BMES375: Computational Bioengineering

Teaching staff

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Course objectives

- Refresh and Strengthen MATLAB programming skills
  - Advanced data types: cell array, logical array….
  - Advanced functions:
  - MATLAB toolbox

- Explore some mathematical and statistical tools
  - Matrix algebra
  - Differential equations
  - Clustering analysis…..
  - Statistical analysis…..

- Gain basic knowledge in some biological systems
  - Genome Sequencing
  - Gene Expression,
  - Enzymatic pathway
  - Clinical data…..

- Different data types from different data sources
  - Text, Excel
  - Relational database
  - Gene expression from NIH database
  - DNA sequencing

BMES375: Schedule

Schedule: **One lecture (Attendance is required)**
Two recitations

Lectures:
Mondays 5-7 pm (In person)

Recitations:
Tuesdays and Wednesdays 5-7pm (In person and ZOOM online)

Office hours:
Tuesday 10-11 am (ZOOM or Microsoft Teams online)
Friday 10-11 am (ZOOM or Microsoft Teams online)
By email appointment (BMES375 in subject)

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Weekly assignment

Weekly homework (100 points each, 10 weeks)

- **100 points each (10 weeks), except Relational database (50 points)**
- **No midterm or final.**
- **Due every week Tuesday or Wed. by 5pm**
- **Part of week 9 homework will be a take-home programming (40 points), due at 5pm Dec. 7th.**
- **A short essay comparing python and matlab (25 points)**
- **Your grade will be calculated as the percentage**

Bonus:

- **Covert one of the MATLAB assignments to Python (25 points)**

Score%	<59	59	63	67	69	73	77	79	83	87	89	92	98
Letter Grade	F	D-	D	D+	C-	C	C+	B-	B	B+	A-	A	A+

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Tentative assignment schedule

Week	Topic		Tasks
1	MATLAB: hw1hivdrug		Assignment #1
2	MATLAB: hw2hivcognitive		Assignment #2
3	MATLAB: hw3symbolicmath/gene expression/clustering analysis		Assignment #3
4	MATLAB: relational database		Assignment #4
5	MATLAB: hw5db_weight_loss		Assignment #5
6	MATLAB: hw6pathway		Assignment #6
7	MATLAB: hw7geo(microarray gene expression)		Assignment #7
8	MATLAB: hw8sequencing_fastq_QC/human genomics		Assignment #8
9	MATLAB: hw9sequencing_aligment_bam-sam, part of take-home exam		Assignment #9
10	Python:python1a_py4matlabbers		Assignment #10
10	Python:Python1b_hw_bioinformatics		Assignment #10
11	Python:Python2a_regression		Assignment #11
11	Python:Python2b_Intergration and Ordinary differential equation		Assignment #11
11	Python:Python2c_sympy		Assignment #11
	A short assay		
	Bonus		

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Homework due/Grading

BMES375-A-Syllabus.FA-21.pdf
submissionguidelines_FA-21.pdf
rubrics_FA-21.pdf

Homework due:
Homework are due before the following recitations.

If you are in recitation 1 (Tuesday, Sept. 21st), you need to submit your hw1 before 5pm on next Tuesday (Sept. 28th) recitation.

For students in recitation 2, submit hw1 before next Wed. (Sept. 29th) recitation.

You will get your grades back before the next lecture (Monday, Oct. 4th).

Submit your homework on blackboard

Additional Grading Rules:

You must work within ONEDRIVE folder for your assignments. Create a Drexel OneDrive folder for the course named: "bmes375.FirstnameLastname.abc123". Then share your bmes375 OneDrive folder with Edit permissions given to: Jadhav,Tanaya tj474@drexel.edu and Wong,Jessica jsw328@drexel.edu. They will run your codes.

Submit your hws in both MATLAB livescript and pdf files on blackboard

Submission not compliant: -5% penalty. Student did not work on the homework within OneDrive folder or the submitted file does not match that in the OneDrive.

Late Penalty: -1%/hour penalty. Blackboard submission time will be used as the time of submission.

Criteria	Unacceptable	Below Avg	Average	Above Avg	Excellent
Correctness **Weight 50.00%**	0 % Analysis methods are irrelevant to the problem being solved.	70 %	80 % The general idea is correct, but there are errors in application to the data. Conclusions are supported only visually or the statistical tests are inadequate.	90 %	100 % All questions are answered correctly. Most appropriate analysis methods are used. Conclusions are supported both visually and using statistical tests.
Result Formatting **Weight 20.00%**	0 % No figure caption and no title sentence. All descriptive text (axis labels and tick-labels) is too small to read or poorly formatted. Color is not used or is not used properly.	70 %	80 % Any of the required elements are missing. Figure title sentence is too verbose or is not supported by the data. Some descriptive text (axis labels and tick-labels) are not large enough to read and or are not properly formatted. Color is used but does not improve understanding.	90 %	100 % The figure caption explains: 1. What is plotted (ie, what does each dot represent?). 2. Units of each axis. 3. What any specific colors or shapes indicate. Figure title sentence is concise and logically flows from the figure. All descriptive text (axis labels and tick-labels) are large enough to read and are properly formatted. Color is used properly to draw the viewer's eye to the relevant conclusion.
Code Formatting **Weight 20.00%**	0 % Variable names are obscure and do not represent the data they contain. Code would be entirely opaque to even an experienced coder.	70 %	80 % Variable names are too long. Some areas of the code would be incomprehensible to an average scientist in the field.	90 %	100 % Variables are named concisely and logically. Commonly used variables are explained. Code is commented enough that an average scientist in the field could understand it.
Code Efficiency **Weight 10.00%**	0 % Code is needlessly inefficient.	70 %	80 % Code has one or more warnings that are mentioned by the Matlab editor and/or employs multi-nested for-loops.	90 %	100 % Code is vectorized, uses in-built functions, avoids for-loops, matrices are pre-allocated, etc.

All assignments on blackboard and should be downloaded from blackboard to a single local folder

Blackboard

	FILE TYPE	NAME	EDITED	SIZE
		Bookmark Items	Download Package	Copy	Move	Delete
☐		hw1_template.mlx	Jun 15, 2020 8:19:56 PM	161.1 KB
☐		installation and upgrade.pptx	Jun 15, 2020 8:19:57 PM	157.7 KB
☐		patientdata.xlsx	Jun 15, 2020 8:19:57 PM	56.0 KB

Bookmark Items   Download Package   Copy   Move   Delete

MATLAB

> This PC > Local Disk (C:) > Teaching > BMES 375-2020-summer > hw1

Name	Date modified	Type	Size
hw1_template	6/15/2020 8:10 PM	MATLAB Live Script	162 KB
installation and upgrade	6/15/2020 8:15 PM	Microsoft PowerPo...	158 KB
patientdata	6/15/2020 8:10 PM	Microsoft Excel W...	56 KB

Installation and Upgrade

- Update MATLAB to at least MATLAB R2018a,b including the toolbox (bioinformatics, database)

- Install Jupyter using anaconda with Python 3.7 version https://www.anaconda.com/download/
  Installing Jupyter Notebook using Anaconda

  We **strongly recommend** installing Python and Jupyter using the Anaconda Distribution, which includes Python, the Jupyter Notebook, and other commonly used packages for scientific computing and data science.
  First, download Anaconda. We recommend downloading Anaconda's latest Python 3 version.
  Second, install the version of Anaconda which you downloaded, following the instructions on the download page.
  Congratulations, you have installed Jupyter Notebook! To run the notebook, run the following command at the Terminal (Mac/Linux) or Command Prompt (Windows):

- DB Browser for SQLite https://sqlitebrowser.org/dl/
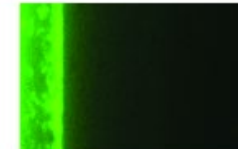
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Interesting Facts About Matlab and Python

MATLAB :
Facts (users, where is the company, revenue, number of employees)
https://en.wikipedia.org/wiki/MathWorks
https://en.wikipedia.org/wiki/MATLAB

Python:
Facts (users, history, who are using python, employment opportunities…..)
https://en.wikipedia.org/wiki/Python_(programming_language)
https://opensource.com/article/18/5/numbers-python-community-trends

Write a short essay (text, video, image, audio) comparing matlab and pytho

MATLAB live script in Live editor
interactive programming environment

Expectations

- Attend classes, punctuality

- Class participation

- Finish assignments on time

- Gain basic knowledge on several biological systems

- Improve your MATLAB and Python skills

- Mathematical and statistical analysis
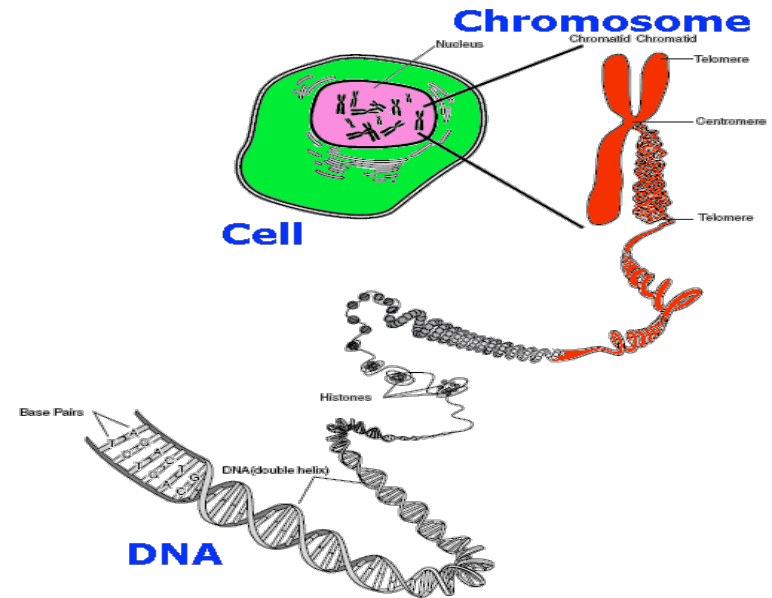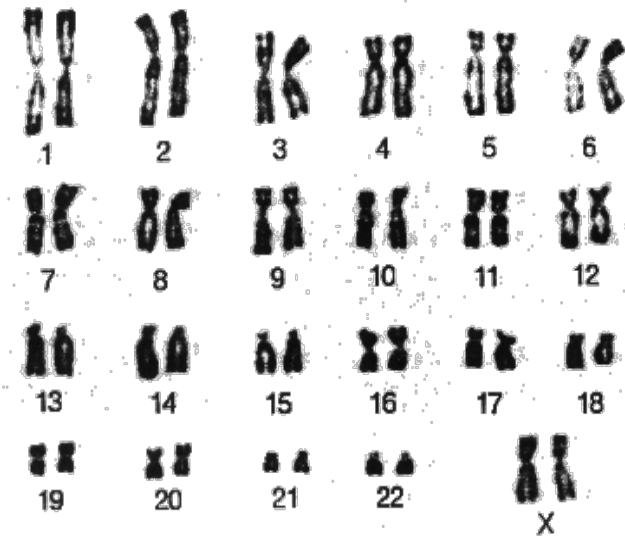
Human Genome

When was the discovery of the structure of DNA awarded the Nobel Prize?
What is the size of human genome in base pairs

Barcoding the Whole Genome in nano-channel
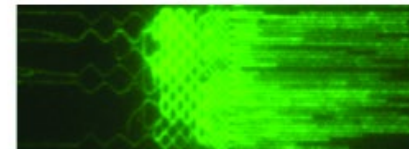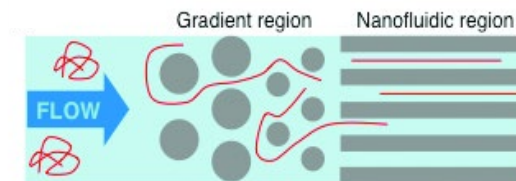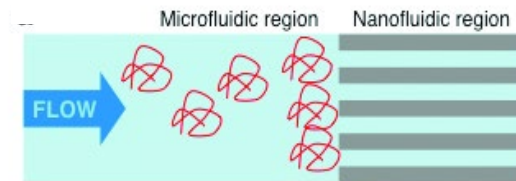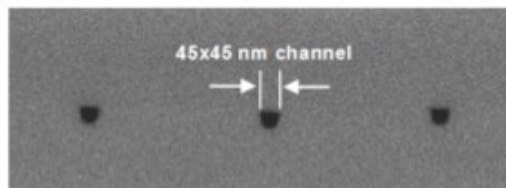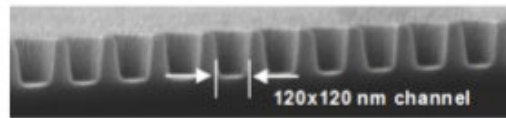
Two color Dual View Imaging System developed for Genomic Barcoding in Nano-channel Array
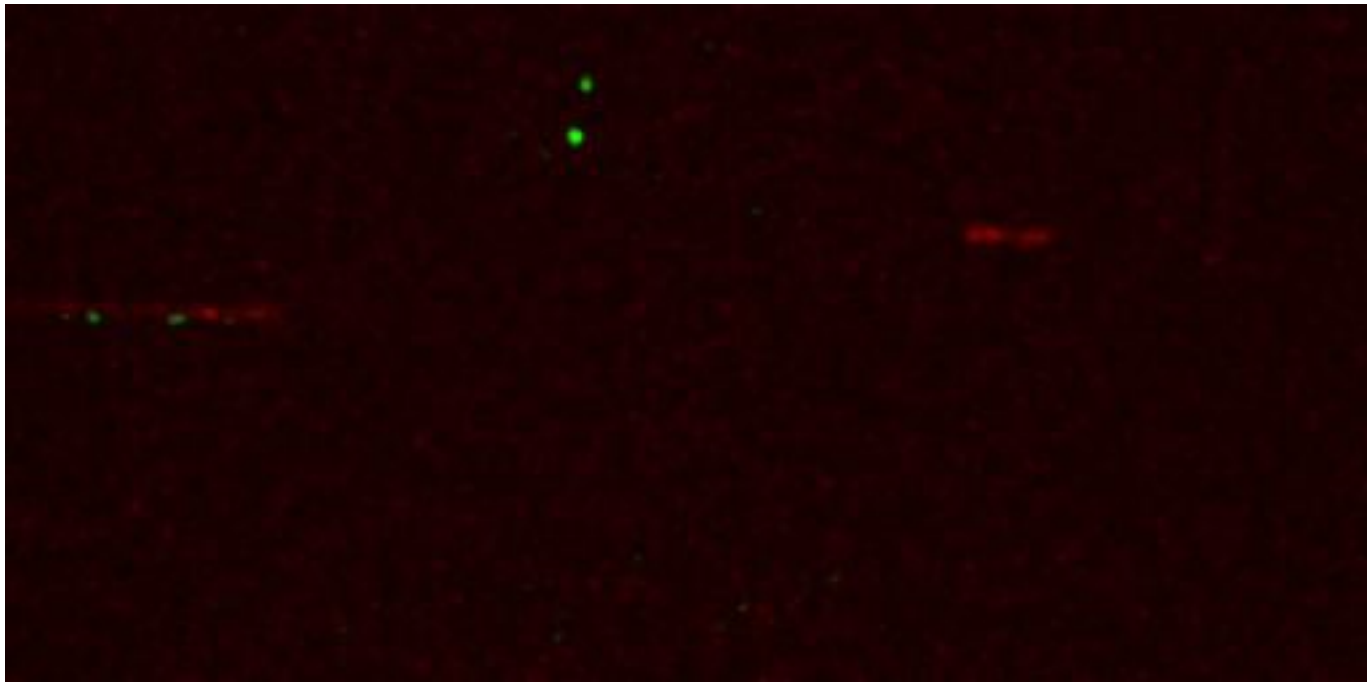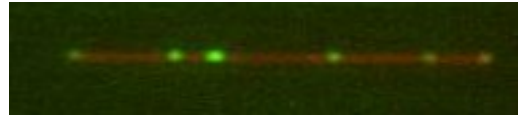
DNA linearization on a patterned glass surface

Median length is 1Mb