



Sources

Friday, July 23, 2021 11:49 AM

- [How it Works: Proximo Hi-C Genome Scaffolding](#)
 - Short overview of Hi-C
- [2020 STAT115 Lect15.1 HiC Introduction](#)
 - Lecture on Hi-C
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- raoetal2014
 - Inspiration for the summer project about Hi-C and visualization
- <https://docs.python.org/3/library/venv.html>
 - Information about Python virtual environments
- 
- CHIA_PET
 - Paper about a method of dna analysis similar to Hi-C which was mentioned in the raoetal2014 paper
- [2019 STAT115 Lect14.1 Chromatin Interaction HiC](#)
 - Another lecture on Hi-C
- <https://github.com/aidenlab/juicer/wiki/Juicer-Tools-Quick-Start>
 - Guide for setting up Juicer for creating Hi-C files
- [Juicebox Guide](#)
 - Guide for setting up Juicebox for viewing Hi-C files as a plot
- <https://github.com/aidenlab/straw>
- <https://aidenlab.gitbook.io/juicebox/accessing-raw-data>
 - Guides for setting up Straw for extracting data from Juicebox
- <https://bioconductor.org/packages/devel/bioc/vignettes/HiCBricks/inst/doc/IntroductionToHiCBricks.html>
 - Guide for setting up the Bioconductor, an R library used for large Hi-C dataset analysis
- <https://www.datanovia.com/en/blog/how-to-install-ggplot2-in-r/>
 - Guide for setting up ggplot2 used for plotting data in Rstudio
- <https://docs.ris.wustl.edu/doc/compute/workshops/ris-docker-basics.html>
 - Guide for setting up Docker on wustl for running python, r, and git jobs on the wustl servers
- <https://packaging.python.org/guides/installing-using-pip-and-virtual-environments/>
 - guide for installing pip and venv
- https://hub.docker.com/_/python?tab=tags&page=1&ordering=last_updated
 - python docker images
- <https://scikit-learn.org/stable/install.html>
 - guide for installing a python package for predictive data analysis
- <https://scikit-learn.org/stable/modules/mixture.html>
 - information about the Gaussian Mixture method
- <https://github.com/aidenlab/Juicebox/wiki/Download>
 - download page for Juicebox for visualizing hic files
- <http://bioinfo.au.tsinghua.edu.cn/member/nadhir/HiC3DViewer/>
 - 3D viewer for Hi-C data models
- https://en.wikipedia.org/wiki/Chromosome_conformation_capture

information about 3C techniques

- <https://www.genome.gov/genetics-glossary/Shotgun-Sequencing#:~:text=Shotgun%20sequencing%20is%20a%20laboratory,fragments%20that%20are%20sequenced%20individually.>

information about shotgun sequencing, used for piecing together a dna sequence after fragmentation

- <https://www.genome.gov/genetics-glossary/DNA-Sequencing>

information about dna sequencing

- <https://machinelearningmastery.com/clustering-algorithms-with-python/>

list of clustering algorithms for analyzing genome data

- <https://seaborn.pydata.org/generated/seaborn.clustermap.html#seaborn.clustermap>

information about a python extension for plotting

- [Introduction to Clustering](#)

overview of clustering data

- [Seaborn clustermap | How the clustermap works and what is the clustermap?](#)

clustermap tutorial

[Videos/22_clustermap.ipynb at master · kimfetti/Videos · GitHub](#)

code from video

- <https://pypi.org/project/fastcluster/>

python library for fast clustering in python

- <https://stackoverflow.com/questions/26551662/import-text-to-pandas-with-multiple-delimiters>

regex expression for giving pandas two delimiter options

- http://www.btechsmartclass.com/data_structures/sparse-matrix.html

Sparse matrices

- <https://docs.scipy.org/doc/scipy/reference/generated/scipy.sparse.eye.html>

sparse.eye used for sparse matrices

- <https://cmdlinetips.com/2019/02/how-to-visualize-sparse-matrix-in-python/>

Sparse matrices in python

- https://matplotlib.org/stable/api/as_gen/matplotlib.pyplot.spy.html

Visualizing sparse matrices in python

- <https://stackoverflow.com/questions/37173892/convert-from-csv-to-array-in-python>

csv to array python

- <https://www.digitalocean.com/community/tutorials/how-to-debug-python-with-an-interactive-console>

python interactive console

- <https://docs.scipy.org/doc/scipy/reference/generated/scipy.spatial.distance.pdist.html#scipy.spatial.distance.pdist>

metrics

- <https://docs.scipy.org/doc/scipy/reference/generated/scipy.cluster.hierarchy.linkage.html#scipy.cluster.hierarchy.linkage>

methods

- <https://stackoverflow.com/questions/61816216/seaborn-clustermap-with-two-row-colors>

clustermaps with bedgraphs

- <https://docs.python.org/3/library/parser.html>

<https://docs.python.org/3/library/argparse.html>

<https://numpy.org/doc/stable/reference/generated/numpy.roll.html>

python libraries for commenting the hic demo code

- [https://en.wikipedia.org/wiki/DNA_\(cytosine-5\)-methyltransferase_3A](https://en.wikipedia.org/wiki/DNA_(cytosine-5)-methyltransferase_3A)

DNAMT3A (from lab meeting presentation)

- <https://en.wikipedia.org/wiki/NPM1>

NPM1

- <https://stackoverflow.com/questions/899103/writing-a-list-to-a-file-with-python/899176>

trying to find another way to view the lists from the python code

- <https://pandas.pydata.org/docs/reference/api/pandas.DataFrame.isin.html>

python library for checking if element is in a dataframe

- [Chromosome conformation capture - Wikipedia](#)
 - How hi-c data is collected
- <https://genomebiology.biomedcentral.com/articles/10.1186/s13059-015-0741-y>
 - hi-c and a/b compartments
- <https://www.kite.com/python/answers/how-to-save-a-numpy-array-to-a-text-file-in-python#:~:text=Use%20numpy.,to%20the%20opened%20file%20fname%20.>
 - write and read arrays to and from files
- <https://www.geeksforgeeks.org/file-flush-method-in-python/>
 - force prints to print on time
- <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3149993/>
- <https://genomebiology.biomedcentral.com/articles/10.1186/s13059-017-1253-8>
 - papers on hic
- <https://pubmed.ncbi.nlm.nih.gov/20461051/>
 - hic abstract
- <https://stackoverflow.com/questions/62473426/display-legend-of-seaborn-clustermap-corresponding-to-the-row-colors>
 - add key for bedgraphs on plot
- <https://stackoverflow.com/questions/4918425/subtract-a-value-from-every-number-in-a-list-in-python>
 - subtract 1 from each element in list python
- <https://docs.ris.wustl.edu/doc/storage/globus.html>
 - move files between computer and server
- <https://www.geeksforgeeks.org/python-perform-append-at-beginning-of-list/>
 - add to beginning of list python
- <https://cvxopt.org/userguide/matrices.html>
 - sparse and dense matrices
- <https://note.nkmk.me/en/python-check-int-float/>
 - check if integer python
- <https://docs.python.org/3/library/csv.html>
 - python write to csv
- https://docs.scipy.org/doc/scipy/reference/generated/scipy.sparse.coo_matrix.html
 - formatting data for a matrix
- https://seaborn.pydata.org/examples/structured_heatmap.html
 - python heatmap
- <https://stackoverflow.com/questions/11106536/adding-row-column-headers-to-numpy-arrays>
 - numpy indices and columns
- <https://pandas.pydata.org/pandas-docs/stable/reference/api/pandas.DataFrame.drop.html>
 - pandas remove from dataframe
- <https://realpython.com/python-csv/>
 - read and write csv files pandas
- <https://stackoverflow.com/questions/7664826/how-to-get-flat-clustering-corresponding-to-color-clusters-in-the-dendrogram-cre>
 - clustering colors
- <https://www.geeksforgeeks.org/python-map-function/>
 - python map
- <https://seaborn.pydata.org/generated/seaborn.clustermap.html>
 - clustermap
- <https://stackoverflow.com/questions/16096627/selecting-a-row-of-pandas-series-dataframe-by-integer-index>
 - get row from dataframe
- <https://pandas.pydata.org/docs/reference/api/pandas.DataFrame.html#>
 - pandas dataframe
- <https://www.educative.io/edpresso/how-to-convert-a-list-to-an-array-in-python>
 - list to array

- <https://stackoverflow.com/questions/40593205/index-4-is-out-of-bounds-for-axis-1-with-size-4-code-with-double-sum>
 - numpy indexing
- <https://riptutorial.com/matplotlib/example/32429/multiple-legends-on-the-same-axes>
 - multiple legends for matplotlib
- https://matplotlib.org/3.1.1/api/_as_gen/matplotlib.pyplot.title.html
 - add title to matplotlib
- <https://numpy.org/doc/stable/reference/generated/numpy.vstack.html>
 - numpy vstack
- <https://stackoverflow.com/questions/13851535/how-to-delete-rows-from-a-pandas-dataframe-based-on-a-conditional-expression>
 - pandas dataframe delete row with condition
- https://matplotlib.org/stable/api/_as_gen/matplotlib.pyplot.text.html
 - matplotlib textbox
- <https://stackoverflow.com/questions/11469228/replace-and-overwrite-instead-of-appending/11469328>
 - read/write to file simple python
- <https://stackoverflow.com/questions/8924173/how-do-i-print-bold-text-in-python/8930747>
 - python bold text
 - print '\033[1m' + 'Hello' + '\033[0m'
- <https://www.geeksforgeeks.org/write-a-dictionary-to-a-file-in-python/>
 - write dictionary to file python
- <https://stackoverflow.com/questions/1904394/read-only-the-first-line-of-a-file>
 - read first line of file
- <https://www.tutorialspoint.com/How-to-create-a-Python-dictionary-from-text-file>
 - turn text file contents into dictionary
- <https://stackoverflow.com/questions/30765493/how-to-slice-in-python-all-but-the-last-n-items-when-n-may-be-zero>
 - slice index
- <https://stackoverflow.com/questions/25584124/oserror-errno-22-invalid-argument-when-use-open-in-python>
 - when storage1 was down, the program was in the middle of running and could not find the file to write to
- <https://numpy.org/doc/stable/reference/generated/numpy.matrix.transpose.html>
 - transpose matrix
- https://www.w3schools.com/python/python_strings.asp
 - ("whatever" not in string) checks if substring not in the string
- <https://www.displayr.com/what-is-hierarchical-clustering/>
- https://en.wikipedia.org/wiki/Hierarchical_clustering
- <https://stackoverflow.com/questions/9838861/scipy-linkage-format>
 - hierarchical clustering
- <https://stackoverflow.com/questions/15741759/find-maximum-value-of-a-column-and-return-the-corresponding-row-values-using-pan>
 - return row from max columns
- <https://realpython.com/python-debugging-pdb/>
 - pdb debugger
- <https://stackoverflow.com/questions/23216512/python-make-string-equal-length>
 - add spaces to end of string for uniformity
- <https://www.geeksforgeeks.org/python-append-to-a-file/>
 - append to file python
- <https://stackoverflow.com/questions/6731119/python-pdb-skip-loop>
 - skip to end of loop pdb
- <https://stackoverflow.com/questions/15599639/what-is-the-perfect-counterpart-in-python-for-while->

[not-eof](#)

- for line in file
- <https://stackoverflow.com/questions/1215208/how-might-i-remove-duplicate-lines-from-a-file>
 - remove duplicates from file python
- https://www.w3schools.com/python/python_file_remove.asp
 - delete file python
- <https://stackoverflow.com/questions/27123125/sorting-a-text-file-alphabetically-python>
 - alphabetize file python
- <https://www.genengnews.com/topics/omics/human-genome-modeled-in-3d-via-proximity-pair-analysis/>
 - Image 1
- <https://science.sciencemag.org/content/326/5950/289.figures-only>
 - Image 2