeom 34% \
        -script quit
    create xdialog /control/Injection -label "Injection (amperes)" \
        -value 0.0 -script "set_inject <widget>"
    create xtoggle /control/feedback  -script toggle_feedback
    setfield /control/feedback offlabel "Feedback OFF" \
        onlabel "Feedback ON" state 1
    xshow /control
end

function make_Vmgraph
    float vmin = -0.100
    float vmax = 0.05
    create xform /data [265,50,350,350]
    create xlabel /data/label -hgeom 10% -label "Simple Neuron Model"
    create xgraph /data/voltage  -hgeom 90%  -title "Membrane Potential"
    setfield ^ XUnits sec YUnits Volts
    setfield ^ xmax {tmax} ymin {vmin} ymax {vmax}
    xshow /data
end

function set_inject(dialog)
    str dialog
    setfield /cell/soma inject {getfield {dialog} value}
end

function make_condgraph
    create xform /condgraphs [620,50,475,350]
    pushe /condgraphs
    create xgraph channel_Gk -hgeom 100% -title "Channel Conductance"
    setfield channel_Gk xmin 0 xmax {tmax} ymin 0 ymax {gmax*10}
    setfield channel_Gk XUnits "sec" YUnits "Gk (Siemen)"
```

```
    pope
    xshow /condgraphs
end

function toggle_feedback
    int msgnum
    if ({getfield /control/feedback state} == 0)
        deletemsg  /cell/soma/spike 0 -out
        echo "Feedback connection deleted"
    else
        addmsg /cell/soma/spike /cell/dend/Ex_channel SPIKE
        msgnum = {getfield /cell/dend/Ex_channel nsynapses} - 1
        setfield /cell/dend/Ex_channel \
            synapse[{msgnum}].weight 10 synapse[{msgnum}].delay 0.005
        echo "Feedback connection added"
    end
end

//==============================
//         Main Script
//==============================

// create the neuron "/cell"
makeneuron /cell {soma_l} {soma_d} {dend_l} {dend_d}
setfield /cell/soma inject 0.0

// make the control panel
make_control

// make the graph to display soma Vm and pass messages to the graph
make_Vmgraph
addmsg /cell/soma /data/voltage PLOT Vm *volts *red

makeinput /cell/dend/Ex_channel

make_condgraph
addmsg /cell/dend/Ex_channel /condgraphs/channel_Gk PLOT Gk *Gk *black

// finally, we add some feedback from the axon to the dendrite
addmsg /cell/soma/spike /cell/dend/Ex_channel SPIKE
setfield /cell/dend/Ex_channel \
    synapse[1].weight 10 synapse[1].delay 0.005

check
reset
```

B.4 tutorial5.g

```
//genesis  -  tutorial5.g - GENESIS Version 2.0

/*=====================================================================
  A sample script which uses the cell reader to create a
   multicompartmental neuron with synaptic input.  SI units are used.
  ====================================================================*/

// Create a library of prototype elements to be used by the cell reader
include protodefs

float gmax = 5e-10              // maximum synaptic conductance (Siemen)

float tmax = 0.1                // simulation time in sec
float dt = 0.00005              // simulation time step in sec
setclock  0  {dt}               // set the simulation clock

//==============================
//      Function Definitions
//==============================

function step_tmax
    step {tmax} -time
end

function makeinput(path)
    str path
    int msgnum
    create randomspike /randomspike
    setfield ^ min_amp 1.0 max_amp 1.0 rate 200 reset 1 reset_value 0
    addmsg /randomspike {path} SPIKE
    msgnum = {getfield {path} nsynapses} - 1
    setfield {path} \
        synapse[{msgnum}].weight 1 synapse[{msgnum}].delay 0
    addmsg /randomspike /data/voltage \
        PLOTSCALE state  *input *blue  0.01     0
//                       title  color  scale  offset
end

//==============================
//    Graphics Functions
//==============================

function make_control
    create xform /control [10,50,250,145]
    create xlabel /control/label -hgeom 50 -bg cyan -label "CONTROL PANEL"
    create xbutton /control/RESET -wgeom 33%       -script reset
    create xbutton /control/RUN  -xgeom 0:RESET -ygeom 0:label -wgeom 33% \
```

```
        -script step_tmax
    create xbutton /control/QUIT -xgeom 0:RUN -ygeom 0:label -wgeom 34% \
        -script quit
    create xdialog /control/Injection -label "Injection (amperes)" \
        -value 0.0 -script "set_inject <widget>"
    create xtoggle /control/feedback  -script toggle_feedback
    setfield /control/feedback offlabel "Feedback OFF" \
        onlabel "Feedback ON" state 1
    xshow /control
end

function make_Vmgraph
    float vmin = -0.100
    float vmax = 0.05
    create xform /data [265,50,350,350]
    create xlabel /data/label -hgeom 10% -label "Simple Neuron Model"
    create xgraph /data/voltage  -hgeom 90%  -title "Membrane Potential"
    setfield ^ XUnits sec YUnits Volts
    setfield ^ xmax {tmax} ymin {vmin} ymax {vmax}
    xshow /data
end

function set_inject(dialog)
    str dialog
    setfield /cell/soma inject {getfield {dialog} value}
end

function make_condgraph
    create xform /condgraphs [620,50,475,350]
    pushe /condgraphs
    create xgraph channel_Gk -hgeom 100% -title "Channel Conductance"
    setfield channel_Gk xmin 0 xmax {tmax} ymin 0 ymax {gmax*10}
    setfield channel_Gk XUnits "sec" YUnits "Gk (siemens)"
    pope
    xshow /condgraphs
end

function toggle_feedback
    int msgnum
    if ({getfield /control/feedback state} == 0)
        deletemsg  /cell/soma/spike 0 -out
        echo "Feedback connection deleted"
    else
        addmsg /cell/soma/spike /cell/dend/Ex_channel SPIKE
        msgnum = {getfield /cell/dend/Ex_channel nsynapses} - 1
        setfield /cell/dend/Ex_channel \
            synapse[{msgnum}].weight 10 synapse[{msgnum}].delay 0.005
        echo "Feedback connection added"
    end
```

```
end

//==============================
//         Main Script
//==============================
// Build the cell from a parameter file using the cell reader
readcell cell.p /cell

setfield /cell/soma inject 0.0

// make the control panel
make_control

// make the graph to display soma Vm and pass messages to the graph
make_Vmgraph
addmsg /cell/soma /data/voltage PLOT Vm *volts *red

makeinput /cell/dend/Ex_channel        // Create synaptic inputs

// Make synaptic conductance graph and pass message to the graph
make_condgraph
addmsg /cell/dend/Ex_channel /condgraphs/channel_Gk PLOT Gk *Gk *black

// finally, we add some feedback from the axon to the dendrite
addmsg /cell/soma/spike /cell/dend/Ex_channel SPIKE
setfield /cell/dend/Ex_channel \
    synapse[1].weight 10 synapse[1].delay 0.005

check
reset
```

B.5 hhchan.g

```
// genesis 2.0

/* FILE INFORMATION
** hh_channel implementation of squid giant axon voltage-dependent
** channels, according to :
** A.L.Hodgkin and A.F.Huxley, J.Physiol(Lond) 117, pp 500-544 (1952)
**
** This file depends on functions and constants defined in library.g
*/

// CONSTANTS
float EREST_ACT = -0.060 /* granule cell resting potl */
float ENA = 0.045
float EK = -0.090
float SOMA_A = 1e-9             /* Square meters */
```

```
int EXPONENTIAL =   1
int SIGMOID     =   2
int LINOID      =   3

/*****************************************************************************
Some conventions in using the HH_CHANNELS

HH_CONVENTIONS
==============
Activation state variable is called x for all channels
Inactivation state variable is called y for all channels
In the traditional hh notations: x=m, y=h for Na channel; x=n for K_channel

There are three functional forms for alpha and beta for each state variable:
FORM 1: alpha(v) = A exp((v-V0)/B)                  (EXPONENTIAL)
FORM 2: alpha(v) = A / (exp((v-V0)/B) + 1)          (SIGMOID)
FORM 3: alpha(v) = A (v-V0) / (exp((v-V0)/B) - 1)   (LINOID)
The same functional forms are used for beta.
In the simulator, the FORM, A, B and V0 are designated by:
X_alpha_FORM, X_alpha_A, X_alpha_B, X_alpha_V0  alpha function for state var x
X_beta_FORM,  X_beta_A,  X_beta_B,  X_beta_V0   beta  function for state var x
Y_alpha_FORM, Y_alpha_A, Y_alpha_B, Y_alpha_V0  alpha function for state var y
Y_beta_FORM,  Y_beta_A,  Y_beta_B,  Y_beta_V0   beta  function for state var y

The conductance is calculated as g = Gbar*x^Xpower * y^Ypower
For a squid axon Na channel: Xpower = 3, Ypower = 1 (m^3 h)
                 K  channel: Xpower = 4, Ypower = 0 (n^4)

These are linked to the soma by two messages :
addmsg /soma/hh_channel /soma CHANNEL Gk Ek
addmsg /soma /soma/hh_channel VOLTAGE Vm

*****************************************************************************/

// Original Hodgkin-Huxley squid parameters, implemented as hh_channel elements

//======================================================================
//                        ACTIVE SQUID NA CHANNEL
//      A.L.Hodgkin and A.F.Huxley, J.Physiol(Lond) 117, pp 500-544 (1952)
//======================================================================
function make_Na_squid_hh
        if ({exists Na_squid_hh})
                return
        end

        create          hh_channel      Na_squid_hh
        setfield Na_squid_hh \
                Ek              {ENA} \                 // V
```

```
                Gbar            { 1.2e3 * SOMA_A } \            // S
                Xpower          3.0 \
                Ypower          1.0 \
                X_alpha_FORM    {LINOID} \
                X_alpha_A       -0.1e6 \                        // 1/V-sec
                X_alpha_B       -0.010 \                        // V
                X_alpha_V0      { 0.025 + EREST_ACT } \         // V
                X_beta_FORM     {EXPONENTIAL} \
                X_beta_A        4.0e3 \                         // 1/sec
                X_beta_B        -18.0e-3 \                      // V
                X_beta_V0       { 0.0 + EREST_ACT } \           // V
                Y_alpha_FORM    {EXPONENTIAL} \
                Y_alpha_A       70.0 \                          // 1/sec
                Y_alpha_B       -20.0e-3 \                      // V
                Y_alpha_V0      { 0.0 + EREST_ACT } \           // V
                Y_beta_FORM     {SIGMOID} \
                Y_beta_A        1.0e3 \                         // 1/sec
                Y_beta_B        -10.0e-3 \                      // V
                Y_beta_V0       { 30.0e-3 + EREST_ACT }         // V
end

//=======================================================================
//                        ACTIVE K CHANNEL - SQUID
//      A.L.Hodgkin and A.F.Huxley, J.Physiol(Lond) 117, pp 500-544 (1952)
//=======================================================================
function make_K_squid_hh
        if ({exists K_squid_hh})
                return
        end

        create          hh_channel      K_squid_hh
        setfield K_squid_hh \
                Ek              {EK} \                          // V
                Gbar            {360.0*SOMA_A} \                // S
                Xpower          4.0 \
                Ypower          0.0 \
                X_alpha_FORM    {LINOID} \
                X_alpha_A       -10.0e3 \                       // 1/V-sec
                X_alpha_B       -10.0e-3 \                      // V
                X_alpha_V0      {10.0e-3+EREST_ACT} \           // V
                X_beta_FORM     {EXPONENTIAL} \
                X_beta_A        125.0 \                         // 1/sec
                X_beta_B        -80.0e-3 \                      // V
                X_beta_V0       {0.0+EREST_ACT}                 // V
end
```

B.6 hhchan_K.g

```
//genesis - hhchan_K.g - creates an extended object for a H-H K channel

// Define some constants to define the form of the rate constant equation
int EXPONENTIAL =   1
int SIGMOID     =   2
int LINOID      =   3

//  Original Hodgkin-Huxley squid parameters
float EREST_ACT = -0.070
float EK = -0.082

create          hh_channel      K_squid_hh
setfield K_squid_hh \
        Ek              {EK} \                          // V
        Gbar            0.0  \
        Xpower          4.0 \
        Ypower          0.0 \
        X_alpha_FORM    {LINOID} \
        X_alpha_A       -10.0e3 \                       // 1/V-sec
        X_alpha_B       -10.0e-3 \                      // V
        X_alpha_V0      {10.0e-3+EREST_ACT} \           // V
        X_beta_FORM     {EXPONENTIAL} \
        X_beta_A        125.0 \                         // 1/sec
        X_beta_B        -80.0e-3 \                      // V
        X_beta_V0       {0.0+EREST_ACT}                 // V

addfield        K_squid_hh      gdens           // conductance density
setfield        K_squid_hh      gdens           360.0   // S/m^2

setfieldprot K_squid_hh -hidden  Xpower Ypower X_alpha_FORM \
    X_alpha_A X_alpha_B X_alpha_V0 X_beta_FORM X_beta_A \
    X_beta_B X_beta_V0 Y_alpha_FORM Y_alpha_A Y_alpha_B \
    Y_alpha_V0 Y_beta_FORM Y_beta_A Y_beta_B Y_beta_V0
setfieldprot K_squid_hh -readonly Gbar

function K_squid_hh_SET(action, field, newvalue)
    float newvalue
    float PI = 3.14159
    if (field == "gdens")
        setfield . Gbar {PI*{getfield .. dia}*{getfield .. len}*newvalue}
    end
    return 0    // indicate that SET action isn't yet complete
end
addaction K_squid_hh SET K_squid_hh_SET

function K_squid_hh_CREATE(action, parent, object, elm)
    float PI = 3.14159
```

```
    if (!{isa compartment ..})
        echo K_squid_hh must be the child of a compartment
        return 0
    end
    setfield . Gbar {PI*{getfield .. dia}*{getfield .. len}*{getfield . gdens}}
    addmsg . .. CHANNEL Gk Ek
    addmsg .. . VOLTAGE Vm
    return 1
end
addaction K_squid_hh CREATE K_squid_hh_CREATE

addobject K_squid_hh K_squid_hh -author "J. R. Hacker" \
    -description "Hodgkin-Huxley Active K Squid Channel - SI units"
```

B.7 userprefs.g

```
// genesis

// Customized userprefs.g to run the "Tutorial 5" simulation with neurokit

/*********************************************************************
**
**      DO NOT EDIT THIS FILE IN THE neurokit DIRECTORY!
**
**      Make a copy of this file in every directory that contains .p
**      files and edit the copies, in order to customize neurokit for
**      different simulations. When you run neurokit from other
**      directories, the simulator will look for the local version of
**      userprefs.g, and if it cannot find it there will look for the
**      default in the neurokit directory.
**
**      There are three aspects to customisation :
**
**      1       Include the appropriate script files from the /neuron/prototype
**              directory and from wherever you have defined new prototype
**              elements.
**
**      2       Invoke the functions that make the prototypes you want for
**              your simulation.
**
**      3       Put your preferences for the user_variables defined in
**              defaults.g in the copies of this file.
**
*********************************************************************/

echo Using local user preferences

/*********************************************************************
```

```
**      1       Including script files for prototype functions
*************************************************************************/

/* file for standard compartments */
include compartments

/* file for Hodgkin-Huxley Squid Na and K channels */
include hhchan

/* file for synaptic channels */
include synchans

/* file which makes a spike generator */
include protospike

/************************************************************************
**      2  Invoking functions to make prototypes in the /library element
************************************************************************/

/* To ensure that all subsequent elements are made in the library */
        pushe /library

        make_cylind_compartment         /* makes "compartment" */

/* Assign some constants to override those used in hhchan.g */
EREST_ACT = -0.07       // resting membrane potential (volts)
ENA   = 0.045           // sodium equilibrium potential
EK    = -0.082          // potassium equilibrium potential

make_Na_squid_hh     /* makes "Na_squid_hh" */

make_K_squid_hh      /* makes "K_squid_hh" */

make_Ex_channel      /* synchan with Ek = 0.045, tau1 = tau2 = 3 msec */

/* In case we need it later, put an inhibitory GABA-activated channel
   in the library, too */

make_Inh_channel    /* synchan: Ek = -0.082, tau1 = tau2 = 20 msec */

make_spike      /* Make a spike generator element */

pope /          /* return to the root element */

/************************************************************************
**      3       Setting preferences for user-variables.
************************************************************************/

/* See defaults.g for default values of these */
```

```
str user_help = "../neurokit/README"

user_cell = "/cell"
user_pfile = "cell.p"

user_runtime = 0.1
user_dt = 50e-6  // 0.05 msec
user_refresh = 5

// These are used for the two buttons which can be used to enter a value
// in the "Syn Type" dialog box
user_syntype1 = "Ex_channel"
user_syntype2 = "Inh_channel"

user_inject = 0.3  // default injection current (nA)

// Set the scales for the graphs in the two cell windows
user_ymin1 = -0.1
user_ymax1 = 0.05
user_xmax1 = 0.1
user_xmax2 = 0.1
user_ymin2 = 0.0
user_ymax2 = 5e-9

/*  This displays the second cell window and plots the "Gk" field of the
    "Inh_channel" channel for the compartment in which a recording electrode
    has been planted.  The default values of the field and path
    are "Vm" and ".", meaning to plot the Vm field for the compartment
    which is selected for recording.
*/

user_numxouts = 2
user_field2     = "Gk"
user_path2 = "Ex_channel"
```

B.8 cellproto.g

```
// genesis 2.0 - prototype cell for the Netkit example
float EREST_ACT = -0.065

function make_cell
    create compartment /proto/cell
        setfield /proto/cell \
                        Rm 3.2e9 \
                        Cm 6.3e-12 \
                        Ra 16e6 \
                        Em -0.065
```

```
    create tabchannel /proto/cell/Na // set up the Na channel
        setfield /proto/cell/Na \
            Ek 0.045    Gbar 8e-7   Xpower 3    Ypower 1    Zpower 0
        setupalpha /proto/cell/Na X \ // setting up the X gate
                {320e3 * (0.013 + EREST_ACT)}  \
                -320e3 -1.0 {-1.0 * (0.013 + EREST_ACT)} -0.004 \
                {-280e3 * (0.040 + EREST_ACT) }  \
                280e3 -1.0 {-1.0 * (0.040 + EREST_ACT) } 5.0e-3 \
                    -size 1000 -range -0.1 0.05

        setupalpha /proto/cell/Na Y \ // setting up the Y gate
                128 0 0 {-1.0 * (0.017 + EREST_ACT)} 0.018 \
                4e3 0 1 {-1.0 * (0.040 + EREST_ACT)} -5e-3 \
                    -size 1000 -range -0.1 0.05

    create tabchannel /proto/cell/K // set up the K channel
        setfield /proto/cell/K \
            Ek -0.090   Gbar 2.4e-7   Xpower 4   Ypower 0   Zpower 0
        setupalpha /proto/cell/K X \ // setting up the X gate
                {32e3 * (0.015 + EREST_ACT) } \
                -32e3 -1 {-1.0 * (0.015 + EREST_ACT)} -5e-3, \
                 500 0 0 {-1.0 * (0.010 + EREST_ACT) } 40e-3 \
                     -size 1000 -range -0.1 0.05

    addmsg /proto/cell /proto/cell/Na VOLTAGE Vm
    addmsg /proto/cell/Na /proto/cell CHANNEL Gk Ek

    addmsg /proto/cell /proto/cell/K VOLTAGE Vm
    addmsg /proto/cell/K /proto/cell CHANNEL Gk Ek

    create spikegen /proto/cell/axon
    setfield /proto/cell/axon abs_refract 0.001 thresh 0.0 output_amp 1
    addmsg /proto/cell /proto/cell/axon INPUT Vm

    create synchan /proto/cell/glu
        setfield /proto/cell/glu \
            tau1  2e-3      tau2  2e-3 \
            gmax  1e-7      Ek    0.045
    addmsg /proto/cell /proto/cell/glu VOLTAGE Vm
    addmsg /proto/cell/glu /proto/cell CHANNEL Gk Ek

    create synchan /proto/cell/GABA
        setfield /proto/cell/GABA \
            tau1  20e-3     tau2  20e-3 \
            gmax   2e-8     Ek    -0.090
    addmsg /proto/cell /proto/cell/GABA VOLTAGE Vm
    addmsg /proto/cell/GABA /proto/cell CHANNEL Gk Ek
end
```

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Index of GENESIS Commands

Index of GENESIS Objects

Index