| What_molecule | What_technique_is_used_for_the | What_molecular_aspec | Is_there_a_spec | What_type_of_c | What_preferences | Do_you_need_a | description | tutorials_and_tool_links |
|---|---|---|---|---|---|---|---|---|
| DNA | ATAC-seq | Chromatin accessibility | None | Concepts | command line | y | ATAC-seq is a method for determining chromatin accessibility a | https://informatics.fas.harvard.edu/atac-seq-guidelines.html |
| DNA | DNA | Chromatin accessibility | None | Raw | command line | what | ATAC-seq is a method for determining chromatin accessibility a | https://informatics.fas.harvard.edu/atac-seq-guidelines.html |
| DNA | ATAC-seq | Chromatin accessibility | None | Concepts | None | None | This is a slide deck that explains the concepts behind ATAC-se | https://training.galaxyproject.org/training-material/topics/epigenetics/tutorials/atac-seq/slides.html#1 |
| DNA | ATAC-seq | Chromatin accessibility | None | Raw | None | None | This is a slide deck that explains the concepts behind ATAC-se | https://training.galaxyproject.org/training-material/topics/epigenetics/tutorials/atac-seq/tutorial.html |
| DNA | Bisulfite sequencing | Methylation | None | Concepts | caper | None | This standard ENCODE ATAC-seq pipeline shows how ATAC-s | https://github.com/ENCODE-DCC/atac-seq-pipeline |
| DNA | Bisulfite sequencing | Methylation | None | Raw | mint | None | The mint pipeline analyzes single-end reads coming from sequencing | https://github.com/sartorlab/mint/blob/master/README.md |
| DNA | Bisulfite sequencing | Methylation | None | Raw | galaxy | None | This pipeline in Galaxy shows how methylation sequence data | https://training.galaxyproject.org/training-material/topics/epigenetics/tutorials/methylation-seq/tutorial.html |
| RNA | Bulk RNA-seq | Gene expression | Bulk | Concepts | none | None | These slides describe the concept behind bulk RNA-seq data | https://drive.google.com/file/d/1A9gNDIuD_c3ppF2k6vY3b0Vg5KZjchzp/view |
| RNA | Bulk RNA-seq | Gene expression | Bulk | Raw | R | None | This GitHub training RMarkdown based files show how one ca | https://github.com/AlexsLemonade/training-modules/blob/master/RNA-seq/README.md |
| RNA | Bulk RNA-seq | Gene expression | Bulk | Raw | R | None | This Data Carpentries lesson walks through the steps that nee | https://scienceparkstudygroup.github.io/rna-seq-lesson/aio/index.html |
| RNA | Bulk RNA-seq | Gene expression | Bulk | Concepts | galaxy | y | These Galaxy slides describe transcriptomics conceptual | https://training.galaxyproject.org/training-material/topics/transcriptomics/slides/introduction.html#1 |
| RNA | Bulk RNA-seq | Gene expression | Bulk | Summary reads | galaxy | y | These Galaxy slides describe how RNA-seq counts can be con | https://training.galaxyproject.org/training-material/topics/transcriptomics/tutorials/rna-seq-counts-to-genes/tutorial.html |
| RNA | Bulk RNA-seq | Gene expression | Bulk | Raw | galaxy | y | These Galaxy slides describe how RNA-seq reads can be conv | https://training.galaxyproject.org/training-material/topics/transcriptomics/tutorials/rna-seq-reads-to-counts/tutorial.html |
| RNA | Bulk RNA-seq | Gene expression | None | None | R | n | The EdgeR package helps downstream RNA-seq be analyzed. | https://www.bioconductor.org/packages/devel/bioc/vignettes/edgeR/inst/doc/edgeRUsersGuide.pdf |
| DNA | Chip-seq | DNA-protein binding | None | Raw | R | n | This book describes how to analyze ChiP-seq data. | http://bioconductor.org/books/3.14/csawBook/ |
| DNA | Chip-seq | DNA-protein binding | None | Raw | command line | n | This GitHub repository has files related to a workshop that des | https://nbisweden.github.io/workshop-archive/workshop-ChIP-seq/2018-11-07/labs/lab-processing.html |
| DNA | Chip-seq | DNA-protein binding | None | Concepts | command line | n | This webpage describes considerations one should think of wh | https://learn.gencore.bio.nyu.edu/chipseq-analysis/chip-seq-considerations/ |
| DNA | Chip-seq or ATAC-seq | DNA-protein binding | None | Concepts | none | n | These slides describe epigenomics assays: ChIP-seq and ATA | https://physiology.med.cornell.edu/faculty/skrabanek/lab/angsd/lecture_notes/13_lecture.pdf |
| DNA | DNA-seq | Base sequence | WGS/WXS | Concepts | command line | n | The GATK4 tool set allows you to process whole genome sequ | https://gatk.broadinstitute.org/hc/en-us/articles/360036194592-Getting-started-with-GATK4 |
| DNA | DNA-seq | Base sequence | WGS/WXS | Concepts | command line | None | This webpage also discusses how to use the GATK4 variant ca | https://gencore.bio.nyu.edu/variant-calling-pipeline-gatk4/ |
| DNA | DNA-seq | Base sequence | None | Raw | command line | None | CNVnator is a tool for CNV discovery and genotyping from de | https://github.com/abyzovlab/CNVnator |
| DNA | DNA-seq | Base sequence | WGS/WXS | Concepts | command line | n | This Galaxy training material discusses sequence analysis on a | https://training.galaxyproject.org/training-material/topics/sequence-analysis/ |
| DNA | DNA-seq | Base sequence | WGS/WXS | Concepts | galaxy | y | This Galaxy training material discusses variant analysis on a co | https://training.galaxyproject.org/training-material/topics/variant-analysis/ |
| DNA | DNA-seq | Base sequence | WGS/WXS | Concepts | command line | y | This webpage describes bioinformatics workflow for Whole G | https://www.cd-genomics.com/bioinformatics-workflow-for-whole-genome-sequencing.html |
| DNA | DNA-seq | Base sequence | WGS/WXS | Concepts | GensearchNGS | y | DNAseq Workflow in a Diagnostic Context and an Example of a Use | https://www.hindawi.com/journals/bmri/2015/403497/ |
| DNA | DNA-seq | Base sequence | WGS/WXS | Concepts | FastQC | n | A description of what a standard DNA-sequencing entails at ai | https://www.kolabtree.com/blog/a-step-by-step-guide-to-dna-sequencing-data-analysis/ |
| DNA | DNA-seq | Base sequence | WGS/WXS | Concepts | many | None | From FastQ data to high confidence variant calls: the Genome | https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4243306/pdf/nihms531590.pdf |
| RNA | Gene expression array | Gene expression | None | Summary stats | R | None | This training material from Alex's Lemonade Stand Foundation | https://alexslemonade.github.io/refinebio-examples/02-microarray/00-intro-to-microarray.html |
| RNA | Gene expression array | Gene expression | Bulk | Raw | R | None | The limma package helps analyze gene expression microarray | https://www.bioconductor.org/packages/devel/bioc/vignettes/limma/inst/doc/usersguide.pdf |
| RNA | Gene expression array | Gene expression | Bulk | Raw | R | None | This bioconductor tutorial shows how to normalize and proces | https://www.bioconductor.org/packages/release/workflows/vignettes/maEndToEnd/inst/doc/MA-Workflow.html |
| DNA | Hi-C | 3D structure | None | Raw | many | y | This Galaxy tutorial shows how to analyze HiC data | https://training.galaxyproject.org/training-material/topics/epigenetics/tutorials/hicexplorer/tutorial.html |
| DNA | Hi-C | 3D structure | None | None | many | y | This Galaxy tutorial shows how to analyze HiC data | https://training.galaxyproject.org/training-material/topics/epigenetics/tutorials/hicexplorer/tutorial.html |
| DNA | Hi-C | 3D structure | None | Concepts | command line | None | These slides describe the concepts behind HiC data | https://qcb.ucla.edu/wp-content/uploads/sites/14/2017/02/Workshop-10-HiC-D1.pdf |
| DNA | Hi-C | 3D structure | None | Raw | command line | None | The snakePipes HIC workflow allows users to process their HiC | https://snakepipes.readthedocs.io/en/latest/content/workflows/HiC.html |
| DNA | Methylation chip | Methylation | None | Concepts | command line | None | This Galaxy tutorial shows how to analyze epigenetic data | https://training.galaxyproject.org/training-material/topics/epigenetics/tutorials/ewas-suite/tutorial.html |
| DNA | Methylation chip | Methylation | None | Summary reads | R | None | This bioconductor tutorial shows how to normalize and proces | https://www.bioconductor.org/packages/release/workflows/vignettes/methylationArrayAnalysis/inst/doc/methylationArrayAnalysis.html |
| Protein | proteomics mass spec | Mass spec | None | Raw | many | n | This Galaxy tutorial shows how to analyze proteomics data | https://training.galaxyproject.org/training-material/topics/proteomics/ |
| Protein | proteomics mass spec | Mass spec | none | Concepts | many | n | This set of Galaxy training slides show information about prote | https://training.galaxyproject.org/training-material/topics/proteomics/slides/introduction.html#1 |
| Protein | proteomics mass spec | Mass spec | none | Raw | R | None | This Bioconductor pacakge shows how to analyze proteomic c | https://www.bioconductor.org/packages/release/workflows/vignettes/proteomics/inst/doc/proteomics.html |
| RNA | RNA-seq | Gene expression | Bulk | Summary reads | R | None | This training material from Alex's Lemonade Stand Foundation | https://alexslemonade.github.io/refinebio-examples/03-rnaseq/00-intro-to-rnaseq.html |
| RNA | RNA-seq | Gene expression | micro-RNA | Summary reads | R | None | Evaluate the performance of depth normalization methods in r | https://github.com/LXQin/PRECISION.seq |
| RNA | RNA-seq | Gene expression | micro-RNA | Summary reads | R | None | DANA is an approach for assessing the performance of norma | https://lxqin.github.io/DANA/ |
| RNA | RNA-seq | Gene expression | Bulk | Summary reads | R | None | This bioconductor tutorial describes | https://www.bioconductor.org/packages/devel/workflows/vignettes/rnaseqGene/inst/doc/rnaseqGene.html |
| RNA | RNA-seq | Gene expression | Bulk | Summary reads | R | None | A guide to creating design matrices for gene expression exper | https://www.bioconductor.org/packages/release/workflows/vignettes/RNAseq123/inst/doc/designmatrices.html |
| RNA | RNA-seq | Gene expression | Bulk | Raw | R | None | Swimming downstream: statistical analysis of differential trans | https://www.bioconductor.org/packages/release/workflows/vignettes/rnaseqDTU/inst/doc/rnaseqDTU.html |
| RNA | RNA-seq | Gene expression | Bulk | Summary reads | R | None | This bioconductor tutorial shows how to use EdgeR to perform | https://www.bioconductor.org/packages/release/workflows/vignettes/RnaSeqGeneEdgeRQL/inst/doc/edgeRQL.html |
| RNA | RNA-seq | Gene expression | Bulk | Raw | none | None | This webpage discusses how to properly handle bulk RNA-seq | https://rnaseq.uoregon.edu/ |
| RNA | RNA-seq | Gene expression | Bulk | Concepts | none | None | This webpage describes the underlying principles behind RNA | https://geneticeducation.co.in/rna-sequencing-principle-steps-methods-and-applications/ |
| RNA | RNA-seq | Gene expression | None | None | None | None | WebMeV application is useful for data visualization | https://web-mev.github.io/quickstart/ |
| RNA | RNA-seq | Gene expression | Single-cell | Raw | R | None | This bioconductor tutorial shows how to use R to analyze singl | http://bioconductor.org/books/3.15/OSCA.intro/ |
| RNA | RNA-seq | Gene expression | Single-cell | Raw | R | None | This bioconductor tutorial shows advanced techniques for ana | http://bioconductor.org/books/3.15/OSCA.advanced/ |
| RNA | RNA-seq | Gene expression | Single-cell | Raw | Python | None | SCGV is an interactive graphical tool for single-cell genomics | https://github.com/KrasnitzLab/SCGV |
| RNA | Single-cell RNA-seq | Gene expression | Single-cell | Concepts | none | None | This set of slides from Alex's Lemonade Stand Foundation des | https://drive.google.com/file/d/186niFprBKlCNsF53WpIhKbilMLawu-ms/view |
| RNA | Single-cell RNA-seq | Gene expression | Single-cell | Raw | R | None | This training material from Alex's Lemonade Stand Foundation | https://github.com/AlexsLemonade/training-modules/blob/master/scRNA-seq/README.md |
| RNA | Single-cell RNA-seq | Gene expression | Single-cell | Raw | R | None | This training material from NYU shows how to analyze single c | https://learn.gencore.bio.nyu.edu/single-cell-rnaseq/prerequisites/ |
| RNA | Single-cell RNA-seq | Gene expression | Single-cell | Raw | command line | None | These documentation guides from Salmon show how to analy | https://salmon.readthedocs.io/en/latest/alevin.html |
| RNA | Single-cell RNA-seq | Gene expression | Single-cell | Concepts | none | None | This Galaxy tutorial describes the concepts underlying single-c | https://training.galaxyproject.org/training-material/topics/transcriptomics/tutorials/scrna-intro/slides.html#1 |
| RNA | Single-cell RNA-seq | Gene expression | Single-cell | Raw | none | None | This Galaxy tutorial shows the basics of analyzing single-cell RI | https://training.galaxyproject.org/training-material/topics/transcriptomics/tutorials/scrna-preprocessing/tutorial.html |
| RNA | Single-cell RNA-seq | Gene expression | Single-cell | Raw | R | None | This book walks through the details of using single-cell RNA-se | https://www.singlecellcourse.org/ |
| RNA | Single-cell RNA-seq | Gene expression | Single-cell | Summary reads | R | None | Seurat is a useful R package for downstream analysis of single | https://satijalab.org/seurat/articles/get_started.html |
| RNA | Single-cell RNA-seq | Gene expression | Single-cell | Summary reads | R | None | scater is a useful R package for visualization of single-cell RNA | https://bioconductor.org/packages/devel/bioc/vignettes/scater/inst/doc/overview.html |
| RNA | Single-cell RNA-seq | Gene expression | Single-cell | Summary reads | R | None | scran is a useful R package for normalization of single-cell RNA | https://bioconductor.org/packages/devel/bioc/vignettes/scran/inst/doc/scran.html |

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|---|---|---|---|---|
| DNA-seq | | https://training.galaxyproject.org/training-material/topics/sequence-analysis/ | | |
| DNA-seq | | https://docs.gdc.cancer.gov/Data/Bioinformatics_Pipelines/DNA_Seq_Variant_Calling_Pipeline/ | | |
| DNA-seq | | https://www.nature.com/articles/s41598-018-25022-6 | | |
| DNA-seq | | https://genpipes.readthedocs.io/en/latest/user_guide/pipelines/gp_dnaseq.html | | |
| RNA-seq | | https://github.com/jhudsl/GDSCN_Book_Statistics_for_Genomics_RNA-seq | | |
| RNA-seq | summarized | https://github.com/AlexsLemonade/refinebio-examples | | |
| RNA | | https://github.com/AlexsLemonade/RNA-Seq-Exercises | | |
| RNA | | https://rnabio.org/ | | |
| RNA | un-processed | https://h3abionet.github.io/H3ABionet-SOPs/RNA-Seq | | |
| RNA | either | https://training.galaxyproject.org/training-material/topics/transcriptomics/ | | |
| RNA | | https://www.genepattern.org/rna-seq-analysis | | |
| DNA methylation | | https://training.galaxyproject.org/training-material/topics/epigenetics/ | | |
| ChiP-Seq | | https://training.galaxyproject.org/training-material/topics/epigenetics/ | | |
| ATAC-seq | | https://training.galaxyproject.org/training-material/topics/epigenetics/ | | |
| HiC | | https://training.galaxyproject.org/training-material/topics/epigenetics/ | | |
| Bulk RNA-seq | un-processed | https://github.com/AlexsLemonade/training-modules/tree/master/RNA-seq | | |
| single cell RNA-seq | un-processed | https://github.com/AlexsLemonade/training-modules/tree/master/scRNA-seq | | |
| ChIP-Seq | | https://www.coursera.org/lecture/network-biology/chip-seq-analysis-part-1-6TcVH | | |
| ChIP-Seq | | https://hbctraining.github.io/Intro-to-ChIPseq/schedule/2-day.html | | |
| proteomics | | https://www.genepattern.org/modules?taskType=Proteomics | | |
| RNA array | | | | |
| DNA array | | | | |
| non-coding | | | | |
| targeted sequencing | | | | |