Tentative Reading List

Textbook:

Ian J. Goodfellow, Yoshua Bengio and Aaron Courville, *Deep Learning*, MIT Press, 2016
https://www.deeplearningbook.org

Papers:

1. Zhou, Jian et al. "Deep learning sequence-based ab initio prediction of variant effects on expression and disease risk." *Nature genetics* vol. 50,8 (2018): 1171-1179. doi:10.1038/s41588-018-0160-6
2. Hwang, B., Lee, J.H. & Bang, D. "Single-cell RNA sequencing technologies and bioinformatics pipelines". *Exp Mol Med* **50,** 96 (2018).
3. Zhou, J., Troyanskaya, O. "Predicting effects of noncoding variants with deep learning–based sequence model". *Nat Methods* **12,** 931–934 (2015).
4. Li, X., Kim, Y., Tsang, E. *et al.* "The impact of rare variation on gene expression across tissues". *Nature* **550,** 239–243 (2017).
5. Edwards, Stacey L et al. "Beyond GWASs: illuminating the dark road from association to function." *American journal of human genetics* vol. 93,5 (2013): 779-97.
6. Eraslan, G., Avsec, Ž., Gagneur, J. *et al.* "Deep learning: new computational modelling techniques for genomics". *Nat Rev Genet***20,** 389–403 (2019).
7. Alipanahi, B., Delong, A., Weirauch, M. *et al.* "Predicting the sequence specificities of DNA- and RNA-binding proteins by deep learning". *Nat Biotechnol* **33,** 831–838 (2015).
8. Kreimer, Anat et al. "Predicting gene expression in massively parallel reporter assays: A comparative study." *Human mutation* vol. 38,9 (2017): 1240-1250.
9. Trung Nghia Vu, Ha-Nam Nguyen, Stefano Calza, Krishna R Kalari, Liewei Wang, Yudi Pawitan, "Cell-level somatic mutation detection from single-cell RNA sequencing", *Bioinformatics*, Volume 35, Issue 22, 15 November 2019, Pages 4679–4687
10. Vieth, B., Parekh, S., Ziegenhain, C. *et al.* "A systematic evaluation of single cell RNA-seq analysis pipelines". *Nat Commun* **10,** 4667 (2019).