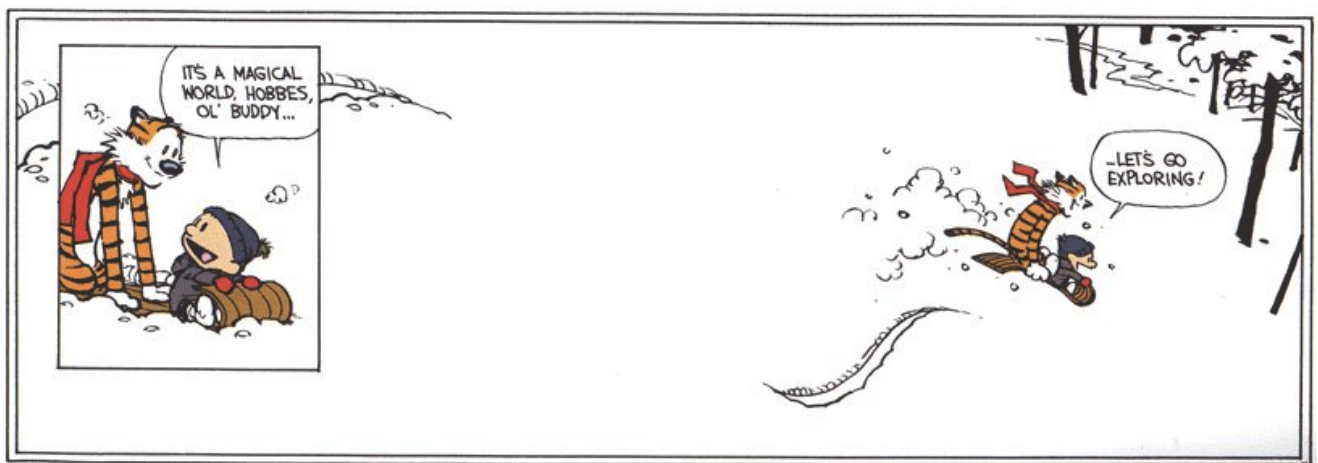


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Exciting catch phrase!

Alternative Title

Author | Subtitle

Thanks

To someone.

Began: July 16, 2012
Updated: March 23, 2013

Table of Contents

Part I	2
Intro Examples	3
Citations	4
El mundo real	4
Lists	5
Lists	5
Terms	5
Code	6
R	6
FASTA	12
FASTA	12
Problems	13
Problems	13
Equations	14
Equations	14
End of Preview	15
Appendix	16
Table	17
Figures	18
References	21
Index	22

Figures

1	Exciting catch phrase!	1
2	Figure 2 Native Americans (a) Pueblo Bonito was an.... (b) Located in Peru. (c) The different type of game hunted in the Americas. (d) The cenote, which were seen as sacred by the Maya.	18
3	Figure 3 Map of Civilizations Discussed Image of the Americas with locations of the cultures discussed in the text. We start with the Algonquin and then discuss the Cahokia, Hisatsinom, Olmec, Maya, Aztec, Chavin, Inca, and Tehuelche.	19
4	Figure 4 Response regulation General concept of integrating temperature information and formulating a response.	20

Tables

1	Kidney Proteins	17
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Part I

Intro Examples

El mundo real

Lorem ipsum dolor sit amet (**Table 1**), consectetur adipiscing elit.⁵ Integer ut arcu risus. Etiam tincidunt aliquet quam nec dignissim (**Fig. 3**). Nam commodo nibh in dui volutpat molestie. Praesent elit dolor, congue in molestie id, ultricies quis leo. Nulla libero dolor, lacinia in vestibulum vestibulum, sagittis ut turpis. Quisque laoreet nisi ut nulla congue ut rhoncus mi imperdiet. **Etiam bibendum** mauris eget purus laoreet egestas.² Vivamus eget justo nec augue facilisis scelerisque. Aenean sit amet quam eget odio aliquet rutrum. Cras gravida, risus id volutpat vehicula, risus nibh malesuada nisi, at suscipit lorem sem eu est. Aenean sit amet arcu sed augue pulvinar aliquet in non urna. Donec tincidunt vehicula est at accumsan. Integer purus lacus, adipiscing eget dictum non, commodo non arcu. Donec adipiscing luctus massa, non placerat sem dignissim vitae. Pellentesque habitant morbi tristique senectus et netus et malesuada fames ac turpis egestas.^{1,9}

Nunc condimentum **Nunc condimentum** auctor tellus non porttitor.^{4,7} Quisque felis lorem, pellentesque sed sodales id, adipiscing sit amet lacus. Morbi et ultrices dui. Praesent consectetur tempor lorem, at luctus est suscipit in. Sed sapien turpis, accumsan eget laoreet nec, hendrerit sed neque. Proin vitae diam lectus, in ullamcorper nulla.⁸ Aenean sollicitudin odio eu metus auctor ut sodales neque semper. Maecenas bibendum, tellus eu consectetur pellentesque, magna metus convallis libero, a porttitor justo turpis nec dui.^{3,6}

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Lists

Example of making list automated, saving space and reducing errors.

Terms

endocrine chemicals <ul style="list-style-type: none">• proteins• steroid hormones• amine hormones• testosterone• insulin• thyroxine• epinephrine• tropic hormones• thyrotropin• luteinizing hormone• follicle-stimulating	chemicals <ul style="list-style-type: none">• hormone<ul style="list-style-type: none">• corticotropin• growth hormone• prolactin• melanocyte-stimulating hormone• enkephalins• endorphins• POMC• receptor tyrosine kinases<ul style="list-style-type: none">• dimerization• autophosphorylation• SH2 domains• EGFR• Ras• Raf• MEK• ERK• SOS• Sevenless• Drk/Grb2• Ras-GAP• Ras-GEF• cAMP• signal amplification• cGMP• guanylyl cyclase• phospholipids• calmodulin• protein-tyrosine phosphatase• serine/threonine kinase• intracellular signal transduction• NF-κB• IκB
---	--

R

Proposed pseudo-code for hierarchical neural networks.

Listing 1: hierarchical neural networks in R

```
# Load neural net library
library(nnet)
library(neuralnet)

# Load trained neural nets
source("model.training.NN.hierarchical.v1")
trainedNeuralNets = NNtrained()

# Load data
source("data.run.NN.hierarchical")
this.data = NNdata()

# define the number of loops before an error has occurred
error.loop.value = 3

neuralNet <- function(neuralNetFxn, this.loop.input){
  # this function runs specific level of a hierarchal neural network then
  # recursively calls the next layer
  # base case is defined when a parent neural net has no children

  # run the initial neural net on the input
  # classifications is a tuple of probabilities for being in given class
  list(classifications,subfunctions) := neuralNetFxn(this.loop.input)

  # set the threshold
  threshold = this.loop.threshold.value

  # get index of next neural net function to be called
  subidx = max(find.col(classifications>threshold))

  # each neural net function outputs a list of functions that can further be
  # called
  subfunctions = [...
    fearNN(),
    runNN(),
    thinkNN(),
    ...]
```

```

#
next.NN.fxn = subfunctions[[subidx]]

# base case, if no more children, exit loop, else
# recursively call the next neural network
if(next.NN.fxn(children=TRUE)){
    return(classifications,next.NN.fxn)
}else if(){
    neuralNet(next.NN.fxn,this.loop.input)
}
}

main <- function(inputData,trainedNeuralNets,run.count){
    # get root neural net by passing no argument to trained neural nets
    root.NN = trainedNeuralNets()

    # Run the neural net hierarchical function until reach end node
    list(classification, id.NN) := neuralNet(root.NN,inputData)

    # Check that we have reached a neural net without children, else call main()
    again
    if(id.NN(children=TRUE)&run.count<error.loop.value){
        main(inputData,trainedNeuralNets,run.count+1)
    }else if(){
        return(NULL)
    }

    # Let user know choice
    print(classification)

    # Return classification, used later if integrated into system
    return(list(classification,id.NN))
}

# start the program
main(this.data,trainedNeuralNets,run.count=0)

```

A playlist maker for python, see more concise implementation in bash.

Listing 2: python playlist maker

```

#!/Python27/env python
#Biafra Ahanonu
#2012.12.02

#Makes .m3u extended playlist at first level folders in a directory

```

```

#Modules used
import os,re,time
#Import settings from settings.py
from settings import *
#Help filter out duplicates
from sets import Set

def folderBrowser():
    #Opens a folder
    import Tkinter, tkFileDialog
    root = Tkinter.Tk()
    root.withdraw()
    dir =
        tkFileDialog.askdirectory(parent=root,initialdir=DEFAULT_DIR,title='Please
        select a directory')
    return dir

def fileTree(dir,relDir):
    #Crawls through a directory and finds audio files, returns list of files
    print dir

    #Variable to save files to
    filesToSave = []

    #Valid mp3 files
    validFiles = set(VALID_AUDIO_FORMATS)

    #Crawl through directory
    for dirname, dirnames, filenames in os.walk(dir):

        #Crawl through each directory in a folder
        for subdirname in dirnames:
            #Next level relative path
            relDir2 = os.path.join(relDir,subdirname)

            #Evaluate each file in directory, if audio, add to playlist
            for filename in os.listdir(os.path.join(dir,subdirname)):
                #If there is an intersection, means valid extension, add
                to playlist
                if validFiles.intersection(set(filename.split('.'))):
                    filesToSave.append(os.path.join(relDir2,filename))

            #Recursion here
            #After finding all file in a subdirectory, crawl through its
            folders

```

```

        filesToSave=filesToSave+fileTree(os.path.join(dir,subdirname),relDir2)

#Finally, get files in root directory, see above for explanation of
    details
    for filename in os.listdir(os.path.join(dir,'')):
        if validFiles.intersection(set(filename.split('.'))):
            filesToSave.append(os.path.join(relDir,filename))

#Break the loop so we don't crawl through subdirectories and add
    playlists there
    break

#Return files found
    return filesToSave

def saveFilesToPlaylist(files,dir,dirname,CURRENT_DIR):
    #Saves a list of files to a playlist

    #Open connection, uses root as name for playlist
    try:
        playlist =
            open(os.path.join(CURRENT_DIR,dirname,dirname+PLAYLIST_ID_TAG+'.m3u'),'w')
    except Exception, e:
        return

    #Output playlist location
    print os.path.join(CURRENT_DIR,dirname,dirname+PLAYLIST_ID_TAG+'.m3u')

    #Extended M3U format used here
    if EXTENDED_M3U == 1:
        playlist.write('#EXTM3U\n')

    #Remove duplicates
    files = sorted(set(files))

    #Loop through each file
    for filename in files:
        if EXTENDED_M3U == 1:
            actualFilename = os.path.basename(filename)
            #Split then rejoin, remove extension
            filenameName = actualFilename.split('.')
            filenameName = '.'.join(filenameName[0:-1])
            #Add name based filename
            try:
                playlist.write('#EXTINF:'+filenameName+'\n')
            except Exception, e:
                continue

```

```

        #Write relative location of file
        playlist.write(os.path.join(filename)+'\n')

    #Close file id
    playlist.close()

def main():
    #Ask user for folder
    dir = folderBrowser()
    #If no folder given, use default
    CURRENT_DIR = dir or DEFAULT_DIR
    #Print the current directory
    print CURRENT_DIR

    #Log all the playlist created
    logFileName = os.path.basename(CURRENT_DIR)
    logFile = open(logFileName+'.log','w')

    #Change to directory
    os.chdir(CURRENT_DIR)

    #Walk along each first level folder in directory
    for dirname, dirnames, filenames in os.walk('.'):
        print dirname
        for subdirname in dirnames:
            #Basename of the current directory
            dirnameTitle = os.path.basename(subdirname)

            #Get all files under first level folder
            filesToSave = fileTree(subdirname, '')

            #Save files to playlist, using top-most folder
            saveFilesToPlaylist(filesToSave, subdirname, dirnameTitle, CURRENT_DIR)

            #Add playlist to log
            logFile.write(os.path.join(CURRENT_DIR, dirnameTitle, dirnameTitle+PLAYLIST))

        #Break the loop so we don't crawl through subdirectories and add
        #playlists there
        break

    #Close connection to log file
    logFile.close()

#We are in main, run
if __name__ == '__main__':

```

```
main()
```

FASTA

Example use of the fasta formatting for protein sequences.

FASTA sequences

D₁a dopamine receptor | Homo sapiens | Humans

```
MRTLNTSAMDGTLVVERDFSVRLTACFLSLILSTLLGNTLVCAAVIRFRHURSKVTNFFVISLAVSDLLVAVLMPWKAVAEIAGFWPFGSFCNIWVAFDIMCSTASILNLCVISVDRYWAISSPFRYERKMTPKAAFILI  
SVAWTLISVLSFIPVQLSWHKAKPTSPSDGNATSLAETIDNCDSSLSRTYAISSSVISFYIPVAIMIVTYTRIYRIAGKQIRRIAALERAADVHAKNCCQTTTGNGKPVCECSQPESSEFKMSFKRETKVLKTLNVIMGVFVCCWL  
PFFILNCILPFCGSGETQPFCDISNTFDVFWVFGWANSSLNPIYAFNADFRKAFSTLLGCYRLCPATNNAIETVSINNINGAAMFSSHHEPRGSISKECNLVYLIPHAVGSSDLKKEEAAGIARPLEKLSVALSVILDYD  
TDVLSLEKIQPITQNGQHPT
```

Problems

If there is any confusion about the questions, shoot me an email or talk to me after class.

1. Look at (Fig. ??), why is the heart rate of the iguana different at the same temperature?
In the first case the body temperature is decreasing while in the second case the iguana raises its heart rate to increase blood flow, which leads to increased body temperature.
2. How does increasing heart rate while in direct sunlight help warm the body? More blood can flow to the skin and be warmed.
3. What does it mean for the Q10 of the metabolic rate of an animal to be 2? To be 1? the animal consumes half as much oxygen per hour at 20C as it does at 30C. In the case of 1, it doesn't change.

Equations

Example of several equations chosen at random from different works. Illustrates the use of the **lbpeq** macro.

$$E = \frac{1}{2} \sum_{q=1}^n \sum_{k=1}^K [y_k(x^q, w) - t_k^q]^2 \tag{1}$$

$$y_j(x) = \sum_{i=0}^n w_{i,j} \phi(x)_i \tag{2}$$

$$\phi(x)_i = \exp(-\frac{x - \mu_i^2}{2\omega_i^2}) \tag{3}$$

$$M + Q_{abs} = \epsilon \sigma T_r^4 + h_c(T_r - T_a) + E + C \tag{4}$$

End of Preview

Appendix

Additional figures and tables are included. References and index found at the end.

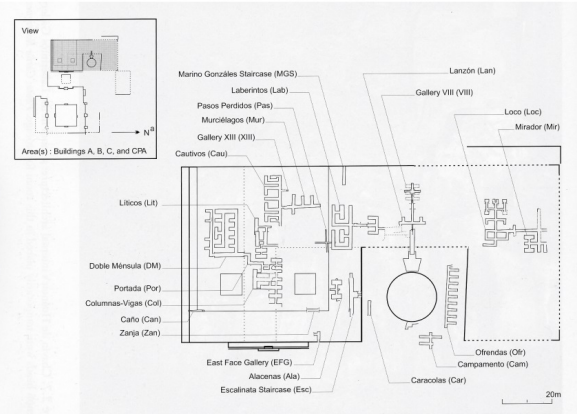
Name	Type	%Δ	Onset	Localization
YAP	protein	60	E18	Nuclear->Cytoplasm
Hippo	protein	40	E18	Cytoplasm
agmatine	metabolite	20	?	Ex->Cytoplasm
Lim1	protein	-50	E9.5	Cytoplasm
FoxC1/2	protein	-10	E11.5	Cytoplasm

Table 1 | Hypothetical list of kidney proteins and metabolites These were identified after removal of housekeeping and injury genes. %Δ is protein or metabolite level change from **onset** to cessation of kidney growth. Onset time is part hypothetical, part from the literature.

Figures



(a) fig



(b) fig



(c) fig



(d) fig

Figure 2 | Native Americans

(a) Pueblo Bonito was an.... (b) Located in Peru. (c) The different type of game hunted in the Americas. (d) The cenote, which were seen as sacred by the Maya.

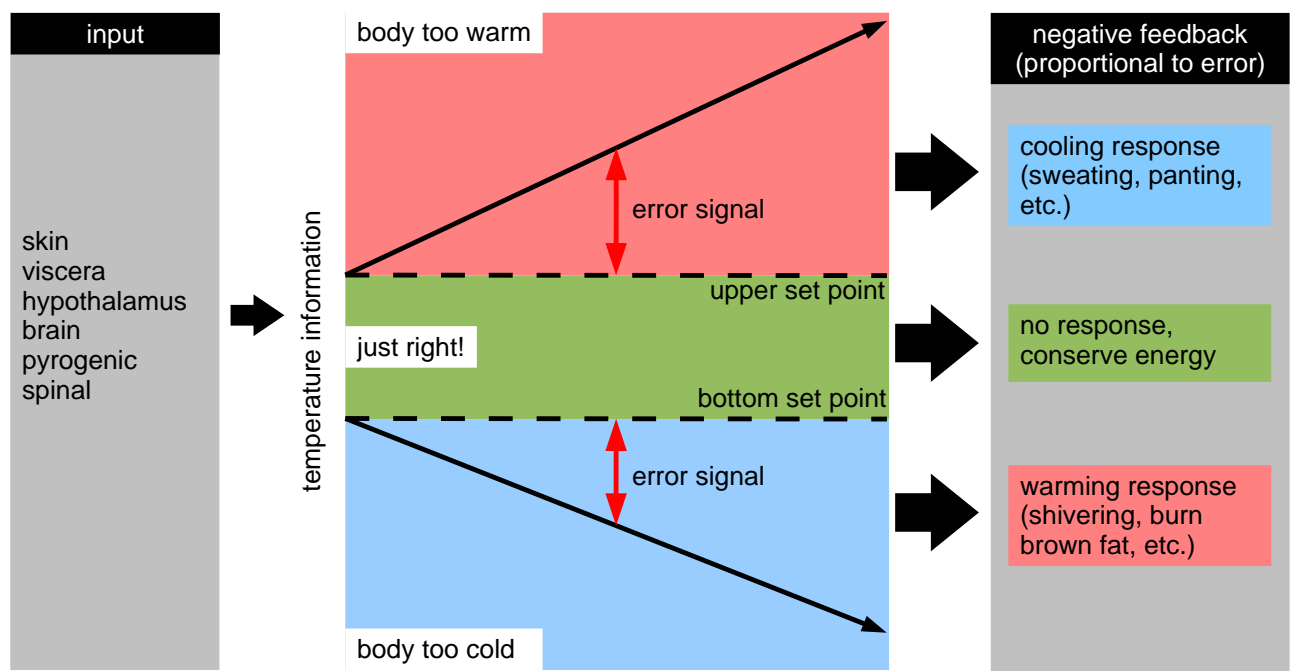


Figure 4 | Response regulation

General concept of integrating temperature information and formulating a response.

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-
- amine hormones, 5
 - autophosphorylation, 5
 - calmodulin, 5
 - cAMP, 5
 - cGMP, 5
 - corticotropin, 5
 - dimerization, 5
 - Drk/Grb2, 5
 - EGFR, 5
 - El mundo real, 4
 - endorphins, 5
 - enkephalins, 5
 - epinephrine, 5
 - Equations, 14
 - ERK, 5
 - Etiam bibendum, 4
 - FASTA, 12
 - follicle-stimulating hormone, 5
 - growth hormone, 5
 - guanylyl cyclase, 5
 - I κ B, 5
 - insulin, 5
 - intracellular signal transduction, 5
 - Lists, 5
 - Lorem ipsum, 4
 - luteinizing hormone, 5
 - MEK, 5
 - melanocyte-stimulating hormone, 5
 - metabolite, 17
 - NF- κ B, 5
 - Nunc
 - Nunc condimentum, 4
 - phospholipids, 5
 - POMC, 5
 - Problems, 13
 - prolactin, 5
 - protein-tyrosine phosphatase, 5
 - proteins, 5
 - R, 6
 - Raf, 5
 - Ras, 5
 - Ras-GAP, 5
 - Ras-GEF, 5
 - serine/threonine kinase, 5
 - Sevenless, 5
 - SH2 domains, 5
 - signal amplification, 5
 - SOS, 5
 - steroid hormones, 5
 - Terms, 5
 - testosterone, 5
 - thyrotropin, 5
 - thyroxine, 5
 - tropic hormones, 5