🧬 ML for Genomics

🦎 [Lecture 1: Biological Background](#)

🧬 [Lecture 2: Gene Variation and Predicting TF Binding Sites](#)

📊 [Lecture 3: Predicting TF Binding Sites & Chromatin Accessibility](#)

🧋 [Lecture 4: Predicting Chromatin Accessibility](#)

🍥 [Lecture 5: Chromatin and Protein Folding](#)

🧃 [Lecture 6: Cell-Type Deconvolution](#)

🥚 [Lecture 7: Intro to Single Cell Transcriptomics and Dropout Imputation](#)

🍄 [Lecture 8: Batch correction, clustering, differential gene expression and cell type annotation in scRNA-seq](#)

💫 [Lecture 9: Trajectory Analysis from scRNA-seq](#)

🌌 [Lecture 10: Spatial Omics](#)

🧬 [Lecture 11: Integration of Different Single Cell Data Types](#)

After Lecture Papers 🕐

[Week 1: Base-resolution models of transcription-factor binding reveal soft motif syntax](#)

[Week 3: Deep learning sequence-based ab initio prediction of variant effects on expression and disease risk](#)

[Week 5: Benchmarking of cell type deconvolution pipelines for transcriptomics data](#)