

Happy Belly Bioinformatics: an open-source resource dedicated to helping biologists utilize bioinformatics

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Software

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Summary

Statement of need: Our civilization's ability to generate data has far surpassed our current, collective capabilities to efficiently access and utilize it. And while the necessary educational infrastructure is trying to adapt and grow as quickly as possible, many graduate students, postdocs, faculty, and other researchers have found ourselves in situations where self-education with little direction is the only option available. This can make it very difficult to get through the initial steep learning curve of beginning to use bioinformatics effectively – particularly when this is expected to happen alongside all of our other research and educational responsibilities.

There are fortunately many resources available online. For example [Codecademy](#) offers free, online lessons focused on learning several different languages from scratch. And more geared towards the sciences, [The Carpentries](#) is an international organization largely powered by volunteers designing and maintaining lessons for in-person workshops that are then openly available. Unfortunately, the plethora of things out there to possibly learn is also very overwhelming when starting out as it can be difficult to know what will be important to us and therefore where to begin.

[Happy Belly Bioinformatics](#) is a website designed and maintained specifically around the goal of helping biologists be able to learn and apply bioinformatics as needed in our research. It has been directly born out of my personal experience of, like many of us these days, being a biologist thrust into the computational world with little or no guidance/advice/resources in my surrounding lab/department/environment. The underlying educational philosophy of the site is that learning a small set of baseline, fundamental skills and concepts that will directly aid in our research is what is important – rather than, for example, sitting down and trying to master a specific programming language without any direct application to our work.

While [Happy Belly Bioinformatics](#) is suitable for use in group-educational activities such as workshop-type environments, part of what makes it stand out from other resources is that each lesson is designed to be completely self-contained with all of the information an in-person instructor might convey being written out in a very personal and conversational form. This often includes personal anecdotes and components/realizations that I found important in the building and shaping of my own mental landscape while navigating the skills and topics being covered. Currently covered areas span foundational skills such as a crash course in working at a [Unix-like command line](#) – with 5 separate modules ending with [6 commands worth knowing about](#) and a primer on [variables and for loops](#) – and working in R (e.g. [an introduction to R](#) and a more detailed look at [indexing in R](#)). Additionally, and also what makes [Happy Belly Bioinformatics](#) differ from most other resources, the site also holds highly comprehensive walkthroughs of common applications in current microbial ecology, e.g.: [an amplicon/marker-gene tutorial](#) that covers a full workflow from

processing through to examples of many standard, initial analyses; walking through a [de novo genome assembly and assessment](#); and [recovering Metagenome-Assembled Genomes \(MAGs\) from metagenomes](#).

[Happy Belly Bioinformatics](#) helps researchers bridge the gap from having little or no current experience to being comfortable with a baseline set of fundamental skills through comprehensive, heavily annotated, and self-contained tutorials. This equips us as researchers to then develop our sphere of capabilities in any and all directions as needed, without there any longer being a technical bottleneck on our science.