References for final project

1. (2015, April 28). Analyze your own microarray data in R/Bioconductor. Bioconductor. Retrieved April 22, 2024, from <https://wiki.bits.vib.be/index.php/Analyze_your_own_microarray_data_in_R/Bioconductor#GCRMA_in_oligo>
2. (2019, March 19). Run affy package encounts clariomdhumancdf error. Bioconductor. Retrieved April 23, 2024, from <https://support.bioconductor.org/p/118573/>
3. (n.d.). Transcriptome Analysis Console (TAC) Software. Thermofisher. Retrieved March 2, 2024, from <https://www.thermofisher.com/ca/en/home/life-science/microarray-analysis/microarray-analysis-instruments-software-services/microarray-analysis-software/affymetrix-transcriptome-analysis-console-software.html>
4. (n.d.). Mastering Microarray Data Analysis: A Step-by-Step R/Bioconductor Tutorial. Omics Tutorials. <https://omicstutorials.com/mastering-microarray-data-analysis-a-step-by-step-r-bioconductor-tutorial/#Chip_pseudo_images_in_affy>
5. (2015, April 28). How to create chip pseudo-images. Bioconductor. Retrieved April 25, 2024, from <https://wiki.bits.vib.be/index.php/How_to_create_chip_pseudo-images#Chip_pseudo_images_in_oligotutorial/#Chip_pseudo_images_in_affy>
6. (n.d.). Microarray normalization. Carnegie Mellon Univesity. <https://www.cs.cmu.edu/~epxing/Class/10810/lecture/recitation7.pdf#pagemode=thumbs>
7. (n.d.). Microarray Data processing with RMA. GTK Teaching. <https://gtk-teaching.github.io/Microarrays-R/05-DataNormalisation/index.html>
8. Irizarry, R. A., Hobbs, B., Collin, F., Beazer-Barclay, Y. D., Antonellis, K. J., Scherf, U., & Speed, T. P. (2003). Exploration, normalization, and summaries of high density oligonucleotide array probe level data. Biostatistics (Oxford, England), 4(2), 249–264. doi:10.1093/biostatistics/4.2.249
9. Zhao, Y., Wong, L., & Goh, W. W. B. (2020). How to do quantile normalization correctly for gene expression data analyses. Scientific Reports, 10(1), 15534. doi:10.1038/s41598-020-72664-6
10. Giorgi, F.M., Bolger, A.M., Lohse, M. *et al.* Algorithm-driven Artifacts in median polish summarization of Microarray data. *BMC Bioinformatics* 11, 553 (2010). <https://doi.org/10.1186/1471-2105-11-553>
11. (2019). Transcriptome Analysis Console (TAC) 4.0.2. AppliedBiosystems. Retrieved April 25, 2024, from <https://assets.thermofisher.com/TFS-Assets/LSG/manuals/tac_user_manual.pdf>
12. (n.d.). Microarray normalization using Signal Space Transformation with probe Guanine Cytosine Count Correction. Affymetrix. <https://tools.thermofisher.cn/content/sfs/brochures/sst_gccn_whitepaper.pdf>
13. (2022). Passage Number Effects in Cell Lines. ATCC. <https://www.atcc.org/resources/technical-documents/passage-number-effects-in-cell-lines#:~:text=Cell%20lines%20at%20high%20passage,compared%20to%20lower%20passage%20cells>.
14. (n.d.). Mitomycin C ready made solution. Milipore Sigma. <https://www.sigmaaldrich.com/CA/en/product/sigma/m5353>
15. McDermaid, A., Monier, B., Zhao, J., Liu, B., & Ma, Q. (2019). Interpretation of differential gene expression results of RNA-seq data: review and integration. Briefings in Bioinformatics, 20(6), 2044–2054. doi:10.1093/bib/bby067
16. Yang, Y. H., Dudoit, S., Luu, P., Lin, D. M., Peng, V., Ngai, J., & Speed, T. P. (2002). Normalization for cDNA microarray data: a robust composite method addressing single and multiple slide systematic variation. Nucleic Acids Research, 30(4), e15. doi:10.1093/nar/30.4.e15
17. Desai, S. D. (2015). ISG15: A double edged sword in cancer. Oncoimmunology, 4(12), e1052935. doi:10.1080/2162402X.2015.1052935
18. Liu, M., Guo, S., & Stiles, J. K. (2011). The emerging role of CXCL10 in cancer (Review). Oncology Letters, 2(4), 583–589. doi:10.3892/ol.2011.300
19. Fleith, R. C., Mears, H. V., Leong, X. Y., Sanford, T. J., Emmott, E., Graham, S. C., … Sweeney, T. R. (2018). IFIT3 and IFIT2/3 promote IFIT1-mediated translation inhibition by enhancing binding to non-self RNA. Nucleic Acids Research, 46(10), 5269–5285. doi:10.1093/nar/gky191
20. Pidugu, V. K., Pidugu, H. B., Wu, M.-M., Liu, C.-J., & Lee, T.-C. (2019). Emerging functions of human IFIT proteins in cancer. Frontiers in Molecular Biosciences, 6, 148. doi:10.3389/fmolb.2019.00148
21. van de Wiel, M. A., Te Beest, D. E., & Münch, M. M. (2019). Learning from a lot: Empirical Bayes for high‐dimensional model‐based prediction. Scandinavian Journal of Statistics, Theory and Applications, 46(1), 2–25. doi:10.1111/sjos.12335
22. Mossman, K. L., Macgregor, P. F., Rozmus, J. J., Goryachev, A. B., Edwards, A. M., & Smiley, J. R. (2001). Herpes simplex virus triggers and then disarms a host antiviral response. Journal of Virology, 75(2), 750–758. doi:10.1128/JVI.75.2.750-758.2001