# Jacob McPherson, PharmD

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# Contents

# 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:

```
bookdown::render_book()
```

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/.

## 1.3   Preview book

As you work, you may start a local server to live preview this HTML book. This preview will update as you edit the book when you save individual .Rmd files. You can start the server in a work session by using the RStudio add-in "Preview book", or from the R console:

```
bookdown::serve_book()
```

# 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_in teractive_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://gith ub.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.natu re.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/inde x.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/vegan devs/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.tidyve rse.org/,

Wickham's '*ggplot2'* https://ggplot2-book.org/,

Wilke's *'Fundamentals of Data Visualization'* https://clauswilke.com/datav iz/,

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

**DEFINNITELY** give the ggplot2 extensions gallery https://exts.ggplot2.t idyverse.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.htm
l),) 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.qiagenbioi
nformatics.com/manuals/clcmgm/300/index.php?manual=Intro
duction_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/clcmg
m/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/ind
ex.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.qiagenbioinf
ormatics.com/manuals/clcmgm/300/index.php?manual=Filter_Samples_Ba
sed_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_Abun
dance.html);) OTU abundance analysis](https://resources.qiagenbioinformati
cs.com/manuals/clcmgm/300/index.php?manual=Abundance_analysis.html))
**but I prefer R for this;**

OTU nucleotide alignment with MUSCLE](https://resources.qiagenbioinforma
tics.com/manuals/clcmgm/300/index.php?manual=Align_OTUs_with_M
USCLE.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/clcgenomicswork bench/current/index.php?manual),) input for the alpha- and beta-diversity workflow](https://resources.qiagenbioinformatics.com/manuals/clcmgm/30 0/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/micr obial-sequencing-methods/shotgun-metagenomic-sequencing.html))

In CLC, whole metagenome shotgun sequencing functional analysis](https:// resources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?manu al=Functional_analysis.html)) first includes the user *de novo* assembling a metagenome,](https://resources.qiagenbioinformatics.com/manuals/clcmg m/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/30 0/index.php?manual=Annotate_CDS_with_Best_BLAST_Hit.html#sec: annotate_cds_with_blast),) Pfam domains,](https://resources.qiagenbioinfor matics.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/manua ls/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://re sources.qiagenbioinformatics.com/manuals/clcmgm/300/index.php?ma nual=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.qiagenbioinf ormatics.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.ed u/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?&c ategory=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.cryoemce nters.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/nano imaging/))

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) |

Intro to Bioinformatics by QIIME2_YT

Intro to QIIME2 Playlist including Importing & Demultiplexing, Denoising/Clustering (DADA2 by The Callahan Lab), Taxonomic Classification, Rarefaction and PhylogeneticReconstruction, Alphaand Beta-Diversity and Longitudinal Studies in Qiime2