**Genomic data science**

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| 1 | What is data science  R basics, Rstudio, Rmarkdown | Rmarkdown  Exercise in R (2.10) |
| 2 | Reproducible research  What is gene expression, RNA-seq  Types of data: FASTQ, microarray, counts, normalized  Normalization: upperquantile, CPM, FPKM, RPKM, TPM  Analyzing gene expression data: correlations, clustering, PCA | Github, Github with Rstudio  Exercise in gene expression (8.5.1) |
| 3 | Differential expression, fold-ratio, p-values, volcano plot  Normalization – upper quantile, RUVseq | Exercise in gene expression (8.5.2) |
| 4 | Functional enrichment analysis | Exercise in gene expression (8.5.3) |
| 5 | Processing raw data – QC, alignment, quantification  Microarray | Exercise in gene expression (8.5.4) |
| 6 | Pharmacogenomics - DepMap  Cell type deconvolution | DepMap  xCell |
| 7 | Cancer genomics – TCGA  Survival analysis | TCGA |
| 8 | Intro to machine learning  Clustering – knn, hierarchical  Regression – linear, logistic | Application of ML in gene expression |
| 10 | Single-cell RNA-seq  Dimensionality reduction – PCA, tSNE, UMAP | scRNA-seq |
| 11 | Single-cell RNA-seq |  |
| 12 | Shiny apps | Shiny |
| 13 | Project description |  |