Jacob McPherson, PharmD

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Chapter 1

About

This is a *sample* book written in **Markdown**. You can use anything that Pandoc's Markdown supports; for example, a math equation $a^2 + b^2 = c^2$.

1.1 Usage

Each **bookdown** chapter is an .Rmd file, and each .Rmd file can contain one (and only one) chapter. A chapter *must* start with a first-level heading: `# A good chapter`, and can contain one (and only one) first-level heading.

Use second-level and higher headings within chapters like: `## A short section` or `### An even shorter section`.

The `index.Rmd` file is required, and is also your first book chapter. It will be the homepage when you render the book.

1.2 Render book

You can render the HTML version of this example book without changing anything:

1. Find the **Build** pane in the RStudio IDE, and
2. Click on **Build Book**, then select your output format, or select "All formats" if you'd like to use multiple formats from the same book source files.

Or build the book from the R console:

To render this example to PDF as a `bookdown::pdf_book`, you'll need to install XeLaTeX. You are recommended to install TinyTeX (which includes XeLaTeX): https://yihui.org/tinytex/.

Chapter 2

Statistics

2.1 Introductory R

The official CRAN '*Intro2R'* https://cran.r-project.org/doc/manuals/r-release/R-intro.html,

Wickham and Grolemund's *'R4DS'* https://r4ds.had.co.nz/,

Douglas et al.'s '*Intro2R'* https://intro2r.com/

2.2 Advanced R

Wickham's *'Advanced R'* https://adv-r.hadley.nz/,

Wickham & Bryan's *'R Packages'* https://r-pkgs.org/,

Jeroen Janssens's *'DS at the CL'* https://www.datascienceatthecommandline.com/1e/,

Other readings can include the RMarkdown and Bookdown readings:

Xie, Dervieux & Riederer's *'R Markdown Cookbook'* https://bookdown.org/yihui/rmarkdown-cookbook/ and Xie, Allaire & Grolemund's R Markdown: '*The Definitive Guide'* https://bookdown.org/yihui/rmarkdown/,

Xie's *'bookdown'* https://bookdown.org/yihui/bookdown/ & *'blogdown'* https://bookdown.org/yihui/blogdown/

Lovelace, Nowosad & Muenchow's *'Geocomputation in R'* https://geocompr.robinlovelace.net/,

Fay et al.'s *'Engineering Production-Grade Shiny Apps'* https://engineering-shiny.org/

2.3 Introductory Statistical Programming

I've found W. Chang's *'Cookbook for R'* http://www.cookbook-r.com/, UCLA's Intro to R https://stats.oarc.ucla.edu/stat/data/intro_r/intro_r_interactive_flat.html & BU's Basic Statistical Analysis https://sphweb.bumc.bu.edu/otlt/MPH-Modules/BS/R/R-Manual/R-Manual_print.html the best single-page introduction for teaching R for statistics

Once you learn R and want a blend of R and statistical theory, A. Swoeney's https://antoinesoetewey.com/ excellent 'Stats and R' Blogdownhttps://github.com/AntoineSoetewey/statsandr provides a PDF in 'What statistical test should I do?' https://statsandr.com/blog/files/overview-statistical-tests-statsandr.pdf that users click the end-node links to follow.

More theory can be found at *Statistics for Biologists* https://www.nature.com/collections/qghhqm and its sub-page *Points of Significance* https://www.nature.com/collections/qghhqm/pointsofsignificance

Handbook of Statistical Analyses Using R HSAUR 3rd ed. https://rdrr.io/cran/HSAUR3/ entirely available online as individual chapter PDFs, with the associated HSAUR3 https://cran.r-project.org/web/packages/HSAUR3/index.html package in CRAN with Vignettes and official documentation reference manual https://cran.r-project.org/web/packages/HSAUR3/HSAUR3.pdf

2.4 Intermediate Statistical Programming

Regression: I've struggled to find reputable open-sourced pages of regression education, let alone incorporation in R, but the PSU STAT 501 https://online.stat.psu.edu/stat501/ has caught my attention

Ecology statistics with Oksanen's *vegan* GitHub https://github.com/vegandevs/vegan, rdocumentation https://rdocumentation.org/packages/vegan and CRAN https://cran.r-project.org/web/packages/vegan/index.html

2.5 Advanced Statistical Programming

High dimensional statistics can be learned from Borg & Groenen's '*Modern Multidmensional Scaling'* https://link.springer.com/book/10.1007/0-387-28981-X

2.6 Data Visualization

Data visualization should use ggplot2 from the Tidyverse https://www.tidyverse.org/,

Wickham's '*ggplot2'* https://ggplot2-book.org/, Wilke's *'Fundamentals of Data Visualization'* https://clauswilke.com/dataviz/,

W. Chang's *'R Graphics Cookbook'* 2e https://r-graphics.org/, and

DEFINNITELY give the ggplot2 extensions gallery https://exts.ggplot2.tidyverse.org/gallery/ a peek, that I most highly recommend Patil's *ggstatplot* https://github.com/IndrajeetPatil/ggstatsplot/

Chapter 3

Genomics

3.1 **Scientific Programming: Bioinformatics & Computational Biology**

3.1.1 Genomics

National Center for Biotechnology and Information (NCBI)](https://ncbiinsights.ncbi.nlm.nih.gov/))

The Bacterial and Viral Bioinformatics Resource Center (BVBRC)](https://www.bv-brc.org/))

European Molecular Biology Laboratories (EMBL)](https://www.embl.org/)) European Bioinformatics Institute (EBI)](https://www.ebi.ac.uk/research))

QIAGEN's Knowledge Hub,](https://www.qiagen.com/us/knowledge-and-support/knowledge-hub),) Bench Guide](https://www.qiagen.com/us/knowledge-and-support/knowledge-hub/bench-guide)) and Digital Insights,](https://digitalinsights.qiagen.com/),)

Swiss Institute for Bioinformatics (SIB)](https://www.sib.swiss/)) which Geert van Geest](https://github.com/GeertvanGeest)) introduced me to the SIB's AWS-Docker](https://github.com/sib-swiss/AWS-docker)) for getting RStudio Server, Jupyter and VSCode running on an AWS EC2 using Docker

Thermo Fisher's Learning Centers](https://www.thermofisher.com/us/en/home/technical-resources/learning-centers.html)) and

Education Connect,](https://www.thermofisher.com/us/en/home/digital-science/thermo-fisher-connect.html),)

Illumina,](https://www.illumina.com/science/education.html),) The user manual for the k-mer trees](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=Create_K_mer_Tree.html)) and SNP trees](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=Create_SNP_Tree.html)) are relatively more straight forward **WHEN USING WORKFLOWS**. Nonetheless, their visualization could use improvement; I naturally turn to **python** for bioinformatics and **R** for visualization

3.1.2 Metagenomics

16s rRNA gene sequencing with Illumina,](https://www.illumina.com/areas-of-interest/microbiology/microbial-sequencing-methods/16s-rrna-sequencing.html),) which feeds into either the current gold-standard open-source (python) tool QIIME2](https://qiime2.org/)) by Bolyen *et al.* 2019,](https://www.nature.com/articles/s41587-019-0209-9),) the superseded (C++) gold-standard tool, Mothur](https://github.com/mothur/mothur)) by Schloss *et al.* 2009,](https://journals.asm.org/doi/10.1128/AEM.01541-09),) which has a 16S rRNA gene sequencing tutorial](https://training.galaxyproject.org/archive/2021-10-01/topics/metagenomics/tutorials/mothur-miseq-sop/tutorial.html))

16s rRNA gene sequencing with CLC](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=Introduction_Metagenomics.html)) with associated white paper:](https://digitalinsights.qiagen.com/wp-content/uploads/2016/05/Characterizing-the-Microbiome-through-Targeted-Sequencing-of-Bacterial-16S-rRNA-and-Fungal-ITS-Regions_White-Paper_QIAGEN-Bioinformatics_0518_ww.pdf):) The CLC workflow for 16S follows an amplicon-based OTU clustering workflow](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=Amplicon_based_OTU_clustering.html)) that uses read trimming using their 'clc_quality_trim' program,](https://resources.qiagenbioinformatics.com/manuals/clcassemblycell/400/index.php?manual=Quality_trimming.html),) but **I would rather use** trimmomatic](http://www.usadellab.org/cms/?page=trimmomatic)) by Bolger, Lihse & Usadel, 2014;](https://pubmed.ncbi.nlm.nih.gov/24695404/);) filtering samples based on the number of reads;](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=Filter_Samples_Based_on_Number_Reads.html);) *de novo* or reference-based [OTU clustering] https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=OTU_clustering removal of low abundance OTUs;](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=Remove_OTUs_with_Low_Abundance.html);) OTU abundance analysis](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=Abundance_analysis.html)) **but I prefer R for this;**

OTU nucleotide alignment with MUSCLE](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=Align_OTUs_with_MUSCLE.html)) by Edgar, 2004](https://academic.oup.com/nar/article/32/

5/1792/2380623?login=true)) to generate a maximum likelihood phylogenetic tree,](http://resources.qiagenbioinformatics.com/manuals/clcgenomicsworkbench/current/index.php?manual),) input for the alpha- and beta-diversity workflow](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=Estimate_Alpha_Beta_Diversities_workflow.html)) **but I prefer vegan](https://vegandevs.github.io/vegan/index.html)) for this**

The microbial , PICRUST2,](https://github.com/picrust/picrust2),) and the interactive Human Microbiome Project (iHMP)](https://portal.hmpdacc.org/))

Illumina SGS](https://www.illumina.com/areas-of-interest/microbiology/microbial-sequencing-methods/shotgun-metagenomic-sequencing.html))

In CLC, whole metagenome shotgun sequencing functional analysis](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=Functional_analysis.html)) first includes the user *de novo* assembling a metagenome,](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=De_Novo_Assemble_Metagenome.html#sec:de_novo_assemble_metagenome),) followed by annotation of the coding sequence (CDS) track with

BLAST,](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=Annotate_CDS_with_Best_BLAST_Hit.html#sec:annotate_cds_with_blast),) Pfam domains,](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=Annotate_CDS_with_Pfam_Domains.html#sec:annotate_cds_with_pfam),) and/or

Gene Ontology (GO).](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=Download_GO_Database.html#sec:download_go).) Then you map the original reads back to the annotated contigs using the 'Map Reads to Reference' in the Build Functional Profile](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=Build_Functional_Profile.html#sec:functional_profile)) tool. The resulting output can be visualized using stacked bar charts and sunburst plots in Visualization of the OTU abundance table](https://resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manual=Visualization_OTU_abundance_tables.html#sec:visualizationotu)) **but as you guessed, I prefer R for this.** As you might expect, **I might use** the open-source Linux OS (python) tool PICRUSt2](https://github.com/picrust/picrust2)) by Douglas *et al.* 2020](https://www.nature.com/articles/s41587-020-0548-6)) to do this too.

Chapter 4

Pharmacology

4.1 Receptor Theory

Terry Kenakin's 'A Pharmacology Primer' https://www.sciencedirect.com/book/9780128139578/a-pharmacology-primer

Pharmacological Reviews https://pharmrev.aspetjournals.org/

Nature Reviews Drug Discovery https://www.nature.com/nrd/

British Journal of Pharmacology (BPJ) https://bpspubs.onlinelibrary.wiley.com/journal/14765381

Journal of Pharmacology and Experimental Therapeutics (JPET) https://www.aspet.org/aspet/journals/the-journal-of-pharmacology-and-experimental-therapeutics

Chapter 5

Favorite Journals

Academic Journals starting with

SCOUPS](https://www.scopus.com/)) that typically directs me to

Nature,](https://www.nature.com/),)

Science,](https://www.science.org/),)

Nature Medicine,](https://www.nature.com/nm/),)

Science Translational Medicine](https://www.science.org/journal/stm))

Laboratory methods in

Nature Methods,](https://www.nature.com/nmeth/),)

Nature Protocols,](https://www.nature.com/nprot/),) and

Springer|Nature Experiments](https://experiments.springernature.com/))

Cellular, Molecular Biology in

Bruce Albert's 'Molecular Biology of the Cell'](https://brucealberts.ucsf.edu/current-projects/molecular-biology-of-the-cell/))

Nature Reviews Molecular Cell Biology,](https://www.nature.com/nrm/),)

Cell Press,](https://www.cell.com/),)

Nature Structural & Molecular Biology,](https://www.nature.com/nsmb/),)

Signal Transduction and Targeted Therapy,](https://www.nature.com/sigtrans/),) and

Science Signaling](https://www.science.org/journal/signaling))

Clinical microbiology, metagenomics and microbial ecology (microbiome sciences) in

Manual of Clinical Microbiology](https://www.amazon.com/Clinical-Microbiology-Twelfth-Michael-Pfaller/dp/1555819834))

Principles of Virology](https://www.amazon.com/Principles-Virology-Multi-ASM-Books/dp/1683670329/))

Nature Reviews Microbiology,](https://www.nature.com/nrmicro/),)

Clinical Microbiology Reviews,](https://journals.asm.org/journal/cmr),)

Journal of Clinical Microbiology (J Clin Micro),](https://journals.asm.org/journal/jcm),)

Nature Microbiology,](https://www.nature.com/nmicrobiol/),)

International Society for Microbial Ecology Journal (ISMEJ),](https://www.nature.com/ismej/),)

Cell Host & Microbe,](https://www.cell.com/cell-host-microbe/),) the

Nature subject/Microbiology](https://www.nature.com/subjects/microbiology/nature)) which includes the more narrow subjects

Nature subject/Microbiome,](https://www.nature.com/subjects/microbiome/nature),)

Nature subject/Communities,](https://www.nature.com/subjects/communities/nature),)

Nature subject/Metagenomics,](https://www.nature.com/subjects/metagenomics/nature),) and the ecology & evolution journals

Annual Review of Ecology, Evolution and Systematics,](https://www.annualreviews.org/journal/ecolsys),) and

Nature Ecology and Evolution](https://www.nature.com/natecolevol/))

Infectious Diseases and antimicrobial stewardship pharmacy practice in

Antimicrobial Agents and Chemotherapy (AAC),](https://journals.asm.org/journal/aac),)

Nature subject/Antimicrobials,](https://www.nature.com/subjects/antimicrobials/nature),)

Clinical Infectious Diseases (CID),](https://academic.oup.com/cid),)

The Lancet Infectious Diseases,](https://www.thelancet.com/journals/laninf/home),)

NEJM Infectious Diseases,](https://www.nejm.org/infectious-disease),) and the CDC's

Morbidity and Mortality Weekly Report (MMWR)](https://www.cdc.gov/mmwr/)) and

Emerging Infectious Diseases (EID)](https://wwwnc.cdc.gov/eid/))

Nucleic Acid Biochemistry

Baxevanis, Bader & Wishart's 'Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins',](https://www.amazon.com/Bioinformatics-Practical-Guide-Analysis-Proteins/dp/1119335582/),)

Bioinformatics,](https://academic.oup.com/bioinformatics/),)

Nature Genetics,](https://www.nature.com/ng/),)

Nature Reviews Genetics,](https://www.nature.com/nrg/),)

Genome Biology,](https://genomebiology.biomedcentral.com/),)

Nucleic Acids Research,](https://academic.oup.com/nar/),) the

Annual Review of Genetics,](https://www.annualreviews.org/journal/genet),) and the

Annual Review of Genomics and Human Genetics](https://www.annualreviews.org/journal/genom))

Immunology in

Nature Immunology,](https://www.nature.com/ni/),)

Nature Reviews Immunology,](https://www.nature.com/nri/),)

Science Immunology,](https://www.science.org/toc/sciimmunol/current),) and

Mucosal Immunology](https://www.nature.com/mi/))

Artificial Intelligence in

Nature Machine Intelligence,](https://www.nature.com/natmachintell/),)

Science Robototics,](https://www.science.org/journal/scirobotics),) the

IEEE Transactions on Pattern Analysis and Machine Intelligence,](https://ieeexplore.ieee.org/xpl/RecentIssue.jsp?punumber=34),)

IEEE Transactions on Neural Networks and Learning Systems,](https://ieeexplore.ieee.org/xpl/RecentIssue.jsp?punumber=5962385),) the

International Journal of Intelligent Systems](https://onlinelibrary.wiley.com/journal/1098111x))

Information Sciences,](https://www.journals.elsevier.com/information-sciences),) the

Physics of Life Review,](https://www.sciencedirect.com/journal/physics-of-life-reviews),)

Artificial Intelligence Review,](https://www.springer.com/journal/10462),) *Knowledge-Based Systems*,](https://www.journals.elsevier.com/knowledge-based-systems),)

Neural Networks,](https://www.journals.elsevier.com/neural-networks),)

Neural Computing and Applications,](https://www.springer.com/journal/521),) the

International Journal of Computer Vision,](https://www.springer.com/journal/11263),) and the journal

Pattern Recognition](https://www.sciencedirect.com/journal/pattern-recognition))

Chapter 6

Artificial Intelligence

Artificial Intelligence in

Nature Machine Intelligence,](https://www.nature.com/natmachintell/),)

Science Robototics,](https://www.science.org/journal/scirobotics),) the

IEEE Transactions on Pattern Analysis and Machine Intelligence,](https://ieeexplore.ieee.org/xpl/RecentIssue.jsp?punumber=34),)

IEEE Transactions on Neural Networks and Learning Systems,](https://ieeexplore.ieee.org/xpl/RecentIssue.jsp?punumber=5962385),) the

International Journal of Intelligent Systems](https://onlinelibrary.wiley.com/journal/1098111x))

Information Sciences,](https://www.journals.elsevier.com/information-sciences),) the

Physics of Life Review,](https://www.sciencedirect.com/journal/physics-of-life-reviews),)

Artificial Intelligence Review,](https://www.springer.com/journal/10462),)

Knowledge-Based Systems,](https://www.journals.elsevier.com/knowledge-based-systems),)

Neural Networks,](https://www.journals.elsevier.com/neural-networks),)

Neural Computing and Applications,](https://www.springer.com/journal/521),) the

International Journal of Computer Vision,](https://www.springer.com/journal/11263),) and the journal

Pattern Recognition](https://www.sciencedirect.com/journal/pattern-recognition))

DeepMind](https://github.com/deepmind)) is an excellent gold-standard for the capability of deep-learning in the biological sciences, AlphaFold](https://github.com/deepmind/alphafold)) and the other amazing discoveries](https://github.com/deepmind/deepmind-research)) at DeepMind. The AlphaFold Colab](https://colab.research.google.com/github/deepmind/alphafold/blob/main/notebooks/AlphaFold.ipynb)) is also freely available as a simplified implementation.

RoseTTAfold](https://github.com/RosettaCommons/RoseTTAFold)) by Baek et al., 2021](https://www.science.org/doi/10.1126/science.abj8754)) and OmegaFold](https://twitter.com/peng_illinois/status/1538536909814874113))

I think AWS SageMaker](https://docs.aws.amazon.com/sagemaker/latest/dg/how-it-works-training.html)) is best for its freedom of scalability; requires knowledge of AWS Data Science,](https://github.com/data-science-on-aws/data-science-on-aws),) and a review of the Sagemaker Workshop](https://github.com/awslabs/amazon-sagemaker-workshop)) and Examples](https://github.com/aws/amazon-sagemaker-examples))

The Microsoft DoWhy](https://github.com/py-why/dowhy)) library for causal inference](https://www.microsoft.com/en-us/research/blog/dowhy-a-library-for-causal-inference/)) recently popped on my radar

Further reading can be found at

Keras,](https://github.com/keras-team/keras),)

TensorFlow,](https://github.com/tensorflow/tensorflow),)

Scikit-Learn,](https://github.com/scikit-learn/scikit-learn),)

'An Intro to Statistical Learning'](https://www.statlearning.com/))

A. Geron's *Hands-On Machine-Learning*, 3rd ed.](https://github.com/ageron/handson-ml3))

F. Chollet's *Deep-Learning with Python*](https://github.com/fchollet/deep-learning-with-python-notebooks))

Nvidia's 'Deep-Learning Examples' in Python](https://github.com/NVIDIA/DeepLearningExamples))

Machine Learning with R](https://machinelearningmastery.com/machine-learning-with-r/))

'Deep learning with R' 2nd ed.](https://livebook.manning.com/book/deep-learning-with-r-second-edition/welcome/v-1/1))

Chapter 7

Computer Science

7.1 Computer science communities

R,](https://www.r-project.org/),)

RStudio,](https://www.rstudio.com/),)

Tidyverse,](https://www.tidyverse.org/),)

Bookdown,](https://bookdown.org/),)

Python,](https://www.python.org/),)

BioPython,](https://biopython.org/),)

Anaconda](https://www.anaconda.com/)) ,

Julia,](https://julialang.org/),)

Docker,](https://www.docker.com/),)

Git,](https://git-scm.com/),)

GitHub **Co-pilot**,](https://github.com/features/copilot),)

LaTeX,](https://www.latex-project.org/),)

VSCode,](https://code.visualstudio.com/),)

AWS,](https://aws.amazon.com/),)

Ubuntu](https://www.ubuntu.com))

7.2 Containerization Learning Resources

The Official Docker Labs](https://github.com/docker/labs)) by Docker,](https:

//github.com/docker),)

The #1 Docker Labs](https://dockerlabs.collabnix.com/)) and Kubernetes Labs](https://collabnix.github.io/kubelabs/)) by Collabnix,](https://github.com/collabnix/),)

Containerization Training](https://container.training/)) by J. Petazzo,](https://github.com/jpetazzo/),)

The Docker *for beginniners* Curriculum](https://docker-curriculum.com/)) by P. Srivastav](https://github.com/prakhar1989/))

7.3 **Academic Programming**

Read in Zotero](https://github.com/zotero/zotero)) and cite using citr](https://github.com/crsh/citr)) for RStudio; optional: VSCode using Citation Picker](https://github.com/mblode/vscode-zotero)) and Better BibTeX](https://github.com/retorquere/zotero-better-bibtex))

**I made a public Zotero](https://www.zotero.org/groups/4734738/jacobs_public_papers/library))

for your reading enjoyment**

Chapter 8

Structural Biology

Structural biology is The Holy Grail of pharmacology; the dynamic states of pharmacological target activation/inactivation as determined by receptor theory

8.1 Cryogenic electronic microscopy (CryoEM)

The Theoretical and Computational Biophysics Group (TCBG) provides tutorial-based training](https://www.ks.uiuc.edu/Training/Tutorials/)) and a database of software for 3D molecular building,](https://www.ks.uiuc.edu/Development/biosoftdb/biosoft.cgi?&category=3),) dynamics](https://www.ks.uiuc.edu/Development/biosoftdb/biosoft.cgi?&category=2)) and visualization](https://www.ks.uiuc.edu/Development/biosoftdb/biosoft.cgi?&category=1))

Further resources can be found notably at the EMBLI-EBI,](https://www.ebi.ac.uk/training/search-results?query=structural-biology),) Stanford

The NIH established the following CryoEM Centers](https://www.cryoemcenters.org/cryoem-centers/)) through awards](https://www.nih.gov/news-events/news-releases/nih-funds-three-national-cryo-em-service-centers-training-new-microscopists)) to the

National Center for CryoEM Access and Training (NCCAT)](https://nccat.nysbc.org/)) at the New York Structural Biology Center (NYSBC),](https://nysbc.org/),) the

Pacific Northwest Center for Cryo-EM](https://pncc.labworks.org/)) at the Pacific Northwest National Laboratory(PNNL),](https://www.pnnl.gov/),) the

Stanford-SLACC Cryo-EM Center](https://cryoem-s2c2.slac.stanford.edu/)) at the National Accelerator Laboratory](https://www6.slac.stanford.edu/))

Online learning resources include:

Thermo Fisher's EM-Learning](https://em-learning.com/)) and

CryoEM Learning Center](https://www.thermofisher.com/us/en/home/electron-microscopy/life-sciences/learning-center.html)) by

Grant Jensen, CalTech,](https://cryo-em-course.caltech.edu/),) and

Matthijn Vos, the Pasteur Institute](https://research.pasteur.fr/en/team/nanoimaging/))

Yale CryoEM,](https://cryoem.yale.edu/cryo-em/workshops-and-online-courses),)

UNC CryoEM Core](https://www.med.unc.edu/cryo-em/)) lists resources available,](https://www.med.unc.edu/cryo-em/cryoem-links-and-resources/),) and

NIGMS National Resource for Automated Molecular Microscopy (NRAMM)](https://nramm.nysbc.org/workshops-and-courses/))

8.2 X-Ray Crystallography

Chapter 9

References:

9.1 Genomics

Pereira, et al. 2020 ‘Bioinformatics and Computational Tools for Next-Generation Sequencing Analysis in Clinical Genetics’

	Wet-lab Protocols	Dry-Lab Protocols
Thermo Fisher	Protocols	
QIAGEN	Bench Guide	
Illumina	NGS for Beginners, NGS Glossary, & NGS Workflow Steps DNA/RNA Isolation Considerations, Library Quality Control, NGS Library Preparation & Library Prep Automation, Sequencing Platforms, Sequencing Methods Explorer, Sequencing by Synthesis	Bioinformatics, Cloud NGS Data Bokulich et al., Nature Methods 2013 FastQ_format, Phred Scores, FastQC (NIAID YT and Tutorial) Trimmomatic (NIAID YT)