

CORE LESSONS

Linux provides the foundation to handle big data. In this core unit, the basics of the Linux OS will be learned on one's own computer. Users will also learn to analyze and visualize big data via the statistical package, R.



INTRODUCTION TO LINUX

Modules 1-5

- MODULE 1: Installing Ubuntu on a Virtual Machine
- MODULE 2: Commands, Navigation, and Permissions
- MODULE 3: Finding and Downloading Data

<https://www.cst.temple.edu/~robie/playbigdata/assets/pages/modules-main.html>,

https://www.youtube.com/playlist?list=PLckPQEKYlbxebubMWdjcGR7K_ukm35ZjN,

Training Courses



As part of its work with the Babraham Institute, the Bioinformatics group runs a regular series of training courses on many aspects of bioinformatics.

These courses are run regularly on the Babraham site but we are also able to come out and present them on other sites and also deliver them remotely. You can see the [list](#) options for running courses on your site.

You can also sign up to our [mailing list](#) to get the latest training news delivered direct to your inbox every couple of months.

Where possible we also aim to make the material from our courses publicly available so that anyone who wants to can download them for their own use.

Below is a list of the courses we currently run. Where they are available there is a link to the training manual and course exercises.

Core Bioinformatics Skills

[Distance Courses](#)

<https://www.bioinformatics.babraham.ac.uk/training.html>,

EVOLUTION AND GENOMICS

Intensive and immersive training opportunities

WORKSHOPS LEARNING PEOPLE APPLY INFORMA

LEARNING

The Learning section of this website is where you will be able to locate the Learning Activities used during the [Workshops](#). Please select a focus area from the list below to be taken to individual learning activities.

- [UNIX Tutorial](#)
- [Genomics](#)
- [Phylogenetics](#)
- [Population and Speciation Genomics](#)
- [Population genetics](#)
- [Programming](#)
- [Workshop software installation](#)

<https://evomics.org/learning/>,

Sed - An Introduction and Tutorial by Bruce Barnett

[Home](#) [Unix/Linux ▼](#) [Security ▼](#) [Misc ▼](#) [References ▼](#) [Magic](#) [Search](#) [About](#) [Donate](#)

Last modified: Tue Jul 25 11:54:15 2023

[Donations ensure I keep this web site up and running. Thank you!](#)

I would appreciate it if you occasionally [buy me a coffee](#) or if you prefer, my [Ko-fi page is here](#)

My Venmo account is @Bruce-Barnett-31

[Click here to donate via paypal, and Thank you for the support](#)

Donate



Check out my [Sed Reference Chart \(pdf\)](#)

[Quick Links](#)

As a convenience, and to make my site more mobile-friendly, I moved my quick links to a new page: [Click Here](#)

[Table of Contents](#)

Note - You can click on the table of contents sections to jump to that section.

<https://www.grymoire.com/Unix/Sed.html>,

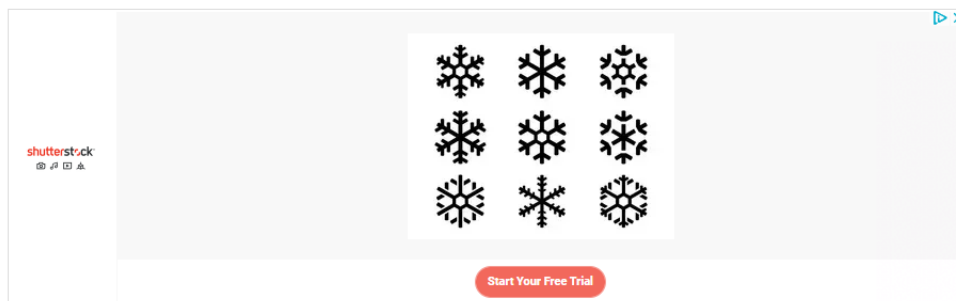
Reason I am here

Naomi Cavallero

Article Index

Tags

AWK GTF! How to Analyze a Transcriptome Like a Pro – Part 1



16 September 2013







This post belongs to a 3-part series on AWK: **Part 1** - [Part 2](#) - [Part 3](#)

The goal of this tutorial is to show a few of the cool things that the Unix tool AWK can do with tabular data. We will focus on extracting useful information from a [transcriptome](#)—because bioinformatics is cool—, but AWK can do its wonders with any kind of text file.

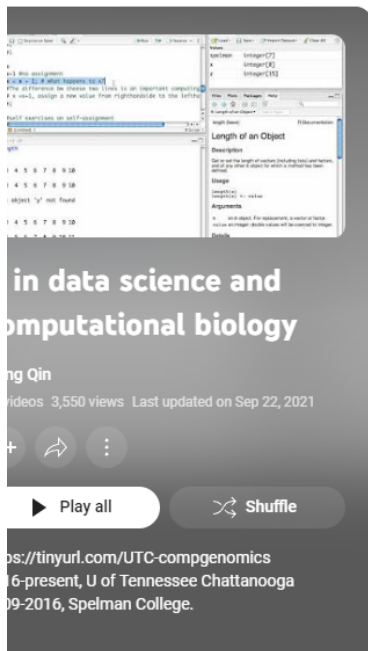
The tutorial has been carefully designed to make it easy for you to play along. So feel free to copy and paste the commands in your Unix terminal.

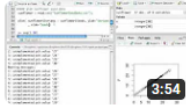
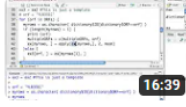
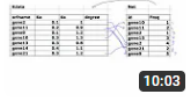

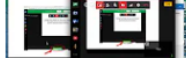
<https://reasoniamhere.com/2013/09/16/awk-gtf-how-to-analyze-a-transcriptome-like-a-pro-part-1/>,



- Search
- 1  **Installing R, RStudio, and RTools for Windows**
Nolan Bentley • 120 views • 1 year ago
 - 2  **Installing R and RStudio for iOS**
Nolan Bentley • 130 views • 1 year ago
 - 3  **A tour of RStudio Part 1**
Nolan Bentley • 175 views • 1 year ago
 - 4  **A tour of RStudio Part 2**
Nolan Bentley • 117 views • 1 year ago
 - 5  **Working directory and file paths in R**
Nolan Bentley • 120 views • 1 year ago
 - 6  **Importing data into RStudio**
Nolan Bentley • 172 views • 1 year ago

<https://www.youtube.com/playlist?list=PL1O4yAimiWhj6rxLgRLVOE76jXHGq0Vrf>



- Search
- 16 unavailable videos are hidden
- 1  **Convert an Excel file to csv, read into R and plot**
Hong Qin • 86K views • 11 years ago
 - 2  **Retrieve and analyze a gene expression data set from NCBI GEO in R**
Hong Qin • 38K views • 11 years ago
 - 3  **How to use R match() function to merge different data sets**
Hong Qin • 28K views • 11 years ago
 - 4  **Hierarchical Clustering by hclust in R on a distance matrix between four cities**
Hong Qin • 28K views • 11 years ago
 - 5  **How to use Youtube to live-record a Powerpoint presentation**
Hong Qin • 23K views • 8 years ago

<https://www.youtube.com/playlist?list=PLA54E692040796EA5>

adv-r.hadley.nz

How do I import m... CoreMIS - PSIS CHOPCHOP auburn Gmail YouTube Maps Login - Authenticate

Advanced R

Table of contents

Welcome

Preface

1 Introduction

Foundations

Introduction

2 Names and values

3 Vectors

4 Subsetting

5 Control flow

6 Functions

7 Environments

8 Conditions

Functional programming


Introduction

Welcome

This is the website for 2nd edition of "Advanced R", a book in Chapman & Hall's R Series. The book is designed primarily for R users who want to improve their programming skills and understanding of the language. It should also be useful for programmers coming to R from other languages, as help you to understand why R works the way it does.

If you're looking for the 1st edition, you can find it at <http://adv-r.had.co.nz/>.

License

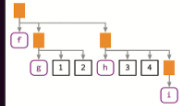


This work, as a whole, is licensed under a Creative Commons Attribution-NonCommercial-ShareAlike 4.0 International Licence

The R Series

Advanced R

Second Edition



Hadley Wickham

CRC Press

A CHAPMAN & HALL BOOK

On this page

Welcome

License

Other books


View source

Edit this page

<https://adv-r.hadley.nz/>,

theanalysisfactor.com/

How do I import m... CoreMIS - PSIS CHOPCHOP auburn Gmail YouTube Maps Login - Authenticate



subscribe to StatWise newsletter

our programs

statistical resources

blog

about

contact

log

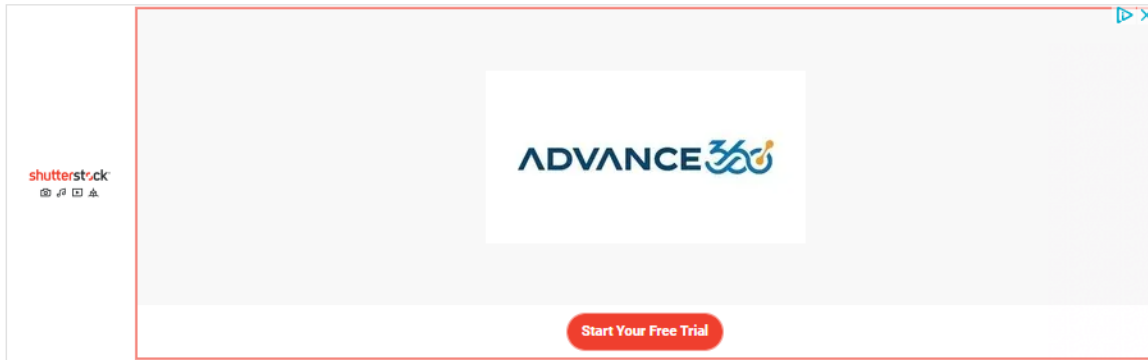
learn R

The statistical programming language R is becoming a popular means for analyzing data. But it's not always easy to use. We have a number of resources about learning and using R, including a several-part tutorial blog series.



<https://www.theanalysisfactor.com/r/>,

Switching Between Long and Wide Formats in R



26 September 2013

This is a basic tutorial in R for switching between the two most common data formats: wide and long. The example dataset we will use is made up of [RT-PCR](#) threshold cycle (Ct) values under two conditions (A and B), with two replicates each.

Download the file by running this in your command line:

<https://reasoniamhere.com/2013/09/26/switching-between-long-and-wide-formats-in-r/>,

<https://sites.google.com/a/bioinformatics.ucr.edu/sites/system/errors/ProxiedWebpaceNotFound?host=manuals.bioinformatics.ucr.edu&webpace=bioinformatics-manuals>

>Computational Genomics

Course Summary and Objectives:

High-throughput sequencing technology has made it possible to obtain large scale genetic data sets for almost any organism, creating a need for computational tools and skill sets to process these data. While the bioinformatics workflows for processing raw data into SNPs are typically well delineated, the path for analyzing and interpreting the resulting SNP data set can be less clear. In this workshop, students learn about classical population genetics statistics that test the neutral theory of evolution, and then get hands-on experience writing their own R code to perform each analysis on a realistic sample SNP data set. Emphasis is placed on programming fundamentals and algorithm design: skills that extend beyond the specific calculations learned in class. At the end of the semester, each student completes an independent project that consists of running an analysis on their own, often using their own data, and presenting their findings to the class.

Intro to R basics

- Syllabus
- R-tutorial
- Overview of course structure
- Introduction to R syntax, data objects, indexing, and loops.

VCF Format and Finding Genotypes

- VCF Format Exercises
- Download Exercise Solution
- Basics of next-gen sequencing, Standard raw data pipelines to call SNPs and produce VCF files.

Hardy-Weinberg Equilibrium

- Hardy-Weinberg Exercises
- Download Exercise Solution
- Review principle of HWE; calculating observed and expected frequencies; assumptions.

<https://eacooper400.github.io/compGen8900.html>,



[Home](#) [Recent Issues](#) [Back Issues](#)

[Search Back Issues](#) 

Are Clusters Races? A Discussion of the Rhetorical Appropriation of Rosenberg et al.'s "Genetic Structure of Human Populations"

Melissa Wills, Department of English, Voorhies Hall, One Shields Avenue, University of California, Davis, CA 95616, USA

EMAIL: MAWILLS@UCDAVIS.EDU

SUBJECT TERMS

[Clusters](#)

[Genetics](#)

[Popular Science](#)

[Populations](#)



<https://quod.lib.umich.edu/cgi/t/text/text-idx?cc=ptb;c=ptb;c=ptpbio;idno=6959004.0009.012;view=text;rgn=main;xc=1;g=ptpbio>,

An introduction to ggplot2

February 2015, by Sean C. Anderson

This page will help you teach yourself how to rapidly explore data with the ggplot2 R package. It was written as a self-study component for the FISH554 class at the University of Washington.

Work your way through this page. When you want to check your work, or if you get stuck on an exercise, just click on the button [R source](#) and you'll see the R source code that created a figure.

Learning objectives

By the end you should be able to:

- Understand the basic grammar of ggplot2 (data, geoms, aesthetics, facets).
- Make quick exploratory plots of your multidimensional data.
- Have an idea about how to start customizing ggplot2 figures.
- Know how to find help on ggplot2 when you run into problems.

ggplot2 for rapid data exploration

ggplot2 is an R package by Hadley Wickham and Winston Chang that implements Wilkinson's Grammar of Graphics. The emphasis of ggplot2 is on rapid exploration of data, and especially high-dimensional data. Think of base graphic functions as drawing with data (examples of base graphic functions are `plot()`, `points()`, and `lines()`). With base graphics, you have complete control over every pixel in a plot but it can take a lot of time and code to produce a plot.

Although ggplot2 can be fully customized, it reaches a point of diminishing returns. I tend to use ggplot2 and base graphics for what they excel at: ggplot2 for rapid data exploration and base graphics for polished and fully-customized plots for publication.

<https://seananderson.ca/ggplot2-fish554/>

[An introduction to ggplot2](#)

[Learning objectives](#)

[ggplot2 for rapid data exploration](#)

[Basics of the grammar](#)

[Loading the data](#)

[Geoms](#)

[Aesthetics](#)

[Facets \(small multiples\)](#)

[Customizing ggplot2](#)

[More examples](#)

[Some final notes](#)

[Feedback](#)

Fundamentals of Data Visualization

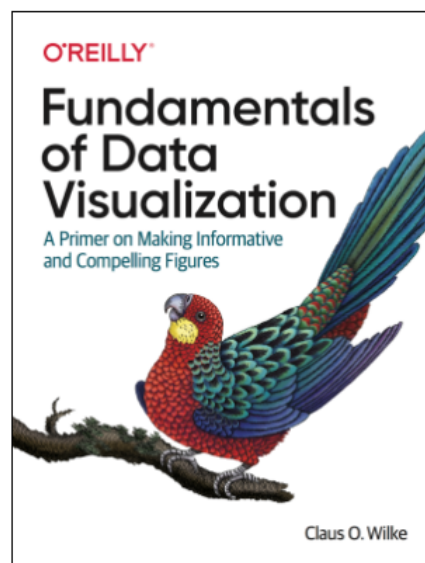
Claus O. Wilke

Welcome

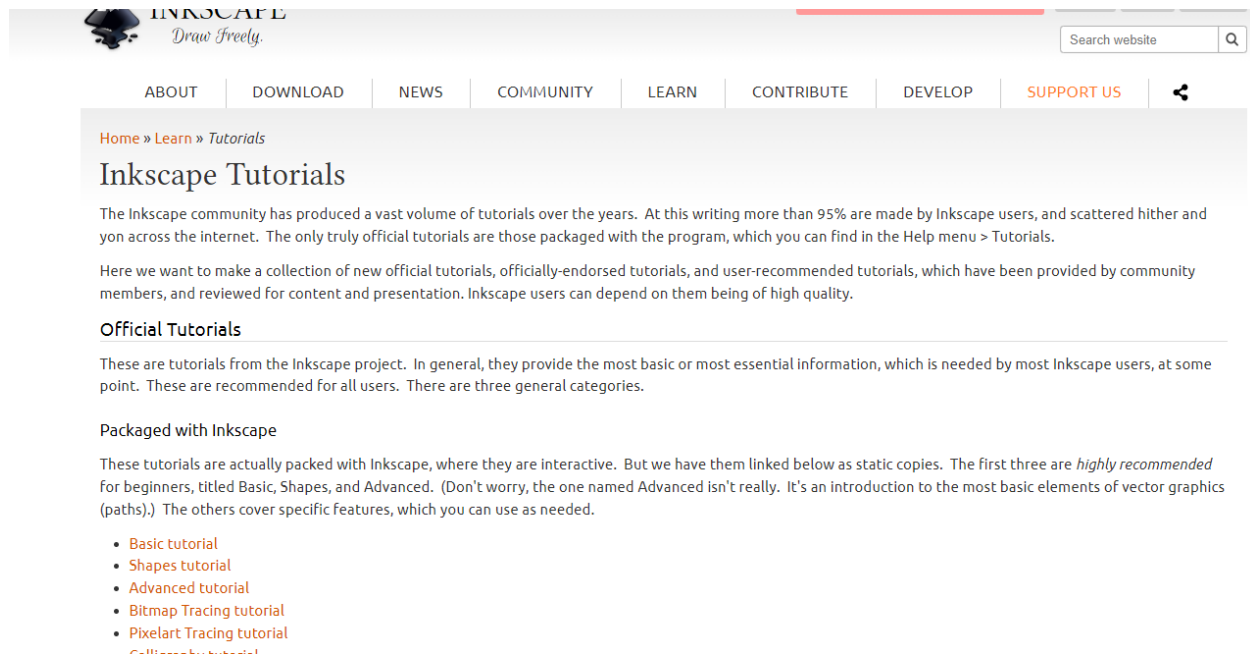
This is the website for the book "Fundamentals of Data Visualization," published by O'Reilly Media, Inc. The website contains the complete author manuscript before final copy-editing and other quality control. If you would like to order an official hardcopy or ebook, you can do so at various resellers, including [Amazon](#), [Barnes and Noble](#), [Google Play](#), or [Powells](#).

The book is meant as a guide to making visualizations that accurately reflect the data, tell a story, and look professional. It has grown out of my experience of working with students and postdocs in my laboratory on thousands of data visualizations. Over the years, I have noticed that the same issues arise over and over. I have attempted to collect my accumulated knowledge from these interactions in the form of this book.

The entire book is written in R Markdown, using RStudio as my text editor and the **bookdown** package to



<https://clauswilke.com/dataviz/>,



The screenshot shows the Inkscape website's 'Tutorials' page. At the top is the Inkscape logo with the tagline 'Draw Freely.' and a search bar. A navigation menu includes links for ABOUT, DOWNLOAD, NEWS, COMMUNITY, LEARN, CONTRIBUTE, DEVELOP, and SUPPORT US. The main heading is 'Inkscape Tutorials', with a breadcrumb trail 'Home » Learn » Tutorials'. The text explains that the Inkscape community has produced a vast volume of tutorials, with over 95% made by users. It mentions that the only truly official tutorials are those packaged with the program. The page then introduces a collection of new official tutorials, officially-endorsed tutorials, and user-recommended tutorials. It lists three general categories: Official Tutorials, Packaged with Inkscape, and User-recommended Tutorials. Under 'Official Tutorials', it states these are from the Inkscape project and provide basic or essential information. Under 'Packaged with Inkscape', it notes these are interactive and linked as static copies. A list of tutorials is provided, including 'Basic tutorial', 'Shapes tutorial', 'Advanced tutorial', 'Bitmap Tracing tutorial', and 'Pixelart Tracing tutorial'.

<https://clauswilke.com/dataviz/>,

INKSCAPE
Draw Freely.

Search website

ABOUT | DOWNLOAD | NEWS | COMMUNITY | LEARN | CONTRIBUTE | DEVELOP | **SUPPORT US**

Home » Learn » Tutorials

Inkscape Tutorials

The Inkscape community has produced a vast volume of tutorials over the years. At this writing more than 95% are made by Inkscape users, and scattered hither and yon across the internet. The only truly official tutorials are those packaged with the program, which you can find in the Help menu > Tutorials.

Here we want to make a collection of new official tutorials, officially-endorsed tutorials, and user-recommended tutorials, which have been provided by community members, and reviewed for content and presentation. Inkscape users can depend on them being of high quality.

Official Tutorials

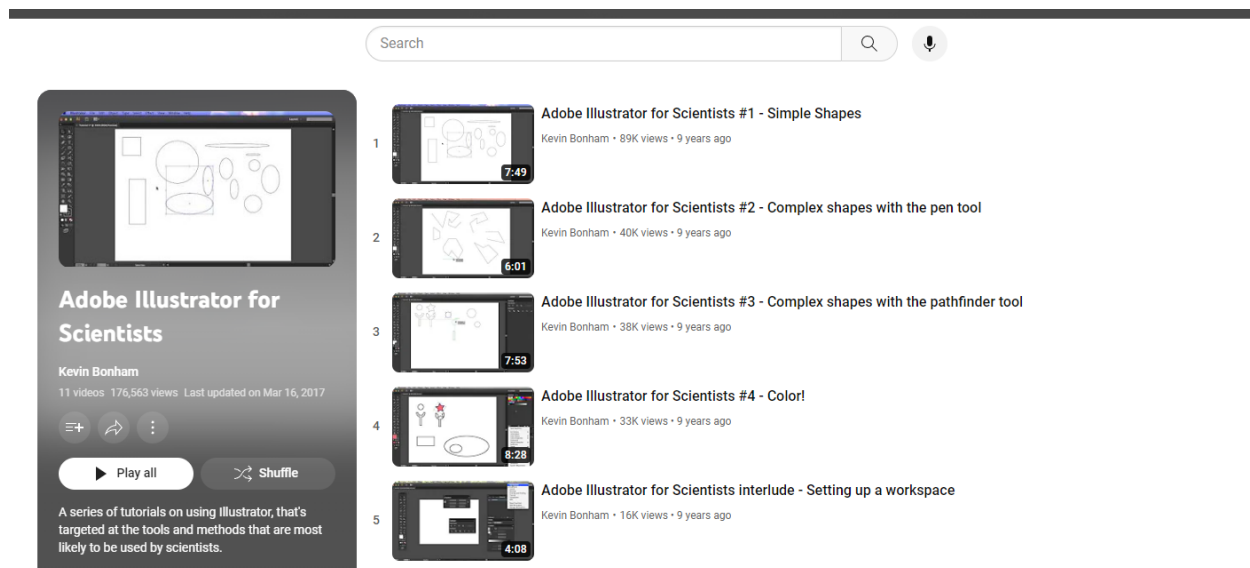
These are tutorials from the Inkscape project. In general, they provide the most basic or most essential information, which is needed by most Inkscape users, at some point. These are recommended for all users. There are three general categories.

Packaged with Inkscape

These tutorials are actually packed with Inkscape, where they are interactive. But we have them linked below as static copies. The first three are *highly recommended* for beginners, titled Basic, Shapes, and Advanced. (Don't worry, the one named Advanced isn't really. It's an introduction to the most basic elements of vector graphics (paths).) The others cover specific features, which you can use as needed.

- [Basic tutorial](#)
- [Shapes tutorial](#)
- [Advanced tutorial](#)
- [Bitmap Tracing tutorial](#)
- [Pixelart Tracing tutorial](#)
- [Calligraphic tutorial](#)

<https://inkscape.org/learn/tutorials/>,



The screenshot shows a YouTube playlist titled 'Adobe Illustrator for Scientists' by Kevin Bonham. The playlist has 11 videos and 176,563 views, last updated on Mar 16, 2017. The video thumbnails show various vector graphics and shapes. The playlist includes videos on simple shapes, complex shapes with the pen tool, complex shapes with the pathfinder tool, color, and setting up a workspace.

Search

Adobe Illustrator for Scientists


Kevin Bonham
11 videos 176,563 views Last updated on Mar 16, 2017

Play all Shuffle

A series of tutorials on using Illustrator, that's targeted at the tools and methods that are most likely to be used by scientists.

- 1 **Adobe Illustrator for Scientists #1 - Simple Shapes**
Kevin Bonham • 89K views • 9 years ago
7:49
- 2 **Adobe Illustrator for Scientists #2 - Complex shapes with the pen tool**
Kevin Bonham • 40K views • 9 years ago
6:01
- 3 **Adobe Illustrator for Scientists #3 - Complex shapes with the pathfinder tool**
Kevin Bonham • 38K views • 9 years ago
7:53
- 4 **Adobe Illustrator for Scientists #4 - Color!**
Kevin Bonham • 33K views • 9 years ago
8:28
- 5 **Adobe Illustrator for Scientists interlude - Setting up a workspace**
Kevin Bonham • 16K views • 9 years ago
4:08

<https://www.youtube.com/playlist?list=PLhKpKEPEAAuYIsyjnIN2YXztNo7BrZVxQ,\>



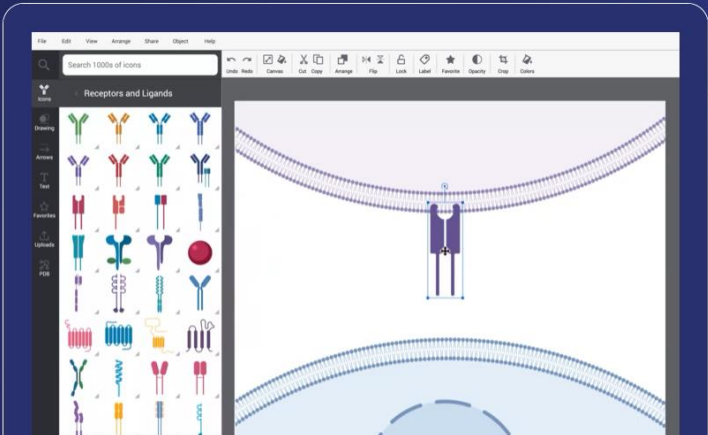
[Features](#)
[Webinars](#)
[Icon Library](#)
[Pricing](#)
[Learning Hub](#)
[Testimonials](#)
[Sign in](#)
[Sign up free](#)

Create Professional Science Figures in Minutes

Browse thousands of pre-made icons and templates from more than 30 fields of life sciences.

SIGN UP FREE


Available online for any computer. No download required.



[https://auburn.instructure.com/courses/1518755/modules/items/27501315,](https://auburn.instructure.com/courses/1518755/modules/items/27501315)

[gatk.broadinstitute.org/hc/en-us](#)


[How do I import m...](#)
[CoreMIS - PSIS](#)
[CHOPCHOP](#)
[auburn](#)
[Gmail](#)
[YouTube](#)
[Maps](#)
[Login - Authenticate](#)



[User Guide](#)
[Tool Index](#)
[Blog](#)
[Forum](#)
[DRAGEN-GATK](#)
[Events](#)
[Download GATK4](#)
[Sign in](#)


Genome Analysis Toolkit

Variant Discovery in High-Throughput Sequencing Data




Developed in the Data Sciences Platform at the [Broad Institute](#), the toolkit offers a wide variety of tools with a primary focus on variant discovery and genotyping. Its powerful processing engine and high-performance computing features make it capable of taking on projects of any size. [Learn more](#)


Find answers to your questions. Stay up to date on the latest topics. Ask questions and help others.




Getting Started
Best practices, tutorials, and other info to get you started




Technical Documentation
Algorithms, glossary, and other detailed resources




Announcements
Blog and events



Tool Index
Purpose, usage and options for each tool



Forum
Ask our team for help and report issues



GATK Showcase on Terra
Check out these fully configured workspaces

[https://gatk.broadinstitute.org/hc/en-us,](https://gatk.broadinstitute.org/hc/en-us)



Case Studies

This page contains a collection of Case Studies in Computational Genomics, mostly based on classic papers, and I Davis, University of Bristol and University of Milano.


Currently most case studies are based on the use of Matlab, but we are planning to add examples of analysis using in hearing from you.

The current list (see the navigation menu on the left) includes analysis of sequence and expression data, and aims

CASE STUDIES

Bird Flu
SARS
HIV
Neanderthal
Chlamydia
Evening Element
Cell Cycle

[https://computationalgenomics.blogs.bristol.ac.uk/case_studies,](https://computationalgenomics.blogs.bristol.ac.uk/case_studies)



Category **Discussion**

Category:Training

To search this page: press **Ctrl + F** (on mac: **Cmd + F**) and enter the query term in the search box.
[Browse Categories](#)

Pages in category "Training"

The following 52 pages are in this category, out of 52 total.

B

- Basic bioinformatics concepts, databases and tools
- BioGPS
- BioMart
- Bioperl introductory training


C

- CI C Bio Main Workbench

I

- Hands-on introduction to NGS variant analysis-2016
- Hands-on introduction to NGS variant analysis-2017
- Hands-on introduction to NGS variant analysis-2018
- Hands-on introduction to NGS variant analysis-2020
- Image Ethics and Poster Design
- Ingenuity Pathway Analysis (IPA) training
- Initiating GMP and Release

[https://wiki.bits.vib.be/index.php/Category:Training,](https://wiki.bits.vib.be/index.php/Category:Training)


OSFHOME

[Search](#)
[Support](#)
[Donate](#)
[Sign Up](#)
[Sign In](#)

[Genomics workflows and teaching activ...](#)
[Metadata](#)
[Files](#)
[Wiki](#)
[Analytics](#)
[Registrations](#)

[Home](#)

[Toggle view:](#)
[View](#)
[Compare](#)

Menu

Project Wiki Pages

Home

View

Wiki Version: (Current) Shannon McDermott: 2019-07-25 12:55:28+00:00 UTC

Read this first!

I teach general biology and genetics at a community college. In summer of 2019, I took a sabbatical of sorts via an ROA (Research Opportunity Award) to work in a research lab. I went to Duke University and worked in Mohamed Noor's lab to learn next-gen sequence analysis. I was disappointed in the lack of transparency and documentation in some of the programs/tools I was using, and starting writing up my own workflows and my own documentation. I include two versions of that documentation here. One is the full version, with all the issues I ran into and all of my mistakes. The second is the clean version - no indication of any problems, just clean workflows.

Note that these were written initially for other members of the Noor lab, and so may contain Duke-specific or Noor lab-specific information that is irrelevant to you.


Also note, I am not a bioinformatician. I am not a computer programmer. My lab notebooks are written for others like me. However, to use many of these tools, you will need to learn some basic Linux. I recommend doing that before starting any genomic analysis.

One of the primary goals of that summer was to develop a genomics-based teaching activity, so that is also included here. This project does NOT require knowing Linux, and does not require installation of any programs - everything is run through the browser. It is intended for sophomore-level undergraduates in a Genetics course. Do I love how I've done it? No, but it's a good starting point. It contains all the instructions, so if you choose to use it, how you present it is up to you.

Everything here is CC-BY licensed, which means you can download and change anything you want to fit your needs, so long as you attribute myself as the original author.

Included:

<https://osf.io/unt8g/wiki/home/>,



[Training](#)
[Hands-On](#)
[How-To](#)
[White Papers](#)

[Resources](#)
[Q&A](#)
[Tool-Boxes](#)
[Overview Pages](#)
[Scripts](#)
[File Formats](#)
[Browse Categories](#)


[Toolbox](#)
[What links here](#)
[Related changes](#)
[Special pages](#)
[Printable version](#)

[Page](#)
[Discussion](#)

NGS data analysis

This wiki page is dedicated to the series of trainings that will lead you through the various Have fun solving the exercises!

[Main_Page]

 *Because most of you have used or will use the Illumina platform to generate their data, we will us*

Contents [hide]

1 Training 1: Introduction to the analysis of NGS data
1.1 Slides
1.2 Exercises
1.2.1 Archive
1.3 FAQ

https://wiki.bits.vib.be/index.php/NGS_data_analysis,

These web pages have moved, as of 31 August 2023.

If you want to find:

The PHYLIP web pages, go here: <https://phylipweb.github.io/phylip/>

The LAMARC web pages, go here: <https://lamarcweb.github.io/lamarcweb/>

Joe Felsenstein's web pages, go here: <https://felsenst.github.io/>

Keep these addresses in mind, in case you need to go back to them.
It will take search engines such as Google a while to realize
That these are the main locations of those pages.

ance with University of Washington requirements for web sites hosted at the University: [Privacy](#) [T](#)

<https://evolution.gs.washington.edu/module1/index.html>,

Harvard FAS Informatics

[About](#)

[Cores](#)

[Employment](#)

[Faq](#)

[Software](#)

[Tutorials](#)

[Archives](#)

Harvard FAS Tutorials and Training

FAS Informatics provides a number of training sessions on everything from basic Linux to transcript assembly.

Materials for training sessions, analysis tutorials, HOWTOs, and short help documents can be found below.

Be sure to check out the training available from [Research Computing](#) as well.

RSEM example on Odyssey

An example of quantifying RNA-seq expression with RSEM on Odyssey cluster

Short Introduction to bwa

This tutorial provides a basic overview of using bwa to align fastas to a reference genome

<https://informatics.fas.harvard.edu/category/tutorials.html>,

[nature](#) > collection

Collection | 09 May 2017

Statistics for Biologists

There is no disputing the importance of statistical analysis in biological research, but too often it is considered only after an experiment is complete, which may be too late.

This collection highlights important statistical issues that biologists should be aware of and provides practical advice to help them improve their work.

Nature Methods' [Points of Significance](#) column on statistics explains many key statistical and experimental design concepts. [Other resources](#) include an online plotting tool and links to statistics guides from other publishers.

Image Credit: Erin DeWalt

<https://www.nature.com/collections/qghhqm>,



Springer has released 65 Machine Learning and Data books for free



Uri Eliabayev · Follow

Published in Towards Data Science · 4 min read · Apr 26, 2020

<https://towardsdatascience.com/springer-has-released-65-machine-learning-and-data-books-for-free-961f8181f189>,



Volume 23 (2015)
Archive (1993-2014)
Index
Interactive Computing Archive
Data Archive
Resources
Editorial Board
Guidelines for Authors
Guidelines for Data Contributors
Guidelines for Readers/Data Users
Home Page
Contact JSE
ASA Publications
Search JSE

An International Journal on the Teaching and Learning of Statistics

JSE Data Archive

[4cdata.txt](#) (the basic data file)
[4c1data.txt](#) (includes indicator or "dummy" variables)
[4c.txt](#) (the documentation file)

NAME: Pricing the C's of Diamond Stones
TYPE: Observational Regression Analysis Data
SIZE: 308 observations, 5 variables

The [article associated with this dataset](#) appears in the *Journal of Statistics Education*, Volume 9, Number 2 (July 2001).

SUBMITTED BY:
Singfat Chu
Faculty of Business Administration
National University of Singapore
10 Kent Ridge Crescent
Singapore 119260
fbachuc1@nus.sg

[93cars.dat.txt](#) (the basic data file)

https://jse.amstat.org/jse_data_archive.htm,

kaggle


Competitions Datasets Models Code Discussions Courses ...

Sign In

Register

Level up with the largest AI & ML community

Join over 16M+ machine learners to share, stress test, and stay up-to-date on all the latest ML techniques and technologies. Discover a huge repository of community-published models, data & code for your next project.

 Register with Google

Register with Email



<https://www.kaggle.com/>,