Winter Quarter 2022, Schedule of papers

Week 1 (January 4) – Basic principles and issues relevant to RNA seq data

Discussion leader(s): Taylor Johnson

Primary paper(s):

Lowe, R., Shirley, N., Bleackley, M., Dolan, S., & Shafee, T. (2017). Transcriptomics technologies. PLoS computational biology, 13(5), e1005457.

Secondary paper(s):

Oshlack, A., Robinson, M. D., & Young, M. D. (2010). From RNA-seq reads to differential expression results. Genome biology, 11(12), 1-10.

Week 2 (January 11) – Normalization of RNA-seq data

Discussion leader(s): Nobu Masaki

Primary paper(s):

Vallejos, C. A., Risso, D., Scialdone, A., Dudoit, S., & Marioni, J. C. (2017). Normalizing single-cell RNA sequencing data: challenges and opportunities. Nature methods, 14(6), 565-571.

Secondary paper(s):

Robinson, M. D., & Oshlack, A. (2010). A scaling normalization method for differential expression analysis of RNA-seq data. Genome biology, 11(3), 1-9.

Additional reading:

Lytal, N., Ran, D., & An, L. (2020). Normalization methods on single-cell RNA-seq data: an empirical survey. *Frontiers in genetics*, *11*, 41.

Week 3 (January 18) – Batch effects & technical noise

Discussion leader(s): Elena Romero

Primary paper(s):

Leek, J. T., Scharpf, R. B., Bravo, H. C., Simcha, D., Langmead, B., Johnson, W. E., ... & Irizarry, R. A. (2010). Tackling the widespread and critical impact of batch effects in high-throughput data. Nature Reviews Genetics, 11(10), 733-739.

Brennecke, P., Anders, S., Kim, J. K., Kołodziejczyk, A. A., Zhang, X., Proserpio, V., ... & Heisler, M. G. (2013). Accounting for technical noise in single-cell RNA-seq experiments. Nature methods, 10(11), 1093-1095.

Additional reading:

Tran, H. T. N., Ang, K. S., Chevrier, M., Zhang, X., Lee, N. Y. S., Goh, M., & Chen, J. (2020). A benchmark of batch-effect correction methods for single-cell RNA sequencing data. Genome biology, 21(1), 1-32.

Week 4 (January 25) – Spatial reconstruction of single cell experiments

Discussion leader(s): Hang Yin and Nicholas Irons

Primary paper(s):

Satija, R., Farrell, J. A., Gennert, D., Schier, A. F., & Regev, A. (2015). Spatial reconstruction of single-cell gene expression data. Nature biotechnology, 33(5), 495-502.

Secondary paper(s):

Duò, A., Robinson, M. D., & Soneson, C. (2018). A systematic performance evaluation of clustering methods for single-cell RNA-seq data. F1000Research, 7.

Additional reading:

Kiselev, V. Y., Andrews, T. S., & Hemberg, M. (2019). Challenges in unsupervised clustering of single-cell RNA-seq data. Nature Reviews Genetics, 20(5), 273-282.

Sun, S., Zhu, J., Ma, Y., & Zhou, X. (2019). Accuracy, robustness and scalability of dimensionality reduction methods for single-cell RNA-seq analysis. Genome biology, 20(1), 1-21.

Week 5 (February 1) – RNA-seq application to real data - 1

Discussion leader(s): Hanley Kingston

Primary paper(s):

Puram, S. V., Tirosh, I., Parikh, A. S., Patel, A. P., Yizhak, K., Gillespie, S., ... & Bernstein, B. E. (2017). Single-cell transcriptomic analysis of primary and metastatic tumor ecosystems in head and neck cancer. Cell, 171(7), 1611-1624.

Week 6 (February 8) – Capstone project presentation

Discussion leader(s): Sanne Aalbers

Primary paper(s):

Willems, T., Zielinski, D., Yuan, J., Gordon, A., Gymrek, M., & Erlich, Y. (2017). Genome-wide profiling of heritable and de novo STR variations. *Nature methods, 14*(6), 590-592.

Week 7 (February 15) – Stochasticity in gene expression and RNA splicing

Discussion leader(s): Seth Temple

Primary paper(s):

Marinov, G. K., Williams, B. A., McCue, K., Schroth, G. P., Gertz, J., Myers, R. M., & Wold, B. J. (2014). From single-cell to cell-pool transcriptomes: stochasticity in gene expression and RNA splicing. Genome research, 24(3), 496-510.

Week 8 (February 22) – Differential alternative splicing

Discussion leader(s): Diane Xue and Amanda Kunkle

Primary paper(s):

Shen, S., Park, J. W., Lu, Z. X., Lin, L., Henry, M. D., Wu, Y. N., ... & Xing, Y. (2014). rMATS: robust and flexible detection of differential alternative splicing from replicate RNA-Seq data. Proceedings of the National Academy of Sciences, 111(51), E5593-E5601.

Week 9 (March 1) – Imputation, errors & missing data

Discussion leader(s): Zorian Thornton

Primary paper(s):

Li, W. V., & Li, J. J. (2018). An accurate and robust imputation method scImpute for single-cell RNA-seq data. Nature communications, 9(1), 1-9.

Secondary paper(s):

Patruno, L., Maspero, D., Craighero, F., Angaroni, F., Antoniotti, M., & Graudenzi, A. (2021). A review of computational strategies for denoising and imputation of single-cell transcriptomic data. Briefings in Bioinformatics, 22(4), bbaa222.

Week 10 (March 8) – RNA-seq application to real data - 2

Discussion leader(s): Ruoyi Cai

Primary paper(s): Zhou, Y. et al (2020) Human and mouse single-nucleus transcriptomics reveal TREM2-dependent and TREM2-independent cellular responses in Alzheimer's disease. Nature Medicine, 26(1):131-142.