The Best Thesis Anyone Has Ever Seen

by

Greggory H. Rothmeier

A Thesis Submitted in Partial Fulfillment of the Requirements for the Degree of

Masters of Science

in the College of Arts and Sciences

Georgia State University

2012

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Greggory H. Rothmeier

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Committee:	Mukesh Dhamala
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Dedication

Mama.

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Date

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Dick Miller
Department Chair

Chapter 1

Introduction

Chapter 2

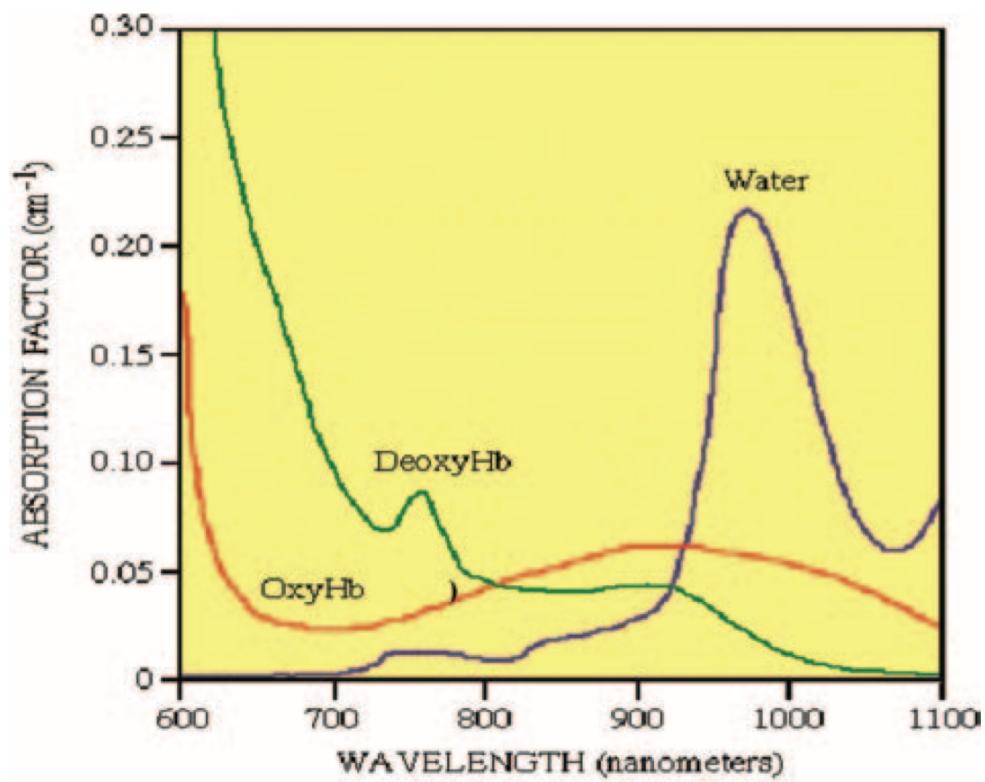# Functional Near-Infrared Spectroscopy (fNIRS)

Figure 2.1: Absorption spectra of water, Hb and Dhb. From [1] and [3]

Chapter 3

Calculating Temperature Changes using fMRI BOLD Response

Lorem ipsum dolor sit amet, consectetur adipiscing elit. Nullam felis justo, consequat vel semper eu, bibendum sed lectus. Fusce ultricies mi sit amet ante imperdiet eget posuere turpis volutpat. Nulla facilisi. Nulla convallis, erat et mattis bibendum, nunc velit tincidunt nisl, ac luctus massa tellus nec lectus. Pellentesque habitant morbi tristique senectus et netus et malesuada fames ac turpis egestas. Nam at venenatis sapien. In vel tortor dapibus tortor porta aliquam a sit amet diam. Nullam feugiat dignissim scelerisque. Donec rhoncus sapien eget lacus eleifend vitae adipiscing arcu mollis. Donec vel tincidunt nibh. Duis placerat scelerisque velit. Integer elementum nisl vel mi sollicitudin dictum non vel dolor. Cras consectetur consequat metus, a malesuada quam tincidunt vitae. Etiam fermentum metus nibh. Sed sollicitudin convallis faucibus. Nunc tincidunt ultricies orci, in aliquam purus interdum fermentum. [4]

3.1 What is BOLD

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3.2 What does BOLD have to do with Temperature?

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Chapter 4

Conclusion

Bibliography

[1] M Cope. The development of a near infrared spectroscopy system and its application for non invasive monitoring of cerebral blood and tissue oxygenation in the newborn infants. *London University*, 1991.

[2] Gigi Galiana, Rosa T. Branca, Elizabeth R. Jenista, and Warren S. Warren. Accurate temperature imaging based on intermolecular coherences in magnetic resonance. *Science*, 322(5900):421–424, 2008.

[3] B. L. Horecker. The absorption spectra of hemoglobin and its derivatives in the visible and near infra-red regions. *The Journal of Biological Chemistry*, 1942.

[4] Roberto C. Sotero and Yasser Iturria-Medina. From blood oxygen level dependent (bold) signals to brain temperature maps. *Bulletin of Mathematical Biology*, 73(11):2731–2747, 2011.

Calculating the Temperature Change

```matlab
function temperatureOut = tempCalcChangingMetabolismFlow(tissue,bloodT,
    airT,nt,tmax,pastCalc,start,stop,amplitudeMet,amplitudeFlow,region,
    savesteps)
% tempCalcChaning Metabolism  How does changin metabolism affect things?
%    tissue: holds all of the strucual information
%    bloodT: Temperature of the blood
%    airT:   Temperature of the surrounding ait
%    nt:      Number of time steps
%    tmax:    Total amount of time the simulation should run over
%
%    region: logical matrix same size as head
%    start:   units of steps
%    stop: units of steps
%
%    Writen by Greggory Rothmeier (greggroth@gmail.com)
%    Georgia State University Dept. Physics and Astronomy
%    May, 2011
%#codegen


%%   Default Values
if nargin<2,  bloodT = 37;         end
if nargin<3,  airT = 24;           end
if nargin<4,  nt = 3;              end
if nargin<5,  tmax = 1;            end
if nargin<6,  pastCalc = 0;        end   %  Voxel size (m)
if nargin<7,  start = 10;          end   %  in steps
if nargin<8,  stop = 20;           end   %  in steps
if nargin<9,  amplitudeMet = 1.2;  end   %  normalized
if nargin<10, amplitudeFlow = 1.2; end   %  normalized
if nargin<11, savesteps = 1;       end

```

```matlab
30
31   dx = 2*10^-3;
32   if nt<(2*tmax),
33       warning('Time step size is not large enough.  Results will be
            unreliable.  Consider increasing the number of steps or reducing
            tmax.')
34   end
35
36
37   % Constants used that aren't already stored in tissue
38   [xmax ymax zmax t] = size(tissue);
39   clear t;
40   dt = tmax/(nt-1);
41   % rhoBlood = 1057;
42   % wBlood = 1000;
43   % cBlood = 3600;
44
45   statusbar = waitbar(0,'Initializing');
46
47   %%  Maps
48   %   Creates a map that identifies where there is tissue
49   %   the condition squeeze(tissue(:,:,:,)~=airIndex picks out the elements
        that are
50   %   tissue
51
52   temperatureOut = ones(ceil((nt-1)/savesteps),xmax,ymax,zmax,'single');
53   temperature = ones(2,xmax,ymax,zmax,'single')*airT;
54   if pastCalc == 0
55       temperature(1,squeeze(tissue(:,:,:,1))~=1) = bloodT;
56   else
57       temperature(1,:,:,:) = pastCalc(end,:,:,:);
58       % temperature(1,:,:,:) = pastCalc;
```

```matlab
59  end
60  temperatureOut(1,:,:,:) = temperature(1,:,:,:);
61  metabMultiplier = ones([xmax ymax zmax],'single');
62  flowMultiplier = ones([xmax ymax zmax],'single');
63
64  %%  Do Work.
65  %   This is a vectorized version of the next section.  For the love of
        god
66  %   don't make any changes to this without first looking below to make
        sure
67  %   you know what you're changing.  This is [nearly] impossible to
68  %   understand, so take your time and don't break it.
69  %   data is stored in 'tissue' as such :
70  %   [tissuetype 0 Qm c rho k w];  <--  second element is blank for all.
71  %   [    1      2 3 4  5  6 7
72
73  %  This makes an array that has smoothed out variations in k by averaging
74  %  all of the k's around each voxel (including itself).  This is a
75  %  hap-hazard solution to the problem that if you only take the value of
        k
76  %  for the voxel without considering what surrounds it, it doesn't matter
77  %  whether the head is surrounded by air, water or anything else.  Since
78  %  water is a better thermal conductor than air, we need a way of
79  %  accounting for this.  This is one way:
80  averagedk = (circshift(tissue(:,:,:,6),[1 0 0])+circshift(tissue(:,:,:,6)
        ,[-1 0 0])+circshift(tissue(:,:,:,6),[0 1 0])+circshift(tissue(:,:,:,6)
        ,[0 -1 0])+circshift(tissue(:,:,:,6),[0 0 1])+circshift(tissue(:,:,:,6)
        ,[0 0 -1])+tissue(:,:,:,6))/7;
81  rhoblood = 1057;
82  cblood = 3600;
83
84  %%  Only saves every 4 steps
```

```matlab
85  tic
86  for t2 = 1:nt-1
87      waitbar(t2/(nt-1),statusbar,sprintf('%d%%',round(t2/(nt-1)*100)));
88      if (start<t2) && (t2<stop)   %  for __ steps
89          metabMultiplier(region) = amplitudeMet;   %  region is hardcoded
                here
90          flowMultiplier(region) = amplitudeFlow;
91      elseif t2==stop %  once the period is over, reset it back to ones
92          metabMultiplier(region) = 1;
93          flowMultiplier(region) = 1;
94      end
95
96      temperature(2,:,:,:) = squeeze(temperature(1,:,:,:)) + ...
97          dt/(tissue(:,:,:,5).*tissue(:,:,:,4)).* ...
98          ((averagedk/dx^2).*...
99          (circshift(squeeze(temperature(1,:,:,:)),[1 0 0])-2*squeeze(
               temperature(1,:,:,:))+circshift(squeeze(temperature(1,:,:,:))
               ,[-1 0 0])+...   % shift along x
100          circshift(squeeze(temperature(1,:,:,:)),[0 1 0])-2*squeeze(
               temperature(1,:,:,:))+circshift(squeeze(temperature(1,:,:,:))
               ,[0 -1 0])+...   % shift along y
101          circshift(squeeze(temperature(1,:,:,:)),[0 0 1])-2*squeeze(
               temperature(1,:,:,:))+circshift(squeeze(temperature(1,:,:,:))
               ,[0 0 -1]))...   % shift along z
102          -(1/6000)*rhoblood*flowMultiplier.*tissue(:,:,:,7)*cblood.*(
               squeeze(temperature(1,:,:,:))-bloodT)+metabMultiplier.*
               tissue(:,:,:,3));
103      %   resets the air temperature back since it's also modified above,
            but
104      %   it needs to be kept constant throughout the calculations
105      temperature(2,squeeze(tissue(:,:,:,1))==1) = airT;
106      temperatureOut(ceil(t2/savesteps),:,:,:) = temperature(2,:,:,:);
```

11

```
107     temperature (1,:,:,:) = temperature (2,:,:,:);  % moves 2 back to 1

108     end

109     close ( statusbar );

110     toc

111     %%  Keeps all of the data

112     %   Note: Make sure that temperature () has enough preallocated space

113     %{

114     tic

115     for t2 = 1: nt -1

116         %tic

117         waitbar ( t2 /( nt -1) , statusbar , sprintf ( '%d%%' , round ( t2 /( nt -1) *100) ) );

118         if ( start < t2 ) && ( t2 < stop )   %  for 10 steps

119             metabMultiplier ( region ) = amplitudeMet;    %  region is hardcoded
                    here

120             flowMultiplier ( region ) = amplitudeFlow;

121         elseif t2 == stop %  once the period is over , reset it back to ones

122             metabMultiplier ( region ) = 1;

123             flowMultiplier ( region ) = 1;

124         end

125         temperature ( t2 +1 ,:,:,:) = squeeze ( temperature ( t2 ,:,:,:) ) + ...

126             dt /( tissue (:,:,:,5) .* tissue (:,:,:,4) ).* ...

127             (( averagedk / dx ^2) .*...

128             ( circshift ( squeeze ( temperature ( t2 ,:,:,:) ) ,[1 0 0]) -2* squeeze (
                    temperature ( t2 ,:,:,:) )+ circshift ( squeeze ( temperature ( t2 ,:,:,:) )
                    ,[ -1 0 0]) +...  % shift along x

129              circshift ( squeeze ( temperature ( t2 ,:,:,:) ) ,[0 1 0]) -2* squeeze (
                    temperature ( t2 ,:,:,:) )+ circshift ( squeeze ( temperature ( t2 ,:,:,:)
                    ) ,[0 -1 0]) +...  % shift along y

130              circshift ( squeeze ( temperature ( t2 ,:,:,:) ) ,[0 0 1]) -2* squeeze (
                    temperature ( t2 ,:,:,:) )+ circshift ( squeeze ( temperature ( t2 ,:,:,:)
                    ) ,[0 0 -1]) )...  % shift along z
```

```matlab
131                -(1/6000)*rhoblood*flowMultiplier.*tissue(:,:,:,7)*cblood.*(
                      squeeze(temperature(t2,:,:,:))-bloodT)+metabMultiplier.*
                      tissue(:,:,:,3));
132        %   resets the air temperature back since it's also modified above,
              but
133        %   it needs to be kept constant throughout the calculations
134        temperature(t2+1,squeeze(tissue(:,:,:,1))==1) = airT;
135        %dispTimeLeft(1,1,nt-1,t2)
136    end
137    close(statusbar);
138    toc
139    %}

141    %% Old Code
142    %   This is what used to be used.  It's much slower (~60 times slower),
          but
143    %   it's much easier to understand compared to the above code.  If any
144    %   changes need to be made above, first look through this code to ensure
145    %   you understand what's happening before making changes.  It's really
          easy
146    %   to mess up the code above and nearly impossible to figure out where.

148    %   good luck.


151    %{
152    for t2 = 1:nt-1
153        for x2 = 2:xmax-1
154            for y2 = 2:ymax-1
155                for z2 = 2:zmax-1
156                    if tissue(x2,y2,z2,1) ~= 1,
```

```matlab
157                          temperature(t2+1,x2,y2,z2) = temperature(t2,x2,y2,z2)
                                + (dt/(tissue(x2,y2,z2,5)*tissue(x2,y2,z2,4)))*((
                                tissue(x2,y2,z2,6)/dx^2)*...
158                          (temperature(t2,x2+1,y2,z2)-2*temperature(t2,x2,y2,
                                z2)+temperature(t2,x2-1,y2,z2)+...
159                          temperature(t2,x2,y2+1,z2)-2*temperature(t2,x2,y2,
                                z2)+temperature(t2,x2,y2-1,z2)+...
160                          temperature(t2,x2,y2,z2+1)-2*temperature(t2,x2,y2,
                                z2)+temperature(t2,x2,y2,z2-1))...
161                          -(1/6000)*rhoBlood*wBlood*cBlood*(temperature(t2,x2
                                ,y2,z2)-bloodT)+tissue(x2,y2,z2,3));
162                      end
163                  end
164              end
165          end
166      end
167  %}
168
169
170  end
```

Calculating The Equilibrium Temperature