The hoc programming language

Based on Kernighan and Pike's "high-order calculator"

Used in

- most published NEURON models
- most NEURON models currently under development
- almost all NEURON models currently available from ModelDB
- NEURON's standard run system and GUI tools
 UNIX / Linux / OS X: nrnxx/share/nrn/lib/hoc
 MSWin: nrnxx\lib\hoc

Where to learn more:

- Programmer's Reference link at http://www.neuron.yale.edu/neuron/
- The NEURON Book (especially chapters 12 and 13), papers about NEURON
- standard run system and GUI tools
- session files, hoc code exported from CellBuilder, Network Builder
- your own programming experiments

Kernighan and Pike's hoc: scalars, arrays, strings, procedures, functions

NEURON adds:

Domain-specific features

- -- specification of model properties (geometry, topology, biophysics)
- -- event delivery system for synaptic connections, artificial spiking cells, and simulation flow control
- -- selection of numerical integration method
- -- elementary initialization and simulation execution
- -- parallel simulation of cell and/or network models

Objects

-- built-in and user-specified classes

Graphics

- -- interactive plots of variables vs. time, distance ("space plot") or another variable (phase plane)
- shape plots (2D renderings of 3D shapes, may show a variable in false color)
- -- customizable GUI for building, analyzing, and using models

And it's

- extendable via NMODL, Channel Builder
- Interoperable with Python

Starting

UNIX / Linux / OS X / MSWin via the rxvt terminal nrniv at the system prompt

OS X / MSWin double click on the nrngui icon

Result:

bash-4.1\$ nrniv

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oc>

Stopping and exiting

Stopping runaway code

^C halts execution "safely"
^C^C halts "immediately"

Exiting hoc

Getting code into NEURON

Built-in microemacs

oc>em starts it
See em in the Programmer's Reference, and
http://www.neuron.yale.edu/neuron/static/docs/help/emacs.txt

Program files

Plain text (ASCII)

OS X: drag & drop hoc file onto nrngui icon

MSWin: double click on hoc file in Windows Explorer

If NEURONMainMenu toolbar ("NMM") exists

NMM / File / load hoc or NMM / File / load session

xopen("filename") reads filename on every call

load_file("filename") reads filename only once per session

Interactive code entry

Type commands at the oc> prompt

Interactive code entry

Particularly useful for

- revising and debugging small chunks of code
- using "toy examples" to understand hoc syntax

Keyboard arrow keys:

 \uparrow goes back in command history ("recalls commands"), \downarrow goes forward \leftarrow , \rightarrow moves cursor by 1 character, \uparrow by 1 word

EMACS-style cursor control:

^P goes back in command history, ^N forward

^A moves cursor to line start, ^E to end

^B moves back 1 character, ^F forward

esc B moves back 1 word, esc F forward

^K kills to end of line and copies to buffer, ^Y pastes from buffer

Basic hoc syntax

Similar to C but no semicolons

Numbers

Numeric values are double precision floating point.

Interpreter

(user input **bold**): Remarks:

oc>**1+0.2** note immediate evaluation

1.2

oc>1e-3 scientific notation

0.001

oc>1E-3

0.001

oc>**PI** a built-in variable

3.1415927 (treat it like a constant)

User-created names

May refer to

- a number ("ordinary" variable or "scalar")
- an array of numbers
- a string
- a function or procedure
- a class ("template")
- an object reference

Naming rules

- start with an alpha character [A-Za-z]
- contain alphanumeric characters or underscore _ [A-Za-z0-9_]
- < 100 characters long
- must not conflict with keywords or built-in functions
 - --see Programmer's Reference entries on keywords-general, functions-general, keywords-neuron, and functions-neuron
- scope is global except for
 - --variables declared local in a procedure or function
 - --variables declared in a template "visibility" (public / private)

Create a scalar by assigning a value to a new name.

Anything that isn't a scalar must be defined before use.

```
oc>double y[3]
oc>for i=0,2 y[i]=sqrt(i)
oc>for i=0,2 print y[i]
0
1
1.4142136

oc>strdef hello
oc>hello="hi"
oc>hello
hi
```

Notes:

- indices start at 0
- if *name* is an array, *name* is a shortcut for *name*[0]

```
oc>print y
0
```

A defined name cannot be redefined as something else.

```
oc>strdef y
/usr/local/nrn/i686/bin/nrniv: y already declared
 near line 31
 strdef v
oc>proc hello() { print "hi" }
/usr/local/nrn/i686/bin/nrniv: syntax error
 near line 32
 proc hello() { print "hi" }
          Λ
However, the body of a proc or func can be changed.
oc>proc foo() { print x^3 }
oc>foo()
8
oc>proc foo() { print x, exp(-x) }
oc>foo()
2 0.13533528
```

Expression: a combination of numbers, variables, operators, and functions that, when "executed," produces ("returns") a value of some type (number, string, object class).

```
1
x+2
sin(PI*0.4)
```

Statement: contains one or more expressions

```
Simple statements
  x=3 // assignment statement
  xopen("cell.hoc") // function call
```

Compound statements

```
{ a=5 b=sqrt(a) } // works, hard to read
{ // one statement/line is better
  a=5
  b=sqrt(a)
}
if (x<1) print "tiny" else print "big"</pre>
```

Program: a sequence of one or more statements

Statements that span multiple lines

Interactive code entry:

Comments

```
// a one-line comment
/* another way to comment */
/* a comment
that spans two
or more lines */
```

Indentation

Do whatever you like, but make it readable.

```
{
    x = 5.1
    y = sqrt(3)
    print x*y
}
is better than
    { x = 5.1 y = sqrt(3) print x*y }
```

Operator precedence

operator	example	comment
()	2*(x+0.1)	grouping
Λ	x^2	exponentiation
- !	-3, !x	unaryminus, not
* / %	5%3	multiply, divide, remainder
+ -		add, subtract
> >= < <= != ==	x==2	logical comparison
&&	(x>1) && (x<2)	AND
	(x<0) (x>1e6)	OR
=	x=2	assignment

Assignment statements

$$x = expression$$

Two shortcuts:

$$x += a$$
 same as $x = x+a$

$$x *= a$$
 same as $x = x*a$

Note: no space between + and =, or * and =

Logical expressions and comparisons

Problem: roundoff error.

Does x^2 equal 2?

4.4408921e-16

How to deal with this?

float_epsilon sets the threshold for deciding equality/inequality

So even though roundoff error makes sqrt(2)^2 - 2 nonzero,

Flow control

```
if (expr) stmt
if (expr) stmt1 else stmt2
while (expr) stmt
for (stmt1; expr2; stmt3) stmt
for var = expr1, expr2 stmt
for iterator_name ( . . . ) stmt
Examples:
i = 0
while (i<10) { i+=1 print i }
for (i=0; i<10; i+=1) print i
for i=0,9 print i
```

What if you typed = when you meant == ?

... and it really will be 3.

Why? Assignment inside () returns a value oc>(x=3)
3

if (number) treats a nonzero number as "true"

Flow control: iterator

```
// this is included in stdlib.hoc
iterator case() { local i
  for i=2, numarg() {
    $&1 = $1
    iterator_statement
// next line requires scalar x to exist
for case(&x, 1, -1, E, R) print x
produces this output:
1
-1
2.7182818
8.31441
oc>
```

Functions and procedures

Arguments to funcs and procs

- scalars, strings or objects
- retrieved by position

	Name of <i>n</i> th	
Variable type	argument	Call by
scalar	\$ <i>n</i>	value
scalar pointer	\$& <i>n</i>	reference
string	\$s <i>n</i>	reference
object reference	\$o <i>n</i>	reference

```
Example: scalar and string as arguments
oc>proc printerr() { print "Error ", $1, "-- ", $s2 }
oc>printerr(3, "file not open")
Error -- file not open
Example: updating and reporting a count. Note call by reference.
  tally=0
  proc count() {
    $&2+=1 // affects arg 2
    print $s1, $&2
  for i=0,2 count("updated count--", &tally)
produces this result:
  updated count--1
  updated count--2
  updated count -- 3
```

Local variables

- temporary--exist only while the proc or func is executed
- scope is local to the proc or func,
 no conflict with globals that have the same names

Declare as part of the proc *name* { line.

```
i=10
proc squares() { local i
   for i=1,$1 print i*i
}
squares(3)
print "i is ", i
produces this result:
1
4
9
i is 10
```

Classes, objects, and object references in hoc

Class: a type or category.

Object: a specific instance of a type.

Object reference: a label or alias for an object,

not the object itself. Similar to pointer.

In hoc there are no "free-standing" objects.

- If an object exists, there must also be an objref that refers to it.
- If an object's reference count drops to 0, the object is destroyed.

Creating and destroying an object

```
oc>objref cells // make new objref
oc>cells
       NULLobject
oc>cells = new List() // make new List object
OC>
                     // and associate cells with it
oc>cells
                     // verify
       List[8]
                     // just making sure . . .
oc>List[8]
       List[8]
oc>objref b // make another objref
oc>b
       NULLobject
oc>b = cells
                     // associate b with the same List object
                     // verify the association
oc>b
       List[8]
```

```
oc>objref b
                      // break link between b and List[8]
oc>b
                      // verify
        NULLobject
oc>cells
                      // make sure cells is still associated
        List[8]
oc>objref cells // break link between cells and List[8]
oc>cells
                      // verify
        NULLobject
oc>// the List's reference count should now be 0
                     // does the object still exist?
oc>List[8]
/usr/local/nrn/i686/bin/nrniv: Object ID doesn't exist: List[8]
near line 15
List[8]
        Λ
```

Using an objref as an argument

```
func totalarea() { local tmp
   tmp = 0 // clear any leftover value
   for $01.all for (x,0) tmp += area(x)
   return tmp
}
print "total area of ", cell, "is ", totalarea(cell)
```

Using call by reference to modify an object

```
proc scalediam() {
  for $01.all diam *= $2
}
scalediam(cell, 2) // doubles diam of cell's sections
```

obfunc: a function that returns an object

```
// creates customized Graph that plots user-specified variable vs. time
             name of variable to be plotted
// $s1
// $2 and $3 y axis min and max
// $4 and $5 screen coordinates of left upper corner
// $6 and $7 graph width and height
// assumes standard run system, so tstop and graphList[0] exist
GWIDTH=300.48 // default width and height of entire graph
GHEIGHT=200.32
obfunc makegraph() { localobj gtmp
  gtmp = new Graph(0) // creates but does not display
  gtmp.size(0,tstop,$2,$3) // axis scaling
  gtmp.view(0, $2, tstop, $3-$2, $4, $5, $6, $7) // draws on the screen
    // with user-specified location and size
  graphList[0].append(gtmp) // so it updates at integer multiples of dt
  gtmp.addexpr($s1, 1, 1, 0.8, 0.9, 2)
 return atmp
obiref a
g = makegraph("soma.v(0.5)", -80, 40, 300, 150, GWIDTH, GHEIGHT)
```

Comment: note use of localobj

Analyzing a program

Understanding how existing programs work is key to

- debugging and maintenance
- modifying them to handle other tasks
- learning by example

Case study: a hoc file generated by the CellBuilder Aims:

- discover how the program works
- identify the programming tactics and strategies that are used in it

cell.hoc part 1 of 2

```
proc celldef() {
  topol()
  subsets()
  geom()
  biophys()
  geom_nseg()
create soma, dend
proc topol() { local i
  connect dend(0), soma(1)
  basic_shape()
proc basic_shape() {
  soma {pt3dclear() pt3dadd(0, 0, 0, 1) pt3dadd(15, 0, 0, 1)}
  dend {pt3dclear() pt3dadd(15, 0, 0, 1) pt3dadd(90, 0, 0, 1)}
}
objref all
proc subsets() { local i
  objref all
  all = new SectionList()
    soma all.append()
    dend all.append()
}
```

cell.hoc part 2 of 2

```
proc geom() {
  forsec all { }
  soma { L = 10 \text{ diam} = 10 }
  dend { L = 1000 \text{ diam} = 1 }
proc geom_nseg() {
  forsec all \{ nseg = int((L/(0.1*lambda_f(100))+.999)/2)*2 + 1 \}
}
proc biophys() {
  forsec all {
    cm = 1
  soma {
    insert hh
      gnabar_hh = 0.12
      gkbar_hh = 0.036
      gl_hh = 0.0003
      el hh = -54.3
  dend {
    insert pas
      g_pas = 0.0001
      e_pas = -65
access soma
celldef()
```

```
The first thing the hoc interpreter encounters
proc celldef() {
  topol()
                          when it reads cell.hoc: a procedure definition.
  subsets()
                          None of the statements in celldef() will do
  geom()
                          anything until some other statement is
  biophys()
                          executed that calls it.
  geom_nseg()
                          Will that ever happen? Remains to be seen.
create soma, dend
proc topol() { local i
  connect dend(0), soma(1)
  basic shape()
proc basic_shape() {
  soma {pt3dclear() pt3dadd(0, 0, 0, 1) pt3dadd(15, 0, 0, 1)}
  dend {pt3dclear() pt3dadd(15, 0, 0, 1) pt3dadd(90, 0, 0, 1)}
}
objref all
proc subsets() { local i
  objref all
  all = new SectionList()
    soma all.append()
    dend all.append()
}
```

```
proc celldef() {
  topol()
  subsets()
  geom()
  biophys()
  geom_nseg()
}

create soma, dend
```

The first statement in cell.hoc that is actually executed. Time to start building an outline.

```
proc topol() { local i
   connect dend(0), soma(1)
   basic_shape()
}
proc basic_shape() {
   soma {pt3dclear() pt3dadd(0, 0, 0, 1) pt3dadd(15, 0, 0, 1)}
   dend {pt3dclear() pt3dadd(15, 0, 0, 1) pt3dadd(90, 0, 0, 1)}
}
objref all
proc subsets() { local i
   objref all
   all = new SectionList()
      soma all.append()
      dend all.append()
}
```

We need a way to record our discoveries that is quick and easy to set up, and quick and easy to understand.

An outline that summarizes the sequence of program execution is sufficient for most cases.

create soma, dend

```
proc celldef() {
  topol()
  subsets()
  geom()
  biophys()
  geom_nseg()
create soma, dend
proc topol() { local i
                                 More procedure definitions.
  connect dend(0), soma(1)
                                 Skip them for now--we're looking for
  basic_shape()
                                 the next statement that is executed.
proc basic_shape() {
  soma {pt3dclear() pt3dadd(0, 0, 0, 1) pt3dadd(15, 0, 0, 1)}
  dend {pt3dclear() pt3dadd(15, 0, 0, 1) pt3dadd(90, 0, 0, 1)}
}
objref all
proc subsets() { local i
  objref all
  all = new SectionList()
    soma all.append()
    dend all.append()
}
```

```
proc celldef() {
  topol()
  subsets()
  geom()
  biophys()
  geom_nseg()
create soma, dend
proc topol() { local i
  connect dend(0), soma(1)
  basic_shape()
proc basic_shape() {
  soma {pt3dclear() pt3dadd(0, 0, 0, 1) pt3dadd(15, 0, 0, 1)}
  dend {pt3dclear() pt3dadd(15, 0, 0, 1) pt3dadd(90, 0, 0, 1)}
}
objref all
proc subsets() { local i
  objref all
                                 add it to the outline.
  all = new SectionList()
    soma all.append()
```

dend all.append()

}

Not very exciting--just a declaration of what kind of variable all is--but let's

And skip the definition of proc subsets(); we're still looking for the next instruction that is executed.

The updated outline.

create soma, dend
objref all

```
proc geom() {
  forsec all { }
                                       Three more procedure definitions.
  soma { L = 10 \ diam = 10 \ }
                                       For now, jump over these . . .
  dend { L = 1000 \text{ diam} = 1 }
proc geom_nseg() {
  forsec all \{ nseg = int((L/(0.1*lambda_f(100))+.999)/2)*2 + 1 \}
proc biophys() {
  forsec all {
    cm = 1
  soma {
    insert hh
      gnabar_hh = 0.12
      gkbar_hh = 0.036
      gl_hh = 0.0003
      el hh = -54.3
  dend {
    insert pas
      g_{pas} = 0.0001
      e_{pas} = -65
access soma
               to this bonanza--two executed statements in a row!
               The pace quickens . . .
celldef()
```

The latest version of the outline.

```
create soma, dend
objref all
access soma
celldef()
```

We have to examine proc celldef() to find out what happens next.

```
proc celldef() {
                     celldef() makes a lot of things happen.
  topol()
  subsets()
                     Let's add these to our outline.
  geom()
  biophys()
  geom_nseg()
}
create soma, dend
proc topol() { local i
  connect dend(0), soma(1)
  basic shape()
proc basic_shape() {
  soma {pt3dclear() pt3dadd(0, 0, 0, 1) pt3dadd(15, 0, 0, 1)}
  dend {pt3dclear() pt3dadd(15, 0, 0, 1) pt3dadd(90, 0, 0, 1)}
}
objref all
proc subsets() { local i
  objref all
  all = new SectionList()
    soma all.append()
    dend all.append()
}
```

celldef() really expands the outline-look at all the procs it calls:

Next we examine each of these five procs to see what they do, and discover if they call any other procs or funcs.

```
proc celldef() {
                      Working our way through proc celldef() . . .
  topol()
  subsets()
                      First it calls topol()
  geom()
  biophys()
  geom_nseg()
create soma, dend
                               topol() sets up the topology of the model,
proc topol() { local i
                               then calls basic_shape().
  connect dend(0), soma(1)
                               Time to revise the execution outline again.
  basic_shape()
                               An aside: why is there an unused local i?
proc basic shape() {
  soma {pt3dclear() pt3dadd(0, 0, 0, 1) pt3dadd(15, 0, 0, 1)}
  dend {pt3dclear() pt3dadd(15, 0, 0, 1) pt3dadd(90, 0, 0, 1)}
}
                               basic_shape() specifies how the model
objref all
                               would look in a CellBuilder.
proc subsets() { local i
                               Note the use of "section stack" syntax to
  objref all
                               specify the currently accessed section.
  all = new SectionList()
                               Also note the compound statements.
    soma all.append()
    dend all.append()
                               Will soma length and diameter really be
}
                               15 um and 1 um, respectively?
```

The revised outline.

```
create soma, dend
objref all
access soma
celldef()
  topol()
   basic_shape() indented because called by topol()
  subsets()
  geom()
  biophys()
  geom_nseg()
```

Next we examine subsets()

```
proc celldef() {
  topol()
  subsets()
  geom()
  biophys()
  geom_nseg()
create soma, dend
proc topol() { local i
  connect dend(0), soma(1)
  basic_shape()
proc basic shape() {
  soma {pt3dclear() pt3dadd(0, 0, 0, 1) pt3dadd(15, 0, 0, 1)}
  dend {pt3dclear() pt3dadd(15, 0, 0, 1) pt3dadd(90, 0, 0, 1)}
}
                              So this is where the various subsets
objref all
                              (SectionLists, actually) are assembled.
proc subsets() { local i
                              Why is it useful to execute objref all
  objref all
  all = new SectionList()
                              inside this proc?
    soma all.append()
                              Why not just do objref all at the top level
    dend all.append()
                              of the interpreter (i.e. outside of any proc
}
                              or func or object), and be done with it?
```

```
proc celldef() {
  topol()
  subsets()
  geom()
  biophys()
 geom_nseg()
                                    geom() specifies the lengths and diameters
                                    of the model's sections.
                                    Also, more examples of section stack syntax
proc geom() {
                                    to specify the currently accessed section.
  forsec all { }
                                   Why is there a forsec all { }
  soma { L = 10 diam = 10 }
  dend { L = 1000 diam = 1 } that doesn't do anything?
proc geom_nseg() {
 forsec all \{ nseg = int((L/(0.1*lambda_f(100))+.999)/2)*2 + 1 \}
proc biophys() {
  forsec all {
    cm = 1
  soma {
```

```
proc celldef() {
  topol()
                        Hmm. geom_nseg() is defined before biophys(),
  subsets()
  geom()
                        but biophys() is called before geom_nseg().
  biophys()
                        Why is that?
  geom_nseg()
}
proc biophys() {
  forsec all {
                           More section stack syntax.
    cm = 1
                           Applying it to a bunch of statements grouped by { }
  soma {
                           saves a lot of typing.
    insert hh
      gnabar_hh = 0.12
      gkbar_hh = 0.036
      gl_hh = 0.0003
      el hh = -54.3
  dend {
    insert pas
      g_{pas} = 0.0001
      e_pas = -65
```

The complete outline.

```
create soma, dend
objref all
access soma
celldef()
  topol()
    basic_shape()
  subsets()
  geom()
  biophys()
  geom_nseg()
    lambda_f()
```

So what can you do now?

Change

- number and names of sections
- model topology
- section geometry
- section biophysics
- discretization strategy

Analyze

- other code generated by the CellBuilder or other GUI tools, e.g. cell classes exported from the CellBuilder, network models exported from the Network Builder
- ses files saved from the GUI, e.g. the RunControl panel
- code mined from the hoc library (not just stdlib.hoc and stdrun.hoc) to discover how to create special-purpose GUI tools and solve more complex problems.

Practical suggestions

Strategy: design programs to have a modular structure. Code that consists of short, relatively simple procedures or functions is easier to develop, debug, and understand.

Tactics: before writing any code, write an outline that breaks the task into manageable steps. Any step that requires more than a couple of statements is a candidate for implementing as a proc or func.

In retrospect, proc celldef() was pretty close to being the outline of cell.hoc