BIOINFORMATICS EDA

1. pySeqRNA – an automated Python package for RNA sequencing data analysis

<https://www.rna-seqblog.com/pyseqrna-an-automated-python-package-for-rna-sequencing-data-analysis/>

1. Predictor de mutaciones patológicas para una familia de proteínas

<http://openaccess.uoc.edu/webapps/o2/bitstream/10609/97847/6/msalinerodTFM0619memoria.pdf>

1. PDB\_EDA package

<https://pypi.org/project/pdb-eda/>

1. Biopython

<https://aprenderly.com/doc/1216112/biopython-b%C3%A1sico>

1. Youtube

<https://www.youtube.com/watch?v=7hjd5AsJ0Jw>

1. Medium

<https://medium.com/swlh/python-tools-for-single-cell-rna-seq-analysis-fe89539972bc>

1. Research gate

<https://www.researchgate.net/figure/The-workflow-of-Python-RNA-Seq-data-analysis-The-diagram-shows-the-main-steps-and_fig1_318404237>

1. RNA seq excercies

<https://schatz-lab.org/teaching/exercises/rnaseq/>

1. KAGGLE

<https://www.kaggle.com/kevinarvai/genetic-variant-classifications-eda>

1. A comprehensive introduction to your genome with the SciPy Stack

<https://www.toptal.com/python/comprehensive-introduction-your-genome-scipy>

1. Bio python

http://biopython.org/DIST/docs/tutorial/Tutorial.html

1. KAGGLE My human genome

<https://www.kaggle.com/adnanawan/23andme-snp-analysis>

**ISCHAEMIC HEART DISEASE**

* IMPORTANCIA DEL CASO DE USO

The top 10 causes of death – WHO

https://www.who.int/news-room/fact-sheets/detail/the-top-10-causes-of-death

* JUSTIFICAR BUSINESS CASE

**The value of prevention**

<https://www.health.harvard.edu/heart-health/the-value-of-prevention>

* WHAT TO WORK WITH
* Zeeshan-ul-hassan Usmani Genome 6,000 Base-Pairs of Phenotype SNPs - Complete Raw Data KAGGLE
* Find information about what are the genes that encode for heart disease
* <https://www.revespcardiol.org/en-the-genetics-ischemic-heart-disease-articulo-S188558571730289X>
* <https://academic.oup.com/eurheartj/article/37/43/3267/2658448>
* <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5935119/>

OTHER

Predict life-expectancy base don genome

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3405107/>

<https://www.bionews.org.uk/page_140916>

<https://futurism.com/neoscope/lifespan-score-prediction-dna>

Predict age from the transcriptome of human dermal fibroblasts

<https://github.com/jasongfleischer/Predicting-age-from-the-transcriptome-of-human-dermal-fibroblasts>

Age and life expectancy clocks based on machine learning analysis of mouse frailty

<https://www.nature.com/articles/s41467-020-18446-0>

Complete genomics

<https://www.completegenomics.com/public-data/69-genomes/>

<https://www.completegenomics.com/documents/PublicGenomes.pdf>

My genome:

* 23 and me

<https://you.23andme.com/covid19-study/>

* Myheritage

<https://www.myheritage.es/>

Ethical use of data ?¿

<https://computerhoy.com/reportajes/life/muy-divertido-pedir-analisis-genetico-adn-pero-detras-esconde-negocio-millonario-561193>

All sources should be cited, the \verb|\autocite| command from Bib\LaTeX\ is the best to use. For example, the command \verb|\autocite{BrandonD.G2008Mcom}| is typeset as \autocite{BrandonD.G2008Mcom}. Some other commands can be useful, these can be investigated in section~3.9 of the \href{http://mirror.ox.ac.uk/sites/ctan.org/macros/latex/contrib/biblatex/doc/biblatex.pdf}{Bib\LaTeX\ user manual}.