[Week 1 (3/23) – Introduction to Python (data types, indexing, variables)](https://zoom.us/rec/play/upMrIr-orDM3E9KX4wSDC_BwW465K6Ks0XMbqaAMz0eyVncEN1SkZeFDZZ6m494yQ2A1VrRRIedbOqQ?continueMode=true&_x_zm_rtaid=7vVkZDK2TwGMX5oPadx1lw.1588784054265.d044caa7fa16a8b5e8e6ecfd5147b5a0&_x_zm_rhtaid=763)

*Associated Files:*

* 200323\_python\_tutorial\_WIP

200323\_python\_tutorial

Week 2 (3/30) – Using Python and Pandas to analyze behavior data, day 1

*Associated Files:*

* 200330\_python\_behavior\_data\_tutorial
* 200330\_python\_behavior\_data\_tutorial\_WIP
* sucrose\_pref\_sample\_data.xlsx

[Week 3 (4/6) – Using Python and Pandas to analyze behavior data, day 2](https://duke.zoom.us/rec/play/uZZ-db_7-Gk3GdLEuQSDB_N7W47sJ_2s2yUZ_PQInRu8V3MEMAfzb-AQY-uKLGJddZn0JWHEZnU1NYr4?continueMode=true&_x_zm_rtaid=7vVkZDK2TwGMX5oPadx1lw.1588784054265.d044caa7fa16a8b5e8e6ecfd5147b5a0&_x_zm_rhtaid=763)

*Associated Files:*

* 200406\_python\_behavior\_data\_tutorial\_2
* sociability\_sample\_data.xlsx

[Week 4 (4/13) – Using Python and Pandas to clean, manipulate, and visualize sample RNAseq data](https://duke.zoom.us/rec/play/vMUsIuyvqTI3HNOdswSDBfFxW469f6ysh3Ud-vpbzUeyWiIHNwbyNbBGN7Es0hnTnvgcvvASYtL9ivBJ?continueMode=true&_x_zm_rtaid=7vVkZDK2TwGMX5oPadx1lw.1588784054265.d044caa7fa16a8b5e8e6ecfd5147b5a0&_x_zm_rhtaid=763)

(PW: N6=6X#5&)

*Associated Files:*

* 200413\_python\_tutorial\_hw\_empty
* 200413\_python\_tutorial\_hw\_solns
* gocke2016\_taxonomy\_mouse\_striatum\_GSE82187.csv

[Week 5 (4/20) – Introduction to R, RStudio, and dplyr](https://duke.zoom.us/rec/play/6MJ7Ier9rmo3TNKSuQSDAaQvW47sK6-sg3RP_fcFnkjkW3UBMQCmNbMTM7DjZAzJMfLaLM5nzgUQAKF1?continueMode=true&_x_zm_rtaid=7vVkZDK2TwGMX5oPadx1lw.1588784054265.d044caa7fa16a8b5e8e6ecfd5147b5a0&_x_zm_rhtaid=763)

*Associated Files:*

* 200420\_r\_dplyr\_tutorial

[Week 6 (4/27) – Introduction to GGplot in R](https://duke.zoom.us/rec/play/68EuJb2rq2g3GYaXuQSDUPQvW43pKf2s0yUa-fYFxB28BngFOlejN7YSNrEVVyrVaqoP4vRFNIVb7eQl?continueMode=true&_x_zm_rtaid=7vVkZDK2TwGMX5oPadx1lw.1588784054265.d044caa7fa16a8b5e8e6ecfd5147b5a0&_x_zm_rhtaid=763)

*Associated Files:*

* 200427\_r\_ggplot\_tutorial
* 200427\_ggplot\_tutorial\_slides

[Week 7 (5/4) – Using R, dplyr, and GGplot to clean and visualize sample RNAseq data](https://duke.zoom.us/rec/play/vMYuIr2rrjw3GdzB5QSDCqN8W9Tve_-shHRK_aEIyUuyUnVVZgLwZbAbZLfpx9FC1N_mEWL-0V_Lk2Vf?continueMode=true&_x_zm_rtaid=7vVkZDK2TwGMX5oPadx1lw.1588784054265.d044caa7fa16a8b5e8e6ecfd5147b5a0&_x_zm_rhtaid=763)

*Associated Files:*

* 200504\_ggplot\_tutorial\_rnaseq
* 200504\_ggplot\_tutorial\_rnaseq\_WIP
* gocke2016\_taxonomy\_mouse\_striatum\_GSE82187.csv

[Week 8 (5/11) – Deep dive into GGplot and making different types of visualizations](https://duke.zoom.us/rec/play/78V-c7r5q243G9HHuQSDA6UqW46_eq-s0SYar_NcyxuyVyICM1uiZrMTa-K-tv0c9n6bSwxvzHLT_Meu?continueMode=true&_x_zm_rtaid=d5FWXtUFT3yZ0flDoyO1sQ.1589213924802.96ca31097fd476e32def57e49a9d2727&_x_zm_rhtaid=527)

*Associated Files:*

* 200511\_ggplot\_tutorial\_rnaseq\_plotting
* gocke2016\_taxonomy\_mouse\_striatum\_GSE82187.csv

[Week 9 (5/18) – Using Seurat to cluster cells from scRNAseq](https://duke.zoom.us/rec/play/78YsdO_7pz43EtSd4wSDUPF8W9S1Kv2sgCZI_vIEzkzkUHAEZ1H1MOEWYrQ2MZEs3VKvMmM0Hc_7zuoO?continueMode=true&_x_zm_rtaid=xIqih6M7SjO_WnXrocXblA.1589818665990.765169ce36f9ee309c1b7b1a29fb0623&_x_zm_rhtaid=956)

*Associated Files:*

* 200518\_seurat\_tutorial\_striatum\_data
* gocke2016\_taxonomy\_mouse\_striatum\_GSE82187.csv

[Week 10 (6/01) – Installing third party packages and using them in Python](https://duke.zoom.us/rec/play/usIoI--g-jg3E9TAswSDAqItW427fa-s23Ab_PYKmh68BiQLZlvybrJANOtDV38bPr605zuDtGX53Si6?continueMode=true&_x_zm_rtaid=ggRMZShwTQmu7Fhge4MTHg.1591294756849.47a33ea84d5f7169bb48caa193355dff&_x_zm_rhtaid=163)

*Associated Files:*

* 200604\_developmental\_index.ipynb
* 200601\_developmental\_index\_WIP.ipynb
* mathys2017\_microglia\_cpk25\_GSE103334.csv
* unique\_data\_microglia\_index\_gene\_list.csv