

**Fall 2006 Genomics Exam #2**  
**Sequence Variations and Microarrays**

There is no time limit on this test, though I don't want you to spend too much time on it. I have tried to design an exam that will take much less time than exams in the past. You do not need to read any additional papers other than the ones I send to you. There are 2 pages, including this cover sheet, for this test. You will have to answer 6 Discovery Questions and 2 original questions. I expect the original questions will take you more time than the Discovery Questions. You are not allowed discuss the test with anyone until all exams are turned in by 11:30 am on Monday October 30. **PAPER COPIES OF YOUR EXAM ANSWERS ARE DUE AT CLASS TIME ON MONDAY OCTOBER 30.** *I will be attending a meeting about a new science magnet high school, so please turn in your exams to my office/lab.* You may use a calculator, a ruler, your notes, the book, and the internet. You may take it in as many blocks of time as you want. Submit your paper and electronic versions before 11:30 am (eastern time zone:-).

The **answers to the questions must be typed in a Word file and emailed to me as an attachment.** Be sure to backup your test answers just in case (I suggest a thumb drive or other removable medium). You will need to capture screen images as a part of your answers which you may do without seeking permission since your test answers will not be in the public domain. Remember to explain your thoughts in your own words and use screen shots to support your answers. **Screen shots without *your* words are worth very few points.**

***DO NOT READ or DOWNLOAD ANY NEW PAPERS FOR THIS EXAM. RELY ONLY ON THE FIGURES PROVIDED IN THIS EXAM, YOUR EXPERIENCE, AND YOUR SKILLS.***

**-3 pts if you do not follow this direction.**

**Please do not write or type your name on any page other than this cover page.**

Staple all your pages (INCLUDING THE TEST PAGES) together when finished with the exam.

Name (please print):

Write out the full pledge and sign:

How long did this exam take you to complete (excluding typing)?

For this part of your exam, answer these 6 Discovery Questions. Be sure to support your answers with data and explain your logic.

Chapter 4, Math Minute 4.2 #3

Chapter 4, Math Minute 4.4 #4

Chapter 4 #16

Chapter 4 #21

Chapter 6 #33

Chapter 7 #39

1) I am emailing you a recent paper (Lamb et al., 2006) from *Science*. Read as much of this as you feel you need to answer this question. Interpret Figure 1 using your own words. Your target audience is a Bio111 student. Be sure to include the goal of what is shown in Figure 1, as well as how it would be applied in the real world. You must use one example from the paper to enhance your answer.

**Key Points:**

Define query genes

Address Affy chips

Generate gene rankings for perturbogens (and define term)

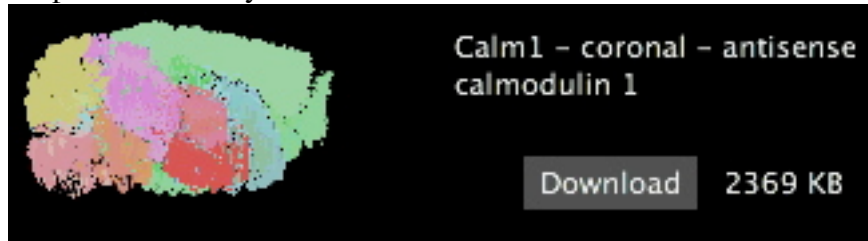
Discuss database and how it is searched.

Discuss display and how results are used.

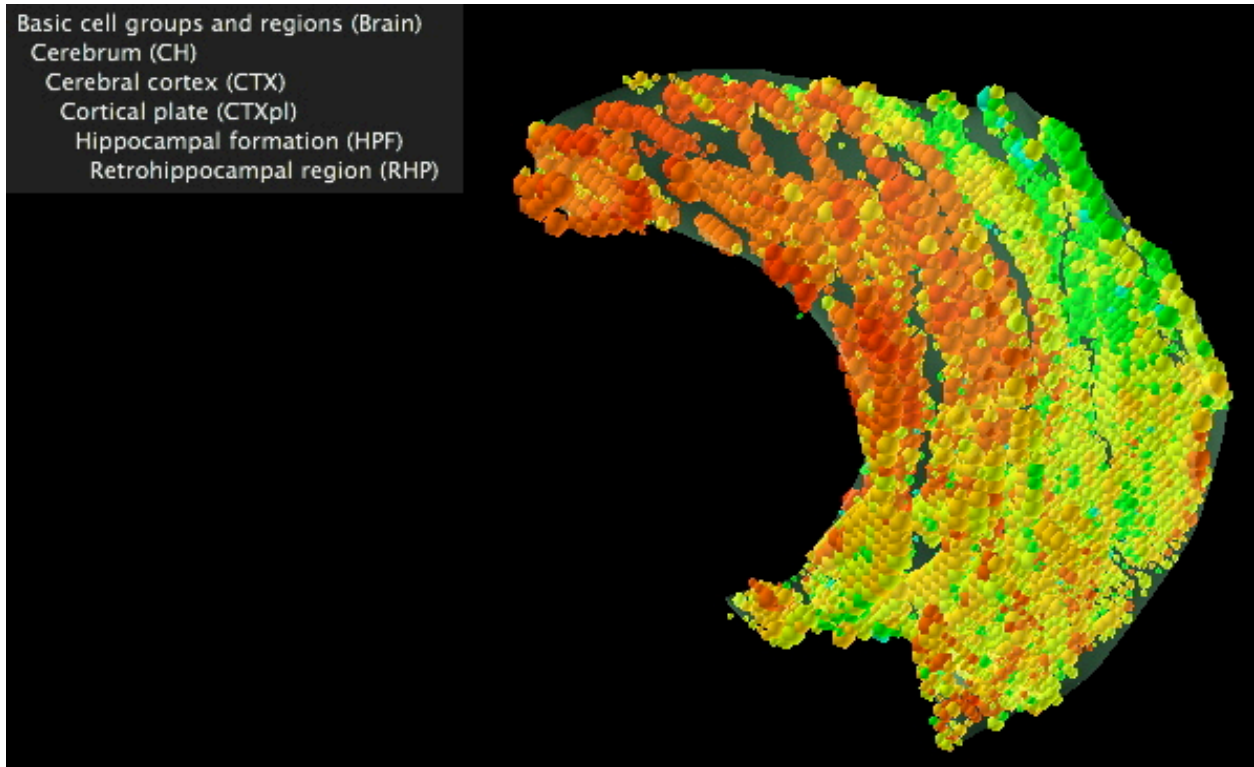
2) For this question, I am emailing a news summary PDF that describes a new microarray visualization tool. If you want to use this program on the Macintosh computers in class, you must download the zipped file from a folder on the Public Drive:

<Public/Biology/Campbell/Genomics/Brain Explorer.zip>. If you want to download the software onto your Windows computer, you can do so using the URL in the summary. Read the summary PDF, install the software, then answer these questions:

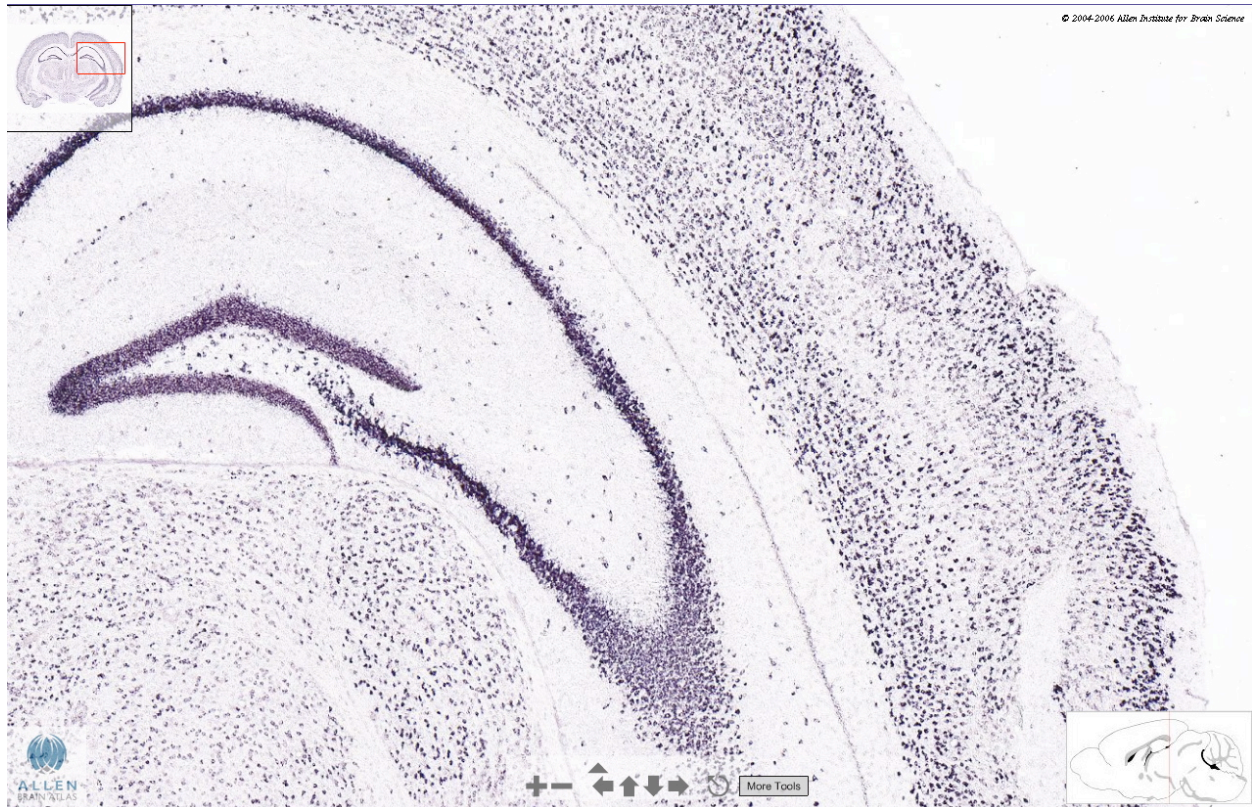
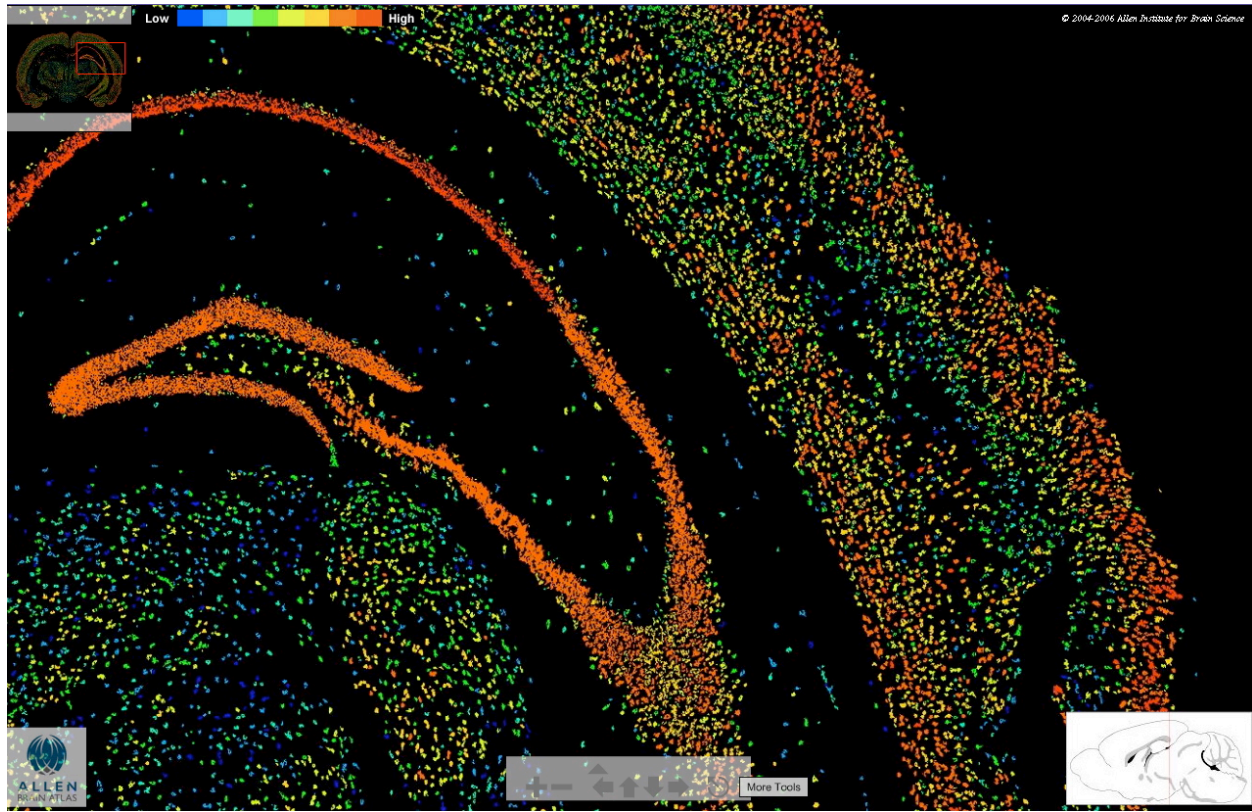
a. search for the calmodulin gene (which we will study in chapter 8) and download the first data set provided from your search. Be sure to tell me the name of the dataset you selected.

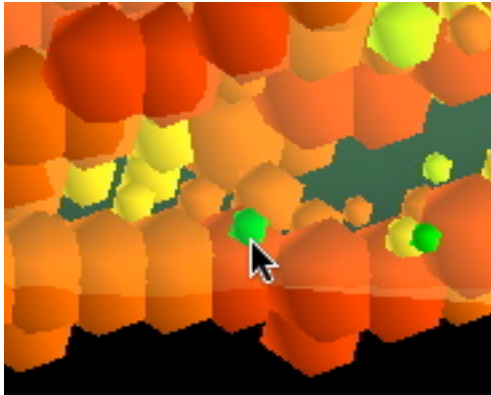


b. show me a screen shot for each section of the hippocampus that expresses high levels of calmodulin. Be sure to show me both expression levels and cellular structures. Choose one cell and show me the data from this cell.



Postpiriform transition area	<input type="checkbox"/>	<input type="checkbox"/>
▼ Hippocampal formation (HPF)	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
▼ Hippocampal region (HIP)	<input type="checkbox"/>	<input checked="" type="checkbox"/>
Ammon's Horn (CA)	<input type="checkbox"/>	<input checked="" type="checkbox"/>
Dentate gyrus (DG)	<input type="checkbox"/>	<input checked="" type="checkbox"/>
▼ Retrohippocampal region (RHP)	<input type="checkbox"/>	<input checked="" type="checkbox"/>
Subiculum (SUB)	<input type="checkbox"/>	<input checked="" type="checkbox"/>
▼ Cerebral nuclei (CNU)	<input type="checkbox"/>	<input type="checkbox"/>





Gene: Calm1  
 Annotation: Ammon's Horn (CA)  
 #Expressors: 5  
 Cell Diameter: 112.653  $\mu\text{m}$   
 Grid Area Spanned: 4%  
 Expression Level: 226.2  
 Grid ID: 306378 (78, 35, 28)  
 Section: 214 Location: 5208, 1864

c. Now download the standard sample data from the original Brain-Map web site. View these data and find a structure that is highly induced for the gene shown. What is the structure and what is the gene's function?

Gene: Tmem16b  
 Annotation: No Annotation (NA)  
 #Expressors: 16  
 Cell Diameter: 287.446  $\mu\text{m}$   
 Grid Area Spanned: 15%  
 Expression Level: 237.875  
 Grid ID: 644912 (127, 69, 59)  
 Section: 25 Location: 2716, 5368

Gene: Tmem16b  
 Annotation: Lateral septal complex (LSX)  
 #Expressors: 13  
 Cell Diameter: 154.675  $\mu\text{m}$   
 Grid Area Spanned: 19%  
 Expression Level: 235.846  
 Grid ID: 585924 (58, 31, 54)  
 Section: 301 Location: 5260, 2504

d. Provide the sequence of the probe used for this, and the experimental details about the mouse. Verify that the sequence used for this experiment would really bind to the gene they claim, and no others.

Needed to compare only with mouse to look for paralogs.

GCAGCCCAGAGTTCCTGAACACAGCAACAACAGGATGAAAAACCTCT  
 CCTACCCATTCTCCAGGGAAAAAATGTACCTGTATAACATCCAGGAA  
 AAGGACACCTTCTTTGACAATGCTACCCGGAGCCGCATTGTACACGA  
 GATTCTGAAGCGGACGGCCTGTTCTCGAGCCAACAACACGATGGGTA  
 TTA ACTCTCTAATAGCAAACAATATCTACGAGGCTGCCTACCCGCTT  
 CATGATGGTGAATATGACAGTCCAGGGGATGACATGAATGACAGAAA  
 GCTGCTGTATCAGGAATGGGCACGCTATGGAGTGTTTTACAAATTC  
 AACCCATTGACCTCATCAGGAAGTATTTTGGAGAGAAAATTGGGCTA

TATTTTGCTTGGCTGGGGTTGTATACATCATTCTGATCCCATCTTC  
TGTCATAGGCGTGATTGTGTTTCTTTATGGATGTGCAACAATCGAGG  
AAGATATCCCAGCAAAGAGATGTGTGACCACCAGAATGCCTTCACC  
ATGTGTCCCCTGTGTGACAAGTCCTGTGACTATTGGAACCTCAGCTC  
AGCCTGTGGGACTGCACGGGCCAGTCATCTGTTTGACAATCCAGCCA  
CCGTCTTCTTTCCATCTTCATGGCTCTGTGGGCTACCATGTTTCTG  
GAAAAGTGGAAAGAGACTCCAGATGCGGTTGGGCTACTTCTGGGACCT  
GACTGGGATCGAAGAGGAAGAAGAACGTTCCCAGGAACACTCTCGGC  
CTGAATATGAAACCAAAGTACGAGAGAAACTGTTAAAGGAGAGTGGC  
AAGTCAGCGGTTTCAGAAGCTGGA

e. Choose a disease from OMIM that could benefit from this brain map in general and explain how you would use the map to further this research. For this answer, use a numbered list of the steps and make a new number for each main step.

You should have chosen something that gives a phenotype in mice, and ideally check for that gene in Brain Map. Then look for cells that express that gene and try to correlate phenotype with cell expression. Ultimately, compare wt and diseased mouse expression levels. One person chose mdx mouse as a great example.