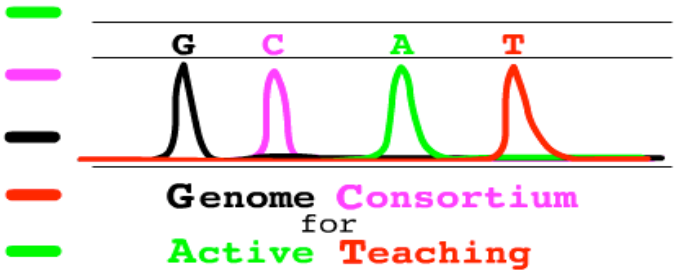

2008-2009 GCAT Assessment
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Students

Students that responded to some portion of the GCAT survey were separated into one of three groups: used GCAT materials, did not use GCAT materials (control), and don't know. Students who belonged to the 'don't know' group received this label because students with the same professor did not consistently identify with either of the two groups above (GCAT or control) and the faculty member failed to respond to the post- survey. Therefore this data was removed from further analysis. Displayed below is a table detailing the participation of student respondents to the pre- and post- GCAT surveys. The fourth column ("Both N") indicates the number of students in each group who completed both the pre- and post- surveys and who also took the surveys more than one week apart.

Group	Pre-test N	Post-Test N	Both N
GCAT	556	414	355
Control	346	204	183
Don't Know	162	15	0

I. Pre- GCAT Assessment

Demographic Information

The following demographic information is representative of the 556 students that used GCAT materials and completed the pre- GCAT survey. Participating GCAT students reported attending 40 colleges and universities. The majority of the students are pursuing a degree in biology (75.2%), and an additional 11.0% are completing pre-medical coursework. The majority of the participants were seniors (59.4%), followed by juniors (25.9%). Students also reported if the course using the GCAT materials was required for their academic major; for 30.9% of the students, the class was not a requirement. Basic demographic information is provided in the table below.*

Gender (%)		*School Year* (%)	
Male	43.0	Freshman	0.5
Female	56.8	Sophomore	9.9
		Junior	25.9
Race/Ethnicity (%)		Senior	59.4
American Indian/Alaskan Native	2.0	Other	4.3
Asian	10.6		
Black/African American	7.0	*Academic Major* (%)	
Caucasian/White	67.3	Biology	75.2
Hispanic/Latino	8.8	Chemistry	7.9
Multi Racial	3.1	Education	0.2
Other	6.1	Math/Computer Sci.	0.2
		Physics	0.2
Overall GPA (%)		Pre-medicine	11.0
3.50-4.00	41.2	Psychology	0.9
3.00-3.49	37.2	Non-science	0.2
2.50-2.99	17.8	Other	4.1
2.00-2.49	3.6		
1.50-1.99	0.2		

* Not every demographic item's percentages add up to 100% due to students who chose not to respond to some items or who selected multiple options on the same item.

Prior Laboratory Research Experience

Prior to the GCAT program, almost all 556 students had some type of research experience (98.0%). The majority of students had introductory laboratory experience (92.4%). Students' self-reported laboratory research experiences are listed below and they were allowed to give more than one response.

Prior Experience (%)			
Introductory lab	92.4	Thesis project	17.3
Upper level lab	28.8	Summer research	29.5
Independent study	24.5	None	1.4

Completed Coursework

The 556 students reported which courses they had completed from the list below. The most common course was Introductory Biology (95.9%). Few students had taken Neuroscience (6.1%) or Bioinformatics (6.3%) classes. Only one student reported taking none of the following classes.

Courses Completed (%)			
Introductory Biology	95.9	Statistics	62.6
Genetics	61.7	Physics	66.7
Microbiology	38.1	Molecular Biology/Genetics	48.0
Immunology	18.2	Cell Biology	59.5
Inorganic Chemistry	44.2	Biochemistry	41.7
Organic Chemistry	81.7	Genomics	10.8
Developmental Biology	17.4	Bioinformatics	6.3
Neuroscience	6.1	Probability	10.3
Calculus	79.1	None of the above	0.2

Graduate Education Intentions

The following table outlines the fields into which the same 556 students anticipate that they will continue education after undergraduate school. The most popular fields were related to Medicine (49.1%), and Biology: Cell, Molecular, Genetics, Biochemistry (37.9%).

Intentions (%)			
Don't intend to continue education	2.5	Law	0.9
Biology: Behavior, Ecology of Field Biology	9.0	Chemistry	5.4
Biology: Cell, Molecular, Genetics, Biochemistry	37.9	Physics	0.5
Medicine	49.1	Education	3.6
Math/Computer Science	1.1	Non-science	2.5
		Don't know	7.0

Degree Intentions

In the pre- survey, the 556 students also indicated their plans for continuing education after undergraduate school. The highest percentage of students (25.7%) reported that they planned to go to medical school for an M.D., followed closely behind by 22.7% of students who indicated their intentions to go to graduate school for a Ph.D. in a science-related field.

Plan (%)			
Ph.D (science)	22.7	Teaching certification	2.7
M.A. (science)	15.6	Volunteer then school	3.1
M.A. or Ph.D. (non-science)	1.8	Volunteer, no school	0.2
M.D.	25.7	Work then school	10.8
M.D./Ph.D.	12.6	Work (science), no school	4.1
School (other health prof.)	17.3	Non-science career, no school	0.5
Professional degree	1.3	Prefer not to answer	4.1

II. Post- GCAT Assessment

GCAT Laboratory Experience

The following information is representative of the 414 students that used GCAT materials and completed the post- GCAT survey. After their GCAT semester, students indicated if they had been successful in performing the GCAT activities listed below. The activity in which students were most successful was scanning their microarray chips (74.4%). At least 50% of the students were able to complete each of the four tasks listed below.

GCAT Activity (%)	
Make your own probe	51.4
Able to get the chips scanned	74.4
Obtain useable data from the chips	62.8
Analyze your own data	62.6

Analysis Software

In the post- survey, the same 414 students indicated which software program they used to analyze microarray chip data. An overwhelming majority of the students (77.8%) indicated that they had used MAGIC Tool for data analysis.

Software Used (%)	
MAGIC Tool	77.8
GenePix	5.1
Scananalyze	5.1
JTreeView	0.7
GeneSpring	1.9
Other	3.9
N/A	6.5

GCAT Activity Effectiveness

The 414 GCAT students who participated in the post-survey also rated the effectiveness of each of the following activities on a 7-point scale where 1 = *not effective at all*, 4 = *moderately effective* and 7 = *highly effective*. Students who rated an activity "not applicable" were excluded from calculations of mean scores, which causes the sample size for each activity to be less than 414.

GCAT Activity	Mean	St. Dev.	N
Practicing data analysis before I began analyzing my own data	5.31	1.47	325
Isolating RNA or genomic DNA used to produce probe	5.43	1.39	327
Producing the fluorescently-labeled probe	5.36	1.42	313
Hybridizing the probe with the spotted DNA	5.48	1.41	334
Designing my own experiment	5.11	1.72	246
Analyzing data from public domain source	5.33	1.50	303
Reading papers that used DNA microarrays	5.30	1.66	127

Students assigned an average effectiveness value of 5.33 (*SD* = 0.12) to all of the GCAT activities. Mean scores on individual activities ranged from 5.11 to 5.48, which demonstrates that students did not judge any activity to be drastically more or less effective than others. Additionally, all of the average ratings are above 4.0 on the 7-point scale, indicating that students judged all of the activities to be more than moderately effective. All activities should remain in the GCAT curriculum.

Student Knowledge

Eleven knowledge questions were presented in identical forms on the pre- and post-GCAT surveys. Students were instructed to answer without the use of notes or friends, and questions presented hypothetical scenarios pertaining to gene expression and microarray experimentation techniques. The following analysis only includes the responses of the 355

students who participated in both pre- and post- GCAT knowledge tests, and who also took the surveys more than one week apart. These 355 students represent 39 different classes. Correct response rates for each item, students' knowledge gains, and effect sizes are found in the table on the following page.

On the pre- survey knowledge test, correct response rates for each question were all below 50%. The mean number of test items that students got correct before GCAT was 3.87 (*SD* = 2.36). Item 5 was particularly difficult for student participants; only 4.5% of students answered this item correctly on the pre-program survey. There was improvement in knowledge scores after the GCAT program; the mean correct number across all the test items after GCAT was 5.50 (*SD* = 2.21). Correct responses for each item increased on average by 14.9%. Questions 1 and 4 showed particularly large gains of improvement: 34.7% and 29.6%, respectively. Knowledge gain and final performance were lowest on item 5 (9.0% increase from pre-, 13.5% correct at post- assessment); subject matter for this question relates to gene expression ratios using a graph. Future GCAT faculty and students should devote more time to this area. Furthermore, fewer than half of the student participants were able to answer items 2, 3, 5, 6, and 8 correctly after the GCAT program, indicating other areas of microarray experimentation and gene expression where improvements could be made in student knowledge. A dependent samples t-test indicates that statistically significant gains were observed from pre- to post- assessment regarding the knowledge questions ($t(354) = 13.23$, $p < 0.001$, $d = 0.70$).

Question	Subject Matter	% Correct Before GCAT	% Correct After GCAT	% Increase	Effect Size
1	Microarray experimentation - RNA	33.2	67.9	34.7	0.60
2	Microarray experimentation	36.3	48.2	11.9	0.19
3	Microarray experimentation - DNA	37.5	45.1	7.6	0.13
4	Microarray experimentation - bacteria	42.5	72.1	29.6	0.52
5	Gene expression ratios using a graph	4.5	13.5	9.0	0.28
6	Gene expression - probability	17.5	27.9	10.4	0.23
7	Gene expression - gene clusters	39.7	55.5	15.8	0.26
8	Gene expression using DNA microarray	36.9	47.3	10.4	0.19
9	Gene expression in catabolic pathway	42.8	51.5	8.7	0.15
10	Gene expression using microarray data	46.8	57.2	10.4	0.18
11	Gene expression - microarray technique	49.3	64.2	14.9	0.25

*All differences were statistically significant. Effect size indexed using *d* (standardized mean difference).

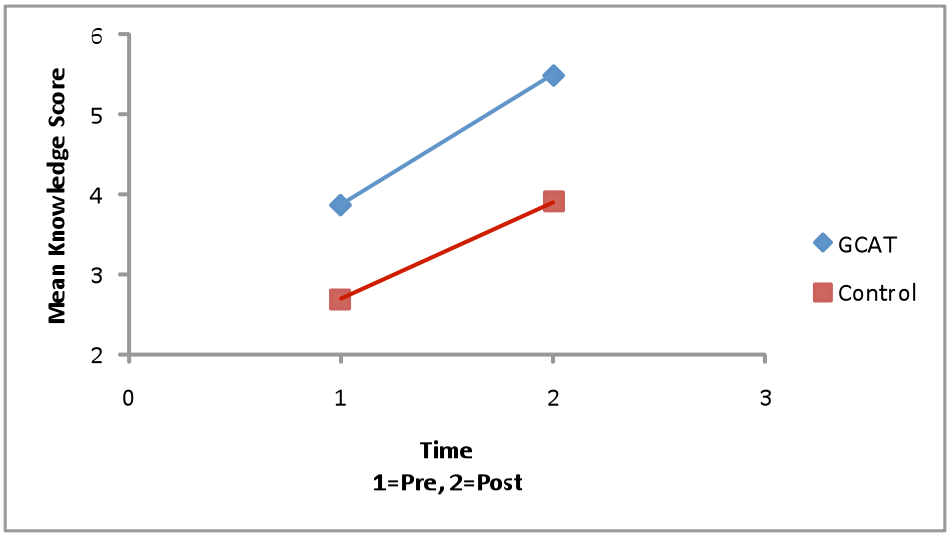
Control Group

In the control group, 183 students (representing ten different classes) completed both pre- and post- GCAT assessments. Lectures and reading assignments in the control classes were congruent with other classes who used GCAT materials, but the control class did not conduct laboratory experiments. Pre - and post- assessment scores on the knowledge test were examined in order to verify the effectiveness of the GCAT program. The following table compares the mean number of test items that students got correct on the pre- and post- assessments and the amount of change experienced during these two testing times.

Group	Pre-	Post-	Difference
GCAT	3.87	5.50	1.63
Control	2.69	3.90	1.21

The GCAT group had higher pre- and post- assessment means than the control group and improved approximately 1.35 times as much as the control group. In order to determine whether the GCAT group improved significantly more than the control group, a mixed 2x2 analysis of

variance was conducted, with time (pre- and post-) being the within-subjects factor and group (GCAT or control) as the between-subjects factor. The ANOVA showed a significant main effect of time, $F(1,536) = 187.94$, $p < .001$, Eta squared = 0.260. This result indicates that there was significant change in knowledge test scores from pre- to post- assessment collapsing across group. A significant Time x Group interaction was also obtained, $F(1,536) = 4.227$, $p = 0.04$, but this is a very weak effect (Eta squared = 0.008). The rate of improvement from pre- to post-assessment significantly differed between the GCAT group and the control group. As displayed in the following graph, both groups improved over time, but the rate of improvement for the GCAT group was significantly greater than that of the control group over the course of the semester. Given the wide variety of activities that different classes may have engaged in and the fact that not all of the topics included in the knowledge test would be covered in individual classes, this result is promising for the GCAT program.



Student Interests

Both the 355 GCAT students and the 183 control students rated how interested they were in genomics, life sciences, math/computer science, and research on a 10-point scale in the pre-

and post- GCAT surveys, where 1 = *not interested at all* and 10 = *extremely interested.* Displayed below is a table with the average interest score for each area on the pre- and post-assessments.

		GCAT				**Control**	
	Pre	Post	Difference		Pre	Post	Difference
Genomics	7.34	7.2	-0.14		6.71	6.32	-0.39
Life Sciences	8.14	7.97	-0.17		8.32	8.14	-0.18
Math/Computer Science	5.09	5.38	0.29		5.30	5.63	0.33
Research	7.64	7.5	-0.14		6.79	6.74	-0.05

Four 2x2 mixed ANOVAs were performed in order to identify any statistically significant differences in interest between the GCAT group and the control group. For all four areas, the results showed no statistically significant difference between the GCAT group and the control group in terms of change in interest from pre- to post- assessment. Collapsing across groups, on only one item (Math/Computer Science) did interest significantly increase from pre- to post-assessment, $F(1,529) = 8.08$, $p = 0.005$, though this is a weak effect (Eta squared = 0.015). The interaction of group and time was still non-significant, $F(1,529) = 0.042$, $p = 0.839$. Overall, the GCAT program has no significant effect on self-reported change in interest in genomics, life sciences, math/computer science, and research.

Faculty

56 faculty members responded to some part of the post- GCAT survey, 42 of which reporting that they used GCAT materials and the remaining 15 being in the control group (one professor had one class using GCAT materials and another class in the control group). 11 professors responded to the survey twice due to their participation in both semesters of the 2008-2009 school year. Taking the repeats into account, there were 52 responses from faculty members with classes using GCAT materials.

From the 52 classes using GCAT materials, more than half of the faculty responses reported having fewer than 10 students using GCAT microarrays. Only 11.5% of the faculty reported having more than 20 students using GCAT microarrays. The average number of microarrays used was 6.48 (*SD* = 4.65). The average number of students who got useable data was 5.21 (*SD* = 5.53).

Selection of GCAT Activities, Time Spent on GCAT Activities, and Assessment of Students' Knowledge

Faculty members were asked to indicate which activities students participated in using GCAT materials and how many hours were allocated to each activity. They were also asked about the methods used to assess students' knowledge of genomic course material. Unfortunately, due to a possible data collection malfunction, there are no results to analyze at this time.

Funding and Implementation

Of the 34 (out of 52) GCAT faculty who responded to the survey questions on funding, 28 reported receiving departmental funding in order to utilize GCAT materials. Three faculty members were supported by institutional funds, and the remaining three indicated that they received no funding to use the GCAT materials. Based on 48 responses, the average amount of funding received was $1862.92 (*SD* = $2698.49). All 52 GCAT faculty members responded to the survey question on implementation, and 76.9% of the professors did not feel that their implementation of GCAT materials was limited by computer resources.

Professors' Evaluation of GCAT

After the GCAT program, professors rated their agreement with the following statements on a 5-point scale, where *1 = strongly disagree* and *5 = strongly agree*. Overall, the GCAT program was rated very favorably. Nearly 80% of the faculty respondents strongly agreed (score of 5) with the statement "Overall, I had a positive experience using GCAT".

	Mean	St. Dev.
I would have access to microarray technology WITHOUT GCAT.	1.85	1.27
The online protocols available on the GCAT website were useful.	4.55	0.73
The GCAT-listserve (GCAT-L) was helpful.	4.50	0.68
The collection of other GCAT members as a support network was a significant factor in launching microarray technology on my campus.	4.27	0.84
Overall, I had a positive experience using GCAT.	4.71	0.57
I would use GCAT again in the future.	4.69	0.67

Additional Recommendations

This year, the GCAT program made great strides in recruiting control groups. Compared to last year, there were many more control students who took both the pre- and post- surveys (183 as opposed to 58). Faculty members seem to have done a much better job at encouraging students in the control group to fill out both surveys, but even more improvement can be made. Efforts to further increase the sample size of the control group will allow the comparison with the GCAT group to be made even more easily. In the GCAT group, there are also still many students who do not complete both pre- and post- surveys, meaning that many students' data could not be analyzed. This year, 244 GCAT students' data could not be used because of the students' failure to complete both pre- and post- assessments or because they did not do so with an appropriate time period between the two (e.g. took the surveys less than one week apart). Therefore, continued efforts should be made to ensure participation by all students throughout the GCAT survey process.

Furthermore, a large amount of data (about 160 students) was discarded because students with the same professor were unable to consistently identify with one group (either GCAT or control) and faculty failed to respond to the post faculty survey. Any gains we can make in improving faculty responses would also dramatically improve our sample size. Additionally, faculty members should be reminded to instruct their students that the pre- assessment should be taken before the administration of the GCAT materials and that the post- assessment should be taken after the completion of the course. There were still some students that were completing both of the surveys within hours of each other and had to be removed from analysis.

Faculty Comments 2008-2009

Please provide any suggestions for future improvements in GCAT in the space provided.
None. It is amazing to see GCAT growth! Thanks for the opportunity.
My spring class was used as a control group and the report information described in here is related to the research student's work that I had this past academic year.
Students struggled with the limited information available on the mouse chip gene list while using Magic Tool. I am not sure if there is anything that can be done about that, but there is an area that needs improvement and/or some creativity on my part.
Since I have used the arrays in class only once a year (though this summer I plan to let my research students use them) I manage to forget how to use MagicTool in the interim. I would love to see more extensive help files and more written (or Flashed) about data exploration and presentation - the 'why' and the meaning, as well as the techniques - which are the hardest things to grasp quickly and to hold onto after the workshop.
This year I used the Carolina simulation kit to introduce the concept of DNA microarrays to my BIO311 Molecular Biology class. The students took the online pre-assessment before coming to lab. I lectured for about 30 minutes on the technique, then the students did the simulation and we spent about 30 minutes discussing data analysis, using the Quantifying Gene Chip Colors website from Malcolm's class at Davidson. Our lab met Tuesday afternoon before Thanksgiving, and the wet lab activity was perfect for the situation - it was easy, fast, and fun. I look forward to taking the GCAT training course this summer and incorporating real microarray analysis into my course next year!
I would love to have access to yeast microarrays that contain intergenic regions.
I thought the project went extremely well. I believe the students learned a lot from this experience.
I really like GCAT and it has opened up tremendous research opportunities for me and for the students working with me. It took me awhile to get good microarray data, but now a lot of students are doing fantastic publishable arrays in my research group. THANKS
The requirements for the assesments should be more transparent to the instructor. I had no knowledge of questions that were to be presented to the students and was unaware of other details. I was unaware that spelling of my name was important for tallying of the assesment results.
This is a fantastic resource for undergraduate teaching! I've only used GCAT once and therefore don't have many data points to suggest improvements at this time. I will use it again this fall (2009) and look forward to it. thank you
I just want to note that I'm filling this out for the course in spring,2008 when four students took Genetic Regulation in Eukaryotes. I evidently missed filling it out that semester. I will teach it next semester to six students.
See if we can get a next generation sequencer to look at expression in new ways.
I find the website a bit disorganized. It is often hard to find what I am looking for and I end up

doing a google search for what I need to find the right GCAT page.
I really have no suggestions for improvement. My first implementing of microarrays was this semester in a course (Intro to Biochem) that I had not anticipated using these materials. However, in an effort to get up to speed for a full experimental implementation next semester in Molecular Biology, I had 10 students perform certain wet lab activities (tcRNA isolation) and simulate cDNA synthesis and microarray hybridization. We focused our attention on the use of MagicTool in the handling of DeRisi tiff files and the generation of data for purposes of filtering and analysis. I developed a set of activities and instructions that I believed would achieve my objectives. Students were guided in the gridding, segmentation, etc. Once they shared files, their exploration of the data become open ended. I believe this worked quite well and student enthusiasm was apparent. Many have commented on how this was among the most interesting activities they have done. I have yet to read their papers (just submitted) so I can't be certain beyond my impressions at this point.
The only difficulty we experienced was compatibility between MagicTool and recent releases of Java. This was a problem for PC users who had new laptops. Our IT had also upgraded Java on the CPUs in the classrooms so MagicTool would not permit me to demonstrate gridding and segmentation. I circumvented the problem with the use of a laptop that I knew everything would run on. It was a while before IT figured out the problem by contacting Laurie Heyer. Otherwise, all worked well. Students were quick to pick up the use of MagicTool and think about their hypotheses and how to effectively filter their data. As a group, they cultured yeast to observe the diauxic shift and allow cells to senesce. So there were different questions that the data could be 'milked for' although students were limited in time to explore the data. Two groups also designed independent projects that required mouse arrays. One group did not get to the hybridization of the arrays due to difficulties they experienced in culturing murine myoblasts, differentiating myotubes in culture and isolating the tcRNA. They had to switch gears. The other group cultured murine hepatocytes to examine gene expression in response to a known activator of apoptosis in relation to extracts that had been developed and tested in relation to cytotoxic behavior on breast carcinoma cell lines. This was quite interesting and the students 'stumbled on' some potentially hepatoprotective effects as well.
This assessment assumes that I used the microarrays in the class when instead we were using them in Inependent study (Under grad research); perhaps a different assessment might be good for those of use using using them in a traditional classroom setting. It is awesome to be in GCAT and have such a wonderful network of colleagues.
Although this may be logistically difficulty, two semi-annual (instead of just one annual) deadlines for requesting microarrays would allow better planning for spring courses.
it all worked very smoothly. The only wish I have is for a less expensive (the dyes not the chips) system in which the students could become more proficient in the protocol. We practice things like pipetting and coverslip dropping, but I was not able to persuade them that the practice is important. Even showing the array Heather and I made last summer in CA that looked like Wolverine had been at it did not seem to make the desired impression. Other than that, I cannot thank you all and especially Peggy, Laurie and Malcolm (and of course your students) for all of your hard work.
more decriptions of the varying techniques to do microarrays
More help in troubleshooting work, especially with bacterial microarrays.
I use the Genisphere microarray simulation in my genetics course so 30-40 students are involved. I show them microarray data from immunology courses and the literature. They design their

own experiment. This year I had an honors student use the 4 arrays.
I would love to see more statistical analysis tools available on Magic Tool - perhaps Lowness Regression, a way to do t-tests on the data... or maybe someone who is an expert in using SAM could write up a protocol for our website.
As time and resources permit, a more detailed instruction manual covering all of the options of MagicTool, and how to make the best use of them, would be helpful.
If it were possible to order arrays separately for the spring semester, we would have a much better idea of the number we would need. It is hard to predict how many students I'll have 6 months in the future.
I appreciate being part of the GCAT process very much. I would enjoy having a place where students working on microarray based research projects could easily talk to each other via the GCAT platform (but separate from the faculty based listserv. I would like to implement a virual presentation area better where students would more routinely post their results at the end of a semester or project.
I have not suggestions for improvements. Our problems were of our own creation, one of our slides dried out on the first attempt. We were able to correct the problem for a second trial which was 100% successful. Also, in the second try the students performed the experiment from beginning to end completely independently.
This was the first semester I was able to use GCAT microarrays in my Gene Expression course. I had eight students, mostly juniors and seniors. The students designed their experiments for human tissue culture cells, I designed the experiments for the yeast cells. The students isolated mRNA, and followed the protocols for microarray hybridization and analysis. With my background in yeast, I really should have had the students BEGIN with the yeast experiment. But, they were more interested in human, so we started there. We got usable data, but not as usable as we did with the second set of arrays, which were yeast. I found that two three hour class periods per week were sufficient, although not every student was able to come and help with the washes. The students really enjoyed the analysis, finding affected genes and the exploration involved in learning more about those genes.
I am having a hard time justify the cost of the arrays in my class. Perhaps a grant to secure funds to bring down costs of labeling kits.

If you have a website or a course webpage that you would be willing to share with the rest of the GCAT community (a link will be created on the GCAT website) please provide the url address below.
http://www.openwetware.org/wiki/Dahlquist
http://pages.pomona.edu/~llh04747/genreg.html
http://www.wiu.edu/biology/faculty/musser.php
http://hildysanders.stevensonuniversity.org/

What activities did you do related to genomics with your class?
This was a course in Developmental Biology. In the lab, my students examined microarray expression data from the Arbeitman et al, Science 2002 paper on gene expression through the life cycle of Drosophila. The students learned the mathematical basis of hierarchical clustering by

working through some sample data step-by-step in Excel, and answered questions about the Eisen et al., 1998 paper to practice interpreting clustergrams. They were given a table of Red/Green expression ratios for ~2500 genes in the Drosophila genome across all the timepoints (I had pre-filtered the data for quality and for genes that had gene expression log-ratios were greater than some cutoff value from zero.) [data from Arbeitman et al., 2002] Students used Mike Eisen's Cluster to hierarchically cluster the data. Students used Alok Saldhana's Java Treeview to browse the data, draw conclusions, devise hypotheses about clusters and genes of interest. Students wrote a paper reporting analysis results, and also shared data with class via oral presentations.
My student's research project was focused on confirming previous experimental data and moving the project forward for the next stage in analysis. We discussed the general methods, advantages and disadvantages of microarray procedures. She used semi-quantitative and qPCR procedures to confirm previous microarray data. Her seminar will be comparing the various techniques to study gene expression.
I did not use GCAT arrays in a class, but had an undergraduate research student begin a project with the goal of screening arrays next semester.
I used the GCAT materials with my research lab group, so all of the genomics related activities were related to student research.
Learned the basics of genomics and how they work in a biological sense.
Discussed microarrays; described history of microarray technique; discussed use of microarray data
Discussed genomics as related to Cell Biology, including parts of several chapters in the textbook. We also did DNA sequencing and two basic bioinformatics computer labs in the Cell Biology Laboratory. Students were required to access the DNA mIcroarray tutorial.
This class was lecture only. We used a textbook, papers, and some online resources only.
Discussion
We used MAGIC TOOL to analyze data from last year.
We used the microarray simulation kit from Carolina.
class room activities I did use the web site.
None
A student summarized how microarrays work. One student who had worked with microarrays in the summer at a different institution analyzed his data and is in the process of using qRT-PCR to validate the microarray results. He's been summarizing his project to the class. In addition, over the course of the semester, we've looked at a number of papers where genomic level data was presented - mostly used to characterize the microbes associated with an environment and their metabolism.
Just introductory genetics.

Why did you not use GCAT materials?
Given the time that I budgeted for this project, my goal was to focus on data analysis and interpretation of gene expression rather than the technical activity of doing the hybridizations and extracting the data. I didn't use MAGIC because I am more familiar and at-ease with Cluster and Java Treeview, and I knew that they would be easy for my students to use.
We didn't get far enough on the project to perform teh next set of microarrays planned.
I actually did use the GCAT materials, but in undergraduate research rather than class.

It is not incorporated into our class assignments.
The microarrays are for E coli, not for the current research involving Vibrio
The logistics were too difficult to coordinate with inexperienced TA's running the 3 lab sections and the requirement for long processing times on consecutive days (we have used the 3 DNA kits in the past when I taught the labs personally). I may do some microarray analysis in molecular biology, but we could not devote enough time for it in Cell Biology. Also, my students lab tech nique is not sufficiently robust at the start of the semester. By the time I trust their pipetting, it is late in the semester.
No lab with this course.
Too large a class and budget cuts.
Ran out of time and money.
I'm not comfortable with the isolation of mRNA; the protocol is difficult for my students and the kits are expensive.
taught lecture portion
Because I did not like teaching.
My seminar is currently focused on the molecular biology of symbiosis. We have been analyzing aspects of the sea anemone Aiptasia and its symbiotic dinoflagellate, Symbiodinium. There are a number of ESTs for both organisms and I believe that there are some chips made by folks at UC Merced and JGI but not currently available through GCAT. I didn't actually think about asking whether we could get some through GCAT, mostly because I didn't have specific experiments in mind to do microarrays with. Many of the most straightforward experiments have been done, and so I would need to think hard about what experiments would be worthwhile - as opposed to analyzing and utilizing the data of others. Also, my colleague Amy Vollmer has been using them, and I'd like to give students the option for a different experimental experience.
It is an intro for majors course, and it is the diversity, ecology, evolution half of the year long course.

What would make it more likely for you to use GCAT materials in the future?
If I decided that using MAGIC was a better choice, I might do so. If my teaching goals for this Developmental Biology lab changed such that a hands-on hybridization was needed, then of course I would wish to use GCAT microarrays.
I do plan on using GCAT meterials in the future.
I will likely expand my work with GCAT to include my teaching labs in the future-- GCAT doesn't need to do anything more to promote the work, I just needed time to transition my teaching lab.
I do think I will expand my use of GCAT materials after attending the workshop this summer-- most likely as part of my biochem 2 lab course.
For my future studies in genomics and bioinformatics.
Switching back to E coli, which is unlikely but possible
I may try again in Molecular Biology where the students may have better lab experience/technique. The labs are very expensive with a high probability for failure if their pipetting technique is not good. But I would say that time is the most critical limiting factor. My students are mathematically challeneged, in general, so even just the analysis will require a large amount of time.

I do not want to work with microarrays now. I am moving to synthetic biology and genome annotations.
I use them in a smaller class I teach in the summer that is funded by NSF. Even with the break in prices, microarrays are too expensive for a class of more than 50 students.
I need to test the protocols and have something work before I incorporate it into the class.
New equipment here (speed vac, etc.). Bigger supply budget.
Availability of chips for organisms of interest. Time to think about interesting problems that could be addressed by microarray experiments in my current experimental system.
NA

Please explain why you think your class belongs in the control group.
Actually, I don't know whether they belong in the control group or not, since they did learn some things about microarrays and participated in cluster analysis. In email conversations, Malcolm suggested I simply describe what I did in this course.
My student has only a cursory understanding of microarray technology, procedures, and data analysis. She has received no training specifically focused on the use or intepretation of arrays or array data.
I only have one student involved, and he learned about microarrays, but did no actual screening this semester.
It actually does not-- at least one of my research students will reply based on his GCAT experience in my lab this year.
The class should be included in the control group because we don't know anything regarding genomics (assuming no one in the class studied it in another class.
Other than the above information, they would not be expected to have additional information on microarrays.
We only covered microarrays in a minimal manner. We did cover genomics approaches to some extent and I continually refer to the importance of gene expression throughout the class. So I believe that they should have a good appreciation for the usefulness of microarrays, but they have not experienced the hands-on aspects and the benefits of that for learning.
We studied microarray methods, results, and applications. We did not use any wet lab or MAGIC Tool.
Because we did not use microarrays or discuss it beyond a statement that they exist. These students are general genetics students and will eventually get to try them in upper level courses
We did the simulation (and they took the pre-test).
Because they did not learn anything.
They didn't use chips themselves. However, one person did use them himself in the summer at a different institution. In addition, there is another faculty member at my same institution using them in her course.
My class did not talk about genomics or mircoarrays in any real capacity.